

| Barcode | Quant | EXHinterp | SUCCESS | EXH | Qant after MCONC | Fold difference between quants | XAMP1 | XAMP2 | INTERP for NCIDD upload - was there another sample that could have been uploaded? | Link - warm (w), cold (c), unlinked (u) | | | | |
|---------|--------|-----------|---------|---|------------------|--------------------------------|-------|-------|---|---|--|--|--|--|
| | 0.0056 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion | 0.0113 | 2.02 | y | | y | c | | | | |
| | 0.0063 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion | 0.0082 | 1.30 | y | | y | c | | | | |
| | 0.0067 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution | 0.0122 | 1.82 | y | | y | c | | | | |
| | 0.0085 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0148 | 1.74 | y | | y | c | | | | |
| | 0.0093 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0185 | 1.99 | n | | y | c | | | | |
| | 0.0111 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.038 | 3.42 | n | | y | c | | | | |
| | 0.0057 | SUCCESS | 1 | Two person mixed DNA profile 2 person mixed profile - conditioned on | 0.0068 | 1.19 | y | | y | u | | | | |
| | 0.0068 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile DNA profile removed from NCIDD | 0.0102 | 1.50 | y | | y | u | | | | |
| | 0.015 | SUCCESS | 1 | Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 Single evidence sample excluded | 0.0262 | 1.75 | y | | y | u | | | | |
| | 0.0015 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile DNA profile removed from NCIDD | 0.0035 | 2.33 | y | | y | w | | | | |
| | 0.0024 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded Excluded from mixed DNA profile | 0.0042 | 1.75 | y | | y | w | | | | |
| | 0.0035 | SUCCESS | 1 | Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.005 | 1.43 | y | | y | w | | | | |
| | 0.0039 | SUCCESS | 1 | Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion | 0.013 | 3.33 | y | | y | w | | | | |
| | 0.0064 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile | 0.0125 | 1.95 | y | | y | w | | | | |
| | 0.0066 | SUCCESS | 1 | Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile | 0.0077 | 1.17 | n | | y | w | | | | |
| | 0.0072 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0115 | 1.60 | y | | y | w | | | | |
| | 0.0082 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Micro positive for sperm. Submitted-Results pending | 0.0089 | 1.09 | y | | y | w | | | | |

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|--------|---------|---|---|--------|------|---|--|--|---|---|--|--|------------|--|----|
| 0.0091 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution | 0.025 | 2.75 | n | | | y | w | | | | | |
| 0.0091 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information NCIDD upload single source DNA profile | 0.0101 | 1.11 | n | | | y | w | | | | | |
| 0.0093 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion | 0.0254 | 2.73 | n | | | y | w | | | | | |
| 0.0095 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion | 0.0061 | 0.64 | n | | | y | w | | | | | |
| 0.0105 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0058 | 0.55 | n | | | y | w | | | | | |
| 0.0111 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile | 0.016 | 1.44 | y | | | y | w | | | SS Assumed | | 22 |
| 0.0112 | SUCCESS | 1 | Submitted as cells Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile Possible sub-threshold information | 0.0184 | 1.64 | n | | | y | w | | | | | |
| 0.0133 | SUCCESS | 1 | Submitted-results pending. Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile Possible sub-threshold information | 0.0313 | 2.35 | n | | | y | w | | | | | |
| 0.0019 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0018 | 0.95 | y | | | n | c | | | | | |
| 0.0032 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution | 0.0041 | 1.28 | y | | | n | c | | | | | |
| 0.0038 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0055 | 1.45 | y | | | n | c | | | | | |
| 0.0056 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0063 | 1.13 | y | | | n | c | | | | | |
| 0.0067 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile SS DNA profile 9 loci and above LR > 100 billion | 0.008 | 1.19 | y | | | n | c | | | | | |
| 0.0068 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0138 | 2.03 | y | | | n | c | | | | | |
| 0.0072 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0145 | 2.01 | y | | | n | c | | | | | |
| 0.0097 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded | 0.0095 | 0.98 | y | | | n | c | | | | | |
| 0.0106 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0149 | 1.41 | n | | | n | c | | | | | |
| 0.0113 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0181 | 1.60 | n | | | n | c | | | | | |
| 0.0113 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information | 0.0115 | 1.02 | n | | | n | c | | | | | |
| 0.0123 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution | 0.0092 | 0.75 | n | | | n | c | | | | | |

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|--------|---------|---|--|--------|------|---|---------|-------|--|---|---|--|--|--|--|
| 0.0129 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile | 0.0127 | 0.98 | n | | | | n | c | | | | |
| 0.0134 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion | 0.0104 | 0.78 | n | | | | n | c | | | | |
| 0.0134 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0274 | 2.04 | y | | | | n | c | | | | |
| 0.0142 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information | 0.0144 | 1.01 | n | | | | n | c | | | | |
| 0.0143 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded Possible sub-threshold information | 0.0132 | 0.92 | n | | | | n | c | | | | |
| 0.0145 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0104 | 0.72 | y | | | | n | c | | | | |
| 0.0019 | SUCCESS | 1 | Hair located. Submitted-results pending Single source DNA profile NCIDD upload single source DNA profile | 0.0034 | 1.79 | y | | | | n | u | | | | |
| 0.0028 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0055 | 1.96 | y | | | | n | u | | | | |
| 0.0041 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0064 | 1.56 | y | | | | n | u | | | | |
| 0.0043 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0062 | 1.44 | y | | | | n | u | | | | |
| 0.0046 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile | 0.0075 | 1.63 | y | | | | n | u | | | | |
| 0.0051 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0372 | 7.29 | n | | | | n | u | | | | |
| 0.0051 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0048 | 0.94 | y | | | | n | u | | | | |
| 0.0055 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution Excluded from mixed DNA profile | 0.124 | | y | 2154.55 | 22.55 | | n | u | | | | |
| 0.0063 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Mixture-low support for contrib or supports non contrib | 0.006 | 0.95 | y | | | | n | u | | | | |
| 0.0065 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed DNA - inconclusive Excluded from mixed DNA profile 3 person mix - supports non contribution 3 person mix - supports non contribution | 0.0109 | 1.68 | y | | | | n | u | | | | |
| 0.0067 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0086 | 1.28 | y | | | | n | u | | | | |

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|--------|---------|---|--|--------|------|---|---|--|--|---|---|--|--|--|--|
| 0.0069 | SUCCESS | 1 | Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Two person mixed DNA profile Excluded from mixed DNA profile Intel report required for further interpretation 2 person mix profile - support for contrib > 100 billion | 0.008 | 1.16 | y | | | | n | u | | | | |
| 0.0074 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0151 | 2.04 | y | | | | n | u | | | | |
| 0.0086 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0182 | 2.12 | y | y | | | n | u | | | | |
| 0.0129 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information | 0.0241 | 1.87 | n | | | | n | u | | | | |
| 0.0135 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile | 0.0101 | 0.75 | n | | | | n | u | | | | |
| 0.0135 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0123 | 0.91 | y | | | | n | u | | | | |
| 0.0135 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Single evidence sample excluded | 0.0067 | 0.50 | y | | | | n | u | | | | |
| 0.0139 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile NCIDD upload - mixed DNA profile Excluded from mixed DNA profile | 0.0541 | 3.89 | y | | | | n | u | | | | |
| 0.0142 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Suspect check inconclusive - mixed DNA profile Suspect check - supports non contribution | 0.0148 | 1.04 | n | | | | n | u | | | | |
| 0.0146 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0082 | 0.56 | n | | | | n | u | | | | |
| 0.015 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0194 | 1.29 | y | | | | n | u | | | | |
| 0.0032 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0051 | 1.59 | n | | | | n | w | | | | |
| 0.0063 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0134 | 2.13 | n | | | | n | w | | | | |
| 0.0067 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending presump Saliva test positive Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion | 0.0082 | 1.22 | y | | | | n | w | | | | |
| 0.0082 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0093 | 1.13 | y | | | | n | w | | | | |
| 0.0088 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0151 | 1.72 | y | | | | n | w | | | | |
| 0.0088 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0086 | 0.98 | y | | | | n | w | | | | |
| 0.0096 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile | 0.0048 | 0.50 | y | | | | n | w | | | | |

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|--------|---------|---|--|--------|------|---|--|--|---|---|--|--|--|--|
| 0.0104 | SUCCESS | 1 | Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0118 | 1.13 | y | | | n | w | | | | |
| 0.0118 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0081 | 0.69 | n | | | n | w | | | | |
| 0.0121 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0059 | 0.49 | y | | | n | w | | | | |
| 0.0122 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0161 | 1.32 | y | | | n | w | | | | |
| 0.0124 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0246 | 1.98 | n | | | n | w | | | | |
| 0.0126 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded | 0.0099 | 0.79 | n | | | n | w | | | | |
| 0.0126 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion | 0.0147 | 1.17 | n | | | n | w | | | | |
| 0.014 | SUCCESS | 1 | Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information | 0.0183 | 1.31 | n | | | n | w | | | | |
| 0.0148 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution | 0.0042 | 0.28 | n | | | n | w | | | | |
| 0.0011 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.0025 | 2.27 | n | | | | | | | | |
| 0.0012 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.0064 | 5.33 | n | | | | | | | | |
| 0.0015 | SUCCESS | 1 | Submitted as cells Single Source DNA profile - assumed known contributor | 0.0051 | 3.40 | y | | | | | | | | |
| 0.0015 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Semen not detected Single source DNA profile Single source DNA profile < 9 loci LR 1000 - 10 000 | 0.003 | 2.00 | n | | | | | | | | |
| 0.0016 | SUCCESS | 1 | Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Two person mixed DNA profile No statistical interpretation performed | 0.0039 | 2.44 | y | | | | | | | | |
| 0.0017 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Single source DNA profile < NCIDD matching stringency Single Source DNA profile - assumed known contributor | 0.0012 | 0.71 | y | | | | | | | | |
| 0.0018 | SUCCESS | 1 | Hair located. Submitted-results pending Interim result - sample undergoing rework Two person mixed DNA profile 2 person mix - supports non contribution 2 person mix profile - support for contrib > 100 billion | 0.0027 | 1.50 | y | | | | | | | | |
| 0.0019 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending Presump Saliva test negative Single Source DNA profile - assumed known contributor | 0.0047 | 2.47 | n | | | | | | | | |
| 0.0019 | SUCCESS | 1 | Presumptive blood test pos. Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor | 0.0026 | 1.37 | n | | | | | | | | |
| 0.0022 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Single Source DNA profile - assumed known contributor | 0.0059 | 2.68 | n | | | | | | | | |

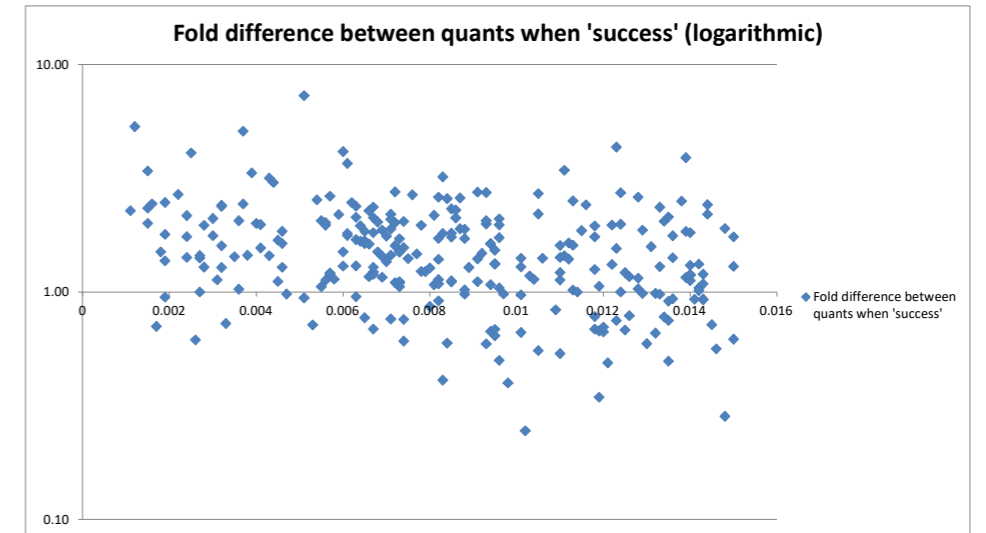
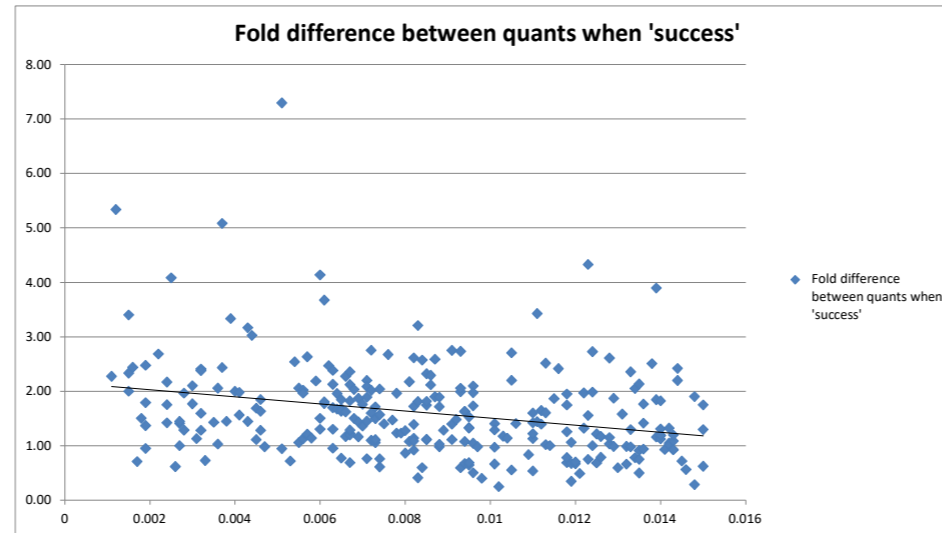
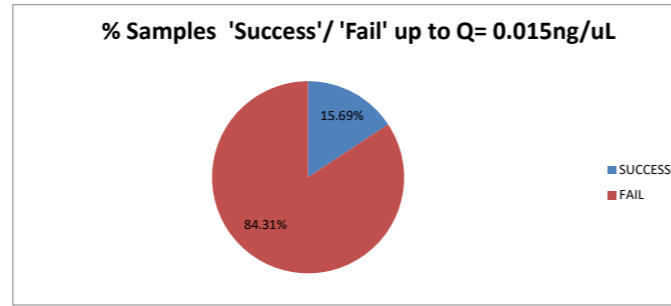
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|--------|---------|---|---|--------|------|---|---------|-------|--|--|--|--|--|--|
| 0.0023 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion | 0.0795 | | y | 3356.52 | 34.57 | | | | | | |
| 0.0024 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib | 0.0052 | 2.17 | y | | | | | | | | |
| 0.0024 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix - support for contrib 1 million - 1 billion | 0.0034 | 1.42 | n | | | | | | | | |
| 0.0025 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.0102 | 4.08 | y | | | | | | | | |
| 0.0026 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending presump Saliva test positive SS | 0.0016 | 0.62 | n | | | | | | | | |
| 0.0027 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor Possible sub-threshold information | 0.0038 | 1.41 | y | | | | | | | | |
| 0.0027 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion | 0.0027 | 1.00 | y | | | | | | | | |
| 0.0027 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.0039 | 1.44 | n | | | | | | | | |
| 0.0028 | SUCCESS | 1 | Hair located. Submitted-results pending Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - supports non contribution | 0.0036 | 1.29 | y | | | | | | | | |
| 0.003 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information | 0.0063 | 2.10 | n | | | | | | | | |
| 0.003 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion | 0.0053 | 1.77 | y | | | | | | | | |
| 0.0031 | SUCCESS | 1 | SS DNA profile 9 loci and above LR > 100 billion | 0.0035 | 1.13 | n | | | | | | | | |
| 0.0032 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile | 0.0077 | 2.41 | y | | | | | | | | |
| 0.0032 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile | 0.0076 | 2.38 | y | | | | | | | | |
| 0.0033 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Single Source DNA profile - assumed known contributor | 0.0024 | 0.73 | n | | | | | | | | |
| 0.0036 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Single source 20 loci DNA profile LR > 100 billion | 0.0074 | 2.06 | n | | | | | | | | |
| 0.0036 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor | 0.0037 | 1.03 | y | | | | | | | | |
| 0.0037 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Single evidence sample excluded | 0.0188 | 5.08 | y | | | | | | | | |
| 0.0037 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile 2 person mix profile - support for contrib > 100 billion | 0.009 | 2.43 | y | | | | | | | | |
| 0.004 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile 2 person mix profile - support for contrib > 100 billion | 0.008 | 2.00 | y | | | | | | | | |

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|--------|---------|---|--|--------|------|---|---|--|--|--|--|--|--|--|
| 0.0041 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor | 0.0081 | 1.98 | n | | | | | | | | |
| 0.0043 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Single evidence sample excluded | 0.0136 | 3.16 | y | | | | | | | | |
| 0.0044 | SUCCESS | 1 | Submitted as cells Single source DNA profile | 0.0133 | 3.02 | y | | | | | | | | |
| 0.0045 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile 2 person mix - supports non contribution | 0.0076 | 1.69 | y | y | | | | | | | |
| 0.0045 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed | 0.005 | 1.11 | y | | | | | | | | |
| 0.0046 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending Presump Saliva test negative Three person mixed DNA profile 3 person mixed profile - conditioned on No statistical interpretation performed 3 person mix remaining - low support for contrib Single evidence sample excluded | 0.0085 | 1.85 | y | | | | | | | | |
| 0.0046 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on No statistical interpretation performed 3 person mix remaining - supports non contribution | 0.0059 | 1.28 | y | | | | | | | | |
| 0.0047 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion | 0.0046 | 0.98 | y | | | | | | | | |
| 0.0053 | SUCCESS | 1 | Submitted-results pending. Single Source DNA profile - assumed known contributor | 0.0038 | 0.72 | n | | | | | | | | |
| 0.0054 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile | 0.0137 | 2.54 | y | | | | | | | | |
| 0.0055 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion | 0.0058 | 1.05 | n | | | | | | | | |
| 0.0055 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Single source DNA profile NCIDD upload single source DNA profile SS DNA profile 9 loci and above LR > 100 billion DNA profile removed from NCIDD | 0.0113 | 2.05 | n | | | | | | | | |
| 0.0056 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.011 | 1.96 | n | | | | | | | | |
| 0.0057 | SUCCESS | 1 | Submitted-results pending. Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Possible sub-threshold information 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution | 0.0069 | 1.21 | y | | | | | | | | |
| 0.0057 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile | 0.015 | 2.63 | y | | | | | | | | |
| 0.0058 | SUCCESS | 1 | Submitted as cells Single source DNA profile Possible sub-threshold information | 0.0066 | 1.14 | n | | | | | | | | |
| 0.0059 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion | 0.0129 | 2.19 | n | | | | | | | | |

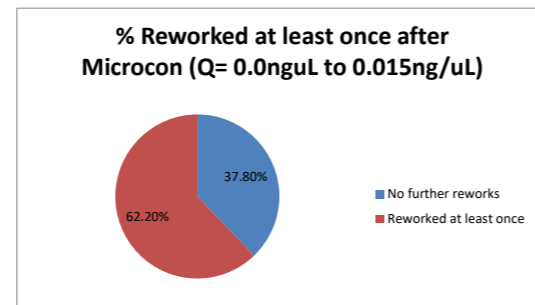
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|--------|---------|---|---|--------|------|---|---|--|--|--|--|--|--|--|
| 0.0069 | SUCCESS | 1 | Presumptive blood test pos. Submitted-results pending. Single Source DNA profile - assumed known contributor | 0.0129 | 1.87 | y | | | | | | | | |
| 0.0069 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information | 0.0099 | 1.43 | y | | | | | | | | |
| 0.007 | SUCCESS | 1 | Submitted-results pending. Single Source DNA profile - assumed known contributor | 0.0095 | 1.36 | n | | | | | | | | |
| 0.007 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded | 0.0123 | 1.76 | y | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Single Source DNA profile - assumed known contributor | 0.0156 | 2.20 | n | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information | 0.0134 | 1.89 | n | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - low support for contribution Excluded from mixed DNA profile | 0.0148 | 2.08 | y | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion | 0.0103 | 1.45 | n | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Presumptive blood test pos. Submitted-results pending. Single source DNA profile | 0.0054 | 0.76 | y | y | | | | | | | |
| 0.0072 | SUCCESS | 1 | Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person rem- support for contrib 1 million to 1 billion | 0.0079 | 1.10 | y | | | | | | | | |
| 0.0072 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed | 0.0198 | 2.75 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib | 0.0125 | 1.71 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile | 0.008 | 1.10 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed | 0.0077 | 1.05 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion | 0.0081 | 1.11 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending SS DNA profile 9 loci and above LR > 100 billion | 0.0109 | 1.49 | n | | | | | | | | |
| 0.0074 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion | 0.0045 | 0.61 | y | | | | | | | | |
| 0.0074 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed | 0.0056 | 0.76 | n | | | | | | | | |
| 0.0074 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib | 0.0116 | 1.57 | y | | | | | | | | |
| 0.0075 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending presump Saliva test positive Three person mixed DNA profile No statistical interpretation performed | 0.0105 | 1.40 | y | | | | | | | | |

| | | | | | | | | | | | | | | |
|--------|---------|---|--|--------|------|---|--|--|--|--|--|--|--|--|
| 0.0085 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information | 0.0094 | 1.11 | y | | | | | | | | |
| 0.0085 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution | 0.0154 | 1.81 | y | | | | | | | | |
| 0.0085 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - support for contrib 100 000 to 1 million 2 person mix - supports non contribution Single evidence sample excluded | 0.0095 | 1.12 | y | | | | | | | | |
| 0.0086 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix - low support for contribution 3 person mixed DNA - inconclusive | 0.0197 | 2.29 | y | | | | | | | | |
| 0.0087 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution | 0.0225 | 2.59 | y | | | | | | | | |
| 0.0087 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded | 0.0165 | 1.90 | y | | | | | | | | |
| 0.0088 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion | 0.009 | 1.02 | y | | | | | | | | |
| 0.0088 | SUCCESS | 1 | Submitted-results pending. Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Single evidence sample excluded | 0.0166 | 1.89 | y | | | | | | | | |
| 0.0089 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed | 0.0114 | 1.28 | n | | | | | | | | |
| 0.0091 | SUCCESS | 1 | consistent elsewhere | 0.0127 | 1.40 | n | | | | | | | | |
| 0.0092 | SUCCESS | 1 | P SS | 0.0136 | 1.48 | n | | | | | | | | |
| 0.0093 | SUCCESS | 1 | P SS | 0.0055 | 0.59 | y | | | | | | | | |
| 0.0093 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0191 | 2.05 | n | | | | | | | | |
| 0.0094 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 1 million - 1 billion 3 person mix - support for contribution 100 to 1000 | 0.0063 | 0.67 | y | | | | | | | | |
| 0.0094 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion 3 person mix remaining - supports non contribution | 0.0153 | 1.63 | n | | | | | | | | |
| 0.0094 | SUCCESS | 1 | 3p | 0.0101 | 1.07 | y | | | | | | | | |
| 0.0094 | SUCCESS | 1 | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution 3 person mix - supports non contribution | 0.0153 | 1.63 | n | | | | | | | | |
| 0.0095 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution | 0.0145 | 1.53 | y | | | | | | | | |

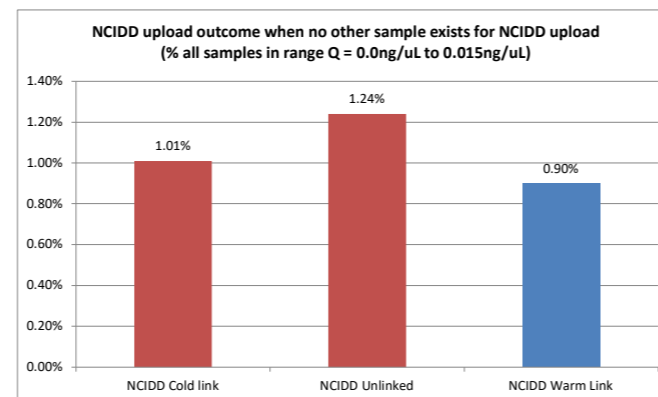
| % Samples Success/ Fail up to Q= 0.015ng/uL | | |
|---|--------|---------------------------|
| | | No. Samples: Total = 1778 |
| SUCCESS | 15.69% | 279 |
| FAIL | 84.31% | 1499 |



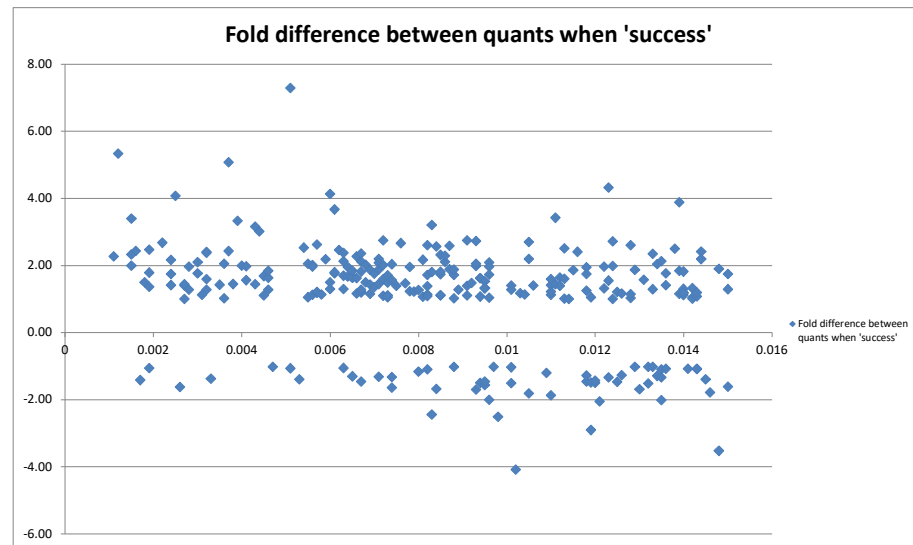
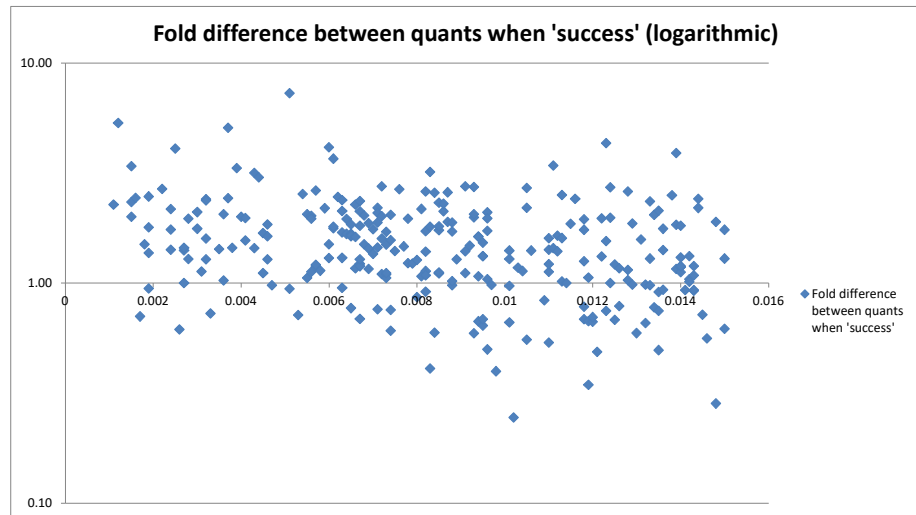
| % Reworked at least once after Microcon (Q= 0.0ng/uL to 0.015ng/uL) | | |
|---|--|--------|
| No further reworks | | 37.80% |
| Reworked at least once | | 62.20% |



| Number of samples (where no other sample could be uploaded) | | | |
|---|-------------------------|-------|----|
| % No other samples to Upload from the range = 56 | | | |
| Total samples in range = 1778 | 0.00ng/uL to 0.015ng/uL | | |
| NCIDD Cold link | | 1.01% | 18 |
| NCIDD Unlinked | | 1.24% | 22 |
| NCIDD Warm Link | | 0.90% | 16 |



| Quant | Fold difference between quants when 'success' | Fold difference between quants when 'success' |
|--------|---|---|
| 0.0011 | 2.27 | 2.27 |
| 0.0012 | 5.33 | 5.33 |
| 0.0015 | 2.33 | 2.33 |
| 0.0015 | 3.40 | 3.40 |
| 0.0015 | 2.00 | 2.00 |
| 0.0016 | 2.44 | 2.44 |
| 0.0017 | 0.71 | -1.416667 |
| 0.0018 | 1.50 | 1.50 |
| 0.0019 | 1.79 | 1.79 |
| 0.0019 | 0.95 | -1.055556 |
| 0.0019 | 2.47 | 2.47 |
| 0.0019 | 1.37 | 1.37 |
| 0.0022 | 2.68 | 2.68 |
| 0.0023 | | |
| 0.0024 | 1.75 | 1.75 |
| 0.0024 | 2.17 | 2.17 |
| 0.0024 | 1.42 | 1.42 |
| 0.0025 | 4.08 | 4.08 |
| 0.0026 | 0.62 | -1.625 |
| 0.0027 | 1.41 | 1.41 |
| 0.0027 | 1.00 | 1.00 |
| 0.0027 | 1.44 | 1.44 |
| 0.0028 | 1.96 | 1.96 |
| 0.0028 | 1.29 | 1.29 |
| 0.003 | 2.10 | 2.10 |
| 0.003 | 1.77 | 1.77 |
| 0.0031 | 1.13 | 1.13 |
| 0.0032 | 1.59 | 1.59 |
| 0.0032 | 1.28 | 1.28 |
| 0.0032 | 2.41 | 2.41 |
| 0.0032 | 2.38 | 2.38 |
| 0.0033 | 0.73 | -1.375 |
| 0.0035 | 1.43 | 1.43 |
| 0.0036 | 2.06 | 2.06 |
| 0.0036 | 1.03 | 1.03 |
| 0.0037 | 5.08 | 5.08 |
| 0.0037 | 2.43 | 2.43 |
| 0.0038 | 1.45 | 1.45 |
| 0.0039 | 3.33 | 3.33 |
| 0.004 | 2.00 | 2.00 |
| 0.0041 | 1.56 | 1.56 |
| 0.0041 | 1.98 | 1.98 |
| 0.0043 | 1.44 | 1.44 |
| 0.0043 | 3.16 | 3.16 |
| 0.0044 | 3.02 | 3.02 |
| 0.0045 | 1.69 | 1.69 |
| 0.0045 | 1.11 | 1.11 |
| 0.0046 | 1.63 | 1.63 |
| 0.0046 | 1.85 | 1.85 |
| 0.0046 | 1.28 | 1.28 |
| 0.0047 | 0.98 | -1.021739 |
| 0.0051 | 7.29 | 7.29 |
| 0.0051 | 0.94 | -1.0625 |
| 0.0053 | 0.72 | -1.394737 |
| 0.0054 | 2.54 | 2.54 |
| 0.0055 | | |
| 0.0055 | 1.05 | 1.05 |
| 0.0055 | 2.05 | 2.05 |
| 0.0056 | 1.13 | 1.13 |
| 0.0056 | 2.02 | 2.02 |
| 0.0056 | 1.96 | 1.96 |
| 0.0057 | 1.19 | 1.19 |
| 0.0057 | 1.21 | 1.21 |
| 0.0057 | 2.63 | 2.63 |
| 0.0058 | 1.14 | 1.14 |
| 0.0059 | 2.19 | 2.19 |
| 0.006 | 1.50 | 1.50 |
| 0.006 | 4.13 | 4.13 |
| 0.006 | 1.30 | 1.30 |
| 0.0061 | 1.77 | 1.77 |
| 0.0061 | 3.67 | 3.67 |
| 0.0061 | 1.80 | 1.80 |
| 0.0062 | 2.47 | 2.47 |
| 0.0063 | 0.95 | -1.05 |
| 0.0063 | 2.13 | 2.13 |
| 0.0063 | 1.30 | 1.30 |
| 0.0063 | 2.38 | 2.38 |
| 0.0063 | 1.70 | 1.70 |
| 0.0064 | 1.95 | 1.95 |
| 0.0064 | 1.67 | 1.67 |
| 0.0065 | 1.68 | 1.68 |
| 0.0065 | 1.63 | 1.63 |
| 0.0065 | 0.77 | -1.3 |
| 0.0065 | 1.65 | 1.65 |
| 0.0065 | 1.85 | 1.85 |
| 0.0066 | 1.17 | 1.17 |
| 0.0066 | 1.62 | 1.62 |
| 0.0066 | 2.27 | 2.27 |
| 0.0067 | 1.22 | 1.22 |
| 0.0067 | 1.19 | 1.19 |
| 0.0067 | 1.28 | 1.28 |



| | | |
|--------|------|-----------|
| 0.0067 | 1.82 | 1.82 |
| 0.0067 | 0.69 | -1.456522 |
| 0.0067 | 2.12 | 2.12 |
| 0.0067 | 2.36 | 2.36 |
| 0.0068 | 2.03 | 2.03 |
| 0.0068 | 1.50 | 1.50 |
| 0.0069 | 1.16 | 1.16 |
| 0.0069 | 1.87 | 1.87 |
| 0.0069 | 1.43 | 1.43 |
| 0.007 | 1.36 | 1.36 |
| 0.007 | 1.76 | 1.76 |
| 0.0071 | 2.20 | 2.20 |
| 0.0071 | 1.89 | 1.89 |
| 0.0071 | 2.08 | 2.08 |
| 0.0071 | 1.45 | 1.45 |
| 0.0071 | 0.76 | -1.314815 |
| 0.0072 | 2.01 | 2.01 |
| 0.0072 | 1.60 | 1.60 |
| 0.0072 | 1.10 | 1.10 |
| 0.0072 | 2.75 | 2.75 |
| 0.0073 | 1.71 | 1.71 |
| 0.0073 | 1.10 | 1.10 |
| 0.0073 | 1.05 | 1.05 |
| 0.0073 | 1.11 | 1.11 |
| 0.0073 | 1.49 | 1.49 |
| 0.0074 | 2.04 | 2.04 |
| 0.0074 | 0.61 | -1.644444 |
| 0.0074 | 0.76 | -1.321429 |
| 0.0074 | 1.57 | 1.57 |
| 0.0075 | 1.40 | 1.40 |
| 0.0076 | 2.67 | 2.67 |
| 0.0077 | 1.47 | 1.47 |
| 0.0078 | 1.96 | 1.96 |
| 0.0078 | 1.23 | 1.23 |
| 0.0079 | 1.23 | 1.23 |
| 0.008 | 1.27 | 1.27 |
| 0.008 | 0.86 | -1.15942 |
| 0.0081 | 1.07 | 1.07 |
| 0.0081 | 2.17 | 2.17 |
| 0.0082 | 1.13 | 1.13 |
| 0.0082 | 1.09 | 1.09 |
| 0.0082 | 1.72 | 1.72 |
| 0.0082 | 2.61 | 2.61 |
| 0.0082 | 0.91 | -1.093333 |
| 0.0082 | 1.39 | 1.39 |
| 0.0083 | 3.20 | 3.20 |
| 0.0083 | 1.81 | 1.81 |
| 0.0083 | 0.41 | -2.441176 |
| 0.0084 | 2.57 | 2.57 |
| 0.0084 | 0.60 | -1.68 |
| 0.0085 | 1.74 | 1.74 |
| 0.0085 | 2.32 | 2.32 |
| 0.0085 | 1.11 | 1.11 |
| 0.0085 | 1.81 | 1.81 |
| 0.0085 | 1.12 | 1.12 |
| 0.0086 | 2.12 | 2.12 |
| 0.0086 | 2.29 | 2.29 |
| 0.0087 | 2.59 | 2.59 |
| 0.0087 | 1.90 | 1.90 |
| 0.0088 | 1.72 | 1.72 |
| 0.0088 | 0.98 | -1.023256 |
| 0.0088 | 1.02 | 1.02 |
| 0.0088 | 1.89 | 1.89 |
| 0.0089 | 1.28 | 1.28 |
| 0.0091 | 1.40 | 1.40 |
| 0.0091 | 2.75 | 2.75 |
| 0.0091 | 1.11 | 1.11 |
| 0.0092 | 1.48 | 1.48 |
| 0.0093 | 1.99 | 1.99 |
| 0.0093 | 2.73 | 2.73 |
| 0.0093 | 0.59 | -1.690909 |
| 0.0093 | 2.05 | 2.05 |
| 0.0094 | 0.67 | -1.492063 |
| 0.0094 | 1.63 | 1.63 |
| 0.0094 | 1.07 | 1.07 |
| 0.0094 | 1.63 | 1.63 |
| 0.0095 | 0.64 | -1.557377 |
| 0.0095 | 1.53 | 1.53 |
| 0.0095 | 1.33 | 1.33 |
| 0.0095 | 1.33 | 1.33 |
| 0.0095 | 0.68 | -1.461538 |
| 0.0096 | 0.50 | -2 |
| 0.0096 | 2.09 | 2.09 |
| 0.0096 | 1.04 | 1.04 |
| 0.0096 | 1.97 | 1.97 |
| 0.0096 | 1.73 | 1.73 |
| 0.0097 | 0.98 | -1.021053 |
| 0.0098 | 0.40 | -2.512821 |
| 0.0101 | 0.97 | -1.030612 |
| 0.0101 | 1.41 | 1.41 |
| 0.0101 | 0.66 | -1.507463 |
| 0.0101 | 1.29 | 1.29 |
| 0.0102 | 0.25 | -4.08 |
| 0.0103 | 1.17 | 1.17 |
| 0.0104 | 1.13 | 1.13 |
| 0.0105 | 2.20 | 2.20 |

| | | | | |
|--------|------|-----------|------|----------|
| 0.0105 | 2.70 | 2.70 | | |
| 0.0105 | 0.55 | -1.810345 | | |
| 0.0106 | 1.41 | 1.41 | | |
| 0.0109 | 0.83 | -1.197802 | | |
| 0.011 | 1.42 | 1.42 | | |
| 0.011 | 1.60 | 1.60 | | |
| 0.011 | 1.13 | 1.13 | | |
| 0.011 | 0.54 | -1.864407 | | |
| 0.011 | 1.22 | 1.22 | | |
| 0.0111 | 3.42 | 3.42 | | |
| 0.0111 | 1.44 | 1.44 | | |
| 0.0112 | 1.64 | 1.64 | | |
| 0.0112 | 1.39 | 1.39 | | |
| 0.0113 | 1.60 | 1.60 | | |
| 0.0113 | 2.51 | 2.51 | | |
| 0.0113 | 1.02 | 1.02 | | |
| 0.0114 | 1.00 | 1.00 | | |
| 0.0115 | 1.86 | 1.86 | | |
| 0.0116 | 2.41 | 2.41 | | |
| 0.0118 | 0.69 | -1.45679 | | |
| 0.0118 | 1.25 | 1.25 | | |
| 0.0118 | 1.75 | 1.75 | | |
| 0.0118 | 1.95 | 1.95 | | |
| 0.0118 | 0.78 | -1.282609 | | |
| 0.0119 | | | 0.02 | -46.2963 |
| 0.0119 | 0.67 | -1.4875 | | |
| 0.0119 | 1.06 | 1.06 | | |
| 0.0119 | 0.34 | -2.902439 | | |
| 0.012 | 0.67 | -1.5 | | |
| 0.012 | 0.70 | -1.428571 | | |
| 0.0121 | 0.49 | -2.050847 | | |
| 0.0122 | 1.32 | 1.32 | | |
| 0.0122 | 1.97 | 1.97 | | |
| 0.0123 | 4.33 | 4.33 | | |
| 0.0123 | 1.55 | 1.55 | | |
| 0.0123 | 0.75 | -1.336956 | | |
| 0.0124 | 1.00 | 1.00 | | |
| 0.0124 | 2.73 | 2.73 | | |
| 0.0124 | 1.98 | 1.98 | | |
| 0.0125 | 1.22 | 1.22 | | |
| 0.0125 | 0.68 | -1.470588 | | |
| 0.0126 | 0.79 | -1.272727 | | |
| 0.0126 | 1.17 | 1.17 | | |
| 0.0128 | 2.61 | 2.61 | | |
| 0.0128 | 1.03 | 1.03 | | |
| 0.0128 | 1.15 | 1.15 | | |
| 0.0129 | 0.98 | -1.015748 | | |
| 0.0129 | 1.87 | 1.87 | | |
| 0.013 | 0.59 | -1.688312 | | |
| 0.0131 | 1.58 | 1.58 | | |
| 0.0132 | 0.98 | -1.015385 | | |
| 0.0132 | 0.66 | -1.517241 | | |
| 0.0133 | 0.98 | -1.023077 | | |
| 0.0133 | 1.29 | 1.29 | | |
| 0.0133 | 2.35 | 2.35 | | |
| 0.0134 | 0.78 | -1.288461 | | |
| 0.0134 | 2.04 | 2.04 | | |
| 0.0135 | 0.75 | -1.336634 | | |
| 0.0135 | 0.91 | -1.097561 | | |
| 0.0135 | 2.13 | 2.13 | | |
| 0.0135 | 0.50 | -2.014925 | | |
| 0.0136 | 0.93 | -1.070866 | | |
| 0.0136 | 1.76 | 1.76 | | |
| 0.0136 | 1.41 | 1.41 | | |
| 0.0138 | 2.51 | 2.51 | | |
| 0.0139 | 1.84 | 1.84 | | |
| 0.0139 | 1.16 | 1.16 | | |
| 0.0139 | 3.89 | 3.89 | | |
| 0.014 | 1.19 | 1.19 | | |
| 0.014 | 1.82 | 1.82 | | |
| 0.014 | 1.19 | 1.19 | | |
| 0.014 | 1.31 | 1.31 | | |
| 0.014 | 1.12 | 1.12 | | |
| 0.014 | 1.19 | 1.19 | | |
| 0.0141 | 0.93 | -1.076336 | | |
| 0.0142 | 1.32 | 1.32 | | |
| 0.0142 | 1.04 | 1.04 | | |
| 0.0142 | 1.01 | 1.01 | | |
| 0.0143 | 0.92 | -1.083333 | | |
| 0.0143 | 1.08 | 1.08 | | |
| 0.0143 | 0.93 | -1.075188 | | |
| 0.0143 | 1.20 | 1.20 | | |
| 0.0144 | 2.19 | 2.19 | | |
| 0.0144 | 2.42 | 2.42 | | |
| 0.0145 | 0.72 | -1.394231 | | |
| 0.0146 | 0.56 | -1.780488 | | |
| 0.0148 | 1.90 | 1.90 | | |
| 0.0148 | 0.28 | -3.52381 | | |
| 0.015 | 1.29 | 1.29 | | |
| 0.015 | 1.75 | 1.75 | | |
| 0.015 | 0.62 | -1.612903 | | |

Paula Brisotto

From: Paula Brisotto
Sent: Tuesday, 18 July 2017 4:43 PM
To: [REDACTED]
Subject: Options for Volume crime processing

Hi Scott,

I have not booked a meeting regarding the options for volume crime processing as discussed on the phone yesterday, as I wanted to ensure you had time available before setting up a meeting with Paul Csoban and Justin. Unfortunately, Paul's calendar is filling up for Thursday, and I am away on Friday and Monday. I am not here tomorrow (Wednesdays are my non-work day) and therefore I will be unable to follow up on a meeting. If you wish to proceed with a meeting for Thursday, Sandy (Paul's ESO) may be able to accommodate this – however we will need to liaise with Justin to ensure some of the meetings Justin and I have booked for Thursday are rescheduled. Otherwise, we can organise a meeting for next week – Cathie returns on Tuesday.

Please let me know, and I will action anything I can on Thursday.

Sandy's contact information is

Sandy Sinclair

ESO to Executive Director

Forensic and Scientific Services

Health Support Queensland, **Department of Health**

Thanks,
Paula

**Paula Brisotto**

A/Managing Scientist

Police Services Stream

Forensic & Scientific Services,

Health Support Queensland, **Department of Health**

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

Paula Brisotto

From: Justin Howes
Sent: Wednesday, 19 July 2017 8:30 AM
To: Sandy Sinclair
Cc: Paula Brisotto; Paul Csoban
Subject: FW: Options for Volume crime processing

Hi Sandy

As per below, can you please organise a 1hr meeting at FSS for Cathie, Paul, A/Supt McLaren and optional for Paula and myself – we will discuss with Cathie if she needs us present.

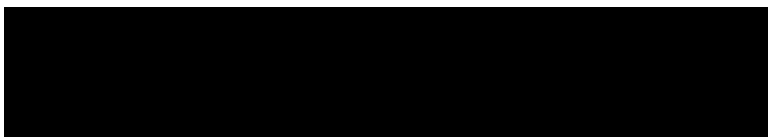
Please schedule for Fri (28 July) if possible. If not, please try for Wed.

Thankyou
Justin

**Justin Howes**

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

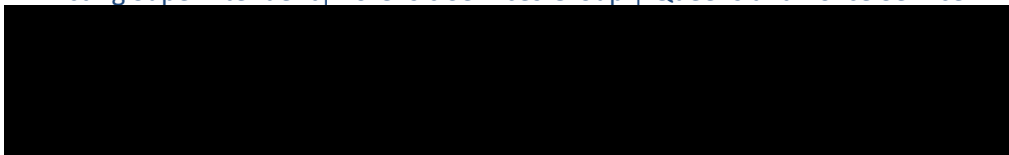
From: [redacted] [mailto:[redacted]]
Sent: Wednesday, 19 July 2017 7:03 AM
To: Paula Brisotto; Justin Howes
Cc: Paul Csoban
Subject: RE: Options for Volume crime processing

Paula thank you for the email and for the briefing and options paper regarding P+. If it's OK I'd like to meet next week to discuss the options moving forward as well as what impact, if any, these changes will have to our funding arrangements.

I'm available all day Wednesday and Friday that week.

Scott McLaren

Acting Superintendent | Forensic Services Group | Queensland Police Service





From: Paula Brisotto [mailto: [REDACTED]]
Sent: Tuesday, 18 July 2017 4:43 PM
To: McLaren.ScottA[OSC] < [REDACTED]>
Subject: Options for Volume crime processing

Hi Scott,

I have not booked a meeting regarding the options for volume crime processing as discussed on the phone yesterday, as I wanted to ensure you had time available before setting up a meeting with Paul Csoban and Justin. Unfortunately, Paul's calendar is filling up for Thursday, and I am away on Friday and Monday. I am not here tomorrow (Wednesdays are my non-work day) and therefore I will be unable to follow up on a meeting. If you wish to proceed with a meeting for Thursday, Sandy (Paul's ESO) may be able to accommodate this – however we will need to liaise with Justin to ensure some of the meetings Justin and I have booked for Thursday are rescheduled. Otherwise, we can organise a meeting for next week – Cathie returns on Tuesday.

Please let me know, and I will action anything I can on Thursday.

Sandy's contact information is

Sandy Sinclair

ESO to Executive Director

Forensic and Scientific Services

Health Support Queensland, **Department of Health**

Thanks,
Paula



Paula Brisotto

A/Managing Scientist

Police Services Stream

Forensic & Scientific Services,

Health Support Queensland, **Department of Health**

HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

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Minutes

Forensic DNA Analysis Management Team Meeting

Date: 20 July 2017
Time: 11:00am – 12.30pm
Venue: FSS CR611

1. Present

| | |
|-----------------------------------|------------------------|
| Allan McNevin (ARM) | Luke Ryan (LBR) |
| Justin Howes (JAH) | Matthew Hunt (MOH) |
| Kirsten Scott (KDS) (Chairperson) | Paula Brisotto (PMB) |
| Kerry-Anne Lancaster (KAL) | Sharon Johnstone (SMJ) |
| Kylie Rika (KDR) | Wendy Harmer (WAH) |

2. Apologies – Cathie Allen (CJA)

Agenda items

| Item | Topic |
|------|---|
| 1.0 | Confirmation of previous minutes – WAH |
| 2.0 | Conflicts of Interest – Nil. Agenda sent out prior to meeting, if any conflicts exist, these are to be discussed with chair prior to meeting. |
| 3.0 | Action Register – See below |
| 4.0 | <p>Standing items</p> <p>4.1 Workplace Health & Safety Issues – Everyone</p> <ul style="list-style-type: none"> - Tour for Paul Belchambers occurred in DNA and Chem. SAB felt successful. - Email sent during the week re liquids in bin - Risk assessment performed by AAQ on requirement for advance resus training. RA found still require use of Oxygen. - Emergency Evacuation Drill. Only issue noted, staff above in BI3 (Level 2) bulking up thoroughfare – other exit used. <p>4.2 Sub-Team Updates</p> <p>Evidence Recovery:</p> <ul style="list-style-type: none"> - About 95% FR, mostly additional in-tubes for AUSLAB cases. - Little behind with whole items with staff on long-term leave. - Feedback provided to QPS (Jamie Cook, Dave Neville) on crime scene envelope photo issues. Most common issue is not the whole envelope in the photos – being looked at by QPS. - QPS adding one cig butt per envelope – process being implemented at QPS. |

- Some minor FR changes to auto-wording. Waiting on supt amylase batch EXH lines.
- Some learning points – tasks created but no Officer number added. Ends up going to unallocated list (CM or Review).

Analytical:

- Qiasymphony AS in use now and going well.
- To order the last 5 P+ kits in existence

Quality & Projects:

- All staff trained in ER using FR.
- PDFing improved – thanks to MLM for finding internet-speed issue within Adobe as likely cause for slow pdf process. Almost up to date with pdfing and Gilling.

Reporting 1:

- Continuing with R1/2 focus on CM/PDA and feeding statements when required.
- Gradually getting more staff exposed to FR and moving to review stage.

Reporting 2:

- Defence request with urgency – CV, eggs, calculation explanations, STRmix overview

Intelligence:

- All LKRs in FR. Few bugs occurring and reported for extremely old data (related to previous interface (pre 2007) samples). Some responses to come.
- Trying to focus on PDA but staff absences has affected amount of time allocated to this.

Admin:

- Last week had first casefile creation request.
- 31 July, WAH to go on leave and trying to find backfill.

Managing Scientist:

- 17 July teleconf with FASS (PMB, JAH, MG) on Business Continuity Plan between the jurisdictions. Who does what if lab shut down etc? At concept stage for now.

BSAG update

- meeting in a few weeks. Likely that MPS and Familial testing will dominate.
- JAH providing feedback on Forensic Foundations proficiency test, and feedback from statistics panel discussion.

4.3 Project Updates

FR Project update

- Issue this morning with SOE update – not FR issue, related to QHealth.
- Information received from Terry regarding who to contact if issues are found.

#173 B – verification of STARlet B (LBR)

- Signed. MPII to be moved out and decommissioned.

Project #181 – Sensitivity of Sperm microscopy – awaiting feedback from CJA.

Project #177 – 3500xL mixtures – 06.07.2017 - has been on hold due to FR UAT and implementation.

- KDR to assess if implementation plan for Mgt Team can be written by EJC for next Mgt meeting.

Project #184 – JAH - re-evaluation of microcons.

- No progress.

Project #185 – LBR – Quantstudio 5

- On hold until LBR back from leave.

Project #152 – Y filer plus validation

- Signed and to be removed.

MPS as Investigative Tool RSS18-004 (LBR)

- Panel provided feedback in research plan to ask for resubmission as 'proof of concept' and to appoint a research supervisor (KDS).
- LBR to speak to Dr Glenn Graham re this. NB. Illumina Miseq in their lab so a side by side comparison could be added to this project.
- Team based funding approved rather than Grant Pool Funding.
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#175 C – validation of STARlet C – for CE. On hold pending STARlet B verification (22.06.2017)

- Revised project plan to be finalised and sent around. Moved to 'in progress'.
- Amp normally, take amp seal off, put perforated seal on for prepping, then add normal seal on and into freezer.

Projects on-hold

Project #146 – GlobalFiler – LBR

On hold until new size standard has been completed (17.03.2016)

Project #172 – Phadebas testing from suspension in ERT – ARM

Pending outcome of project on how suspensions are made. (12.05.2016)

5.0

New business

5.1 CaPE Brisbane Workshops – Performance & Reasonable Management Action (WAH)

– was anyone interested in attending a session?

- Tuesday 25 July 2017 : KDR on waiting list
- Thursday 17 August 2017 : KDR, MOH on waiting list
- Thursday 28 September 2017
- Wednesday 4 October 2017 : full
- Thursday 14 December 2017 : LBR registered

Where:

██████████ 1 William Street, Brisbane, QLD 4000

Time: 1:30pm–5:00pm

Cost: Free

About

The Conduct and Performance Excellence (CaPE) Service, Public Service Commission invites you to a workshop on Performance and Reasonable Management Action.

The workshop is for human resources practitioners and public service leaders at all levels.

The workshop provides an overview of:

- Recent legislative changes impacting the management of conduct and performance
- Obligations:
 - of managers in addressing conduct and performance issues
 - of employees regarding conduct and performance
- Reasonable management action vs Workplace bullying
- Hints and tips for addressing performance and conduct issues
- Responding to common workplace conflict issues

Register here (<https://www.eventbrite.com.au/e/cape-brisbane-workshops-performance-and-reasonable-management-action-tickets-34840999367>)

Contact

Organiser: Public Service Commission

Phone: (07) [REDACTED]

Email: [REDACTED] ([mailto:\[REDACTED\]](mailto:[REDACTED]))

5.2 Modifying Test Quant Procedure (LBR)

- Looking at lot numbers and receipts and trying to be consistent with test-amp procedures.
- LBR to email proposal to Mgt Team to vote on.

5.3 Forensic Foundations Proficiency Test outcomes/feedback (ARM) brought forward from previous meeting.

- 4 refs and crime scene samples.
- Arrived as extracts and quant values – arrived at room temp.
- paperwork had typos and many blank pages.
- high quants and degradation observed – not unexpected given received at room temp.
- results SS and mixtures.
- the idea was good in that it is not a binary CTS process, but requires STRmix.
- was offered to the lab as a free test – originally we declined as it was more expensive.

5.4 Proflex trial (LBR) - Thermofisher

- New 9700 replacement. Checkerboard plate from STARlet B validation run and duplicate plate run as well.
- To be continued by LBR (report)

6.0**New business – for noting**

Nil

- **Next Meeting**

Date: Thursday 3 August 2017

Venue: CR611

ACTION REGISTER

| Minutes Reference | Item Number | Subject | Action | Action Officer | Status |
|-------------------|-------------|--------------------|--|-----------------------------|--|
| 07/07/2016 | 5.2 | DNA Profiling Kits | <p>JAH to prepare a matrix / table for Mgmt to consider</p> <p>10/11/2016 Updated information: JAH, LBR and ARM met with thermofisherscientific (AB) – Identifiler/ID+ is their biggest selling kit, and it is the chemistry that Globalfiler is built on (ID+ has the buffer that was then used for GF)</p> <p>24/11 – JAH to have one more conversation</p> <p>19/01 – CJA, PMB and JAH to have follow up meeting</p> <p>25/05 – CJA has spoken to Paul Csoban regarding options paper. Next step is to organise meeting with QPS.</p> | <p>Mgmt Team</p> <p>PMB</p> | <p>27/10/2016 Read doc and feedback when you can.</p> <p>Ongoing – JAH to finalise</p> <p>08/12 – no update</p> <p>22/12 – to progress early new year</p> <p>19/01 – ongoing</p> <p>02/02 – ongoing</p> <p>16/02 – appt sent for next week.</p> <p>16/03 – appt to be re-sent</p> <p>04/04- meeting set for today</p> <p>13/04 – meeting held and CJA to write Options paper</p> <p>27/04 –PMB to follow-up</p> <p>11/05/2017 – CJA to follow up.</p> <p>25/05/2017 – see action</p> <p>22/06 – nil progress</p> <p>06/07 – nil progress. PMB to speak to PC.</p> <p>20/07 – meeting booked with QPS A/Supt 28 July.</p> |
| 19/01/2017 | 4.1 | WH&S Issues | <p>Follow up on immunity for staff for immunisations given >10 years ago? CJA to follow up on policy relating to existing staff, for provision of information to team.</p> <p>Email from CJA 30/05 – recommendation for staff to have titres checked. Email through [REDACTED] to [REDACTED] to book.</p> | CJA | <p>02/02 – awaiting reply from Infection Control Officer</p> <p>16/03 – no update</p> <p>04/04 – followed up with no response to date.</p> <p>13/04 – no update</p> |

| | | | | | |
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| | | | 22/06/2017 – query regarding if Forensic DNA Analysis as a team should book a clinic, or this should be campus wide. See item 4.1. PNC to follow up with Leadership team | PNC PMB | 27/04/2017 – no update 11/05/2017 – CJA to follow up 22/06/2017 – see 4.1 PNC to follow up 06/07/2017 – QE2 has clinics twice per month. Need to clarify if booster shots to be provided. 20/07 – clinics at QE2 monthly. Boosters would be provided if required based on titre checks. |
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| | | | | | |
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| | | | | KDR | <p>AHU filtering in place, smell should be throughout the level and not workstation specific. Practical action: photos, time - KDR to follow up with incident reporter.</p> <p>20/07 – staff member followed up with, to be monitored – photos, call Martin Bradford when smell sensed.</p> <p>COMPLETE</p> |
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Date: 20 July 2017
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Contact

Organiser: Public Service Commission

Phone: (07) [REDACTED]

Email: [REDACTED] ([mailto:\[REDACTED\]](mailto:[REDACTED]))

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New business – for noting

Nil

• Next Meeting

Date: Thursday 3 August 2017

Venue: CR611

ACTION REGISTER

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Paula Brisotto

From: Cathie Allen
Sent: Wednesday, 6 September 2017 2:24 PM
To: Justin Howes; Paula Brisotto
Subject: VOLume Crime profiling kit

Follow Up Flag: Follow up
Flag Status: Completed

Hi Paula and Justin

I've followed up with Supt Dale Freiberg and she has advised that the QPS wishes to proceed with Volume Crime samples being processed with PP21.

Paula – can you please set up a project to valid a new Profiling Kit as a Business Continuity plan.

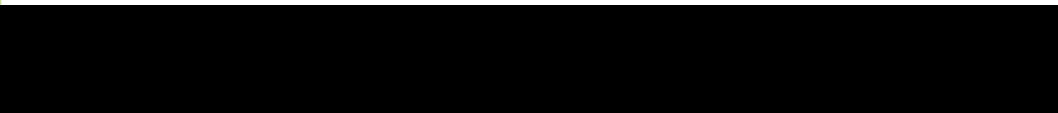
Justin – can you please set up a project to assess the current reporting strategies and how these may be adapted / reduced for Volume Crime so that enhancements can be added to the FR for Volume.

Cheers
Cathie

**Cathie Allen**

Managing Scientist – Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

Paula Brisotto

From: Paula Brisotto
Sent: Friday, 29 September 2017 3:18 PM
To: Adam Kaity; Adrian Pippia; Alanna Darmanin; Alicia Quartermain; Allan McNevin; Allison Lloyd; Amanda Reeves; Amy Cheng; Angela Adamson; Angelina Keller; Anita Sandanasamy; Anne Finch; Belinda Andersen; Biljana Micic; Cassandra James; Cathie Allen; Cecilia Iannuzzi; Chantal Angus; Chelsea Savage; Cindy Chang; Claire Gallagher; Deborah Nicoletti; Emma Caunt; FSS DNA Analysis Admin; Generosa Lundie; Hannah Pattison; Helen Williams; Ingrid Moeller; Jacqui Wilson; Janine Seymour-Murray; Josie Entwistle; Julie Brooks; Justin Howes; Kerry-Anne Lancaster; Kevin Avdic; Kirsten Scott; Kylie Rika; Lai-Wan Le; Lisa Benstead; Lisa Farrelly; Luke Harmer; Luke Ryan; Matthew Hunt; Megan Mathieson; Melissa Cipollone; Michael Goodrich; Michael Hart; Michael Ward; Michelle Margetts; Nicole Gardiner; Paige Rosekrans; Paula Brisotto; Penelope Taylor; Pierre Acedo; Rhys Parry; Ryu Eba; Sandra McKean; Sharelle Nydam; Sharon Byrne; Sharon Cummings; Sharon Johnstone; Susan Brady; Suzanne Sanderson; Tegan Dwyer; Thomas Nurthen; Timothy Gardam; Valerie Caldwell; Vicki Jarrett; Wendy Harmer; Yvonne Connolly
Subject: Volume Crime processing

Hi all,

As you are all aware, Thermo Fisher Scientific has discontinued production of Profiler Plus kits. Forensic DNA Analysis has been provided with sufficient supply to continue processing Volume Crime samples in Profiler Plus until ~January 2018.

In deciding a way forward for Volume crime processing, the following options were considered:

Option 1:

Re-introduce PP21 and STRmix™ for Volume Crime samples.

Option 2

Validate and implement if appropriate an alternative kit for Volume Crime casework on the 3500xL Genetic Analyser, for use with STRmix (a number of kits were discussed including Identifiler® Plus, Globalfiler and Fusion).

All options and considerations were discussed within the Management team, and presented to the superintendent of the Forensic Services Branch, Supt Dale Freiberg, and Insp Scott McLaren.

The QPS have provided support for using PP21 with STRmix for Volume Crime samples.

Key considerations in this decision were:

- No validation would be required, as Volume Crime samples will use the same kit and technology as current Major crime samples.
- ANZPAA Board approved 18 STR DNA loci to be the core DNA markers for Australia in April 2012. PP21 for all case type is consistent with this direction.
- Since January 2017, CODIS core loci (US labs) set at 20 Loci which PP21 is closer to achieving concordance with (than ID Plus).
- STRmix would be used for Volume Crime samples irrespective of the kit chosen.
- TAT may be impacted for Volume Crime processing.
 - o Given the aim of processing Volume Crime samples is getting DNA profiles to NCIDD quickly for the QPS to aid in their investigations, workflow changes will be the focus of the next few month to streamline the process for loading and reporting of Volume Crime results.
- PP21 is currently only validated for processing on the 3130xL genetic Analyser. Validation is currently progressing for processing on the 3500xL.

- Microcon project proposal is progressing, which aims to re-evaluate the number of samples proceeding to auto-microcon.
- STRmix v2.5 will further streamline the process.

The next steps forward are:

1. Validate PP21 for casework on the 3500xL Genetic Analyser (progressing).
2. Verify STRmix v2.5
3. Implement changes if proposed by Microcon project (once approved)
4. Design and implement workflow changes for PP21 volume crime samples
5. Validate Globalfiler as a Business Continuity measure (partially validated).

Please feel free to discuss any of this content with your line managers.

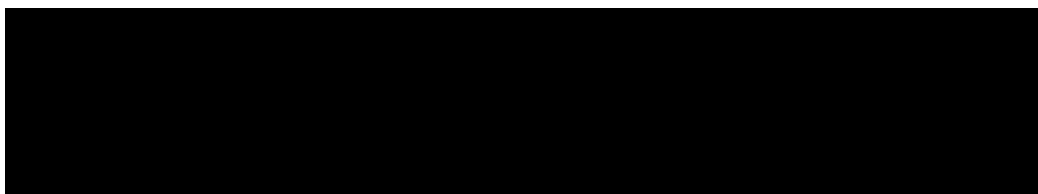
Regards,

Paula and Justin.



Paula Brisotto

Team Leader – Evidence Recovery and Quality Team, Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

Forensic and Scientific Services

An assessment of the ability to obtain DNA profiles when further work is requested on samples with low-level Quantification values.

Justin Howes and Cathie Allen
09 June 2022

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1. Summary

All casework DNA extracts that had an initial quantification result between zero and 0.0088ng/μL and underwent a concentration step using the Microcon® process during the period 2018-2021 (inclusive) were evaluated. The final interpretation result, after one or more amplifications post-concentration, were categorised into two broad categories of 'suitable' for comparison purposes or 'unsuitable' for comparison purposes.

The findings of this evaluation are presented for the Queensland Police Service to consider options on processing pathways.

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2. Definitions and Abbreviations

bdna: Consulting service responsible for the maintenance and management of the Forensic Register

DIFP: DNA Insufficient for Further Processing

FSS: Forensic and Scientific Services

NCIDD: National Criminal Investigation DNA Database.

NDNAD: No DNA Detected

PP21: PowerPlex® 21 amplification system

QPS: Queensland Police Service.

Quant: Quantification – assessment of quantity or concentration of DNA in a sample

Suitable: In this report, this word is applied to DNA profile information that was suitable for comparing to reference DNA profiles and other casework samples.

Unsuitable: In this report, this word is applied to DNA profile information that was obtained that was unsuitable for comparing to reference DNA profiles and other casework samples. This includes final results (ie. after reworks) of 'Complex unsuitable for comparison purposes', 'Partial unsuitable for comparison purposes', 'No DNA profile', 'No DNA detected' and 'DNA insufficient for further processing'.

3. Background

Microcon® Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane [1].

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of extract from approximately 100uL to ≤35 µL for amplification with PP21 amplification kit.

Project #184 assessed the suitability of DNA profiles for comparison purpose for Priority 2 (P2) cases reported in 2016 and provided options to QPS to consider. Following this consideration, QPS approved a new workflow that was implemented in February 2018, where all P2 and Priority 3 (P3) crime scene samples with Quant values less than 0.0088ng/µL were reported as follows:

0 < Quant < 0.001ng: No DNA Detected

0.001ng/µL < Quant < 0.0088ng/µL: DNA insufficient for further processing

Priority 1 (P1) samples with Quant values in this range were to undergo Microcon® concentration and proceed to amplification.

This QPS-approved workflow enabled extracts with Quant values less than 0.0088ng/µL to remain available for processing upon request. QPS could request specific extracts to be reactivated and processed, initially with a Microcon® concentration step. Similarly, the workflow afforded Forensic DNA Analysis case managers the ability to request reactivation of specific extracts based on their assessment of the findings in the case. The aim of the approved workflow was to provide information in the form of a result based on the initial Quant value to QPS Forensic Officers, to facilitate an opportunity to assess the ongoing need for further processing of these samples in light of the receipt of other results in the case, and in the context of the ongoing investigation. The extract would be held indefinitely and therefore continue to be available for further processing if requested.

Since implementation of the workflow, a number of samples have been selected by QPS or Forensic DNA Analysis scientists for further processing during 2018-2021. There are a number of reasons for reactivation of processing including but not limited to, only samples for the case (eg P3 cases), some samples selected based on presumptive findings (eg. 'Micro-positive for sperm'), or some samples might have been selected based on Quant value after discussion with a scientist (eg. select the highest Quant sample from a group of samples).

4. Data interrogation

Priority 1, 2 and 3 crime scene samples (ie. excluding Quality controls, samples flagged as Quality Failure, and environmental samples) submitted for analytical processing between 2018 and 2021 were assessed for suitability for comparison purposes.

Samples were requested of bdna to be provided in MS Excel format with the following information:

- Forensic Register (FR) number
- Exhibit barcode
- Date of submission for DNA profiling (based on result line: 'Submitted – Results Pending')
- Analytical priority
- Date of result line NDNAD
- Quant Batch ID when reported as NDNAD and well
 - o Quantification data (TSAQty, TSAIPCCT, TLAQty, TSADegIndex, TSALOWQT)
- Date of result line DIFP
- Quant Batch ID when reported as DIFP and well
 - o Quantification data (TSAQty, TSAIPCCT, TLAQty, TSADegIndex, TSALOWQT)
- Microcon® request date

- Quant Batch ID after Microcon®
 - o Quantification data (TSAQty, TSAIPCCT, TLAQty, TSADegIndex, TSALOWQT)
- Result mnemonics

In addition to an MS Excel worksheet with the above information, a worksheet of total numbers of samples from 2018-2021 was also obtained.

Samples that were in progress at the time of data interrogation were excluded from assessment.

4.1 Total numbers of 'No DNA Detected' (NDNAD) and 'DNA Insufficient for Further Processing' (DIFP)

Intent

To assess how many samples were received from QPS in the calendar years 2018-2021 that were initially reported as NDNAD and DIFP.

Data Analysis

Raw data was assessed for Priority 1, 2 and 3 crime scene samples. The data represents the number of samples that were triaged and available for further processing upon request.

4.2 Assessment of suitability for comparison purposes

Intent

To assess the final reported results of samples that were selected for further processing by either QPS or FSS scientists during 2018-2021.

Data Analysis

Results were assigned 'suitable' or 'unsuitable' based on final result type after Microcon® concentration and amplification.

To enable data interrogation, 'suitable' results were ascribed a numerical value of '1' and 'unsuitable' results were ascribed the numerical value of '-1'.

The sample's priorities were assessed to determine the breakdown of the number of samples of each priority that were requested for further processing.

The total number of samples initiated by QPS as opposed to Forensic DNA Analysis scientists was not assessed.

The number of further reworks (after the Microcon® concentration) were not assessed; the final result outcome based on any number of reworks was evaluated.

The type of concentration (eg. 'full-microcon', or to ~35uL) for each sample was not assessed.

4.3 Assessment of suitability for NCIDD searching

Intent

To assess whether the final results after further processing satisfied the criteria for loading to the NCIDD in the relevant case.

Data Analysis

Results were interrogated to determine if the reactivated sample's profiles satisfied the criteria for loading and searching on the NCIDD.

The data was assessed further to determine if the sample that was reactivated produced the only result in that case suitable for loading to NCIDD.

5. Results and Discussion

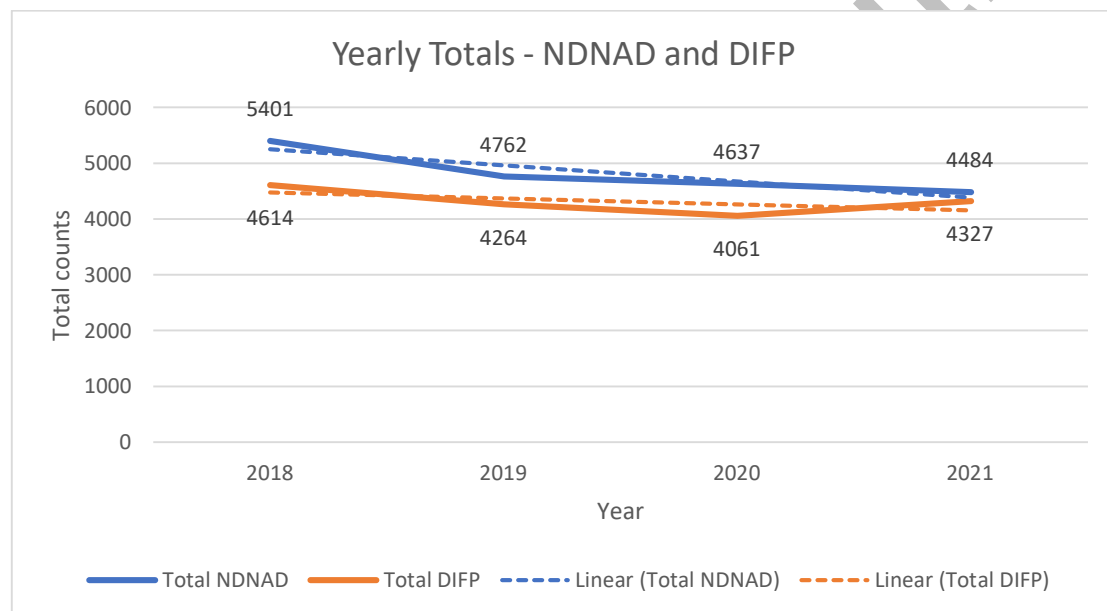
5.1 Total numbers of NDNAD and DIFP

The total number of results reported in the calendar years as NDNAD or DIFP are in Table 1. In total across the data collection period, there were 36550 crime scene samples that resulted in Quant values less than 0.0088ng/µL.

There is no obviously discernible difference between the years other than a decrease in the number of NDNAD in 2018 to 2021 by almost 1000 results. The trend can be observed in Figure 1. This could be due to the improvement of collection procedures over time by QPS, or the improved triage of samples for submission for testing. This means there could have been an improvement in the selection of samples for DNA testing over time (eg. taking high-source DNA samples such as possible blood as a preference) and that could have resulted in samples with higher Quant values being processed and less low-Quant samples received.

Table 1: Total number and percentage (of total) per year and priority

| Year | Priority | Count NDNAD | % Total per year NDNAD | Count DIFP | % Total per year DIFP | Total | Total NDNAD per year | Total DIFP per year | Total per year |
|------|----------|-------------|------------------------|------------|-----------------------|-------|----------------------|---------------------|----------------|
| 2018 | 1 | 40 | 0.40 | 37 | 0.37 | 77 | 5401 | 4614 | 10015 |
| | 2 | 3246 | 32.41 | 1649 | 16.47 | 4895 | | | |
| | 3 | 2115 | 21.12 | 2928 | 29.24 | 5043 | | | |
| 2019 | 1 | 15 | 0.17 | 0 | 0.00 | 15 | 4762 | 4264 | 9026 |
| | 2 | 3126 | 34.63 | 1632 | 18.08 | 4758 | | | |
| | 3 | 1621 | 17.96 | 2632 | 29.16 | 4253 | | | |
| 2020 | 1 | 8 | 0.09 | 0 | 0.00 | 8 | 4637 | 4061 | 8698 |
| | 2 | 3168 | 36.42 | 1714 | 19.71 | 4882 | | | |
| | 3 | 1461 | 16.80 | 2347 | 26.98 | 3808 | | | |
| 2021 | 1 | 10 | 0.11 | 0 | 0.00 | 10 | 4484 | 4327 | 8811 |
| | 2 | 2938 | 33.34 | 1891 | 21.46 | 4829 | | | |
| | 3 | 1536 | 17.43 | 2436 | 27.65 | 3972 | | | |

**Figure { SEQ Figure * ARABIC } : Yearly Totals - NDNAD and DIFP**

The total number of NDNAD and DIFP results per year as a function of testing priority can be seen in Figure 2. The data shows that there were a larger number of NDNAD results issued for P2 cases than P3 cases. There were less DIFP results issued for P2 samples than P3. The reasons could be related to the triage process for P3 cases in that if there is an ability to submit suspected blood samples for instance, then that is preferred over trace samples (eg. tapelifts). These samples, if indeed from a blood source, could contain more DNA to submit for testing. This could lead to less NDNAD and more samples higher than the detection threshold of 0.001ng/ μ L.

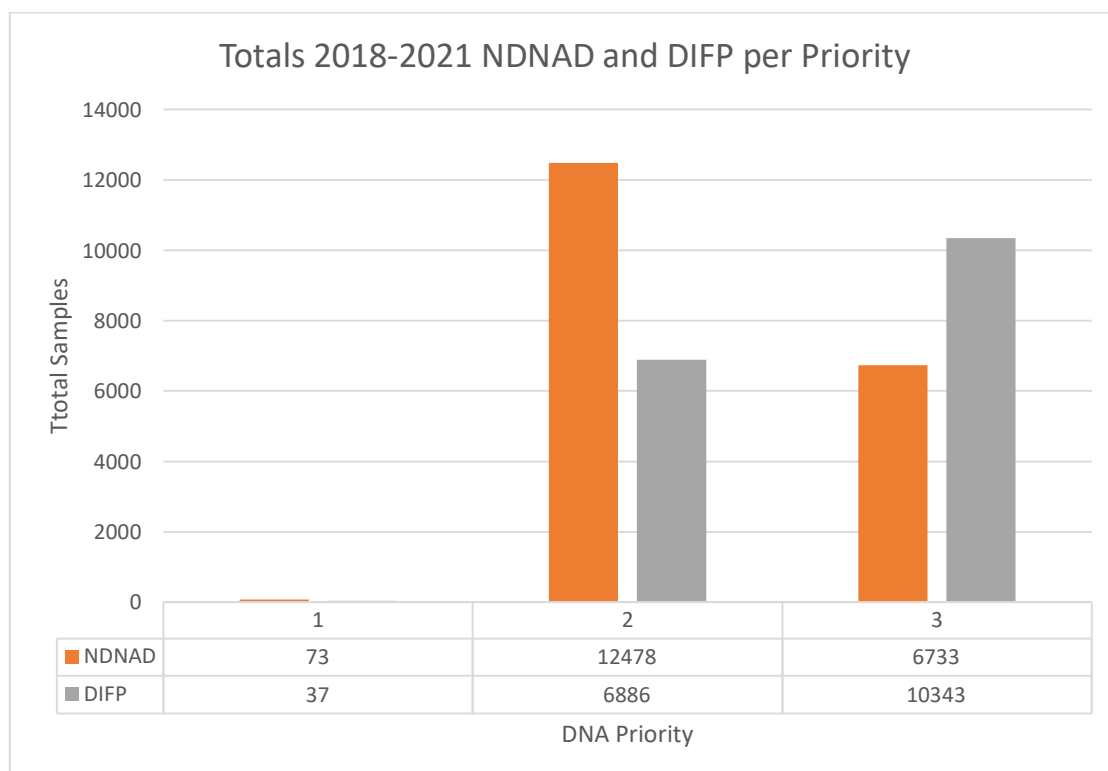


Figure { SEQ Figure * ARABIC } : Total NDNAD and DIFP as a function of priority

The QPS-approved workflow for P1 samples that yielded results in the Quant range between 0.001ng/μL and 0.0088ng/μL is to automatically concentrate and proceed to amplification. The number of P1 samples in the data (represented by Figure 2) could be samples that had the result line issued prior to the standard 'auto-Microcon' process or were requested for P1 testing after processing had already commenced.

5.2 Assessment of suitability for comparison purposes

The data obtained was assessed for suitability for comparison purposes based on the final result after Microcon® concentration. The total number of samples requested for further processing in 2018-2021 was 650 samples. This equates to 1.78% of samples with Quant values <0.0088ng/μL that were selected for further processing during the data collection period.

The data was assessed for the percentage of samples requested from each processing priority. The vast majority of samples for further processing were of P2 (Figure 3). This finding is not unexpected given the higher priority of these samples.

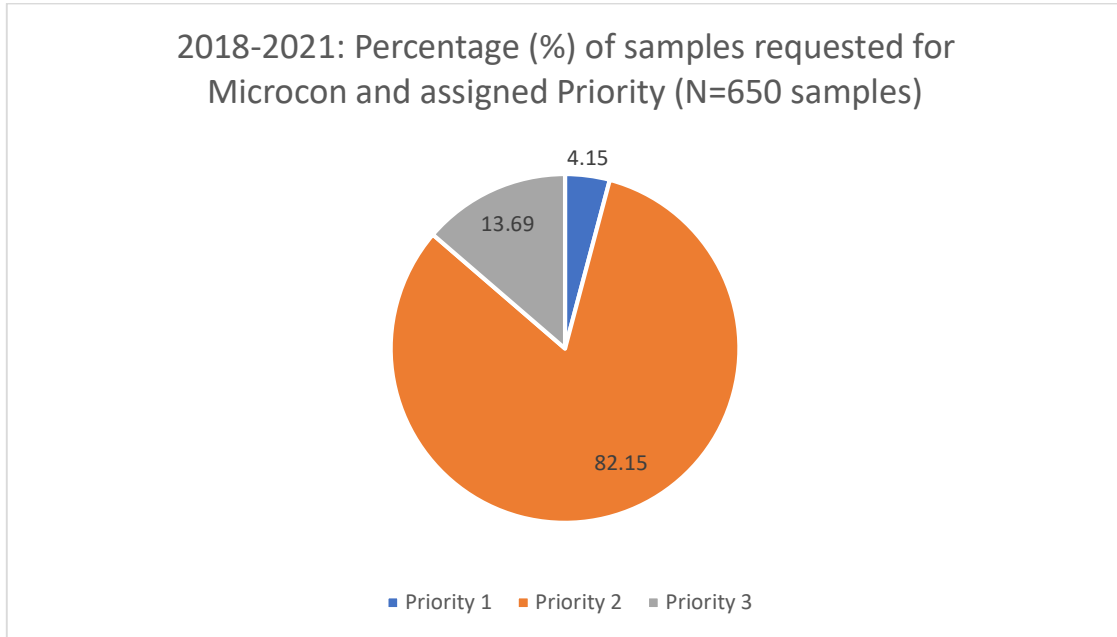


Figure { SEQ Figure * ARABIC }: Percentage of samples requested for further processing according to Priority

Of the 650 samples assessed, 165 resulted in 'suitable' for comparison purposes, and the remaining 485 were reported as 'unsuitable' for comparison after concentration. This represents 25.4% and 74.6% respectively of requests for further processing in the data collection period (Figure 4).

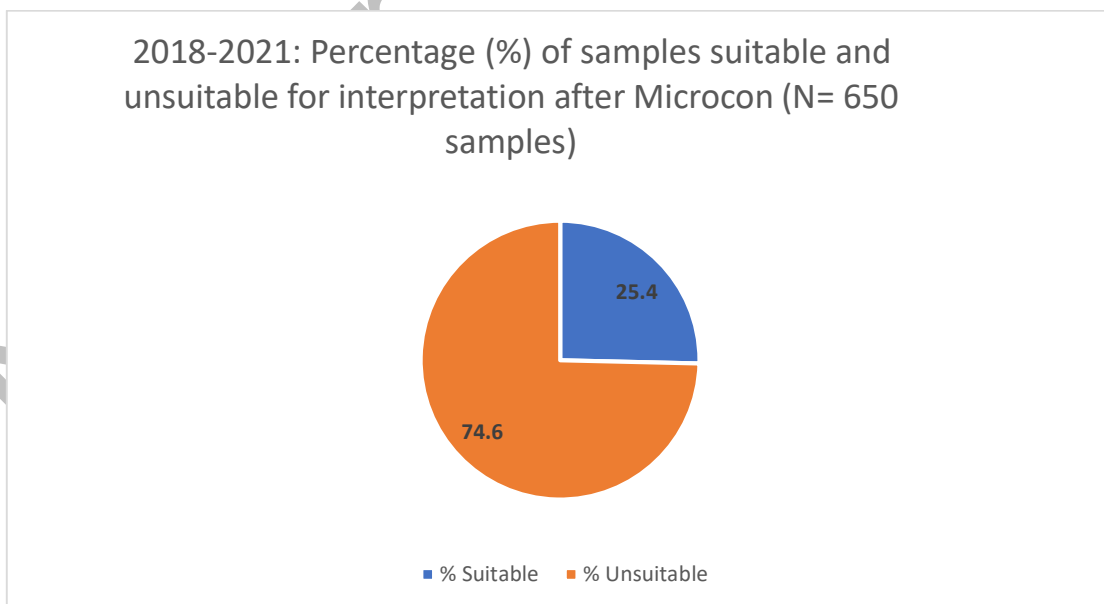


Figure { SEQ Figure * ARABIC }: Percentage of samples 'suitable' and 'unsuitable' for comparison

The percentage of samples deemed 'suitable' for comparison was greater than the findings in Project #184 which found approximately 10% of samples resulted in 'unsuitable' interpretations.

It must be noted that the dataset used in this assessment is different to the data in the previous project. This data evaluation was based on samples that were actively selected for further processing, that is, they were assessed by either QPS or Forensic DNA Analysis as samples that had indications that there might be some value in further processing. This could have either been determined through discussion between QPS and Forensic DNA Analysis scientists or by the scientists independently. Selections for further processing may be based on a number of considerations using the Forensic DNA Analysis scientists experience and knowledge of Quant values and profile behaviour, taking into account higher Quant samples, samples with less degradation, and/or samples with higher percentage of Y-chromosome (in sexual assault samples).

The data in this assessment also includes P3 data. The previous assessments did not include P3 data as those samples were processed with Profiler Plus amplification kit at that time. All cases undergo a pre-FSS triage process by QPS, especially P3 cases (volume crime) where there is a limit on the number of samples submitted for DNA testing. This triaging process exists to focus efforts and resources on samples that might have an improved chance of obtaining DNA profiles eg. possible blood stains.

The data in Project #184 did not include interpretations where the DNA profile result was deemed to have come from at least four contributors. Four-person mixed DNA profile interpretations commenced in August 2018. Prior to this time, if a DNA profile was considered to have originated from at least four contributors, it was reported as 'complex unsuitable for comparison purposes'. Of the 165 samples that were deemed suitable for comparison purposes, nine of these were four-person mixtures. This means approximately 5.5% of the total samples deemed to be suitable for comparison in this assessment would have been considered to be unsuitable for comparison within the assessment of Project #184.

Figures 5 and 6 show the spread of 'suitable' and 'unsuitable' results as a function of the original Quant value. As expected, the number of samples yielding 'suitable' results improved as the Quant value increased. Figure 6 shows the number of samples that yielded 'suitable' and 'unsuitable' results where the Quant values are grouped into 0.001ng/μL intervals. The last interval (0.008-0.0088ng/μL) shows there were more results 'suitable' than 'unsuitable' out of the 34 samples in this range. Prior to this interval, when samples were selected for

further processing, the final interpretation outcome was more likely to be 'unsuitable'.

There was one sample that had an initial Quant value less than 0.001ng/μL that was processed further to then yield a 'suitable' result. This result was an incomplete single source DNA profile that matched the assumed contributor of the DNA profile [REDACTED] refers).

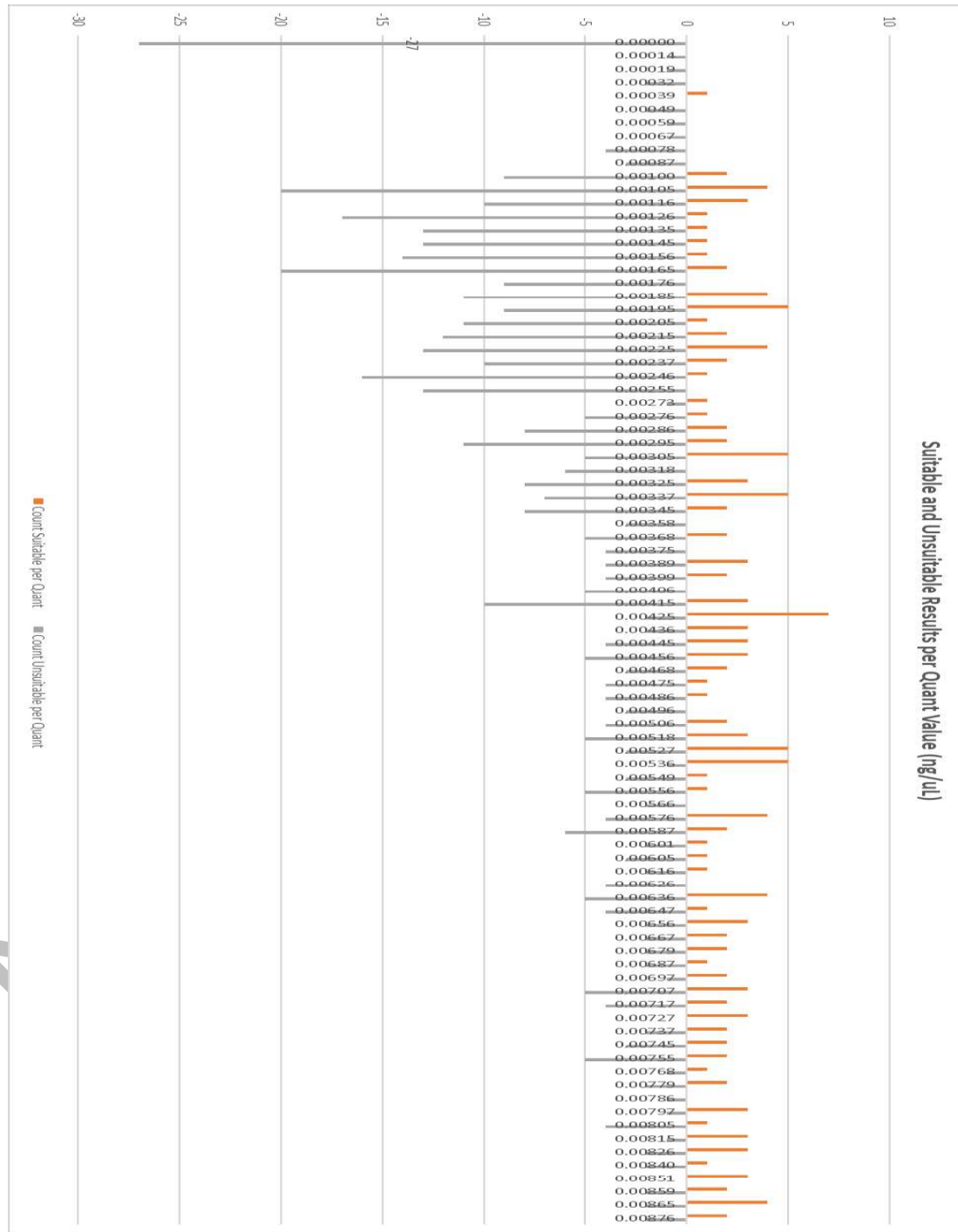


Figure { SEQ Figure * ARABIC } : Results per Quant value (ng/μL)

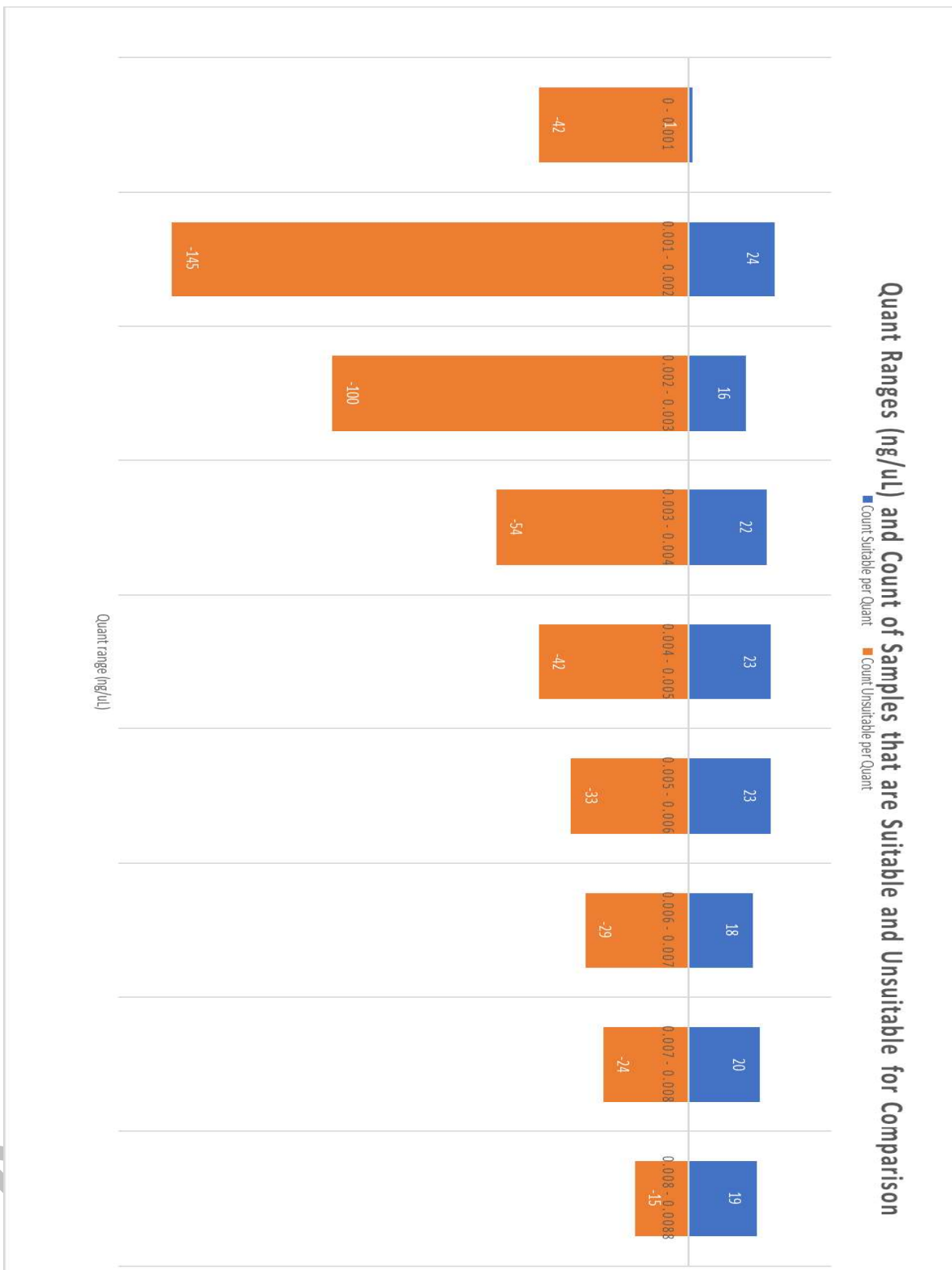


Figure { SEQ Figure * ARABIC }: Count of sample results per Quant value range (ng/µL)

5.3 Assessment of suitability for NCIDD searching

The data was interrogated to determine what percentage of samples, where results were deemed to be 'suitable' for comparison purposes, resulted in an outcome that involved NCIDD.

Of the 165 results that were 'suitable' for comparison after further processing, 41 had an interpretation that involved an NCIDD upload. This represents 6.3% of total samples selected for further processing. Where results of this type were obtained, the cases were assessed to see if there were other samples in the case that also satisfied the criteria for NCIDD upload. This was to determine what the risk might be if the sample (with the NCIDD upload) was not selected for further processing – would there be another sample with the same DNA profile that satisfied the criteria for an NCIDD upload? The data showed that of the 41 samples for NCIDD, in 32 situations there were no other samples matching the same contributor that could have been loaded to NCIDD (Table 2).

Table { SEQ Table * ARABIC }: Suitable samples for comparison and NCIDD

| | Count | Percentage (%) of samples in range reworked (N= 650) |
|----------------------------|-------|--|
| Total Suitable Samples | 165 | 25.4 |
| Total NCIDD Upload samples | 41 | 6.3 |
| No Other samples for NCIDD | 32 | 4.9 |

The data was separated according to processing Priority (Figure 7). In the data set interrogated, there were no P1 samples that were selected for further processing and resulted in an NCIDD upload.

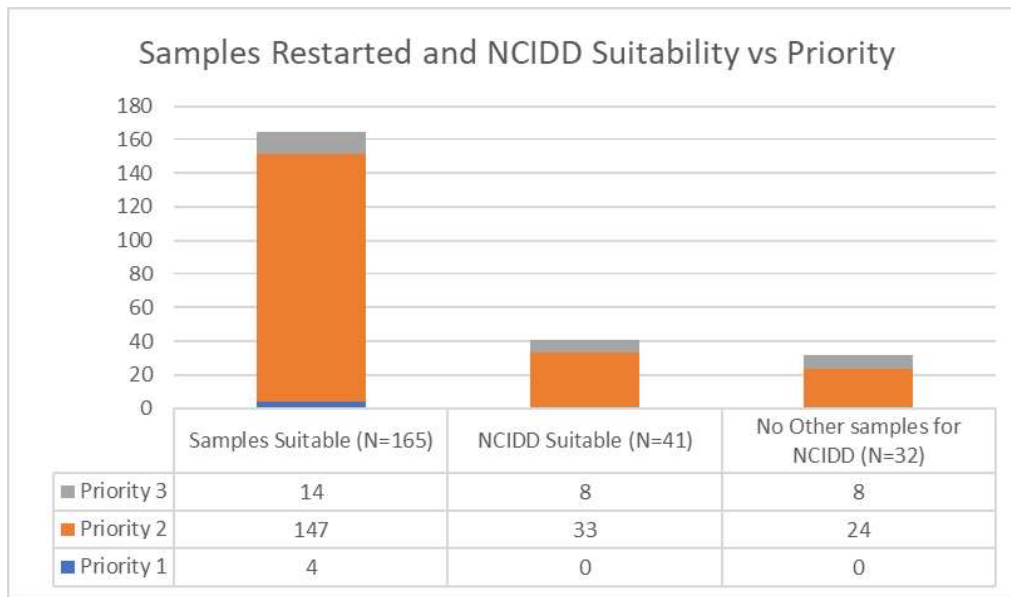


Figure { SEQ Figure * ARABIC }: Suitable samples for comparison and NCIDD with Priority

All P3 samples that yielded 'suitable' DNA profiles for NCIDD did not have other samples in the case where the matching contributor could be uploaded. This is not unexpected given the triage of samples pre-submission to FSS as it is not unusual to receive only one sample per P3 case.

6. Further considerations

In considering options moving forward, some key elements to consider include, but are not limited to:

- Turnaround time:
 - There may be an increased time and cost pressure on the analytical system to process samples in a new range (if one is determined) with or without a concentration step (and beyond).
 - More samples processed through amplification and analysis will mean more samples with DNA profiles for interpretation. In addition to consumable and laboratory staff cost to process, there will be additional time for laboratory and reporting staff to release results (of any type).

- A triage step in the analytical workflow permits the reallocation of staff time, and resources to samples with higher DNA yield, thus improving the turnaround time for results on those samples.

- The opportunity to conserve DNA extract for further processing with other technologies should that be considered (eg. Y-STR analysis, Low Copy Number analysis, Minifiler, MPS);
 - o If samples proceed to a concentration process and beyond, including assessment for further processing post-amplification, there will be less DNA extract available for further processing with other DNA technology.

- The improved ability to provide quick results to QPS (using the Forensic Register at Quantification stage) where there are indications of low levels of DNA detected, thus enabling QPS Forensic Officers the ability to consider further strategies (eg. further sampling of parent items, request for further processing) within context of the investigation.

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Justin Howes

From: Justin Howes
Sent: Wednesday, 7 February 2018 3:18 PM
To: Adrian Pippia; Alicia Quartermain; Allison Lloyd; Amanda Reeves; Angela Adamson; Angelina Keller; Anne Finch; Cassandra James; Claire Gallagher; Deborah Nicoletti; Emma Caunt; Hannah Pattison; Helen Williams; Ingrid Moeller; Jacqui Wilson; Josie Entwistle; Justin Howes; Kylie Rika; Lisa Benstead; Matthew Hunt; Penelope Taylor; Rhys Parry; Sharon Johnstone; Susan Brady; Thomas Nurthen; Timothy Gardam
Subject: Auto-microcons

Hi all

On the back of case manager's anecdotal feedback and our lab's second round of datamining of samples that underwent the auto-microcon process, an Options Paper was presented to QPS Superintendent of Forensic Services Dale Frieberg on ways forward for QPS to consider – continue with auto-microcon process, or cease auto-microcons.

QPS have advised the laboratory that they do not wish for our efforts to be put to the auto-microcon process (including the efforts in interpretation) for Priority 1 or 2 samples.

This means samples in the range 0.001ng/uL (LOD) - 0.0088ng/uL will be reported at Quant stage as 'DNA Insufficient for Further Processing'. This is consistent with the process in place for P3 samples. The manual Microcon process may be performed upon QPS request.

To report in a statement, the following wording could be used:

Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.

This is slightly different to the wording written in 2012/13 for these samples (P3) but after some consultation, appears a good starting point.

An enhancement has been requested to enable this to occur from 12 February. Reactivating samples for further post-extraction processing, if requested from QPS, will be directed to Luke via an FR Request. If there are changes to the 12 February date, I will let you know. As usual, appropriate comments to SOPs will follow.

Regards
 Justin



Justin Howes

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
 Health Support Queensland, **Department of Health**



Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.



HealthSupport
Queensland

Project Proposal #184

Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon[®] Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

August 2017

Justin Howes and Cathie Allen

Project Proposal #184 Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon[®] Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

Published by the State of Queensland (Queensland Health), July 2017



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Version history

| Version | Date | Changed by | Description |
|---------|------------|--------------|-------------------|
| 1.0 | 31/08/2017 | Justin Howes | Document Created. |
| | | | |
| | | | |

Document sign off

This document has been approved by:

| Name | Position | Signature | Date |
|--------------|--------------------|------------|-----------|
| Cathie Allen | Managing Scientist | [REDACTED] | 04/09/17. |

The following officers have endorsed this document

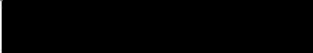
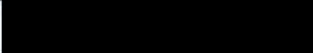
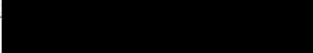
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1. Purpose and Scope

1.1. Background

Microcon[®] Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane^[1].

The use of Microcon[®] filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of extract from approximately 100uL to $\leq 20\mu\text{L}$ for amplification with AmpF ϕ STR[®] Profiler Plus[®], and to $\leq 35\mu\text{L}$ for amplification with PowerPlex[®] 21 system (PP21).

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of $< 0.132\text{ng}$ were found to exhibit marked stochastic effects after amplification^[2]. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process).

Anecdotally, the suitability to provide the Queensland Police Service (QPS) with DNA profile intelligence from extracts that have been concentrated has been noted to be limited. Furthermore, extracts that are of low quant value that have been automatically concentrated have been observed to rarely yield DNA information for QPS.

NB. Project #163 – *Assessment of results obtained from 'automatic-microcon' samples*^[3] was conducted to evaluate the results of samples that were processed with the 'auto-microcon' process. A recommendation of this project was to re-evaluate after the introduction of the Forensic Register in conjunction with the use of Quantifiler[®] Trio DNA Quantification Kit.

This recommendation was based on the perceived ease of retrieving data from the FR as opposed to AUSLAB, and with the thought that the FR would soon be implemented. For the purposes of this project, it is not considered essential to have the FR implemented if the data can be retrieved from AUSLAB. However, it is considered important that the data be spanning a sufficient period of processing, and be based on the same Quantification system namely the Quantifiler[®] Trio DNA Quantification Kit.

1.2. Purpose

The purpose of this project is to evaluate the suitability for interpretation of DNA profiles that may be obtained after the post-extraction concentration step using the Microcon[®] centrifugal filter devices. This evaluation will include an assessment of those samples that underwent the 'auto-microcon' process.

1.3. Scope

This evaluation will be based on a data mine of extracts in the year 2016 that were concentrated with Microcon[®] centrifugal filter devices, and will assess the 'suitability' of PP21 profile outcomes as a function of quant values obtained from using the Quantifiler[®] Trio DNA Quantification Kit.

This evaluation will look at two data sets as a function of the quantification value:

1. PP21 DNA profile outcomes from extracts that were processed through the 'auto-microcon' process;
2. PP21 DNA profile outcomes from all extracts that were concentrated with the Microcon[®] filter devices.

1.4. Definitions

Auto-microcon: Samples with extracts quantified in the range 0.001ng/ μ L to 0.0088ng/ μ L that were automatically processed for a concentration step using Microcon[®] centrifugal filter devices.

NCIDD: National Criminal Investigation DNA Database

2. Governance

Project Personnel

- Project Manager: Justin Howes – Team Leader, Forensic Reporting and Intelligence Team.

Decision Making Group

- The Management Team (including the Project Manager), are the decision making group for this project and may use the defined acceptance criteria in this project to cease part or all of the

experimentation at any stage. The Decision Making Group may also make modifications to this Experimental Design as required, however this must be documented and retained with the original approved Experimental Design.

Reporting

The Project Manager will provide a fortnightly project status update to the Decision Making Group at the Management Team meetings and by exception as required.

3. Resources

The following resources are required for this validation/project:

Forensic DNA Analysis staff and computer time to retrieve data from AUSLAB and to use Microsoft Excel.

4. Methods

4.1. Data retrieval from AUSLAB (LIMS)

The data date range is to encompass all samples quantified with Quantifiler[®] Trio DNA Quantification Kit in 2016, with the following criteria:

1. Quantification value above the Limit of Detection (Quantification) for the Quantifiler[®] Trio DNA Quantification Kit (ie. 0.001ng/ μ L);
2. Extracts to be from samples with DNA Priority 2 (High Priority – PP21 amplification kit);
3. Extracts to have undergone a concentration step using Microcon[®] centrifugal filter devices;
4. Exhibit report outcome (interpretation).

Data will be exported to Microsoft Excel for interrogation.

4.2. Data interrogation

The data will be interrogated by assessing the DNA profile outcome results reported as Exhibit Report lines (from AUSLAB) as a function of the quantification value.

The data will exclude samples that have not returned a DNA profile result, Quality samples (including environmental monitoring samples), have no quant value in the data export, or have quality issues noted.

The DNA profile outcome will be assessed as either 'fail' or 'success' with the following definitions:

1. 'Fail': DNA profile interpretation outcomes of 'Complex unsuitable for interpretation', 'No DNA profile', 'Partial unsuitable for interpretation', 'No DNA Detected';
2. 'Success': All other DNA profile outcomes.

5. Experimental Design

5.1. Experiment 1: Assessment of 'auto-microcon' results

Intent

Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.

Data Analysis

The samples applicable to this experiment will have quantification values in the range 0.001ng/ μ L to 0.0088ng/ μ L.

DNA profile interpretation outcomes will be grouped into either 'success' or 'fail' as a function of the quantification value.

A percentage of samples that fall into these categories will be determined.

Of the DNA profile interpretation outcomes of 'success', the type of outcome will be broken down further to determine:

1. The percentage of these samples that were reworked; and,

2. The percentage of samples that led to an upload of DNA information to NCIDD, including the amount of reworking required for this upload.

Assessment Criteria

The Decision Making Group will determine if the percentages obtained are significant enough to inform a new workflow strategy in consultation with QPS.

Factors to consider include, but not limited to:

1. Effect on turnaround time for samples in this range considering the success/fail results;
2. Effect on intelligence provision that is provided to QPS from DNA profiles uploaded to NCIDD for samples in this range;
3. Cost of processing samples (including reworks where appropriate) including staff and consumables considering the success/fail results;
4. Opportunity cost of not being able to process other samples that could lead to meaningful information for QPS, including processing with further techniques (eg. Y-STR profiling).

5.2. Experiment 2: Assessment of all DNA profile results from extracts that have had a concentration step.

Intent

Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 and underwent a post-extraction concentration step using Microcon[®] centrifugal filter devices.

Data Analysis

The samples applicable to this experiment will have quantification values above 0.001ng/ μ L.

DNA profile interpretation outcomes will be grouped into either 'success' or 'fail' as a function of the quantification value.

A percentage of samples that fall into these categories will be determined.

Of the DNA profile interpretation outcomes of 'success', the type of outcome will be broken down further to determine:

1. The percentage of these samples that were reworked; and,
2. The percentage of samples that led to an upload of DNA information to NCIDD, including the amount of reworking required for this upload.

Assessment Criteria

The Decision Making Group will determine if the percentages obtained are significant enough to inform a new workflow strategy in consultation with QPS.

Factors to consider include, but not limited to:

1. Effect on turnaround time for samples in this range considering the success/fail results;
2. Effect on intelligence provision that is provided to QPS from DNA profiles uploaded to NCIDD for samples in this range;
3. Cost of processing samples (including reworks where appropriate) including staff and consumables considering the success/fail results;
4. Opportunity cost of not being able to process other samples that could lead to meaningful information for QPS, including processing with further techniques (eg. Y-STR profiling).

5.3. Experiment 3: Datamine of the difference in pre- and post-Microcon[®] Quantification values

Intent

Evaluate the difference between the values obtained from the Quantification process in samples that have had a Microcon[®] concentration step applied.

As this is purely a datamining experiment, only the samples that have yielded a result of 'success' will be examined.

Data Analysis

The samples applicable to this experiment will have quantification values above 0.001ng/ μ L where the final result has been 'success'.

Assessment Criteria

The Decision Making Group will determine if the differences are satisfactorily correlating with expectations.

The Decision Making Group may use this information to decide if the Microcon® concentrating step is worthwhile in keeping as a post-extraction processing step, or to look into other providers of similar technology.

6. Results and Data Compilation

The assessment criteria for each experiment will be used to make an overall assessment as to whether there is sufficient information to inform a new workflow strategy for low quant samples.

The decision points will be based on two data groups:

1. Samples in the 'auto-microcon' range;
2. Samples in an extended quant range (and what that extended range may be).

The Decision Making Group is responsible for assessing the need for further work to assist in making a decision, and will inform the Project Manager.

A final report will be produced which will compile all analyses, conclusion and recommendations.

7. References

- [1] QIS 19544v11 – Concentration of DNA Extracts Using Microcon Centrifugal Filter Devices
- [2] PowerPlex® 21– Amplification of Extracted DNA Validation. Megan Mathieson, Thomas Nurthen, Cathie Allen. December 2012. Forensic DNA Analysis.
- [3] Project #163 - Assessment of results obtained from 'automatic-microcon' samples. Josie Entwistle, Allison Lloyd, Kylie Rika, Thomas Nurthen, Cathie Allen. August 2015. Forensic DNA Analysis.

No. **K 20405**



QUEENSLAND POLICE

OFFICIAL DIARY

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PARTICULARS OF DUTY AND PLACES VISITED

Discussion re: options Paper
 re: 'auto-microcen' process for
 Priority 2 (major Quine) samples.
 Selection - option 2. Followed up
 with email to Cathie / Paul confirming

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|------|------------|------|
| TRUE | 0.005 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.009 Auto | |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.005 Auto | |
| TRUE | 0.009 Auto | |
| TRUE | 0.008 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |

| | | |
|------|------------|---------|
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.007 Auto | SUCCESS |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.007 Auto | SUCCESS |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |

| | | |
|------|------------|------|
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| | | |
| TRUE | 0.005 Auto | |
| TRUE | 0.006 Auto | FAIL |
| | | |
| TRUE | 0.005 Auto | |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.006 Auto | |
| | | |
| TRUE | 0.008 Auto | |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |

| | | |
|------|------------|---------|
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.002 Auto | |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | SUCCESS |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | |

| | | |
|------|------------|---------|
| TRUE | 0.008 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.003 Auto | SUCCESS |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.005 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.002 Auto | |
| TRUE | 0.005 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.006 Auto | |
| TRUE | 0.005 Auto | |
| TRUE | 0.004 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.005 Auto | |
| TRUE | 0.005 Auto | FAIL |

| | | |
|------|------------|------|
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.002 Auto | |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.009 Auto | |
| TRUE | 0.002 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |

| | | |
|------|------------|------|
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.005 Auto | |
| TRUE | 0.002 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.008 Auto | |
| TRUE | 0.008 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |

| | | |
|------|------------|---------|
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | SUCCESS |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |

| | | |
|------|------------|---------|
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.004 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | SUCCESS |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |

| | | |
|------|------------|---------|
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.005 Auto | SUCCESS |
| TRUE | 0.007 Auto | FAIL |

| | | |
|------|------------|------|
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |

| | | |
|------|------------|------|
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.009 Auto | |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.006 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.008 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |

| | | |
|------|------------|---------|
| TRUE | 0.007 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.007 Auto | SUCCESS |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |

| | | |
|------|------------|------|
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |

| | | |
|------|------------|------|
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.005 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.002 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.006 Auto | |

| | | |
|------|------------|---------|
| TRUE | 0.007 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.008 Auto | SUCCESS |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | SUCCESS |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |

| | | |
|------|------------|------|
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.002 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.002 Auto | |
| TRUE | 0.004 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |

| | | |
|------|------------|---------|
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.002 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.002 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.007 Auto | SUCCESS |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.009 Auto | |
| TRUE | 0.005 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.008 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.004 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |

| | | |
|------|------------|------|
| TRUE | 0.008 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.005 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.002 Auto | |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.002 Auto | |
| TRUE | 0.004 Auto | |
| TRUE | 0.006 Auto | |
| TRUE | 0.009 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.009 Auto | |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.005 Auto | |
| TRUE | 0.008 Auto | FAIL |

| | | |
|------|------------|---------|
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.004 Auto | |
| TRUE | 0.006 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.008 Auto | SUCCESS |
| TRUE | 0.009 Auto | SUCCESS |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | |
| TRUE | 0.007 Auto | FAIL |

| | | |
|------|------------|---------|
| TRUE | 0.003 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.009 Auto | |
| TRUE | 0.007 Auto | SUCCESS |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.004 Auto | SUCCESS |
| TRUE | 0.003 Auto | FAIL |

| | | |
|------|------------|---------|
| TRUE | 0.004 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.005 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.004 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | SUCCESS |

| | | |
|------|------------|------|
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.002 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |

| | | |
|------|------------|------|
| TRUE | 0.004 Auto | |
| TRUE | 0.008 Auto | |
| TRUE | 0.004 Auto | |
| TRUE | 0.005 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.006 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.002 Auto | |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.009 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |

TRUE 0.007 Auto SUCCESS

TRUE 0.005 Auto SUCCESS
TRUE 0.004 Auto

TRUE 0.005 Auto
TRUE 0.002 Auto

TRUE 0.005 Auto FAIL
TRUE 0.004 Auto FAIL

TRUE 0.005 Auto FAIL
TRUE 0.005 Auto

TRUE 0.004 Auto FAIL

TRUE 0.006 Auto FAIL

TRUE 0.007 Auto
TRUE 0.008 Auto

TRUE 0.009 Auto

TRUE 0.005 Auto FAIL

TRUE 0.002 Auto FAIL

TRUE 0.004 Auto FAIL

TRUE 0.008 Auto FAIL

TRUE 0.008 Auto FAIL

TRUE 0.004 Auto FAIL

TRUE 0.008 Auto FAIL

TRUE 0.005 Auto FAIL

TRUE 0.004 Auto FAIL

TRUE 0.005 Auto FAIL
TRUE 0.007 Auto

TRUE 0.007 Auto FAIL

| | | |
|------|------------|------|
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.004 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.002 Auto | |
| TRUE | 0.002 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.002 Auto | FAIL |

| | | |
|------|------------|------|
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.002 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.003 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.004 Auto | |

| | | |
|------|------------|------|
| TRUE | 0.003 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.008 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.004 Auto | |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.009 Auto | FAIL |
| TRUE | 0.005 Auto | |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.002 Auto | |
| TRUE | 0.004 Auto | |

| | | |
|------|------------|---------|
| TRUE | 0.009 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.004 Auto | |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | SUCCESS |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.007 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.003 Auto | |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.008 Auto | |
| TRUE | 0.005 Auto | |
| TRUE | 0.004 Auto | |
| TRUE | 0.002 Auto | |
| TRUE | 0.006 Auto | |
| TRUE | 0.009 Auto | |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.007 Auto | |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |

| | | |
|------|--------------|---------|
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.003 Auto | FAIL |
| TRUE | 0.004 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.008 Auto | FAIL |
| TRUE | 0.002 Auto | FAIL |
| TRUE | 0.004 Auto | |
| TRUE | 0.005 Auto | FAIL |
| TRUE | 0.006 Auto | |
| TRUE | 0.007 Auto | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.009 Manual | |
| TRUE | 0.002 Manual | SUCCESS |
| TRUE | 0.001 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.029 Manual | FAIL |
| TRUE | 0 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.019 Manual | FAIL |

| | | | |
|------|-------|--------|---------|
| TRUE | 0.038 | Manual | |
| TRUE | 0 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.023 | Manual | |
| TRUE | 0.013 | Manual | FAIL |
| TRUE | 0.016 | Manual | FAIL |
| TRUE | 0.03 | Manual | FAIL |
| TRUE | 0.03 | Manual | FAIL |
| TRUE | 0.021 | Manual | FAIL |
| TRUE | 0.021 | Manual | FAIL |
| TRUE | 0.025 | Manual | SUCCESS |
| TRUE | 0.029 | Manual | |
| TRUE | 0.013 | Manual | FAIL |
| TRUE | 0.002 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.015 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.021 | Manual | SUCCESS |
| TRUE | 0.001 | Manual | FAIL |

| | | |
|------|--------------|------|
| TRUE | 0.026 Manual | FAIL |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.021 Manual | FAIL |
| TRUE | 3E-04 Manual | FAIL |
| TRUE | 4E-04 Manual | FAIL |
| TRUE | 0.019 Manual | FAIL |
| TRUE | 0.021 Manual | |
| TRUE | 0.026 Manual | |
| TRUE | 0.023 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.028 Manual | FAIL |
| TRUE | 0.032 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.02 Manual | |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.016 Manual | |

| | | | |
|------|-------|--------|------|
| TRUE | 0.017 | Manual | |
| TRUE | 0.017 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.009 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 3E-04 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.032 | Manual | FAIL |
| TRUE | 0.03 | Manual | |
| TRUE | 0.035 | Manual | FAIL |
| TRUE | 0.009 | Manual | |
| TRUE | 0.033 | Manual | FAIL |
| TRUE | 0.022 | Manual | |
| TRUE | 0.014 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |

| | | |
|------|--------------|------|
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.017 Manual | |
| TRUE | 0.002 Manual | |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0 Manual | |
| TRUE | 0.02 Manual | FAIL |
| TRUE | 0.022 Manual | FAIL |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.024 Manual | FAIL |
| TRUE | 0.019 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.017 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | |

| | | | |
|------|-------|--------|---------|
| TRUE | 0.002 | Manual | |
| TRUE | 0.01 | Manual | SUCCESS |
| TRUE | 0.027 | Manual | |
| TRUE | 0.016 | Manual | FAIL |
| TRUE | 0.026 | Manual | FAIL |
| TRUE | 0.02 | Manual | FAIL |
| TRUE | 0.021 | Manual | |
| TRUE | 0.011 | Manual | FAIL |
| TRUE | 0.033 | Manual | FAIL |
| TRUE | 0.013 | Manual | FAIL |
| TRUE | 0.017 | Manual | FAIL |
| TRUE | 0.014 | Manual | |
| TRUE | 0.014 | Manual | FAIL |
| TRUE | 0.026 | Manual | |
| TRUE | 0.002 | Manual | |
| TRUE | 0.014 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.015 | Manual | FAIL |
| TRUE | 0.022 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.018 | Manual | FAIL |
| TRUE | 0.018 | Manual | |

| | | |
|------|--------------|---------|
| TRUE | 0.028 Manual | FAIL |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.016 Manual | FAIL |
| TRUE | 0.02 Manual | |
| TRUE | 0.013 Manual | |
| TRUE | 0.002 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0 Manual | FAIL |
| TRUE | 0.023 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.012 Manual | |
| TRUE | 0.027 Manual | |
| TRUE | 0.023 Manual | FAIL |
| TRUE | 0.014 Manual | |
| TRUE | 0.016 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.012 Manual | |
| TRUE | 0.015 Manual | SUCCESS |

| | | |
|------|--------------|---------|
| TRUE | 0.017 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.02 Manual | FAIL |
| TRUE | 0.017 Manual | |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 7E-04 Manual | FAIL |
| TRUE | 0.018 Manual | FAIL |
| TRUE | 2E-04 Manual | FAIL |
| TRUE | 0.014 Manual | |
| TRUE | 0 Manual | FAIL |
| TRUE | 0.014 Manual | SUCCESS |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.013 Manual | |
| TRUE | 0 Manual | FAIL |
| TRUE | 2E-04 Manual | FAIL |
| TRUE | 0.026 Manual | FAIL |
| TRUE | 3E-04 Manual | |

TRUE 0.016 Manual
TRUE 0.009 Manual

TRUE 0.016 Manual
TRUE 0.018 Manual

TRUE 0.025 Manual FAIL

TRUE 0.002 Manual FAIL

TRUE 0.001 Manual FAIL

TRUE 0.002 Manual FAIL

TRUE 0.01 Manual FAIL

TRUE 0.015 Manual FAIL

TRUE 0.019 Manual FAIL

TRUE 0.018 Manual FAIL

TRUE 0.016 Manual

TRUE 0.018 Manual FAIL

TRUE 0.023 Manual FAIL

TRUE 0.024 Manual FAIL

TRUE 0.013 Manual

TRUE 0.02 Manual

TRUE 0.017 Manual

| | | | |
|------|-------|--------|---------|
| TRUE | 0.012 | Manual | |
| TRUE | 0.027 | Manual | |
| TRUE | 0.016 | Manual | FAIL |
| TRUE | 0.032 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.02 | Manual | SUCCESS |
| TRUE | 0.031 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | |
| TRUE | 0.074 | Manual | |
| TRUE | 0.002 | Manual | |
| TRUE | 0.009 | Manual | FAIL |
| TRUE | 0.026 | Manual | |
| TRUE | 0.024 | Manual | FAIL |
| TRUE | 0.022 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.026 | Manual | FAIL |
| TRUE | 0.013 | Manual | FAIL |

| | | |
|------|--------------|---------|
| TRUE | 0.01 Manual | |
| TRUE | 0.018 Manual | |
| TRUE | 0.011 Manual | |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.024 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.017 Manual | SUCCESS |
| TRUE | 0.009 Manual | |
| TRUE | 0.022 Manual | |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.032 Manual | FAIL |
| TRUE | 0.021 Manual | FAIL |

| | | |
|------|--------------|---------|
| TRUE | 0.018 Manual | FAIL |
| TRUE | 0.025 Manual | FAIL |
| TRUE | 0.017 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.019 Manual | FAIL |
| TRUE | 0.012 Manual | SUCCESS |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.014 Manual | |
| TRUE | 0.037 Manual | FAIL |
| TRUE | 0.017 Manual | SUCCESS |
| TRUE | 0.009 Manual | |
| TRUE | 0.015 Manual | |
| TRUE | 0.016 Manual | |
| TRUE | 0.011 Manual | SUCCESS |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.009 Manual | |
| TRUE | 0.01 Manual | |
| TRUE | 0.022 Manual | |
| TRUE | 0.02 Manual | |

| | | |
|------|--------------|------|
| TRUE | 0.022 Manual | FAIL |
| TRUE | 0.022 Manual | FAIL |
| TRUE | 0.025 Manual | |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.026 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.025 Manual | |
| TRUE | 0.022 Manual | |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 8E-04 Manual | |
| TRUE | 7E-04 Manual | FAIL |
| TRUE | 2E-04 Manual | FAIL |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.021 Manual | |
| TRUE | 0.017 Manual | FAIL |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.029 Manual | |
| TRUE | 0.002 Manual | |
| TRUE | 0.019 Manual | FAIL |
| TRUE | 0.035 Manual | FAIL |
| TRUE | 0.025 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |

| | | |
|------|--------------|---------|
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.014 Manual | |
| TRUE | 0.029 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.028 Manual | |
| TRUE | 0.018 Manual | FAIL |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.027 Manual | FAIL |
| TRUE | 0.061 Manual | |
| TRUE | 0.01 Manual | |
| TRUE | 0.025 Manual | FAIL |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.011 Manual | SUCCESS |
| TRUE | 0.029 Manual | |
| TRUE | 0.016 Manual | |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.016 Manual | FAIL |

| | | | |
|------|-------|--------|------|
| TRUE | 0.001 | Manual | |
| TRUE | 0.013 | Manual | |
| TRUE | 0.029 | Manual | |
| TRUE | 0.024 | Manual | |
| TRUE | 0.02 | Manual | |
| TRUE | 0.019 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | |
| TRUE | 0.014 | Manual | FAIL |
| TRUE | 0.001 | Manual | |
| TRUE | 0.016 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.019 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | |
| TRUE | 0.015 | Manual | FAIL |
| TRUE | 0.023 | Manual | FAIL |
| TRUE | 0.014 | Manual | |
| TRUE | 0.024 | Manual | |
| TRUE | 0.015 | Manual | |
| TRUE | 0.012 | Manual | FAIL |
| TRUE | 0.027 | Manual | |
| TRUE | 0 | Manual | FAIL |

| | | | |
|------|-------|--------|------|
| TRUE | 0 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.028 | Manual | FAIL |
| TRUE | 0.023 | Manual | |
| TRUE | 0.014 | Manual | FAIL |
| TRUE | 0.015 | Manual | |
| TRUE | 0.011 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.014 | Manual | |
| TRUE | 0.002 | Manual | |
| TRUE | 0.013 | Manual | FAIL |
| TRUE | 0 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.02 | Manual | |
| TRUE | 0.015 | Manual | |
| TRUE | 0.002 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |

| | | |
|------|--------------|---------|
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.011 Manual | SUCCESS |
| TRUE | 0.014 Manual | |
| TRUE | 0.022 Manual | FAIL |
| TRUE | 0.012 Manual | |
| TRUE | 0.025 Manual | FAIL |
| TRUE | 0.011 Manual | |
| TRUE | 0.033 Manual | SUCCESS |
| TRUE | 0.02 Manual | |
| TRUE | 0.033 Manual | FAIL |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.021 Manual | FAIL |
| TRUE | 0.033 Manual | |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.025 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |

| | | |
|------|--------------|---------|
| TRUE | 0.029 Manual | |
| TRUE | 0.013 Manual | SUCCESS |
| TRUE | 0.013 Manual | |
| TRUE | 0.018 Manual | SUCCESS |
| TRUE | 8E-04 Manual | FAIL |
| TRUE | 3E-04 Manual | FAIL |
| TRUE | 0.021 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.012 Manual | |
| TRUE | 0.012 Manual | |
| TRUE | 4E-04 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.019 Manual | FAIL |
| TRUE | 0.009 Manual | SUCCESS |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.022 Manual | FAIL |
| TRUE | 0.053 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.016 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |

| | | |
|------|--------------|------|
| TRUE | 0.009 Manual | |
| TRUE | 0.015 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.025 Manual | FAIL |
| TRUE | 2E-04 Manual | FAIL |
| TRUE | 0.021 Manual | |
| TRUE | 0.028 Manual | FAIL |
| TRUE | 0.014 Manual | |
| TRUE | 0.02 Manual | |
| TRUE | 0.023 Manual | |
| TRUE | 0.025 Manual | |
| TRUE | 0.012 Manual | |
| TRUE | 0.016 Manual | |
| TRUE | 0 Manual | |
| TRUE | 0.002 Manual | |
| TRUE | 0.001 Manual | FAIL |

| | | |
|------|--------------|---------|
| TRUE | 0.012 Manual | SUCCESS |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.017 Manual | |
| TRUE | 0.017 Manual | |
| TRUE | 0.032 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.013 Manual | |
| TRUE | 0.023 Manual | |
| TRUE | 0.018 Manual | SUCCESS |
| TRUE | 0.002 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.013 Manual | |
| TRUE | 0.019 Manual | FAIL |
| TRUE | 0.009 Manual | |
| TRUE | 0.013 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.032 Manual | |
| TRUE | 0.026 Manual | |
| TRUE | 0 Manual | |
| TRUE | 0 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |

TRUE 0.013 Manual SUCCESS

TRUE 0.01 Manual FAIL

TRUE 0.012 Manual

TRUE 0.035 Manual

TRUE 0.015 Manual FAIL

TRUE 0.001 Manual FAIL

TRUE 0.002 Manual FAIL

TRUE 0.017 Manual SUCCESS

TRUE 0.012 Manual FAIL

TRUE 0.011 Manual FAIL

TRUE 0.009 Manual FAIL

TRUE 0.021 Manual FAIL

TRUE 0.002 Manual FAIL

TRUE 0.014 Manual FAIL

TRUE 0.022 Manual FAIL

TRUE 0.028 Manual FAIL

TRUE 0.014 Manual FAIL

TRUE 0.009 Manual FAIL

TRUE 0.015 Manual FAIL

TRUE 0.025 Manual

TRUE 0.002 Manual FAIL

TRUE 0.026 Manual

| | | | |
|------|-------|--------|---------|
| TRUE | 0.012 | Manual | FAIL |
| TRUE | 0.028 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.021 | Manual | |
| TRUE | 0.021 | Manual | FAIL |
| TRUE | 0.016 | Manual | FAIL |
| TRUE | 0.04 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.011 | Manual | |
| TRUE | 0.009 | Manual | |
| TRUE | 0.03 | Manual | |
| TRUE | 0.009 | Manual | |
| TRUE | 0.032 | Manual | SUCCESS |
| TRUE | 0.024 | Manual | |
| TRUE | 0.025 | Manual | |
| TRUE | 0.016 | Manual | FAIL |
| TRUE | 0.04 | Manual | FAIL |
| TRUE | 0.01 | Manual | FAIL |

| | | |
|------|--------------|---------|
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0 Manual | |
| TRUE | 0.022 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.014 Manual | |
| TRUE | 0.038 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.023 Manual | |
| TRUE | 0.032 Manual | FAIL |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.028 Manual | SUCCESS |
| TRUE | 0.009 Manual | |
| TRUE | 0.022 Manual | |
| TRUE | 0.023 Manual | |
| TRUE | 0.02 Manual | |
| TRUE | 0.026 Manual | FAIL |
| TRUE | 0.024 Manual | FAIL |
| TRUE | 0.022 Manual | |
| TRUE | 0.025 Manual | FAIL |
| TRUE | 0.014 Manual | FAIL |

| | | | |
|------|-------|--------|------|
| TRUE | 0.012 | Manual | FAIL |
| TRUE | 0.019 | Manual | FAIL |
| TRUE | 0.016 | Manual | FAIL |
| TRUE | 0.016 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | |
| TRUE | 0.002 | Manual | |
| TRUE | 0.002 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.032 | Manual | |
| TRUE | 0.027 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.018 | Manual | FAIL |
| TRUE | 0.02 | Manual | |

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|------|-------|--------|---------|
| TRUE | 0.01 | Manual | |
| TRUE | 0.091 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.023 | Manual | FAIL |
| TRUE | 0.01 | Manual | FAIL |
| TRUE | 0.021 | Manual | |
| TRUE | 0.022 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 6E-04 | Manual | |
| TRUE | 9E-04 | Manual | |
| TRUE | 0.011 | Manual | FAIL |
| TRUE | 0.014 | Manual | FAIL |
| TRUE | 0.019 | Manual | |
| TRUE | 0 | Manual | |
| TRUE | 0.01 | Manual | SUCCESS |
| TRUE | 0.001 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0 | Manual | |
| TRUE | 0 | Manual | |
| TRUE | 0.016 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |

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|------|-------|--------|---------|
| TRUE | 0.001 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.015 | Manual | SUCCESS |
| TRUE | 0.033 | Manual | |
| TRUE | 0.01 | Manual | FAIL |
| TRUE | 0.035 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0 | Manual | |
| TRUE | 0 | Manual | FAIL |
| TRUE | 0 | Manual | |
| TRUE | 2E-04 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.011 | Manual | FAIL |
| TRUE | 0.011 | Manual | FAIL |
| TRUE | 0.002 | Manual | |
| TRUE | 0.001 | Manual | |
| TRUE | 0.012 | Manual | FAIL |
| TRUE | 0.002 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | |
| TRUE | 0.02 | Manual | FAIL |
| TRUE | 0.002 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |

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|------|--------------|------|
| TRUE | 0.001 Manual | |
| TRUE | 0.012 Manual | |
| TRUE | 0.018 Manual | |
| TRUE | 0.002 Manual | |
| TRUE | 4E-04 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.023 Manual | FAIL |
| TRUE | 0.023 Manual | FAIL |
| TRUE | 0.012 Manual | |
| TRUE | 0.032 Manual | FAIL |
| TRUE | 0.027 Manual | |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.025 Manual | |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |

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|------|-------|--------|------|
| TRUE | 0.001 | Manual | |
| TRUE | 0.01 | Manual | |
| TRUE | 0.013 | Manual | |
| TRUE | 0.011 | Manual | |
| TRUE | 0.024 | Manual | |
| TRUE | 0.014 | Manual | |
| TRUE | 0.001 | Manual | |
| TRUE | 0.017 | Manual | FAIL |
| TRUE | 0.013 | Manual | FAIL |
| TRUE | 0.032 | Manual | |
| TRUE | 0.023 | Manual | |
| TRUE | 0.029 | Manual | |
| TRUE | 0.027 | Manual | |
| TRUE | 0.001 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.024 | Manual | |
| TRUE | 0.015 | Manual | FAIL |
| TRUE | 0.018 | Manual | FAIL |
| TRUE | 0.023 | Manual | |
| TRUE | 0.011 | Manual | |
| TRUE | 0.01 | Manual | |
| TRUE | 0.019 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |

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|------|-------|--------|------|
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.012 | Manual | FAIL |
| TRUE | 0 | Manual | |
| TRUE | 0.015 | Manual | |
| TRUE | 0.011 | Manual | FAIL |
| TRUE | 0.012 | Manual | |
| TRUE | 0 | Manual | |
| TRUE | 0 | Manual | |
| TRUE | 0 | Manual | |
| TRUE | 0 | Manual | |
| TRUE | 0.013 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | |
| TRUE | 0.001 | Manual | |
| TRUE | 0 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.015 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.009 | Manual | FAIL |
| TRUE | 0.016 | Manual | |

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| TRUE | 0.035 Manual | |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.026 Manual | |
| TRUE | 0.014 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.012 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.013 Manual | |
| TRUE | 0.011 Manual | SUCCESS |
| TRUE | 0.03 Manual | |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.011 Manual | |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.002 Manual | SUCCESS |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.023 Manual | |
| TRUE | 0.029 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.017 Manual | FAIL |
| TRUE | 0.011 Manual | SUCCESS |

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|------|--------------|---------|
| TRUE | 0.02 Manual | FAIL |
| TRUE | 0.02 Manual | |
| TRUE | 0.002 Manual | SUCCESS |
| TRUE | 0.032 Manual | |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.033 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 5E-04 Manual | |
| TRUE | 3E-04 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0 Manual | |
| TRUE | 0.02 Manual | |
| TRUE | 0.015 Manual | |
| TRUE | 0.012 Manual | |
| TRUE | 0.018 Manual | FAIL |
| TRUE | 0 Manual | |
| TRUE | 0.025 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.013 Manual | |
| TRUE | 0.002 Manual | FAIL |

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| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.019 Manual | FAIL |
| TRUE | 0.016 Manual | |
| TRUE | 0.02 Manual | FAIL |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.02 Manual | |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.009 Manual | SUCCESS |
| TRUE | 0.024 Manual | SUCCESS |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.01 Manual | |
| TRUE | 0.014 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.058 Manual | |

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| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.009 Manual | SUCCESS |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.01 Manual | |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.021 Manual | FAIL |
| TRUE | 0.016 Manual | FAIL |
| TRUE | 0.016 Manual | FAIL |
| TRUE | 0.014 Manual | |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.02 Manual | FAIL |
| TRUE | 0.014 Manual | |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.014 Manual | |
| TRUE | 0.022 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.029 Manual | FAIL |

TRUE 0.03 Manual FAIL

TRUE 0.012 Manual

TRUE 0.012 Manual FAIL

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TRUE 0.017 Manual

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TRUE 0.025 Manual FAIL

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| TRUE | 0.018 Manual | |
| TRUE | 0.018 Manual | |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.018 Manual | |
| TRUE | 0.02 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.016 Manual | FAIL |
| TRUE | 0.014 Manual | |
| TRUE | 0.013 Manual | |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.02 Manual | |
| TRUE | 0.019 Manual | FAIL |
| TRUE | 0.025 Manual | FAIL |
| TRUE | 0.014 Manual | |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0 Manual | |
| TRUE | 0 Manual | |
| TRUE | 2E-04 Manual | FAIL |
| TRUE | 7E-04 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 2E-04 Manual | |
| TRUE | 2E-04 Manual | |
| TRUE | 0 Manual | |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |

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| TRUE | 0.018 Manual | SUCCESS |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.01 Manual | |
| TRUE | 0.01 Manual | |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.012 Manual | |
| TRUE | 0.014 Manual | |
| TRUE | 0.022 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.002 Manual | |
| TRUE | 0.014 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.015 Manual | |
| TRUE | 0.021 Manual | FAIL |
| TRUE | 0.024 Manual | |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |

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|------|-------|--------|---------|
| TRUE | 0.016 | Manual | FAIL |
| TRUE | 0 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.016 | Manual | FAIL |
| TRUE | 0.024 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.01 | Manual | FAIL |
| TRUE | 0.024 | Manual | |
| TRUE | 0.032 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.014 | Manual | SUCCESS |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | |
| TRUE | 0.002 | Manual | |
| TRUE | 0.01 | Manual | FAIL |
| TRUE | 0.018 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.024 | Manual | FAIL |
| TRUE | 0.032 | Manual | FAIL |
| TRUE | 0.026 | Manual | FAIL |
| TRUE | 0.027 | Manual | FAIL |

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| TRUE | 0.027 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.017 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.014 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 5E-04 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 2E-04 Manual | FAIL |
| TRUE | 3E-04 Manual | FAIL |
| TRUE | 0.024 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.031 Manual | |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.029 Manual | |
| TRUE | 0.025 Manual | |
| TRUE | 0.02 Manual | FAIL |

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|------|--------------|---------|
| TRUE | 0.024 Manual | |
| TRUE | 0.03 Manual | |
| TRUE | 0.026 Manual | FAIL |
| TRUE | 0.012 Manual | |
| TRUE | 0.021 Manual | |
| TRUE | 0.02 Manual | |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.016 Manual | |
| TRUE | 0.021 Manual | FAIL |
| TRUE | 0.027 Manual | SUCCESS |
| TRUE | 0.014 Manual | SUCCESS |
| TRUE | 0.012 Manual | |
| TRUE | 0.021 Manual | FAIL |
| TRUE | 0.016 Manual | FAIL |
| TRUE | 0.009 Manual | |
| TRUE | 0.029 Manual | |
| TRUE | 0.021 Manual | |
| TRUE | 0.012 Manual | FAIL |

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|------|-------|--------|------|
| TRUE | 0.012 | Manual | FAIL |
| TRUE | 0.019 | Manual | |
| TRUE | 0.013 | Manual | |
| TRUE | 0.01 | Manual | FAIL |
| TRUE | 0.009 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.047 | Manual | |
| TRUE | 0.03 | Manual | |
| TRUE | 0.017 | Manual | FAIL |
| TRUE | 0.028 | Manual | |
| TRUE | 0.023 | Manual | FAIL |
| TRUE | 0.027 | Manual | |
| TRUE | 0.015 | Manual | FAIL |
| TRUE | 0.023 | Manual | |
| TRUE | 0.03 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.022 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |

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|------|--------------|------|
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.022 Manual | FAIL |
| TRUE | 0.016 Manual | |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.031 Manual | |
| TRUE | 0.009 Manual | |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.026 Manual | FAIL |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 2E-04 Manual | FAIL |
| TRUE | 5E-04 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.012 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.019 Manual | |
| TRUE | 0.029 Manual | |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.012 Manual | |
| TRUE | 0.012 Manual | |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |

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|------|--------------|------|
| TRUE | 0.014 Manual | |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.039 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.011 Manual | |
| TRUE | 0.016 Manual | |
| TRUE | 0.016 Manual | |
| TRUE | 0.002 Manual | |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.031 Manual | FAIL |
| TRUE | 0.025 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.016 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | |

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|------|-------|--------|------|
| TRUE | 0.03 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.013 | Manual | |
| TRUE | 0.023 | Manual | |
| TRUE | 0.012 | Manual | FAIL |
| TRUE | 0.012 | Manual | |
| TRUE | 0.032 | Manual | |
| TRUE | 0.013 | Manual | FAIL |
| TRUE | 0.01 | Manual | |
| TRUE | 0.012 | Manual | |
| TRUE | 0.011 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.01 | Manual | |
| TRUE | 0.01 | Manual | FAIL |
| TRUE | 0.02 | Manual | |
| TRUE | 0.012 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.026 | Manual | |
| TRUE | 0.036 | Manual | FAIL |

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|------|-------|--------|---------|
| TRUE | 0.015 | Manual | FAIL |
| TRUE | 0.009 | Manual | |
| TRUE | 0.031 | Manual | |
| TRUE | 0.027 | Manual | |
| TRUE | 0.01 | Manual | |
| TRUE | 0.023 | Manual | |
| TRUE | 0.018 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | |
| TRUE | 7E-04 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.001 | Manual | |
| TRUE | 0.013 | Manual | |
| TRUE | 0.018 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.024 | Manual | FAIL |
| TRUE | 0.013 | Manual | FAIL |
| TRUE | 0.002 | Manual | |
| TRUE | 0.014 | Manual | SUCCESS |
| TRUE | 0.022 | Manual | |

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|------|--------------|------|
| TRUE | 0.018 Manual | FAIL |
| TRUE | 0.02 Manual | FAIL |
| TRUE | 0.011 Manual | |
| TRUE | 0.002 Manual | |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.009 Manual | |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.028 Manual | |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.017 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.002 Manual | |
| TRUE | 0.009 Manual | |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.015 Manual | |
| TRUE | 0.02 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.014 Manual | |

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| TRUE | 0.013 Manual | |
| TRUE | 0.033 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.03 Manual | |
| TRUE | 0.023 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.03 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.018 Manual | FAIL |
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| TRUE | 0.01 Manual | FAIL |
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| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
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| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
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| TRUE | 0.02 | Manual | FAIL |
| TRUE | 0.012 | Manual | FAIL |
| TRUE | 0.021 | Manual | |
| TRUE | 0.001 | Manual | FAIL |
| TRUE | 0.01 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.002 | Manual | |
| TRUE | 0.001 | Manual | |
| TRUE | 0.002 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.019 | Manual | FAIL |
| TRUE | 0.02 | Manual | FAIL |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.01 | Manual | FAIL |
| TRUE | 0.017 | Manual | FAIL |
| TRUE | 0.009 | Manual | FAIL |
| TRUE | 0.013 | Manual | SUCCESS |
| TRUE | 0.013 | Manual | FAIL |
| TRUE | 0.002 | Manual | |
| TRUE | 0.002 | Manual | FAIL |
| TRUE | 0.019 | Manual | FAIL |
| TRUE | 2E-04 | Manual | |
| TRUE | 4E-04 | Manual | FAIL |
| TRUE | 0.021 | Manual | |
| TRUE | 0.019 | Manual | |
| TRUE | 0.021 | Manual | FAIL |
| TRUE | 0.015 | Manual | FAIL |
| TRUE | 0.021 | Manual | FAIL |

TRUE 0.031 Manual SUCCESS

TRUE 0.031 Manual FAIL

TRUE 0.021 Manual

TRUE 0.023 Manual FAIL

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| TRUE | 0.009 Manual | |
| TRUE | 0.02 Manual | |
| TRUE | 0.023 Manual | |
| TRUE | 0.016 Manual | SUCCESS |
| TRUE | 0.017 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.011 Manual | |
| TRUE | 0.01 Manual | |
| TRUE | 0.017 Manual | FAIL |
| TRUE | 0.012 Manual | |
| TRUE | 0.024 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.016 Manual | SUCCESS |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.014 Manual | |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | |

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| TRUE | 0.009 Manual | |
| TRUE | 0.017 Manual | |
| TRUE | 0.023 Manual | |
| TRUE | 0.028 Manual | |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.009 Manual | |
| TRUE | 0.03 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.037 Manual | |
| TRUE | 0.02 Manual | |
| TRUE | 0.019 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.012 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.002 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.002 Manual | |
| TRUE | 0.014 Manual | |
| TRUE | 0.022 Manual | |
| TRUE | 0.015 Manual | |
| TRUE | 0.031 Manual | |
| TRUE | 0.002 Manual | |
| TRUE | 0.02 Manual | FAIL |

TRUE 0.024 Manual FAIL

TRUE 0.001 Manual

TRUE 0.002 Manual

TRUE 0.019 Manual FAIL

TRUE 0.031 Manual

TRUE 0.031 Manual

TRUE 5E-04 Manual FAIL

TRUE 2E-04 Manual

TRUE 3E-04 Manual

TRUE 0.024 Manual

TRUE 0.001 Manual

TRUE 0.001 Manual

| | | |
|------|--------------|---------|
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.018 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.015 Manual | FAIL |
| TRUE | 0.016 Manual | FAIL |
| TRUE | 0.02 Manual | |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.009 Manual | |
| TRUE | 0.014 Manual | |
| TRUE | 0.022 Manual | FAIL |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.022 Manual | SUCCESS |
| TRUE | 0.017 Manual | FAIL |
| TRUE | 0.02 Manual | FAIL |
| TRUE | 0.015 Manual | |
| TRUE | 0.027 Manual | |
| TRUE | 0.002 Manual | |
| TRUE | 0.002 Manual | |

| | | |
|------|--------------|---------|
| TRUE | 0.013 Manual | SUCCESS |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.03 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.001 Manual | |
| TRUE | 0.011 Manual | |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.013 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 7E-04 Manual | FAIL |
| TRUE | 0.036 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 9E-04 Manual | FAIL |
| TRUE | 6E-04 Manual | FAIL |
| TRUE | 0.028 Manual | FAIL |
| TRUE | 0.028 Manual | |
| TRUE | 0.01 Manual | |
| TRUE | 0.016 Manual | |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |

| | | |
|------|--------------|---------|
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.017 Manual | |
| TRUE | 0.02 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.012 Manual | FAIL |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.018 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.001 Manual | FAIL |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.002 Manual | |
| TRUE | 0.045 Manual | SUCCESS |
| TRUE | 0.002 Manual | FAIL |
| TRUE | 0.001 Manual | |
| TRUE | 0.031 Manual | FAIL |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.022 Manual | FAIL |
| TRUE | 0.018 Manual | FAIL |
| TRUE | 0.021 Manual | FAIL |
| TRUE | 0.035 Manual | FAIL |
| TRUE | 0.025 Manual | FAIL |
| TRUE | 0.026 Manual | FAIL |

| | | |
|-------|--------------|------|
| TRUE | 0.009 Manual | FAIL |
| TRUE | 0.014 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.016 Manual | FAIL |
| TRUE | 0.029 Manual | FAIL |
| TRUE | 0.019 Manual | FAIL |
| TRUE | 0.018 Manual | |
| TRUE | 0.016 Manual | FAIL |
| TRUE | 0.011 Manual | FAIL |
| TRUE | 0.01 Manual | FAIL |
| TRUE | 0.021 Manual | FAIL |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | FAIL |
| FALSE | 0 n/a | FAIL |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | FAIL |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | FAIL |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | FAIL |

| | | |
|-------|-------|------|
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | FAIL |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
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| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |

| | | |
|-------|-------|------|
| FALSE | 0 n/a | FAIL |
|-------|-------|------|

| | |
|-------|-------|
| FALSE | 0 n/a |
| FALSE | 0 n/a |
| FALSE | 0 n/a |
| FALSE | 0 n/a |
| FALSE | 0 n/a |
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| FALSE | 0 n/a |
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| FALSE | 0 n/a |
| FALSE | 0 n/a |
| FALSE | 0 n/a |
| FALSE | 0 n/a |

| | | |
|-------|-------|---------|
| FALSE | 0 n/a | SUCCESS |
| FALSE | 0 n/a | |
| FALSE | 0 n/a | |

| | |
|-------|-------|
| FALSE | 0 n/a |
| FALSE | 0 n/a |

FALSE 0 n/a FAIL

FALSE 0 n/a FAIL

FALSE 0 n/a FAIL

FALSE 0 n/a FAIL

FALSE 0 n/a

FALSE 0 n/a

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FALSE 0 n/a

FALSE 0 n/a

FALSE 0 n/a

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FALSE 0 n/a

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FALSE 0 n/a

FALSE 0 n/a

FALSE 0 n/a

FALSE 0 n/a FAIL

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FALSE 0 n/a

FALSE 0 n/a

FALSE 0 n/a

EXH

Submitted-results pending.

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Two person mixed DNA profile

2 person mixed profile - conditioned on

Single evidence sample excluded

Excluded from mixed DNA profile

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Single source 20 loci DNA profile LR > 100 billion

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Single source DNA profile

NCIDD upload single source DNA profile

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted as cells

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

No DNA detected

This sample has undergone further processing

Complex mixed profile unsuitable for interp or comparison

Submitted as cells

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells
QPS advised no further work required - results available
Submitted as cells
QPS advised no further work required - results available
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Quality flag identified, on hold awaiting advice from QPS
Quality control failure, refer to QPS
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Single evidence sample excluded
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
QPS advised no further work required - results available
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells
Single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Hair located. Submitted-results pending
Complex mixed profile unsuitable for interp or comparison
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
2 person mix - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - low support for contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVM - Complex mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
Excluded from mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Presump. PSA test positive, no sperm found
Two person mixed DNA profile
2 person mixed profile - conditioned on
2 person mix rem - support for contribution > 100 billion
Micro positive for sperm. Submitted-Results pending
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted for cells. Presumptive saliva test pending.
Presump Saliva test negative
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Submitted-results pending.

Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Micro positive for sperm. Submitted-Results pending
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Semen not detected
Submitted as cells
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Presump. PSA test positive, no sperm found
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Two person mixed DNA profile
Excluded from mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells
Single source DNA profile
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Excluded from mixed DNA profile
2 person mix - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Two person mixed DNA profile
2 person mixed profile - conditioned on
2 person rem- support for contrib 1 million to 1 billion
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix - low support for contribution
3 person mixed DNA - inconclusive
Submitted-results pending.
Quality flag identified, on hold awaiting advice from QPS
Quality control failure, refer to QPS
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
NCIDD upload single source DNA profile
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Single source DNA profile
Single source 20 loci DNA profile LR > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Semen not detected
Submitted as cells
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Presump. PSA test positive, no sperm found
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
2 person mix - support for contrib 100 000 to 1 million
2 person mix - supports non contribution
Single evidence sample excluded

Presump. PSA test positive, no sperm found
Complex mixed profile unsuitable for interp or comparison

Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
Excluded from mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Two person mixed DNA profile
Excluded from mixed DNA profile
2 person mix profile - support for contrib > 100 billion

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells, Presump saliva test pending
Presump Saliva test negative
Three person mixed DNA profile
3 person mixed profile - conditioned on
No statistical interpretation performed
3 person mix remaining - low support for contrib
Single evidence sample excluded
presump Saliva test positive
Complex mixed profile unsuitable for interp or comparison
Three person mixed DNA profile
3 person mixed profile - conditioned on
No statistical interpretation performed
3 person mix remaining - supports non contribution
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Quality flag identified, on hold awaiting advice from QPS
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Single source 20 loci DNA profile LR > 100 billion
Complex mixed profile unsuitable for interp or comparison

Submitted as cells, Presump saliva test pending
presump Saliva test positive
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 Person Mix Rem contrib unsuitable for NCIDD
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
Possible sub-threshold information

Submitted-results pending.
Single source DNA profile
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
SS DNA profile 9 loci and above LR > 100 billion
NCIDD upload single source DNA profile
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Single Source DNA profile - assumed known contributor

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Micro positive for sperm. Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison

Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Micro positive for sperm. Submitted-Results pending
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
2 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells, Presump saliva test pending
presump Saliva test positive
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Presump saliva positive. Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison
Two person mixed DNA profile
Single evidence sample excluded
Single evidence sample excluded
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
3 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Single evidence sample excluded
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
3 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Single evidence sample excluded
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
NCIDD upload single source DNA profile
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Semen not detected
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
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Complex mixed profile unsuitable for interp or comparison
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Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
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Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Submitted-results pending.
Micro positive for sperm. Submitted-Results pending
Three person mixed DNA profile
Possible sub-threshold information
3 person mixed profile - conditioned on
3 person mix remaining - supports non contribution

Two person mixed DNA profile
2 person mixed profile - conditioned on
Single evidence sample excluded
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Micro positive for sperm. Submitted-Results pending
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Two person mixed DNA profile
No statistical interpretation performed
Submitted for cells. Presumptive saliva test pending.
presump Saliva test positive
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison

Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Mixture-low support for contrib or supports non contrib
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
Mixture-low support for contrib or supports non contrib
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
Mixture-low support for contrib or supports non contrib
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison

Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Micro positive for sperm. Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Micro neg for sperm
Single Source DNA profile - assumed known contributor
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
SS DNA profile 9 loci and above LR > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
Single evidence sample excluded
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix rem - support for contribution > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Micro neg for sperm
Single Source DNA profile - assumed known contributor

Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Excluded from mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Micro positive for sperm. Submitted-Results pending
Single source DNA profile
NCIDD upload single source DNA profile
Single source 20 loci DNA profile LR > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
SS DNA profile 9 loci and above LR > 100 billion
NCIDD upload single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
Single evidence sample excluded
2 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Micro neg for sperm
Single Source DNA profile - assumed known contributor
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted as cells, Presump saliva test pending
presump Saliva test positive
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Quality flag identified, on hold awaiting advice from QPS
Quality control failure, refer to QPS
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted as cells, Presump saliva test pending
presump Saliva test positive
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Micro neg for sperm
Single Source DNA profile - assumed known contributor

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
NCIDD upload single source DNA profile
Possible sub-threshold information
Submitted-results pending.
SS DNA profile 9 loci and above LR > 100 billion
NCIDD upload single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted for cells. Presumptive saliva test pending.
Presump Saliva test negative
Complex mixed profile unsuitable for interp or comparison
Submitted for cells. Presumptive saliva test pending.
Presump Saliva test negative
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Interim result- mixed profile obtained. Rework Reqd
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Micro positive for sperm. Submitted-Results pending
No DNA profile - possible sub-threshold peaks
Micro positive for sperm. Submitted-Results pending
SS DNA profile 9 loci and above LR > 100 billion
Submitted-results pending.
Micro positive for sperm. Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Micro positive for sperm. Submitted-Results pending
No DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells, Presump saliva test pending
Presump Saliva test negative
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes

Single source 20 loci DNA profile LR > 100 billion
NCIDD upload single source DNA profile
Possible sub-threshold information
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA detected
Single Source DNA profile - assumed known contributor

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Interim result - sample undergoing rework
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Presumptive blood test pos. Submitted-results pending.
Single Source DNA profile - assumed known contributor

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Micro positive for sperm. Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

presump Saliva test positive

Partial DNA profile unsuitable for comparison purposes
Presumptive blood test pos. Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Micro positive for sperm. Submitted-Results pending
Single Source DNA profile - assumed known contributor

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Presumptive blood test pos. Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Submitted as cells
Single source DNA profile
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Hair located. Submitted-results pending
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
SS DNA profile 9 loci and above LR > 100 billion

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Micro positive for sperm. Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
SS DNA profile 9 loci and above LR > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison

Presumptive blood test pos. Submitted-results pending.
Presump. PSA test positive, no sperm found
Complex mixed profile unsuitable for interp or comparison
Single Source DNA profile - assumed known contributor
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Micro neg for sperm
Single Source DNA profile - assumed known contributor

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Hair located. Submitted-results pending
Single source 20 loci DNA profile LR > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Sample processed and final results under
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
Possible sub-threshold information
Submitted-results pending.
Two person mixed DNA profile
2 person mix - support for contrib 1 million - 1 billion

Submitted-results pending.
Single source DNA profile
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Presumptive blood test pos. Submitted-results pending.
Micro positive for sperm. Submitted-Results pending
Single Source DNA profile - assumed known contributor
Possible sub-threshold information
Submitted-results pending.
Micro positive for sperm. Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Micro positive for sperm. Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Micro neg for sperm

Single source DNA profile- unsuitable for NCIDD searching
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Submitted-results pending.
Submitted-results pending.
Submitted-results pending.

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Quality flag identified, on hold awaiting advice from QPS
Quality control failure, refer to QPS
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Interim result- mixed profile obtained. Rework Reqd
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA detected
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison
Presump. PSA test positive, no sperm found
Single source DNA profile < NCIDD matching stringency
Single Source DNA profile - assumed known contributor
Submitted-results pending.
No DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix - supports non contribution
Submitted-results pending.
No DNA detected
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
Possible sub-threshold information
NCIDD upload single source DNA profile
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVM- Complex mixture unsuitable for interp or comparison
ENVM - Partial profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
Mixture-low support for contrib or supports non contrib
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Single evidence sample excluded
Submitted-results pending.
Three person mixed DNA profile
3 person mix - support for contrib 10 000 - 100 000
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
No DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Two person mixed DNA profile
2 person mixed profile - conditioned on
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Excluded from mixed DNA profile
Single evidence sample excluded

Submitted-results pending.
Three person mixed DNA profile
3 person mix - supports non contribution
3 person mix - support for contrib 10 000 - 100 000
3 person mix - supports non contribution
Sample undergone further work - conditioned
3 person mixed profile - conditioned on
2 person mix rem - support for contrib 10 000 to 100 000
2 person mix remaining - supports non contribution
2 person mix remaining - supports non contribution
3 person mix rem - support for contrib 10 000 to 100 000
3 person mix remaining - supports non contribution
3 person mix remaining - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
No DNA detected
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - low support for contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
Single evidence sample excluded
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Single evidence sample excluded

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted for cells. Presumptive saliva test pending.
presump Saliva test positive
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Single evidence sample excluded
Semen not detected
Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Semen not detected
Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Semen not detected
Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Submitted-results pending.
Quality flag identified, on hold awaiting advice from QPS
Quality control failure, refer to QPS
Submitted-results pending.
Single source DNA profile
SS DNA profile 9 loci and above LR > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVM - Partial profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - low support for contribution

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVM - Partial profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix rem - support for contribution > 100 billion
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile

Submitted as cells, Presump saliva test pending
presump Saliva test positive
Two person mixed DNA profile
2 person mixed profile - conditioned on
2 person mix rem - support for contribution > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix - support for contrib 10 000 - 100 000
Mixture-low support for contrib or supports non contrib
Submitted for cells. Presumptive saliva test pending.
Presump Saliva test negative
Two person mixed DNA profile
Single evidence sample excluded
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVM- Complex mixture unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVM - Partial profile unsuitable for comparison purposes
Micro positive for sperm. Submitted-Results pending
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining - supports non contribution
Two person mixed DNA profile
2 person mixed profile - conditioned on
Single evidence sample excluded
Possible sub-threshold information
ENVM- Complex mixture unsuitable for interp or comparison
Submitted as cells
Single source DNA profile
NCIDD upload single source DNA profile
Single Source DNA profile - assumed known contributor
DNA profile removed from NCIDD
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
3 person mix profile - support for contrib > 100 billion
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
ENVM- Complex mixture unsuitable for interp or comparison
ENVM - Partial profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVM - No DNA profile

Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Semen not detected
Submitted as cells
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix rem - support for contribution > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Single source DNA profile
NCIDD Intel upload - single source partial profile
NCIDD upload single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Suspect check - low support or non contrib
Suspect check - supports non contribution
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Suspect check - low support or non contrib
Suspect check - supports non contribution
Submitted-results pending.
Two person mixed DNA profile
Mixture-low support for contrib or supports non contrib
2 person mix profile - support for contrib > 100 billion
Excluded from mixed DNA profile
Suspect check - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
Mixture-low support for contrib or supports non contrib
3 person mix - support for contrib 1 million - 1 billion
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile

Submitted-results pending.
Single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Presump. PSA test positive, no sperm found
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
Submitted-results pending.
Two person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Micro positive for sperm. Submitted-Results pending
No DNA detected
This sample has undergone further processing
Partial DNA profile unsuitable for comparison purposes
ENVN- Complex mixture unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
2 person mix profile - support for contrib > 100 billion
Excluded from mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
Cond mix rem-low supp for contrib or supp non contrib

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - support for contrib 100 000 to 1 million
Mixture-low support for contrib or supports non contrib
Excluded from mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells, Presump saliva test pending
presump Saliva test positive
Two person mixed DNA profile
2 person mixed profile - conditioned on
2 person mix rem - support for contribution > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Presump. PSA test positive, no sperm found
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Possible sub-threshold information
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
2 person mix remaining - supports non contribution
Submitted as cells
Two person mixed DNA profile
2 person mix - supports non contribution
Sample undergone further work - conditioned
Two person mixed DNA profile
2 person mixed profile - conditioned on
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
2 person mixed profile - conditioned on
Mix remaining DNA contrib unsuitable for NCIDD searching

Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Micro positive for sperm. Submitted-Results pending
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining - supports non contribution
Presumptive blood test pos. Submitted-results pending.
Two person mixed DNA profile
2 person mixed profile - conditioned on
2 person mix rem - support for contribution > 100 billion
Submitted-results pending.
Two person mixed DNA profile
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Interim result - sample undergoing rework
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Interim result - sample undergoing rework
Quality flag identified, on hold awaiting advice from QPS
Quality control failure, refer to QPS
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Micro positive for sperm. Submitted-Results pending
QPS advised no further work required - results available
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
Possible sub-threshold information
Submitted-results pending.
No DNA detected
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
No DNA detected
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison
Hair located. Submitted-results pending
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Three person mixed DNA profile
No statistical interpretation performed
Sample undergone further work - conditioned
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Single evidence sample excluded
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
No DNA profile
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVM- Complex mixture unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Single evidence sample excluded
Submitted-results pending.
Two person mixed DNA profile
Submitted as cells
Single Source DNA profile - assumed known contributor
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells
Single Source DNA profile - assumed known contributor
NCIDD upload single source DNA profile
Possible sub-threshold information
Three person mixed DNA profile
3 person mixed profile - conditioned on
Single evidence sample excluded
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single Source DNA profile - assumed known contributor
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
DNA profile removed from NCIDD
Submitted-results pending.
Single source DNA profile
Single source 20 loci DNA profile LR > 100 billion
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells, Presump saliva test pending
Presump Saliva test negative
Single Source DNA profile - assumed known contributor
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix rem - support for contribution > 100 billion
Submitted as cells, Presump saliva test pending
presump Saliva test positive
Submitted-results pending.
Single source DNA profile
Possible sub-threshold information
NCIDD upload single source DNA profile

Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Possible sub-threshold information
Single source 20 loci DNA profile LR > 100 billion
Complex mixed profile unsuitable for interp or comparison
DNA profile removed from NCIDD
ENVM- Complex mixture unsuitable for interp or comparison
ENVM - Partial profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

ENVM - Partial profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Possible sub-threshold information
Complex mixed profile unsuitable for interp or comparison
DNA profile removed from NCIDD
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells, Presump saliva test pending
presump Saliva test positive
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining - supports non contribution
Submitted-results pending.
No DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Semen not detected
Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVN- Complex mixture unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person rem- support for contrib 1 billion-100 billion
Submitted-results pending.
Three person mixed DNA profile
Excluded from mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - support for contribution 100 to 1000

Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix profile - support for contrib > 100 billion
3 person mix rem - support for contribution > 100 billion
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion

Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
NCIDD upload single source DNA profile
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Single evidence sample excluded
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
Possible sub-threshold information
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Three person mixed DNA profile

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Presump. PSA test positive, no sperm found
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Micro positive for sperm. Submitted-Results pending
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Micro positive for sperm. Submitted-Results pending
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - support for contrib 1 million - 1 billion
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix rem - support for contribution > 100 billion
3 person mix remaining - supports non contribution
Submitted-results pending.
Two person mixed DNA profile
2 person mixed profile - conditioned on
Possible sub-threshold information
Micro positive for sperm. Submitted-Results pending
Single source 20 loci DNA profile LR > 100 billion
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile
Submitted-results pending.
No DNA profile
Submitted-results pending.
No DNA profile
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - support for contrib 1 million - 1 billion
Excluded from mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
2 person mix- support for contrib 1 billion - 100 billion
2 person mix profile - support for contrib > 100 billion

Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Excluded from mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
Excluded from mixed DNA profile
Submitted-results pending.
Two person mixed DNA profile
2 person mixed profile - conditioned on
Mix remaining DNA contrib unsuitable for NCIDD searching
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVN -Partial DNA profile
ENVN -Partial DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining - supports non contribution

Micro positive for sperm. Submitted-Results pending
SS DNA profile 9 loci and above LR > 100 billion
NCIDD upload single source DNA profile
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.
No DNA profile
Possible sub-threshold information
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
2 person mix - support for contrib 1 million - 1 billion
2 person mix profile - support for contrib > 100 billion
Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
ENVM -Partial DNA profile
ENVM - Partial profile unsuitable for comparison purposes
ENVM - No DNA profile
ENVM - Partial profile unsuitable for comparison purposes
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Labelling discrepancy
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Submitted for cells. Presumptive saliva test pending.
presump Saliva test positive
Two person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Quality flag identified, on hold awaiting advice from QPS
Quality control failure, refer to QPS
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Semen not detected
Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Semen not detected
Submitted as cells
Three person mixed DNA profile
3 person mixed profile - conditioned on
Cond mix rem-low supp for contrib or supp non contrib
Sample on hold - awaiting advice
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
2 person mixed profile - conditioned on
Mix remaining DNA contrib unsuitable for NCIDD searching
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Complex mixed profile unsuitable for interp or comparison

Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
No DNA profile
SS DNA profile 9 loci and above LR > 100 billion
Possible sub-threshold information

Three person mixed DNA profile
3 person mixed profile - conditioned on
Cond mix rem-low supp for contrib or supp non contrib
Two person mixed DNA profile
2 person mixed profile - conditioned on
Excluded from mixed DNA profile
Mix Rem DNA contrib < NCIDD matching Stringency
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix- support for contrib 1 billion - 100 billion
Excluded from mixed DNA profile
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - support for contribution 1000 to 10 000
3 person mix - support for contribution 100 to 1000
3 person mix - low support for contribution

Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Intel report required for further interpretation
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - support for contrib 1 million - 1 billion
Mixture-low support for contrib or supports non contrib

Presump. PSA test positive, no sperm found
Two person mixed DNA profile
2 person mixed profile - conditioned on
2 person rem - support for contrib 1 billion -100 billion
Two person mixed DNA profile
2 person mixed profile - conditioned on
2 person mix rem - support for contribution > 100 billion
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Semen not detected
Submitted as cells
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA detected

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
No DNA detected
This sample has undergone further processing
No DNA profile
Submitted-results pending.
No DNA detected
This sample has undergone further processing
No DNA profile
Possible sub-threshold information
Submitted-results pending.
No DNA detected
This sample has undergone further processing
No DNA profile
Possible sub-threshold information
Submitted-results pending.
No DNA detected
This sample has undergone further processing
No DNA profile
Submitted-results pending.
Single Source DNA profile - assumed known contributor
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
No DNA profile - possible sub-threshold peaks

Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix - supports non contribution

Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
NCIDD upload single source DNA profile
Submitted as cells
Two person mixed DNA profile
2 person mixed profile - conditioned on
2 person mix rem - support for contribution > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Hair located. Submitted-results pending
Single source DNA profile
NCIDD upload single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix - low support for contribution
Submitted-results pending.
SS DNA profile 9 loci and above LR > 100 billion
NCIDD upload single source DNA profile
DNA profile removed from NCIDD
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Single evidence sample excluded
3 person mix - support for contribution 100 to 1000
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 Person Mix Rem contrib unsuitable for NCIDD
3 person mix remaining - low support for contrib
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVM -Partial DNA profile
ENVM -Partial DNA profile
ENVM -Partial DNA profile

Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
3 person mix profile - support for contrib > 100 billion
Excluded from mixed DNA profile
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
3 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Submitted for cells. Presumptive saliva test pending.
Presump Saliva test negative
Complex mixed profile unsuitable for interp or comparison

Submitted for cells. Presumptive saliva test pending.
Presump Saliva test negative
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Single evidence sample excluded
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Three person mixed DNA profile
Excluded from mixed DNA profile
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
3 person mix profile - support for contrib > 100 billion
Excluded from mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Possible sub-threshold information
Single source 20 loci DNA profile LR > 100 billion
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
SS DNA profile 9 loci and above LR > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Presump. PSA test positive, no sperm found
Two person mixed DNA profile
2 person mixed profile - conditioned on
2 person rem- support for contrib 1 million to 1 billion
Submitted for cells. Presumptive saliva test pending.
Presump Saliva test negative
Complex mixed profile unsuitable for interp or comparison
Submitted for cells. Presumptive saliva test pending.
Presump Saliva test negative
Complex mixed profile unsuitable for interp or comparison
Submitted for cells. Presumptive saliva test pending.
presump Saliva test positive
Complex mixed profile unsuitable for interp or comparison
Submitted for cells. Presumptive saliva test pending.
presump Saliva test positive
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - support for contribution 1000 to 10 000
3 person mix - supports non contribution

Semen not detected
Submitted as cells
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
Possible sub-threshold information
NCIDD upload single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
Single evidence sample excluded
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
Single evidence sample excluded
3 Person Mix Rem contrib unsuitable for NCIDD
Submitted-results pending.
Two person mixed DNA profile
Suspect check inconclusive - mixed DNA profile
Suspect check - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Two person mixed DNA profile
2 person mixed profile - conditioned on
2 person mix rem - support for contribution > 100 billion
Possible sub-threshold information

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells, Presump saliva test pending
Presump Saliva test negative
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Micro positive for sperm. Submitted-Results pending
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix profile - support for contrib > 100 billion
3 person mix - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion

Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Micro positive for sperm. Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison
This sample has undergone further processing
Two person mixed DNA profile
2 person mixed profile - conditioned on
2 person mix rem - support for contribution > 100 billion
Possible sub-threshold information
Two person mixed DNA profile
2 person mixed profile - conditioned on
2 person mix rem - support for contribution > 100 billion
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
Possible sub-threshold information
Submitted-results pending.
SS DNA profile 9 loci and above LR > 100 billion
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Micro positive for sperm. Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Suspect Check Actioned - No Match
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVM - No DNA profile

ENVM - Partial profile unsuitable for comparison purposes
ENVM - No DNA profile
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Hair located. Submitted-results pending
Single Source DNA profile - assumed known contributor
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Single source DNA profile
Possible sub-threshold information
Single Source DNA profile - assumed known contributor
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
Possible sub-threshold information

Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA detected
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Cond mix rem-low supp for contrib or supp non contrib
3 person mixed profile - conditioned on
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining- support for contrib 1000 to 10000
3 person mix remaining - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Possible sub-threshold information
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Micro neg for sperm
Two person mixed DNA profile
2 person mixed profile - conditioned on
Mix remaining DNA contrib unsuitable for NCIDD searching

Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Excluded from mixed DNA profile
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted as cells, Presump saliva test pending
Presump Saliva test negative
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVM - Partial profile unsuitable for comparison purposes
ENVM - Partial profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Hair located. Submitted-results pending
Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted as cells
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - support for contrib 1 million - 1 billion
Micro positive for sperm. Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - support for contribution 100 to 1000
3 person mix - supports non contribution
Submitted as cells
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Three person mixed DNA profile
3 person mix - support for contrib 10 000 - 100 000
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Single Source DNA profile - assumed known contributor
Micro positive for sperm. Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix rem - support for contribution > 100 billion
Submitted-results pending.
Two person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Possible sub-threshold information
Submitted-results pending.
Single source DNA profile
Possible sub-threshold information
NCIDD upload single source DNA profile
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
2 person mix - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Micro positive for sperm. Submitted-Results pending
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - supports non contribution

Submitted-results pending.
Two person mixed DNA profile
2 person mix - support for contrib 1 million - 1 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
Possible sub-threshold information
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted for cells. Presumptive saliva test pending.
Presump Saliva test negative
Partial DNA profile unsuitable for comparison purposes
Submitted for cells. Presumptive saliva test pending.
Presump Saliva test negative
Complex mixed profile unsuitable for interp or comparison
Submitted as cells, Presump saliva test pending
Presump Saliva test negative
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
Single evidence sample excluded
2 person mix profile - support for contrib > 100 billion
This sample has undergone further processing
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix rem - support for contribution > 100 billion
Submitted-results pending.
Single source DNA profile
Possible sub-threshold information
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source 20 loci DNA profile LR > 100 billion
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Three person mixed DNA profile
3 person mixed profile - conditioned on
Single evidence sample excluded
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
Single source 20 loci DNA profile LR > 100 billion
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison

Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.

Micro neg for sperm

Single Source DNA profile - assumed known contributor
Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.

No DNA profile

Possible sub-threshold information

Submitted-results pending.

Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

No DNA profile - possible sub-threshold peaks

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Three person mixed DNA profile

3 person mix - support for contribution 1000 to 10 000

Submitted-results pending.

Single source DNA profile

Possible sub-threshold information

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

ENVM - Partial profile unsuitable for comparison purposes

ENVM - Partial profile unsuitable for comparison purposes

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Submitted-results pending.

No DNA profile - possible sub-threshold peaks

Two person mixed DNA profile

2 person mixed profile - conditioned on

Excluded from mixed DNA profile

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Micro positive for sperm. Submitted-Results pending
Three person mixed DNA profile
Single evidence sample excluded
3 person mix - supports non contribution
Submitted-results pending.
Three person mixed DNA profile
3 person mix- support for contrib 1 billion - 100 billion
3 person mix profile - support for contrib > 100 billion
Excluded from mixed DNA profile
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - low support for contribution
Excluded from mixed DNA profile
Hair located. Submitted-results pending
Interim result - sample undergoing rework
Two person mixed DNA profile
2 person mix - supports non contribution
2 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Single Source DNA profile - assumed known contributor
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Semen not detected
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Micro positive for sperm. Submitted-Results pending
Single source 20 loci DNA profile LR > 100 billion
Possible sub-threshold information
Three person mixed DNA profile
3 person mixed profile - conditioned on
Remaining contribution - inconclusive
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining- support for contrib 1000 to 10000
Single evidence sample excluded
3 person mix remaining - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
Submitted-results pending.
Two person mixed DNA profile
2 person mix - supports non contribution
Hair located. Submitted-results pending
Complex mixed profile unsuitable for interp or comparison
No DNA profile - possible sub-threshold peaks
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - support for contrib 100 000 to 1 million
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix rem - support for contribution > 100 billion
Submitted-results pending.

Submitted-results pending.
Single Source DNA profile - assumed known contributor
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Presump saliva positive. Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison

ENVN -Partial DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
Three person mixed DNA profile
Mixture-low support for contrib or supports non contrib
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Micro neg for sperm
Semen not detected
Single source DNA profile
Single source DNA profile < 9 loci LR 1000 - 10 000
Submitted-results pending.
Two person mixed DNA profile
Single source DNA profile
NCIDD upload single source DNA profile
Possible sub-threshold information

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Single evidence sample excluded
Micro positive for sperm. Submitted-Results pending
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Hair located. Submitted-results pending
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining - low support for contrib
Submitted as cells, Presump saliva test pending
Presump Saliva test negative
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
ENVM- Complex mixture unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
No DNA detected
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Three person mixed DNA profile
3 person mix - support for contribution 1000 to 10 000
Single evidence sample excluded
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Interim result- mixed profile obtained. Rework Reqd
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Excluded from mixed DNA profile
3 person mix profile - support for contrib > 100 billion

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Excluded from mixed DNA profile
Submitted-results pending.
Micro neg for sperm
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
No DNA profile - possible sub-threshold peaks

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
This sample has undergone further processing
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Possible sub-threshold information
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
ENVM - No DNA profile
ENVM - Partial profile unsuitable for comparison purposes
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Single evidence sample excluded
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Single Source DNA profile - assumed known contributor
Possible sub-threshold information
NCIDD upload single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
2 person mix - supports non contribution
Three person mixed DNA profile
3 person mixed profile - conditioned on
Single evidence sample excluded
presump Saliva test positive
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining - support for contrib 100 to 1000
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Single evidence sample excluded
3 person mix profile - support for contrib > 100 billion
Micro positive for sperm. Submitted-Results pending
Two person mixed DNA profile
NCIDD upload - mixed DNA profile
Excluded from mixed DNA profile

Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib

Micro positive for sperm. Submitted-Results pending
Three person mixed DNA profile
Mixture-low support for contrib or supports non contrib
3 person mix - support for contrib 1 million - 1 billion
3 person mix - support for contribution 100 to 1000
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Three person mixed DNA profile
3 person mix - supports non contribution
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Possible sub-threshold information

Micro positive for sperm. Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Micro positive for sperm. Submitted-Results pending
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining - low support for contrib
3 person mix remaining - supports non contribution

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Micro positive for sperm. Submitted-Results pending
Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.
Semen not detected
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
No DNA profile - possible sub-threshold peaks

Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - low support for contribution
3 person mix - supports non contribution

Submitted-results pending.
Two person mixed DNA profile
2 person mix - supports non contribution

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile

Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Micro positive for sperm. Submitted-Results pending
Single source 20 loci DNA profile LR > 100 billion
Possible sub-threshold information
Presumptive blood test pos. Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion

Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
No DNA profile
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
2 person mix - low support for contribution
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
2 person mix - low support for contribution
Submitted-results pending.
Submitted-results pending.

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
No DNA profile - possible sub-threshold peaks

Suspect Check Actioned - No Match
Suspect Check Actioned - No Match
Suspect Check Actioned - No Match
Suspect Check Actioned - No Match
Suspect check - low support for contribution
Micro positive for sperm. Submitted-Results pending
Interim result- mixed profile obtained. Rework Reqd
Two person mixed DNA profile
2 person mixed profile - conditioned on
Excluded from mixed DNA profile
Mix remaining DNA contrib unsuitable for NCIDD searching
Suspect Check Actioned - No Match
Suspect Check Actioned - No Match
Suspect Check Actioned - No Match
Suspect Check Actioned - No Match
Suspect check - supports non contribution
Suspect check - supports non contribution
Suspect check - supports non contribution
Suspect check - supports non contribution
Suspect check - supports non contribution
Suspect check - supports non contribution
Three person mixed DNA profile
3 person mixed profile - conditioned on
Suspect check- support for contribution 10 000 to 100 000
Mixture-low support for contrib or supports non contrib
Suspect check - supports non contribution
Suspect check - supports non contribution

Submitted-results pending.
Presump. PSA test positive, no sperm found
Partial DNA profile unsuitable for comparison purposes

Interim result- mixed profile obtained. Rework Reqd
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining - supports non contribution
3 person mix remaining - supports non contribution
Single evidence sample excluded
Suspect check - support for contrib 100 000 - 1 million
Suspect check - supports non contribution
Suspect check - supports non contribution
Suspect Check Actioned - No Match
Suspect Check Actioned - No Match
Suspect Check Actioned - No Match
Suspect check - supports non contribution
Suspect check - supports non contribution
Suspect Check Actioned - No Match
Micro positive for sperm. Submitted-Results pending
Submitted-results pending.
No DNA profile - possible sub-threshold peaks

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
Submitted for cells. Presumptive saliva test pending.
Presump Saliva test negative
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
Mixture-low support for contrib or supports non contrib
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Single source DNA profile
Possible sub-threshold information
NCIDD upload single source DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
Mixture-low support for contrib or supports non contrib
Suspect check - low support or non contrib
Suspect check - low support or non contrib
Suspect check - low support or non contrib
Submitted-results pending.
Micro neg for sperm
Micro positive for sperm. Submitted-Results pending

Submitted-results pending.
Single Source DNA profile - assumed known contributor
NCIDD upload single source DNA profile
Possible sub-threshold information
Submitted-results pending.
Interim result- mixed profile obtained. Rework Reqd
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
Submitted-results pending.
Submitted-results pending.
Sample processed and final results under
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes

Submitted-results pending.
No DNA profile - possible sub-threshold peaks
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Complex mixed profile unsuitable for interp or comparison
Presumptive blood test pos. Submitted-results pending.
Micro neg for sperm
Single Source DNA profile - assumed known contributor
ENVM- Complex mixture unsuitable for interp or comparison

Submitted-results pending.
Micro neg for sperm
Complex mixed profile unsuitable for interp or comparison
ENVM - Partial profile unsuitable for comparison purposes
ENVM - Partial profile unsuitable for comparison purposes
Submitted for cells. Presumptive saliva test pending.
presump Saliva test positive
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mix - support for contrib 1 million - 1 billion
Excluded from mixed DNA profile
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Single source DNA profile
NCIDD upload single source DNA profile
Presump saliva positive. Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
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Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
Mixture-low support for contrib or supports non contrib
Single evidence sample excluded
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Micro neg for sperm
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Presump saliva positive. Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix - low support for contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted as cells
Submitted-results pending.
QPS advised no further work required - results available

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

ENVM - Partial profile unsuitable for comparison purposes

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Three person mixed DNA profile
3 person mix - supports non contribution
Sample undergone further work - conditioned
3 person mixed profile - conditioned on
3 person mix remaining - supports non contribution
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining - supports non contribution
Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
Submitted-results pending.
Three person mixed DNA profile
3 person mixed profile - conditioned on
3 person mix remaining - supports non contribution

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
DNA insufficient for further processing
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Interim result - sample undergoing rework
Single source DNA profile
NCIDD upload single source DNA profile
Possible sub-threshold information

Submitted-results pending.
Three person mixed DNA profile
3 person mix profile - support for contrib > 100 billion
3 person mix- support for contrib 1 billion - 100 billion
3 person mix - supports non contribution
3 person mix - supports non contribution
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Interim result - sample undergoing rework
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Interim result- Partial profile undergoing rework
Single source DNA profile
SS DNA profile 9 loci and above LR > 100 billion

Submitted as cells
Single source DNA profile
NCIDD Intel upload - single source partial profile
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison
DNA profile removed from NCIDD

Hair located. Submitted-results pending
No DNA detected
This sample has undergone further processing
No DNA profile

Submitted as cells
No DNA detected
This sample has undergone further processing
No DNA profile - possible sub-threshold peaks

Submitted-results pending.
Three person mixed DNA profile
No statistical interpretation performed
3 person mix profile - support for contrib > 100 billion
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
No DNA profile - possible sub-threshold peaks

Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison
Submitted-results pending.
Partial DNA profile unsuitable for comparison purposes
This sample has undergone further processing
Complex mixed profile unsuitable for interp or comparison

Submitted-results pending.
9 loci DNA profile- NCIDD- possible sub-threshold peaks
9 loci DNA profile- NCIDD- possible sub-threshold peaks
This sample has undergone further processing
Two person mixed DNA profile
2 person mix profile - support for contrib > 100 billion
DNA profile removed from NCIDD
Submitted-results pending.
Complex mixed profile unsuitable for interp or comparison

Partial DNA profile

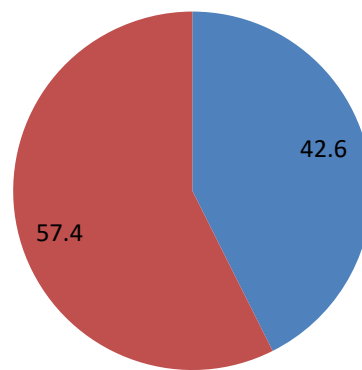
MANUAL MICROCON CHARTS

n=752 samples = all samples

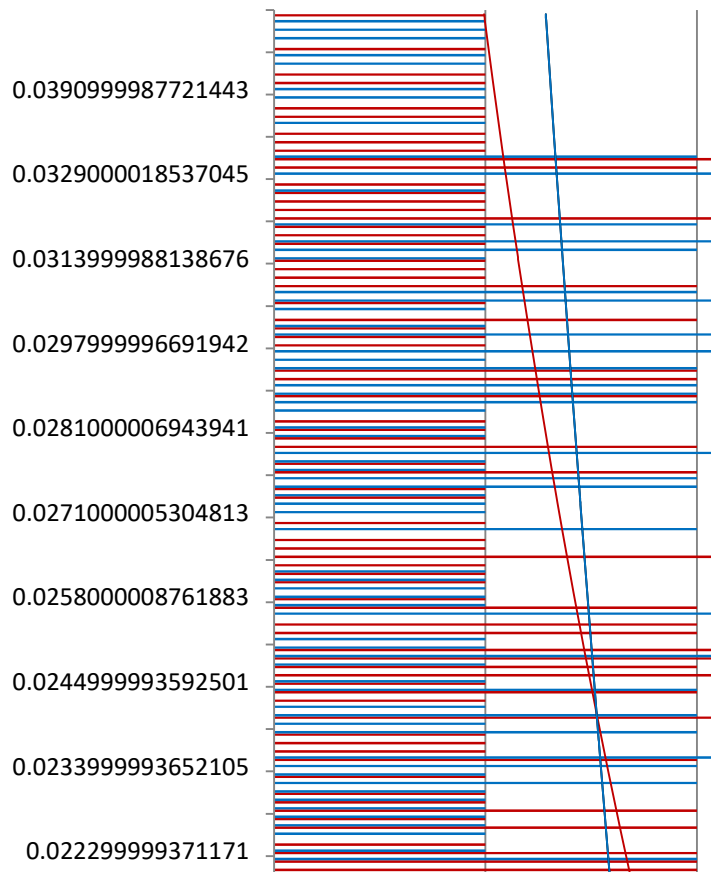
SUCCESS
FAIL

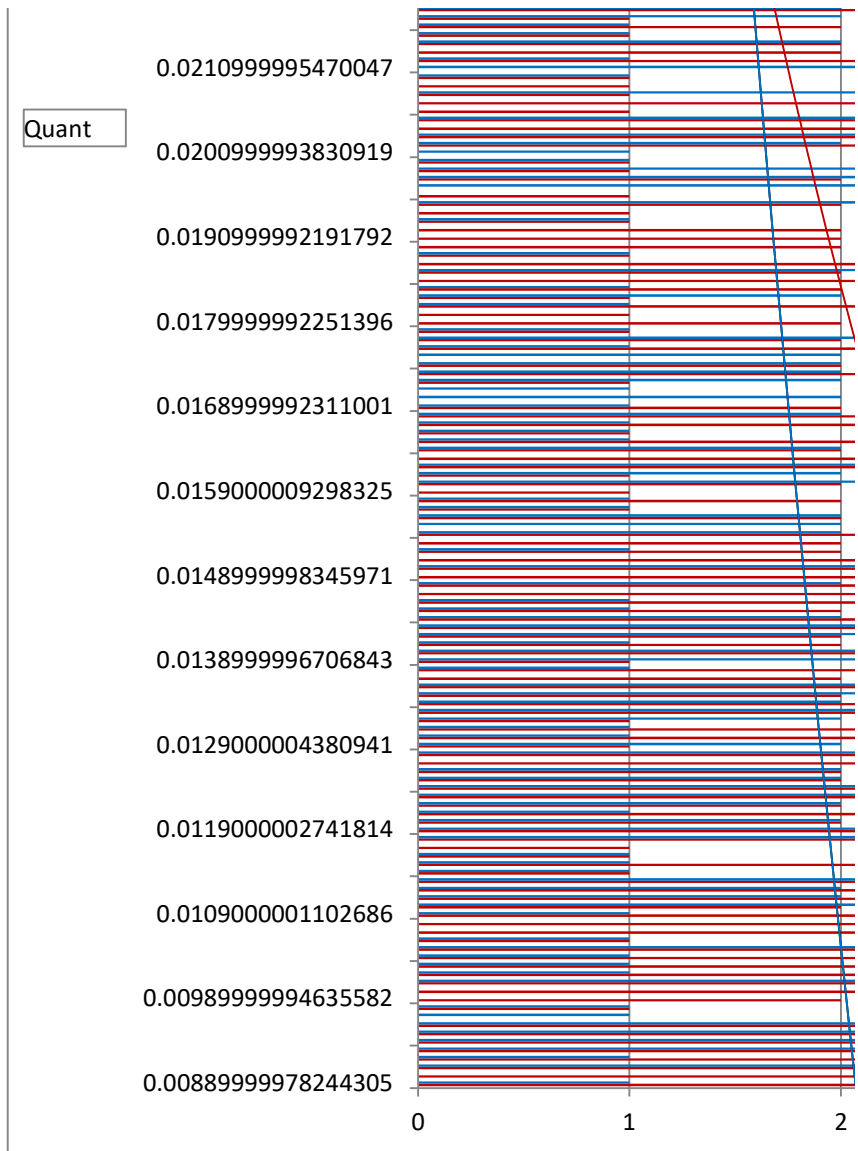
%Success/Fail
42.6
57.4

% Success/Fail of 'Manual' Microcor



Count of Success or Fail





AUTO-MICROCON CHARTS

Difference ('fold') between pre and post MCONC Quants when SUCCESS
 - removed 2 data points as outliers:
 34 fold, 22 fold

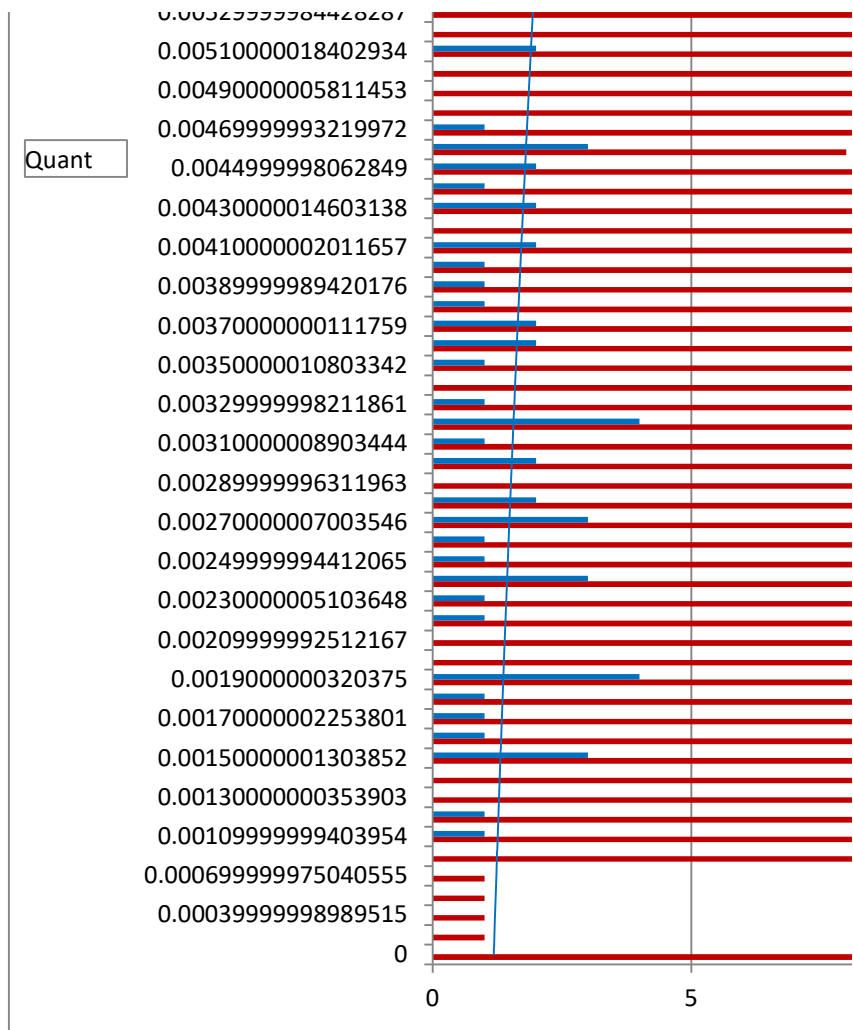


| | | % Success |
|---------|------|-----------|
| SUCCESS | 154 | 10.60% |
| FAIL | 1295 | 89.40% |

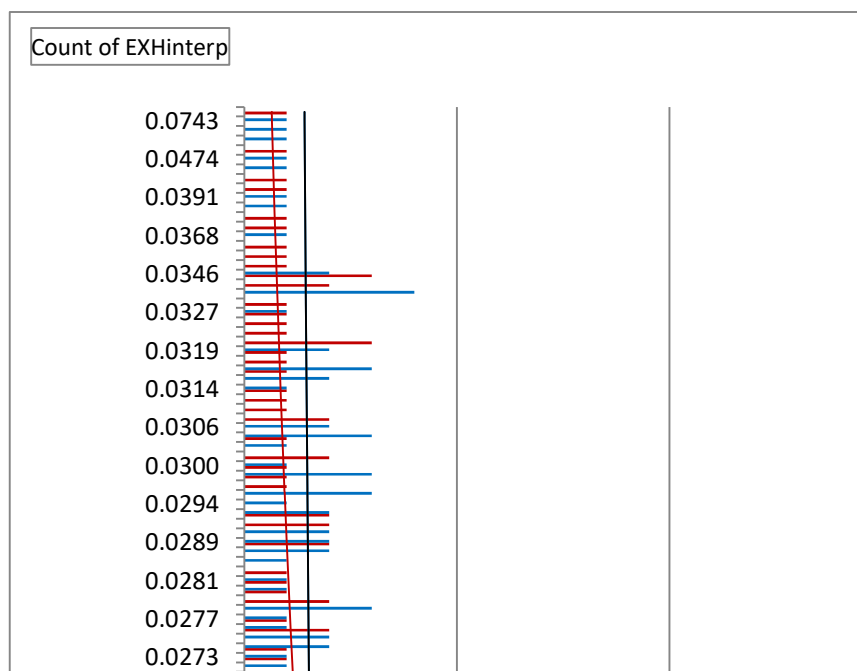


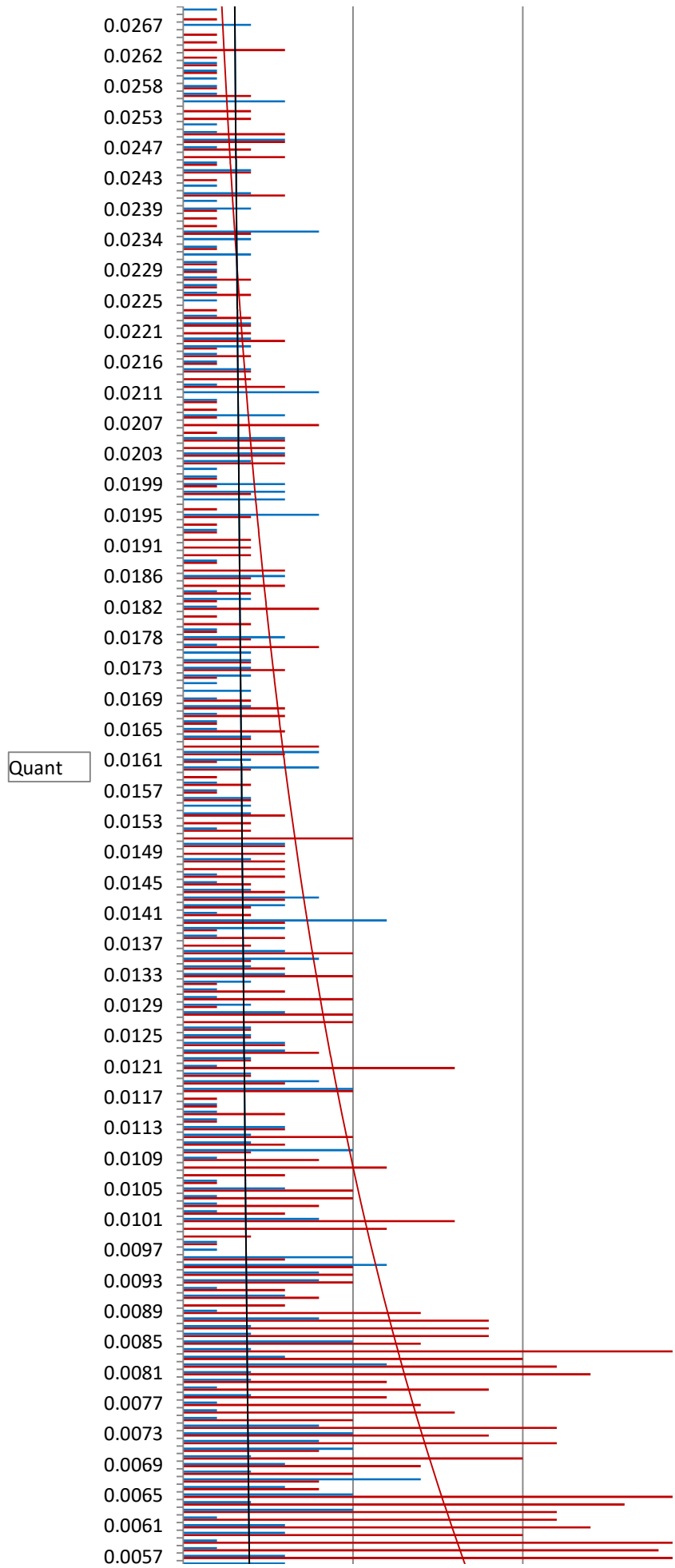
Original Quant vs No. samples and Success/Fail

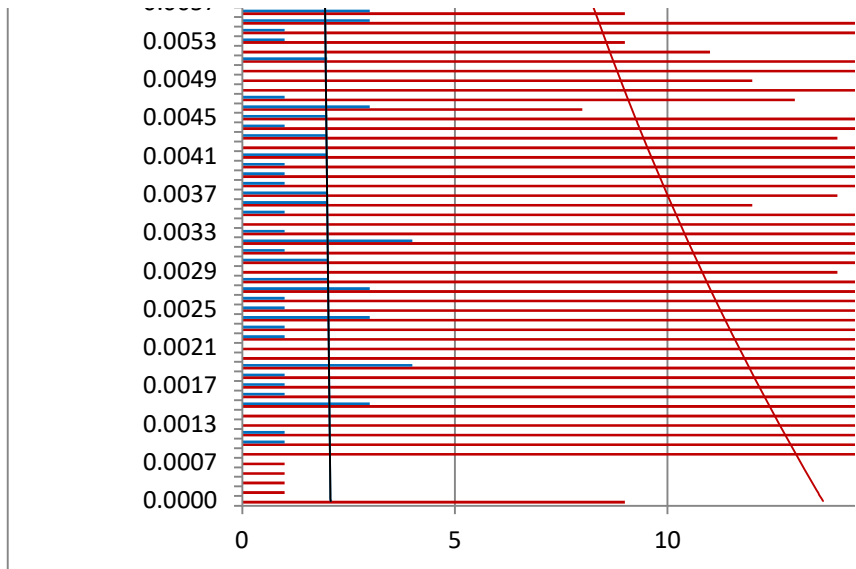




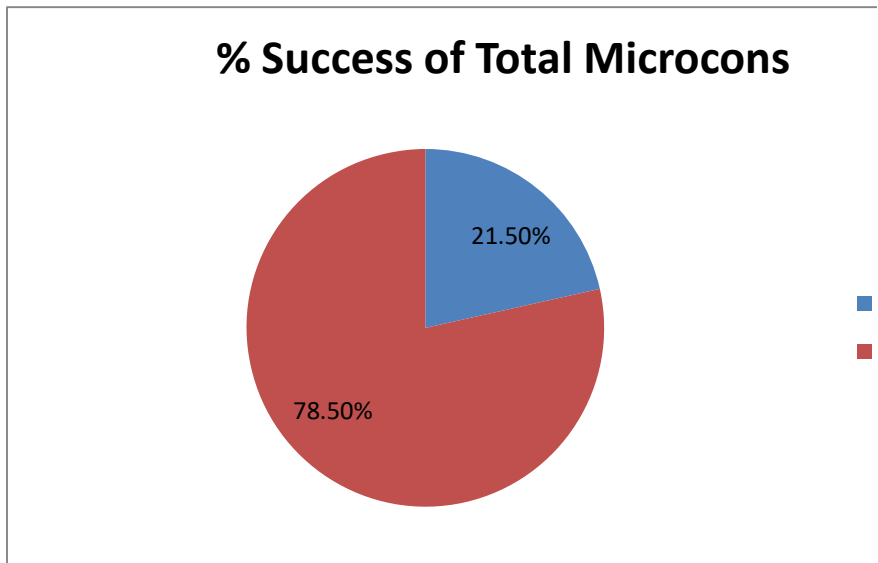
COMBINED / TOTAL DATA







| | | % Success |
|---------|------|-----------|
| SUCCESS | 474 | 21.50% |
| FAIL | 1727 | 78.50% |



n=226 = 0.02ng/uL < SAMPLES > 0.033ng/uL

% Success/Fail

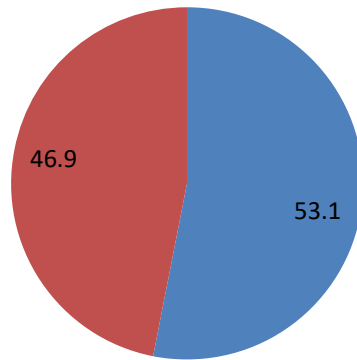
SUCCESS 53.1

FAIL 46.9

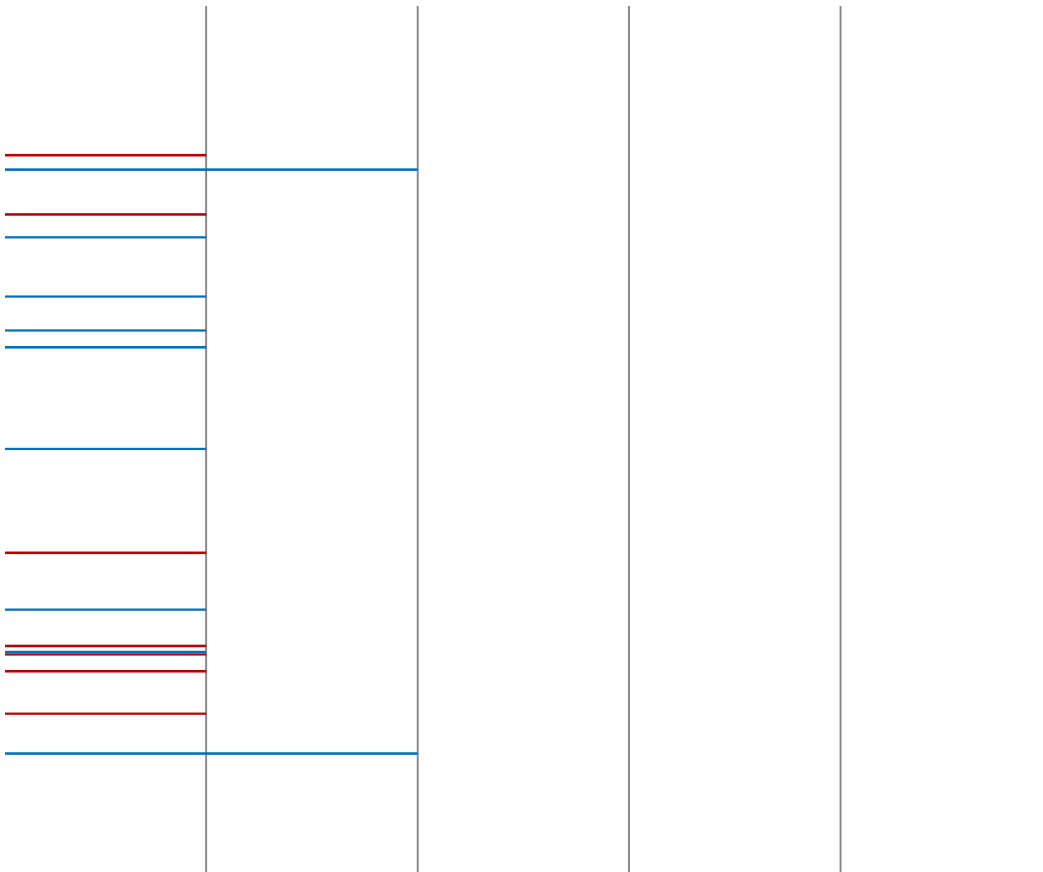
1S

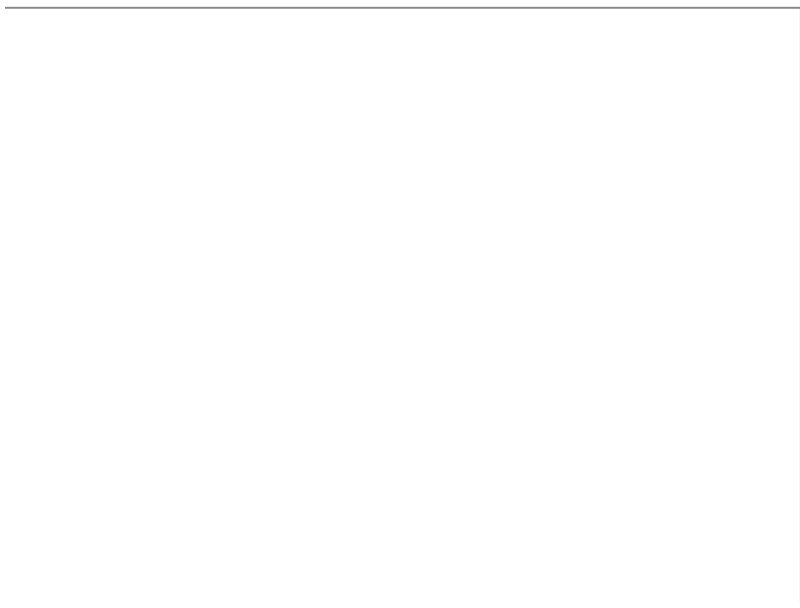
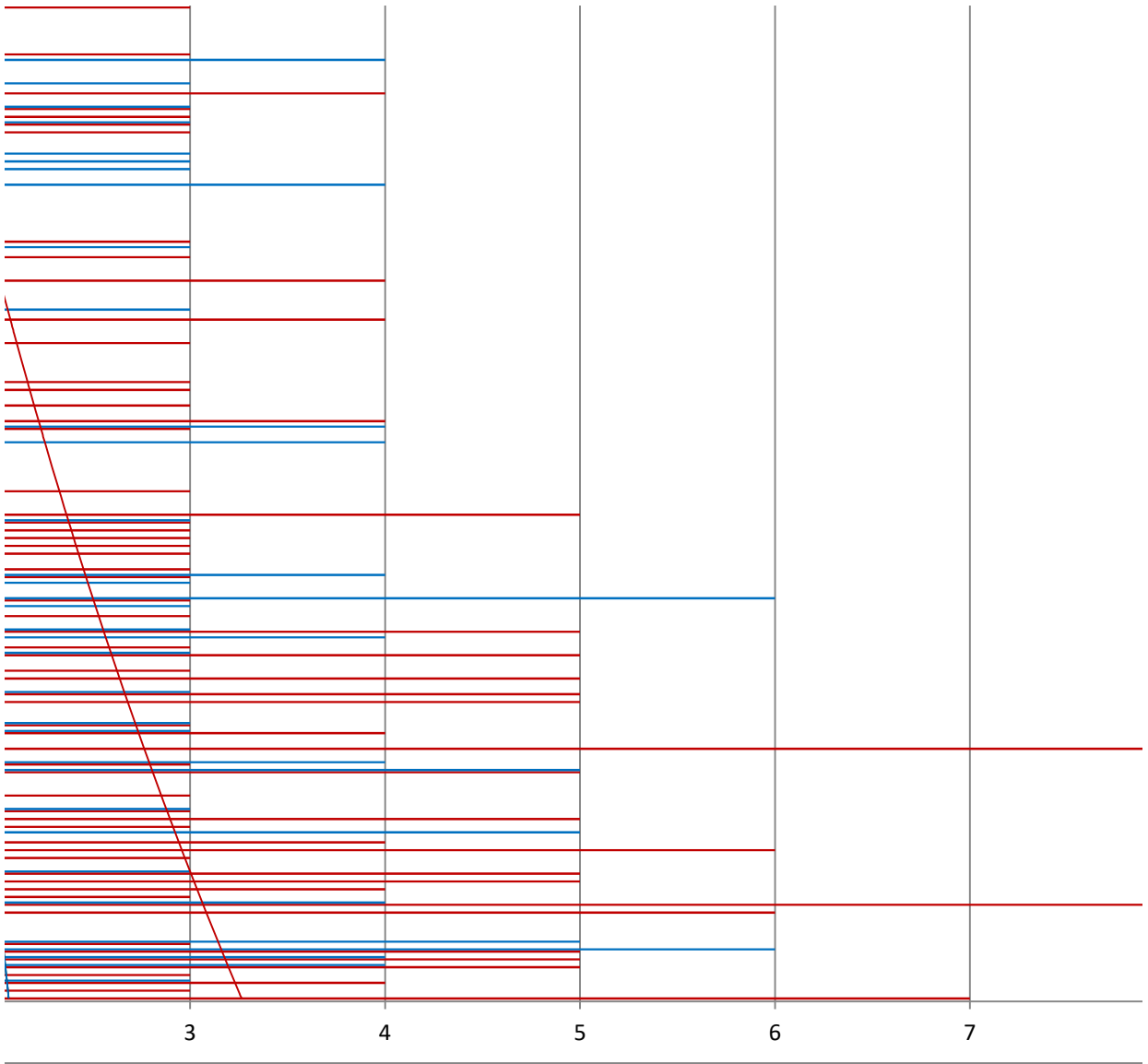
■ SUCCESS
■ FAIL

% Success/Fail of Manual Microcons where samples are in the range
0.02ng/uL to 0.033ng/uL

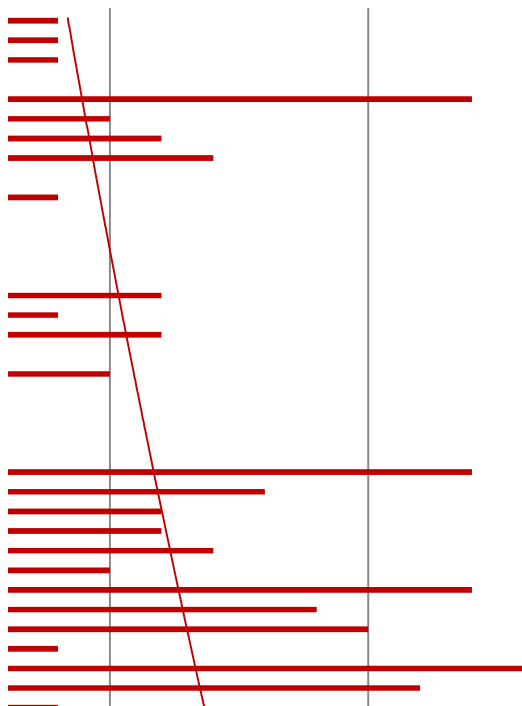
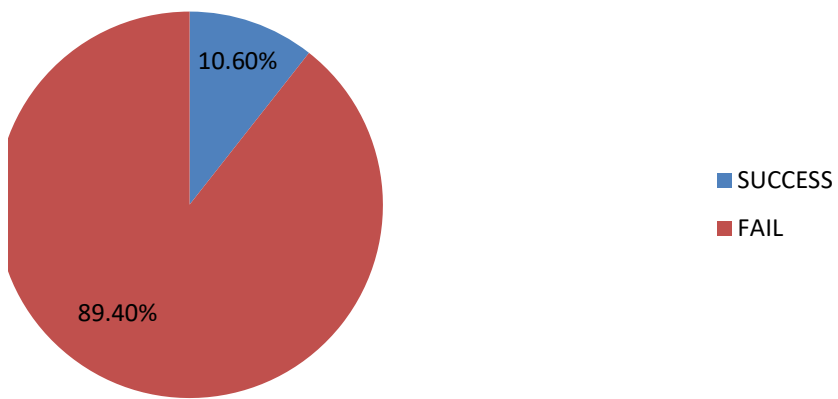


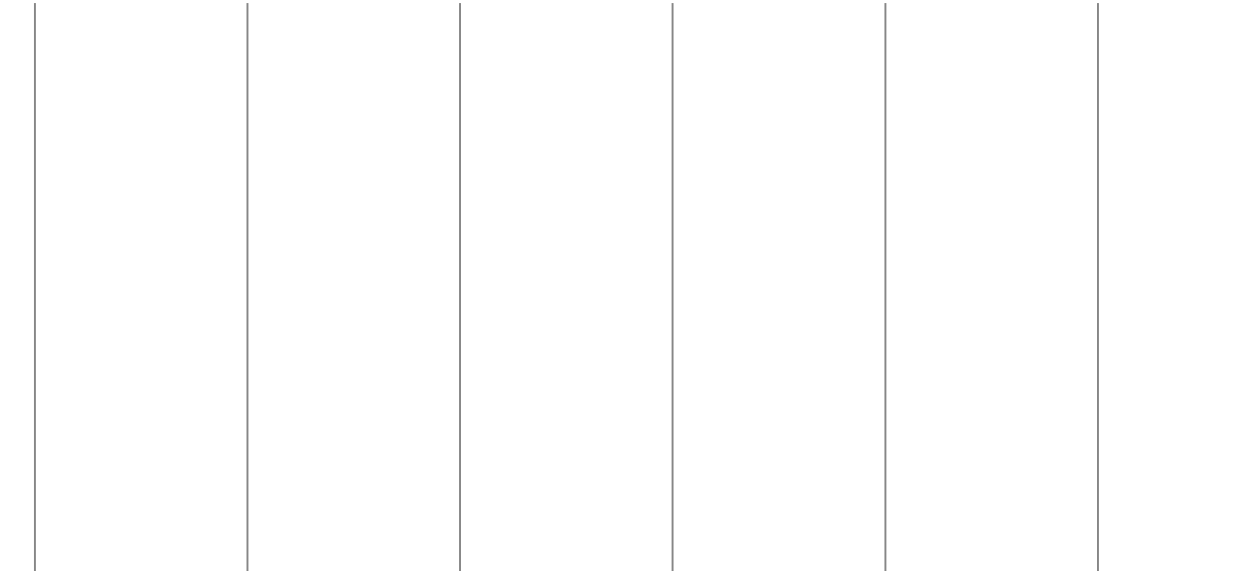
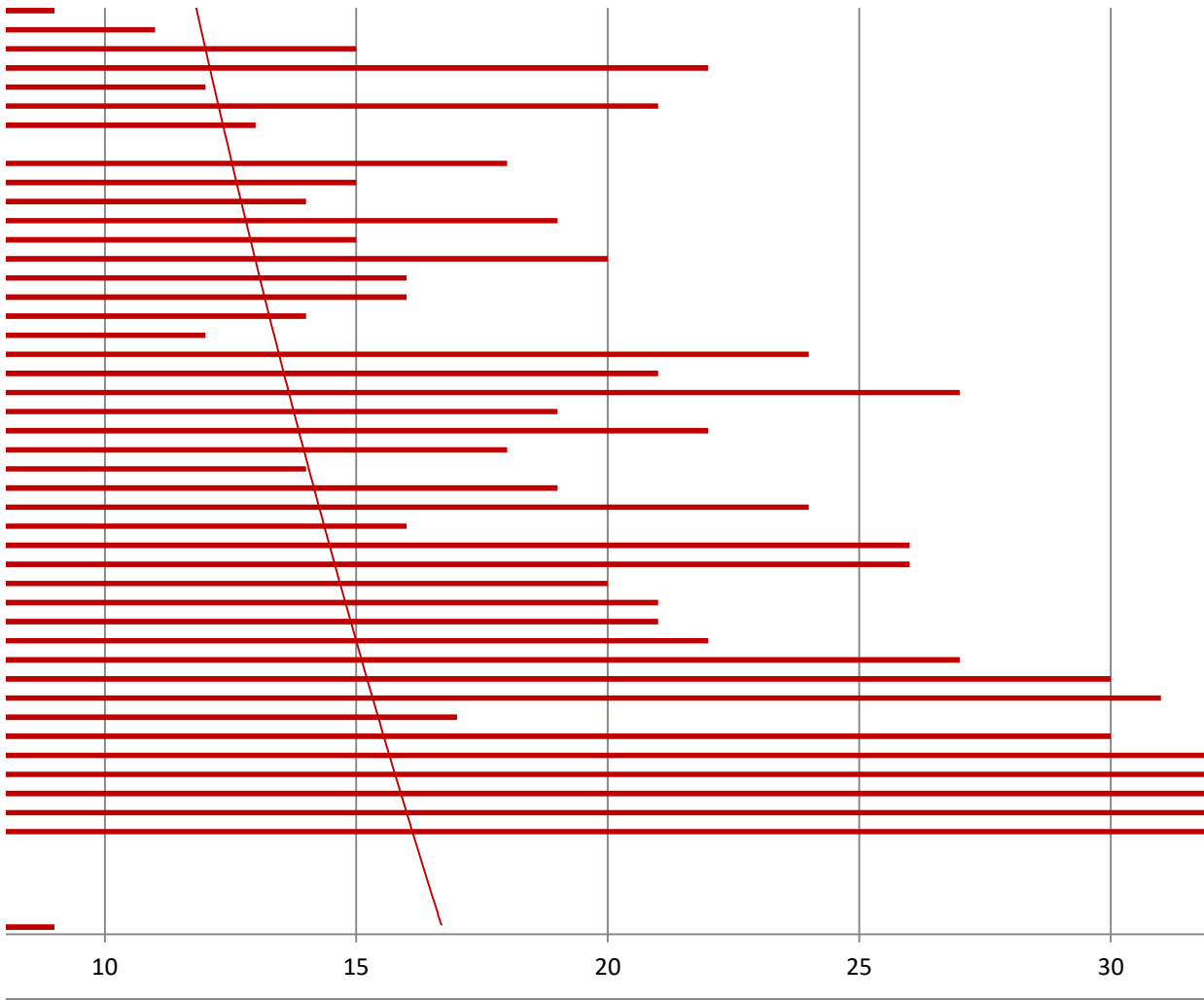
■ SUC
■ FAIL

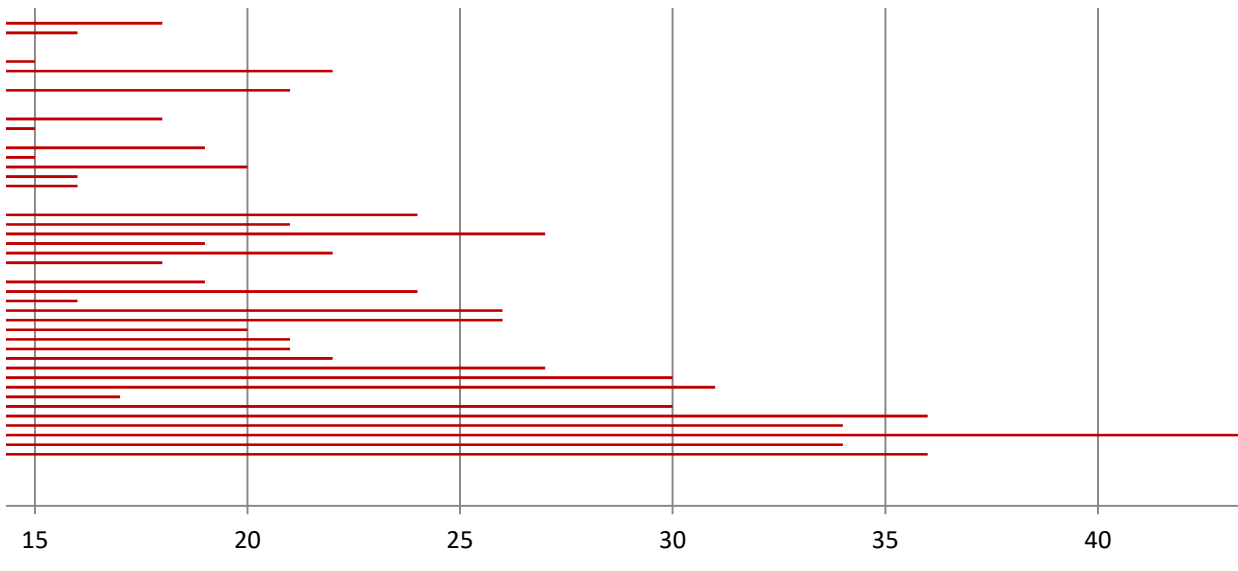




Success' of 'Auto-Microcon' Process









SUCCESS
FAIL

EXHinterp

 SUCCESS

 FAIL

 Expon. (FAIL)

 Expon. (SUCCESS)

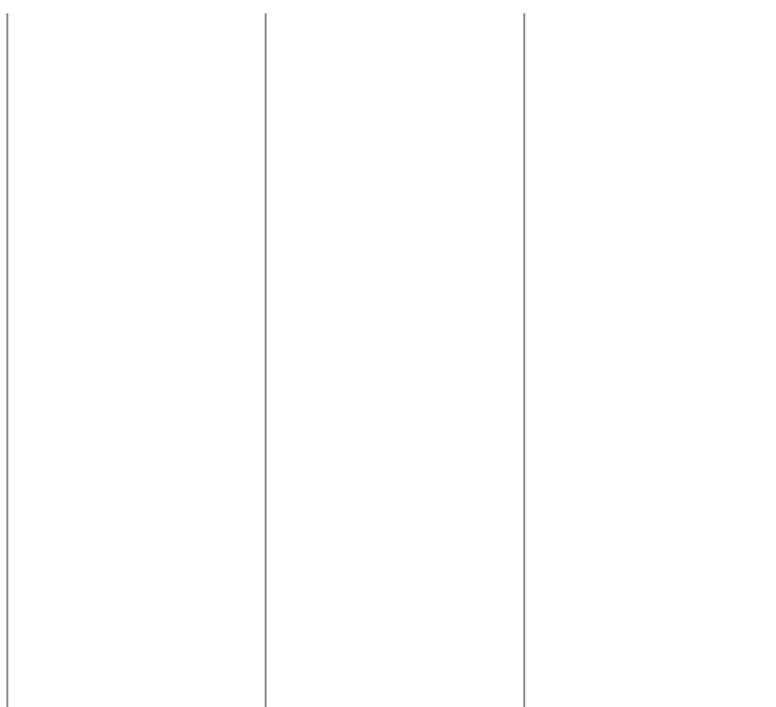
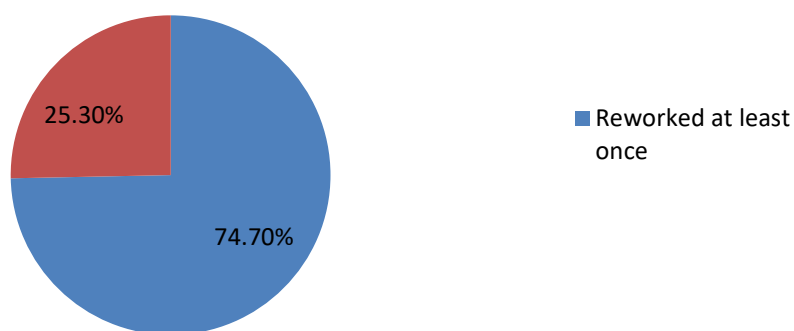
8

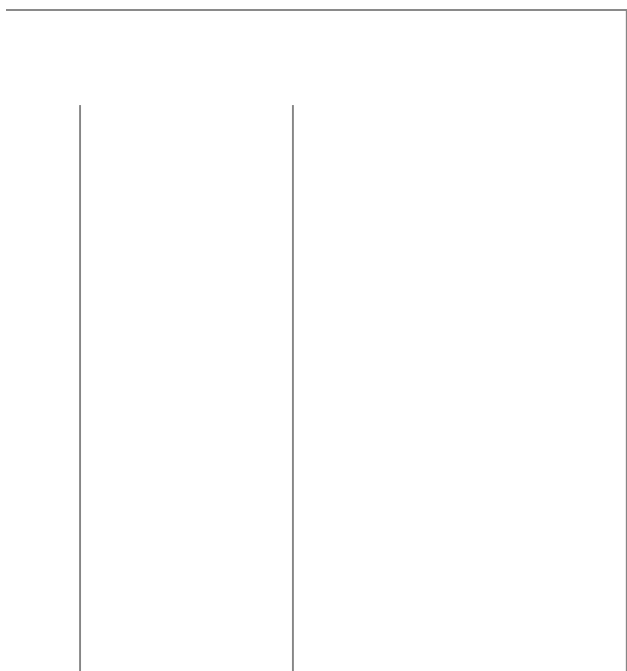
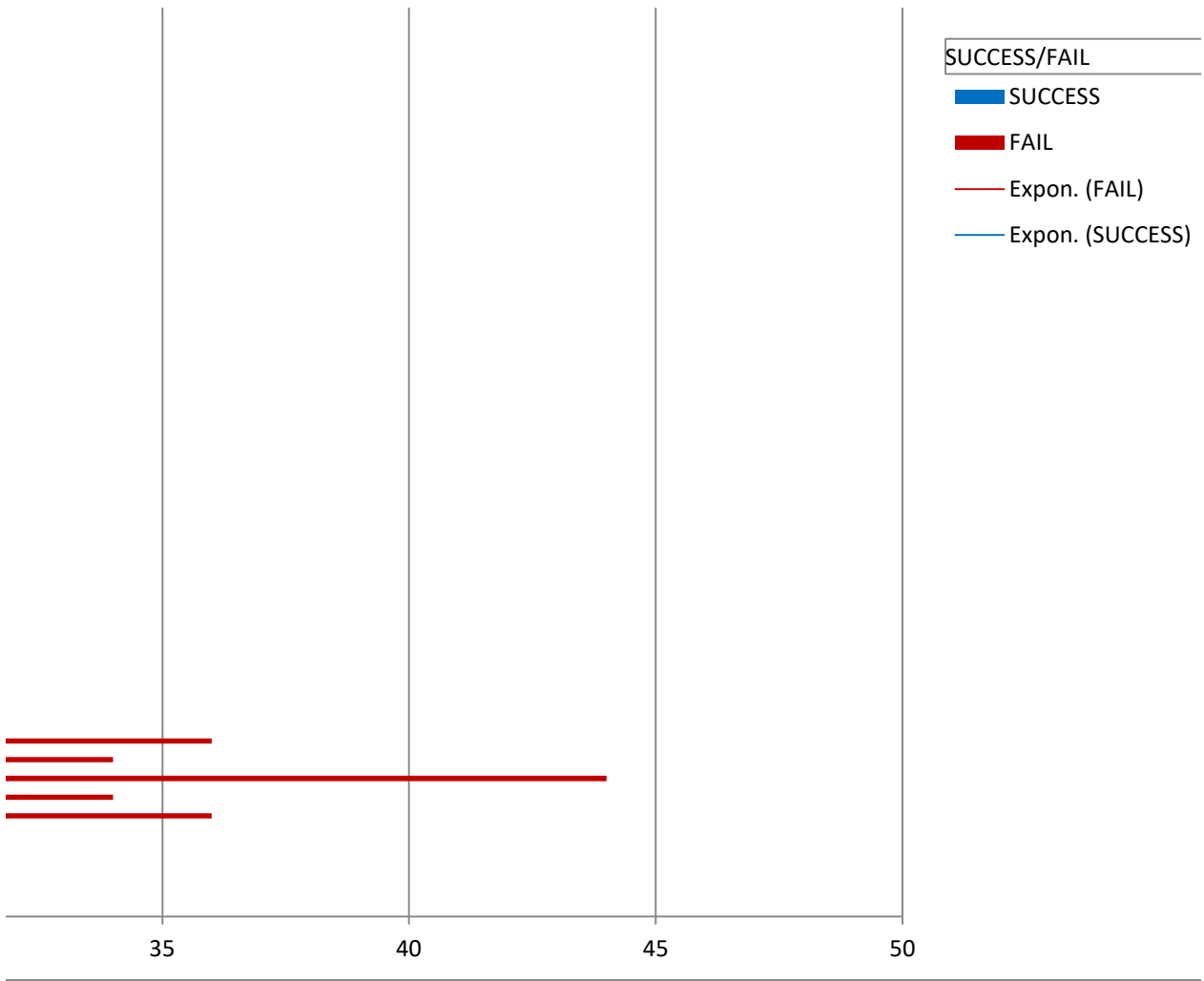
9




| rework after MCONC when SUCCESS | count | % |
|------------------------------------|-------|--------|
| Reworked at least once | 115 | 74.70% |
| Not Reworked | 39 | 25.30% |

% Samples reworked after 'Auto-Microcon' (when 'successful')







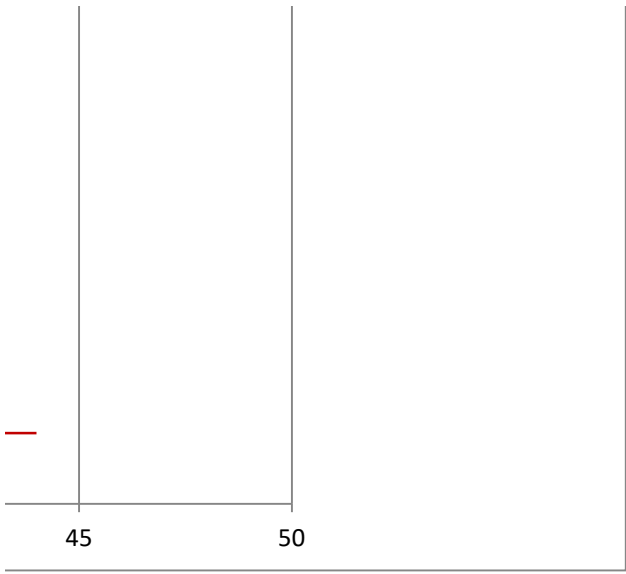
SUCCESS/FAIL

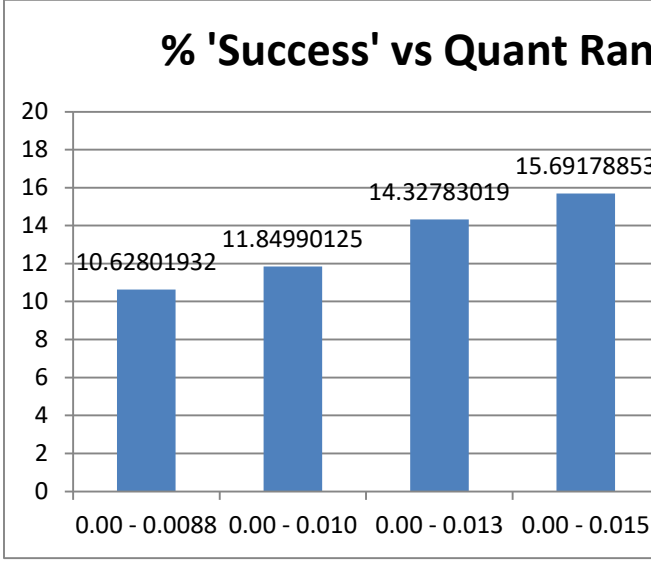
 SUCCESS

 FAIL

 Expon. (FAIL)

 Expon. (SUCCESS)

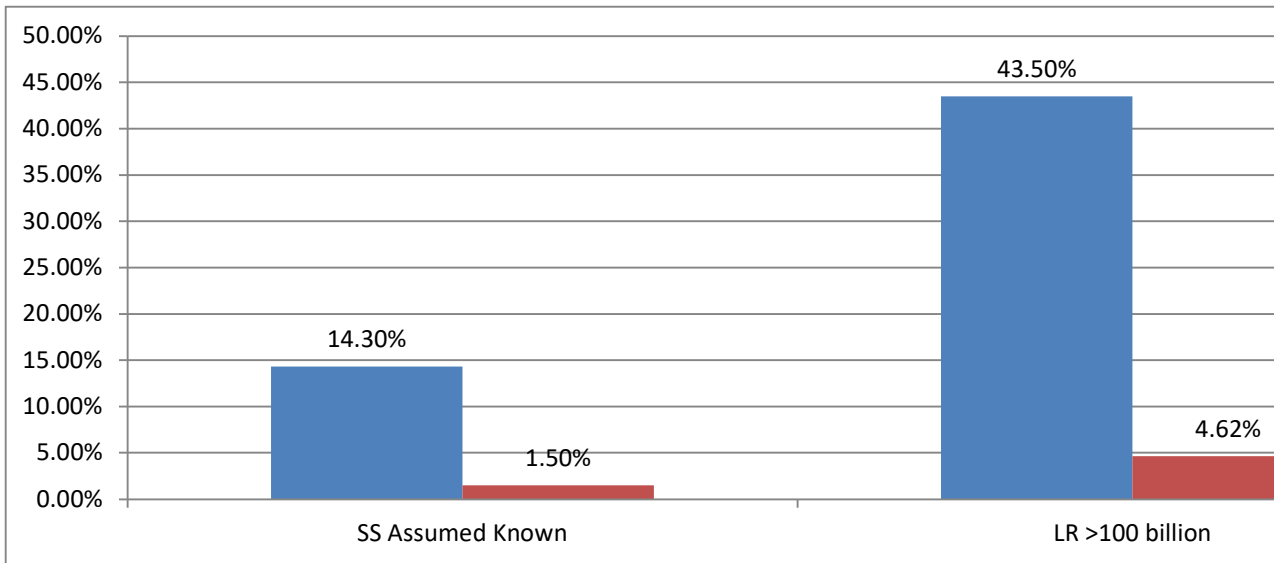




| No. samples | No. samples 'success' | % 'Success' |
|-------------|-----------------------|-------------|
| 1449 | 154 | 10.62801932 |
| 1519 | 180 | 11.84990125 |
| 1696 | 243 | 14.32783019 |
| 1778 | 279 | 15.69178853 |
| 1933 | 345 | 17.84790481 |

SS Assumed Known
LR >100 billion

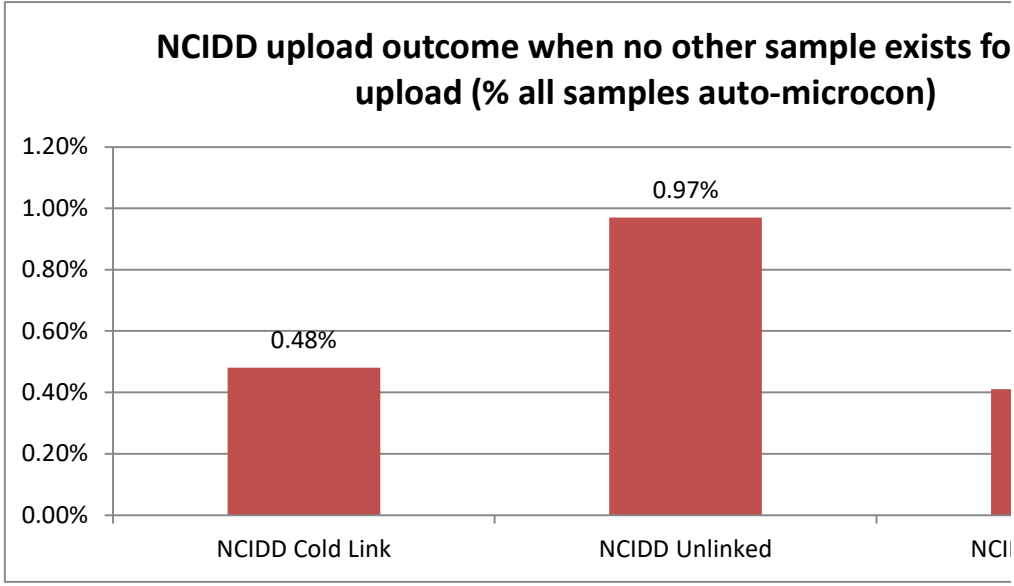
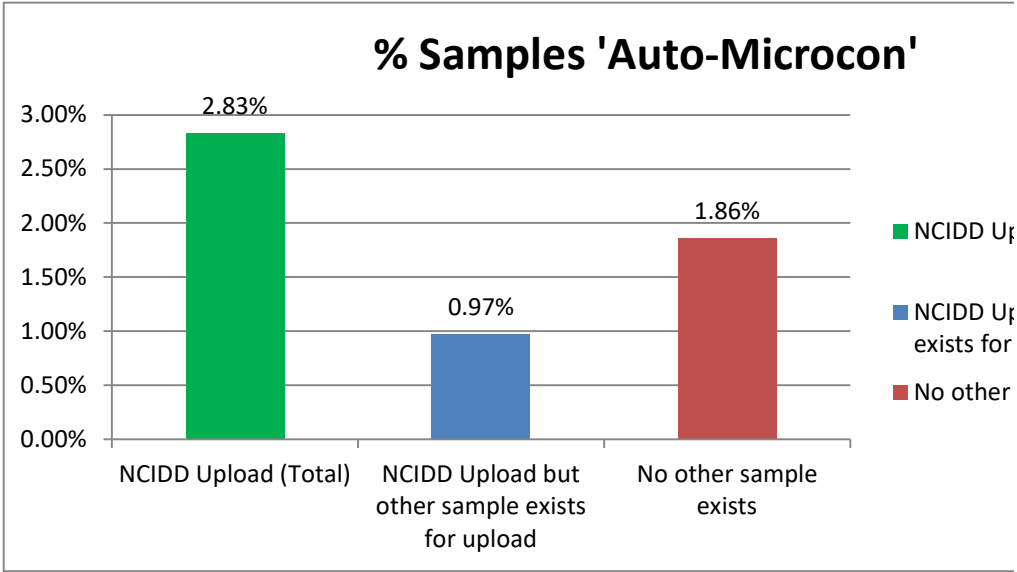
% Samples when 'Successful'
14.30%
43.50%



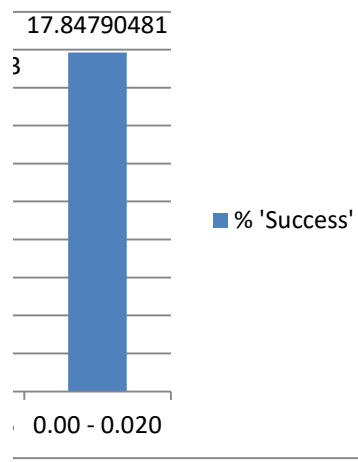
| | Number of samples | % Samples 'Auto-Microcon' |
|--|-------------------|---------------------------|
| NCIDD Upload (Total) | 41 | 2.83% |
| NCIDD Upload but other sample exists for upload | 14 | 0.97% |
| No other sample exists | 27 | 1.86% |

| | Number of samples (where no other sample could be uploaded) | % Samples 'Auto-Microcon' |
|------------------------|---|---------------------------|
| NCIDD Cold Link | 7 | 0.48% |
| NCIDD Unlinked | 14 | 0.97% |
| NCIDD Warm Link | 6 | 0.41% |

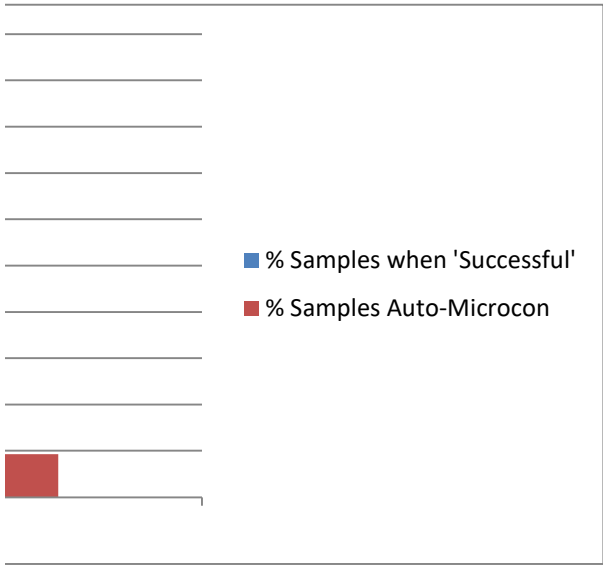
]



Age (ng/uL)



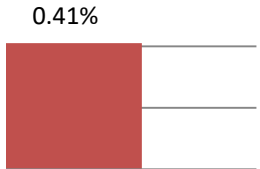
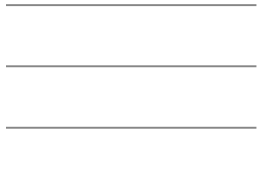
% Samples Auto-Microcon
1.50%
4.62%



upload (Total)

upload but other sample
upload
sample exists

or NCIDD



DD Warm Link

| Quant | EXHinterp | XAMP1 | XAMP2 | 3356.52 | 34.57 | Link - INTERP for NCIDD upload - warm (w), was there another sample cold (c), that could have been uploaded? (u) |
|--------|-----------|-------|-------|---------|-------|---|
| 0.0023 | SUCCESS | y | | | | |
| 0.0074 | SUCCESS | y | | n | | u |
| 0.0046 | SUCCESS | y | | n | | u |
| 0.0032 | SUCCESS | n | | n | | w |
| 0.0032 | SUCCESS | y | | n | | c |
| 0.0038 | SUCCESS | y | | n | | c |
| 0.0068 | SUCCESS | y | | n | | c |
| 0.0063 | SUCCESS | y | | n | | u |
| 0.0072 | SUCCESS | y | | n | | c |
| 0.0067 | SUCCESS | y | | n | | w |
| 0.0019 | SUCCESS | y | | n | | u |
| 0.0067 | SUCCESS | y | | n | | c |
| 0.0051 | SUCCESS | n | | n | | u |
| 0.0086 | SUCCESS | y | y | n | | u |
| 0.0019 | SUCCESS | y | | n | | c |
| 0.0088 | SUCCESS | y | | n | | w |

| | | | | | |
|----------------|---|---------|-------|-----|-----|
| 0.0063 SUCCESS | n | | | n | w |
| 0.0065 SUCCESS | y | | | n | u |
| 0.0067 SUCCESS | y | | | n | u |
| 0.0069 SUCCESS | y | | | n | u |
| 0.0055 SUCCESS | y | 2154.55 | 22.55 | n | u |
| 0.0088 SUCCESS | y | | | n | w |
| 0.0056 SUCCESS | y | | | n | c |
| 0.0051 SUCCESS | y | | | n | u |
| 0.0041 SUCCESS | y | | | n | u |
| 0.0028 SUCCESS | y | | | n | u |
| 0.0043 SUCCESS | y | | | n | u |
| 0.0082 SUCCESS | y | | | n | w |
| 0.0055 SUCCESS | n | | | n/a | n/a |
| 0.0085 SUCCESS | y | | | y | c |
| 0.0066 SUCCESS | n | | | y | w |

| | | | |
|----------------|---|---|---|
| 0.0015 SUCCESS | y | y | w |
| 0.0056 SUCCESS | y | y | c |
| 0.0082 SUCCESS | y | y | w |
| 0.0039 SUCCESS | y | y | w |
| 0.0072 SUCCESS | y | y | w |
| 0.0024 SUCCESS | y | y | w |
| 0.0064 SUCCESS | y | y | w |
| 0.0063 SUCCESS | y | y | c |
| 0.0068 SUCCESS | y | y | u |
| 0.0067 SUCCESS | y | y | c |
| 0.0035 SUCCESS | y | y | w |
| 0.0057 SUCCESS | y | y | u |
| 0.0016 FAIL | | | |
| 0.0047 SUCCESS | y | | |
| 0.0048 FAIL | | | |

0.0072 FAIL

0.0026 FAIL

0.0012 FAIL

0 FAIL

0.0031 FAIL

0.0086 SUCCESS y

0.0063 FAIL

0.004 FAIL

0.001 FAIL

0.0046 FAIL

0.0047 FAIL

0.0039 FAIL

0.0054 SUCCESS y

0.0025 FAIL

0.0017 FAIL

0.0018 FAIL

0.0028 FAIL

0.0034 FAIL

0.0012 FAIL

0.0014 FAIL

0.0043 FAIL

0.0042 FAIL

0.0031 FAIL

0.0021 FAIL

0.0026 FAIL

0.0043 SUCCESS y

0.0037 SUCCESS y

0.0074 SUCCESS y

0.0041 FAIL

0.0082 FAIL

0.0041 FAIL

0 FAIL

0.0052 FAIL

0.0058 FAIL

0.0015 FAIL

0.0034 FAIL

0.0066 FAIL

0.0054 FAIL

0.006 FAIL

0.0042 FAIL

0.0018 FAIL

0.005 FAIL

0.005 FAIL

0.0035 FAIL

0.0012 SUCCESS n

0.0057 FAIL

0.0062 SUCCESS n

0.0022 FAIL

0.0074 FAIL

0.0021 FAIL

0.0082 FAIL

0.006 FAIL

0.0086 FAIL

0.0086 FAIL

0.0059 FAIL

0.0017 FAIL

0.0024 FAIL

0.0015 FAIL

0.0058 FAIL

0.0041 FAIL

0.0033 FAIL

0.0014 FAIL

0.0059 FAIL

0.0028 FAIL

0.0067 FAIL

0.0063 FAIL

0.0017 SUCCESS y

0.0065 FAIL

0.0044 SUCCESS y

0.0023 FAIL

0.0007 FAIL

| | | | |
|----------------|---|---|--|
| 0.0071 SUCCESS | n | | |
| 0.0068 FAIL | | | |
| 0.0059 FAIL | | | |
| 0.0088 FAIL | | | |
| 0.0064 SUCCESS | y | y | |
| 0.0039 FAIL | | | |
| 0.0019 FAIL | | | |
| 0.0035 FAIL | | | |
| 0.0087 FAIL | | | |
| 0.0057 SUCCESS | y | | |
| 0.0083 SUCCESS | y | | |
| 0.0084 FAIL | | | |
| 0.007 FAIL | | | |
| 0.0022 FAIL | | | |
| 0.0019 FAIL | | | |
| 0.0063 FAIL | | | |
| 0.0032 SUCCESS | y | | |
| 0.0013 FAIL | | | |
| 0.0033 FAIL | | | |
| 0.0052 FAIL | | | |
| 0.0082 SUCCESS | y | | |
| 0.0029 FAIL | | | |

0.0067 SUCCESS y
0.0013 FAIL

0.001 FAIL

0.004 FAIL

0.0045 FAIL

0.0068 FAIL

0.0055 FAIL

0.0057 FAIL

0.0082 FAIL

0.0023 FAIL

0.0071 SUCCESS n

0.0044 FAIL

0.001 FAIL

0.0024 FAIL

0.007 FAIL

0.0026 FAIL

0.0043 FAIL

0.002 FAIL

0.0059 FAIL

0.0014 FAIL

0.003 FAIL

0.0046 FAIL

0.0061 FAIL

0.0064 FAIL

0.0029 FAIL

0.0086 FAIL

0.0087 FAIL

0.0062 FAIL

0.0026 FAIL

0.0079 FAIL

0.0014 FAIL

0.0012 FAIL

0.007 FAIL

0.0059 FAIL

0.0074 FAIL

0.0018 FAIL

0.002 FAIL

0.0036 FAIL

0.0013 FAIL

0.0024 FAIL

0.0072 FAIL

0.004 FAIL

0.0025 FAIL

0.0082 FAIL

0.0087 SUCCESS y

0.0025 FAIL

0.001 FAIL

0.0013 FAIL

0.0074 FAIL

0.0014 FAIL

0.0045 FAIL

0.0014 FAIL

0.0037 FAIL

0.0034 FAIL

0.0061 FAIL

0.002 FAIL

0.0058 FAIL

0.0011 FAIL

0.0023 FAIL

0.004 SUCCESS y

0.0058 FAIL

0.0084 FAIL

0.006 SUCCESS n

0.0031 FAIL

0.0026 FAIL

0.004 FAIL

0.0013 FAIL

0.0022 FAIL

0.006 FAIL

0.0017 FAIL

0.0036 FAIL

0.0023 FAIL

0.0055 FAIL

0.0057 FAIL

0.0033 FAIL

0.0021 FAIL

0.001 FAIL

0.002 FAIL

0.0065 FAIL

0.0025 FAIL

0.0053 FAIL

0.0016 FAIL

0.0035 FAIL

0.0053 FAIL

0.0025 FAIL

0.0036 SUCCESS n

0.0039 FAIL

0.0072 FAIL

0.0012 FAIL

0.0063 FAIL

0.0047 FAIL

0.0057 FAIL

0.004 FAIL

0.005 FAIL

0.0084 FAIL

0.0037 FAIL

0.0019 FAIL

0.0077 FAIL

0.0039 FAIL

0.005 FAIL

0.0087 SUCCESS y

0.0037 FAIL

0.0082 FAIL

0.0081 SUCCESS y

0.0068 FAIL
0.0045 FAIL
0.0015 FAIL
0.0042 FAIL
0.0011 FAIL
0.0051 FAIL
0.0059 FAIL
0.0011 FAIL
0.0014 FAIL
0.0012 FAIL
0.0085 FAIL
0.0037 FAIL
0.0046 FAIL
0.007 FAIL
0.0055 FAIL
0.002 FAIL
0.008 FAIL
0.0084 FAIL
0.0058 FAIL
0.0017 FAIL
0.0019 FAIL
0.0065 SUCCESS n
0.0048 FAIL
0.0041 FAIL
0.0014 FAIL
0.0037 FAIL
0.0021 FAIL
0.0026 FAIL

0.0011 FAIL

0.0041 FAIL

0.0017 FAIL

0.0084 FAIL

0.0064 FAIL

0.0038 FAIL

0.0057 FAIL

0.0014 FAIL

0.0012 FAIL

0.0012 FAIL

0.0015 FAIL

0.0027 FAIL

0.0058 FAIL

0.0051 FAIL

0.0016 FAIL

0.0032 SUCCESS y

0.0077 FAIL

0.003 FAIL

0.0078 FAIL

0.0084 FAIL

0.0012 FAIL

0.0013 FAIL

0.0028 FAIL

0.0024 FAIL

0.0075 FAIL

0.005 FAIL

0.0043 FAIL

0.0035 FAIL

0.0017 FAIL

0.0017 FAIL

0.0035 FAIL

0.0044 FAIL

0.0019 FAIL

0.004 FAIL

0.0026 FAIL

0.0014 FAIL

0.0017 FAIL

0.0018 FAIL

0.0014 FAIL

0.0051 FAIL

0.001 FAIL

0.0033 FAIL

0.004 FAIL

0.0035 FAIL

0.0025 FAIL

0.0081 FAIL

0.0059 FAIL

0.0059 FAIL

0.0056 FAIL

0.0018 FAIL

0.0079 FAIL

0.0033 FAIL

0.0042 FAIL

0.0018 FAIL

0.0024 FAIL

0.0018 FAIL

0.004 FAIL

0.0027 FAIL

0.0063 FAIL

0.0084 FAIL

0.0079 SUCCESS y

0.0087 FAIL

0.0032 FAIL

0.003 FAIL

0.0043 FAIL

0.0047 FAIL

0.0019 FAIL

0.0013 FAIL

0.002 FAIL

0.0035 FAIL

0.0058 FAIL

0.0024 FAIL

0.0018 FAIL

0.0038 FAIL

0.0017 FAIL

0.0011 FAIL

0.0014 FAIL

0.0071 FAIL

0.0019 FAIL

0.0011 FAIL

0.0051 FAIL

0.0084 FAIL

0.0033 FAIL

0.0022 FAIL

0.0084 FAIL

0.0019 FAIL

0.0014 FAIL

0.0014 FAIL

0.0055 FAIL

0.0048 FAIL

0.006 FAIL

0.0027 FAIL

0.0064 FAIL

0.0055 FAIL

0.0086 FAIL

0.0065 FAIL

0.0015 FAIL

0.0038 FAIL

0.0054 FAIL

0.0025 FAIL

0.0034 FAIL

0.0045 FAIL

0.0032 FAIL

0.0033 FAIL

0.0052 FAIL

0.0012 FAIL

0.0059 FAIL

0.0027 FAIL

0.0035 FAIL

0.0048 FAIL

0.0031 FAIL

0.0039 FAIL

0.0087 FAIL

0.0074 FAIL

0.0083 FAIL

0.0073 FAIL

0.0041 FAIL

0.0055 FAIL

0.0055 FAIL

0.0024 FAIL

0.0074 FAIL

0.0044 FAIL

0.0017 FAIL

0.0012 FAIL

0.0081 FAIL

0.0052 FAIL

0.0024 FAIL

0.0077 FAIL

0.0065 SUCCESS y

0.0088 FAIL

0.008 FAIL

0.0057 FAIL

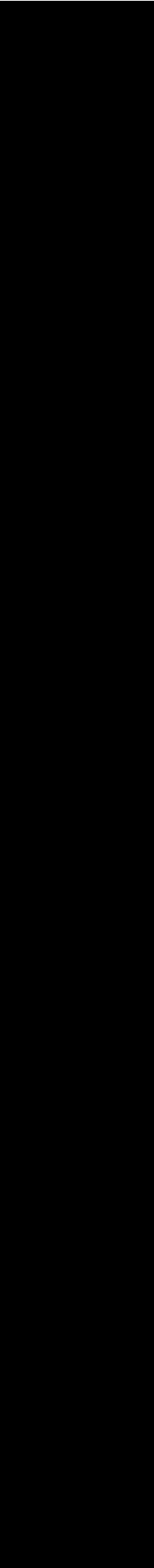
0.0015 FAIL

0.0078 FAIL

0.002 FAIL

0.0042 FAIL

0.0013 FAIL



0.0053 FAIL

0.002 FAIL

0.0025 FAIL

0.0049 FAIL

0.0055 FAIL

0.0022 FAIL

0.0028 FAIL

0.0033 FAIL

0.0065 FAIL

0.0067 FAIL

0.0021 FAIL

0.0071 FAIL

0.0015 FAIL

0.0033 FAIL

0.0029 FAIL

0.0018 FAIL

0.0044 FAIL

0.0013 FAIL

0.0084 FAIL

0.0017 FAIL

0.0042 FAIL

0.0033 FAIL

0.001 FAIL

0.003 FAIL

0.0036 FAIL

0.0011 FAIL

0.0064 FAIL

0.0016 FAIL

0.0011 FAIL

0.0022 FAIL

0.0065 FAIL

0.0034 FAIL

0.0019 FAIL

0.0079 FAIL

0.0031 FAIL

0.002 FAIL

0.0058 FAIL

0.0023 FAIL

0.0056 FAIL

0.0028 FAIL

0.0049 FAIL

0.0044 FAIL

0.0029 FAIL

0.0084 FAIL

0 FAIL

0 FAIL

0.0081 SUCCESS y

0.0018 FAIL

0.0028 FAIL

0.0028 SUCCESS y

0.0073 SUCCESS y

0.0058 SUCCESS n

0.0033 SUCCESS n

0.0016 FAIL

0.0015 SUCCESS y

0.0019 SUCCESS n

0.0018 SUCCESS y

0.0025 FAIL

0.0081 FAIL

0.0022 FAIL

0.0018 FAIL

0.0016 FAIL

0.0012 FAIL

0.0023 FAIL

0.0015 SUCCESS n

0.0035 FAIL

0.0031 FAIL

0.0061 SUCCESS n

0.0037 FAIL

0.0025 FAIL

0.0081 FAIL

0.0012 FAIL

0.0041 SUCCESS n

0.0024 FAIL

0.0012 FAIL

0.0079 FAIL

0.0072 SUCCESS y

0.0011 FAIL

0.0018 FAIL

0.0022 FAIL

0.0066 FAIL

0.0065 FAIL

0.0085 SUCCESS y

0.0078 SUCCESS y

0.0055 SUCCESS n

0.0088 SUCCESS y

0.0072 FAIL

0.0075 SUCCESS y

0.0053 SUCCESS n

0.0015 FAIL

0.0024 SUCCESS y

0.0004 FAIL

0.0057 FAIL

0.0076 FAIL

0.0036 FAIL

0.0012 FAIL

0.0082 SUCCESS y

0.0052 FAIL

0.0051 FAIL

0.0015 FAIL

0.0038 FAIL
0.005 FAIL
0.0045 FAIL
0.0026 FAIL
0.002 FAIL

0.0018 FAIL

0.007 SUCCESS n
0.0011 FAIL
0.0081 FAIL

0.001 FAIL

0.0069 SUCCESS y
0.0022 FAIL

0.0085 SUCCESS y

0.0021 FAIL

0.0013 FAIL

0.0005 FAIL

0.0024 SUCCESS n
0.0082 FAIL

0.0018 FAIL
0.0024 FAIL

0.0026 FAIL
0.0063 SUCCESS y

0.006 SUCCESS y

0.0081 FAIL
0.0061 FAIL

0.006 FAIL
0.0047 FAIL

0.005 FAIL
0.0011 FAIL

0.0024 FAIL
0.0032 FAIL

0.0019 FAIL
0.0083 SUCCESS y

0.0088 SUCCESS y
0.0015 FAIL
0.0025 SUCCESS y
0.0049 FAIL
0.0031 FAIL

0.0021 FAIL

0.0083 FAIL

0.0081 FAIL

0.0032 FAIL

0.0071 FAIL

0.0017 FAIL

0.0024 FAIL

0.002 FAIL

0.0034 FAIL

0.0024 FAIL

0.0024 FAIL

0.0054 FAIL

0.0022 FAIL

0.0084 FAIL

0.0014 FAIL

0.0014 FAIL

0.0051 FAIL

0.0027 FAIL

0.0024 FAIL

0.0045 SUCCESS y y

0.002 FAIL

0.0079 FAIL

0.0048 FAIL

0.0043 FAIL

0.0023 FAIL

0.0027 FAIL

0.0036 FAIL

0.0027 FAIL

0.0085 FAIL

0.0057 FAIL

0.007 FAIL

0.0017 FAIL

0.0011 FAIL

0.0038 FAIL

0.0064 FAIL

0.0021 FAIL

0.0014 FAIL

0.0034 FAIL

0.0013 FAIL

0.0045 FAIL

0.0049 FAIL

0.0048 FAIL

0.005 FAIL

0.0046 FAIL

0.002 FAIL

0.0018 FAIL

0.0044 FAIL

0.0035 FAIL

0.0013 FAIL

0.0049 FAIL

0.0084 FAIL

0.001 FAIL

0.0075 FAIL

0.0025 FAIL

0.0034 FAIL

0.006 FAIL

0.001 FAIL

0.0041 FAIL

0.0066 SUCCESS y

0.0019 FAIL

0.0024 FAIL

0.0011 FAIL

0.003 FAIL

0.0034 FAIL

0.0015 FAIL

0.003 FAIL

0.0061 FAIL

0.0035 FAIL

0.0027 FAIL

0.0036 FAIL

0.0065 FAIL

0.0048 FAIL

0.003 FAIL

0.0033 FAIL

0.0003 FAIL

0.0011 FAIL

0.0015 FAIL

0.0061 SUCCESS y

0.0031 FAIL

0.0043 FAIL

0.0012 FAIL

0.0048 FAIL

0.0014 FAIL

0.0019 FAIL

0.0017 FAIL

0.0016 FAIL

0.0029 FAIL

0.0031 FAIL

0.0026 FAIL

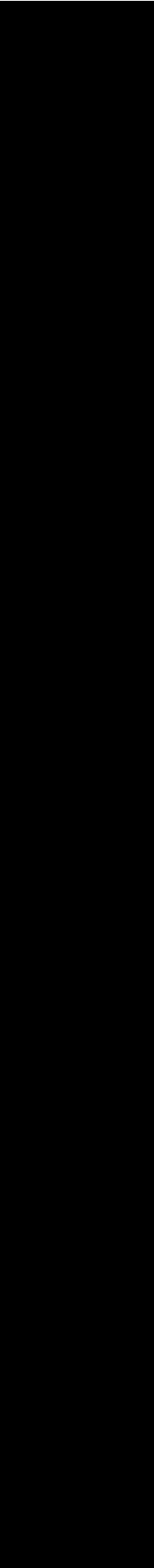
0.0022 FAIL

0.0012 FAIL

0.0034 FAIL

0.0063 SUCCESS y

0.0081 FAIL



0.0058 FAIL

0.0057 FAIL

0.0054 FAIL

0.0021 FAIL

0.0021 FAIL

0.0076 FAIL

0.0047 FAIL

0.0055 FAIL

0.0021 FAIL

0.0011 FAIL

0.001 FAIL

0.0031 FAIL

0.0027 FAIL

0.0012 FAIL

0.0062 FAIL

0.0011 FAIL

0.0026 FAIL

0.0038 FAIL

0.0032 FAIL

0.0012 FAIL

0.0065 FAIL

0.0035 FAIL

0.0023 FAIL

0.0025 FAIL

0.0016 FAIL

0.007 FAIL

0.0016 SUCCESS y

0.0017 FAIL

0.003 SUCCESS n

0.0087 FAIL

0.0043 FAIL

0.0017 FAIL

0.0028 FAIL

0.0083 FAIL

0.0027 FAIL

0.0042 FAIL

0.005 FAIL

0.003 FAIL

0.0073 FAIL

0.0053 FAIL

0.0015 FAIL

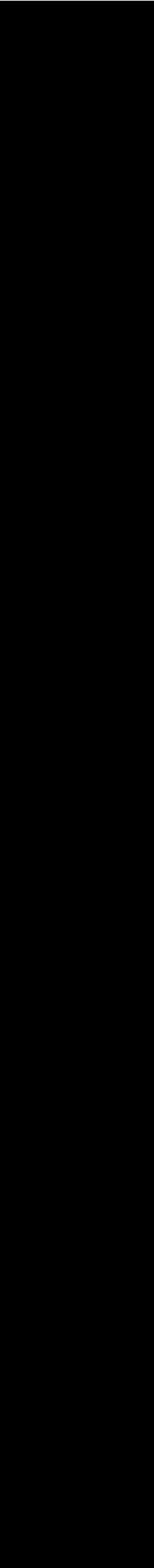
0.0039 FAIL

0 FAIL

0 FAIL

0 FAIL

0 FAIL



0.0029 FAIL

0.0056 FAIL

0.0027 FAIL

0.0064 FAIL

0.0055 FAIL

0.0045 FAIL

0.0013 FAIL

0.0057 FAIL

0.0087 FAIL

0.0029 FAIL

0.0035 FAIL

0.004 FAIL

0.0032 FAIL

0.002 FAIL

0.0048 FAIL

0.0051 FAIL

0.004 FAIL

0.0042 FAIL

0.0039 FAIL

0.0047 FAIL

0.0062 FAIL

0.001 FAIL

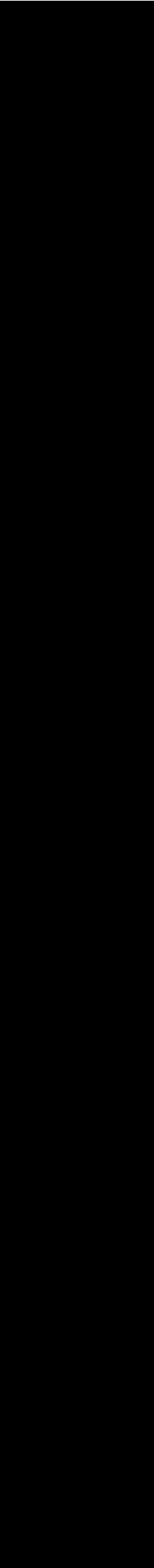
0.0059 FAIL

0.0027 FAIL

0.0021 FAIL

0.0019 FAIL

0.006 FAIL



0.0056 FAIL

0.0032 FAIL

0.0076 FAIL

0.0087 FAIL

0.005 FAIL

0.0078 FAIL

0.0015 FAIL

0.0034 FAIL

0.002 FAIL

0.0013 FAIL

0.0026 FAIL

0.0031 FAIL

0.002 FAIL

0.0024 FAIL

0.0018 FAIL

0.0041 FAIL

0.0028 FAIL

0.0053 FAIL

0.0045 FAIL

0.0022 FAIL

0.006 FAIL

0.0036 FAIL

0.0056 FAIL

0.0015 FAIL

0.0028 FAIL

0.0025 FAIL

0.008 SUCCESS y

0.001 FAIL

0.0019 FAIL

0.0024 FAIL

0.0047 FAIL

0.0059 FAIL

0.0061 FAIL

0.0041 FAIL

0.0063 FAIL

0.0039 FAIL

0.0069 FAIL

0.001 FAIL

0.0012 FAIL

0.008 FAIL

0.0063 FAIL

0.0051 FAIL

0.0066 FAIL

0.001 FAIL

0.0054 FAIL

0.0021 FAIL

0.0052 FAIL

0.0014 FAIL

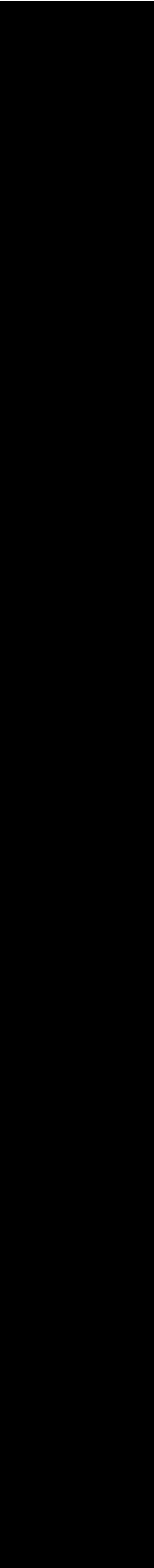
0.0036 FAIL

0.0074 FAIL

0.0034 FAIL

0.0041 FAIL

0.002 FAIL



0.0049 FAIL

0.0018 FAIL

0.0033 FAIL

0.0028 FAIL

0.0043 FAIL

0.0016 FAIL

0.0037 FAIL

0.0013 FAIL

0.0047 FAIL

0.0029 FAIL

0.003 FAIL

0.0041 FAIL

0.0017 FAIL

0.0078 FAIL

0.005 FAIL

0.0032 FAIL

0.0034 FAIL

0.0059 FAIL

0.0034 FAIL

0.0086 FAIL

0.0015 FAIL

0.0013 FAIL

0.0054 FAIL

0.0083 FAIL

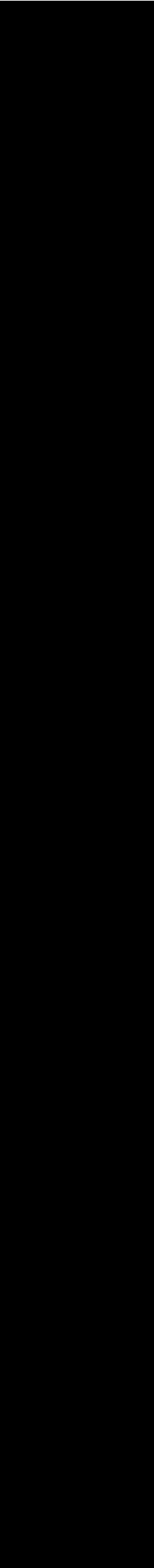
0.0023 FAIL

0.003 FAIL

0.0026 FAIL

0.0015 FAIL

0.0036 FAIL
0.0014 FAIL
0.0011 FAIL
0.0032 FAIL
0.0061 SUCCESS y
0.0074 SUCCESS n
0.0064 FAIL
0.0085 FAIL
0.0012 FAIL
0.0019 FAIL
0.0032 FAIL
0.0028 FAIL
0.0055 FAIL
0.0032 FAIL
0.0074 FAIL
0.0027 FAIL
0.0031 FAIL
0.0043 FAIL
0.0065 FAIL
0.0082 SUCCESS y
0.0025 FAIL
0.0051 FAIL
0.0019 FAIL
0.0045 FAIL
0.0069 FAIL
0.0032 FAIL



0.0013 FAIL

0.0021 FAIL

0.0014 FAIL

0.0023 FAIL

0.0013 FAIL

0.0021 FAIL

0.0038 FAIL

0.0044 FAIL

0.0018 FAIL

0.0034 FAIL

0.0029 FAIL

0.0011 FAIL

0.0013 FAIL

0.0024 FAIL

0.0012 FAIL

0.0028 FAIL

0.0057 FAIL

0.0017 FAIL

0.0049 FAIL

0.0062 FAIL

0.0012 FAIL

0.0063 FAIL

0.0011 FAIL

0.0073 FAIL



0.0046 FAIL

0.0065 FAIL

0.0051 FAIL

0.0058 FAIL

0.001 FAIL

0.0019 FAIL

0.0033 FAIL

0.0056 FAIL

0.0024 FAIL

0.001 FAIL

0.0016 FAIL

0.0033 FAIL

0.0014 FAIL

0.0073 FAIL

0.0011 FAIL

0.0062 FAIL

0.0025 FAIL

0.0025 FAIL

0.0042 FAIL

0.0078 FAIL

0.0018 FAIL

0.0015 FAIL

0.0053 FAIL

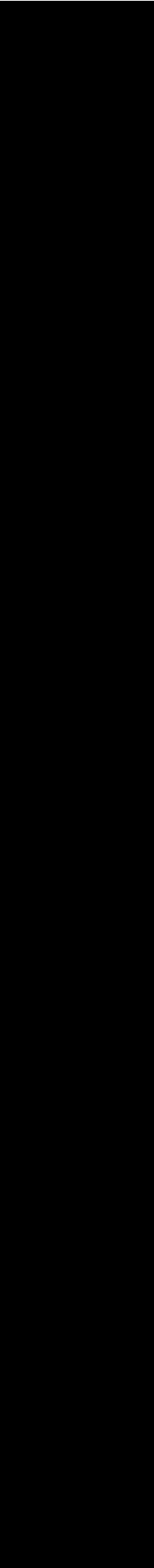
0.0035 FAIL

0.0042 FAIL

0.0035 FAIL

0.0086 FAIL

0.0012 FAIL



0.0088 FAIL

0.0073 FAIL

0.0071 FAIL

0.0026 FAIL

0.0029 FAIL

0.0037 FAIL

0.0025 FAIL

0.0027 FAIL

0.0017 FAIL

0.0083 FAIL

0.0014 FAIL

0.0031 FAIL

0.0011 FAIL

0.0018 FAIL

0.0013 FAIL

0.0025 FAIL

0.0033 FAIL

0.0041 FAIL

0.0013 FAIL

0.005 FAIL

0.0042 FAIL

0.0054 FAIL

0.0042 FAIL

0.0015 FAIL

0.0047 FAIL

0.0047 FAIL

0.0028 FAIL

0.003 FAIL

0.0015 FAIL

0.0063 FAIL

0.0052 FAIL

0.0067 FAIL

0.0038 FAIL

0.0012 FAIL

0.001 FAIL

0.005 FAIL

0.0085 SUCCESS y

0.005 FAIL

0.0044 FAIL

0.0021 FAIL

0.0049 FAIL

0.0028 FAIL

0.0042 FAIL

0.0023 FAIL

0.0025 FAIL

0.0017 FAIL

0.0049 FAIL

0.0066 FAIL

0.004 FAIL

0.0042 FAIL

0.0082 FAIL

0.0021 FAIL

0.001 FAIL

0.0018 FAIL

0.0074 FAIL

0.0055 FAIL

0.0037 FAIL

0.0018 FAIL

0.0062 FAIL

0.0025 FAIL

0.0029 FAIL

0.0055 FAIL

0.0073 SUCCESS y

0.0067 FAIL

0.0035 FAIL

0.0059 SUCCESS n

0.0069 SUCCESS y

0.0079 FAIL

0.0035 FAIL

0.0085 FAIL

0.004 FAIL

0.0048 FAIL

0.0012 FAIL

0.0035 FAIL

0.0011 FAIL

0.0032 FAIL

0.0018 FAIL

0.0013 FAIL

0.0045 FAIL

0.0012 FAIL

0.0023 FAIL

0.0045 SUCCESS y

0.002 FAIL

0.0076 FAIL

0.0037 FAIL

0.0035 FAIL

0.0045 FAIL

0.0052 FAIL

0.0011 FAIL

0.0057 FAIL

0.0038 FAIL

0.0031 FAIL

0.0032 FAIL

0.003 FAIL

0.0073 SUCCESS y

0.0011 FAIL

0.0034 FAIL

0.0035 FAIL

0.0031 FAIL

0.0031 FAIL

0.0013 FAIL

0.001 FAIL

0.0072 FAIL

0.0028 FAIL

0.001 FAIL

0.0018 FAIL

0.0027 FAIL

0.003 FAIL

0.0069 FAIL

0.0033 FAIL

0.0044 FAIL

0.002 FAIL

0.0011 FAIL

0.0017 FAIL

0.0061 FAIL

0.0023 FAIL

0.0072 FAIL

0.007 FAIL

0.0014 FAIL

0.0077 FAIL

0.0075 FAIL

0.0065 FAIL

0.0062 FAIL

0.0058 FAIL

0.0086 FAIL

0.001 FAIL

0.0066 SUCCESS y

0.0067 SUCCESS y

0.0013 FAIL

0.0048 FAIL

0.0042 FAIL

0.0045 FAIL

0.0072 FAIL

0.005 FAIL

0.0075 FAIL

0.0012 FAIL

0.0081 FAIL

0.0056 FAIL

0.001 FAIL

0.0076 FAIL

0.0064 FAIL

0.0048 FAIL

0.0055 FAIL

0.004 FAIL

0.005 FAIL

0.0036 FAIL

0.0015 FAIL

0.0084 FAIL

0.0026 FAIL

0.0016 FAIL

0.0044 FAIL

0.0012 FAIL

0.0023 FAIL

0.0047 FAIL

0.0022 FAIL

0.0012 FAIL

0.001 FAIL

0.0012 FAIL

0.0039 FAIL

0.0044 FAIL

0.0039 FAIL

0.0029 FAIL

0.0012 FAIL

0.0037 FAIL

0.0053 FAIL

0.0043 FAIL

0.007 FAIL

0.0083 FAIL

0.001 FAIL

0.0081 FAIL

0.0014 FAIL

0.0088 FAIL

0.0024 FAIL

0.0045 FAIL

0.0086 FAIL

0.0062 FAIL

0.0032 FAIL

0.0046 FAIL

0.0029 FAIL

0.0076 FAIL

0.003 SUCCESS y

0.0014 FAIL

0.0022 FAIL

0.0076 FAIL

0.0048 FAIL

0.0049 FAIL

0.0033 FAIL

0.0031 FAIL

0.0088 FAIL

0.0039 FAIL

0.005 FAIL

0.008 FAIL

0.0064 FAIL

0.0064 FAIL

0.0033 FAIL

0.0025 FAIL

0.0065 FAIL

0.0058 FAIL

0.0087 FAIL

0.0074 FAIL

0.002 FAIL

0.0085 FAIL

0.0068 FAIL

0.0042 FAIL

0.0032 FAIL

0.0054 FAIL

0.0081 FAIL

0.0046 FAIL

0.004 FAIL
0.0061 FAIL
0.0017 FAIL
0.0079 FAIL
0.0033 FAIL
0.0057 SUCCESS y
0.0041 FAIL
0.0072 FAIL
0.0019 FAIL
0.0011 FAIL
0.0036 FAIL
0.0065 FAIL
0.0014 FAIL
0.0016 FAIL
0.0069 FAIL

0.0015 FAIL
0.0014 FAIL
0.0061 FAIL
0.0026 FAIL
0.0012 FAIL
0.0037 FAIL
0.0042 FAIL
0.0032 FAIL

0.0037 SUCCESS y
0.0083 FAIL
0.0054 FAIL

0.0042 FAIL

0.0015 FAIL

0.0012 FAIL

0.0019 FAIL

0.0073 FAIL

0.003 FAIL

0.0064 FAIL

0.0047 FAIL

0.0034 FAIL

0.0041 FAIL

0.0027 FAIL

0.0012 FAIL

0.0027 FAIL

0.0065 FAIL

0.0032 FAIL

0.0045 FAIL

0.0077 FAIL

0.0057 FAIL

0.0016 FAIL

0.0039 FAIL

0.0062 FAIL

0.0033 FAIL

0.0071 SUCCESS y

0.0021 FAIL

0.0018 FAIL

0.0044 FAIL

0.005 FAIL

0.0081 FAIL

0.005 FAIL

0.0083 FAIL

0.0054 FAIL

0.001 FAIL

0.0016 FAIL

0.0013 FAIL

0.0028 FAIL

0.0059 FAIL

0.0034 FAIL

0.0017 FAIL

0.0054 FAIL

0.0019 FAIL

0.008 FAIL

0.0017 FAIL

0.0055 FAIL

0.0061 FAIL

0.003 FAIL

0.0065 SUCCESS y

0.004 FAIL

0.0014 FAIL

0.0011 FAIL

0.0056 FAIL

0.0085 FAIL

0.0078 FAIL

0.0051 FAIL

0.0022 FAIL

0.0025 FAIL

0.0084 SUCCESS y

0.0054 FAIL

0.0072 FAIL

0.0017 FAIL

0.0015 FAIL

0.0017 FAIL

0.0019 FAIL

0.0025 FAIL

0.0077 SUCCESS n

0.002 FAIL

0.0028 FAIL

0.0022 FAIL

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0.0014 FAIL

0.0033 FAIL

0.0019 FAIL

0.0017 FAIL

0.0011 FAIL

0.0033 FAIL

0.0018 FAIL

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0.001 FAIL

0.0051 FAIL

0.0072 SUCCESS y

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0.0019 FAIL

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0.0043 FAIL

0.0079 FAIL

0.006 FAIL

0.003 FAIL

0.0035 FAIL

0.0045 FAIL

0.0072 FAIL

0.0051 FAIL

0.0083 FAIL

0.0076 FAIL

0.0038 FAIL

0.0069 FAIL

0.0049 FAIL

0.0074 FAIL

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0.0012 FAIL

0.0064 FAIL

0.0079 FAIL

0.0035 FAIL

0.0012 FAIL

0.0069 FAIL

0.0058 FAIL

0.001 FAIL

0.0048 FAIL

0.006 SUCCESS n

0.0027 FAIL

0.0051 FAIL

0.0059 FAIL

0.0022 FAIL

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0.0013 FAIL

0.007 FAIL

0.0068 FAIL

0.0073 FAIL

0.0023 FAIL

0.0033 FAIL

0.001 FAIL

0.0014 FAIL

0.0078 SUCCESS y

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0.0015 FAIL

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0.007 SUCCESS y

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0.0011 FAIL

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0.0054 FAIL

0.0057 FAIL

0.0046 FAIL

0.005 FAIL

0.0015 FAIL

0.0014 FAIL

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0.0037 FAIL

0.0031 FAIL

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0.001 FAIL

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0.0057 FAIL

0.0017 FAIL

0.0022 FAIL

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0.0012 FAIL

0.0061 FAIL

0.0047 FAIL

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0.0045 FAIL

0.0038 FAIL

0.008 FAIL

0.004 FAIL

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0.0024 FAIL

0.0084 SUCCESS y

0.0055 FAIL

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0.0031 FAIL
0.001 FAIL
0.0017 FAIL
0.0013 FAIL
0.0065 FAIL
0.004 FAIL
0.0059 FAIL
0.0033 FAIL
0.0027 FAIL
0.0073 SUCCESS y
0.0025 FAIL
0.0041 FAIL
0.0011 FAIL
0.0039 FAIL
0.0065 FAIL
0.005 FAIL
0.0018 FAIL
0.001 FAIL
0.0039 FAIL
0.0012 FAIL
0.0074 SUCCESS y
0.005 FAIL
0.0055 FAIL
0.0054 FAIL
0.0013 FAIL
0.0067 SUCCESS y

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|----------------|---|
| 0.0019 FAIL | |
| 0.0022 SUCCESS | n |
| 0.0014 FAIL | |
| 0.0033 FAIL | |
| 0.0045 FAIL | |
| 0.0011 FAIL | |
| 0.0082 SUCCESS | n |
| 0.0019 SUCCESS | n |
| 0.0032 FAIL | |
| 0.0013 FAIL | |
| 0.0038 FAIL | |
| 0.0024 FAIL | |
| 0.0012 FAIL | |
| 0.0023 FAIL | |
| 0.0085 SUCCESS | y |
| 0.0048 FAIL | |
| 0.0046 SUCCESS | y |
| 0.0058 FAIL | |
| 0.0046 SUCCESS | y |
| 0.0056 FAIL | |
| 0.0088 FAIL | |
| 0.001 FAIL | |
| 0.0031 SUCCESS | n |
| 0.0017 FAIL | |
| 0.001 FAIL | |
| 0.0043 FAIL | |

0.0023 FAIL

0.0071 SUCCESS n

0.0031 FAIL

0.0034 FAIL

0.0088 FAIL

0.0019 FAIL

0.0035 FAIL

0.0027 SUCCESS y

0.0027 SUCCESS y

0.0036 SUCCESS y

0.0019 FAIL

0.0011 SUCCESS n

0.003 FAIL

0.0015 FAIL

0.0023 FAIL

0.0083 SUCCESS n

0.0071 SUCCESS y y

0.0026 SUCCESS n

0.0012 FAIL

0.0034 FAIL

0.0073 SUCCESS n

0.0027 SUCCESS n

0.0053 FAIL

0.0011 FAIL

0.0048 FAIL

0.0065 SUCCESS y

0.0086 FAIL

0.0076 SUCCESS n

0.0015 FAIL

0.0022 FAIL

0.0056 SUCCESS n

0.008 SUCCESS Y

0.0049 FAIL

0.0045 FAIL

0.0048 FAIL

0.0012 FAIL

0.0011 FAIL

0.0077 FAIL

0.0073 FAIL

0.0013 FAIL

0.0021 FAIL

0.0044 FAIL

0.0048 FAIL

0.0064 FAIL

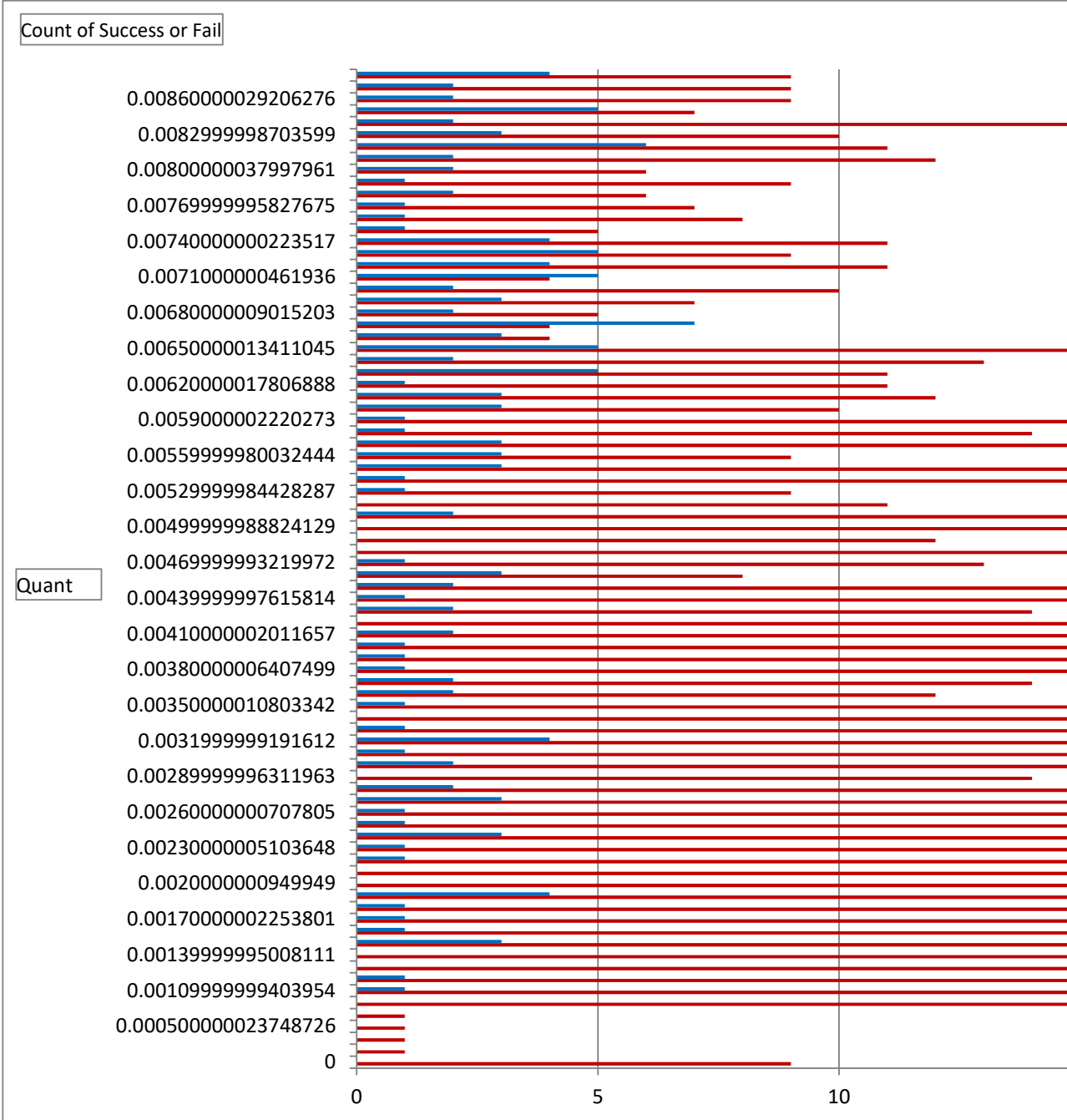
0.0031 FAIL

0.0013 FAIL

0.0012 FAIL

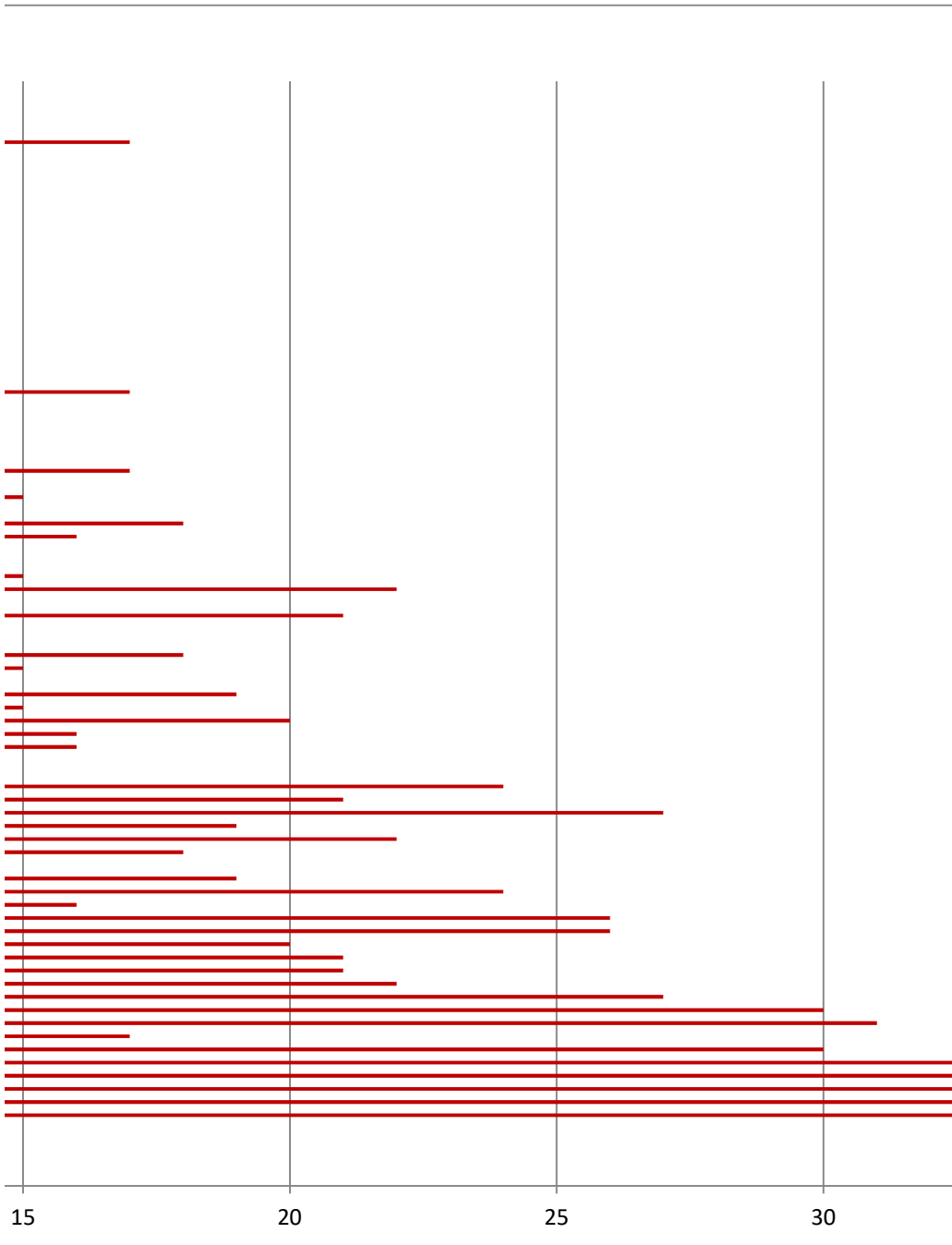
0.004 FAIL

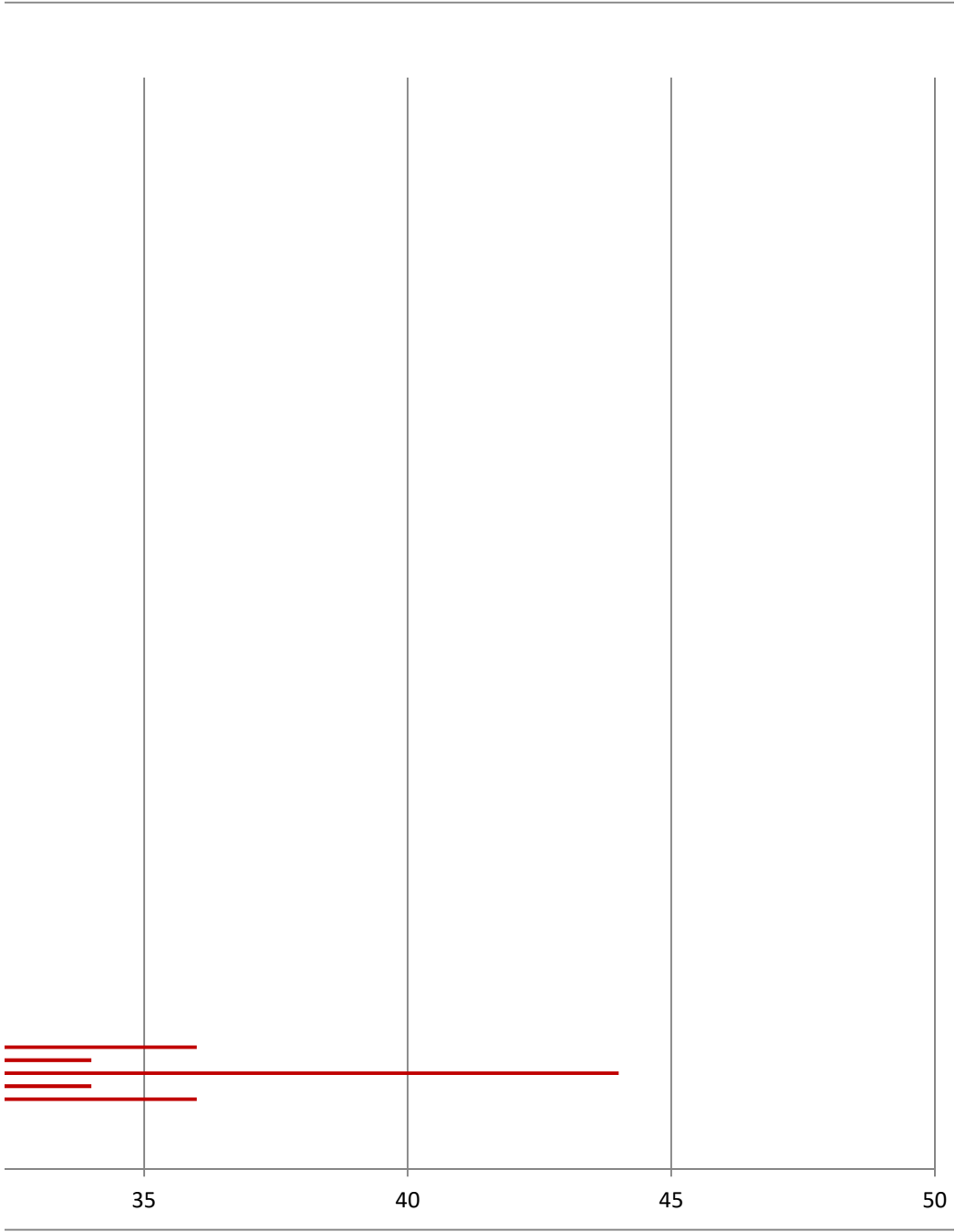
| Count of Success or Column Labels | FAIL | SUC Grand Total |
|-----------------------------------|------|-----------------|
| 0 | 9 | 9 |
| 0.0003 | 1 | 1 |
| 0.0004 | 1 | 1 |
| 0.0005 | 1 | 1 |
| 0.0007 | 1 | 1 |



| | | | |
|--------|----|---|----|
| 0.0051 | 15 | 2 | 17 |
| 0.0052 | 11 | | 11 |
| 0.0053 | 9 | 1 | 10 |
| 0.0054 | 16 | 1 | 17 |
| 0.0055 | 18 | 3 | 21 |
| 0.0056 | 9 | 3 | 12 |
| 0.0057 | 15 | 3 | 18 |
| 0.0058 | 14 | 1 | 15 |
| 0.0059 | 17 | 1 | 18 |

| | | | |
|--------------------|-------------|------------|-------------|
| 0.006 | 10 | 3 | 13 |
| 0.0061 | 12 | 3 | 15 |
| 0.0062 | 11 | 1 | 12 |
| 0.0063 | 11 | 5 | 16 |
| 0.0064 | 13 | 2 | 15 |
| 0.0065 | 17 | 5 | 22 |
| 0.0066 | 4 | 3 | 7 |
| 0.0067 | 4 | 7 | 11 |
| 0.0068 | 5 | 2 | 7 |
| 0.0069 | 7 | 3 | 10 |
| 0.007 | 10 | 2 | 12 |
| 0.0071 | 4 | 5 | 9 |
| 0.0072 | 11 | 4 | 15 |
| 0.0073 | 9 | 5 | 14 |
| 0.0074 | 11 | 4 | 15 |
| 0.0075 | 5 | 1 | 6 |
| 0.0076 | 8 | 1 | 9 |
| 0.0077 | 7 | 1 | 8 |
| 0.0078 | 6 | 2 | 8 |
| 0.0079 | 9 | 1 | 10 |
| 0.008 | 6 | 2 | 8 |
| 0.0081 | 12 | 2 | 14 |
| 0.0082 | 11 | 6 | 17 |
| 0.0083 | 10 | 3 | 13 |
| 0.0084 | 17 | 2 | 19 |
| 0.0085 | 7 | 5 | 12 |
| 0.0086 | 9 | 2 | 11 |
| 0.0087 | 9 | 2 | 11 |
| 0.0088 | 9 | 4 | 13 |
| Grand Total | 1295 | 154 | 1449 |





SUCCESS/FAIL

■ SUCCESS

■ FAIL

| | | |
|--------|---------|----|
| 0.0025 | FAIL | -1 |
| 0.0025 | FAIL | -1 |
| 0.0025 | FAIL | -1 |
| 0.0025 | FAIL | -1 |
| 0.0025 | FAIL | -1 |
| 0.0025 | FAIL | -1 |
| 0.0025 | FAIL | -1 |
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| 0.0025 | FAIL | -1 |
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| 0.0025 | SUCCESS | 1 |
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| 0.0027 | FAIL | -1 |
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| 0.0027 | FAIL | -1 |
| 0.0027 | FAIL | -1 |
| 0.0027 | FAIL | -1 |
| 0.0027 | SUCCESS | 1 |
| 0.0027 | SUCCESS | 1 |
| 0.0027 | SUCCESS | 1 |

| | | |
|--------|---------|----|
| 0.0065 | FAIL | -1 |
| 0.0065 | FAIL | -1 |
| 0.0065 | FAIL | -1 |
| 0.0065 | FAIL | -1 |
| 0.0065 | FAIL | -1 |
| 0.0065 | FAIL | -1 |
| 0.0065 | SUCCESS | 1 |
| 0.0065 | SUCCESS | 1 |
| 0.0065 | SUCCESS | 1 |
| 0.0065 | SUCCESS | 1 |
| 0.0065 | SUCCESS | 1 |
| 0.0066 | FAIL | -1 |
| 0.0066 | FAIL | -1 |
| 0.0066 | FAIL | -1 |
| 0.0066 | FAIL | -1 |
| 0.0066 | SUCCESS | 1 |
| 0.0066 | SUCCESS | 1 |
| 0.0066 | SUCCESS | 1 |
| 0.0067 | FAIL | -1 |
| 0.0067 | FAIL | -1 |
| 0.0067 | FAIL | -1 |
| 0.0067 | FAIL | -1 |
| 0.0067 | SUCCESS | 1 |
| 0.0067 | SUCCESS | 1 |
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| 0.0067 | SUCCESS | 1 |
| 0.0067 | SUCCESS | 1 |
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| 0.0068 | FAIL | -1 |
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| 0.0068 | FAIL | -1 |
| 0.0068 | SUCCESS | 1 |
| 0.0068 | SUCCESS | 1 |
| 0.0069 | FAIL | -1 |
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| 0.0069 | FAIL | -1 |
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| 0.0069 | FAIL | -1 |
| 0.0069 | FAIL | -1 |
| 0.0069 | SUCCESS | 1 |
| 0.0069 | SUCCESS | 1 |
| 0.0069 | SUCCESS | 1 |
| 0.0070 | FAIL | -1 |
| 0.0070 | FAIL | -1 |
| 0.0070 | FAIL | -1 |
| 0.0070 | FAIL | -1 |
| 0.0070 | FAIL | -1 |
| 0.0070 | FAIL | -1 |
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| 0.0070 | FAIL | -1 |
| 0.0070 | FAIL | -1 |
| 0.0070 | SUCCESS | 1 |
| 0.0070 | SUCCESS | 1 |
| 0.0071 | FAIL | -1 |

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|--------|---------|----|
| 0.0071 | FAIL | -1 |
| 0.0071 | FAIL | -1 |
| 0.0071 | FAIL | -1 |
| 0.0071 | SUCCESS | 1 |
| 0.0071 | SUCCESS | 1 |
| 0.0071 | SUCCESS | 1 |
| 0.0071 | SUCCESS | 1 |
| 0.0071 | SUCCESS | 1 |
| 0.0072 | FAIL | -1 |
| 0.0072 | FAIL | -1 |
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| 0.0072 | SUCCESS | 1 |
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| 0.0073 | SUCCESS | 1 |
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| 0.0074 | FAIL | -1 |
| 0.0074 | SUCCESS | 1 |
| 0.0074 | SUCCESS | 1 |
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| 0.0075 | FAIL | -1 |
| 0.0075 | FAIL | -1 |
| 0.0075 | FAIL | -1 |
| 0.0075 | SUCCESS | 1 |
| 0.0076 | FAIL | -1 |

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|--------|---------|----|
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| 0.0076 | SUCCESS | 1 |
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| 0.0079 | SUCCESS | 1 |
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| 0.0084 | FAIL | -1 |
| 0.0084 | FAIL | -1 |
| 0.0084 | FAIL | -1 |
| 0.0084 | FAIL | -1 |
| 0.0084 | FAIL | -1 |
| 0.0084 | FAIL | -1 |
| 0.0084 | FAIL | -1 |
| 0.0084 | SUCCESS | 1 |
| 0.0084 | SUCCESS | 1 |
| 0.0085 | FAIL | -1 |
| 0.0085 | FAIL | -1 |
| 0.0085 | FAIL | -1 |
| 0.0085 | FAIL | -1 |
| 0.0085 | FAIL | -1 |
| 0.0085 | FAIL | -1 |
| 0.0085 | FAIL | -1 |
| 0.0085 | FAIL | -1 |
| 0.0085 | SUCCESS | 1 |
| 0.0085 | SUCCESS | 1 |
| 0.0085 | SUCCESS | 1 |
| 0.0085 | SUCCESS | 1 |
| 0.0085 | SUCCESS | 1 |
| 0.0086 | FAIL | -1 |

| | | |
|--------|---------|----|
| 0.0086 | FAIL | -1 |
| 0.0086 | FAIL | -1 |
| 0.0086 | FAIL | -1 |
| 0.0086 | FAIL | -1 |
| 0.0086 | FAIL | -1 |
| 0.0086 | FAIL | -1 |
| 0.0086 | FAIL | -1 |
| 0.0086 | FAIL | -1 |
| 0.0086 | SUCCESS | 1 |
| 0.0086 | SUCCESS | 1 |
| 0.0087 | FAIL | -1 |
| 0.0087 | FAIL | -1 |
| 0.0087 | FAIL | -1 |
| 0.0087 | FAIL | -1 |
| 0.0087 | FAIL | -1 |
| 0.0087 | FAIL | -1 |
| 0.0087 | FAIL | -1 |
| 0.0087 | FAIL | -1 |
| 0.0087 | FAIL | -1 |
| 0.0087 | FAIL | -1 |
| 0.0087 | FAIL | -1 |
| 0.0087 | SUCCESS | 1 |
| 0.0087 | SUCCESS | 1 |
| 0.0088 | FAIL | -1 |
| 0.0088 | FAIL | -1 |
| 0.0088 | FAIL | -1 |
| 0.0088 | FAIL | -1 |
| 0.0088 | FAIL | -1 |
| 0.0088 | FAIL | -1 |
| 0.0088 | FAIL | -1 |
| 0.0088 | FAIL | -1 |
| 0.0088 | FAIL | -1 |
| 0.0088 | SUCCESS | 1 |
| 0.0088 | SUCCESS | 1 |
| 0.0088 | SUCCESS | 1 |
| 0.0088 | SUCCESS | 1 |

| Barcode | Quant | EXHinter | Sample type | Sampled Substrate type | ? Possible biological type | Profile type |
|---------|--------|----------|-------------|------------------------|----------------------------|--------------|
| | 0.0011 | SUCCESS | swab | LVS SFRAC | Cells | SS AKC |
| | 0.0012 | SUCCESS | swab | Anal/Rectal SFRAC | Cells | SS AKC |
| | 0.0015 | SUCCESS | swab | PM Body SFRAC | Cells | SS AKC |
| | 0.0015 | SUCCESS | swab | Shoe stain | Blood | SS AKC |
| | 0.0015 | SUCCESS | swab | Perianal | Cells | SS AKC |
| | 0.0016 | SUCCESS | swab | Unknown | Cells | MIX NSIP/LR |
| | 0.0017 | SUCCESS | swab | Anal/Rectal SFRAC | Cells | SS AKC |
| | 0.0018 | SUCCESS | hair | drop sheet | hair | MIX NSIP/LR |
| | 0.0019 | SUCCESS | swab | endocervical SFRAC | Cells | SS AKC |
| | 0.0019 | SUCCESS | swab | penis | Cells | SS AKC |
| | 0.0019 | SUCCESS | hair | drop sheet | hair | SS |
| | 0.0019 | SUCCESS | swab | Wall stain | Blood | SS |
| | 0.0022 | SUCCESS | swab | LVS SFRAC | Cells | SS AKC |
| | 0.0023 | SUCCESS | tapelift | Bag handles | Cells | MIX NSIP/LR |
| | 0.0024 | SUCCESS | swab | penis | Cells | MIX AKC |
| | 0.0024 | SUCCESS | swab | Nail scrapings | Cells | MIX AKC |
| | 0.0024 | SUCCESS | tapelift | wipe SFRAC | Unknown | MIX NSIP/LR |
| | 0.0025 | SUCCESS | swab | buccal/oral SFRAC | Cells | SS AKC |
| | 0.0026 | SUCCESS | swab | penis SFRAC | Cells | SS AKC |
| | 0.0027 | SUCCESS | swab | buccal/oral SFRAC | Cells | SS AKC |
| | 0.0027 | SUCCESS | swab | vulval SFRAC | Unknown | MIX NSIP/LR |
| | 0.0027 | SUCCESS | swab | Cervical SFRAC | Cells | SS AKC |
| | 0.0028 | SUCCESS | hair | drop sheet | hair | MIX NSIP/LR |
| | 0.0028 | SUCCESS | swab | Glasses | Cells | SS AKC |
| | 0.0030 | SUCCESS | swab | Driveway stain | Blood | SS |
| | 0.0030 | SUCCESS | swab | Bottle | Cells | SS |
| | 0.0031 | SUCCESS | tapelift | wipe EFRAC | Cells | SS |
| | 0.0032 | SUCCESS | swab | vehicle headlight | Cells | SS |
| | 0.0032 | SUCCESS | swab | Bottle | Cells | MIX NSIP/LR |
| | 0.0032 | SUCCESS | swab | Bottle | Cells | SS |
| | 0.0032 | SUCCESS | swab | fabric | Blood | SS AKC |
| | 0.0033 | SUCCESS | swab | HVS SFRAC | Cells | SS AKC |
| | 0.0035 | SUCCESS | swab | Anal/Rectal SFRAC | Cells | SS |
| | 0.0036 | SUCCESS | swab | Glove | Cells | MIX NSIP/LR |
| | 0.0036 | SUCCESS | swab | vaginal SFRAC | Cells | SS AKC |
| | 0.0037 | SUCCESS | swab | phone | Cells | MIX NSIP/LR |
| | 0.0037 | SUCCESS | tapelift | Glove | Cells | MIX NSIP/LR |
| | 0.0038 | SUCCESS | swab | Glasses | Cells | SS |
| | 0.0039 | SUCCESS | swab | LVS SFRAC | Unknown | MIX NSIP/LR |
| | 0.0040 | SUCCESS | swab | door | Blood | MIX NSIP/LR |
| | 0.0041 | SUCCESS | swab | Anal/Rectal SFRAC | Cells | SS AKC |
| | 0.0041 | SUCCESS | swab | tape | Cells | SS |
| | 0.0043 | SUCCESS | tapelift | hose | Cells | SS |
| | 0.0043 | SUCCESS | tapelift | Glove | Cells | MIX NSIP/LR |
| | 0.0044 | SUCCESS | cig butt | cig butt | Cells | SS |
| | 0.0045 | SUCCESS | swab | metal | Blood | MIX NSIP/LR |

2p or 3 p mix, suitable for LR's only if obtained

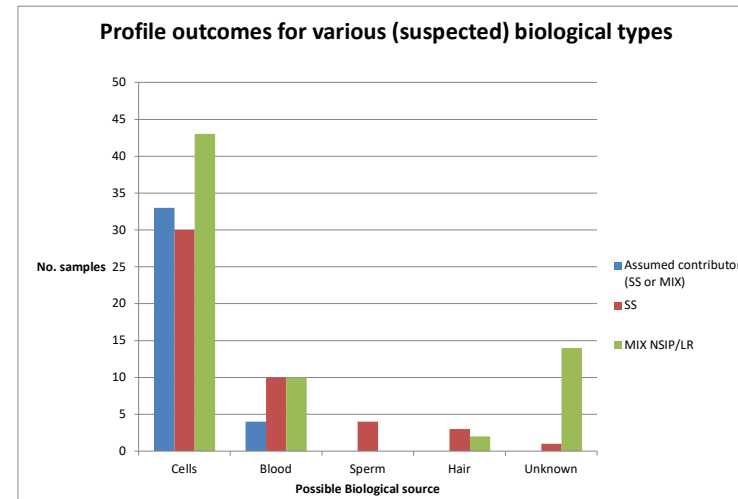
Ownership not known; contribution can't be assumed; matches profile elsewhere eg. UK; profile for NCIDD

Where conditioned and nothing remaining (s/thresh)

Most likely in absence of reference profile, and given other samples in case.

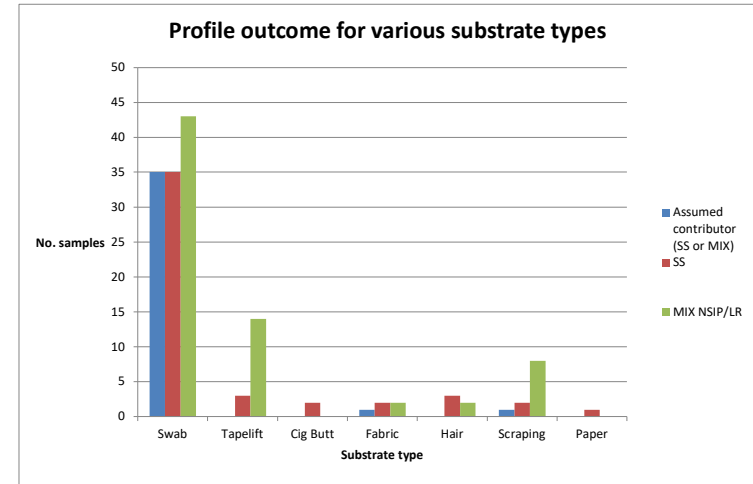
Most likely in absence of reference profile, and given other samples in case.

| | Assumed contributor (SS or MIX) | SS | MIX NSIP/LR |
|---------|---------------------------------|----|-------------|
| Cells | 33 | 30 | 43 |
| Blood | 4 | 10 | 10 |
| Sperm | 0 | 4 | 0 |
| Hair | 0 | 3 | 2 |
| Unknown | 0 | 1 | 14 |



| | Assumed contributor (SS or MIX) | SS | MIX NSIP/LR |
|----------|---------------------------------|----|-------------|
| Swab | 35 | 35 | 43 |
| Tapelift | 0 | 3 | 14 |
| Cig Butt | 0 | 2 | 0 |
| Fabric | 1 | 2 | 2 |
| Hair | 0 | 3 | 2 |
| Scraping | 1 | 2 | 8 |
| Paper | 0 | 1 | 0 |

| | | | | | |
|--------|---------|-----------|-------------------|---------|-------------|
| 0.0045 | SUCCESS | swab | Window sill | Blood | MIX NSIP/LR |
| 0.0046 | SUCCESS | swab | Nipple | Cells | MIX NSIP/LR |
| 0.0046 | SUCCESS | swab | number plate | Cells | MIX NSIP/LR |
| 0.0046 | SUCCESS | swab | Nipple | Cells | MIX NSIP/LR |
| 0.0047 | SUCCESS | tapelift | Window ledge | Cells | MIX NSIP/LR |
| 0.0051 | SUCCESS | swab | Glove | Cells | MIX NSIP/LR |
| 0.0051 | SUCCESS | swab | straw | Cells | SS |
| 0.0053 | SUCCESS | swab | penis SFRAC | Cells | SS AKC |
| 0.0054 | SUCCESS | swab | carpet | Blood | MIX NSIP/LR |
| 0.0055 | SUCCESS | fabric | Clothing SFRAC | Sperm | SS |
| 0.0055 | SUCCESS | swab | HVS SFRAC | Cells | SS AKC |
| 0.0055 | SUCCESS | swab | drink can | Cells | MIX NSIP/LR |
| 0.0056 | SUCCESS | swab | vulval SFRAC | Cells | SS AKC |
| 0.0056 | SUCCESS | swab | toothbrush | Cells | MIX NSIP/LR |
| 0.0056 | SUCCESS | swab | straw | Cells | SS |
| 0.0057 | SUCCESS | swab | Labia SFRAC | Unknown | MIX NSIP/LR |
| 0.0057 | SUCCESS | scrapping | Clothing SFRAC | Unknown | MIX NSIP/LR |
| 0.0057 | SUCCESS | swab | plastic bag | Cells | SS |
| 0.0058 | SUCCESS | swab | Labia | Cells | SS AKC |
| 0.0059 | SUCCESS | fabric | Clothing | Blood | SS |
| 0.0060 | SUCCESS | swab | skin | Cells | SS |
| 0.0060 | SUCCESS | tapelift | knife | Blood | MIX NSIP/LR |
| 0.0060 | SUCCESS | swab | penis | Cells | MIX NSIP/LR |
| 0.0061 | SUCCESS | swab | Nipple | Cells | SS AKC |
| 0.0061 | SUCCESS | swab | clothing | Blood | MIX NSIP/LR |
| 0.0061 | SUCCESS | tapelift | plastic gear knob | Cells | MIX NSIP/LR |
| 0.0062 | SUCCESS | swab | vulval SFRAC | Cells | SS AKC |
| 0.0063 | SUCCESS | swab | glass window | Blood | SS |
| 0.0063 | SUCCESS | swab | bottle | Cells | MIX NSIP/LR |
| 0.0063 | SUCCESS | swab | Driveway stain | Blood | SS |
| 0.0063 | SUCCESS | swab | lighter | Cells | MIX NSIP/LR |
| 0.0063 | SUCCESS | swab | nail | Cells | SS |
| 0.0064 | SUCCESS | scrapping | blanket | Unknown | MIX NSIP/LR |
| 0.0064 | SUCCESS | swab | Bottle | Cells | SS |
| 0.0065 | SUCCESS | swab | tiles | Blood | SS |
| 0.0065 | SUCCESS | swab | firearm | Cells | MIX NSIP/LR |
| 0.0065 | SUCCESS | swab | handle | Cells | MIX NSIP/LR |
| 0.0065 | SUCCESS | tapelift | glasses | Cells | MIX NSIP/LR |
| 0.0065 | SUCCESS | fabric | clothing | Cells | MIX NSIP/LR |
| 0.0066 | SUCCESS | scrapping | SFRAC | Sperm | SS |
| 0.0066 | SUCCESS | swab | bottle | Cells | SS |
| 0.0066 | SUCCESS | swab | plastic | Cells | MIX NSIP/LR |
| 0.0067 | SUCCESS | swab | handle | Blood | SS |
| 0.0067 | SUCCESS | swab | bottle | Cells | SS |
| 0.0067 | SUCCESS | swab | window | Cells | MIX NSIP/LR |
| 0.0067 | SUCCESS | hair | tape | hair | SS |
| 0.0067 | SUCCESS | tapelift | fabric | Cells | MIX NSIP/LR |
| 0.0067 | SUCCESS | tapelift | plastic | Cells | MIX NSIP/LR |
| 0.0067 | SUCCESS | swab | vaginal SFRAC | Unknown | MIX NSIP/LR |
| 0.0068 | SUCCESS | paper | stain | Blood | SS |
| 0.0068 | SUCCESS | swab | knife | Cells | SS |
| 0.0069 | SUCCESS | swab | ring | Blood | MIX NSIP/LR |
| 0.0069 | SUCCESS | swab | Unknown | Cells | SS |
| 0.0069 | SUCCESS | swab | perianal SFRAC | Blood | SS AKC |
| 0.0070 | SUCCESS | swab | penis | Cells | SS AKC |
| 0.0070 | SUCCESS | swab | skin | Cells | MIX AKC |
| 0.0071 | SUCCESS | swab | Nipple | Cells | MIX NSIP/LR |
| 0.0071 | SUCCESS | swab | hand | Cells | SS AKC |
| 0.0071 | SUCCESS | swab | LVS SFRAC | Cells | SS AKC |
| 0.0071 | SUCCESS | swab | needle | Blood | SS |
| 0.0071 | SUCCESS | swab | cup | Cells | MIX NSIP/LR |
| 0.0072 | SUCCESS | swab | penis | Cells | MIX NSIP/LR |
| 0.0072 | SUCCESS | swab | toothbrush | Cells | SS |
| 0.0072 | SUCCESS | swab | plastic bag | Cells | MIX NSIP/LR |
| 0.0072 | SUCCESS | tapelift | glove | Cells | MIX NSIP/LR |
| 0.0073 | SUCCESS | swab | condom SFRAC | Unknown | SS |



| | | | | | |
|-------|---------|-----------|--------------------|---------|-------------|
| .0073 | SUCCESS | tapelift | plastic | Cells | MIX NSIP/LR |
| .0073 | SUCCESS | swab | plastic | Blood | MIX NSIP/LR |
| .0073 | SUCCESS | tapelift | steering wheel | Cells | SS |
| .0073 | SUCCESS | scrapping | fabric SFRAC | Unknown | MIX NSIP/LR |
| .0074 | SUCCESS | swab | clothing | Blood | MIX NSIP/LR |
| .0074 | SUCCESS | swab | shoes | Blood | SS |
| .0074 | SUCCESS | swab | gear knob | Cells | MIX NSIP/LR |
| .0074 | SUCCESS | swab | can | Cells | SS |
| .0075 | SUCCESS | swab | breast | Cells | MIX NSIP/LR |
| .0076 | SUCCESS | scrapping | clothing | Cells | MIX NSIP/LR |
| .0077 | SUCCESS | cig butt | cig butt | Cells | SS |
| .0078 | SUCCESS | swab | glove | Cells | MIX NSIP/LR |
| .0078 | SUCCESS | swab | floor EFRAC | Cells | SS |
| .0079 | SUCCESS | swab | condom packet | Cells | MIX NSIP/LR |
| .0080 | SUCCESS | swab | HVS SFRAC | Cells | SS AKC |
| .0080 | SUCCESS | tapelift | fabric SFRAC | Unknown | MIX NSIP/LR |
| .0081 | SUCCESS | swab | bottle | Cells | SS |
| .0081 | SUCCESS | scrapping | fabric SFRAC | Unknown | MIX NSIP/LR |
| .0082 | SUCCESS | hair | condom | hair | SS |
| .0082 | SUCCESS | tapelift | cartridge | Cells | MIX NSIP/LR |
| .0082 | SUCCESS | scrapping | clothing SFRAC | Unknown | MIX NSIP/LR |
| .0082 | SUCCESS | swab | tool | Cells | SS |
| .0082 | SUCCESS | fabric | clothing | Cells | MIX AKC |
| .0082 | SUCCESS | swab | breast | Cells | MIX NSIP/LR |
| .0083 | SUCCESS | swab | endocervical SFRAC | Cells | SS AKC |
| .0083 | SUCCESS | swab | perianal SFRAC | Sperm | SS |
| .0083 | SUCCESS | scrapping | clothing SFRAC | Cells | MIX AKC |
| .0084 | SUCCESS | swab | can | Cells | SS |
| .0084 | SUCCESS | fabric | clothing | Blood | MIX NSIP/LR |
| .0085 | SUCCESS | scrapping | fabric SFRAC | Unknown | MIX NSIP/LR |
| .0085 | SUCCESS | scrapping | bedding SFRAC | Unknown | MIX NSIP/LR |
| .0085 | SUCCESS | swab | can | Cells | SS |
| .0085 | SUCCESS | swab | can | Cells | MIX NSIP/LR |
| .0085 | SUCCESS | swab | tiles EFRAC | Cells | MIX NSIP/LR |
| .0086 | SUCCESS | swab | bottle | Cells | MIX NSIP/LR |
| .0086 | SUCCESS | swab | penis | Cells | MIX AKC |
| .0087 | SUCCESS | swab | hand | Blood | MIX AKC |
| .0087 | SUCCESS | swab | gun | Cells | MIX NSIP/LR |
| .0088 | SUCCESS | swab | can | Cells | SS |
| .0088 | SUCCESS | scrapping | fabric SFRAC | Sperm | SS |
| .0088 | SUCCESS | swab | straw | Cells | SS |
| .0088 | SUCCESS | swab | HVS SFRAC | Unknown | MIX NSIP/LR |

| ant | EXHinterp | Success (+1) or Fail (-1) | EXH |
|--------|-----------|---------------------------|---|
| | | | Hair located. Submitted-results pending |
| 0.0089 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0089 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0089 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0089 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0089 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0089 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0089 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0089 | SUCCESS | 1 | No statistical interpretation performed |
| 0.009 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.009 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.009 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0091 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0091 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | | | Complex mixed profile unsuitable for interp or comparison This sample has undergone further processing Three person mixed DNA profile |
| 0.0091 | FAIL | -1 | 3 person mix profile - support for contrib > 100 billion |
| 0.0091 | FAIL | -1 | CMPU |
| 0.0091 | SUCCESS | 1 | consistent elsewhere Submitted-results pending. |
| | | | Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information |
| 0.0091 | SUCCESS | 1 | NCIDD upload single source DNA profile Submitted-results pending. |
| | | | Three person mixed DNA profile |
| 0.0091 | SUCCESS | 1 | 3 person mixed profile - conditioned on |
| | | | 3 person mix remaining - supports non contribution Submitted-results pending. |
| 0.0092 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0092 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0092 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison |
| 0.0092 | SUCCESS | 1 | P SS |
| | | | Micro positive for sperm. Submitted-Results pending |
| 0.0093 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0093 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0093 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0093 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0093 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | | | Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information |
| 0.0093 | SUCCESS | 1 | Single source 20 loci DNA profile LR > 100 billion |
| 0.0093 | SUCCESS | 1 | P SS Submitted-results pending. |
| | | | Three person mixed DNA profile |
| 0.0093 | SUCCESS | 1 | 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0093 | SUCCESS | 1 | Two person mixed DNA profile Submitted-results pending. |
| 0.0094 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0094 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison |

| | |
|----------------|---|
| | Submitted-results pending. |
| 0.0094 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0094 FAIL | -1 CMPU |
| 0.0094 FAIL | -1 CMPU |
| 0.0094 SUCCESS | 1 3p Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 1 million - 1 billion |
| 0.0094 SUCCESS | 1 3 person mix - support for contribution 100 to 1000 Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution |
| 0.0094 SUCCESS | 1 3 person mix - supports non contribution Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion |
| 0.0094 SUCCESS | 1 3 person mix remaining - supports non contribution Submitted-results pending. |
| 0.0095 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0095 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0095 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0095 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0095 FAIL | -1 CMPU Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Complex mixed profile unsuitable for interp or comparison |
| 0.0095 SUCCESS | 1 DNA profile removed from NCIDD |
| 0.0095 SUCCESS | 1 3p Micro positive for sperm. Submitted-Results pending |
| 0.0095 SUCCESS | 1 Single source 20 loci DNA profile LR > 100 billion Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0095 SUCCESS | 1 3 person mix - supports non contribution Submitted-results pending. Single source DNA profile |
| 0.0095 SUCCESS | 1 Possible sub-threshold information Submitted-results pending. Three person mixed DNA profile |
| 0.0095 SUCCESS | 1 Mixture-low support for contrib or supports non contrib Submitted-results pending. |
| 0.0096 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0096 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0096 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0096 SUCCESS | 1 cond |
| 0.0096 SUCCESS | 1 ss akc SS DNA profile 9 loci and above LR > 100 billion |
| 0.0096 SUCCESS | 1 Possible sub-threshold information Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Suspect check - low support or non contrib |
| 0.0096 SUCCESS | 1 Suspect check - supports non contribution Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| 0.0096 SUCCESS | 1 Excluded from mixed DNA profile Three person mixed DNA profile 3 person mixed profile - conditioned on |
| 0.0097 SUCCESS | 1 Single evidence sample excluded Submitted-results pending. |
| 0.0098 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Hair located. Submitted-results pending Single Source DNA profile - assumed known contributor |
| 0.0098 SUCCESS | 1 Possible sub-threshold information |

| | |
|----------------|--|
| 0.0099 FAIL | Submitted-results pending. -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0099 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.01 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.01 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.01 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.01 FAIL | -1 cmpu |
| 0.01 FAIL | -1 cmpu |
| 0.0101 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0101 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0101 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0101 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0101 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0101 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0101 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0101 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0101 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0101 SUCCESS | 1 ss Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mixed profile - conditioned on |
| 0.0101 SUCCESS | 1 2 person rem - support for contrib 1 billion -100 billion Submitted-results pending. |
| 0.0101 SUCCESS | 1 Single source DNA profile Submitted-results pending. Single source DNA profile |
| 0.0101 SUCCESS | 1 Possible sub-threshold information Submitted as cells |
| 0.0102 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0102 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0102 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0102 SUCCESS | 1 ss Submitted-results pending. |
| 0.0103 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0103 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0103 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Micro neg for sperm Two person mixed DNA profile 2 person mixed profile - conditioned on |
| 0.0103 FAIL | -1 Mix remaining DNA contrib unsuitable for NCIDD searching Submitted-results pending. Three person mixed DNA profile |
| 0.0103 SUCCESS | 1 No statistical interpretation performed Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative |
| 0.0104 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0104 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0104 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0104 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0104 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

| | |
|----------------|--|
| | Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Three person mixed DNA profile |
| 0.0104 SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0105 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0105 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0105 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0105 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0105 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending SS DNA profile 9 loci and above LR > 100 billion |
| 0.0105 SUCCESS | 1 NCIDD upload single source DNA profile Submitted-results pending. Single source DNA profile |
| 0.0105 SUCCESS | 1 NCIDD upload single source DNA profile |
| 0.0105 SUCCESS | 1 ss Submitted-results pending. |
| 0.0106 FAIL | -1 ENVM- Complex mixture unsuitable for interp or comparison Submitted-results pending. Single source DNA profile |
| 0.0106 SUCCESS | 1 NCIDD upload single source DNA profile Submitted-results pending. |
| 0.0107 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0107 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0107 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Interim result- mixed profile obtained. Rework Reqd Submitted for cells. Presumptive saliva test pending. presump Saliva test positive |
| 0.0108 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0108 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0108 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0108 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0108 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0108 FAIL | -1 cmpu Semen not detected Submitted as cells |
| 0.0109 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0109 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0109 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0109 FAIL | -1 cmpu Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - low support for contrib |
| 0.0109 SUCCESS | 1 3 person mix remaining - supports non contribution Labelling discrepancy Submitted-results pending. |
| 0.011 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.011 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.011 SUCCESS | 1 2p |
| 0.011 SUCCESS | 1 3p |
| 0.011 SUCCESS | 1 2p Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Single evidence sample excluded |
| 0.011 SUCCESS | 1 3 person mix - supports non contribution Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.011 SUCCESS | 1 3 person mix - support for contrib 1 million - 1 billion |

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| 0.0111 | FAIL | Submitted-results pending. -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0111 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0111 | FAIL | -1 Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| 0.0111 | SUCCESS | Single source 20 loci DNA profile LR > 100 billion 1 NCIDD upload single source DNA profile Submitted-results pending. Single source DNA profile |
| 0.0111 | SUCCESS | 1 NCIDD upload single source DNA profile |
| 0.0112 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending |
| 0.0112 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0112 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0112 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0112 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted as cells Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile |
| 0.0112 | SUCCESS | 1 Possible sub-threshold information Submitted-results pending. Two person mixed DNA profile Mixture-low support for contrib or supports non contrib 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile |
| 0.0112 | SUCCESS | 1 Suspect check - supports non contribution Submitted as cells, Presump saliva test pending Presump Saliva test negative |
| 0.0113 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0113 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0113 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile |
| 0.0113 | SUCCESS | 1 Possible sub-threshold information Submitted-results pending. |
| 0.0113 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed Single evidence sample excluded |
| 0.0113 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0114 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| 0.0114 | SUCCESS | 1 Single evidence sample excluded Submitted-results pending. |
| 0.0115 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0115 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0115 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0115 | SUCCESS | 1 Three person mixed DNA profile No statistical interpretation performed Submitted-results pending. |
| 0.0116 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion |
| 0.0116 | SUCCESS | 1 3 person mix - supports non contribution Submitted-results pending. |
| 0.0117 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0118 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

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| 0.0118 FAIL | Submitted-results pending. -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0118 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0118 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0118 FAIL | -1 cmpu Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile |
| 0.0118 SUCCESS | 1 Possible sub-threshold information |
| 0.0118 SUCCESS | 1 ss |
| 0.0118 SUCCESS | 1 2p Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix profile - support for contrib > 100 billion |
| 0.0118 SUCCESS | 1 3 person mix rem - support for contribution > 100 billion Submitted-results pending. Two person mixed DNA profile |
| 0.0118 SUCCESS | 1 2 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0119 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0119 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0119 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0119 SUCCESS | 1 2p |
| 0.0119 SUCCESS | 1 ss Submitted-results pending. Single Source DNA profile - assumed known contributor |
| 0.0119 SUCCESS | 1 Possible sub-threshold information Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0119 SUCCESS | 1 Mixture-low support for contrib or supports non contrib Submitted-results pending. |
| 0.012 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.012 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.012 SUCCESS | 1 mix Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| 0.012 SUCCESS | 1 2 person mix - supports non contribution Submitted-results pending. |
| 0.0121 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0121 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0121 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0121 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0121 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0121 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0121 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0121 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0121 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0121 SUCCESS | SS DNA profile 9 loci and above LR > 100 billion 1 NCIDD upload single source DNA profile Submitted-results pending. |
| 0.0122 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0122 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile |
| 0.0122 SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile |
| 0.0122 SUCCESS | 1 No statistical interpretation performed |

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| 0.0123 FAIL | Submitted-results pending. -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0123 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0123 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0123 FAIL | -1 cmpu |
| 0.0123 SUCCESS | 1 mix Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion |
| 0.0123 SUCCESS | 1 Mixture-low support for contrib or supports non contrib Submitted-results pending. Two person mixed DNA profile |
| 0.0123 SUCCESS | 1 2 person mix - supports non contribution Submitted-results pending. |
| 0.0124 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0124 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0124 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0124 SUCCESS | 1 mix Submitted-results pending. Three person mixed DNA profile |
| 0.0124 SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile |
| 0.0124 SUCCESS | 3 person mix profile - support for contrib > 100 billion 1 Mixture-low support for contrib or supports non contrib Submitted-results pending. |
| 0.0125 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0125 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0125 SUCCESS | 1 mix Submitted-results pending. Three person mixed DNA profile |
| 0.0125 SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Mixture-low support for contrib or supports non contrib |
| 0.0126 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0126 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0126 SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile |
| 0.0126 SUCCESS | 1 Mixture-low support for contrib or supports non contrib Submitted-results pending. Two person mixed DNA profile |
| 0.0126 SUCCESS | 2 person mix profile - support for contrib > 100 billion 1 Single evidence sample excluded Submitted-results pending. |
| 0.0127 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0127 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0127 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0127 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0127 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison This sample has undergone further processing |
| 0.0128 FAIL | Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion -1 Possible sub-threshold information Semen not detected Submitted as cells |
| 0.0128 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0128 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0128 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

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| 0.0128 | FAIL | Submitted-results pending. -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0128 | SUCCESS | Mixture-low support for contrib or supports non contrib 1 3 person mix - support for contrib 100 000 to 1 million Submitted-results pending. |
| 0.0128 | SUCCESS | 1 Single source 20 loci DNA profile LR > 100 billion Submitted-results pending. Single source DNA profile |
| 0.0128 | SUCCESS | 1 Possible sub-threshold information Sample on hold - awaiting advice Submitted-results pending. |
| 0.0129 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile |
| 0.0129 | SUCCESS | 1 Possible sub-threshold information Submitted-results pending. Single source DNA profile Possible sub-threshold information |
| 0.0129 | SUCCESS | 1 NCIDD upload single source DNA profile Submitted-results pending. |
| 0.013 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.013 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.013 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.013 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.013 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.013 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single Source DNA profile - assumed known contributor |
| 0.013 | SUCCESS | 1 Possible sub-threshold information |
| 0.0131 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0131 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0131 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Two person mixed DNA profile |
| 0.0131 | SUCCESS | 1 2 person mix profile - support for contrib > 100 billion Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd |
| 0.0132 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0132 | SUCCESS | 1 mix Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mixed profile - conditioned on |
| 0.0132 | SUCCESS | 1 3 person mix remaining - supports non contribution Submitted-results pending. |
| 0.0133 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0133 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0133 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0133 | FAIL | -1 cmpu |
| 0.0133 | FAIL | -1 cmpu Submitted-results pending. Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile |
| 0.0133 | SUCCESS | 1 Possible sub-threshold information Submitted-results pending. Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion |
| 0.0133 | SUCCESS | 1 Possible sub-threshold information |

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| | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0133 SUCCESS | 1 3 person mix - low support for contribution Submitted-results pending. |
| 0.0134 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0134 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0134 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile |
| 0.0134 SUCCESS | 1 Single source 20 loci DNA profile LR > 100 billion Submitted-results pending. |
| 0.0134 SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0135 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on |
| 0.0135 FAIL | -1 Mix remaining DNA contrib unsuitable for NCIDD searching Submitted-results pending. Single source DNA profile Possible sub-threshold information |
| 0.0135 SUCCESS | 1 NCIDD upload single source DNA profile Submitted-results pending. |
| 0.0135 SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution Mixture-low support for contrib or supports non contrib |
| 0.0135 SUCCESS | 1 3 person mix - low support for contribution Submitted-results pending. Two person mixed DNA profile |
| 0.0135 SUCCESS | 1 Single evidence sample excluded Semen not detected Submitted as cells |
| 0.0136 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0136 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0136 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0136 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0136 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0136 SUCCESS | 1 Three person mixed DNA profile No statistical interpretation performed Submitted as cells Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0136 SUCCESS | 1 Excluded from mixed DNA profile Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 100 000 to 1 million Mixture-low support for contrib or supports non contrib |
| 0.0136 SUCCESS | 1 Excluded from mixed DNA profile Submitted-results pending. |
| 0.0137 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0137 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0138 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0138 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0138 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0138 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on |
| 0.0138 SUCCESS | 1 Single evidence sample excluded |

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| 0.0139 FAIL | Submitted-results pending. -1 Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile NCIDD upload - mixed DNA profile |
| 0.0139 SUCCESS | 1 Excluded from mixed DNA profile Submitted-results pending. Single source DNA profile |
| 0.0139 SUCCESS | 1 SS DNA profile 9 loci and above LR > 100 billion Submitted-results pending. Three person mixed DNA profile |
| 0.0139 SUCCESS | 3 person mixed profile - conditioned on 1 3 person mix remaining - supports non contribution Submitted-results pending. |
| 0.014 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.014 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.014 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.014 SUCCESS | 1 ss Submitted-results pending. Single source DNA profile Possible sub-threshold information |
| 0.014 SUCCESS | 1 Single Source DNA profile - assumed known contributor Submitted-results pending. Two person mixed DNA profile |
| 0.014 SUCCESS | 2 person mix profile - support for contrib > 100 billion 1 2 person mix - low support for contribution Three person mixed DNA profile |
| 0.014 SUCCESS | 3 person mixed profile - conditioned on 1 3 person mix rem - support for contribution > 100 billion Two person mixed DNA profile |
| 0.014 SUCCESS | 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion 1 Possible sub-threshold information |
| 0.014 SUCCESS | Two person mixed DNA profile 2 person mixed profile - conditioned on Excluded from mixed DNA profile |
| 0.014 SUCCESS | 1 Mix Rem DNA contrib < NCIDD matching Stringency Submitted-results pending. |
| 0.0141 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0141 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted as cells Three person mixed DNA profile |
| 0.0141 SUCCESS | 3 person mixed profile - conditioned on 1 3 person rem- support for contrib 1 billion-100 billion |
| 0.0142 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0142 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile |
| 0.0142 SUCCESS | 1 Possible sub-threshold information Presump. PSA test positive, no sperm found Two person mixed DNA profile |
| 0.0142 SUCCESS | 2 person mixed profile - conditioned on 1 2 person rem- support for contrib 1 million to 1 billion Submitted-results pending. Two person mixed DNA profile |
| 0.0142 SUCCESS | Suspect check inconclusive - mixed DNA profile 1 Suspect check - supports non contribution |
| 0.0143 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0143 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0143 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Two person mixed DNA profile Single source DNA profile NCIDD upload single source DNA profile |
| 0.0143 SUCCESS | 1 Possible sub-threshold information |

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| | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded |
| 0.0143 SUCCESS | 1 Possible sub-threshold information Submitted-results pending. |
| 0.0143 SUCCESS | Single source 20 loci DNA profile LR > 100 billion 1 Possible sub-threshold information Submitted-results pending. |
| 0.0143 SUCCESS | Three person mixed DNA profile 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0144 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0144 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0144 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted as cells Single source DNA profile NCIDD upload single source DNA profile Single Source DNA profile - assumed known contributor |
| 0.0144 SUCCESS | 1 DNA profile removed from NCIDD Submitted-results pending. Interim result- mixed profile obtained. Rework Req'd Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile |
| 0.0144 SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0145 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0145 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0145 SUCCESS | Three person mixed DNA profile 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0146 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0146 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0146 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0146 SUCCESS | 1 Single source DNA profile NCIDD upload single source DNA profile Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Two person mixed DNA profile Single evidence sample excluded This sample has undergone further processing |
| 0.0147 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0147 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0147 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0148 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0148 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0148 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0148 SUCCESS | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0148 SUCCESS | Three person mixed DNA profile 3 person mixed profile - conditioned on 1 3 person mix remaining - supports non contribution Submitted-results pending. |
| 0.0149 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

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| | Submitted-results pending. |
| 0.0149 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0149 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.015 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.015 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.015 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.015 SUCCESS | 1 ss Submitted-results pending. |
| 0.015 SUCCESS | 1 Three person mixed DNA profile Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 |
| 0.015 SUCCESS | 1 Single evidence sample excluded Submitted-results pending. |
| 0.0151 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0151 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0151 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0151 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0151 FAIL | -1 cmpu Submitted-results pending. |
| 0.0152 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0152 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0152 SUCCESS | 1 Two person mixed DNA profile Submitted-results pending. |
| 0.0153 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0153 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0154 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0154 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0154 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0154 SUCCESS | 1 NCIDD upload single source DNA profile Submitted-results pending. |
| 0.0154 SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0155 SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0155 SUCCESS | 1 Two person mixed DNA profile Submitted-results pending. |
| 0.0156 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0156 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution |
| 0.0156 SUCCESS | 1 Excluded from mixed DNA profile Submitted-results pending. Three person mixed DNA profile Excluded from mixed DNA profile |
| 0.0156 SUCCESS | 1 Single evidence sample excluded Submitted-results pending. |
| 0.0157 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0157 SUCCESS | 1 3 person mix - supports non contribution Submitted-results pending. |
| 0.0158 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0158 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

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| | | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion 3 person mix - supports non contribution Sample undergone further work - conditioned 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion 3 person mix rem - support for contribution > 100 billion |
| 0.0158 | SUCCESS | 1 Single evidence sample excluded Submitted-results pending. |
| 0.0159 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.016 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.016 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile |
| 0.016 | SUCCESS | 1 Possible sub-threshold information Submitted-results pending. Micro neg for sperm |
| 0.016 | SUCCESS | 1 Single Source DNA profile - assumed known contributor Submitted-results pending. Three person mixed DNA profile |
| 0.016 | SUCCESS | 1 3 person mix - supports non contribution Submitted-results pending. Two person mixed DNA profile |
| 0.016 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. |
| 0.0161 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile |
| 0.0161 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Two person mixed DNA profile |
| 0.0161 | SUCCESS | 1 2 person mix profile - support for contrib > 100 billion Semen not detected Submitted-results pending. |
| 0.0162 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0162 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0162 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source DNA profile |
| 0.0162 | SUCCESS | 1 NCIDD upload single source DNA profile 2 person mix remaining - supports non contribution Submitted as cells Two person mixed DNA profile 2 person mix - supports non contribution Sample undergone further work - conditioned Two person mixed DNA profile |
| 0.0162 | SUCCESS | 1 2 person mixed profile - conditioned on Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 Mixture-low support for contrib or supports non contrib |
| 0.0162 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile 3 person mix- support for contrib 1 billion - 100 billion 3 person mix profile - support for contrib > 100 billion |
| 0.0162 | SUCCESS | 1 Excluded from mixed DNA profile Submitted-results pending. |
| 0.0163 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0163 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0163 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0163 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0164 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

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| 0.0164 FAIL | -1 cmпу |
| 0.0164 SUCCESS | 1 ss |
| | Submitted-results pending. |
| 0.0164 SUCCESS | 1 Three person mixed DNA profile |
| | Submitted-results pending. |
| 0.0165 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0165 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| | Two person mixed DNA profile |
| | 2 person mixed profile - conditioned on |
| 0.0165 FAIL | -1 Mix remaining DNA contrib unsuitable for NCIDD searching |
| | Single evidence sample excluded |
| | Three person mixed DNA profile |
| | 3 person mix profile - support for contrib > 100 billion |
| 0.0165 SUCCESS | 1 3 person mix profile - support for contrib > 100 billion |
| | Submitted-results pending. |
| 0.0166 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| 0.0166 SUCCESS | 1 Single evidence sample excluded |
| | Submitted-results pending. |
| 0.0167 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0167 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0167 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0167 SUCCESS | 1 mix |
| | Submitted-results pending. |
| 0.0168 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0168 FAIL | -1 cmпу |
| 0.0168 FAIL | -1 cmпу |
| | Submitted as cells, Presump saliva test pending |
| | presump Saliva test positive |
| | Two person mixed DNA profile |
| | 2 person mixed profile - conditioned on |
| 0.0168 SUCCESS | 1 2 person mix rem - support for contribution > 100 billion |
| | Two person mixed DNA profile |
| | 2 person mixed profile - conditioned on |
| | 2 person mix rem - support for contribution > 100 billion |
| 0.0168 SUCCESS | 1 Possible sub-threshold information |
| 0.0169 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0169 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| 0.0169 SUCCESS | 1 3 person mix profile - support for contrib > 100 billion |
| | Submitted-results pending. |
| | Single source DNA profile |
| | Possible sub-threshold information |
| | This sample has undergone further processing |
| | Single source 20 loci DNA profile LR > 100 billion |
| | NCIDD upload single source DNA profile |
| 0.017 SUCCESS | 1 Possible sub-threshold information |
| 0.017 SUCCESS | 1 mix |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| | 3 person mix - support for contrib 10 000 - 100 000 |
| 0.0171 SUCCESS | 1 Mixture-low support for contrib or supports non contrib |
| | Submitted-results pending. |
| 0.0172 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0172 SUCCESS | 1 ss |
| | Submitted-results pending. |
| | Two person mixed DNA profile |
| 0.0172 SUCCESS | 1 2 person mix profile - support for contrib > 100 billion |
| | Submitted-results pending. |
| 0.0173 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0173 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0173 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

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| 0.0182 | SUCCESS | Submitted-results pending. 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0183 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source DNA profile |
| 0.0183 | SUCCESS | 1 NCIDD upload single source DNA profile |
| 0.0183 | SUCCESS | 1 mix Submitted-results pending. |
| 0.0184 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0184 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion Complex mixed profile unsuitable for interp or comparison |
| 0.0184 | SUCCESS | 1 DNA profile removed from NCIDD Submitted-results pending. |
| 0.0185 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0185 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0185 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0186 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0186 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion |
| 0.0186 | SUCCESS | 1 Possible sub-threshold information Submitted-results pending. Three person mixed DNA profile |
| 0.0186 | SUCCESS | 1 3 person mix remaining - supports non contribution Two person mixed DNA profile |
| 0.0186 | SUCCESS | 2 person mixed profile - conditioned on |
| 0.0186 | SUCCESS | 1 2 person mix rem - support for contribution > 100 billion Submitted-results pending. |
| 0.0187 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0187 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Suspect Check Actioned - No Match Suspect Check Actioned - No Match Suspect Check Actioned - No Match Suspect Check Actioned - No Match Suspect check - low support for contribution Micro positive for sperm. Submitted-Results pending Interim result- mixed profile obtained. Rework Reqd Two person mixed DNA profile |
| 0.0187 | FAIL | 2 person mixed profile - conditioned on Excluded from mixed DNA profile Mix remaining DNA contrib unsuitable for NCIDD searching Suspect Check Actioned - No Match Suspect Check Actioned - No Match Suspect Check Actioned - No Match |
| 0.0187 | FAIL | -1 Suspect Check Actioned - No Match Submitted-results pending. |
| 0.0189 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion |
| 0.0189 | SUCCESS | 1 Possible sub-threshold information Submitted-results pending. |
| 0.019 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.019 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0191 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0191 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0192 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

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| 0.0192 | FAIL | Submitted-results pending. -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0193 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0193 | SUCCESS | 1 ss |
| 0.0194 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0195 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0195 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0195 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. Three person mixed DNA profile |
| 0.0195 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion |
| 0.0195 | SUCCESS | 1 Excluded from mixed DNA profile Submitted-results pending. |
| 0.0195 | SUCCESS | 1 Two person mixed DNA profile Submitted-results pending. |
| 0.0196 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source DNA profile Single source 20 loci DNA profile LR > 100 billion |
| 0.0197 | SUCCESS | 1 Possible sub-threshold information Submitted-results pending. Three person mixed DNA profile |
| 0.0197 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile Excluded from mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0197 | SUCCESS | 1 3 person mix - support for contribution 100 to 1000 Submitted-results pending. |
| 0.0198 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0198 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile |
| 0.0198 | SUCCESS | 1 3 person mix - support for contrib 10 000 - 100 000 Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0198 | SUCCESS | 1 Mixture-low support for contrib or supports non contrib Two person mixed DNA profile |
| 0.0198 | SUCCESS | 1 2 person mixed profile - conditioned on Submitted as cells |
| 0.0199 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile |
| 0.0199 | SUCCESS | 1 3 person mix - low support for contribution Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0199 | SUCCESS | 1 Mixture-low support for contrib or supports non contrib Submitted-results pending. Three person mixed DNA profile |
| 0.0199 | SUCCESS | 1 Single evidence sample excluded Submitted-results pending. |
| 0.02 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile |
| 0.02 | SUCCESS | 1 Suspect Check Actioned - No Match Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion |
| 0.0201 | SUCCESS | 1 Excluded from mixed DNA profile Submitted-results pending. |
| 0.0202 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

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| 0.0202 | FAIL | Submitted-results pending. -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0202 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source DNA profile NCIDD Intel upload - single source partial profile |
| 0.0202 | SUCCESS | 1 NCIDD upload single source DNA profile Submitted-results pending. |
| 0.0202 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0203 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0203 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile Excluded from mixed DNA profile |
| 0.0203 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0203 | SUCCESS | 1 ss Submitted-results pending. Three person mixed DNA profile |
| 0.0203 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix- support for contrib 1 billion - 100 billion |
| 0.0203 | SUCCESS | 1 2 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0204 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion This sample has undergone further processing |
| 0.0204 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded |
| 0.0204 | FAIL | -1 3 Person Mix Rem contrib unsuitable for NCIDD Submitted-results pending. |
| 0.0205 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0205 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0205 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile |
| 0.0205 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0205 | SUCCESS | 1 Single evidence sample excluded Submitted-results pending. Two person mixed DNA profile |
| 0.0205 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. |
| 0.0206 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0207 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0207 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0207 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0207 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0208 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source DNA profile |
| 0.0208 | SUCCESS | 1 NCIDD upload single source DNA profile Submitted-results pending. Three person mixed DNA profile |
| 0.0208 | SUCCESS | 1 No statistical interpretation performed |

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| | | Two person mixed DNA profile |
| | | 2 person mix profile - support for contrib > 100 billion |
| | | 2 person mix profile - support for contrib > 100 billion |
| | | Excluded from mixed DNA profile |
| 0.0208 | SUCCESS | 1 2 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0209 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.021 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | | Three person mixed DNA profile |
| 0.021 | SUCCESS | 3 person mixed profile - conditioned on 1 Excluded from mixed DNA profile Submitted-results pending. |
| | | Three person mixed DNA profile |
| 0.0211 | SUCCESS | 3 person mixed profile - conditioned on 1 Mixture-low support for contrib or supports non contrib Submitted-results pending. |
| | | Two person mixed DNA profile |
| 0.0211 | SUCCESS | 1 2 person mix - support for contrib 1 million - 1 billion Submitted-results pending. |
| | | Two person mixed DNA profile |
| 0.0211 | SUCCESS | 2 person mix profile - support for contrib > 100 billion |
| | | 1 Single evidence sample excluded |
| | | Two person mixed DNA profile |
| 0.0211 | SUCCESS | 2 person mix profile - support for contrib > 100 billion |
| | | 1 Excluded from mixed DNA profile Submitted-results pending. |
| 0.0212 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0212 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0212 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | | Three person mixed DNA profile |
| 0.0212 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0213 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0213 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0215 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0215 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0215 | SUCCESS | 1 mix |
| 0.0215 | SUCCESS | 1 mix Submitted-results pending. |
| 0.0216 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | | Two person mixed DNA profile |
| 0.0216 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. |
| 0.0218 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | | Two person mixed DNA profile |
| | | 2 person mixed profile - conditioned on |
| 0.0218 | FAIL | -1 Mix remaining DNA contrib unsuitable for NCIDD searching Submitted-results pending. |
| | | Three person mixed DNA profile |
| | | 3 person mix - supports non contribution |
| 0.0218 | SUCCESS | 1 3 person mix - supports non contribution Submitted-results pending. |
| 0.0219 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | | Single source DNA profile |
| | | Possible sub-threshold information |
| 0.0219 | SUCCESS | 1 NCIDD upload single source DNA profile Submitted-results pending. |
| | | Three person mixed DNA profile |
| | | 3 person mixed profile - conditioned on |
| 0.0219 | SUCCESS | 1 Single evidence sample excluded Submitted-results pending. |
| 0.022 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

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| 0.022 FAIL | Submitted-results pending. |
| 0.022 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | -1 cmphu |
| | Submitted-results pending. |
| | Two person mixed DNA profile |
| | 2 person mix profile - support for contrib > 100 billion |
| 0.022 SUCCESS | 1 2 person mix - low support for contribution |
| | Submitted-results pending. |
| | Two person mixed DNA profile |
| 0.022 SUCCESS | 1 No statistical interpretation performed |
| | Submitted-results pending. |
| 0.0221 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0221 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0222 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0222 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0222 SUCCESS | 1 Single source DNA profile |
| | This sample has undergone further processing |
| | Three person mixed DNA profile |
| | 3 person mix profile - support for contrib > 100 billion |
| | 3 person mix - support for contrib 10 000 - 100 000 |
| 0.0222 SUCCESS | 1 Mixture-low support for contrib or supports non contrib |
| | Submitted-results pending. |
| 0.0223 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0223 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0223 SUCCESS | Single source DNA profile |
| | 1 Single source 20 loci DNA profile LR > 100 billion |
| | Submitted-results pending. |
| 0.0224 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| 0.0225 SUCCESS | 1 No statistical interpretation performed |
| | Submitted-results pending. |
| 0.0226 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0226 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Three person mixed DNA profile |
| | 3 person mixed profile - conditioned on |
| 0.0226 SUCCESS | 1 Remaining contribution - inconclusive |
| | Submitted-results pending. |
| 0.0227 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Three person mixed DNA profile |
| | 3 person mix profile - support for contrib > 100 billion |
| | 3 person mix - support for contribution 1000 to 10 000 |
| | 3 person mix - support for contribution 100 to 1000 |
| 0.0227 SUCCESS | 1 3 person mix - low support for contribution |
| | Submitted-results pending. |
| 0.0228 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0228 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Three person mixed DNA profile |
| | No statistical interpretation performed |
| | Sample undergone further work - conditioned |
| | Three person mixed DNA profile |
| | 3 person mixed profile - conditioned on |
| 0.0228 SUCCESS | 1 3 person mix remaining - supports non contribution |
| | Submitted-results pending. |
| 0.0229 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| | Two person mixed DNA profile |
| 0.0229 SUCCESS | 1 2 person mix - supports non contribution |
| | Submitted-results pending. |
| 0.023 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| 0.023 SUCCESS | 1 3 person mix - supports non contribution |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| 0.0231 SUCCESS | 1 No statistical interpretation performed |

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| | | Submitted-results pending. Two person mixed DNA profile |
| 0.0231 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. |
| 0.0232 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion |
| 0.0232 | SUCCESS | 1 Mixture-low support for contrib or supports non contrib |
| 0.0234 | SUCCESS | 1 mix Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion |
| 0.0234 | SUCCESS | 1 Possible sub-threshold information Submitted-results pending. |
| 0.0235 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0235 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 10 000 - 100 000 |
| 0.0235 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion |
| 0.0235 | SUCCESS | 1 mix Submitted-results pending. Three person mixed DNA profile |
| 0.0235 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. |
| 0.0235 | SUCCESS | Three person mixed DNA profile 1 No statistical interpretation performed Submitted-results pending. |
| 0.0236 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 1 million - 1 billion This sample has undergone further processing |
| 0.0238 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0239 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 100 to 1000 |
| 0.0239 | SUCCESS | 1 3 person mix - supports non contribution Three person mixed DNA profile 3 person mixed profile - conditioned on |
| 0.0239 | SUCCESS | 1 Cond mix rem-low supp for contrib or supp non contrib Submitted-results pending. Three person mixed DNA profile Cond mix rem-low supp for contrib or supp non contrib |
| 0.024 | SUCCESS | 1 3 person mixed profile - conditioned on Submitted-results pending. |
| 0.0241 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0241 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0241 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile |
| 0.0241 | SUCCESS | 1 SS DNA profile 9 loci and above LR > 100 billion |

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| | Interim result- mixed profile obtained. Rework Reqd |
| | Three person mixed DNA profile |
| | 3 person mixed profile - conditioned on |
| | 3 person mix remaining - supports non contribution |
| | 3 person mix remaining - supports non contribution |
| | Single evidence sample excluded |
| | Suspect check - support for contrib 100 000 - 1 million |
| | Suspect check - supports non contribution |
| | Suspect check - supports non contribution |
| | Suspect Check Actioned - No Match |
| | Suspect Check Actioned - No Match |
| | Suspect Check Actioned - No Match |
| | Suspect check - supports non contribution |
| | Suspect check - supports non contribution |
| 0.0241 SUCCESS | 1 Suspect Check Actioned - No Match |
| | Submitted-results pending. |
| 0.0242 SUCCESS | 1 Two person mixed DNA profile |
| | Semen not detected |
| | Submitted as cells |
| 0.0243 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0244 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0244 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0244 SUCCESS | 1 Single source DNA profile |
| | Submitted-results pending. |
| 0.0244 SUCCESS | 1 Three person mixed DNA profile |
| | Submitted-results pending. |
| 0.0245 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0245 SUCCESS | 1 ss |
| | Submitted-results pending. |
| 0.0246 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0246 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0246 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0247 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0247 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| 0.0247 SUCCESS | 1 No statistical interpretation performed |
| | Submitted-results pending. |
| 0.0248 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0248 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| | 3 person mixed profile - conditioned on |
| | Mixture-low support for contrib or supports non contrib |
| | Single evidence sample excluded |
| | This sample has undergone further processing |
| 0.0248 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| | Single source 20 loci DNA profile LR > 100 billion |
| | Possible sub-threshold information |
| 0.0248 SUCCESS | 1 NCIDD upload single source DNA profile |
| 0.0248 SUCCESS | 1 mix |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| 0.0248 SUCCESS | 1 No statistical interpretation performed |
| | Submitted-results pending. |
| 0.0249 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0249 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0249 FAIL | -1 cmpu |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| 0.0249 SUCCESS | 1 No statistical interpretation performed |
| | Submitted-results pending. |
| 0.0252 SUCCESS | 1 Three person mixed DNA profile |

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| 0.0253 FAIL | Submitted-results pending. -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0253 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0255 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0255 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0256 SUCCESS | 1 Single evidence sample excluded |
| 0.0256 SUCCESS | 1 mix Submitted-results pending. |
| 0.0256 SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0257 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0257 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Two person mixed DNA profile |
| 0.0257 SUCCESS | 1 2 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0258 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0258 SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0259 SUCCESS | 1 3 person mix - support for contrib 100 000 to 1 million Submitted-results pending. |
| 0.026 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.026 SUCCESS | 1 Single source 20 loci DNA profile LR > 100 billion Submitted-results pending. |
| 0.0261 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0261 SUCCESS | 1 Mixture-low support for contrib or supports non contrib Submitted-results pending. |
| 0.0262 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0263 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0263 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0263 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0265 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0266 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0267 SUCCESS | 1 3 person mix - supports non contribution Submitted-results pending. Three person mixed DNA profile |
| 0.0267 SUCCESS | 1 No statistical interpretation performed Submitted-results pending. |
| 0.027 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile |
| 0.0271 SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion |
| 0.0272 SUCCESS | 1 Possible sub-threshold information Submitted-results pending. |
| 0.0273 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile |
| 0.0273 SUCCESS | 1 Possible sub-threshold information Submitted-results pending. |
| 0.0274 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

| | | |
|--------|---------|--|
| | | Semen not detected |
| | | Submitted as cells |
| | | Three person mixed DNA profile |
| | | 3 person mixed profile - conditioned on |
| 0.0274 | SUCCESS | 1 3 person mix rem - support for contribution > 100 billion |
| | | Three person mixed DNA profile |
| | | 3 person mixed profile - conditioned on |
| 0.0274 | SUCCESS | 1 Single evidence sample excluded |
| | | Semen not detected |
| | | Submitted as cells |
| | | Three person mixed DNA profile |
| | | 3 person mixed profile - conditioned on |
| 0.0275 | SUCCESS | 1 Cond mix rem-low supp for contrib or supp non contrib |
| | | Submitted-results pending. |
| | | Two person mixed DNA profile |
| | | 2 person mix profile - support for contrib > 100 billion |
| | | Mixture-low support for contrib or supports non contrib |
| | | Suspect check - low support or non contrib |
| | | Suspect check - low support or non contrib |
| 0.0275 | SUCCESS | 1 Suspect check - low support or non contrib |
| | | Submitted-results pending. |
| 0.0276 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0276 | FAIL | -1 cmpu |
| | | Submitted-results pending. |
| | | SS DNA profile 9 loci and above LR > 100 billion |
| 0.0276 | SUCCESS | 1 NCIDD upload single source DNA profile |
| | | Submitted-results pending. |
| 0.0277 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | | Submitted as cells, Presump saliva test pending |
| | | presump Saliva test positive |
| | | Two person mixed DNA profile |
| | | 2 person mixed profile - conditioned on |
| 0.0277 | SUCCESS | 1 2 person mix rem - support for contribution > 100 billion |
| | | presump Saliva test positive |
| | | Three person mixed DNA profile |
| | | 3 person mixed profile - conditioned on |
| 0.0278 | SUCCESS | 1 3 person mix remaining - support for contrib 100 to 1000 |
| | | Submitted-results pending. |
| | | Three person mixed DNA profile |
| | | 3 person mixed profile - conditioned on |
| 0.0278 | SUCCESS | 1 3 person mix remaining - low support for contrib |
| | | Submitted-results pending. |
| | | Three person mixed DNA profile |
| | | Single evidence sample excluded |
| 0.0278 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion |
| | | Submitted as cells |
| 0.0279 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | | Submitted-results pending. |
| 0.0279 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | | Submitted-results pending. |
| 0.028 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.028 | SUCCESS | 1 mix |
| | | Submitted-results pending. |
| 0.0281 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | | Submitted-results pending. |
| | | Single source 20 loci DNA profile LR > 100 billion |
| 0.0281 | SUCCESS | 1 Possible sub-threshold information |
| | | Submitted for cells. Presumptive saliva test pending. |
| | | presump Saliva test positive |
| 0.0284 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0285 | SUCCESS | 1 mix |
| | | Submitted-results pending. |
| | | Three person mixed DNA profile |
| | | 3 person mixed profile - conditioned on |
| 0.0287 | SUCCESS | 1 Cond mix rem-low supp for contrib or supp non contrib |
| | | Submitted-results pending. |
| | | Three person mixed DNA profile |
| 0.0287 | SUCCESS | 1 No statistical interpretation performed |
| | | Submitted-results pending. |
| 0.0289 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | | Submitted-results pending. |
| | | Interim result- mixed profile obtained. Rework Req'd |
| 0.0289 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

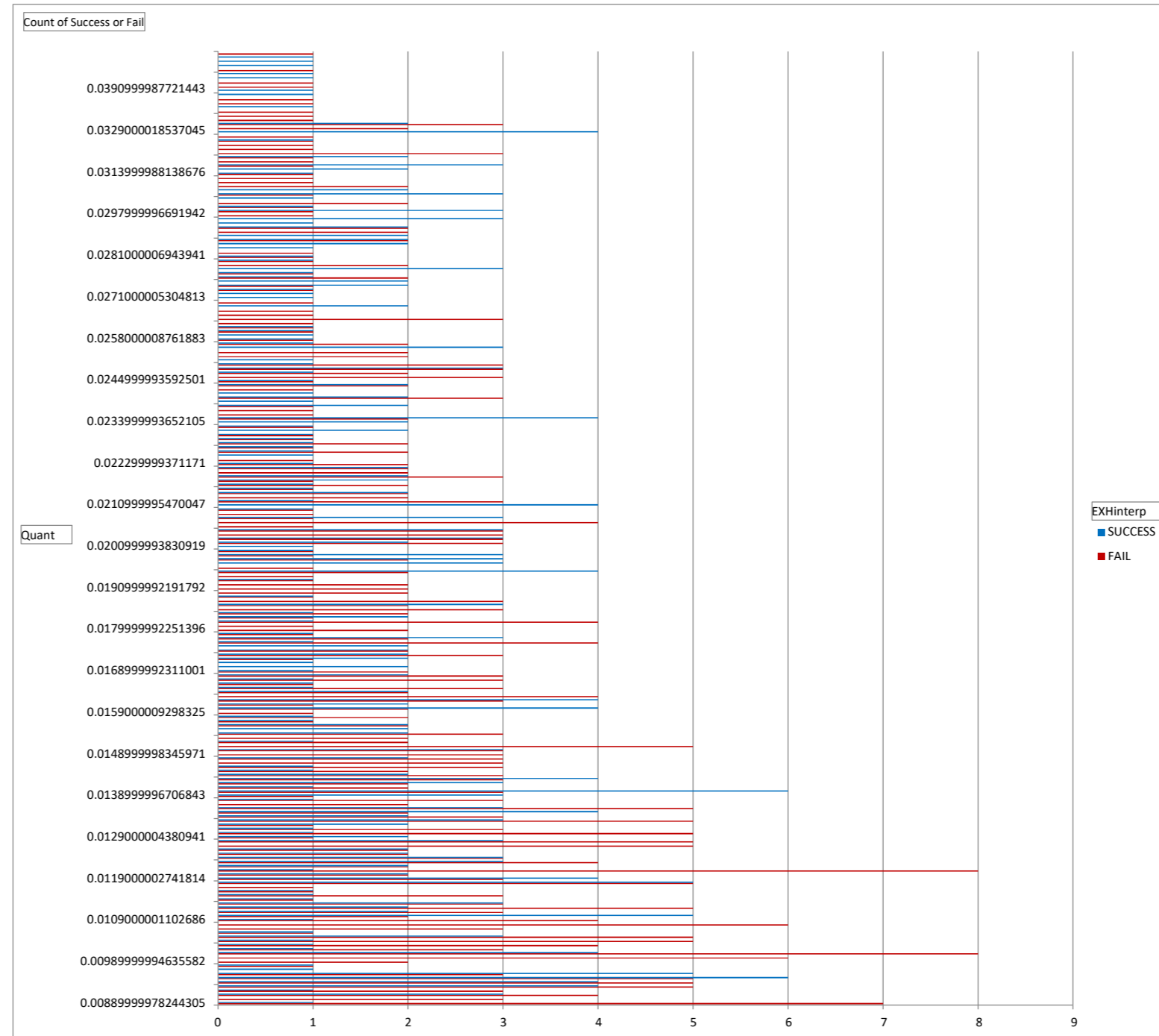
| | | |
|--------|---------|---|
| | | Presumptive blood test pos. Submitted-results pending. Two person mixed DNA profile |
| 0.0289 | SUCCESS | 2 person mixed profile - conditioned on 1 2 person mix rem - support for contribution > 100 billion Submitted-results pending. |
| 0.0289 | SUCCESS | 1 SS DNA profile 9 loci and above LR > 100 billion Submitted-results pending. |
| 0.029 | SUCCESS | 1 Single source 20 loci DNA profile LR > 100 billion Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion Submitted as cells, Presump saliva test pending |
| 0.029 | SUCCESS | 1 presump Saliva test positive Submitted-results pending. |
| 0.0292 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0292 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0293 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0293 | FAIL | -1 cmpu Submitted-results pending. |
| 0.0293 | SUCCESS | 1 Three person mixed DNA profile Two person mixed DNA profile 2 person mixed profile - conditioned on |
| 0.0293 | SUCCESS | 1 Excluded from mixed DNA profile |
| 0.0294 | SUCCESS | 1 mix Submitted as cells Two person mixed DNA profile 2 person mixed profile - conditioned on |
| 0.0296 | SUCCESS | 1 2 person mix rem - support for contribution > 100 billion Submitted-results pending. Single source DNA profile |
| 0.0296 | SUCCESS | 1 Possible sub-threshold information Submitted-results pending. |
| 0.0296 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0298 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0299 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0299 | SUCCESS | 1 mix Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on |
| 0.0299 | SUCCESS | 1 Possible sub-threshold information Submitted-results pending. Two person mixed DNA profile |
| 0.0299 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. |
| 0.03 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.03 | SUCCESS | 1 3 person mix - low support for contribution Submitted-results pending. |
| 0.0301 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0301 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted as cells Three person mixed DNA profile |
| 0.0304 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. |
| 0.0305 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted as cells Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| 0.0305 | SUCCESS | 1 3 person mix - support for contrib 1 million - 1 billion Submitted-results pending. Three person mixed DNA profile |
| 0.0305 | SUCCESS | 1 3 person mix - support for contribution 1000 to 10 000 |

| | |
|----------------|--|
| | Suspect check - supports non contribution |
| | Suspect check - supports non contribution |
| | Suspect check - supports non contribution |
| | Suspect check - supports non contribution |
| | Suspect check - supports non contribution |
| | Suspect check - supports non contribution |
| | Three person mixed DNA profile |
| | 3 person mixed profile - conditioned on |
| | Suspect check- support for contribution 10 000 to 100 000 |
| | Mixture-low support for contrib or supports non contrib |
| | Suspect check - supports non contribution |
| 0.0305 SUCCESS | 1 Suspect check - supports non contribution |
| 0.0306 SUCCESS | 1 ss |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| | 3 person mixed profile - conditioned on |
| 0.0306 SUCCESS | 1 3 person mix rem - support for contribution > 100 billion |
| | Submitted-results pending. |
| 0.0309 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0309 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0311 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0312 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0314 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| | Single Source DNA profile - assumed known contributor |
| | Possible sub-threshold information |
| 0.0314 SUCCESS | 1 NCIDD upload single source DNA profile |
| | Submitted-results pending. |
| | Single source DNA profile |
| 0.0315 SUCCESS | 1 NCIDD upload single source DNA profile |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| | 3 person mixed profile - conditioned on |
| | 3 person mix remaining- support for contrib 1000 to 10000 |
| | Single evidence sample excluded |
| 0.0315 SUCCESS | 1 3 person mix remaining - supports non contribution |
| | Submitted-results pending. |
| 0.0316 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| | 3 person mix profile - support for contrib > 100 billion |
| | 3 person mix - support for contrib 1 million - 1 billion |
| 0.0316 SUCCESS | 1 Excluded from mixed DNA profile |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| | 3 person mix profile - support for contrib > 100 billion |
| | Single evidence sample excluded |
| 0.0316 SUCCESS | 1 3 person mix - support for contribution 100 to 1000 |
| | Submitted-results pending. |
| | Three person mixed DNA profile |
| | 3 person mixed profile - conditioned on |
| | 3 person mix remaining- support for contrib 1000 to 10000 |
| 0.0316 SUCCESS | 1 3 person mix remaining - supports non contribution |
| | Submitted-results pending. |
| 0.0318 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0319 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0319 SUCCESS | 1 Three person mixed DNA profile |
| | Three person mixed DNA profile |
| | 3 person mix profile - support for contrib > 100 billion |
| | 3 person mix- support for contrib 1 billion - 100 billion |
| 0.0319 SUCCESS | 1 Excluded from mixed DNA profile |
| | Submitted-results pending. |
| 0.0321 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0321 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| | Submitted-results pending. |
| 0.0321 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

| | | |
|--------|---------|--|
| 0.0322 | FAIL | Submitted-results pending. -1 Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells |
| 0.0325 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells |
| 0.0327 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - support for contrib 1 million - 1 billion |
| 0.0327 | SUCCESS | 1 2 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 Person Mix Rem contrib unsuitable for NCIDD |
| 0.0328 | FAIL | -1 3 person mix remaining - low support for contrib Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile |
| 0.0329 | SUCCESS | 1 DNA profile removed from NCIDD Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib |
| 0.0329 | SUCCESS | 1 3 person mix - support for contribution 100 to 1000 Submitted-results pending. |
| 0.0329 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| 0.0329 | SUCCESS | 1 2 person mix - supports non contribution Submitted-results pending. |
| 0.033 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.033 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0346 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0346 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0346 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted as cells, Presump saliva test pending Presump Saliva test negative Three person mixed DNA profile 3 person mixed profile - conditioned on |
| 0.0346 | SUCCESS | 1 Single evidence sample excluded Submitted-results pending. Three person mixed DNA profile |
| 0.0346 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0349 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0362 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0364 | FAIL | -1 cmpu Submitted-results pending. |
| 0.0368 | SUCCESS | 1 Three person mixed DNA profile Semen not detected Submitted as cells |
| 0.0369 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0382 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on |
| 0.0384 | SUCCESS | 1 3 person mix - supports non contribution Submitted-results pending. |
| 0.0391 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0396 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0397 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

| | | |
|--------|---------|---|
| 0.0446 | SUCCESS | <p>Submitted-results pending. Single source DNA profile 1 NCIDD upload single source DNA profile Submitted-results pending. Two person mixed DNA profile Single evidence sample excluded 2 person mix profile - support for contrib > 100 billion This sample has undergone further processing Three person mixed DNA profile 3 person mixed profile - conditioned on</p> |
| 0.0474 | SUCCESS | <p>1 3 person mix rem - support for contribution > 100 billion Submitted-results pending.</p> |
| 0.0533 | FAIL | <p>-1 Complex mixed profile unsuitable for interp or comparison Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 1000 to 10 000</p> |
| 0.0577 | SUCCESS | <p>1 3 person mix - supports non contribution Submitted-results pending. Two person mixed DNA profile</p> |
| 0.0611 | SUCCESS | <p>1 2 person mix profile - support for contrib > 100 billion Submitted-results pending.</p> |
| 0.0743 | SUCCESS | <p>1 Single source 20 loci DNA profile LR > 100 billion Submitted-results pending.</p> |
| 0.0907 | FAIL | <p>-1 Complex mixed profile unsuitable for interp or comparison</p> |

| Count of Success or Fail | Column Labels | FAIL | SUCCESS | Grand Total |
|--------------------------|---------------|------|---------|-------------|
| 0.0089 | | 7 | 1 | 8 |
| 0.009 | | 3 | | 3 |
| 0.0091 | | 4 | 3 | 7 |
| 0.0092 | | 3 | 1 | 4 |
| 0.0093 | | 5 | 4 | 9 |
| 0.0094 | | 5 | 4 | 9 |
| 0.0095 | | 5 | 6 | 11 |
| 0.0096 | | 3 | 5 | 8 |
| 0.0097 | | | 1 | 1 |
| 0.0098 | | 1 | 1 | 2 |
| 0.0099 | | 2 | | 2 |
| 0.01 | | 6 | | 6 |
| 0.0101 | | 8 | 4 | 12 |
| 0.0102 | | 3 | 1 | 4 |
| 0.0103 | | 4 | 1 | 5 |
| 0.0104 | | 5 | 1 | 6 |
| 0.0105 | | 5 | 3 | 8 |
| 0.0106 | | 1 | 1 | 2 |
| 0.0107 | | 3 | | 3 |
| 0.0108 | | 6 | | 6 |
| 0.0109 | | 4 | 1 | 5 |
| 0.011 | | 2 | 5 | 7 |
| 0.0111 | | 3 | 2 | 5 |
| 0.0112 | | 5 | 2 | 7 |
| 0.0113 | | 3 | 3 | 6 |
| 0.0114 | | 1 | 1 | 2 |
| 0.0115 | | 3 | 1 | 4 |
| 0.0116 | | 1 | 1 | 2 |
| 0.0117 | | 1 | | 1 |
| 0.0118 | | 5 | 5 | 10 |
| 0.0119 | | 3 | 4 | 7 |
| 0.012 | | 2 | 2 | 4 |
| 0.0121 | | 8 | 1 | 9 |
| 0.0122 | | 2 | 2 | 4 |
| 0.0123 | | 4 | 3 | 7 |
| 0.0124 | | 3 | 3 | 6 |
| 0.0125 | | 2 | 2 | 4 |
| 0.0126 | | 2 | 2 | 4 |
| 0.0127 | | 5 | | 5 |
| 0.0128 | | 5 | 3 | 8 |
| 0.0129 | | 1 | 2 | 3 |
| 0.013 | | 5 | 1 | 6 |
| 0.0131 | | 3 | 1 | 4 |
| 0.0132 | | 1 | 2 | 3 |
| 0.0133 | | 5 | 3 | 8 |
| 0.0134 | | 3 | 2 | 5 |
| 0.0135 | | 2 | 4 | 6 |
| 0.0136 | | 5 | 3 | 8 |
| 0.0137 | | 2 | | 2 |
| 0.0138 | | 3 | 1 | 4 |
| 0.0139 | | 1 | 3 | 4 |
| 0.014 | | 3 | 6 | 9 |
| 0.0141 | | 2 | 1 | 3 |
| 0.0142 | | 2 | 3 | 5 |
| 0.0143 | | 3 | 4 | 7 |
| 0.0144 | | 3 | 2 | 5 |
| 0.0145 | | 2 | 1 | 3 |
| 0.0146 | | 3 | 1 | 4 |
| 0.0147 | | 3 | | 3 |
| 0.0148 | | 3 | 2 | 5 |
| 0.0149 | | 3 | | 3 |
| 0.015 | | 3 | 3 | 6 |
| 0.0151 | | 5 | | 5 |
| 0.0152 | | 2 | 1 | 3 |
| 0.0153 | | 2 | | 2 |
| 0.0154 | | 3 | 2 | 5 |
| 0.0155 | | | 2 | 2 |
| 0.0156 | | 2 | 2 | 4 |
| 0.01569999 | | 1 | 1 | 2 |
| 0.01579999 | | 2 | 1 | 3 |
| 0.01590001 | | 1 | | 1 |
| 0.01600001 | | 2 | 4 | 6 |
| 0.01610001 | | 1 | 2 | 3 |
| 0.0162 | | 3 | 4 | 7 |
| 0.0163 | | 4 | | 4 |
| 0.0164 | | 2 | 2 | 4 |
| 0.0165 | | 3 | 1 | 4 |
| 0.0166 | | 1 | 1 | 2 |
| 0.0167 | | 3 | 1 | 4 |
| 0.01679999 | | 3 | 2 | 5 |
| 0.01689999 | | 2 | 1 | 3 |
| 0.01700001 | | | 2 | 2 |
| 0.01710001 | | | 1 | 1 |
| 0.01720001 | | 1 | 2 | 3 |



| | | | |
|-------------|---|---|---|
| 0.0173 | 3 | 2 | 5 |
| 0.0174 | 2 | 2 | 4 |
| 0.0175 | 2 | 2 | 2 |
| 0.0176 | 4 | 1 | 5 |
| 0.0178 | 2 | 3 | 5 |
| 0.017899999 | 1 | 1 | 2 |
| 0.017999999 | 2 | | 2 |
| 0.018100001 | 1 | | 1 |
| 0.018200001 | 4 | 1 | 5 |
| 0.018300001 | 1 | 2 | 3 |
| 0.0184 | 2 | 1 | 3 |
| 0.0185 | 3 | | 3 |
| 0.0186 | 2 | 3 | 5 |
| 0.0187 | 3 | | 3 |
| 0.0189 | 1 | 1 | 2 |
| 0.018999999 | 2 | | 2 |
| 0.019099999 | 2 | | 2 |
| 0.019200001 | 2 | | 2 |
| 0.019300001 | 1 | 1 | 2 |
| 0.019400001 | 1 | | 1 |
| 0.0195 | 2 | 4 | 6 |
| 0.0196 | 1 | | 1 |
| 0.0197 | | 3 | 3 |
| 0.0198 | 2 | 3 | 5 |
| 0.0199 | 1 | 3 | 4 |
| 0.02 | 1 | 1 | 2 |
| 0.020099999 | | 1 | 1 |
| 0.020199999 | 3 | 2 | 5 |
| 0.020300001 | 3 | 3 | 6 |
| 0.020400001 | 3 | | 3 |
| 0.020500001 | 3 | 3 | 6 |
| 0.0206 | 1 | | 1 |
| 0.0207 | 4 | | 4 |
| 0.0208 | 1 | 3 | 4 |
| 0.0209 | 1 | | 1 |
| 0.021 | 1 | 1 | 2 |
| 0.0211 | | 4 | 4 |
| 0.021199999 | 3 | 1 | 4 |
| 0.021299999 | 2 | | 2 |
| 0.021500001 | 2 | 2 | 4 |
| 0.021600001 | 1 | 1 | 2 |
| 0.0218 | 2 | 1 | 3 |
| 0.0219 | 1 | 2 | 3 |
| 0.022 | 3 | 2 | 5 |
| 0.0221 | 2 | | 2 |
| 0.0222 | 2 | 2 | 4 |
| 0.022299999 | 2 | 1 | 3 |
| 0.022399999 | 1 | | 1 |
| 0.022500001 | | 1 | 1 |
| 0.022600001 | 2 | 1 | 3 |
| 0.022700001 | 1 | 1 | 2 |
| 0.0228 | 2 | 1 | 3 |
| 0.0229 | 1 | 1 | 2 |
| 0.023 | 1 | 1 | 2 |
| 0.0231 | | 2 | 2 |
| 0.0232 | 1 | 1 | 2 |
| 0.023399999 | | 2 | 2 |
| 0.023499999 | 2 | 4 | 6 |
| 0.023600001 | 1 | | 1 |
| 0.023800001 | 1 | | 1 |

| | | | |
|--------------------|------------|------------|------------|
| 0.0239 | 1 | 2 | 3 |
| 0.024 | | 1 | 1 |
| 0.0241 | 3 | 2 | 5 |
| 0.0242 | | 1 | 1 |
| 0.0243 | 1 | | 1 |
| 0.0244 | 2 | 2 | 4 |
| 0.024499999 | 1 | 1 | 2 |
| 0.024599999 | 3 | | 3 |
| 0.024700001 | 2 | 1 | 3 |
| 0.024800001 | 3 | 3 | 6 |
| 0.024900001 | 3 | 1 | 4 |
| 0.0252 | | 1 | 1 |
| 0.0253 | 2 | | 2 |
| 0.0255 | 2 | | 2 |
| 0.025599999 | | 3 | 3 |
| 0.025699999 | 2 | 1 | 3 |
| 0.025800001 | 1 | 1 | 2 |
| 0.025900001 | | 1 | 1 |
| 0.026000001 | 1 | 1 | 2 |
| 0.0261 | 1 | 1 | 2 |
| 0.0262 | 1 | | 1 |
| 0.0263 | 3 | | 3 |
| 0.0265 | 1 | | 1 |
| 0.0266 | 1 | | 1 |
| 0.026699999 | | 2 | 2 |
| 0.027000001 | 1 | | 1 |
| 0.027100001 | | 1 | 1 |
| 0.0272 | | 1 | 1 |
| 0.0273 | 1 | 1 | 2 |
| 0.0274 | 1 | 2 | 3 |
| 0.0275 | | 2 | 2 |
| 0.0276 | 2 | 1 | 3 |
| 0.0277 | 1 | 1 | 2 |
| 0.027799999 | | 3 | 3 |
| 0.027899999 | 2 | | 2 |
| 0.028000001 | 1 | 1 | 2 |
| 0.028100001 | 1 | 1 | 2 |
| 0.0284 | 1 | | 1 |
| 0.0285 | | 1 | 1 |
| 0.0287 | | 2 | 2 |
| 0.028899999 | 2 | 2 | 4 |
| 0.028999999 | | 2 | 2 |
| 0.029200001 | 2 | | 2 |
| 0.029300001 | 2 | 2 | 4 |
| 0.0294 | | 1 | 1 |
| 0.0296 | | 3 | 3 |
| 0.0298 | 1 | | 1 |
| 0.029899999 | 1 | 3 | 4 |
| 0.029999999 | 1 | 1 | 2 |
| 0.030099999 | 2 | | 2 |
| 0.030400001 | | 1 | 1 |
| 0.0305 | 1 | 3 | 4 |
| 0.0306 | | 2 | 2 |
| 0.0309 | 2 | | 2 |
| 0.031099999 | 1 | | 1 |
| 0.031199999 | 1 | | 1 |
| 0.031399999 | 1 | 1 | 2 |
| 0.031500001 | | 2 | 2 |
| 0.031599998 | 1 | 3 | 4 |
| 0.031800002 | 1 | | 1 |
| 0.0319 | 1 | 2 | 3 |
| 0.032099999 | 3 | | 3 |
| 0.032200001 | 1 | | 1 |
| 0.032499999 | 1 | | 1 |
| 0.032699998 | 1 | 1 | 2 |
| 0.0328 | 1 | | 1 |
| 0.032900002 | | 4 | 4 |
| 0.033 | 2 | | 2 |
| 0.034600001 | 3 | 2 | 5 |
| 0.034899998 | 1 | | 1 |
| 0.036200002 | 1 | | 1 |
| 0.036400001 | 1 | | 1 |
| 0.036800001 | | 1 | 1 |
| 0.036899999 | 1 | | 1 |
| 0.038199998 | 1 | | 1 |
| 0.038400002 | | 1 | 1 |
| 0.039099999 | | 1 | 1 |
| 0.0396 | 1 | | 1 |
| 0.039700001 | 1 | | 1 |
| 0.044599999 | | 1 | 1 |
| 0.047400001 | | 1 | 1 |
| 0.053300001 | 1 | | 1 |
| 0.057700001 | | 1 | 1 |
| 0.061099999 | | 1 | 1 |
| 0.074299999 | | 1 | 1 |
| 0.090700001 | 1 | | 1 |
| Grand Total | 432 | 320 | 752 |

| Quant | EXHinterp Success (+1) or Fail (-1) | EXH |
|--------|-------------------------------------|--|
| 0.009 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0112 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0118 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0126 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0131 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0142 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0143 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0169 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0174 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0194 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0255 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Hair located. Submitted-results pending |
| 0.0089 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Labelling discrepancy Submitted-results pending. |
| 0.011 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending |
| 0.0093 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending |
| 0.0112 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison This sample has undergone further processing Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion |
| 0.0128 | FAIL | -1 Possible sub-threshold information Sample on hold - awaiting advice Submitted-results pending. |
| 0.0129 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells |
| 0.0109 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells |
| 0.0128 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells |
| 0.0136 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells |
| 0.0243 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells |
| 0.0325 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells |
| 0.0327 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted as cells |
| 0.0369 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Semen not detected Submitted-results pending. |
| 0.0162 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| 0.0102 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| 0.0174 | FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

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| 0.0199 FAIL | Submitted as cells -1 Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| 0.0279 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted as cells, Presump saliva test pending Presump Saliva test negative |
| 0.0113 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative |
| 0.0104 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Two person mixed DNA profile Single evidence sample excluded This sample has undergone further processing |
| 0.0147 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted for cells. Presumptive saliva test pending. presump Saliva test positive |
| 0.0108 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted for cells. Presumptive saliva test pending. presump Saliva test positive |
| 0.0284 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0089 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0089 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0089 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0089 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0089 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0089 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.009 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.009 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0091 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0091 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0092 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0092 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0092 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0093 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0093 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0093 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0093 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0094 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

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| 0.0314 FAIL | Submitted-results pending. -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0316 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0318 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0319 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0321 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0321 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0321 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0322 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.033 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.033 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0346 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0346 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0346 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0349 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0362 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0382 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0396 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0397 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0533 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| 0.0907 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | Complex mixed profile unsuitable for interp or comparison This sample has undergone further processing Three person mixed DNA profile |
| 0.0091 FAIL | -1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0106 FAIL | -1 ENVM- Complex mixture unsuitable for interp or comparison Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd |
| 0.0107 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd |
| 0.0132 FAIL | -1 Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd |
| 0.0289 FAIL | -1 Complex mixed profile unsuitable for interp or comparison |

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| 0.0103 FAIL | Submitted-results pending. Micro neg for sperm Two person mixed DNA profile 2 person mixed profile - conditioned on -1 Mix remaining DNA contrib unsuitable for NCIDD searching |
| 0.0111 FAIL | Submitted-results pending. -1 Partial DNA profile unsuitable for comparison purposes |
| 0.0204 FAIL | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion This sample has undergone further processing -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0328 FAIL | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 Person Mix Rem contrib unsuitable for NCIDD -1 3 person mix remaining - low support for contrib |
| 0.0248 FAIL | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Mixture-low support for contrib or supports non contrib Single evidence sample excluded This sample has undergone further processing -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0204 FAIL | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded -1 3 Person Mix Rem contrib unsuitable for NCIDD |
| 0.0203 FAIL | Submitted-results pending. Three person mixed DNA profile Excluded from mixed DNA profile -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0238 FAIL | Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 1 million - 1 billion This sample has undergone further processing -1 Complex mixed profile unsuitable for interp or comparison |
| 0.0135 FAIL | Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on -1 Mix remaining DNA contrib unsuitable for NCIDD searching |
| 0.0165 FAIL | Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on -1 Mix remaining DNA contrib unsuitable for NCIDD searching |
| 0.0218 FAIL | Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on -1 Mix remaining DNA contrib unsuitable for NCIDD searching |

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| | Suspect Check Actioned - No Match |
| | Suspect Check Actioned - No Match |
| | Suspect Check Actioned - No Match |
| | Suspect Check Actioned - No Match |
| | Suspect check - low support for contribution |
| | Micro positive for sperm. Submitted-Results pending |
| | Interim result- mixed profile obtained. Rework Reqd |
| | Two person mixed DNA profile |
| | 2 person mixed profile - conditioned on |
| | Excluded from mixed DNA profile |
| | Mix remaining DNA contrib unsuitable for NCIDD searching |
| | Suspect Check Actioned - No Match |
| | Suspect Check Actioned - No Match |
| | Suspect Check Actioned - No Match |
| 0.0187 FAIL | -1 Suspect Check Actioned - No Match |
| 0.0091 FAIL | -1 CMPU |
| 0.0094 FAIL | -1 CMPU |
| 0.0094 FAIL | -1 CMPU |
| 0.0095 FAIL | -1 CMPU |
| 0.01 FAIL | -1 cmpu |
| 0.01 FAIL | -1 cmpu |
| 0.01 FAIL | -1 cmpu |
| 0.0108 FAIL | -1 cmpu |
| 0.0109 FAIL | -1 cmpu |
| 0.0118 FAIL | -1 cmpu |
| 0.0123 FAIL | -1 cmpu |
| 0.0133 FAIL | -1 cmpu |
| 0.0133 FAIL | -1 cmpu |
| 0.0151 FAIL | -1 cmpu |
| 0.0164 FAIL | -1 cmpu |
| 0.0168 FAIL | -1 cmpu |
| 0.0168 FAIL | -1 cmpu |
| 0.0176 FAIL | -1 cmpu |
| 0.0176 FAIL | -1 cmpu |
| 0.022 FAIL | -1 cmpu |
| 0.0249 FAIL | -1 cmpu |
| 0.0276 FAIL | -1 cmpu |
| 0.0293 FAIL | -1 cmpu |
| 0.0364 FAIL | -1 cmpu |
| 0.0091 SUCCESS | 1 consistent elsewhere |
| | Micro positive for sperm. Submitted-Results pending |
| | SS DNA profile 9 loci and above LR > 100 billion |
| 0.0105 SUCCESS | 1 NCIDD upload single source DNA profile |
| | Micro positive for sperm. Submitted-Results pending |
| | Two person mixed DNA profile |
| | NCIDD upload - mixed DNA profile |
| 0.0139 SUCCESS | 1 Excluded from mixed DNA profile |
| | Single source DNA profile |
| | NCIDD upload single source DNA profile |
| | Single Source DNA profile - assumed known contributor |
| 0.0173 SUCCESS | 1 DNA profile removed from NCIDD |
| | Submitted as cells |
| | Single Source DNA profile - assumed known contributor |
| | NCIDD upload single source DNA profile |
| 0.0112 SUCCESS | 1 Possible sub-threshold information |

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| | | Submitted as cells |
| | | Single source DNA profile |
| | | NCIDD upload single source DNA profile |
| | | Single Source DNA profile - assumed known contributor |
| 0.0144 | SUCCESS | 1 DNA profile removed from NCIDD |
| | | Submitted-results pending. |
| 0.029 | SUCCESS | 1 Single source 20 loci DNA profile LR > 100 billion |
| | | Submitted-results pending. |
| | | Single source 20 loci DNA profile LR > 100 billion |
| 0.0111 | SUCCESS | 1 NCIDD upload single source DNA profile |
| | | Submitted-results pending. |
| | | Single source 20 loci DNA profile LR > 100 billion |
| | | NCIDD upload single source DNA profile |
| 0.0118 | SUCCESS | 1 Possible sub-threshold information |
| | | Submitted-results pending. |
| | | Single source 20 loci DNA profile LR > 100 billion |
| | | Possible sub-threshold information |
| 0.0091 | SUCCESS | 1 NCIDD upload single source DNA profile |
| | | Submitted-results pending. |
| | | Single source 20 loci DNA profile LR > 100 billion |
| | | Possible sub-threshold information |
| 0.0248 | SUCCESS | 1 NCIDD upload single source DNA profile |
| | | Submitted-results pending. |
| | | Single Source DNA profile - assumed known contributor |
| | | NCIDD upload single source DNA profile |
| 0.0133 | SUCCESS | 1 Possible sub-threshold information |
| | | Submitted-results pending. |
| | | Single Source DNA profile - assumed known contributor |
| | | Possible sub-threshold information |
| 0.0314 | SUCCESS | 1 NCIDD upload single source DNA profile |
| | | Submitted-results pending. |
| | | Single source DNA profile |
| | | NCIDD Intel upload - single source partial profile |
| 0.0202 | SUCCESS | 1 NCIDD upload single source DNA profile |
| | | Submitted-results pending. |
| | | Single source DNA profile |
| 0.0105 | SUCCESS | 1 NCIDD upload single source DNA profile |
| | | Submitted-results pending. |
| | | Single source DNA profile |
| 0.0106 | SUCCESS | 1 NCIDD upload single source DNA profile |
| | | Submitted-results pending. |
| | | Single source DNA profile |
| 0.0111 | SUCCESS | 1 NCIDD upload single source DNA profile |
| | | Submitted-results pending. |
| | | Single source DNA profile |
| 0.0146 | SUCCESS | 1 NCIDD upload single source DNA profile |
| | | Submitted-results pending. |
| | | Single source DNA profile |
| 0.0154 | SUCCESS | 1 NCIDD upload single source DNA profile |
| | | Submitted-results pending. |
| | | Single source DNA profile |
| 0.0162 | SUCCESS | 1 NCIDD upload single source DNA profile |
| | | Submitted-results pending. |
| | | Single source DNA profile |
| 0.0174 | SUCCESS | 1 NCIDD upload single source DNA profile |
| | | Submitted-results pending. |
| | | Single source DNA profile |
| 0.0178 | SUCCESS | 1 NCIDD upload single source DNA profile |

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| | | Submitted-results pending. Single source DNA profile |
| 0.0183 | SUCCESS | 1 NCIDD upload single source DNA profile Submitted-results pending. Single source DNA profile |
| 0.0208 | SUCCESS | 1 NCIDD upload single source DNA profile Submitted-results pending. Single source DNA profile |
| 0.0315 | SUCCESS | 1 NCIDD upload single source DNA profile Submitted-results pending. Single source DNA profile |
| 0.0446 | SUCCESS | 1 NCIDD upload single source DNA profile Submitted-results pending. Single source DNA profile |
| 0.0329 | SUCCESS | 1 NCIDD upload single source DNA profile DNA profile removed from NCIDD Submitted-results pending. Single source DNA profile |
| 0.0113 | SUCCESS | 1 NCIDD upload single source DNA profile Possible sub-threshold information Submitted-results pending. Single source DNA profile |
| 0.0129 | SUCCESS | 1 NCIDD upload single source DNA profile Possible sub-threshold information Submitted-results pending. Single source DNA profile |
| 0.0142 | SUCCESS | 1 NCIDD upload single source DNA profile Possible sub-threshold information Submitted-results pending. Single source DNA profile |
| 0.016 | SUCCESS | 1 NCIDD upload single source DNA profile Possible sub-threshold information Submitted-results pending. Single source DNA profile |
| 0.0273 | SUCCESS | 1 NCIDD upload single source DNA profile Possible sub-threshold information Submitted-results pending. Single source DNA profile |
| 0.0095 | SUCCESS | 1 NCIDD upload single source DNA profile Possible sub-threshold information Complex mixed profile unsuitable for interp or comparison DNA profile removed from NCIDD Submitted-results pending. Single source DNA profile |
| 0.0093 | SUCCESS | 1 NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion Submitted-results pending. Single source DNA profile |
| 0.0184 | SUCCESS | 1 NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion Complex mixed profile unsuitable for interp or comparison DNA profile removed from NCIDD Submitted-results pending. Single source DNA profile |
| 0.0134 | SUCCESS | 1 NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion |

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| 0.0241 | SUCCESS | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile 1 SS DNA profile 9 loci and above LR > 100 billion |
| 0.0129 | SUCCESS | Submitted-results pending. Single source DNA profile Possible sub-threshold information 1 NCIDD upload single source DNA profile |
| 0.0135 | SUCCESS | Submitted-results pending. Single source DNA profile Possible sub-threshold information 1 NCIDD upload single source DNA profile |
| 0.0219 | SUCCESS | Submitted-results pending. Single source DNA profile Possible sub-threshold information 1 NCIDD upload single source DNA profile |
| 0.017 | SUCCESS | Submitted-results pending. Single source DNA profile Possible sub-threshold information This sample has undergone further processing Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile 1 Possible sub-threshold information |
| 0.0121 | SUCCESS | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion 1 NCIDD upload single source DNA profile |
| 0.0276 | SUCCESS | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion 1 NCIDD upload single source DNA profile |
| 0.0155 | SUCCESS | Submitted-results pending. Three person mixed DNA profile 1 Three person mixed DNA profile |
| 0.0235 | SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contrib 10 000 - 100 000 1 3 person mix profile - support for contrib > 100 billion |
| 0.03 | SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 1 3 person mix - low support for contribution |
| 0.0261 | SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 1 Mixture-low support for contrib or supports non contrib |
| 0.0256 | SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 1 Single evidence sample excluded |
| 0.0384 | SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 1 3 person mix - supports non contribution |
| 0.0091 | SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 1 3 person mix remaining - supports non contribution |
| 0.0211 | SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 1 Mixture-low support for contrib or supports non contrib |

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| | | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on |
| 0.0219 | SUCCESS | 1 Single evidence sample excluded Submitted-results pending. Three person mixed DNA profile |
| 0.0136 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0225 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0166 | SUCCESS | 1 Single evidence sample excluded Submitted-results pending. Two person mixed DNA profile |
| 0.0089 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Two person mixed DNA profile Single source DNA profile NCIDD upload single source DNA profile |
| 0.0143 | SUCCESS | 1 Possible sub-threshold information |
| 0.0092 | SUCCESS | 1 P SS |
| 0.0093 | SUCCESS | 1 P SS |
| 0.0094 | SUCCESS | 1 3p |
| 0.0095 | SUCCESS | 1 3p |
| 0.0096 | SUCCESS | 1 cond |
| 0.0096 | SUCCESS | 1 ss akc |
| 0.0101 | SUCCESS | 1 ss |
| 0.0102 | SUCCESS | 1 ss |
| 0.0105 | SUCCESS | 1 ss |
| 0.011 | SUCCESS | 1 2p |
| 0.011 | SUCCESS | 1 3p |
| 0.011 | SUCCESS | 1 2p |
| 0.0118 | SUCCESS | 1 ss |
| 0.0118 | SUCCESS | 1 2p |
| 0.0119 | SUCCESS | 1 2p |
| 0.0119 | SUCCESS | 1 ss |
| 0.012 | SUCCESS | 1 mix |
| 0.0123 | SUCCESS | 1 mix |
| 0.0124 | SUCCESS | 1 mix |
| 0.0125 | SUCCESS | 1 mix |
| 0.0132 | SUCCESS | 1 mix |
| 0.014 | SUCCESS | 1 ss |
| 0.015 | SUCCESS | 1 ss |
| 0.0164 | SUCCESS | 1 ss |
| 0.0167 | SUCCESS | 1 mix |
| 0.017 | SUCCESS | 1 mix |
| 0.0172 | SUCCESS | 1 ss |
| 0.0175 | SUCCESS | 1 mix |
| 0.0178 | SUCCESS | 1 mix |
| 0.0183 | SUCCESS | 1 mix |
| 0.0193 | SUCCESS | 1 ss |
| 0.0203 | SUCCESS | 1 ss |
| 0.0215 | SUCCESS | 1 mix |
| 0.0215 | SUCCESS | 1 mix |
| 0.0234 | SUCCESS | 1 mix |
| 0.0235 | SUCCESS | 1 mix |
| 0.0245 | SUCCESS | 1 ss |
| 0.0248 | SUCCESS | 1 mix |

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| 0.0256 SUCCESS | 1 mix |
| 0.028 SUCCESS | 1 mix |
| 0.0285 SUCCESS | 1 mix |
| 0.0294 SUCCESS | 1 mix |
| 0.0299 SUCCESS | 1 mix |
| 0.0306 SUCCESS | 1 ss |
| | 2 person mix remaining - supports non contribution |
| | Submitted as cells |
| | Two person mixed DNA profile |
| | 2 person mix - supports non contribution |
| | Sample undergone further work - conditioned |
| | Two person mixed DNA profile |
| 0.0162 SUCCESS | 1 2 person mixed profile - conditioned on |
| | Hair located. Submitted-results pending |
| | Single Source DNA profile - assumed known contributor |
| 0.0098 SUCCESS | 1 Possible sub-threshold information |
| | Interim result- mixed profile obtained. Rework Reqd |
| | Three person mixed DNA profile |
| | 3 person mixed profile - conditioned on |
| | 3 person mix remaining - supports non contribution |
| | 3 person mix remaining - supports non contribution |
| | Single evidence sample excluded |
| | Suspect check - support for contrib 100 000 - 1 million |
| | Suspect check - supports non contribution |
| | Suspect check - supports non contribution |
| | Suspect Check Actioned - No Match |
| | Suspect Check Actioned - No Match |
| | Suspect Check Actioned - No Match |
| | Suspect check - supports non contribution |
| | Suspect check - supports non contribution |
| 0.0241 SUCCESS | 1 Suspect Check Actioned - No Match |
| | Micro positive for sperm. Submitted-Results pending |
| 0.0095 SUCCESS | 1 Single source 20 loci DNA profile LR > 100 billion |
| | Micro positive for sperm. Submitted-Results pending |
| | Single source 20 loci DNA profile LR > 100 billion |
| 0.0189 SUCCESS | 1 Possible sub-threshold information |
| | Micro positive for sperm. Submitted-Results pending |
| | Three person mixed DNA profile |
| | 3 person mix profile - support for contrib > 100 billion |
| 0.0095 SUCCESS | 1 3 person mix - supports non contribution |
| | Micro positive for sperm. Submitted-Results pending |
| | Three person mixed DNA profile |
| | 3 person mix profile - support for contrib > 100 billion |
| | 3 person mix profile - support for contrib > 100 billion |
| 0.0116 SUCCESS | 1 3 person mix - supports non contribution |
| | Micro positive for sperm. Submitted-Results pending |
| | Three person mixed DNA profile |
| | 3 person mixed profile - conditioned on |
| 0.0132 SUCCESS | 1 3 person mix remaining - supports non contribution |
| | Micro positive for sperm. Submitted-Results pending |
| | Three person mixed DNA profile |
| | 3 person mixed profile - conditioned on |
| | 3 person mix remaining - supports non contribution |
| | Two person mixed DNA profile |
| | 2 person mixed profile - conditioned on |
| | Single evidence sample excluded |
| 0.0143 SUCCESS | 1 Possible sub-threshold information |

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| | Micro positive for sperm. Submitted-Results pending |
| | Three person mixed DNA profile |
| | Mixture-low support for contrib or supports non contrib |
| 0.0094 SUCCESS | 3 person mix - support for contrib 1 million - 1 billion |
| | 1 3 person mix - support for contribution 100 to 1000 |
| | Micro positive for sperm. Submitted-Results pending |
| | Three person mixed DNA profile |
| 0.011 SUCCESS | Single evidence sample excluded |
| | 1 3 person mix - supports non contribution |
| | presump Saliva test positive |
| | Three person mixed DNA profile |
| 0.0278 SUCCESS | 3 person mixed profile - conditioned on |
| | 1 3 person mix remaining - support for contrib 100 to 1000 |
| | Presump. PSA test positive, no sperm found |
| | Two person mixed DNA profile |
| 0.0101 SUCCESS | 2 person mixed profile - conditioned on |
| | 1 2 person rem - support for contrib 1 billion -100 billion |
| | Presump. PSA test positive, no sperm found |
| | Two person mixed DNA profile |
| 0.0142 SUCCESS | 2 person mixed profile - conditioned on |
| | 1 2 person rem- support for contrib 1 million to 1 billion |
| | Presumptive blood test pos. Submitted-results pending. |
| | Two person mixed DNA profile |
| 0.0289 SUCCESS | 2 person mixed profile - conditioned on |
| | 1 2 person mix rem - support for contribution > 100 billion |
| | Semen not detected |
| | Submitted as cells |
| | Three person mixed DNA profile |
| 0.0274 SUCCESS | 3 person mixed profile - conditioned on |
| | 1 3 person mix rem - support for contribution > 100 billion |
| | Semen not detected |
| | Submitted as cells |
| | Three person mixed DNA profile |
| 0.0275 SUCCESS | 3 person mixed profile - conditioned on |
| | 1 Cond mix rem-low supp for contrib or supp non contrib |
| | Single evidence sample excluded |
| | Three person mixed DNA profile |
| 0.0165 SUCCESS | 3 person mix profile - support for contrib > 100 billion |
| | 1 3 person mix profile - support for contrib > 100 billion |
| | SS DNA profile 9 loci and above LR > 100 billion |
| 0.0096 SUCCESS | 1 Possible sub-threshold information |
| | Submitted as cells |
| | Three person mixed DNA profile |
| 0.0305 SUCCESS | 3 person mix profile - support for contrib > 100 billion |
| | 1 3 person mix - support for contrib 1 million - 1 billion |
| | Submitted as cells |
| | Three person mixed DNA profile |
| 0.0136 SUCCESS | 3 person mix profile - support for contrib > 100 billion |
| | 1 Excluded from mixed DNA profile |
| | Submitted as cells |
| | Three person mixed DNA profile |
| 0.0141 SUCCESS | 3 person mixed profile - conditioned on |
| | 1 3 person rem- support for contrib 1 billion-100 billion |
| | Submitted as cells |
| 0.0304 SUCCESS | Three person mixed DNA profile |
| | 1 No statistical interpretation performed |

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| | Submitted as cells |
| | Two person mixed DNA profile |
| | 2 person mixed profile - conditioned on |
| 0.0296 SUCCESS | 1 2 person mix rem - support for contribution > 100 billion |
| | Submitted as cells, Presump saliva test pending |
| | Presump Saliva test negative |
| | Three person mixed DNA profile |
| | 3 person mixed profile - conditioned on |
| 0.0346 SUCCESS | 1 Single evidence sample excluded |
| | Submitted as cells, Presump saliva test pending |
| | presump Saliva test positive |
| | Two person mixed DNA profile |
| | 2 person mixed profile - conditioned on |
| 0.0168 SUCCESS | 1 2 person mix rem - support for contribution > 100 billion |
| | Submitted as cells, Presump saliva test pending |
| | presump Saliva test positive |
| | Two person mixed DNA profile |
| | 2 person mixed profile - conditioned on |
| 0.0277 SUCCESS | 1 2 person mix rem - support for contribution > 100 billion |
| | Submitted for cells. Presumptive saliva test pending. |
| | presump Saliva test positive |
| | Three person mixed DNA profile |
| 0.0104 SUCCESS | 1 3 person mix profile - support for contrib > 100 billion |
| | Submitted for cells. Presumptive saliva test pending. |
| | presump Saliva test positive |
| | Three person mixed DNA profile |
| | 3 person mix profile - support for contrib > 100 billion |
| | 3 person mix - support for contribution 1000 to 10 000 |
| 0.0577 SUCCESS | 1 3 person mix - supports non contribution |
| | Submitted-results pending. |
| | Interim result- mixed profile obtained. Rework Reqd |
| | Three person mixed DNA profile |
| | 3 person mix profile - support for contrib > 100 billion |
| | Excluded from mixed DNA profile |
| 0.0144 SUCCESS | 1 3 person mix profile - support for contrib > 100 billion |
| | Submitted-results pending. |
| | Interim result- mixed profile obtained. Rework Reqd |
| | Three person mixed DNA profile |
| | 3 person mix profile - support for contrib > 100 billion |
| | Mixture-low support for contrib or supports non contrib |
| 0.0128 SUCCESS | 1 3 person mix - support for contrib 100 000 to 1 million |
| | Submitted-results pending. |
| | Interim result- mixed profile obtained. Rework Reqd |
| | Three person mixed DNA profile |
| | 3 person mix profile - support for contrib > 100 billion |
| | Mixture-low support for contrib or supports non contrib |
| 0.0329 SUCCESS | 1 3 person mix - support for contribution 100 to 1000 |
| | Submitted-results pending. |
| | Micro neg for sperm |
| 0.016 SUCCESS | 1 Single Source DNA profile - assumed known contributor |
| | Submitted-results pending. |
| | Micro positive for sperm. Submitted-Results pending |
| | Single source 20 loci DNA profile LR > 100 billion |
| 0.0133 SUCCESS | 1 Possible sub-threshold information |
| | Submitted-results pending. |
| 0.0128 SUCCESS | 1 Single source 20 loci DNA profile LR > 100 billion |
| | Submitted-results pending. |
| 0.026 SUCCESS | 1 Single source 20 loci DNA profile LR > 100 billion |

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| 0.0743 | SUCCESS | Submitted-results pending. 1 Single source 20 loci DNA profile LR > 100 billion Submitted-results pending. |
| 0.0143 | SUCCESS | Single source 20 loci DNA profile LR > 100 billion 1 Possible sub-threshold information Submitted-results pending. |
| 0.0186 | SUCCESS | Single source 20 loci DNA profile LR > 100 billion 1 Possible sub-threshold information Submitted-results pending. |
| 0.0234 | SUCCESS | Single source 20 loci DNA profile LR > 100 billion 1 Possible sub-threshold information Submitted-results pending. |
| 0.0272 | SUCCESS | Single source 20 loci DNA profile LR > 100 billion 1 Possible sub-threshold information Submitted-results pending. |
| 0.0281 | SUCCESS | Single source 20 loci DNA profile LR > 100 billion 1 Possible sub-threshold information Submitted-results pending. |
| 0.0101 | SUCCESS | 1 Single source DNA profile Submitted-results pending. |
| 0.0222 | SUCCESS | 1 Single source DNA profile Submitted-results pending. |
| 0.0244 | SUCCESS | 1 Single source DNA profile Submitted-results pending. |
| 0.0119 | SUCCESS | Single Source DNA profile - assumed known contributor 1 Possible sub-threshold information Submitted-results pending. |
| 0.013 | SUCCESS | Single Source DNA profile - assumed known contributor 1 Possible sub-threshold information Submitted-results pending. |
| 0.0175 | SUCCESS | Single Source DNA profile - assumed known contributor 1 Possible sub-threshold information Submitted-results pending. |
| 0.0095 | SUCCESS | Single source DNA profile 1 Possible sub-threshold information Submitted-results pending. |
| 0.0101 | SUCCESS | Single source DNA profile 1 Possible sub-threshold information Submitted-results pending. |
| 0.0128 | SUCCESS | Single source DNA profile 1 Possible sub-threshold information Submitted-results pending. |
| 0.0296 | SUCCESS | Single source DNA profile 1 Possible sub-threshold information Submitted-results pending. |
| 0.014 | SUCCESS | Single source DNA profile Possible sub-threshold information 1 Single Source DNA profile - assumed known contributor Submitted-results pending. |
| 0.0223 | SUCCESS | Single source DNA profile 1 Single source 20 loci DNA profile LR > 100 billion Submitted-results pending. |
| 0.0197 | SUCCESS | Single source 20 loci DNA profile LR > 100 billion 1 Possible sub-threshold information Submitted-results pending. |
| 0.0139 | SUCCESS | Single source DNA profile 1 SS DNA profile 9 loci and above LR > 100 billion |

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|--------|---------|--|
| 0.0289 | SUCCESS | Submitted-results pending. 1 SS DNA profile 9 loci and above LR > 100 billion Submitted-results pending. |
| 0.0113 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0134 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0135 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.015 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0154 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0164 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0182 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0195 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0202 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0244 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0252 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0256 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0258 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0293 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0296 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0319 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0329 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0368 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0391 | SUCCESS | 1 Three person mixed DNA profile Submitted-results pending. |
| 0.0199 | SUCCESS | Three person mixed DNA profile 1 3 person mix - low support for contribution Submitted-results pending. |
| 0.0174 | SUCCESS | Three person mixed DNA profile 3 person mix - support for contrib 1 million - 1 billion 1 Excluded from mixed DNA profile Submitted-results pending. |
| 0.0198 | SUCCESS | Three person mixed DNA profile 1 3 person mix - support for contrib 10 000 - 100 000 Submitted-results pending. |
| 0.0171 | SUCCESS | Three person mixed DNA profile 3 person mix - support for contrib 10 000 - 100 000 1 Mixture-low support for contrib or supports non contrib Submitted-results pending. |
| 0.0305 | SUCCESS | Three person mixed DNA profile 1 3 person mix - support for contribution 1000 to 10 000 |

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| 0.0162 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 Mixture-low support for contrib or supports non contrib 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.016 SUCCESS | Three person mixed DNA profile 1 3 person mix - supports non contribution Submitted-results pending. |
| 0.023 SUCCESS | Three person mixed DNA profile 1 3 person mix - supports non contribution Submitted-results pending. |
| 0.0173 SUCCESS | Three person mixed DNA profile 3 person mix - supports non contribution 3 person mix - support for contrib 10 000 - 100 000 3 person mix - supports non contribution Sample undergone further work - conditioned 3 person mixed profile - conditioned on 2 person mix rem - support for contrib 10 000 to 100 000 2 person mix remaining - supports non contribution 2 person mix remaining - supports non contribution 3 person mix rem - support for contrib 10 000 to 100 000 3 person mix remaining - supports non contribution 1 3 person mix remaining - supports non contribution Submitted-results pending. |
| 0.0218 SUCCESS | Three person mixed DNA profile 3 person mix - supports non contribution 1 3 person mix - supports non contribution Submitted-results pending. |
| 0.0093 SUCCESS | Three person mixed DNA profile 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0122 SUCCESS | Three person mixed DNA profile 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0124 SUCCESS | Three person mixed DNA profile 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0143 SUCCESS | Three person mixed DNA profile 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0145 SUCCESS | Three person mixed DNA profile 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0161 SUCCESS | Three person mixed DNA profile 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0169 SUCCESS | Three person mixed DNA profile 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0176 SUCCESS | Three person mixed DNA profile 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0178 SUCCESS | Three person mixed DNA profile 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| 0.0195 SUCCESS | Three person mixed DNA profile 1 3 person mix profile - support for contrib > 100 billion |

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|--------|---------|---|
| | | Submitted-results pending. Three person mixed DNA profile |
| 0.0197 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile |
| 0.0212 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile |
| 0.0271 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile |
| 0.0346 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile |
| 0.0133 | SUCCESS | 3 person mix profile - support for contrib > 100 billion 1 3 person mix - low support for contribution Submitted-results pending. Three person mixed DNA profile |
| 0.0156 | SUCCESS | 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution 1 Excluded from mixed DNA profile Submitted-results pending. Three person mixed DNA profile |
| 0.0135 | SUCCESS | 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution Mixture-low support for contrib or supports non contrib 1 3 person mix - low support for contribution Submitted-results pending. Three person mixed DNA profile |
| 0.011 | SUCCESS | 3 person mix profile - support for contrib > 100 billion 1 3 person mix - support for contrib 1 million - 1 billion Submitted-results pending. Three person mixed DNA profile |
| 0.0158 | SUCCESS | 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion 3 person mix - supports non contribution Sample undergone further work - conditioned 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion 3 person mix rem - support for contribution > 100 billion 1 Single evidence sample excluded Submitted-results pending. Three person mixed DNA profile |
| 0.0316 | SUCCESS | 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion 1 Excluded from mixed DNA profile Submitted-results pending. Three person mixed DNA profile |
| 0.0259 | SUCCESS | 3 person mix profile - support for contrib > 100 billion 1 3 person mix - support for contrib 100 000 to 1 million Submitted-results pending. Three person mixed DNA profile |
| 0.0239 | SUCCESS | 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 100 to 1000 1 3 person mix - supports non contribution Submitted-results pending. Three person mixed DNA profile |
| 0.0157 | SUCCESS | 3 person mix profile - support for contrib > 100 billion 1 3 person mix - supports non contribution |

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| 0.0267 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 1 3 person mix - supports non contribution |
| 0.0148 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 1 3 person mix profile - support for contrib > 100 billion |
| 0.0119 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 1 Mixture-low support for contrib or supports non contrib |
| 0.0124 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 1 Mixture-low support for contrib or supports non contrib |
| 0.0198 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 1 Mixture-low support for contrib or supports non contrib |
| 0.0199 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 1 Mixture-low support for contrib or supports non contrib |
| 0.0096 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Suspect check - low support or non contrib 1 Suspect check - supports non contribution |
| 0.0179 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Suspect check - low support or non contrib 1 Suspect check - supports non contribution |
| 0.0316 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Single evidence sample excluded 1 3 person mix - support for contribution 100 to 1000 |
| 0.0162 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mix- support for contrib 1 billion - 100 billion 3 person mix profile - support for contrib > 100 billion 1 Excluded from mixed DNA profile |
| 0.0118 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix profile - support for contrib > 100 billion 1 3 person mix rem - support for contribution > 100 billion |
| 0.0306 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 1 3 person mix rem - support for contribution > 100 billion |
| 0.0278 SUCCESS | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 1 3 person mix remaining - low support for contrib |

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|----------------|---|
| | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - low support for contrib |
| 0.0109 SUCCESS | 1 3 person mix remaining - supports non contribution Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on |
| 0.0139 SUCCESS | 1 3 person mix remaining - supports non contribution Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on |
| 0.0148 SUCCESS | 1 3 person mix remaining - supports non contribution Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on |
| 0.0186 SUCCESS | 1 3 person mix remaining - supports non contribution Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on |
| 0.0316 SUCCESS | 1 3 person mix remaining - supports non contribution Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining- support for contrib 1000 to 10000 |
| 0.0315 SUCCESS | 1 3 person mix remaining - supports non contribution Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining- support for contrib 1000 to 10000 Single evidence sample excluded |
| 0.0287 SUCCESS | 1 Cond mix rem-low supp for contrib or supp non contrib Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on |
| 0.021 SUCCESS | 1 Excluded from mixed DNA profile Submitted-results pending. Three person mixed DNA profile Cond mix rem-low supp for contrib or supp non contrib |
| 0.024 SUCCESS | 1 3 person mixed profile - conditioned on Submitted-results pending. Three person mixed DNA profile Excluded from mixed DNA profile |
| 0.0197 SUCCESS | 3 person mix profile - support for contrib > 100 billion 1 3 person mix - support for contribution 100 to 1000 Submitted-results pending. Three person mixed DNA profile Excluded from mixed DNA profile |
| 0.0156 SUCCESS | 1 Single evidence sample excluded Submitted-results pending. Three person mixed DNA profile |
| 0.0095 SUCCESS | 1 Mixture-low support for contrib or supports non contrib Submitted-results pending. Three person mixed DNA profile |
| 0.0125 SUCCESS | Mixture-low support for contrib or supports non contrib 1 3 person mix profile - support for contrib > 100 billion |

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| | | Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib |
| 0.0126 | SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile |
| 0.0103 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0115 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0122 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0203 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0205 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0208 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0231 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0235 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0235 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0247 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0248 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0249 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0267 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| 0.0287 | SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Three person mixed DNA profile |
| | | No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion |
| 0.0195 | SUCCESS | 1 Excluded from mixed DNA profile Submitted-results pending. Three person mixed DNA profile |
| | | No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion |
| 0.0201 | SUCCESS | 1 Excluded from mixed DNA profile |

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|----------------|---|
| 0.0123 SUCCESS | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion 1 Mixture-low support for contrib or supports non contrib Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion |
| 0.0131 SUCCESS | Two person mixed DNA profile 1 2 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed Single evidence sample excluded |
| 0.0113 SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile |
| 0.0199 SUCCESS | 1 Single evidence sample excluded Submitted-results pending. Three person mixed DNA profile |
| 0.0205 SUCCESS | 1 Single evidence sample excluded Submitted-results pending. Three person mixed DNA profile Single evidence sample excluded |
| 0.0278 SUCCESS | 1 3 person mix profile - support for contrib > 100 billion Submitted-results pending. Three person mixed DNA profile |
| 0.02 SUCCESS | 1 Suspect Check Actioned - No Match Submitted-results pending. |
| 0.0093 SUCCESS | 1 Two person mixed DNA profile Submitted-results pending. |
| 0.0152 SUCCESS | 1 Two person mixed DNA profile Submitted-results pending. |
| 0.0155 SUCCESS | 1 Two person mixed DNA profile Submitted-results pending. |
| 0.0195 SUCCESS | 1 Two person mixed DNA profile Submitted-results pending. |
| 0.0242 SUCCESS | 1 Two person mixed DNA profile Submitted-results pending. Two person mixed DNA profile |
| 0.0211 SUCCESS | 1 2 person mix - support for contrib 1 million - 1 billion Submitted-results pending. Two person mixed DNA profile |
| 0.0123 SUCCESS | 1 2 person mix - supports non contribution Submitted-results pending. Two person mixed DNA profile |
| 0.0229 SUCCESS | 1 2 person mix - supports non contribution Submitted-results pending. Two person mixed DNA profile |
| 0.0118 SUCCESS | 1 2 person mix profile - support for contrib > 100 billion Submitted-results pending. Two person mixed DNA profile |
| 0.0161 SUCCESS | 1 2 person mix profile - support for contrib > 100 billion Submitted-results pending. Two person mixed DNA profile |
| 0.0172 SUCCESS | 1 2 person mix profile - support for contrib > 100 billion |

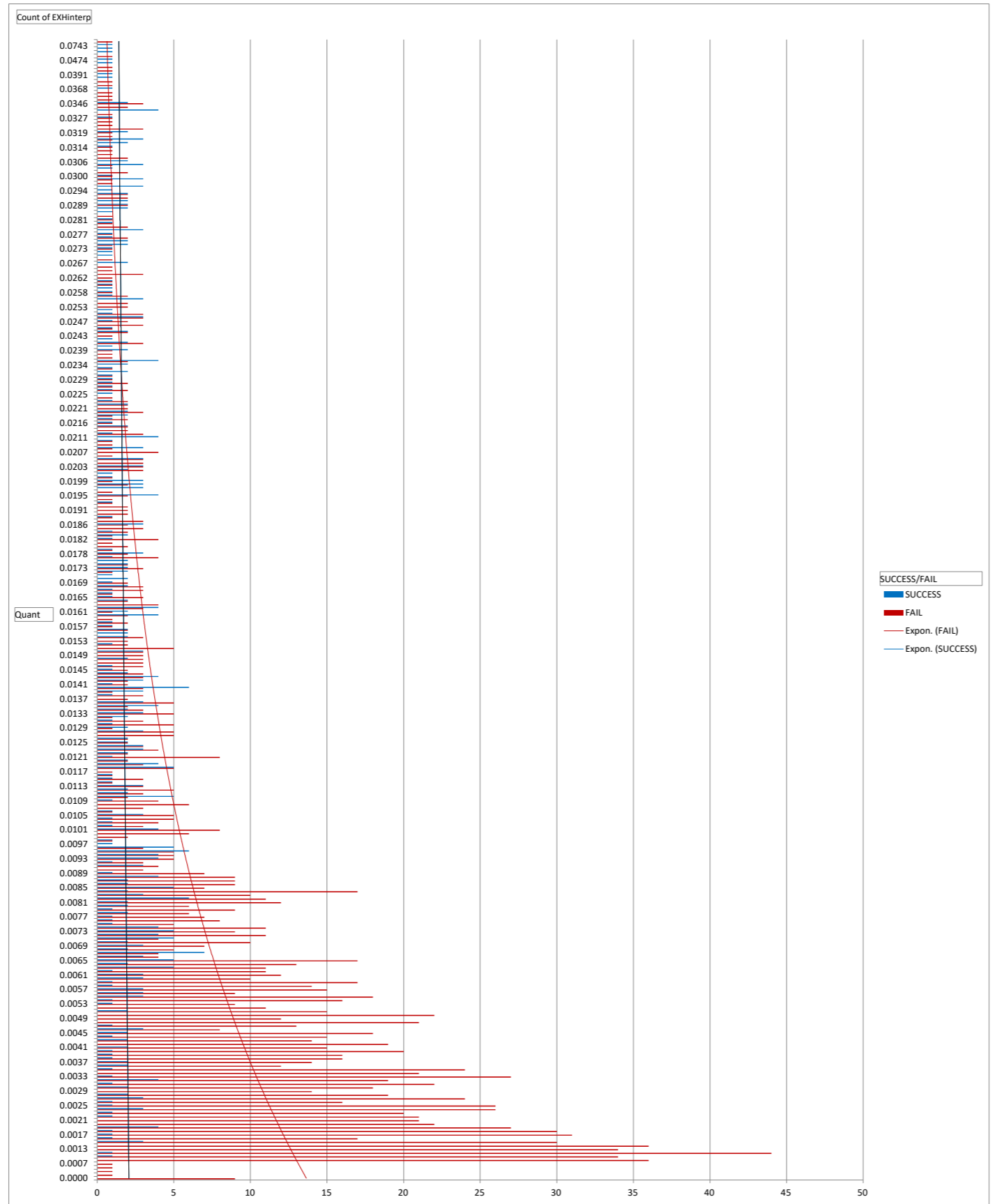
| | | |
|--------|---------|---|
| | | Submitted-results pending. Two person mixed DNA profile |
| 0.0257 | SUCCESS | 1 2 person mix profile - support for contrib > 100 billion Submitted-results pending. Two person mixed DNA profile |
| 0.0611 | SUCCESS | 1 2 person mix profile - support for contrib > 100 billion Submitted-results pending. Two person mixed DNA profile |
| 0.014 | SUCCESS | 2 person mix profile - support for contrib > 100 billion 1 2 person mix - low support for contribution Submitted-results pending. Two person mixed DNA profile |
| 0.022 | SUCCESS | 2 person mix profile - support for contrib > 100 billion 1 2 person mix - low support for contribution Submitted-results pending. Two person mixed DNA profile |
| 0.0327 | SUCCESS | 2 person mix profile - support for contrib > 100 billion 2 person mix - support for contrib 1 million - 1 billion 1 2 person mix profile - support for contrib > 100 billion Submitted-results pending. Two person mixed DNA profile |
| 0.012 | SUCCESS | 2 person mix profile - support for contrib > 100 billion 1 2 person mix - supports non contribution Submitted-results pending. Two person mixed DNA profile |
| 0.0329 | SUCCESS | 2 person mix profile - support for contrib > 100 billion 1 2 person mix - supports non contribution Submitted-results pending. Two person mixed DNA profile |
| 0.0203 | SUCCESS | 2 person mix profile - support for contrib > 100 billion 2 person mix- support for contrib 1 billion - 100 billion 1 2 person mix profile - support for contrib > 100 billion Submitted-results pending. Two person mixed DNA profile |
| 0.0096 | SUCCESS | 2 person mix profile - support for contrib > 100 billion 1 Excluded from mixed DNA profile Submitted-results pending. Two person mixed DNA profile |
| 0.0275 | SUCCESS | 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Suspect check - low support or non contrib Suspect check - low support or non contrib 1 Suspect check - low support or non contrib Submitted-results pending. Two person mixed DNA profile |
| 0.0114 | SUCCESS | 2 person mix profile - support for contrib > 100 billion 1 Single evidence sample excluded Submitted-results pending. Two person mixed DNA profile |
| 0.0126 | SUCCESS | 2 person mix profile - support for contrib > 100 billion 1 Single evidence sample excluded Submitted-results pending. Two person mixed DNA profile |
| 0.0211 | SUCCESS | 2 person mix profile - support for contrib > 100 billion 1 Single evidence sample excluded Submitted-results pending. Two person mixed DNA profile |
| 0.0299 | SUCCESS | 2 person mixed profile - conditioned on 1 Possible sub-threshold information |

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|----------------|---|
| | Submitted-results pending. Two person mixed DNA profile Mixture-low support for contrib or supports non contrib 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile |
| 0.0112 SUCCESS | 1 Suspect check - supports non contribution Submitted-results pending. Two person mixed DNA profile |
| 0.016 SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Two person mixed DNA profile |
| 0.0205 SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Two person mixed DNA profile |
| 0.0216 SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Two person mixed DNA profile |
| 0.022 SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Two person mixed DNA profile |
| 0.0231 SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Two person mixed DNA profile |
| 0.0299 SUCCESS | 1 No statistical interpretation performed Submitted-results pending. Two person mixed DNA profile |
| 0.0135 SUCCESS | 1 Single evidence sample excluded Submitted-results pending. Two person mixed DNA profile Single evidence sample excluded 2 person mix profile - support for contrib > 100 billion This sample has undergone further processing Three person mixed DNA profile 3 person mixed profile - conditioned on |
| 0.0474 SUCCESS | 1 3 person mix rem - support for contribution > 100 billion Submitted-results pending. Two person mixed DNA profile Suspect check inconclusive - mixed DNA profile |
| 0.0142 SUCCESS | 1 Suspect check - supports non contribution Suspect check - supports non contribution Suspect check - supports non contribution Suspect check - supports non contribution Suspect check - supports non contribution Suspect check - supports non contribution Suspect check - supports non contribution Three person mixed DNA profile 3 person mixed profile - conditioned on Suspect check- support for contribution 10 000 to 100 000 Mixture-low support for contrib or supports non contrib Suspect check - supports non contribution |
| 0.0305 SUCCESS | 1 Suspect check - supports non contribution This sample has undergone further processing Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 10 000 - 100 000 |
| 0.0222 SUCCESS | 1 Mixture-low support for contrib or supports non contrib Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 |
| 0.015 SUCCESS | 1 Single evidence sample excluded |

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|----------------|---|
| 0.0094 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution 1 3 person mix - supports non contribution |
| 0.0232 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 1 million - 1 billion 1 Mixture-low support for contrib or supports non contrib |
| 0.0136 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 100 000 to 1 million Mixture-low support for contrib or supports non contrib 1 Excluded from mixed DNA profile |
| 0.0227 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contribution 1000 to 10 000 3 person mix - support for contribution 100 to 1000 1 3 person mix - low support for contribution |
| 0.0319 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix- support for contrib 1 billion - 100 billion 1 Excluded from mixed DNA profile |
| 0.014 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mixed profile - conditioned on 1 3 person mix rem - support for contribution > 100 billion |
| 0.0094 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion 1 3 person mix remaining - supports non contribution |
| 0.029 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion Submitted as cells, Presump saliva test pending 1 presump Saliva test positive |
| 0.0239 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mixed profile - conditioned on 1 Cond mix rem-low supp for contrib or supp non contrib |
| 0.0226 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mixed profile - conditioned on 1 Remaining contribution - inconclusive |
| 0.0097 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mixed profile - conditioned on 1 Single evidence sample excluded |
| 0.0138 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mixed profile - conditioned on 1 Single evidence sample excluded |
| 0.0274 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mixed profile - conditioned on 1 Single evidence sample excluded No statistical interpretation performed Sample undergone further work - conditioned |
| 0.0228 SUCCESS | <ul style="list-style-type: none"> Three person mixed DNA profile 3 person mixed profile - conditioned on 1 3 person mix remaining - supports non contribution |

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|----------------|---|
| 0.0208 SUCCESS | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile 1 2 person mix profile - support for contrib > 100 billion Two person mixed DNA profile |
| 0.0211 SUCCESS | 2 person mix profile - support for contrib > 100 billion 1 Excluded from mixed DNA profile Two person mixed DNA profile |
| 0.0198 SUCCESS | 1 2 person mixed profile - conditioned on Two person mixed DNA profile |
| 0.0186 SUCCESS | 2 person mixed profile - conditioned on 1 2 person mix rem - support for contribution > 100 billion Two person mixed DNA profile |
| 0.014 SUCCESS | 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion 1 Possible sub-threshold information Two person mixed DNA profile |
| 0.0168 SUCCESS | 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion 1 Possible sub-threshold information Two person mixed DNA profile |
| 0.0293 SUCCESS | 2 person mixed profile - conditioned on 1 Excluded from mixed DNA profile Two person mixed DNA profile |
| 0.014 SUCCESS | 2 person mixed profile - conditioned on Excluded from mixed DNA profile 1 Mix Rem DNA contrib < NCIDD matching Stringency |

| Count of EXHinterp | Column Labels | SUC Grand Total |
|--------------------|---------------|-----------------|
| Row Labels | FAIL | |
| 0.0000 | 9 | 9 |
| 0.0003 | 1 | 1 |
| 0.0004 | 1 | 1 |
| 0.0005 | 1 | 1 |
| 0.0007 | 1 | 1 |
| 0.0010 | 36 | 36 |
| 0.0011 | 34 1 | 35 |
| 0.0012 | 44 1 | 45 |
| 0.0013 | 34 | 34 |
| 0.0014 | 36 | 36 |
| 0.0015 | 30 3 | 33 |
| 0.0016 | 17 1 | 18 |
| 0.0017 | 31 1 | 32 |
| 0.0018 | 30 1 | 31 |
| 0.0019 | 27 4 | 31 |
| 0.0020 | 22 | 22 |
| 0.0021 | 21 | 21 |
| 0.0022 | 21 1 | 22 |
| 0.0023 | 20 1 | 21 |
| 0.0024 | 26 3 | 29 |
| 0.0025 | 26 1 | 27 |
| 0.0026 | 16 1 | 17 |
| 0.0027 | 24 3 | 27 |
| 0.0028 | 19 2 | 21 |
| 0.0029 | 14 | 14 |
| 0.0030 | 18 2 | 20 |
| 0.0031 | 22 1 | 23 |
| 0.0032 | 19 4 | 23 |
| 0.0033 | 27 1 | 28 |
| 0.0034 | 21 | 21 |
| 0.0035 | 24 1 | 25 |
| 0.0036 | 12 2 | 14 |
| 0.0037 | 14 2 | 16 |
| 0.0038 | 16 1 | 17 |
| 0.0039 | 16 1 | 17 |
| 0.0040 | 20 1 | 21 |
| 0.0041 | 15 2 | 17 |
| 0.0042 | 19 | 19 |
| 0.0043 | 14 2 | 16 |
| 0.0044 | 15 1 | 16 |
| 0.0045 | 18 2 | 20 |
| 0.0046 | 8 3 | 11 |
| 0.0047 | 13 1 | 14 |
| 0.0048 | 21 | 21 |
| 0.0049 | 12 | 12 |
| 0.0050 | 22 | 22 |
| 0.0051 | 15 2 | 17 |
| 0.0052 | 11 | 11 |
| 0.0053 | 9 1 | 10 |
| 0.0054 | 16 1 | 17 |
| 0.0055 | 18 3 | 21 |
| 0.0056 | 9 3 | 12 |
| 0.0057 | 15 3 | 18 |
| 0.0058 | 14 1 | 15 |
| 0.0059 | 17 1 | 18 |
| 0.0060 | 10 3 | 13 |
| 0.0061 | 12 3 | 15 |
| 0.0062 | 11 1 | 12 |
| 0.0063 | 11 5 | 16 |
| 0.0064 | 13 2 | 15 |
| 0.0065 | 17 5 | 22 |
| 0.0066 | 4 3 | 7 |
| 0.0067 | 4 7 | 11 |
| 0.0068 | 5 2 | 7 |
| 0.0069 | 7 3 | 10 |
| 0.0070 | 10 2 | 12 |
| 0.0071 | 4 5 | 9 |
| 0.0072 | 11 4 | 15 |
| 0.0073 | 9 5 | 14 |
| 0.0074 | 11 4 | 15 |
| 0.0075 | 5 1 | 6 |
| 0.0076 | 8 1 | 9 |
| 0.0077 | 7 1 | 8 |
| 0.0078 | 6 2 | 8 |
| 0.0079 | 9 1 | 10 |
| 0.0080 | 6 2 | 8 |
| 0.0081 | 12 2 | 14 |
| 0.0082 | 11 6 | 17 |
| 0.0083 | 10 3 | 13 |
| 0.0084 | 17 2 | 19 |
| 0.0085 | 7 5 | 12 |
| 0.0086 | 9 2 | 11 |
| 0.0087 | 9 2 | 11 |
| 0.0088 | 9 4 | 13 |
| 0.0089 | 7 1 | 8 |
| 0.0090 | 3 | 3 |
| 0.0091 | 4 3 | 7 |
| 0.0092 | 3 1 | 4 |
| 0.0093 | 5 4 | 9 |
| 0.0094 | 5 4 | 9 |
| 0.0095 | 5 6 | 11 |
| 0.0096 | 3 5 | 8 |
| 0.0097 | 1 | 1 |
| 0.0098 | 1 1 | 2 |
| 0.0099 | 2 | 2 |
| 0.0100 | 6 | 6 |
| 0.0101 | 8 4 | 12 |
| 0.0102 | 3 1 | 4 |
| 0.0103 | 4 1 | 5 |
| 0.0104 | 5 1 | 6 |
| 0.0105 | 5 3 | 8 |
| 0.0106 | 1 1 | 2 |
| 0.0107 | 3 | 3 |
| 0.0108 | 6 | 6 |
| 0.0109 | 4 1 | 5 |



| | | | |
|--------|---|---|----|
| 0.0110 | 2 | 5 | 7 |
| 0.0111 | 3 | 2 | 5 |
| 0.0112 | 5 | 2 | 7 |
| 0.0113 | 3 | 3 | 6 |
| 0.0114 | 1 | 1 | 2 |
| 0.0115 | 3 | 1 | 4 |
| 0.0116 | 1 | 1 | 2 |
| 0.0117 | 1 | | 1 |
| 0.0118 | 5 | 5 | 10 |
| 0.0119 | 3 | 4 | 7 |
| 0.0120 | 2 | 2 | 4 |
| 0.0121 | 8 | 1 | 9 |
| 0.0122 | 2 | 2 | 4 |
| 0.0123 | 4 | 3 | 7 |
| 0.0124 | 3 | 3 | 6 |
| 0.0125 | 2 | 2 | 4 |
| 0.0126 | 2 | 2 | 4 |
| 0.0127 | 5 | | 5 |
| 0.0128 | 5 | 3 | 8 |
| 0.0129 | 1 | 2 | 3 |
| 0.0130 | 5 | 1 | 6 |
| 0.0131 | 3 | 1 | 4 |
| 0.0132 | 1 | 2 | 3 |
| 0.0133 | 5 | 3 | 8 |
| 0.0134 | 3 | 2 | 5 |
| 0.0135 | 2 | 4 | 6 |
| 0.0136 | 5 | 3 | 8 |
| 0.0137 | 2 | | 2 |
| 0.0138 | 3 | 1 | 4 |
| 0.0139 | 1 | 3 | 4 |
| 0.0140 | 3 | 6 | 9 |
| 0.0141 | 2 | 1 | 3 |
| 0.0142 | 2 | 3 | 5 |
| 0.0143 | 3 | 4 | 7 |
| 0.0144 | 3 | 2 | 5 |
| 0.0145 | 2 | 1 | 3 |
| 0.0146 | 3 | 1 | 4 |
| 0.0147 | 3 | | 3 |
| 0.0148 | 3 | 2 | 5 |
| 0.0149 | 3 | | 3 |
| 0.0150 | 3 | 3 | 6 |
| 0.0151 | 5 | | 5 |
| 0.0152 | 2 | 1 | 3 |
| 0.0153 | 2 | | 2 |
| 0.0154 | 3 | 2 | 5 |
| 0.0155 | 2 | 2 | 2 |
| 0.0156 | 2 | 2 | 4 |
| 0.0157 | 1 | 1 | 2 |
| 0.0158 | 2 | 1 | 3 |
| 0.0159 | 1 | | 1 |
| 0.0160 | 2 | 4 | 6 |
| 0.0161 | 1 | 2 | 3 |
| 0.0162 | 3 | 4 | 7 |
| 0.0163 | 4 | | 4 |
| 0.0164 | 2 | 2 | 4 |
| 0.0165 | 3 | 1 | 4 |
| 0.0166 | 1 | 1 | 2 |
| 0.0167 | 3 | 1 | 4 |
| 0.0168 | 3 | 2 | 5 |
| 0.0169 | 2 | 1 | 3 |
| 0.0170 | 2 | | 2 |
| 0.0171 | 1 | | 1 |
| 0.0172 | 1 | 2 | 3 |
| 0.0173 | 3 | 2 | 5 |
| 0.0174 | 2 | 2 | 4 |
| 0.0175 | 2 | | 2 |
| 0.0176 | 4 | 1 | 5 |
| 0.0178 | 2 | 3 | 5 |
| 0.0179 | 1 | 1 | 2 |
| 0.0180 | 2 | | 2 |
| 0.0181 | 1 | | 1 |
| 0.0182 | 4 | 1 | 5 |
| 0.0183 | 1 | 2 | 3 |
| 0.0184 | 2 | 1 | 3 |
| 0.0185 | 3 | | 3 |
| 0.0186 | 2 | 3 | 5 |
| 0.0187 | 3 | | 3 |
| 0.0189 | 1 | 1 | 2 |
| 0.0190 | 2 | | 2 |
| 0.0191 | 2 | | 2 |
| 0.0192 | 2 | | 2 |
| 0.0193 | 1 | 1 | 2 |
| 0.0194 | 1 | | 1 |
| 0.0195 | 2 | 4 | 6 |
| 0.0196 | 1 | | 1 |
| 0.0197 | 3 | | 3 |
| 0.0198 | 2 | 3 | 5 |
| 0.0199 | 1 | 3 | 4 |
| 0.0200 | 1 | 1 | 2 |
| 0.0201 | 1 | | 1 |
| 0.0202 | 3 | 2 | 5 |
| 0.0203 | 3 | 3 | 6 |
| 0.0204 | 3 | | 3 |
| 0.0205 | 3 | 3 | 6 |
| 0.0206 | 1 | | 1 |
| 0.0207 | 4 | | 4 |
| 0.0208 | 1 | 3 | 4 |
| 0.0209 | 1 | | 1 |
| 0.0210 | 1 | 1 | 2 |
| 0.0211 | 4 | | 4 |
| 0.0212 | 3 | 1 | 4 |
| 0.0213 | 2 | | 2 |
| 0.0215 | 2 | 2 | 4 |
| 0.0216 | 1 | 1 | 2 |
| 0.0218 | 2 | 1 | 3 |
| 0.0219 | 1 | 2 | 3 |
| 0.0220 | 3 | 2 | 5 |
| 0.0221 | 2 | | 2 |
| 0.0222 | 2 | 2 | 4 |

| | | | |
|--------------------|-------------|------------|-------------|
| 0.0223 | 2 | 1 | 3 |
| 0.0224 | 1 | | 1 |
| 0.0225 | 1 | 1 | 1 |
| 0.0226 | 2 | 1 | 3 |
| 0.0227 | 1 | 1 | 2 |
| 0.0228 | 2 | 1 | 3 |
| 0.0229 | 1 | 1 | 2 |
| 0.0230 | 1 | 1 | 2 |
| 0.0231 | | 2 | 2 |
| 0.0232 | 1 | 1 | 2 |
| 0.0234 | | 2 | 2 |
| 0.0235 | 2 | 4 | 6 |
| 0.0236 | 1 | | 1 |
| 0.0238 | 1 | | 1 |
| 0.0239 | 1 | 2 | 3 |
| 0.0240 | | 1 | 1 |
| 0.0241 | 3 | 2 | 5 |
| 0.0242 | | 1 | 1 |
| 0.0243 | 1 | | 1 |
| 0.0244 | 2 | 2 | 4 |
| 0.0245 | 1 | 1 | 2 |
| 0.0246 | 3 | | 3 |
| 0.0247 | 2 | 1 | 3 |
| 0.0248 | 3 | 3 | 6 |
| 0.0249 | 3 | 1 | 4 |
| 0.0252 | | 1 | 1 |
| 0.0253 | 2 | | 2 |
| 0.0255 | 2 | | 2 |
| 0.0256 | | 3 | 3 |
| 0.0257 | 2 | 1 | 3 |
| 0.0258 | 1 | 1 | 2 |
| 0.0259 | | 1 | 1 |
| 0.0260 | 1 | 1 | 2 |
| 0.0261 | 1 | 1 | 2 |
| 0.0262 | 1 | | 1 |
| 0.0263 | 3 | | 3 |
| 0.0265 | 1 | | 1 |
| 0.0266 | 1 | | 1 |
| 0.0267 | | 2 | 2 |
| 0.0270 | 1 | | 1 |
| 0.0271 | | 1 | 1 |
| 0.0272 | | 1 | 1 |
| 0.0273 | 1 | 1 | 2 |
| 0.0274 | 1 | 2 | 3 |
| 0.0275 | | 2 | 2 |
| 0.0276 | 2 | 1 | 3 |
| 0.0277 | 1 | 1 | 2 |
| 0.0278 | | 3 | 3 |
| 0.0279 | 2 | | 2 |
| 0.0280 | 1 | 1 | 2 |
| 0.0281 | 1 | 1 | 2 |
| 0.0284 | 1 | | 1 |
| 0.0285 | | 1 | 1 |
| 0.0287 | | 2 | 2 |
| 0.0289 | 2 | 2 | 4 |
| 0.0290 | | 2 | 2 |
| 0.0292 | 2 | | 2 |
| 0.0293 | 2 | 2 | 4 |
| 0.0294 | | 1 | 1 |
| 0.0296 | | 3 | 3 |
| 0.0298 | 1 | | 1 |
| 0.0299 | 1 | 3 | 4 |
| 0.0300 | 1 | 1 | 2 |
| 0.0301 | 2 | | 2 |
| 0.0304 | | 1 | 1 |
| 0.0305 | 1 | 3 | 4 |
| 0.0306 | | 2 | 2 |
| 0.0309 | 2 | | 2 |
| 0.0311 | 1 | | 1 |
| 0.0312 | 1 | | 1 |
| 0.0314 | 1 | 1 | 2 |
| 0.0315 | | 2 | 2 |
| 0.0316 | 1 | 3 | 4 |
| 0.0318 | 1 | | 1 |
| 0.0319 | 1 | 2 | 3 |
| 0.0321 | 3 | | 3 |
| 0.0322 | 1 | | 1 |
| 0.0325 | 1 | | 1 |
| 0.0327 | 1 | 1 | 2 |
| 0.0328 | 1 | | 1 |
| 0.0329 | | 4 | 4 |
| 0.0330 | 2 | | 2 |
| 0.0346 | 3 | 2 | 5 |
| 0.0349 | 1 | | 1 |
| 0.0362 | 1 | | 1 |
| 0.0364 | 1 | | 1 |
| 0.0368 | | 1 | 1 |
| 0.0369 | 1 | | 1 |
| 0.0382 | 1 | | 1 |
| 0.0384 | | 1 | 1 |
| 0.0391 | | 1 | 1 |
| 0.0396 | 1 | | 1 |
| 0.0397 | 1 | | 1 |
| 0.0446 | | 1 | 1 |
| 0.0474 | | 1 | 1 |
| 0.0533 | 1 | | 1 |
| 0.0577 | | 1 | 1 |
| 0.0611 | | 1 | 1 |
| 0.0743 | | 1 | 1 |
| 0.0907 | 1 | | 1 |
| Grand Total | 1727 | 474 | 2201 |

| | | |
|--------|---------|----|
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| 0.0146 | SUCCESS | 1 |
| 0.0147 | FAIL | -1 |
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| 0.0148 | FAIL | -1 |
| 0.0148 | FAIL | -1 |
| 0.0148 | FAIL | -1 |
| 0.0148 | SUCCESS | 1 |
| 0.0148 | SUCCESS | 1 |
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| 0.0150 | FAIL | -1 |
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| 0.0150 | SUCCESS | 1 |
| 0.0150 | SUCCESS | 1 |
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| 0.0154 | FAIL | -1 |
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| 0.0154 | SUCCESS | 1 |
| 0.0155 | SUCCESS | 1 |
| 0.0155 | SUCCESS | 1 |
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| 0.0156 | SUCCESS | 1 |
| 0.0156 | SUCCESS | 1 |
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| 0.0158 | FAIL | -1 |
| 0.0158 | SUCCESS | 1 |
| 0.0159 | FAIL | -1 |
| 0.0160 | FAIL | -1 |
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| 0.0160 | SUCCESS | 1 |
| 0.0160 | SUCCESS | 1 |
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| 0.0161 | SUCCESS | 1 |
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| 0.0162 | SUCCESS | 1 |
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| 0.0163 | FAIL | -1 |
| 0.0163 | FAIL | -1 |
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| 0.0164 | SUCCESS | 1 |
| 0.0165 | FAIL | -1 |
| 0.0165 | FAIL | -1 |
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| 0.0166 | SUCCESS | 1 |
| 0.0167 | FAIL | -1 |
| 0.0167 | FAIL | -1 |
| 0.0167 | FAIL | -1 |
| 0.0167 | SUCCESS | 1 |

| | | |
|--------|---------|----|
| 0.0146 | FAIL | -1 |
| 0.0146 | SUCCESS | 1 |
| 0.0147 | FAIL | -1 |
| 0.0147 | FAIL | -1 |
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| 0.0148 | FAIL | -1 |
| 0.0148 | FAIL | -1 |
| 0.0148 | FAIL | -1 |
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| 0.0148 | SUCCESS | 1 |
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| 0.0149 | FAIL | -1 |
| 0.0150 | FAIL | -1 |
| 0.0150 | FAIL | -1 |
| 0.0150 | FAIL | -1 |
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| 0.0150 | SUCCESS | 1 |
| 0.0150 | SUCCESS | 1 |

| | | |
|--------|---------|----|
| 0.0168 | FAIL | -1 |
| 0.0168 | FAIL | -1 |
| 0.0168 | FAIL | -1 |
| 0.0168 | SUCCESS | 1 |
| 0.0168 | SUCCESS | 1 |
| 0.0169 | FAIL | -1 |
| 0.0169 | FAIL | -1 |
| 0.0169 | SUCCESS | 1 |
| 0.0170 | SUCCESS | 1 |
| 0.0170 | SUCCESS | 1 |
| 0.0171 | SUCCESS | 1 |
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| 0.0172 | SUCCESS | 1 |
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| 0.0173 | SUCCESS | 1 |
| 0.0174 | FAIL | -1 |
| 0.0174 | FAIL | -1 |
| 0.0174 | SUCCESS | 1 |
| 0.0174 | SUCCESS | 1 |
| 0.0175 | SUCCESS | 1 |
| 0.0175 | SUCCESS | 1 |
| 0.0176 | FAIL | -1 |
| 0.0176 | FAIL | -1 |
| 0.0176 | FAIL | -1 |
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| 0.0176 | SUCCESS | 1 |
| 0.0178 | FAIL | -1 |
| 0.0178 | FAIL | -1 |
| 0.0178 | SUCCESS | 1 |
| 0.0178 | SUCCESS | 1 |
| 0.0178 | SUCCESS | 1 |
| 0.0179 | FAIL | -1 |
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| 0.0180 | FAIL | -1 |
| 0.0180 | FAIL | -1 |
| 0.0181 | FAIL | -1 |
| 0.0182 | FAIL | -1 |
| 0.0182 | FAIL | -1 |
| 0.0182 | FAIL | -1 |
| 0.0182 | FAIL | -1 |
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| 0.0185 | FAIL | -1 |
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| 0.0186 | FAIL | -1 |
| 0.0186 | FAIL | -1 |
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| 0.0186 | SUCCESS | 1 |
| 0.0186 | SUCCESS | 1 |
| 0.0187 | FAIL | -1 |
| 0.0187 | FAIL | -1 |
| 0.0187 | FAIL | -1 |
| 0.0189 | FAIL | -1 |
| 0.0189 | SUCCESS | 1 |
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| 0.0192 | FAIL | -1 |
| 0.0192 | FAIL | -1 |
| 0.0193 | FAIL | -1 |
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| 0.0194 | FAIL | -1 |
| 0.0195 | FAIL | -1 |
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| 0.0195 | SUCCESS | 1 |
| 0.0195 | SUCCESS | 1 |
| 0.0195 | SUCCESS | 1 |
| 0.0195 | SUCCESS | 1 |
| 0.0196 | FAIL | -1 |

| | | |
|--------|---------|----|
| 0.0197 | SUCCESS | 1 |
| 0.0197 | SUCCESS | 1 |
| 0.0197 | SUCCESS | 1 |
| 0.0198 | FAIL | -1 |
| 0.0198 | FAIL | -1 |
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| 0.0198 | SUCCESS | 1 |
| 0.0198 | SUCCESS | 1 |
| 0.0199 | FAIL | -1 |
| 0.0199 | SUCCESS | 1 |
| 0.0199 | SUCCESS | 1 |
| 0.0199 | SUCCESS | 1 |
| 0.0200 | FAIL | -1 |
| 0.0200 | SUCCESS | 1 |
| 0.0201 | SUCCESS | 1 |
| 0.0202 | FAIL | -1 |
| 0.0202 | FAIL | -1 |
| 0.0202 | FAIL | -1 |
| 0.0202 | SUCCESS | 1 |
| 0.0202 | SUCCESS | 1 |
| 0.0203 | FAIL | -1 |
| 0.0203 | FAIL | -1 |
| 0.0203 | FAIL | -1 |
| 0.0203 | SUCCESS | 1 |
| 0.0203 | SUCCESS | 1 |
| 0.0203 | SUCCESS | 1 |
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| 0.0204 | FAIL | -1 |
| 0.0205 | FAIL | -1 |
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| 0.0205 | SUCCESS | 1 |
| 0.0205 | SUCCESS | 1 |
| 0.0205 | SUCCESS | 1 |
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| 0.0207 | FAIL | -1 |
| 0.0207 | FAIL | -1 |
| 0.0207 | FAIL | -1 |
| 0.0207 | FAIL | -1 |
| 0.0208 | FAIL | -1 |
| 0.0208 | SUCCESS | 1 |
| 0.0208 | SUCCESS | 1 |
| 0.0208 | SUCCESS | 1 |
| 0.0209 | FAIL | -1 |
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| 0.0210 | SUCCESS | 1 |
| 0.0211 | SUCCESS | 1 |
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| 0.0211 | SUCCESS | 1 |
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| 0.0215 | SUCCESS | 1 |
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| 0.0216 | SUCCESS | 1 |
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| 0.0219 | SUCCESS | 1 |
| 0.0220 | FAIL | -1 |
| 0.0220 | FAIL | -1 |
| 0.0220 | FAIL | -1 |
| 0.0220 | SUCCESS | 1 |
| 0.0220 | SUCCESS | 1 |
| 0.0221 | FAIL | -1 |
| 0.0221 | FAIL | -1 |
| 0.0222 | FAIL | -1 |
| 0.0222 | FAIL | -1 |
| 0.0222 | SUCCESS | 1 |
| 0.0222 | SUCCESS | 1 |

| | | |
|--------|---------|----|
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| 0.0225 | SUCCESS | 1 |
| 0.0226 | FAIL | -1 |
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| 0.0226 | SUCCESS | 1 |
| 0.0227 | FAIL | -1 |
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| 0.0228 | SUCCESS | 1 |
| 0.0229 | FAIL | -1 |
| 0.0229 | SUCCESS | 1 |
| 0.0230 | FAIL | -1 |
| 0.0230 | SUCCESS | 1 |
| 0.0231 | SUCCESS | 1 |
| 0.0231 | SUCCESS | 1 |
| 0.0232 | FAIL | -1 |
| 0.0232 | SUCCESS | 1 |
| 0.0234 | SUCCESS | 1 |
| 0.0234 | SUCCESS | 1 |
| 0.0235 | FAIL | -1 |
| 0.0235 | FAIL | -1 |
| 0.0235 | SUCCESS | 1 |
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| 0.0235 | SUCCESS | 1 |
| 0.0235 | SUCCESS | 1 |
| 0.0236 | FAIL | -1 |
| 0.0238 | FAIL | -1 |
| 0.0239 | FAIL | -1 |
| 0.0239 | SUCCESS | 1 |
| 0.0239 | SUCCESS | 1 |
| 0.0240 | SUCCESS | 1 |
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| 0.0241 | FAIL | -1 |
| 0.0241 | FAIL | -1 |
| 0.0241 | SUCCESS | 1 |
| 0.0241 | SUCCESS | 1 |
| 0.0242 | SUCCESS | 1 |
| 0.0243 | FAIL | -1 |
| 0.0244 | FAIL | -1 |
| 0.0244 | FAIL | -1 |
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| 0.0244 | SUCCESS | 1 |
| 0.0245 | FAIL | -1 |
| 0.0245 | SUCCESS | 1 |
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| 0.0246 | FAIL | -1 |
| 0.0247 | FAIL | -1 |
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| 0.0248 | FAIL | -1 |
| 0.0248 | FAIL | -1 |
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| 0.0248 | SUCCESS | 1 |
| 0.0249 | FAIL | -1 |
| 0.0249 | FAIL | -1 |
| 0.0249 | FAIL | -1 |
| 0.0249 | SUCCESS | 1 |
| 0.0252 | SUCCESS | 1 |
| 0.0253 | FAIL | -1 |
| 0.0253 | FAIL | -1 |
| 0.0255 | FAIL | -1 |
| 0.0255 | FAIL | -1 |
| 0.0256 | SUCCESS | 1 |
| 0.0256 | SUCCESS | 1 |
| 0.0256 | SUCCESS | 1 |
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| 0.0257 | FAIL | -1 |
| 0.0257 | SUCCESS | 1 |
| 0.0258 | FAIL | -1 |
| 0.0258 | SUCCESS | 1 |
| 0.0259 | SUCCESS | 1 |
| 0.0260 | FAIL | -1 |
| 0.0260 | SUCCESS | 1 |

| | | |
|--------|---------|----|
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| 0.0261 | SUCCESS | 1 |
| 0.0262 | FAIL | -1 |
| 0.0263 | FAIL | -1 |
| 0.0263 | FAIL | -1 |
| 0.0263 | FAIL | -1 |
| 0.0265 | FAIL | -1 |
| 0.0266 | FAIL | -1 |
| 0.0267 | SUCCESS | 1 |
| 0.0267 | SUCCESS | 1 |
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| 0.0272 | SUCCESS | 1 |
| 0.0273 | FAIL | -1 |
| 0.0273 | SUCCESS | 1 |
| 0.0274 | FAIL | -1 |
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| 0.0274 | SUCCESS | 1 |
| 0.0275 | SUCCESS | 1 |
| 0.0275 | SUCCESS | 1 |
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| 0.0276 | FAIL | -1 |
| 0.0276 | SUCCESS | 1 |
| 0.0277 | FAIL | -1 |
| 0.0277 | SUCCESS | 1 |
| 0.0278 | SUCCESS | 1 |
| 0.0278 | SUCCESS | 1 |
| 0.0278 | SUCCESS | 1 |
| 0.0279 | FAIL | -1 |
| 0.0279 | FAIL | -1 |
| 0.0280 | FAIL | -1 |
| 0.0280 | SUCCESS | 1 |
| 0.0281 | FAIL | -1 |
| 0.0281 | SUCCESS | 1 |
| 0.0284 | FAIL | -1 |
| 0.0285 | SUCCESS | 1 |
| 0.0287 | SUCCESS | 1 |
| 0.0287 | SUCCESS | 1 |
| 0.0289 | FAIL | -1 |
| 0.0289 | FAIL | -1 |
| 0.0289 | SUCCESS | 1 |
| 0.0289 | SUCCESS | 1 |
| 0.0290 | SUCCESS | 1 |
| 0.0290 | SUCCESS | 1 |
| 0.0292 | FAIL | -1 |
| 0.0292 | FAIL | -1 |
| 0.0293 | FAIL | -1 |
| 0.0293 | FAIL | -1 |
| 0.0293 | SUCCESS | 1 |
| 0.0293 | SUCCESS | 1 |
| 0.0294 | SUCCESS | 1 |
| 0.0296 | SUCCESS | 1 |
| 0.0296 | SUCCESS | 1 |
| 0.0296 | SUCCESS | 1 |
| 0.0298 | FAIL | -1 |
| 0.0299 | FAIL | -1 |
| 0.0299 | SUCCESS | 1 |
| 0.0299 | SUCCESS | 1 |
| 0.0299 | SUCCESS | 1 |
| 0.0300 | FAIL | -1 |
| 0.0300 | SUCCESS | 1 |
| 0.0301 | FAIL | -1 |
| 0.0301 | FAIL | -1 |
| 0.0304 | SUCCESS | 1 |
| 0.0305 | FAIL | -1 |
| 0.0305 | SUCCESS | 1 |
| 0.0305 | SUCCESS | 1 |
| 0.0305 | SUCCESS | 1 |
| 0.0306 | SUCCESS | 1 |
| 0.0306 | SUCCESS | 1 |
| 0.0309 | FAIL | -1 |
| 0.0309 | FAIL | -1 |
| 0.0311 | FAIL | -1 |
| 0.0312 | FAIL | -1 |
| 0.0314 | FAIL | -1 |
| 0.0314 | SUCCESS | 1 |
| 0.0315 | SUCCESS | 1 |
| 0.0315 | SUCCESS | 1 |
| 0.0316 | FAIL | -1 |
| 0.0316 | SUCCESS | 1 |

| | | |
|--------|---------|----|
| 0.0316 | SUCCESS | 1 |
| 0.0316 | SUCCESS | 1 |
| 0.0318 | FAIL | -1 |
| 0.0319 | FAIL | -1 |
| 0.0319 | SUCCESS | 1 |
| 0.0319 | SUCCESS | 1 |
| 0.0321 | FAIL | -1 |
| 0.0321 | FAIL | -1 |
| 0.0321 | FAIL | -1 |
| 0.0322 | FAIL | -1 |
| 0.0325 | FAIL | -1 |
| 0.0327 | FAIL | -1 |
| 0.0327 | SUCCESS | 1 |
| 0.0328 | FAIL | -1 |
| 0.0329 | SUCCESS | 1 |
| 0.0329 | SUCCESS | 1 |
| 0.0329 | SUCCESS | 1 |
| 0.0329 | SUCCESS | 1 |
| 0.0330 | FAIL | -1 |
| 0.0330 | FAIL | -1 |
| 0.0346 | FAIL | -1 |
| 0.0346 | FAIL | -1 |
| 0.0346 | FAIL | -1 |
| 0.0346 | SUCCESS | 1 |
| 0.0346 | SUCCESS | 1 |
| 0.0349 | FAIL | -1 |
| 0.0362 | FAIL | -1 |
| 0.0364 | FAIL | -1 |
| 0.0368 | SUCCESS | 1 |
| 0.0369 | FAIL | -1 |
| 0.0382 | FAIL | -1 |
| 0.0384 | SUCCESS | 1 |
| 0.0391 | SUCCESS | 1 |
| 0.0396 | FAIL | -1 |
| 0.0397 | FAIL | -1 |
| 0.0446 | SUCCESS | 1 |
| 0.0474 | SUCCESS | 1 |
| 0.0533 | FAIL | -1 |
| 0.0577 | SUCCESS | 1 |
| 0.0611 | SUCCESS | 1 |
| 0.0743 | SUCCESS | 1 |
| 0.0907 | FAIL | -1 |

TRUE 0.0046 Auto

Submitted as cells QPS advised no further work required - results available
Submitted as cells QPS advised no further work required - results available

TRUE 0.0022 Auto

Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
Submitted-results pending. QPS advised no further work required - results available

TRUE 0.0088 Auto

TRUE 0.0074 Auto
TRUE 0.0088 Auto
TRUE 0.0037 Auto
TRUE 0.0071 Auto
TRUE 0.0052 Auto

TRUE 0.0031 Auto

Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS
Submitted-results pending. QPS advised no further work required - results available

TRUE 0.0031 Auto
TRUE 0.0036 Auto
TRUE 0.0074 Auto
TRUE 0.0037 Auto

| | | | |
|-----------|------|--------|------|
| 672471318 | TRUE | 0.0055 | Auto |
| 628789678 | TRUE | 0.0073 | Auto |

Submitted-results pending.
Quality flag identified, on hold awaiting advice from QPS
Quality control failure, refer to QPS
Submitted-results pending.

| | | | |
|-----------|------|--------|------|
| 672471327 | TRUE | 0.0029 | Auto |
| 581879272 | TRUE | 0.0024 | Auto |
| 628961957 | TRUE | 0.0073 | Auto |
| 628961941 | TRUE | 0.0029 | Auto |
| 599196283 | TRUE | 0.0041 | Auto |
| 342233157 | TRUE | 0.0038 | Auto |
| 690651009 | TRUE | 0.005 | Auto |
| 581879691 | TRUE | 0.0067 | Auto |
| 688808010 | TRUE | 0.0039 | Auto |
| 688807933 | TRUE | 0.0068 | Auto |
| 599196456 | TRUE | 0.0049 | Auto |
| 688808174 | TRUE | 0.0032 | Auto |
| 690651179 | TRUE | 0.0078 | Auto |
| 690651185 | TRUE | 0.0029 | Auto |
| 688808207 | TRUE | 0.0038 | Auto |
| 599196478 | TRUE | 0.0022 | Auto |
| 688808270 | TRUE | 0.0073 | Auto |
| 581879886 | TRUE | 0.0023 | Auto |
| 688808942 | TRUE | 0.0029 | Auto |
| 688809018 | TRUE | 0.0071 | Auto |
| 688808997 | TRUE | 0.0049 | Auto |
| 688808801 | TRUE | 0.0033 | Auto |
| 688808680 | TRUE | 0.0044 | Auto |
| 690160041 | TRUE | 0.0051 | Auto |
| 690160013 | TRUE | 0.003 | Auto |
| 690160291 | TRUE | 0.0033 | Auto |
| 690160303 | TRUE | 0.0022 | Auto |
| 690160320 | TRUE | 0.0066 | Auto |

Submitted-results pending.
Quality flag identified, on hold awaiting advice from QPS
Quality control failure, refer to QPS
ENVM - Complex mixed DNA profile
Submitted-results pending.
Submitted-results pending.

| | | | |
|-----------|------|--------|------|
| 380300938 | TRUE | 0.0052 | Auto |
| 688809600 | TRUE | 0.0066 | Auto |
| 688809928 | TRUE | 0.0066 | Auto |
| 711157192 | TRUE | 0.0066 | Auto |
| 690161092 | TRUE | 0.0046 | Auto |
| 690161083 | TRUE | 0.0074 | Auto |
| 690161074 | TRUE | 0.0053 | Auto |
| 690161060 | TRUE | 0.0086 | Auto |

Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS

Submitted-results pending.

| | | | |
|-----------|------|--------|------|
| 710948282 | TRUE | 0.0022 | Auto |
| 599197268 | TRUE | 0.0023 | Auto |
| 685693459 | TRUE | 0.0045 | Auto |
| 727530907 | TRUE | 0.0078 | Auto |
| 599197470 | TRUE | 0.0032 | Auto |
| 690161845 | TRUE | 0.0066 | Auto |
| 690161827 | TRUE | 0.0057 | Auto |
| 727531085 | TRUE | 0.0085 | Auto |
| 727555981 | TRUE | 0.0033 | Auto |
| 712137797 | TRUE | 0.0038 | Auto |
| 712137829 | TRUE | 0.008 | Auto |

Submitted-results pending. Quality control failure - results not reportable

Submitted-results pending.

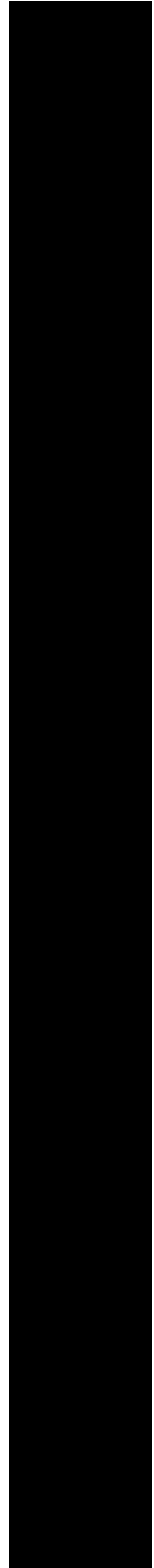
Submitted-results pending.
Submitted-results pending.

| | | | |
|-----------|------|--------|------|
| 711088403 | TRUE | 0.006 | Auto |
| 727531898 | TRUE | 0.0044 | Auto |
| 695315657 | TRUE | 0.0028 | Auto |
| 695321114 | TRUE | 0.0064 | Auto |
| 690162353 | TRUE | 0.0047 | Auto |
| 690636732 | TRUE | 0.0026 | Auto |
| 690636743 | TRUE | 0.0022 | Auto |
| 690162483 | TRUE | 0.0028 | Auto |
| 690162474 | TRUE | 0.0059 | Auto |
| 690162460 | TRUE | 0.0053 | Auto |
| 690162451 | TRUE | 0.0038 | Auto |
| 727532129 | TRUE | 0.0054 | Auto |
| 727532225 | TRUE | 0.0027 | Auto |
| 690162848 | TRUE | 0.0086 | Auto |
| 690162852 | TRUE | 0.0025 | Auto |
| 695321510 | TRUE | 0.0036 | Auto |
| 695321504 | TRUE | 0.0052 | Auto |
| 599195435 | TRUE | 0.0036 | Auto |
| 599195449 | TRUE | 0.0026 | Auto |
| 690163379 | TRUE | 0.008 | Auto |
| 690163385 | TRUE | 0.008 | Auto |
| 599198463 | TRUE | 0.005 | Auto |
| 599198908 | TRUE | 0.0068 | Auto |
| 727534031 | TRUE | 0.0031 | Auto |
| 690164470 | TRUE | 0.0031 | Auto |
| 727534332 | TRUE | 0.0029 | Auto |
| 599199163 | TRUE | 0.0062 | Auto |
| 690164755 | TRUE | 0.0056 | Auto |

Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS

TRUE 0.0054 Auto
TRUE 0.005 Auto
TRUE 0.0072 Auto
TRUE 0.0023 Auto
TRUE 0.0057 Auto
TRUE 0.0066 Auto
TRUE 0.0082 Auto
TRUE 0.0025 Auto
TRUE 0.0045 Auto
TRUE 0.0075 Auto
TRUE 0.0071 Auto
TRUE 0.0023 Auto
TRUE 0.0065 Auto
TRUE 0.0055 Auto
TRUE 0.0074 Auto
TRUE 0.0049 Auto
TRUE 0.0031 Auto
TRUE 0.0045 Auto
TRUE 0.0057 Auto
TRUE 0.0085 Auto
TRUE 0.0088 Auto
TRUE 0.005 Auto
TRUE 0.0039 Auto
TRUE 0.0042 Auto
TRUE 0.003 Auto
TRUE 0.0038 Auto
TRUE 0.0044 Auto
TRUE 0.003 Auto
TRUE 0.0028 Auto
TRUE 0.0037 Auto
TRUE 0.0066 Auto
TRUE 0.0081 Auto
TRUE 0.0033 Auto
TRUE 0.0067 Auto
TRUE 0.0035 Auto
TRUE 0.0033 Auto
TRUE 0.0044 Auto
TRUE 0.005 Auto
TRUE 0.0029 Auto
TRUE 0.006 Auto
TRUE 0.0078 Auto
TRUE 0.0083 Auto
TRUE 0.0045 Auto
TRUE 0.0025 Auto
TRUE 0.0051 Auto
TRUE 0.008 Auto
TRUE 0.0043 Auto
TRUE 0.0036 Auto
TRUE 0.0077 Auto
TRUE 0.0025 Auto
TRUE 0.0029 Auto
TRUE 0.0033 Auto
TRUE 0.0028 Auto
TRUE 0.0039 Auto
TRUE 0.0043 Auto
TRUE 0.0067 Auto
TRUE 0.0034 Auto
TRUE 0.0031 Auto
TRUE 0.0031 Auto
TRUE 0.004 Auto
TRUE 0.0041 Auto
TRUE 0.0026 Auto
TRUE 0.0038 Auto
TRUE 0.0031 Auto
TRUE 0.0044 Auto
TRUE 0.0041 Auto
TRUE 0.0088 Auto
TRUE 0.0037 Auto
TRUE 0.0063 Auto
TRUE 0.0086 Auto
TRUE 0.0037 Auto
TRUE 0.0063 Auto
TRUE 0.0067 Auto

| | | | |
|------|--------|------|---|
| TRUE | 0.0028 | Auto | Submitted-results pending. |
| TRUE | 0.0034 | Auto | Submitted-results pending. |
| TRUE | 0.003 | Auto | Submitted-results pending. |
| TRUE | 0.0059 | Auto | Submitted-results pending. |
| TRUE | 0.0074 | Auto | Submitted-results pending. |
| TRUE | 0.0045 | Auto | Submitted-results pending. |
| TRUE | 0.0055 | Auto | Submitted-results pending. |
| TRUE | 0.0034 | Auto | Submitted-results pending. |
| TRUE | 0.0082 | Auto | Submitted-results pending. |
| TRUE | 0.0054 | Auto | Submitted-results pending. |
| TRUE | 0.0044 | Auto | Submitted-results pending. |
| TRUE | 0.0023 | Auto | Submitted-results pending. |
| TRUE | 0.0042 | Auto | Submitted-results pending. |
| TRUE | 0.0025 | Auto | Hair located. Submitted-results pending |
| | | | Submitte |
| | | | d-results |
| | | | pending. |
| | | | Quality |
| | | | flag |
| | | | identified, |
| | | | on hold |
| | | | awaiting |
| | | | advice |
| | | | from QPS |
| | | | Quality |
| | | | control |
| | | | failure, |
| | | | refer to |
| TRUE | 0.0023 | Auto | QPS |
| | | | Submitte |
| | | | d-results |
| | | | pending. |
| | | | Quality |
| | | | flag |
| | | | identified, |
| | | | on hold |
| | | | awaiting |
| | | | advice |
| | | | from QPS |
| | | | Quality |
| | | | control |
| | | | failure, |
| | | | refer to |
| TRUE | 0.007 | Auto | QPS |
| | | | Submitte |
| | | | d-results |
| | | | pending. |
| | | | Sample |
| | | | processe |
| | | | d and |
| | | | final |
| | | | results |
| | | | under |
| TRUE | 0.0031 | Auto | Submitte |
| | | | d-results |
| | | | pending. |
| | | | Sample |
| | | | processe |
| | | | d and |
| | | | final |
| | | | results |
| | | | under |
| TRUE | 0.0039 | Auto | Submitte |
| | | | d-results |
| | | | pending. |
| | | | Sample |
| | | | processe |
| | | | d and |
| | | | final |
| | | | results |
| | | | under |
| TRUE | 0.0038 | Auto | Micro positive for sperm. Submitted-Results pending |
| TRUE | 0.0044 | Auto | presump Saliva test positive |
| TRUE | 0.007 | Auto | |



| | | | |
|------|-------------|---------|--|
| TRUE | 0.0054 Auto | | Presumptive blood test pos. Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor Submitted for cells. Presumptive saliva test pending. Presump |
| TRUE | 0.0087 Auto | | Saliva test negative Submitted-results pending. Micro neg for sperm Submitted-results pending. Micro neg for sperm Submitted-results pending. Micro neg for sperm Submitted-results pending. Presump |
| TRUE | 0.0046 Auto | | Saliva test negative Micro neg for sperm Single Source DNA profile - assumed known contributor Submitted for cells. Presumptive saliva test pending. Presump |
| TRUE | 0.0022 Auto | | Saliva test negative Micro neg for sperm Submitted-results pending. Micro neg for sperm Submitted-results pending. Micro neg for sperm Submitted-results pending. Presump |
| TRUE | 0.0062 Auto | | Saliva test negative Micro neg for sperm Submitted-results pending. Micro neg for sperm Submitted-results pending. Micro neg for sperm Submitted-results pending. Presump |
| TRUE | 0.0023 Auto | SUCCESS | Saliva test negative Micro neg for sperm Single Source DNA profile - assumed known contributor Submitted for cells. Presumptive saliva test pending. Presump |

Micro positive for sperm. Submitted-Results pending Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100

0.0079 SUCCESS billion

not auto

0.0057 SUCCESS SS DNA profile 9 loci and above LR > 100 billion

not auto

Submitted-results pending.
No DNA detected
This sample has undergone further processing
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Presump saliva positive. Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

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-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

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-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

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-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison
Submitted-results pending.
Complex mixed profile unsuitable for interp or

0 FAIL

-1 comparison

| | | |
|--------|---------------|--|
| 0 FAIL | -1 comparison | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 0 FAIL | -1 comparison | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 0 FAIL | -1 comparison | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 0 FAIL | -1 comparison | Submitted-results pending. DNA insufficient for further processing This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison |
| 0 FAIL | -1 comparison | Submitted-results pending. Interim result - sample undergoing rework Complex mixed profile unsuitable for interp or comparison |
| 0 FAIL | -1 comparison | Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison |
| 0 FAIL | -1 comparison | Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison |
| 0 FAIL | -1 comparison | Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison |
| 0 FAIL | -1 comparison | Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison |
| 0 FAIL | -1 comparison | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison |
| 0 FAIL | -1 comparison | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison |
| 0 FAIL | -1 comparison | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix- support for contrib 1 billion - 100 billion 3 person mix - supports non contribution 3 person mix - supports non contribution This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison |
| 0 FAIL | -1 comparison | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison |

| | | | | |
|----------|------|----------|------|--|
| 7.1E+08 | TRUE | 0 Manual | FAIL | Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for intercomparison |
| 7.1E+08 | TRUE | 0 Manual | FAIL | Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for intercomparison |
| 6.95E+08 | TRUE | 0 Manual | FAIL | |
| 5.99E+08 | TRUE | 0 Manual | FAIL | ENVN - Partial profile unsuitable for comparison purposes |
| 5.99E+08 | TRUE | 0 Manual | FAIL | ENVN- Complex mixture unsuitable for intercomparison |
| 5.82E+08 | TRUE | 0 Manual | FAIL | ENVN- Complex mixture unsuitable for intercomparison |

| | | | | |
|----------|------|----------|------|---|
| | | | | Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison |
| 7.1E+08 | TRUE | 0 Manual | FAIL | Submitted-results pending. No DNA detected This sample has undergone further processing Complex mixed profile unsuitable for interp or comparison |
| 7.1E+08 | TRUE | 0 Manual | FAIL | on |
| 5.99E+08 | TRUE | 0 Manual | FAIL | ENVM- Complex mixture unsuitable for interp or comparison |
| 7.28E+08 | TRUE | 0 Manual | | |
| 7.28E+08 | TRUE | 0 Manual | | |
| 7.28E+08 | TRUE | 0 Manual | | |
| 7.28E+08 | TRUE | 0 Manual | | |
| 5.8E+08 | TRUE | 0 Manual | | |
| 7.28E+08 | TRUE | 0 Manual | | |
| 7.28E+08 | TRUE | 0 Manual | | |
| 7.28E+08 | TRUE | 0 Manual | | ENVM -Partial DNA profile |
| 7.28E+08 | TRUE | 0 Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes |
| 7.28E+08 | TRUE | 0 Manual | | ENVM - No DNA profile |
| | | | | Submitted-results pending. No DNA detected |
| 3.83E+08 | TRUE | 0 Manual | | |

| | | | |
|---------|------|----------|--|
| 7.1E+08 | TRUE | 0 Manual | Submitted-results pending. No DNA detected This sample has undergone further processing No DNA profile Submitted-results pending. No DNA detected This sample has undergone further processing No DNA profile Possible sub-threshold information |
| 7.1E+08 | TRUE | 0 Manual | Submitted-results pending. No DNA detected This sample has undergone further processing No DNA profile Possible sub-threshold information |
| 7.1E+08 | TRUE | 0 Manual | Submitted-results pending. No DNA detected This sample has undergone further processing No DNA profile Possible sub-threshold information |

| | | | | |
|----------|------|--------|--------|---|
| | | | | Submitted- results pending. No DNA detected This sample has undergone further processing No DNA profile |
| 7.1E+08 | TRUE | 0 | Manual | |
| 7.28E+08 | TRUE | 0 | Manual | |
| 7.28E+08 | TRUE | 0 | Manual | |
| 7.28E+08 | TRUE | 0 | Manual | |
| 7.28E+08 | TRUE | 0 | Manual | ENVM - No DNA profile |
| 7.28E+08 | TRUE | 0 | Manual | |
| 7.28E+08 | TRUE | 0 | Manual | |
| | | | | Submitted- results pending. No DNA detected |
| 5.24E+08 | TRUE | 0 | Manual | |
| 5.99E+08 | TRUE | 0.0002 | Manual | FAIL ENVM - Partial profile unsuitable for comparison purposes |
| 5.82E+08 | TRUE | 0.0002 | Manual | FAIL ENVM - Partial profile unsuitable for comparison purposes |
| 7.28E+08 | TRUE | 0.0002 | Manual | FAIL ENVM- Complex mixture unsuitable for interp or comparison |
| 7.28E+08 | TRUE | 0.0002 | Manual | FAIL ENVM- Complex mixture unsuitable for interp or comparison |
| 7.28E+08 | TRUE | 0.0002 | Manual | FAIL ENVM - Partial profile unsuitable for comparison purposes |
| 7.28E+08 | TRUE | 0.0002 | Manual | FAIL ENVM - Partial profile unsuitable for comparison purposes |
| 7.28E+08 | TRUE | 0.0002 | Manual | |
| 7.28E+08 | TRUE | 0.0002 | Manual | |
| 5.99E+08 | TRUE | 0.0002 | Manual | FAIL ENVM - Partial profile unsuitable for comparison purposes |
| 6.9E+08 | TRUE | 0.0002 | Manual | FAIL ENVM - Partial profile unsuitable for comparison purposes |
| 7.27E+08 | TRUE | 0.0002 | Manual | ENVM - No DNA profile |
| 6.9E+08 | TRUE | 0.0002 | Manual | |
| 6.95E+08 | TRUE | 0.0003 | Manual | FAIL ENVM- Complex mixture unsuitable for interp or comparison |
| | | | | Submitted- results pending. No DNA detected |
| 7.1E+08 | TRUE | 0.0003 | Manual | |
| 5.99E+08 | TRUE | 0.0003 | Manual | ENVM - No DNA profile |
| 5.99E+08 | TRUE | 0.0003 | Manual | FAIL ENVM - Partial profile unsuitable for comparison purposes |
| 5.99E+08 | TRUE | 0.0003 | Manual | ENVM -Partial DNA profile |
| 5.99E+08 | TRUE | 0.0003 | Manual | FAIL ENVM - Partial profile unsuitable for comparison purposes |
| 6.9E+08 | TRUE | 0.0003 | Manual | |
| 6.95E+08 | TRUE | 0.0004 | Manual | FAIL ENVM - Partial profile unsuitable for comparison purposes |
| 5.99E+08 | TRUE | 0.0004 | Manual | FAIL ENVM - Partial profile unsuitable for comparison purposes |
| | | | | Submitted- results pending. Complex mixed profile unsuitable for interp or comparison |
| 6.9E+08 | TRUE | 0.0004 | Manual | FAIL on |
| 7.27E+08 | TRUE | 0.0004 | Manual | FAIL ENVM - Partial profile unsuitable for comparison purposes |
| 5.99E+08 | TRUE | 0.0005 | Manual | ENVM -Partial DNA profile |

| | | | | | |
|----------|------|--------|--------|------|---|
| 6.9E+08 | TRUE | 0.0005 | Manual | | |
| 6.9E+08 | TRUE | 0.0005 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes Submitted results pending. Presumptive PSA test positive, no sperm found Partial DNA profile unsuitable for comparison purposes |
| 6.9E+08 | TRUE | 0.0005 | Manual | FAIL | ENVM -Partial DNA profile |
| 7.28E+08 | TRUE | 0.0006 | Manual | | |
| 7.27E+08 | TRUE | 0.0006 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes |
| 5.99E+08 | TRUE | 0.0007 | Manual | FAIL | ENVM- Complex mixture unsuitable for inter or comparison Micro positive for sperm. Submitted Results pending No DNA detected This sample has undergone further processing Partial DNA profile unsuitable for comparison purposes |
| 5.99E+08 | TRUE | 0.0007 | Manual | FAIL | ENVM - No DNA profile |
| 7.28E+08 | TRUE | 0.0007 | Manual | | |
| 6.9E+08 | TRUE | 0.0007 | Manual | | |
| 6.95E+08 | TRUE | 0.0007 | Manual | FAIL | ENVM- Complex mixture unsuitable for inter or comparison |
| 5.99E+08 | TRUE | 0.0008 | Manual | | |
| 5.99E+08 | TRUE | 0.0008 | Manual | FAIL | ENVM- Complex mixture unsuitable for inter or comparison |
| 7.28E+08 | TRUE | 0.0009 | Manual | | |
| 7.27E+08 | TRUE | 0.0009 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes Submitted results pending. Complex mixed profile unsuitable for inter or comparison |
| 7.11E+08 | TRUE | 0.001 | Manual | FAIL | on |

| | | | | | |
|----------|------|-------|--------|------|--|
| 6.63E+08 | TRUE | 0.001 | Manual | | Submitted-results pending. |
| 7.11E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 6.19E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 7.11E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.11E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 6.19E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |

| | | | | | |
|----------|------|-------|--------|------|---|
| 6.29E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.72E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.1E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 4.56E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.1E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |

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|----------|------|-------|--------|------|---|
| 6.86E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.95E+08 | TRUE | 0.001 | Manual | | |
| 7.11E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.89E+08 | TRUE | 0.001 | Manual | | |
| 6.45E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |

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|----------|------|-------|--------|------|--|
| 7.11E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.12E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.28E+08 | TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| 7.28E+08 | TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| 6.9E+08 | TRUE | 0.001 | Manual | | |
| 6.86E+08 | TRUE | 0.001 | Manual | | Submitted-results pending. |
| 5.8E+08 | TRUE | 0.001 | Manual | | |
| 7.11E+08 | TRUE | 0.001 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 7.1E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.11E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.28E+08 | TRUE | 0.001 | Manual | | |
| 7.28E+08 | TRUE | 0.001 | Manual | | |

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|----------|------|-------|--------|------|--|
| 7.11E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.13E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.28E+08 | TRUE | 0.001 | Manual | | |
| 7.13E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.12E+08 | TRUE | 0.001 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 7.28E+08 | TRUE | 0.001 | Manual | | |
| 7.12E+08 | TRUE | 0.001 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 5.99E+08 | TRUE | 0.001 | Manual | | |
| 6.9E+08 | TRUE | 0.001 | Manual | | |

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|----------|------|-------|--------|------|---|
| 6.9E+08 | TRUE | 0.001 | Manual | FAIL | Hair located. Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison. Submitted-results pending. No DNA profile - possible sub-threshold peaks. |
| 7.13E+08 | TRUE | 0.001 | Manual | | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison. |
| 7.11E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. No DNA profile - possible sub-threshold peaks. |
| 6.9E+08 | TRUE | 0.001 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks. |
| 7.12E+08 | TRUE | 0.001 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks. |
| 7.27E+08 | TRUE | 0.001 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks. |
| 7.1E+08 | TRUE | 0.001 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks. |

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|----------|------|--------|--------|------|--|
| 7.11E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.95E+08 | TRUE | 0.001 | Manual | | |
| 7.12E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.12E+08 | TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.73E+08 | TRUE | 0.0011 | Manual | | No DNA profile Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.11E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison |
| 6.86E+08 | TRUE | 0.0011 | Manual | FAIL | purposes |
| 6.89E+08 | TRUE | 0.0011 | Manual | FAIL | ENVN - Partial profile unsuitable for comparison purposes |

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|----------|------|--------|--------|------|---|
| 6.86E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation or comparison |
| 6.55E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation or comparison |
| 7.11E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.1E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation or comparison |
| 7.1E+08 | TRUE | 0.0011 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |

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|----------|------|--------|--------|------|---|
| 7.11E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.11E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.11E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.9E+08 | TRUE | 0.0011 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes |
| 7.12E+08 | TRUE | 0.0011 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 7.11E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |

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|----------|------|--------|--------|------|---|
| 7.1E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes. Micro positive for sperm. Submitted-Results pending. Partial DNA profile unsuitable for comparison purposes. |
| 6.44E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for inter or comparison purposes. Submitted-results pending. Complex mixed profile unsuitable for inter or comparison purposes. |
| 7.12E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. No DNA profile. Possible sub-threshold information. |
| 7.11E+08 | TRUE | 0.0011 | Manual | | |
| 6.91E+08 | TRUE | 0.0011 | Manual | | |
| 6.9E+08 | TRUE | 0.0011 | Manual | | |
| 7.28E+08 | TRUE | 0.0011 | Manual | | |
| 6.95E+08 | TRUE | 0.0011 | Manual | FAIL | Complex mixed profile unsuitable for inter or comparison purposes. Submitted-results pending. No DNA profile. |
| 7.1E+08 | TRUE | 0.0011 | Manual | | |

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|----------|------|--------|--------|------|---|
| 7.12E+08 | TRUE | 0.0011 | Manual | FAIL | Semen not detected Submitted as cells Partial DNA profile unsuitable for comparison purposes Submitted-results pending. No DNA profile - possible sub-threshold peaks Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 6.55E+08 | TRUE | 0.0011 | Manual | | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.11E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.28E+08 | TRUE | 0.0011 | Manual | | |
| 7.28E+08 | TRUE | 0.0011 | Manual | | |
| 7.13E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes Submitted-results pending. Complex mixed profile unsuitable for interpor comparison |
| 7.1E+08 | TRUE | 0.0011 | Manual | FAIL | |

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|----------|------|--------|--------|------|--|
| | | | | | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 6.63E+08 | TRUE | 0.0011 | Manual | FAIL | |
| 7.28E+08 | TRUE | 0.0011 | Manual | | Single Source DNA profile - assumed known contributor |
| 6.9E+08 | TRUE | 0.0011 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| 7.28E+08 | TRUE | 0.0011 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| 5.99E+08 | TRUE | 0.0011 | Manual | | |
| 6.9E+08 | TRUE | 0.0011 | Manual | | |
| 7.27E+08 | TRUE | 0.0011 | Manual | | |
| | | | | | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.11E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Micro neg for sperm Complex mixed profile unsuitable for interp or comparison |
| 7.28E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.12E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|----------|------|--------|--------|------|--|
| 7.27E+08 | TRUE | 0.0011 | Manual | | Submitted-results pending. Semen not detected. No DNA profile - possible sub-threshold peaks. |
| 7.27E+08 | TRUE | 0.0011 | Manual | | |
| 7.11E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes. Submitted-results pending. Sample processed and final results under Submitted-results pending. Complex mixed profile unsuitable for interpretation. |
| 7.13E+08 | TRUE | 0.0011 | Manual | | |
| 6.73E+08 | TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation. |
| 6.9E+08 | TRUE | 0.0011 | Manual | | |
| 3.83E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation. |

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|----------|------|--------|--------|------|---|
| 7.11E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 5.06E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.1E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.1E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.11E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |

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|----------|------|--------|--------|------|---|
| 6.9E+08 | TRUE | 0.0012 | Manual | FAIL | Presump. PSA test positive, no sperm found Complex mixed profile unsuitabl e for interp or comparis on Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |
| 6.85E+08 | TRUE | 0.0012 | Manual | FAIL | Submitte d as cells, Presump saliva test pending presump Saliva test positive Complex mixed profile unsuitabl e for interp or comparis on |
| 7.12E+08 | TRUE | 0.0012 | Manual | FAIL | Submitte d as cells, Presump saliva test pending presump Saliva test positive Complex mixed profile unsuitabl e for interp or comparis on Submitte d-results pending. Partial DNA profile unsuitabl e for comparis on |
| 7.1E+08 | TRUE | 0.0012 | Manual | FAIL | Submitte d as cells, Presump saliva test pending presump Saliva test positive Complex mixed profile unsuitabl e for interp or comparis on Submitte d-results pending. Partial DNA profile unsuitabl e for comparis on purposes |

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|----------|------|--------|--------|------|---|
| 7.11E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.28E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted as cells. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.0012 | Manual | | No DNA profile. Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |

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|----------|------|--------|--------|------|--|
| 7.11E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 6.86E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 6.63E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison purposes |
| 6.63E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.11E+08 | TRUE | 0.0012 | Manual | | No DNA profile - possible sub-threshold peaks |

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|----------|------|--------|--------|------|---|
| 6.9E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.28E+08 | TRUE | 0.0012 | Manual | | |
| 7.11E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.55E+08 | TRUE | 0.0012 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 6.45E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 6.29E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |

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|----------|------|--------|--------|------|---|
| 7.11E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.11E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.11E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted as cells, Presumptive saliva test pending Presumptive Saliva test negative Complex mixed profile unsuitable for intercomparison |
| 7.11E+08 | TRUE | 0.0012 | Manual | FAIL | |
| 6.9E+08 | TRUE | 0.0012 | Manual | | |

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|----------|------|--------|--------|------|--|
| | | | | | Submitted for cells. Presumptive saliva test pending. Presumptive Saliva test negative. Complex mixed profile unsuitable for intercomparison |
| 6.63E+08 | TRUE | 0.0012 | Manual | FAIL | on |
| 7.28E+08 | TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for intercomparison |
| 7.28E+08 | TRUE | 0.0012 | Manual | | |
| 5.8E+08 | TRUE | 0.0012 | Manual | | Single Source DNA profile - assumed known contributor |
| | | | | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 7.11E+08 | TRUE | 0.0012 | Manual | | Submitted-results pending. Partial DNA profile unsuitable for comparison |
| 7.13E+08 | TRUE | 0.0012 | Manual | FAIL | purposes |
| 7.28E+08 | TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for intercomparison |
| | | | | | Presumptive saliva positive. Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.9E+08 | TRUE | 0.0012 | Manual | FAIL | on |
| 6.9E+08 | TRUE | 0.0012 | Manual | | |

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|----------|------|--------|--------|------|--|
| 7.1E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.12E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.12E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 7.12E+08 | TRUE | 0.0012 | Manual | | Presumptive blood test pos. Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 6.9E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |

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|----------|------|--------|--------|------|---|
| 7.12E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 6.9E+08 | TRUE | 0.0012 | Manual | | |
| 7.12E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.91E+08 | TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.45E+08 | TRUE | 0.0013 | Manual | FAIL | No DNA profile |
| 6.03E+08 | TRUE | 0.0013 | Manual | FAIL | Complex mixed profile unsuitable for intercomparison |
| 6.86E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison |
| 7.11E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |

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|----------|------|--------|--------|------|--|
| 7.1E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.1E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for intercomparison purposes |
| 7.11E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.89E+08 | TRUE | 0.0013 | Manual | | |
| 7.11E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.9E+08 | TRUE | 0.0013 | Manual | | |
| 7.11E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |

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|----------|------|--------|--------|------|---|
| 6.29E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes. Semen not detected. Submitted as cells. Complex mixed profile unsuitable for interpretation. |
| 7.11E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation. |
| 7.11E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation. |
| 7.11E+08 | TRUE | 0.0013 | Manual | FAIL | Micro positive for sperm. Submitted-Results pending. Complex mixed profile unsuitable for interpretation. |
| 7.1E+08 | TRUE | 0.0013 | Manual | FAIL | |

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|----------|------|--------|--------|------|--|
| 6.73E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.12E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.11E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.12E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 5.99E+08 | TRUE | 0.0013 | Manual | | ENVM -Partial DNA profile |

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|----------|------|--------|--------|------|--|
| 7.11E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted for cells. Presumptive saliva test pending. Presumptive Saliva test negative. Complex mixed profile unsuitable for interpretation or comparison. |
| 7.11E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted for cells. Presumptive saliva test pending. presumptive Saliva test positive. Complex mixed profile unsuitable for interpretation or comparison. |
| 6.02E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison. |
| 7.28E+08 | TRUE | 0.0013 | Manual | | |
| 7.28E+08 | TRUE | 0.0013 | Manual | | |
| 7.12E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison. |

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|----------|------|--------|--------|------|--|
| 6.63E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted for cells. Presumptive saliva test pending. Presumptive Saliva test negative Partial DNA profile unsuitable for comparison purposes Submitted-results pending. Complex mixed profile unsuitable for inter or comparison |
| 7.72E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. No DNA profile Possible sub-threshold information Submitted-results pending. Partial DNA profile unsuitable for comparison purposes Submitted-results pending. Complex mixed profile unsuitable for inter or comparison |
| 7.13E+08 | TRUE | 0.0013 | Manual | | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes Submitted-results pending. Complex mixed profile unsuitable for inter or comparison |
| 7.1E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for inter or comparison |
| 7.12E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for inter or comparison |
| 7.27E+08 | TRUE | 0.0013 | Manual | FAIL | Complex mixed profile unsuitable for inter or comparison |

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|----------|------|--------|--------|------|--|
| 6.9E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Micro positive for sperm. Submitted-Results pending Partial DNA profile unsuitable for comparison purposes Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 6.29E+08 | TRUE | 0.0013 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 6.9E+08 | TRUE | 0.0013 | Manual | | |
| 7.13E+08 | TRUE | 0.0013 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 7.28E+08 | TRUE | 0.0013 | Manual | | |
| 7.91E+08 | TRUE | 0.0013 | Manual | | Submitted-results pending. Micro neg for sperm Complex mixed profile unsuitable for interper or comparison |
| 7.27E+08 | TRUE | 0.0013 | Manual | FAIL | |

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|----------|------|--------|--------|------|---|
| 6.86E+08 | TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.95E+08 | TRUE | 0.0014 | Manual | | |
| 6.63E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 5.06E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 5.85E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.63E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 5.99E+08 | TRUE | 0.0014 | Manual | | |

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|----------|------|--------|--------|------|---|
| 6.29E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.1E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.1E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.1E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |

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|----------|------|--------|--------|------|---|
| 7.11E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.11E+08 | TRUE | 0.0014 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 6.63E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 6.19E+08 | TRUE | 0.0014 | Manual | | No DNA profile Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.11E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.12E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |

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|----------|------|--------|--------|------|--|
| 7.11E+08 | TRUE | 0.0014 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 7.11E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 6.55E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.11E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 6.64E+08 | TRUE | 0.0014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| 6.29E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |

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|----------|------|--------|--------|------|--|
| 7.11E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted for cells. Presumptive saliva test pending. Presumptive Saliva test negative. Complex mixed profile unsuitable for interpretation or comparison. |
| 6.73E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison. |
| 6.73E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison. |
| 6.73E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison. |
| 7.11E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted for cells. Presumptive saliva test pending. Presumptive Saliva test negative. Complex mixed profile unsuitable for interpretation or comparison. |

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|----------|------|--------|--------|------|--|
| 7.12E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.13E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.11E+08 | TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 7.12E+08 | TRUE | 0.0014 | Manual | | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.12E+08 | TRUE | 0.0014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| 7.27E+08 | TRUE | 0.0014 | Manual | | |
| 7.27E+08 | TRUE | 0.0014 | Manual | FAIL | |

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|----------|------|--------|--------|---|
| | | | | Submitte d-results pending. No DNA profile - possible sub- threshold peaks |
| 7.12E+08 | TRUE | 0.0014 | Manual | |
| 6.95E+08 | TRUE | 0.0014 | Manual | Micro positive for sperm. Submitted-Results pending |
| | | | | Submitte d-results pending. No DNA profile - possible sub- threshold peaks |
| 7.11E+08 | TRUE | 0.0014 | Manual | Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |
| 6.29E+08 | TRUE | 0.0014 | Manual | FAIL |
| | | | | Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |
| 7.13E+08 | TRUE | 0.0014 | Manual | FAIL |
| 6.9E+08 | TRUE | 0.0014 | Manual | |
| | | | | Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |
| 6.85E+08 | TRUE | 0.0015 | Manual | FAIL |

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|----------|------|--------|--------|------|---|
| 6.55E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.03E+08 | TRUE | 0.0015 | Manual | | |
| 6.86E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.1E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 5.85E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |

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|----------|------|--------|--------|------|--|
| 7.1E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Interim result - sample undergoing rework. Complex mixed profile unsuitable for interpretation or comparison. |
| 7.11E+08 | TRUE | 0.0015 | Manual | | Submitted-results pending. No DNA profile. Possible sub-threshold information. |
| 7.11E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison. |
| 6.89E+08 | TRUE | 0.0015 | Manual | | Submitted as cells. Single Source DNA profile - assumed known contributor. |
| 7.11E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison. |

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|----------|------|--------|--------|------|---|
| 7.11E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.0015 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 7.1E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.86E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |

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|----------|------|--------|--------|---------|---|
| 6.63E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.9E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.12E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.9E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.45E+08 | TRUE | 0.0015 | Manual | SUCCESS | NCIDD |
| 7.11E+08 | TRUE | 0.0015 | Manual | | Submitted-results pending. |
| 7.28E+08 | TRUE | 0.0015 | Manual | | |

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|----------|------|--------|--------|------|--|
| 7.11E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.13E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.28E+08 | TRUE | 0.0015 | Manual | FAIL | Hair located. Submitted-results pending Partial DNA profile unsuitable for comparison purposes |
| 7.12E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 6.95E+08 | TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interpretation or comparison |
| 6.9E+08 | TRUE | 0.0015 | Manual | | No DNA profile - possible sub-threshold peaks |
| 5.24E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |

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|----------|------|--------|--------|------|---|
| 6.9E+08 | TRUE | 0.0015 | Manual | | Submitted-results pending. Micro neg for sperm Semen not detected Single source DNA profile Single source DNA profile < 9 loci LR 1000 - 10 000 |
| 7.27E+08 | TRUE | 0.0015 | Manual | | |
| 7.1E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes Submitted-results pending. No DNA profile |
| 7.12E+08 | TRUE | 0.0015 | Manual | | |
| 7.28E+08 | TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.12E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison |
| 7.1E+08 | TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison |
| 7.28E+08 | TRUE | 0.0015 | Manual | | |

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|----------|------|--------|--------|------|---|
| 7.11E+08 | TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.45E+08 | TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.1E+08 | TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 6.91E+08 | TRUE | 0.0016 | Manual | | |
| 7.1E+08 | TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |

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|----------|------|--------|--------|------|---|
| 7.11E+08 | TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 3.42E+08 | TRUE | 0.0016 | Manual | | |
| 6.89E+08 | TRUE | 0.0016 | Manual | FAIL | Hair located. Submitted-results pending. Complex mixed profile unsuitable for inter or comparison |
| 6.86E+08 | TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for inter or comparison |
| 7.11E+08 | TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for inter or comparison |
| 7.12E+08 | TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for inter or comparison |

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|----------|------|---------------|------|---|
| | | | | Submitted-results pending. Complex mixed profile unsuitable for interpretation |
| 7.12E+08 | TRUE | 0.0016 Manual | FAIL | |
| 6.91E+08 | TRUE | 0.0016 Manual | | |
| 6.9E+08 | TRUE | 0.0016 Manual | | |
| | | | | Submitted for cells. Presumptive saliva test pending. presumptive Saliva test positive Two person mixed DNA profile No statistical interpretation performed |
| 7.1E+08 | TRUE | 0.0016 Manual | | Submitted-results pending. Complex mixed profile unsuitable for interpretation |
| 7.12E+08 | TRUE | 0.0016 Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison |
| 3.83E+08 | TRUE | 0.0016 Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.28E+08 | TRUE | 0.0016 Manual | | |

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|----------|------|--------|--------|------|---|
| | | | | | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.12E+08 | TRUE | 0.0016 | Manual | FAIL | |
| 6.9E+08 | TRUE | 0.0016 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| | | | | | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 6.63E+08 | TRUE | 0.0016 | Manual | FAIL | |
| 7.27E+08 | TRUE | 0.0016 | Manual | | |
| | | | | | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.13E+08 | TRUE | 0.0016 | Manual | FAIL | |
| 7.12E+08 | TRUE | 0.0016 | Manual | | Submitted-results pending. |
| | | | | | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 5.06E+08 | TRUE | 0.0017 | Manual | FAIL | |

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|----------|------|--------|--------|---------|---|
| 5.99E+08 | TRUE | 0.0017 | Manual | SUCCESS | Presump. PSA test positive, no sperm found Single source DNA profile < NCIDD matching stringenc y Single Source DNA profile - assumed known contributo |
| 7.11E+08 | TRUE | 0.0017 | Manual | FAIL | Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |
| 7.1E+08 | TRUE | 0.0017 | Manual | FAIL | Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |
| 6.86E+08 | TRUE | 0.0017 | Manual | FAIL | Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |

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|----------|------|--------|--------|------|--|
| 6.45E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 6.86E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 6.91E+08 | TRUE | 0.0017 | Manual | | |
| 7.11E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 6.63E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 6.73E+08 | TRUE | 0.0017 | Manual | | Submitted-results pending. No DNA profile |
| 7.1E+08 | TRUE | 0.0017 | Manual | | |

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|----------|------|--------|--------|------|--|
| 7.1E+08 | TRUE | 0.0017 | Manual | | Submitted-results pending. No DNA profile Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.12E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.11E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.11E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS |
| 6.85E+08 | TRUE | 0.0017 | Manual | | |

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|----------|------|--------|--------|--|
| | | | | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.12E+08 | TRUE | 0.0017 | Manual | FAIL |
| 7.28E+08 | TRUE | 0.0017 | Manual | FAIL |
| 7.28E+08 | TRUE | 0.0017 | Manual | Complex mixed profile unsuitable for interp or comparison |
| | | | | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.12E+08 | TRUE | 0.0017 | Manual | FAIL |
| | | | | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 5.85E+08 | TRUE | 0.0017 | Manual | FAIL |
| | | | | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.13E+08 | TRUE | 0.0017 | Manual | FAIL |
| | | | | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.11E+08 | TRUE | 0.0017 | Manual | FAIL |
| | | | | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|----------|------|--------|--------|------|---|
| 6.63E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.63E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.63E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.13E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.12E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |

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|----------|------|--------|--------|------|---|
| 7.12E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.1E+08 | TRUE | 0.0017 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 7.11E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.63E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.12E+08 | TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.9E+08 | TRUE | 0.0017 | Manual | | |

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|----------|------|--------|--------|------|--|
| 6.73E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.73E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.89E+08 | TRUE | 0.0018 | Manual | FAIL | Complex mixed profile unsuitable for intercomparison |
| 7.1E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 6.86E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Quality flag identified, on hold awaiting advice from QPS |
| 7.1E+08 | TRUE | 0.0018 | Manual | | Quality control failure, refer to QPS |

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|----------|------|--------|--------|------|---|
| 7.11E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation or comparison |
| 7.11E+08 | TRUE | 0.0018 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 6.89E+08 | TRUE | 0.0018 | Manual | | |
| 7.1E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 6.89E+08 | TRUE | 0.0018 | Manual | | |
| 6.73E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation or comparison |
| 6.63E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation or comparison |

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|----------|------|--------|--------|------|--|
| 6.9E+08 | TRUE | 0.0018 | Manual | FAIL | Presump. PSA test positive, no sperm found Complex mixed profile unsuitabl e for interp or comparis on Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |
| 7.12E+08 | TRUE | 0.0018 | Manual | FAIL | Submitte d-results pending. Partial DNA profile unsuitabl e for comparis on Submitte d-results pending. Partial DNA profile unsuitabl e for comparis on |
| 7.11E+08 | TRUE | 0.0018 | Manual | FAIL | purposes Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |
| 7.11E+08 | TRUE | 0.0018 | Manual | FAIL | Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |
| 6.29E+08 | TRUE | 0.0018 | Manual | FAIL | Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |

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|----------|------|--------|--------|------|--|
| 6.73E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.11E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.13E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 6.9E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted as cells, Presumptive saliva test pending Presumptive Saliva test negative Complex mixed profile unsuitable for interpretation or comparison |

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|----------|------|--------|--------|--|
| | | | | Hair located. Submitted-results pending Interim result - sample undergoing rework Two person mixed DNA profile 2 person mix - supports non contribution 2 person mix profile - support for contrib > 100 billion |
| 6.9E+08 | TRUE | 0.0018 | Manual | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| 7.13E+08 | TRUE | 0.0018 | Manual | FAIL |
| 5.73E+08 | TRUE | 0.0018 | Manual | FAIL |
| 6.9E+08 | TRUE | 0.0018 | Manual | FAIL |
| | | | | Complex mixed profile unsuitable for interp or comparison |
| 5.06E+08 | TRUE | 0.0018 | Manual | FAIL |

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|----------|------|--------|--------|------|---|
| 7.11E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.12E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.9E+08 | TRUE | 0.0018 | Manual | | |
| 7.11E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.12E+08 | TRUE | 0.0018 | Manual | | Submitted-results pending. No DNA profile |
| 6.95E+08 | TRUE | 0.0018 | Manual | | |
| 7.12E+08 | TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |

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|----------|------|--------|--------|---------|--|
| 6.9E+08 | TRUE | 0.0018 | Manual | FAIL | Presump saliva positive. Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on Submitte d-results pending. Single source DNA profile NCIDD upload single source DNA |
| 7.11E+08 | TRUE | 0.0019 | Manual | SUCCESS | profile Submitte d-results pending. Partial DNA profile unsuitabl e for comparis on |
| 6.63E+08 | TRUE | 0.0019 | Manual | FAIL | purposes Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |
| 6.73E+08 | TRUE | 0.0019 | Manual | FAIL | Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |
| 7.11E+08 | TRUE | 0.0019 | Manual | FAIL | Submitte d-results pending. Complex mixed profile unsuitabl e for interp or comparis on |

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|----------|------|--------|--------|------|--|
| 7.1E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.89E+08 | TRUE | 0.0019 | Manual | | |
| 7.1E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 5.82E+08 | TRUE | 0.0019 | Manual | | |
| 5.99E+08 | TRUE | 0.0019 | Manual | | |
| 7.1E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.89E+08 | TRUE | 0.0019 | Manual | | Submitted as cells, Presumptive saliva test pending Presumptive Saliva test negative Single Source DNA profile - assumed known contributor |

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|----------|------|--------|--------|------|---|
| 7.11E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.86E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.73E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |

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|----------|------|--------|--------|------|---|
| 7.12E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.12E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 6.63E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.12E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.54E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |

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|----------|------|--------|--------|---------|--|
| 7.11E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 6.02E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 5.99E+08 | TRUE | 0.0019 | Manual | FAIL | Complex mixed profile unsuitable for intercomparison |
| 6.9E+08 | TRUE | 0.0019 | Manual | SUCCESS | Hair located. Submitted-results pending Single source DNA profile NCIDD upload single source DNA profile |
| 7.12E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.12E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |

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|----------|------|--------|--------|------|---|
| 6.73E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation |
| 7.28E+08 | TRUE | 0.0019 | Manual | | |
| 7.28E+08 | TRUE | 0.0019 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes |
| 7.28E+08 | TRUE | 0.0019 | Manual | | |
| 7.11E+08 | TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interpretation Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion |
| 7.28E+08 | TRUE | 0.0019 | Manual | FAIL | |

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|----------|------|---------------|------|---|
| | | | | Submitted as cells, Presumptive saliva test pending |
| 6.95E+08 | TRUE | 0.0019 Manual | FAIL | Presumptive Saliva test negative |
| 7.27E+08 | TRUE | 0.0019 Manual | | Complex mixed profile unsuitable for interpretation or comparison |
| | | | | on Micro positive for sperm. Submitted-Results pending |
| | | | | Micro positive for sperm. Submitted-Results pending |
| | | | | Complex mixed profile unsuitable for interpretation or comparison |
| 7.27E+08 | TRUE | 0.0019 Manual | FAIL | on Submitted-Results pending |
| | | | | Complex mixed profile unsuitable for interpretation or comparison |
| 7.28E+08 | TRUE | 0.0019 Manual | | Submitted-Results pending |
| 6.9E+08 | TRUE | 0.0019 Manual | | Micro neg for sperm |
| | | | | Micro positive for sperm. Submitted-Results pending |
| | | | | Presumptive blood test pos. Submitted-Results pending |
| | | | | Micro neg for sperm |
| | | | | Single Source DNA profile - assumed known contributor |
| 7.27E+08 | TRUE | 0.0019 Manual | | |

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|----------|------|-------|--------|------|---|
| 7.1E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.1E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.63E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.19E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.89E+08 | TRUE | 0.002 | Manual | | |

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|----------|------|-------|--------|------|---|
| 7.1E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.45E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.1E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.1E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |

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|----------|------|-------|--------|------|---|
| 6.86E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.29E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.86E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. No DNA profile Possible sub-threshold information |
| 6.73E+08 | TRUE | 0.002 | Manual | | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.12E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |

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|----------|------|-------|--------|------|---|
| 7.11E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for inter or comparison |
| 7.11E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| 7.1E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for inter or comparison |
| 6.9E+08 | TRUE | 0.002 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes |
| 6.44E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for inter or comparison |
| 7.13E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for inter or comparison |

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|----------|------|--------|--------|------|---|
| 6.86E+08 | TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.27E+08 | TRUE | 0.002 | Manual | | |
| 7.1E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.11E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.86E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 7.1E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpolation |
| 6.91E+08 | TRUE | 0.0021 | Manual | | |

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|----------|------|--------|--------|------|--|
| 7.1E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.1E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 6.63E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 5.82E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.28E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.1E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |

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|----------|------|--------|--------|------|---|
| 7.11E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes. Submitted-results pending. Complex mixed profile unsuitable for intercomparison. |
| 5.06E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted for cells. Presumptive saliva test pending. Presumptive Saliva test negative. Complex mixed profile unsuitable for intercomparison. |
| 7.11E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted for cells. Presumptive saliva test pending. Presumptive Saliva test negative. Complex mixed profile unsuitable for intercomparison. |
| 7.11E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted for cells. Presumptive saliva test pending. Presumptive Saliva test negative. Complex mixed profile unsuitable for intercomparison. |

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|----------|------|--------|--------|------|--|
| 7.1E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.72E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interpretation or comparison |
| 7.11E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| 6.45E+08 | TRUE | 0.0021 | Manual | | Submitted-results pending. No DNA detected |
| 7.13E+08 | TRUE | 0.0021 | Manual | | |
| 6.9E+08 | TRUE | 0.0021 | Manual | | Micro positive for sperm. Submitted-Results pending |
| 6.9E+08 | TRUE | 0.0021 | Manual | FAIL | Complex mixed profile unsuitable for interpretation or comparison |

| | | | | | |
|----------|--------|--------|--------|------|--|
| 6.9E+08 | TRUE | 0.0021 | Manual | | |
| 6.9E+08 | TRUE | 0.0021 | Manual | | |
| | | | | | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.13E+08 | TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for intercomparison |
| 7.12E+08 | TRUE | 0.0021 | Manual | FAIL | on |
| 7.13E+08 | TRUE | 0.0021 | Manual | | Submitted-results pending. |
| 7.12E+08 | 0.0091 | | | | Submitted-results pending. |
| 7.28E+08 | 0.0121 | | | nfa | |
| 7.28E+08 | 0.023 | | | nfa | |
| | | | | | Micro positive for sperm. Submitted-Results pending QPS advised no further work required - results available |
| 6.9E+08 | 0.0155 | | | | available |
| 7.12E+08 | 0.0115 | | | | Submitted-results pending. |
| 7.11E+08 | 0.0119 | | | | Submitted-results pending. |
| 7.12E+08 | 0.0128 | | | | Submitted-results pending. |
| 7.11E+08 | 0.0139 | | | | Submitted-results pending. |
| 6.72E+08 | 0.0141 | | | | Submitted-results pending. |
| 7.11E+08 | 0.0142 | | | | Submitted-results pending. |
| 5.85E+08 | 0.0143 | | | | Submitted-results pending. |
| 7.12E+08 | 0.0146 | | | | Submitted-results pending. |
| 6.86E+08 | 0.0165 | | | | Submitted-results pending. |
| 7.11E+08 | 0.0191 | | | | Submitted-results pending. |
| 7.12E+08 | 0.0195 | | | | Submitted-results pending. |
| 7.13E+08 | 0.0196 | | | | Submitted-results pending. |
| 7.1E+08 | 0.0238 | | | | Submitted-results pending. |
| 7.1E+08 | 0.0247 | | | | Submitted-results pending. |
| 7.13E+08 | 0.0268 | | | | Submitted-results pending. |
| 7.12E+08 | 0.0304 | | | | Submitted-results pending. |
| 7.11E+08 | 0.0305 | | | | Submitted-results pending. |

| | | |
|----------|--------|---|
| 7.1E+08 | 0.0239 | Submitted-results pending. Intel report required for further interpretation |
| 7.1E+08 | 0.016 | Submitted-results pending. Interim result - sample undergoing rework. Quality flag identified, on hold awaiting advice from QPS. Quality control failure, refer to QPS. |
| 6.95E+08 | 0.0181 | Submitted-results pending. Micro neg for sperm |

HSSA | Health Services Support Agency

PowerPlex®21 – Amplification of Extracted DNA Validation

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DNA Analysis, Forensic & Scientific Services

December 2012



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Version history

| Version | Date | Changed by | Description |
|---------|------------|------------|-----------------------|
| 1.0 | 14/12/2012 | | 1 st Issue |

Document sign off

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1 Abstract

To meet Queensland legislative requirements and core business needs, DNA Analysis has validated the PowerPlex® 21 system DNA profiling Kit. All Australian jurisdictions are expected to implement a new DNA profiling kit by the end of 2012. This project came about through the Australian and New Zealand Policing Advisory Agency (ANZPAA).

The loci within the AmpF/STR® Profiler Plus® and AmpF/STR® COfiler® kits, which are currently used in DNA Analysis, are represented within the PowerPlex® 21 system loci. This allows concordance of the kit for direct comparison and matching against existing AmpF/STR® Profiler Plus® crime scene and reference DNA profiles.

This validation has demonstrated that the PowerPlex® 21 system kit is fit for purpose for the amplification of extracted DNA samples processed in the DNA Analysis Unit. A limit of reporting threshold of 40RFU will be adopted for analysis of extracted DNA samples amplified at either 25µL or 12.5µL total PCR volumes.

The sensitivity of this next generation STR kit has greatly increased, however the increased sensitivity does not necessarily result in increased information. The results of this validation indicates that Promega's PowerPlex® 21 system is a very sensitive STR amplification kit, but to reduce the risk of type 2 errors (calling a heterozygous locus homozygous[1]) consideration needs to be given to restricting the range of DNA template added. Single source samples with DNA templates of greater than 0.5ng overload the PowerPlex® 21 system resulting in DNA profiles being unable to be interpreted. Generally samples with lower templates (reaching the often termed 'low copy number' level of 100-150pg) tend to exhibit enhanced stochastic effects as one would expect. Therefore, it should be considered whether samples around this input template level should be amplified given that interpretation of the results could be unwieldy. It would be possible to increase the template levels of samples that fall into this category by post extraction concentration or increase the total PCR volume.

At a total DNA input template of 0.5ng, for 25µL and 12.5µL total PCR volumes, all alleles were detected for the mixtures with ratios of 1:1, 2:1 and 5:1.

The results from this validation support that the Promega PowerPlex®21 System is suitable for analysis of short tandem repeats (STR).

2 Introduction

To meet Queensland legislative requirements and core business needs, DNA Analysis has validated the PowerPlex® 21 system DNA profiling Kit. All Australian jurisdictions are expected to implement a new DNA profiling kit by the end of 2012. This expectation has been directed by ANZPAA, which comprises a Police Commissioner from each jurisdiction.

The initial plan endorsed by the members of the Biological Specialist Advisory Group (BSAG) involved a series of experiments designed to enable each jurisdiction to choose an appropriate STR amplification kit but using the same methodology (national approach to STR kit validation)[2].

This plan included:

1. Sensitivity and amplification volume determination
2. Population studies
3. Concordance
4. Mixture studies
5. Baseline determinations, peak balance, stutter thresholds, minimum reporting threshold and probability of drop in. This last series of experiments were devised by the Statistics Scientific Working Group (StatSWG)[3].

The plans created by BSAG and StatSWG are a significant development with respect to STR validation and interpretation within Australia. In line with current research, these plans involve the move away from a binary approach to DNA profile interpretation to a continuous model. To achieve this, a new DNA profile interpretation software (STRmix™) has been developed by forensic DNA experts & statisticians from Australia and New Zealand forensic laboratories. The validation of the STRmix™ software will be covered in the STRmix™ validation document to be issued subsequent to this report.

The PowerPlex® 21 system[4] is a new short tandem repeat (STR) kit made available to the Australian forensic laboratories in early 2012. The kit has all of the nine loci amplified in AmpF/STR® Profiler Plus®[5] and the six loci amplified in AmpF/STR® COfiler®[6] and an additional seven loci. See Table 1 for kit loci.

Table 1 - Comparison of loci in three different kits

(dye colour indicated by colour text)

| PowerPlex® 21 System | AmpFℓSTR® Profiler Plus® | AmpFℓSTR® COfiler® |
|----------------------|--------------------------|--------------------|
| AMEL | AMEL | AMEL |
| D3S1358 | D3S1358 | D3S1358 |
| D1S1656 | | |
| D6S1043 | | |
| D13S317 | D13S317 | |
| Penta E | | |
| D16S539 | | D16S539 |
| D18S51 | D18S51 | |
| D2S1338 | | |
| CSF1PO | | CSF1PO |
| Penta D | | |
| TH01 | | TH01 |
| vWA | vWA | |
| D21S11 | D21S11 | |
| D7S820 | D7S820 | D7S820 |
| D5S818 | D5S818 | |
| TPOX | | TPOX |
| D8S1179 | D8S1179 | |
| D12S391 | | |
| D19S433 | | |
| FGA | FGA | |

The scope of this validation is to determine for the PowerPlex® 21 system, the limit of detection (LOD), limit of reporting (LOR), the optimal total PCR amplification volume, the range of DNA template, ensure concordance of the PowerPlex® 21 system against the AmpFℓSTR® Profiler Plus® and COfiler® kits, observe the performance of mixed DNA samples and create population datasets required for statistical calculations. Secondary to this, this validation provides the data necessary for STRmix™ validation.

3 Materials

The following materials were used within this validation:

- BSD Duet 600 Series II (BSD Robotics, Brisbane, QLD,AU)
- STORstar instrument (Process Analysis & Automation, Hampshire, GB)
- MultiPROBE II PLUS HT EX with Gripper Integration Platform (PerkinElmer, Downers Grove, IL, US)
- Sterile conductive filtered Roborack 25µL disposable tips (PerkinElmer, Downers Grove, IL, USA)
- 5804 centrifuge (Eppendorf AG, Hamburg, DE)
- 5424 centrifuge (Eppendorf AG, Hamburg, DE)
- Thermomixer (Eppendorf AG, Hamburg, DE)
- MixMate (Eppendorf AG, Hamburg, DE)

- Vortex (Ratek Instruments Pty Ltd, Melbourne, VIC, AU)
- Micro centrifuge (Tomy, Tokyo, JP)
- 1.5mL screw-cap tubes (Axygen Inc. Union City, CA, US)
- Pipettes (Eppendorf, Hamburg, DE and Thermo Fisher Scientific(Finnpipette), Waltham, MA, US)
- Pipette tips (VWR International LLC Radnor, PA, US and Molecular Bioproducts Inc., San Diego, CA, US)
- 96-well PCR plates(Axygen Inc. Union City, CA, US)
- 2.0mL sterile screw-cap tubes (Axygen Inc. Union City, CA, US)
- Plate septas (Axygen Inc. Union City, CA, US)
- Adhesive film (QIAGEN, Hilden, DE)
- FTA™ collection kits (Whatman™ GE Healthcare, Buckinghamshire, GB)
- Positive controls (DNA Analysis Unit, Brisbane, QLD, AU)
- TNE (DNA Analysis Unit, Brisbane, QLD, AU)
- Proteinase K (20mg/mL) (Sigma-Aldrich® Corporation, St Louis, MO, US)
- Dithiothreitol (Sigma-Aldrich® Corporation, St Louis, MO, US)
- Trigen (Medichem International, Kent, GB)
- Ethanol (Recochem Incorporated, Wynnum, QLD,AU)
- Bleach (Ionics Australasia Pty Ltd., Lytton, QLD, AU)
- Amphyl (Rickitt Benckiser Inc. Parsippany, NJ, US)
- Sarcosyl (Sigma-Aldrich® Corporation, St Louis, MO, US)
- Nanopure water (DNA Analysis Unit, Brisbane, QLD, AU)
- Quantifiler™ Human DNA Quantification kits (Life Technologies Applied Biosystems, Foster City, CA, US)
- AB 7500 Real Time PCR System (Life Technologies Applied Biosystems, Foster City, CA, US)
- GeneAmp® PCR system 9700 (Life Technologies Applied Biosystems, Foster City, CA, US)
- ABI 3130x/ Genetic Analyzer (Life Technologies Applied Biosystems, Foster City, CA, US)
- Hi-Di™ Formamide (Life Technologies Applied Biosystems, Foster City, CA, US)
- 3130 POP-4™ Polymer (Life Technologies Applied Biosystems, Foster City, CA, US)
- Running Buffer (Life Technologies Applied Biosystems, Foster City, CA, US)

- DNA IQ™ Casework Pro Kit for Maxwell® 16 (Promega Corp., Madison, WI, US)
- Promega PowerPlex® 21 system (Promega Corp., Madison, WI, US)
- Promega CC5 Internal Lane Standard 500 (Promega Corp., Madison, WI, US)
- Promega PowerPlex 5 Dye Matrix Standard (Promega Corp., Madison, WI, US)
- Promega PowerPlex® 21 Allelic Ladder Mix (Promega Corp., Madison, WI, US)
- 2800M Control DNA, 10ng/μl (Promega Corp., Madison, WI, US)
Water amplification grade (Promega Corp., Madison, WI, US)

4 Methods

4.1 Sample Selection

All samples used in this validation were sourced from the internal DNA Analysis staff DNA database, Collaborative Testing Services (CTS) DNA testing samples, or reference samples that had the National Criminal Investigation DNA Database (NCIDD) categories of Volunteer Unlimited Purpose (VUP) or Suspect (SCT). Permission to use reference samples from NCIDD was obtained from the Queensland Police Service (QPS).

4.2 Selection of Sub-Population Samples

4.2.1 Aboriginal and Torres Strait Islanders Sub-Populations

Aboriginal samples:

Aboriginal samples previously profiled as part of the sub-population dataset for the validation of AmpF[®]STR[®] Profiler Plus[®] loci were recommended as the best samples to use for compilation of the Aboriginal sub-population dataset for the Promega PowerPlex[®]21 system. The samples are self-declared Aboriginal ethnicity and were collected over a number of years.

220 Aboriginal samples were randomly selected from the Aboriginal dataset (545 total) previously profiled with AmpF[®]STR[®] Profiler Plus[®]. Microsoft Excel RANDBETWEEN function was used and duplicates removed until 220 unique samples were identified for profiling.

These 220 samples were originally extracted using Chelex. The extracts for the 220 samples were viewed for sufficient volume. 201 samples with sufficient volume were identified and given new population dataset barcodes.

Torres Straits Islander samples:

A list of FTA™ samples previously profiled with AmpFℓSTR® Profiler Plus® resulting in a full profile and identified as self-declared Torres Strait Islander ethnicity in AUSLAB were compiled to be used for the Aboriginal sub population dataset.

599 samples were listed and after further filtering, including removing duplicates, 249 Torres Strait Islander samples remained. Of the 249 Torres Strait Islander samples listed 223 samples were randomly selected for processing. Samples were given new population dataset barcodes

4.2.2 Caucasian Sub-Population

A list of FTA™ samples previously profiled with AmpFℓSTR® Profiler Plus® resulting in a full profile and identified as Caucasian ethnicity in AUSLAB were compiled to be used for the Caucasian sub-population dataset.

From this list 210 samples were selected and 208 were selected for processing as two were deemed unsuitable. Samples were given new population database barcodes.

4.2.3 South East Asian Sub-Population

A list of FTA™ samples previously profiled with AmpFℓSTR® Profiler Plus® resulting in a full profile and identified as South East Asian ethnicity in AUSLAB were compiled to be used for the South East Asian population dataset.

157 samples were listed and after further filtering 141 South East Asian samples remained. These 141 samples were given new population database barcodes.

4.3 Collection Procedure for FTA™ Cards

Where staff samples were entirely consumed during processing, additional samples were collected. New FTA™ samples were collected using FTA™ Collection kits. A foam swab was used to collect buccal cells from each cheek for one minute then applied to the FTA™ card[7]. The FTA™ card was stored at room temperature until required.

4.4 FTA™ Punching Method

1. PCR Amplification mix was created as required.
2. 25µL (full) or 12.5µL (half) of PCR amplification mix was added to a clean 0.2mL 96 well PCR plate.
3. Plate was sealed and centrifuged to ensure PCR amplification mix was at the bottom of the wells.

4. Each FTA™ sample was punched with the 1.2mm diameter die into the 96 well PCR plate using the BSD Duet 600 Series II.
5. 1µL of 2800M control DNA was added to the Positive control well.
6. 1 x 1.2mm punch of a blank FTA™ card was added to the blank control well
7. Amplification mix without FTA™ card was used as a negative control.
8. The plate was sealed and centrifuged briefly to pull the FTA™ cards to the bottom of the plate wells.

4.5 FTA® Punching Method 2

1. 7.5µL of amplification grade water was added to the required wells.
2. Plate was sealed and centrifuged to ensure the water was at the bottom of the wells.
3. Each FTA® sample was punched with the 1.2mm diameter die into the 96 well PCR plate using the BSD Duet 600 Series II.
4. 1µL of 2800M control DNA was added to the Positive control well.
5. 1 x 1.2mm punch of a blank FTA® card was added to the blank control well
6. PCR Amplification mix without FTA® card was used as a negative control.
7. PCR Amplification mix was created as required and 5µL added to each well.
8. The plate was sealed and centrifuged briefly to pull the FTA® cards to the bottom of the plate wells.

4.6 Punching for Extraction

FTA™ samples were prepared for extraction by punching four paper spots of 3.2mm diameter into 1.5mL/2mL tubes using the BSD Duet 600 according to standard operating procedure 24823 V4.0 “FTA™ Processing and Work Instructions”.

4.7 Extraction

FTA™ samples requiring DNA extraction were processed using the DNA IQ™ Casework Pro Kit for Maxwell®16 according to standard operating procedure 29344 V4.0 “DNA IQ™ Extraction using the Maxwell®16”.

4.8 Preparation of DNA Stock Solutions

Samples used to make dilution series required a stock solution to be prepared. FTA™ samples were selected and punched in duplicate for

extraction (as outlined in section 4.6) then extracted (as outlined in section 4.7). The duplicate samples were pooled into a single tube and quantified twice (as outlined in section 4.9).

4.9 Procedure for Creating a Dilution Series

The samples used to make dilution series were diluted with amplification grade water provided with the Promega PowerPlex®21 System. Spreadsheets for calculating the normalisation and dilution series were written to outline the serial dilutions required to obtain the specified concentrations (refer to Appendix A).

4.10 Quantification

All preparations of reactions were performed using MultiPROBE II plus HT EX platform according to standard operating procedure 19977 V8.0 “Automated Quantification of Extracted DNA using the Quantifiler™ Human DNA Quantitation Kit”.

4.11 Amplification Set up

For the experiments that used extracted DNA, all amplification reactions were performed using a MultiPROBE II plus HT EX platform. A new protocol called PowerPlex 21 amp setup v1.0 was created using WinPrep® software and utilised for amplifications at 25µL and 12.5µL total PCR volumes. The protocol is saved and stored on the C drive of the MultiPROBE II plus HT EX platform computer. Table 2 outlines the components of the amplification mix per sample.

Table 2 - Amplification mix per sample.

| Kit components | Volumes (µL) | Volumes (µL) |
|-----------------------|---------------------|---------------------|
| Master Mix | 5.0 | 2.5 |
| Primer pair | 5.0 | 2.5 |
| Sample | 15 | 7.5 |
| Total Volume | 25 | 12.5 |

4.12 Amplification Conditions

Table 3 lists the PCR cycling conditions used in this validation. All PCR reactions were carried out in 96 well plates (Axygen Inc.) on GeneAmp® 9700 thermal cyclers

Table 3 - PCR cycling conditions used for PowerPlex®21 system

| PowerPlex® 21 Kit | Direct amp | Standard |
|--------------------------|--|--|
| GeneAmp 9700 mode | Max | Max |
| Activation | 25,26 or 27 cycles 96°C for 1 minute | 30 cycles 96°C for 1 minute |
| Cycling | 94°C for 10 seconds 59°C for 1 minute 72°C for 30 seconds | 94°C for 10 seconds 59°C for 1 minute 72°C for 30 seconds |
| Extension | 60°C for 20 minutes | 60°C for 10 minutes |
| | 4°C Soak | 4°C Soak |

4.13 DNA Fragment Analysis

The plates for DNA fragment analysis were prepared as recommended by the manufacturer, using a combination of Hi-Di™ formamide, size standard and sample as outlined below.

Formamide: size standard mixture composed of

[(2.0µl CC5 ILS 500) x (number of injections)] + [(10.0µl Hi-Di™ formamide) x (number of injections)]

Formamide: size standard mixture **12µL**

PCR product or allelic ladder **1µL**

The prepared plate was then centrifuged to remove bubbles, denatured at 95°C for 3 minutes then chilled in an ice block in the freezer for 3 minutes. The prepared plates were then run on a 3130x/ Genetic Analyzer.

The PCR fragments were separated by capillary electrophoresis (CE) using a 3130x/ Genetic Analyzer set up according to manufacturer recommendations outlined in Table 4.

Table 4 - CE Protocol conditions.

| Injection time | Injection voltage | Run time |
|----------------|-------------------|--------------|
| 5s | 3kV | 1500s |

4.14 Profile Interpretation 1

All DNA profiles were analysed with GeneMapper® ID-X v1.1.1. The analysis panel used was PowerPlex_21_IDX_v1.0. The thresholds were set as follows:

1. Heterozygote threshold was set at 40RFU
2. Limit of Detection (negative controls) was set at 16RFU
3. Individual locus stutter thresholds were set as per Promega PowerPlex® 21 Stutter filter
4. Homozygote threshold was set to 200RFU

4.15 Profile Interpretation 2

All DNA profiles were analysed with GeneMapper® ID-X v1.1.1. The analysis panel used was PowerPlex_21_IDX_v1.0. The rules were set as follows:

1. Samples were analysed at 1RFU.
2. All known alleles, forward and back stutter (+/-4bp or +/-5bp) of known alleles, known artefacts and spectral pull-up were removed. As defined by Promega artefact peaks in the N-2bp and/or N+2bp position at D1S1656, D6S1043, D13S317, vWA, D21S11, D7S820, D5S818, D12S391 and D18S51 loci and in the N-1bp position at Amelogenin were also removed.
3. Any peaks determined to be carry over peaks were also removed. Carry-over is defined as the physical transfer of DNA from one injection to the next.

4.16 Profile Interpretation 3

All samples were analysed with GeneMapper ID-X v1.1.1 with the stutter thresholds set to zero. The analysis panel used was PowerPlex_21_IDX_v1.1.

1. Samples were analysed at 20RFU
2. Loci where the two main alleles were one repeat apart were excluded from analysis.

5 Experimental Design

5.1 Sub-Population Datasets

As part of the national approach to implementation of next generation STR amplification kits, the creation of three national sub-population datasets was undertaken. Each jurisdiction contributed DNA profiles for each sub-population Caucasian, Aboriginal and South East Asian to Jo-Anne Bright (ESR) and John Buckleton (ESR) for analysis.

5.1.1 Aboriginal dataset

In this experiment 201 Aboriginal samples were transferred to appropriate tubes and the DNA concentrations determined as outlined in Method 4.10.

The samples were amplified with the recommended DNA template input of 0.5ng in a 25µL total PCR volume. Three plates were amplified using the PowerPlex®21 system kit with each plate including a positive amplification control (2800M DNA) and a negative amplification control (amplification grade water). The three plates were prepared as per Method 4.11.

Standard amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

5.1.2 Torres Strait Islander dataset

In this experiment 223 Torres Strait Islander samples were punched across three 96 well plates as outlined in section 4.4. Each sample had one spot punched, a total PCR volume of 12.5µL and was directly amplified at 26 PCR cycles.

Amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

5.1.3 Caucasian dataset

In this experiment 208 Caucasian samples were punched across three 96 well plates as outlined in section 4.4. Each sample had two spots punched, a total PCR volume of 25µL and was directly amplified at 25 PCR cycles.

Caucasian samples that did not produce a full PowerPlex®21 profile were punched again using 2 spots, a total PCR volume of 25µL and was directly amplified at 26 PCR cycles.

Amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

5.1.4 South East Asian dataset

In this experiment 141 South East Asian samples were punched across two 96 well plates as outlined in section 4.5. Each sample had one spot punched, a total PCR volume of 12.5µL and was directly amplified at 26 PCR cycles.

South East Asian samples that did not produce a full PowerPlex®21 profile were punched for extraction, extracted, quantified and amplified as outlined in Methods 4.6, 4.7, 4.8 and 4.10.

Amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

5.2 Concordance

155 samples purchased from Collaborative Testing Services (CTS) as external Proficiency Tests were used to test the concordance of the PowerPlex® 21 system. These samples had previously been extracted, quantified and amplified with AmpF[®]/STR® Profiler Plus® and AmpF[®]/STR® COfiler® kits.

The samples were amplified with the recommended DNA template input of 0.5ng in a 12.5µL total PCR volume. Two plates were amplified using the PowerPlex®21 system kit with each plate including a positive amplification control (2800M DNA) and a negative amplification control (amplification grade water). The two plates were prepared as outlined in Method 4.11.

Amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13 and 4.14.

The alleles obtained from these samples were compared with the CTS published alleles. Three loci could not be compared as CTS did not publish results for the D12S391, D1S1656 and D6S1043 loci.

5.3 Baseline Determination

To determine the limit of detection (LOD) and the limit of reporting (LOR), the baseline (background) was assessed.

Ten samples from the Caucasian sub-population dataset that exhibited high heterozygosity were used for baseline determination.

The samples were prepared as Methods 4.6, 4.7, 4.8, 4.9, 4.10, 4.11.

Ten samples diluted in ten steps (10x10) outlined in Table 5 were used for the baseline calculations. Each dilution set was amplified at 25µL and 12.5µL total PCR volumes.

50 negative samples were also amplified at 25µL and 12.5µL total PCR volumes.

Table 5 - Total DNA input for each dilution

| Dilution | Total DNA (ng) |
|----------|----------------|
| 1 | 0.500 |
| 2 | 0.447 |
| 3 | 0.394 |
| 4 | 0.342 |
| 5 | 0.289 |
| 6 | 0.236 |
| 7 | 0.183 |
| 8 | 0.131 |
| 9 | 0.078 |
| 10 | 0.025 |

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.12, 4.13, 4.14 and 4.15.

The average peak height RFU (μ_{PK}) for each dye channel was calculated using the AVERAGE function (Arithmetic mean) in Microsoft Excel. The standard deviation (σ_{PK}) was calculated using the STDEV function in Microsoft Excel.

The thresholds were calculated as follows:

The limit of detection (LOD) was calculated from Equation 1[8].

Equation 1

$$\text{LOD} = \mu_{PK} + 3\sigma_{PK}$$

The limit of reporting (LOR) also known as the analytical threshold (AT) was calculated from Equation 2[8].

Equation 2

$$\text{LOR} = \mu_{PK} + 10\sigma_{PK}$$

5.4 Sensitivity 1

This experiment tested the sensitivity of PowerPlex® 21 system at amplification volumes of 25 μ L and 12.5 μ L for DNA template inputs from 4ng to 1pg.

Two staff (one male and one female) with the most heterozygous DNA profile processed with AmpF ℓ STR® Profiler Plus® and AmpF ℓ STR COfiler® kits were selected for testing[9]. Heterozygous loci provide more information with respect to allele drop out and peak balance.

FTA™ cards were collected, processed, extracted, stock solutions prepared, quantified and dilution series prepared as outlined in Methods 4.6, 4.7, 4.8, 4.9 and 4.10.

Each donor had 9 dilutions prepared as outlined in Table 6. These dilutions were amplified in duplicate with a total amplification volume of 25 μ L and 12.5 μ L. Each amplification plate included the kit positive control (2800M DNA) and a negative control (amplification grade water).

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.14.

Table 6 - Total DNA input for sensitivity 1

| DNA Template Input (ng) |
|----------------------------|
| 4 |
| 2 |
| 1 |
| 0.5 |
| 0.1 |
| 0.05 |
| 0.01 |
| 0.005 |
| 0.001 |

5.5 Sensitivity 2

To assess the differences between the two total PCR volumes with respect to low DNA extract concentrations a second sensitivity experiment was performed.

This experiment tested a dilution series of the same samples used in sensitivity 1 at low DNA templates outlined in table 7. Each dilution was amplified in duplicate at 25 μ L and 12.5 μ L.

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.14.

Table 7 - Concentration, DNA template input for each dilution.

| Concentration (ng/ μ L) | Volume of sample added to 25 μ L reaction volume | Total DNA template input (ng) | Volume of Sample added to 12.5 μ L volume reaction | Total DNA template input (ng) |
|-----------------------------|--|-------------------------------|--|-------------------------------|
| 0.01 | 15 | 0.15 | 7.5 | 0.075 |
| 0.005 | 15 | 0.075 | 7.5 | 0.0375 |
| 0.0025 | 15 | 0.0375 | 7.5 | 0.01875 |
| 0.00125 | 15 | 0.01875 | 7.5 | 0.009375 |
| 0.000625 | 15 | 0.009375 | 7.5 | 0.004688 |
| 0.0003125 | 15 | 0.004688 | 7.5 | 0.002344 |
| 0.00015625 | 15 | 0.002344 | 7.5 | 0.001172 |
| 0.000078125 | 15 | 0.001172 | 7.5 | 0.000586 |

5.6 Drop In

50 negative samples were amplified alongside the 10 x10 data at 25 μ L and 12.5 μ L. Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.15.

The negative samples were analysed at 1RFU using GeneMapper ID-X v1.1.1 to determine if any peaks above 20RFU were present. Known artefacts, carry-over and pull-up were removed and not included in the analysis.

5.7 Stutter

To determine the thresholds for forward and back stutter peaks 342 samples from the Aboriginal data set, 10 x10, sensitivity 1 and sensitivity 2 were amplified at 25 μ L and 255 samples from 155 CTS samples, 10 x 10, sensitivity 1 and sensitivity 2 samples were amplified at 12.5 μ L.

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.16.

The stutter ratio (SR) was calculated for each locus as per Equation 3.

Equation 3

$$SR = E_S/E_A$$

SR = Stutter Ratio, E_S = Stutter Height, E_A = Allele Height

The stutter threshold (ST)[4] for each locus was calculated as per Equation 4.

Equation 4

$$ST = \mu_{SR} + 3 \sigma_{SR}$$

ST = Stutter Threshold, μ_{SR} = average stutter ratio, σ_{SR} = standard deviation of stutter ratio.

The stutter results were also processed with a multiple regression analysis by Jo-Anne Bright for use within the STRmix™ validation and STRmix™ settings[10].

5.8 Peak Balance

The samples from the 10 x10 (section 5.4) were used to calculate peak height ratios and an allelic imbalance threshold to be used for reference samples and as a guide for determining the number of contributors to a mixture.

5.8.1 Peak Height Ratio and Allelic imbalance threshold

Peak height ratios for heterozygote loci (1127 alleles for 12.5µL and 1094 alleles for 25 µL total PCR volumes) were determined by dividing the lower peak height by the higher peak height. Loci where the two main alleles were one repeat apart or were homozygous were excluded from analysis.

The peak height ratio (PHR) was calculated for each locus as per equation 5 [11].

Equation 5

$$PHR = LPH / HPH$$

PHR = Peak Height Ratio, LPH = Lower Peak Height, HPH = Higher Peak Height

The average peak heights and standard deviation of peak height ratio were calculated using the Microsoft Excel AVERAGE and STDEV worksheet functions.

The allelic imbalance threshold (AI) was calculated as per Equation 6[12, 13]

Equation 6

$$AI_{TH} = \mu_{PHR} - 3\sigma_{PHR}$$

AI_{TH} = Allelic Imbalance threshold, μ_{PHR} = overall average PHR, σ_{PHR} = standard deviation of the PHR.

5.8.2 Homozygote threshold

The homozygote threshold is the threshold above which you can be confident that a heterozygote locus will not be incorrectly called as a homozygote locus. It was calculated using the following methods

Method 1 – As previously described in the internal validation[14] of peak heights and allelic imbalance thresholds and illustrated below:

Equation 7

$$Th_{Hom} = LOR \times (1 / AI_{TH}) \times 2$$

The LOR used for this calculation is from 5.3 and AI_{TH} was determined in 5.8.2.

Method 2 – As described in the Promega Internal validation guidelines[15] determined from a plot of allelic imbalance versus the lower RFU of a heterozygote pair. The homozygote threshold is assigned at the point at which there is a rapid drop off in peak height ratio.

5.9 Drop Out

To aid in determining the default total PCR volume and template DNA range a series of drop out analyses were performed on the 10 x 10 (section 5.4), sensitivity experiments (sections 5.3 & 5.5) and population datasets (section 5.2).

5.9.1 Drop out 1

The samples from the sensitivity 1 experiment (section 5.3) were used to determine at what RFU the partner of a heterozygote pair drops out. The data was interpreted as outlined in section 4.13. Homozygote peaks, excess samples and no size data were excluded from data analysis. Heat maps were used to summarise the data.

5.9.2 Drop out 2

Samples processed at 25 μ L and 12.5 μ L were analysed to determine the threshold when an allele most frequently drops out.

334 DNA profiles amplified at 25 μ L (from section 5.1.1, 5.3, 5.4 and 5.5) and 279 DNA profiles amplified at 12.5 μ L (from section 5.2, 5.3, 5.4 and 5.5) were analysed as outlined in Method 4.13.

Homozygote peaks, excess samples and no size data were excluded from both sets of data.

5.9.3 Drop out 3

The samples from the 10 x 10 (section 5.4) and sensitivity experiments (section 5.3 & 5.5) experiments (156 samples) were analysed to record the peak height at which a heterozygote paired allele was lost. The data was interpreted as outlined in Method 4.13.

Homozygote peaks, excess samples and no size data were excluded from data analysis.

5.10 Mixture Studies

In experiment 4 samples, two female and two male samples with high heterozygosity were selected, from the Caucasian dataset and CTS samples, to be combined to make mixed DNA samples. The samples were created as Methods 4.3, 4.4, 4.6, 4.7 and 4.10.

One female sample was combined with one male profile to create a two person mixture, the same female sample was combined with the two male samples to create a three person mixture and two female samples and two male samples were combined to create a four person mixture. The amount of sample required from each contributor to create the mixture ratio was calculated using excel spreadsheets, refer to Appendix A. Varying contributor ratios were made for each of the mixture combinations as outlined in table 8. Each mixture combination was amplified in duplicate at a variety of DNA templates.

Amplification, amplification cycling conditions, DNA fragment analysis and profile interpretation was followed as outlined in Methods 4.11, 4.12, 4.13 and 4.16.

Table 8 - Mixture ratios

| Mixture Ratio | Template (ng) | |
|-------------------------|---------------|-------|
| Female:Male | | |
| 50:1 | 0.500 | |
| | 0.250 | |
| | 0.125 | |
| 30:1 | 0.500 | |
| | 20:1 | 0.500 |
| | | 0.250 |
| 10:1 | 0.125 | |
| | 5:1 | 0.500 |
| | | 0.125 |
| 2:1 | 0.500 | |
| | 0.06 | |
| 1:1 | 0.500 | |
| Female:Male:Male | | |
| 20:10:1 | 0.500 | |
| | 0.125 | |
| 10:5:1 | 0.500 | |
| 5:2:1 | 0.500 | |
| | 0.125 | |
| Female:Male:Male:Female | | |
| 5:3:2:1 | 0.500 | |
| | 0.125 | |

The mixture ratio was calculated for each DNA profile and compared to the admixture ratio to determine whether there is any variability and whether the mixture ratio can be expected to hold across the profile.

The DNA profiles were analysed to determine at what ratio the minor contributor would be expected to drop out.

6 Results and Discussion

6.1 Population Datasets

Results were tabulated in the following format Unique Sample ID, Race ID, Marker, Allele 1 and Allele 2. Table 9 summarizes the number of profiles for each sub-population submitted for analysis.

Table 9 - Summary of number of profiles for each sub-population submitted.

| | Caucasian | Aboriginal | SE Asian |
|--------------------------|-------------|-------------|------------|
| DNA Analysis, FSS | 139 | 309 | 126 |
| Dataset total | 1707 | 1778 | 990 |

Data generated for the three sub-population datasets were analysed by Jo Bright and John Buckleton and used in STRmix™ for statistical analysis[16, 17].

6.2 Concordance

All samples (number of alleles = 4644) tested were found to be concordant to the CTS reported DNA profiles. Table 10 displays the number of times a particular allele was seen at each locus within the laboratory.

Different DNA amplification kits may contain different primers for each locus. Comparison of allele calls (concordance) is required to ensure that each kit gives consistent allele designations, as mismatches or null alleles will affect matching on NCIDD or within a case. The current kits used by the DNA Analysis are AmpF \mathbb{I} STR® Profiler Plus® and AmpF \mathbb{I} STR COfiler® DNA amplification kits. Both of these use primers developed by, and manufactured by Life technologies. There are known issues with these kits such as a reverse primer binding mutation at the D8S1179 locus[18], vWA locus[19] and FGA locus[20]. The PowerPlex® 21 kit uses different primer sequences. All alleles tested were found to be concordant. As primer binding mutations and null alleles have been observed within DNA Analysis, any resulting mismatches on NCIDD will need to be retested using PowerPlex® 21.

Table 10 - Observed number of allele concordances

| Allele Size | D3S1358 | D13S317 | Penta E | D16S539 | D18S51 | D2S1338 | CSF1PO | Penta D | TH01 | VWA | D21S11 | D7S820 | D5S818 | TPOX | D8S1179 | D19S433 | FGA |
|-------------|---------|---------|---------|---------|--------|---------|--------|---------|------|-----|--------|--------|--------|------|---------|---------|-----|
| 2.2 | | | | | | | | 5 | | | | | | | | | |
| 3.2 | | | | | | | | 2 | | | | | | | | | |
| 5 | | | 17 | | | | | 5 | 1 | | | | | | | | |
| 6 | | | | | | | | | 44 | | | | | 7 | | | |
| 7 | | | 32 | | | | 4 | 5 | 75 | | | 4 | 3 | 4 | | | |
| 8 | | 23 | 22 | 4 | | | 8 | 9 | 42 | | | 68 | 6 | 133 | 1 | | |
| 9 | | 21 | 10 | 44 | | | 4 | 48 | 50 | | | 28 | 13 | 34 | 4 | | |
| 9.3 | | | | | | | | | 69 | | | | | | | | |
| 10 | | 11 | 25 | 26 | 2 | | 69 | 31 | 3 | | | 80 | 19 | 13 | 11 | 1 | |
| 10.3 | | | | | | | | | 1 | | | | | | | | |
| 11 | | 79 | 26 | 83 | 2 | | 77 | 45 | | 1 | | 65 | 91 | 65 | 14 | 6 | |
| 11.2 | | | | | | | | | | | | | | | | 1 | |
| 12 | 1 | 86 | 40 | 78 | 37 | | 93 | 51 | | | | 26 | 100 | 11 | 37 | 26 | |
| 12.2 | | | | | | | | | | | | | | | | 4 | |
| 13 | 1 | 48 | 27 | 46 | 30 | | 16 | 44 | | 3 | | 9 | 15 | 1 | 96 | 72 | |
| 13.2 | | | | | | | | | | | | | | | | 5 | |
| 14 | 41 | 20 | 15 | 2 | 38 | 1 | 1 | 8 | | 28 | | | 3 | | 71 | 67 | |
| 14.2 | | | | | | | | | | | | | | | | 9 | |
| 15 | 84 | | 12 | | 42 | 1 | | 3 | | 43 | | | | | 43 | 23 | |
| 15.2 | | | | | | | | | | | | | | | | 8 | |
| 16 | 56 | | 13 | | 48 | 14 | | 1 | | 63 | | | | | 10 | 5 | |
| 16.2 | | | | | | | | | | | | | | | | 4 | |
| 17 | 67 | | 10 | | 36 | 46 | | | | 67 | | | | | 1 | | |
| 17.2 | | | | | | | | | | | | | | | | 1 | |
| 18 | 36 | | 6 | | 18 | 19 | | | | 57 | | | | | 1 | | 4 |
| 18.2 | | | | | | | | | | | | | | | | 1 | |
| 19 | 4 | | 2 | | 13 | 33 | | | | 20 | | | | | | | 23 |
| 20 | | | 1 | | 10 | 28 | | | | 2 | | | | | | | 39 |
| 20.2 | | | | | | | | | | | | | | | | | 2 |
| 21 | | | 2 | | 5 | 19 | | | | 2 | | | | | | | 35 |
| 22 | | | 2 | | 2 | 13 | | | | 1 | | | | | | | 56 |
| 22.2 | | | | | | | | | | | | | | | | | 3 |
| 23 | | | | | 1 | 20 | | | | | | | | | | | 48 |
| 24 | | | | | | 13 | | | | | | | | | | | 36 |
| 25 | | | | | | 22 | | | | | | | | | | | 28 |
| 26 | | | | | | 8 | | | | | 3 | | | | | | 10 |
| 27 | | | | | | 1 | | | | | 7 | | | | | | 4 |
| 28 | | | | | | | | | | | 61 | | | | | | |
| 29 | | | | | | | | | | | 47 | | | | | | 1 |
| 29.2 | | | | | | | | | | | 1 | | | | | | |
| 29.3 | | | | | | | | | | | 1 | | | | | | |
| 30 | | | | | | | | | | | 78 | | | | | | |
| 30.2 | | | | | | | | | | | 10 | | | | | | |
| 31 | | | | | | | | | | | 18 | | | | | | |
| 31.2 | | | | | | | | | | | 22 | | | | | | |
| 32 | | | | | | | | | | | 5 | | | | | | |
| 32.2 | | | | | | | | | | | 25 | | | | | | |
| 33.2 | | | | | | | | | | | 9 | | | | | | |
| 35 | | | | | | | | | | | 2 | | | | | | |

6.3 Baseline Determination

The thresholds determined by the baseline experiments are the limit of detection (LOD) and limit of reporting (LOR). The use of thresholds for reporting is essentially a risk assessment[21], if the thresholds are set too low then labelling of artefacts and noise may occur, if set too high then real peaks will not be labelled and information will be lost[1, 11].

Type 1 errors are defined as false labelling of noise peaks. LODs calculated from negative samples may not be optimal for medium-high template samples, as the baseline will differ between positives and negative samples[22].

Type 2 errors are defined as false non-labelling of alleles. If the LOD is set too high, then low level samples may have a heterozygous locus called as a homozygous locus[1, 22-24].

The LOR is the threshold in which a peak can be confidently distinguished from the background fluorescence (baseline). Several methods can be used to determine this threshold.

For the method used here[8] the LOR is derived from the mean baseline plus ten standard deviations (Equation 2).

The LOD is the lowest signal that can be distinguished from the background fluorescence (baseline) and may vary between CE instruments.

Previously in DNA Analysis [14] baseline for the AmpF/STR® Profiler Plus® kit was determined using the BatchExtract software v0.16. The LOD was calculated using Equation 1. This approach of using the mean and three standard deviations would account for 99.73% of baseline fluorescence.

The files generated by GeneMapper ID-X v1.1.1 are not compatible with the BatchExtract software without modification. For this validation an equivalent process for measuring the baseline as described by Promega was used with some modifications to the types of samples used. For this validation samples containing DNA were used to determine baseline fluorescence.

Table 11 shows the results determined from the baseline calculations when the samples were amplified at 25µL. The highest average peak height (5.74RFU) and the highest standard deviation (3.21) was in the TMR (yellow) channel from run 2 on 3130xl A. The TMR (yellow) channel for run 2 on 3130xl A also yielded the highest LOD (15.37) and highest LOR (37.84). The LOD was rounded to 16RFU and the LOR was rounded to 40RFU and is to be used for all dye channels for samples amplified using a total amplification volume of 25µL.

Table 11 - Baseline results for amplifications at 25 μ L

| | | 3130xl A | 3130xl A | 3130xl B | 3130xl B | Overall 3130xl A & B |
|-------------------|---------------|--------------|--------------|--------------|--------------|----------------------|
| | | run 1 | run 2 | run 1 | run 2 | run 1 & 2 |
| Fluorescin (Blue) | μ_{PK} | 2.33 | 2.58 | 1.90 | 1.68 | 2.11 |
| | σ_{PK} | 1.55 | 2.05 | 1.01 | 0.89 | 1.52 |
| | LOD | 6.99 | 8.73 | 4.93 | 4.36 | 6.68 |
| | LOR | 17.86 | 23.07 | 12.01 | 10.59 | 17.35 |
| JOE (Green) | μ_{PK} | 3.51 | 3.83 | 2.25 | 2.16 | 2.94 |
| | σ_{PK} | 2.34 | 2.62 | 1.04 | 1.29 | 2.12 |
| | LOD | 10.54 | 11.68 | 5.37 | 6.02 | 9.30 |
| | LOR | 26.94 | 29.99 | 12.65 | 15.02 | 24.14 |
| TMR (Yellow) | μ_{PK} | 5.29 | 5.74 | 3.33 | 3.07 | 4.32 |
| | σ_{PK} | 2.73 | 3.21 | 1.27 | 1.66 | 2.68 |
| | LOD | 13.47 | 15.37 | 7.15 | 8.05 | 12.37 |
| | LOR | 32.55 | 37.84 | 16.06 | 19.66 | 31.16 |
| CXR (Red) | μ_{PK} | 2.22 | 2.44 | 2.02 | 1.78 | 2.09 |
| | σ_{PK} | 1.36 | 1.54 | 0.89 | 1.01 | 1.35 |
| | LOD | 6.29 | 7.05 | 4.69 | 4.81 | 6.16 |
| | LOR | 15.79 | 17.79 | 10.93 | 11.88 | 15.63 |
| CC5 (Orange) | μ_{PK} | 1.76 | 1.99 | 1.14 | 1.36 | 1.66 |
| | σ_{PK} | 1.30 | 1.80 | 0.44 | 1.39 | 2.44 |
| | LOD | 5.68 | 7.38 | 2.47 | 5.52 | 9.00 |
| | LOR | 14.81 | 19.94 | 5.58 | 15.24 | 26.11 |
| Overall | μ_{PK} | 3.41 | 3.72 | 2.44 | 2.22 | 2.79 |
| | σ_{PK} | 2.45 | 2.80 | 1.33 | 1.39 | 2.29 |
| | LOD | 10.76 | 12.13 | 6.23 | 6.40 | 9.65 |
| | LOR | 27.91 | 31.76 | 15.54 | 16.14 | 25.65 |

Table 12 shows the results determined from the baseline calculations when the samples were amplified at 12.5 μ L. The highest average peak height (6.06RFU) was in the TMR (yellow) channel from the run on 3130xl A and the highest standard deviation (4.41) was in the JOE (green) channel from the run on 3130xl A. The TMR (yellow) channel for the run on 3130xl A yielded the highest LOD (18.50) and the JOE (green) channel yielded the highest LOR (48.60). It was noted on 3130xl A the baseline was raised more than expected compared to other baseline runs on the same instrument and baseline runs on 3130xl B. This could be due to a prolonged period between spectral calibrations, aging reagents and arrays and was taken into consideration when setting thresholds. With natural variations, the results from run to run and instrument may vary, by using the mean + 10SD for the LOR, although the baseline itself may shift, the LOR will always be greater than the LOD even if baseline is either increased or decreased on any given run. By using an “over all” result, the standard deviation is increased due to the difference in fluorescence between instruments, and this then gets factored into the overall LOR.

The highest overall LOD (15.70) was in the TMR (yellow) channel and was rounded to 16RFU and the highest overall LOR (42.27) was in the JOE (green) channel and was rounded to 40RFU.

In an effort to eliminate error and confusion a single LOD and LOR value is to be used for both instruments.

Table 12 - Baseline results for amplifications at 12.5 μ L

| | | 3130xl A 12.5 μ L | 3130xl B 12.5 μ L | Overall 3130xl A & B 12.5 μ L |
|-------------------|---------------|--------------------------|--------------------------|--------------------------------------|
| Fluorescin (Blue) | μ_{PK} | 3.10 | 2.19 | 2.64 |
| | σ_{PK} | 3.66 | 2.72 | 2.99 |
| | LOD | 14.07 | 10.36 | 11.59 |
| | LOR | 39.67 | 29.42 | 32.49 |
| JOE (Green) | μ_{PK} | 4.46 | 2.69 | 3.62 |
| | σ_{PK} | 4.41 | 2.86 | 3.86 |
| | LOD | 17.70 | 11.26 | 15.22 |
| | LOR | 48.60 | 31.28 | 42.27 |
| TMR (Yellow) | μ_{PK} | 6.06 | 3.58 | 4.83 |
| | σ_{PK} | 4.15 | 2.43 | 3.63 |
| | LOD | 18.50 | 10.88 | 15.70 |
| | LOR | 47.52 | 27.92 | 41.08 |
| CXR (Red) | μ_{PK} | 2.87 | 2.10 | 2.49 |
| | σ_{PK} | 2.32 | 1.28 | 1.93 |
| | LOD | 9.84 | 5.94 | 8.27 |
| | LOR | 26.11 | 14.90 | 21.75 |
| CC5 (Orange) | μ_{PK} | 2.38 | 1.66 | 2.02 |
| | σ_{PK} | 2.31 | 1.87 | 2.14 |
| | LOD | 9.33 | 7.26 | 8.84 |
| | LOR | 25.53 | 20.33 | 23.40 |
| Overall | μ_{PK} | 3.94 | 2.54 | 3.32 |
| | σ_{PK} | 3.87 | 2.46 | 3.30 |
| | LOD | 15.56 | 9.91 | 13.21 |
| | LOR | 42.68 | 27.10 | 36.28 |

μ_{PK} = Average peak height, σ_{PK} = Standard Deviation, LOD = limit of detection, LOR = Limit of Reporting

6.4 Sensitivity

All PCR amplification kits are optimised for a particular total reaction volume by the manufacturer; but it is commonplace to reduce the total PCR reaction volume to increase the sensitivity[25-28] and reduce processing costs[27]. Two sensitivity experiments were performed, in addition to the 10x10 (baseline determination) dataset.

To contrast and compare the effect of total PCR volume on DNA profiles, the same dilution series were amplified at two different total PCR volumes (25 μ L and 12.5 μ L) using 30 PCR cycles.

The results for the amplification of the two donors at 25 μ L and 12.5 μ L are summarised in tables 13 and 14 respectively.

Table 13 - Summary of the 2 donors amplified at 25µL

| Donor 1 25µL | Template | Av No. Alleles | Av PH (RFU) | Max PH | Min PH | AV PHR |
|-------------------------|-----------------|---------------------------|------------------------|----------------------|----------------------|-------------------|
| Donor1 | 4ng | N/A | NAD XS | N/A | N/A | N/A |
| Donor1 | 2ng | N/A | XS | N/A | N/A | N/A |
| Donor1 | 1ng | 42 | 2512.56 | 4661.00 | 1456.00 | 90.47 |
| Donor1 | 0.5ng | 42 | 1347.65 | 2492.00 | 172.00 | 85.58 |
| Donor1 | 0.1ng | 42 | 277.47 | 506.00 | 119.00 | 78.78 |
| Donor1 | 50pg | 41 | 153.39 | 387.00 | 48.00 | 67.09 |
| Donor1 | 10pg | 17 | 46.86 | 108.00 | 20.00 | 79.08 |
| Donor1 | 5pg | 6.5 | 39.57 | 78.00 | 20.50 | 0.00 |
| Donor1 | 1pg | 1.5 | 33.83 | 43.00 | 27.00 | 0.00 |
| Donor 2 25µL | Template | Av No. Alleles | Av PH (RFU) | Av Max PH | Av Min PH | AV PHR |
| Donor2 | 4ng | N/A | XS | N/A | N/A | N/A |
| Donor2 | 2ng | N/A | XS | N/A | N/A | N/A |
| Donor2 | 1ng | 42 | 2790.81 | 5126.00 | 1461.00 | 89.19 |
| Donor2 | 0.5ng | 42 | 1344.10 | 2878.00 | 431.00 | 86.91 |
| Donor2 | 0.1ng | 42 | 292.72 | 698.00 | 88.00 | 74.55 |
| Donor2 | 50pg | 41.5 | 157.40 | 479.00 | 47.00 | 68.59 |
| Donor2 | 10pg | 24.5 | 69.69 | 171.00 | 14.25 | 69.60 |
| Donor2 | 5pg | 5.5 | 44.95 | 75.00 | 23.00 | 96.79 |
| Donor2 | 1pg | 6 | 33.62 | 55.00 | 20.00 | 94.85 |

Av = Average, PH = Peak Height, No. = Number, Max = Maximum, Min = Minimum, PHR = Peak Height Ratio

Table 14 - Summary of the 2 donors amplified at 12.5µL.

| Donor 1 12.5µL | Template | Av No. Alleles | Av PH (RFU) | Max PH | Min PH | AV PHR |
|---------------------------|-----------------|---------------------------|------------------------|----------------------|----------------------|-------------------|
| Donor1 | 4ng | N/A | NAD XS | N/A | N/A | N/A |
| Donor1 | 2ng | N/A | XS | N/A | N/A | N/A |
| Donor1 | 1ng | N/A | XS | N/A | N/A | N/A |
| Donor1 | 0.5ng | 42 | 3132.96 | 6719.00 | 1590.00 | 84.41 |
| Donor1 | 0.1ng | 42 | 780.57 | 2444.00 | 180.00 | 74.66 |
| Donor1 | 50pg | 42 | 346.67 | 931.00 | 58.00 | 68.88 |
| Donor1 | 10pg | 27 | 91.95 | 406.00 | 21.00 | 49.76 |
| Donor1 | 5pg | 12 | 48.20 | 91.50 | 20.00 | 71.22 |
| Donor1 | 1pg | 4.5 | 35.80 | 51.00 | 22.00 | 88.24 |
| Donor 2 12.5µL | Template | Av No. Alleles | Av PH (RFU) | Av Max PH | Av Min PH | AV PHR |
| Donor2 | 4ng | N/A | XS | N/A | N/A | N/A |
| Donor2 | 2ng | N/A | XS | N/A | N/A | N/A |
| Donor2 | 1ng | N/A | XS | N/A | N/A | N/A |
| Donor2 | 0.5ng | 42 | 2878.80 | 6159.00 | 1281.00 | 78.29 |
| Donor2 | 0.1ng | 42 | 742.73 | 1612.00 | 140.00 | 68.12 |
| Donor2 | 50pg | 42 | 333.38 | 892.00 | 93.00 | 60.88 |
| Donor2 | 10pg | 25 | 82.33 | 249.00 | 21.00 | 59.05 |
| Donor2 | 5pg | 13.5 | 51.47 | 121.00 | 21.00 | 67.89 |
| Donor2 | 1pg | 0 | 0.00 | 0.00 | 0.00 | 0.00 |

The amplifications at 25µL total PCR volume with DNA templates of 4ng and 2ng for both donors gave excess profiles resulting in the profiles being unable to be interpreted. The results from the excess samples were excluded from the data analysis. The average number of alleles and the

average peak height was similar for both donors when processed with an amplification volume of 25 μ L.

The amplifications at 12.5 μ L with DNA templates of 4ng, 2ng, 1ng and one replicate of the 0.5ng for both donors gave excess results. The results from the excess samples were excluded from the data analysis. The average number of alleles and average peak height was similar for both donors when processed with an amplification volume of 12.5 μ L.

Figure 1 displays the average number of alleles and average peak height ratio obtained for each donor at each template amplified at 25 μ L and 12.5 μ L.

Figure 2 displays the average peak height and average peak height ratio at each DNA template amplified for 25 μ L and 12.5 μ L.

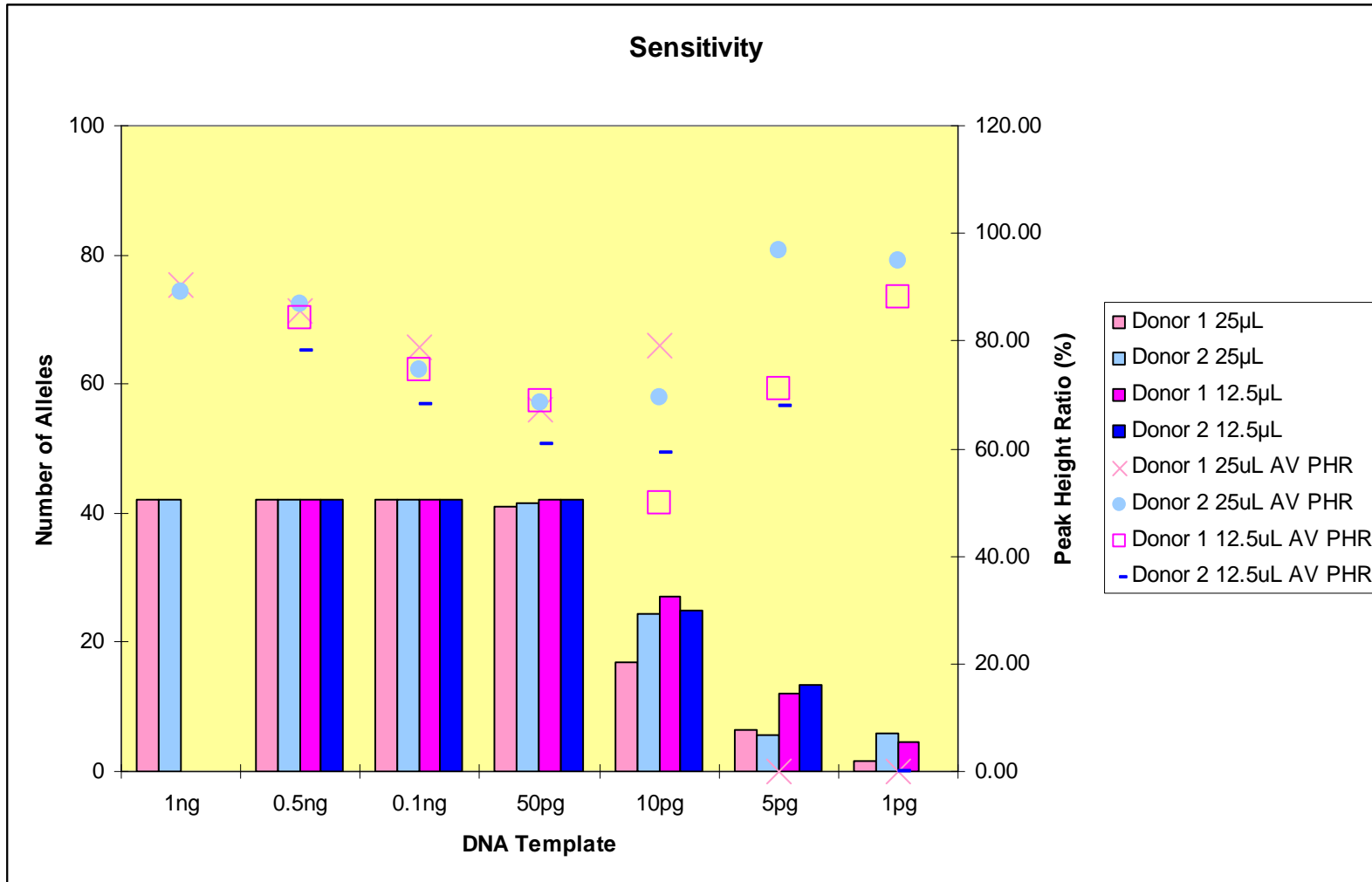


Figure 1 - Average number of alleles for each donor at each DNA template at amplification volumes of 25µL and 12.5µL. AV PHR = Average Peak Height Ratio

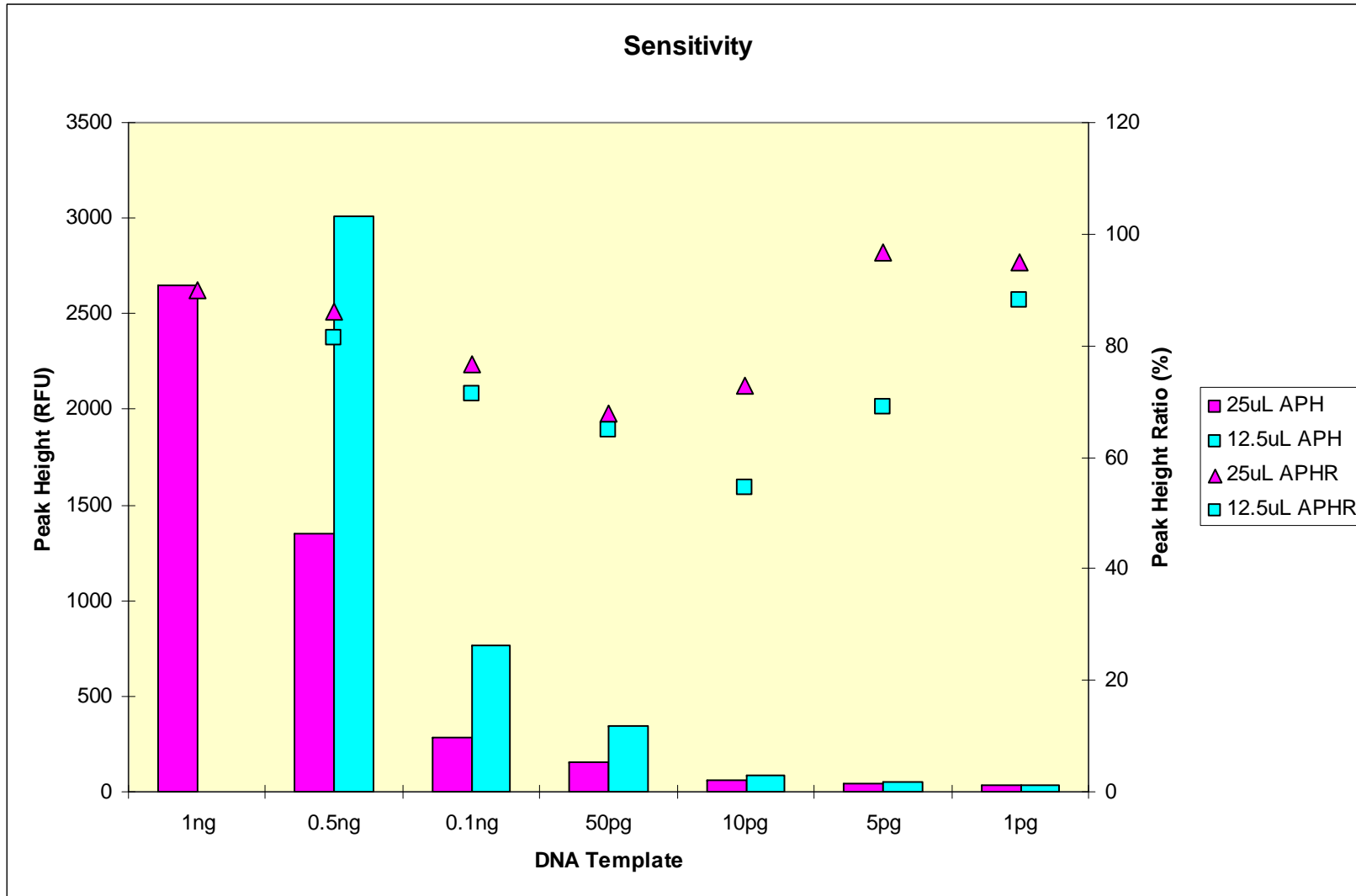


Figure 2 Average peak height and average peak height ratio for each DNA template

A full complement of alleles in the PowerPlex® 21 system was obtained for both donors at total DNA template inputs of 0.5ng and 0.1ng when amplified at both total PCR volumes. As expected the average number of alleles decreased as the DNA template decreased.

For both total PCR volumes, as the total DNA template decreased, the peak heights also decreased. The 12.5µL amplification gave higher peaks heights at the 0.5ng, 0.1ng and 50pg DNA template inputs compared with the 25µL amplification.

The average peak height ratio decreased as the DNA template decreased to 50pg. Below a DNA template of 50pg less heterozygote pairs were observed (as expected) which resulted in the peak height ratio becoming more variable and drop out being observed.

The samples from the 10x10 dataset ranged from template inputs of 0.5ng to 0.025ng. The results of these experiments are concordant with the first sensitivity experiment.

A full complement of alleles in the PowerPlex® 21 system was obtained for all samples between 0.5ng and 0.132ng DNA template inputs when amplified at both total PCR volumes.

The second sensitivity experiment was undertaken to enable direct comparison of the sample concentration when amplified at a total PCR volume of 25µL and 12.5µL rather than comparing the total DNA template input.

Figure 3 shows the results of low concentration samples amplified at 25µL and 12.5µL total PCR volumes with the vertical red line highlighting the limit of detection[29] (quantification) used for the AB 7500 Real Time PCR system. The numbers of alleles obtained at each concentration were counted using the LOR thresholds determined in section 6.4.

The DNA profiles exhibited increased allelic imbalance across different loci when the sample concentration dropped below 0.025ng/µL.

Overall the PowerPlex®21 system is a very sensitive STR amplification kit capable of detecting DNA amounts below what is generally considered low copy number (LCN). The data analyses indicate that the risk of type 2 errors will increase if the DNA template is too low for both total PCR volumes.

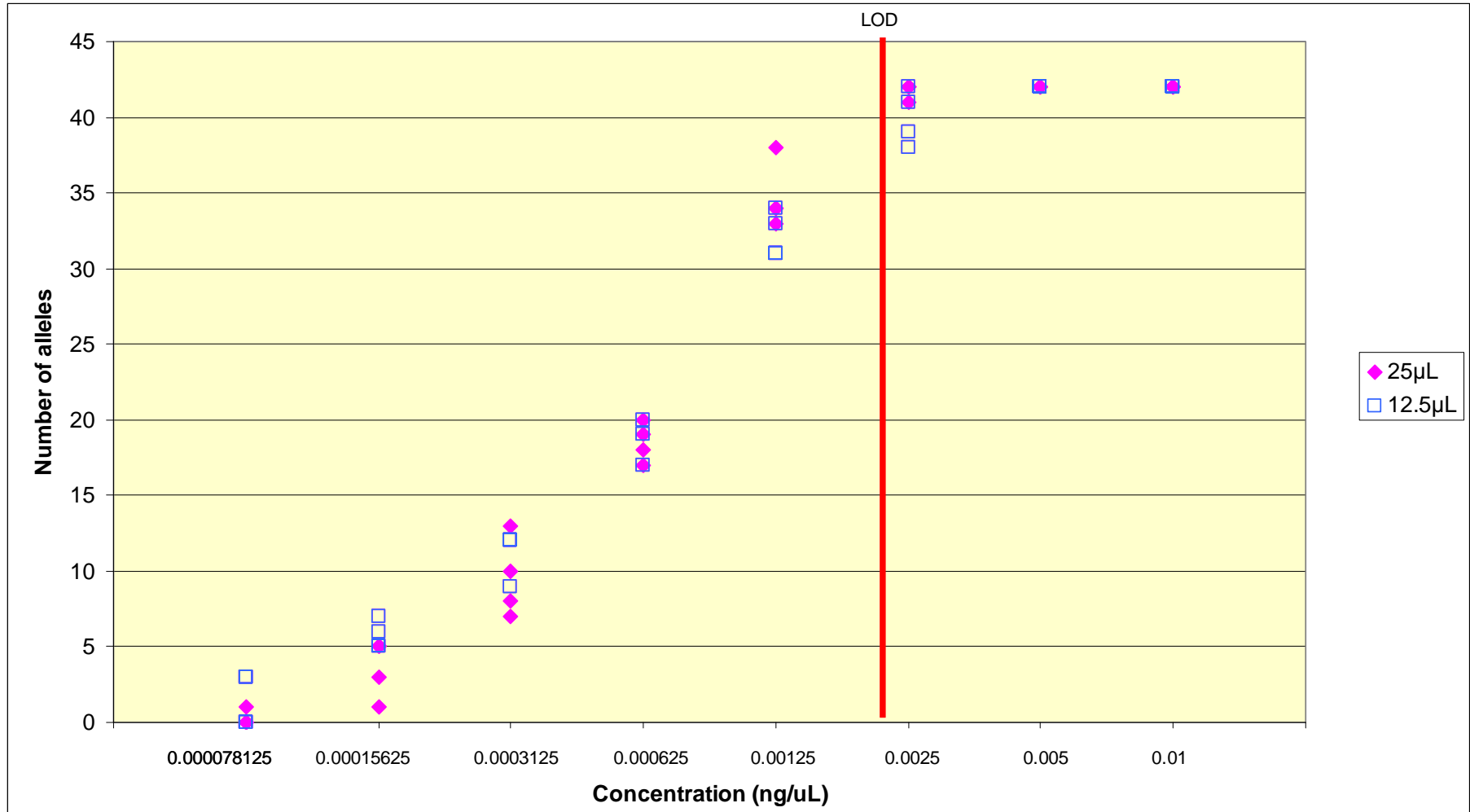


Figure 3 - Comparison of sample concentration vs allele count for 25µL and 12.5µL total PCR volumes.

6.5 Drop In

Allelic drop-in is due to spurious amplification products from unknown DNA, which makes allele drop-in a random event[30, 31]. The phenomenon of allelic drop-in is usually not reproducible and can be detected through testing samples multiple times[32].

For the 25 μ L amplifications processed on both 3130xl instruments 3 drop in events were noted. True drop-in alleles were seen in three negative controls at D16S539 as a 7 allele at 21RFU, D3S1358 as a 21 allele at 19RFU and at TH01 as a 5 allele at 19RFU.

For 12.5 μ L amplifications on both 3130xl instruments no drop in events were noted.

Drop in data was sent to John Buckleton for fit to a Poisson distribution and tested. This data is required for STRmix™ validation and STRmix™ settings.

The rate of drop in events for 25 μ L volume amplifications (3 events in 1050 alleles above 15RFU) was calculated for STRmix™ by John Buckleton, see figure 4.

STRmix™ uses the model for drop-in ae^{-bx} where the values for a and b are the drop-in parameters in STRmix™. John Buckleton's calculations determined that $a=b=0.393$. The maximum drop-in seen at any one locus is determined in RFU; this means that if two peaks were seen at one locus the drop-in would be the total height of both peaks. Since only one drop-in peak was observed at any one locus and the highest of these events was 21RFU, then our drop-in setting for STRmix™ would be 21RFU. Since our LOR was determined to be 40RFU, it seemed reasonable to set the drop-in level to 40RFU.

Although no drop-in events were observed for half volume amplifications, the same parameters will be applied.

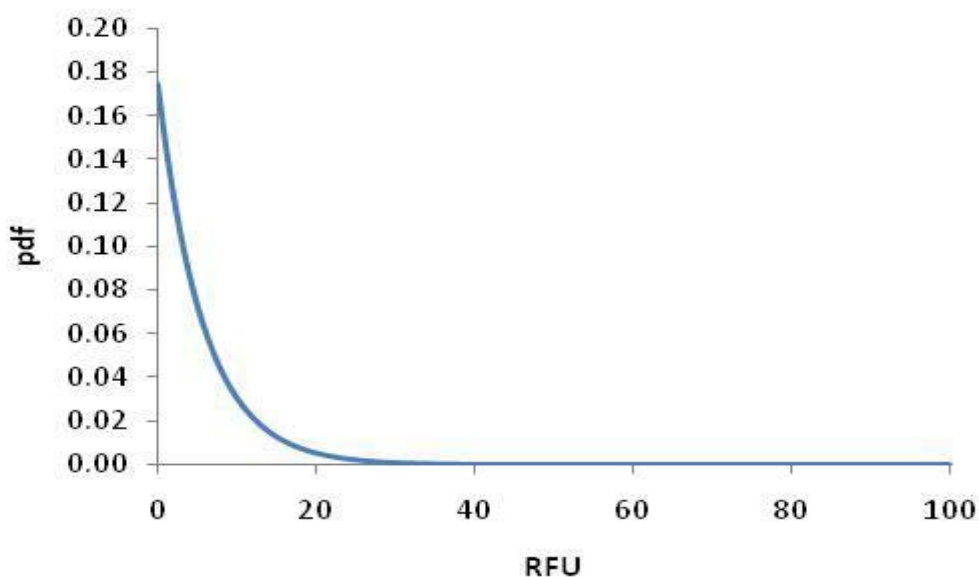


Figure 4 - Probability of Drop in for 25 μ L total PCR volume.

6.6 Stutter

Stutter peaks are Polymerase Chain Reaction (PCR) artefacts commonly observed in all STR analysis[4, 33]. They are usually observed as a peak one repeat unit smaller in size than the true allele peak[33]. The stutter mechanism has been attributed to slippage of the DNA strand during replication.

Over stutter is observed as a peak one repeat unit more in size than the true allele. Figure 5 shows an example of stutter and over stutter.

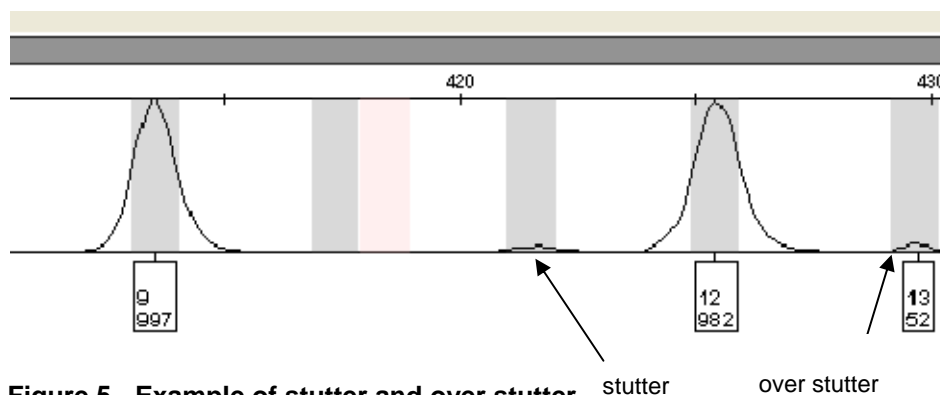


Figure 5 - Example of stutter and over stutter.

Promega supplied a stutter text file (using $\mu + 3\sigma$ [4]) for GeneMapper ID-X v.1.1.1. We have used the same calculation as it incorporates 99.73% of the data assuming normal distribution.

The data for the observed stutter ratios (forward and over) for samples amplified at 25 μ L are listed in table 15 and for 12.5 μ L are listed in table 16.

Over stutter was observed for all loci when amplified at 25 μ L and therefore a threshold was able to be calculated for each locus. Over stutter was not observed for all loci when amplified at 12.5 μ L and therefore a threshold was only able to be calculated for those loci at which over stutter was observed. Over stutter will be continued to be monitored until enough data is obtained to review the thresholds set in this validation.

Most calculated stutter thresholds were higher than the Promega supplied stutter filter file both for 25 μ L and 12.5 μ L. The exceptions were D6S1043, D18D51, D2S1338, and Penta D for 25 μ L and D6S1043, Penta E, D18D51, D2S1338, and Penta D for 12.5 μ L.

When comparing the calculated stutter thresholds for the 25 μ L and 12.5 μ L total PCR volumes, they appear to be similar.

Table 15 - 25µL Calculated stutter thresholds.

| Locus | μ_{SR} | σ_{SR} | Stutter Ratio (%) | μ_{OSR} | σ_{OSR} | Over stutter Ratio (%) |
|---------|------------|---------------|-------------------|-------------|----------------|------------------------|
| D3S1358 | 0.0868 | 0.0184 | 14.2 | 0.0131 | 0.0100 | 4.3 |
| D1S1656 | 0.0910 | 0.0269 | 17.2 | 0.0183 | 0.0163 | 6.7 |
| D6S1043 | 0.0685 | 0.0171 | 12.0 | 0.0164 | 0.0192 | 7.4 |
| D13S317 | 0.0496 | 0.0228 | 11.8 | 0.0185 | 0.0184 | 7.4 |
| Penta E | 0.0457 | 0.0203 | 10.7 | 0.0113 | 0.0018 | 1.7 |
| D16S539 | 0.0686 | 0.0173 | 12.1 | 0.0133 | 0.0099 | 4.3 |
| D18S51 | 0.0873 | 0.0244 | 16.0 | 0.0144 | 0.0116 | 4.9 |
| D2S1338 | 0.0878 | 0.0203 | 14.9 | 0.0196 | 0.0150 | 6.5 |
| CSF1PO | 0.0640 | 0.0244 | 13.7 | 0.0155 | 0.0096 | 4.4 |
| Penta D | 0.0245 | 0.0190 | 8.2 | 0.0306 | 0.0193 | 8.8 |
| TH01 | 0.0325 | 0.0181 | 8.7 | 0.0085 | 0.0041 | 2.1 |
| vWA | 0.0782 | 0.0246 | 15.2 | 0.0157 | 0.0135 | 5.6 |
| D21S11 | 0.0809 | 0.0199 | 14.1 | 0.0175 | 0.0177 | 7.1 |
| D7S820 | 0.0485 | 0.0218 | 11.4 | 0.0207 | 0.0124 | 5.8 |
| D5S818 | 0.0595 | 0.0202 | 12.0 | 0.0165 | 0.0132 | 5.6 |
| TPOX | 0.0381 | 0.0174 | 9.0 | 0.0235 | 0.0130 | 6.3 |
| D8S1179 | 0.0790 | 0.0177 | 13.2 | 0.0176 | 0.0123 | 5.5 |
| D12S391 | 0.0948 | 0.0311 | 18.8 | 0.0146 | 0.0128 | 5.3 |
| D19S433 | 0.0666 | 0.0205 | 12.8 | 0.0211 | 0.0165 | 7.1 |
| FGA | 0.0702 | 0.0227 | 13.8 | 0.0182 | 0.0135 | 5.9 |

Stutter thresholds higher than the recommended stutter thresholds from Promega =

μ_{SR} = mean stutter ratio, σ_{SR} = standard deviation of stutter ratio, μ_{OSR} = mean over stutter ratio, σ_{OSR} = standard deviation of over stutter ratio

Table 16 - 12.5 μ L Calculated stutter thresholds.

| Locus | μ_{SR} | σ_{SR} | Stutter Ratio (%) | μ_{OSR} | σ_{OSR} | Over stutter Ratio (%) |
|---------|------------|---------------|-------------------|-------------|----------------|------------------------|
| D3S1358 | 0.0880 | 0.0194 | 14.6 | 0.0113 | 0.0067 | 3.2 |
| D1S1656 | 0.0909 | 0.0247 | 16.5 | 0.0138 | 0.0055 | 3.0 |
| D6S1043 | 0.0738 | 0.0153 | 12.0 | 0.0141 | 0.0088 | 4.0 |
| D13S317 | 0.0544 | 0.0197 | 11.3 | 0.0148 | 0.0070 | 3.6 |
| Penta E | 0.0389 | 0.0141 | 8.1 | 0.0289 | 0.0111 | 6.2 |
| D16S539 | 0.0690 | 0.0195 | 12.8 | 0.0120 | 0.0049 | 2.7 |
| D18S51 | 0.0827 | 0.0258 | 16.0 | 0.0167 | 0.0125 | 5.4 |
| D2S1338 | 0.0909 | 0.0218 | 15.6 | 0.0298 | 0.0241 | 10.2 |
| CSF1PO | 0.0721 | 0.0258 | 14.9 | 0.0145 | 0.0071 | 3.6 |
| Penta D | 0.0262 | 0.0093 | 5.4 | 0.0324 | 0.0005 | 3.4 |
| TH01 | 0.0252 | 0.0120 | 6.1 | 0.0071 | 0.0000 | 0.0 |
| vWA | 0.0836 | 0.0212 | 14.7 | 0.0149 | 0.0097 | 4.4 |
| D21S11 | 0.0839 | 0.0199 | 14.4 | 0.0256 | 0.0132 | 6.5 |
| D7S820 | 0.0508 | 0.0232 | 12.0 | 0.0250 | 0.0108 | 5.7 |
| D5S818 | 0.0675 | 0.0230 | 13.7 | 0.0163 | 0.0139 | 5.8 |
| TPOX | 0.0346 | 0.0179 | 8.8 | 0.0145 | 0.0000 | 0.0 |
| D8S1179 | 0.0818 | 0.0208 | 14.4 | 0.0173 | 0.0125 | 5.5 |
| D12S391 | 0.1026 | 0.0313 | 19.6 | 0.0135 | 0.0083 | 3.8 |
| D19S433 | 0.0689 | 0.0185 | 12.4 | 0.0129 | 0.0032 | 2.2 |
| FGA | 0.0700 | 0.0218 | 13.5 | 0.0192 | 0.0223 | 8.6 |

6.7 Peak Balance

6.7.1 Peak Height Ratio and Allelic Imbalance Threshold

Peak height ratio (PHR) is the ratio between the two peaks in a heterozygous pair. Under optimal conditions the amplification of a pair of alleles should result in equal peak heights however, input DNA, inhibitors and quality of DNA will affect the amplification [34, 35].

The method used in Equation 4 is recommended in the SWGDAM guidelines [11] and well represented in the literature [36], although other methods have been published by Kelly et al [37].

By assigning a threshold of the mean minus three standard deviations, this incorporates 99.73% of the data, resulting in a conservative threshold. This threshold was rounded up to the nearest RFU. Use of this method to produce a threshold is a low risk to reference samples, as samples that deviate would be reprocessed.

Table 17 shows the summary of PHR and AI_{Th} data calculated. The overall average PHR for 12.5 μ L and 25 μ L total PCR volumes are 78.9% and 80.4% respectively. These values are consistent with other kits listed in the literature [12, 38]. Although the average peak height ratios are similar to those reported in the literature, given the wide standard deviation

observed in our data, the calculated AI_{TH} of 31.1% for 12.5 μ L and 38.6% for 25 μ L reaction volumes are considered low.

Figures 6 and 7 display the data obtained from the 10 x10 experiments for 25 μ L and 12.5 μ L total PCR volumes respectively. For both total PCR volumes, as the amount of DNA input is decreased from the recommended 0.5ng template DNA, the average peak height ratio (μ_{PHR}) decreases and the standard deviation of the peak height ratio (σ_{PHR}) increases.

When the mean PHR are calculated for each DNA template, between 0.183ng and 0.5ng inputs there is no significant difference between total PCR volumes although the standard deviation is higher for the 12.5 μ L total PCR volume, resulting in a much lower threshold. Refer to table 17.

Figures 10 -19 show observed PHR for different template DNA amounts. The PHR range is separated into 0.1 increments plotted against number of allele pairs. Figure 10 is lowest template DNA amount. This shows that at the low template DNA range, the PHR varies unpredictably for both the 25 μ L and 12.5 μ L total PCR volumes. As the template DNA amount increases, the PHR converges towards the ideal of 1.0.

The $\mu_{PHR_{25}}$ at 25pg input was 0.736 and at 0.5ng input was 0.851 compared with the $\mu_{PHR_{12.5}}$, at 25pg input was 0.598 and at 0.5ng was 0.832.

The results of our validation are consistent with previous published findings referring to low template DNA and reduced volume amplifications [13, 34, 39].

Stochastic effects were obvious in this experiment in data from templates below 0.132ng. Stochastic effects are the result of random, uneven amplification of heterozygous allele pairs from low template samples (SWGAM 2010 interpretation) which is displayed by low peak heights or allele/locus dropout. At 0.132ng DNA template is approaching what is usually defined as low copy number (LCN) (~0.100ng to 0.150ng).

Supportive experimental data is displayed in Figure 20 AI_{TH} vs input graph, which displays a rapid drop off the AI_{TH} after 0.132ng DNA template. The calculated AI_{TH} drops below 0 for 0.02475ng DNA template because the standard deviation is so large. The rapid drop off is likely to increase the number of type 2 errors if AI_{TH} is used calculated from the entire dataset due to the large standard deviation. Exclusion of data from templates below 0.132ng increases the μ_{PHR} and decreases σ_{PHR} .

A multiple regression analysis was performed by Jo-Anne Bright, Duncan Taylor and John Buckleton to calculate the peak height variance for use in STRmix™[40].

The peak height ratios calculated here are for use with reference samples that have been amplified from extracted DNA and as a guideline to help determine the number of contributors for mixture interpretation as required for STRmix™ analysis.

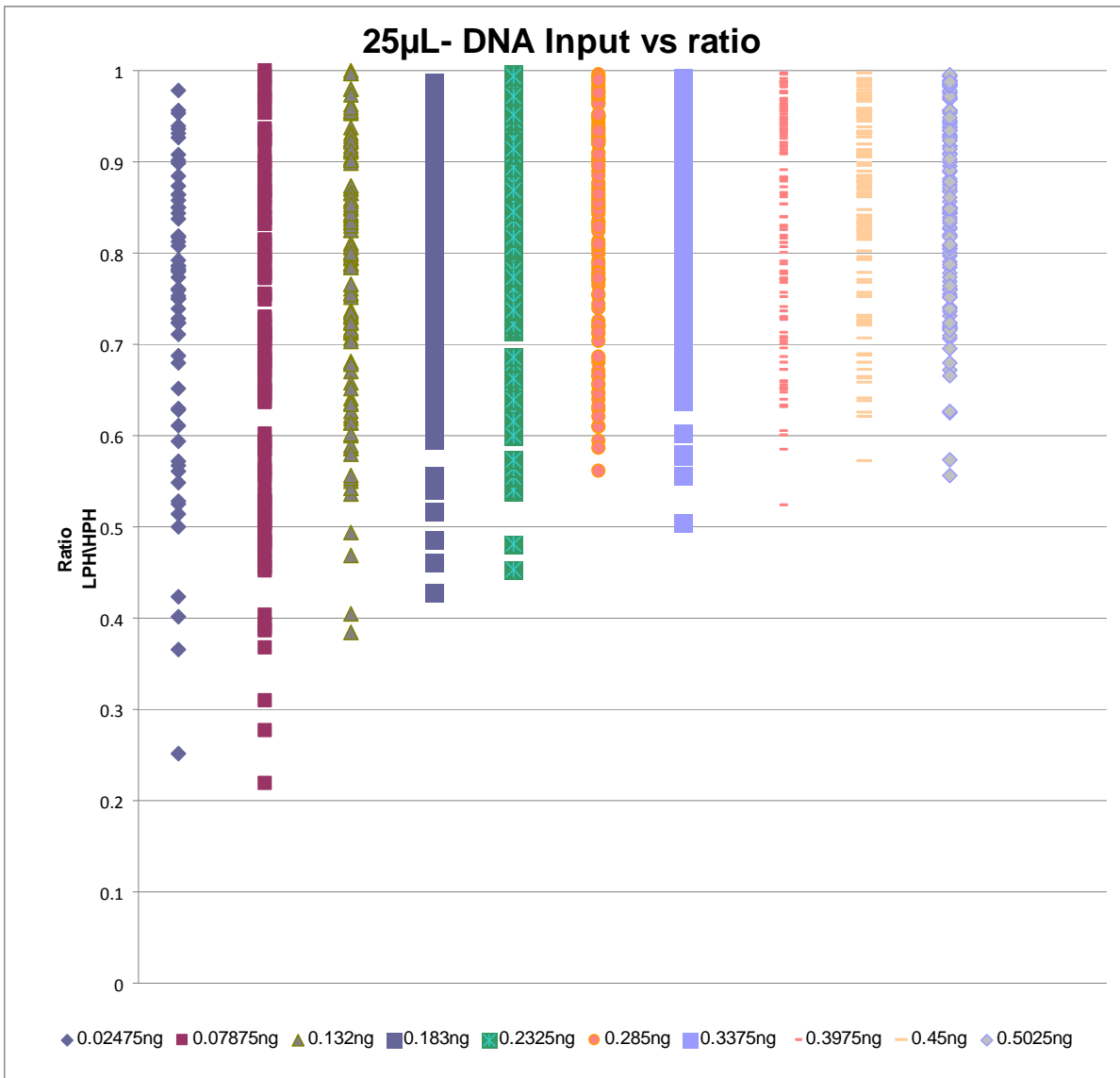


Figure 6 - 25µL total PCR volume, Peak balance vs total input DNA

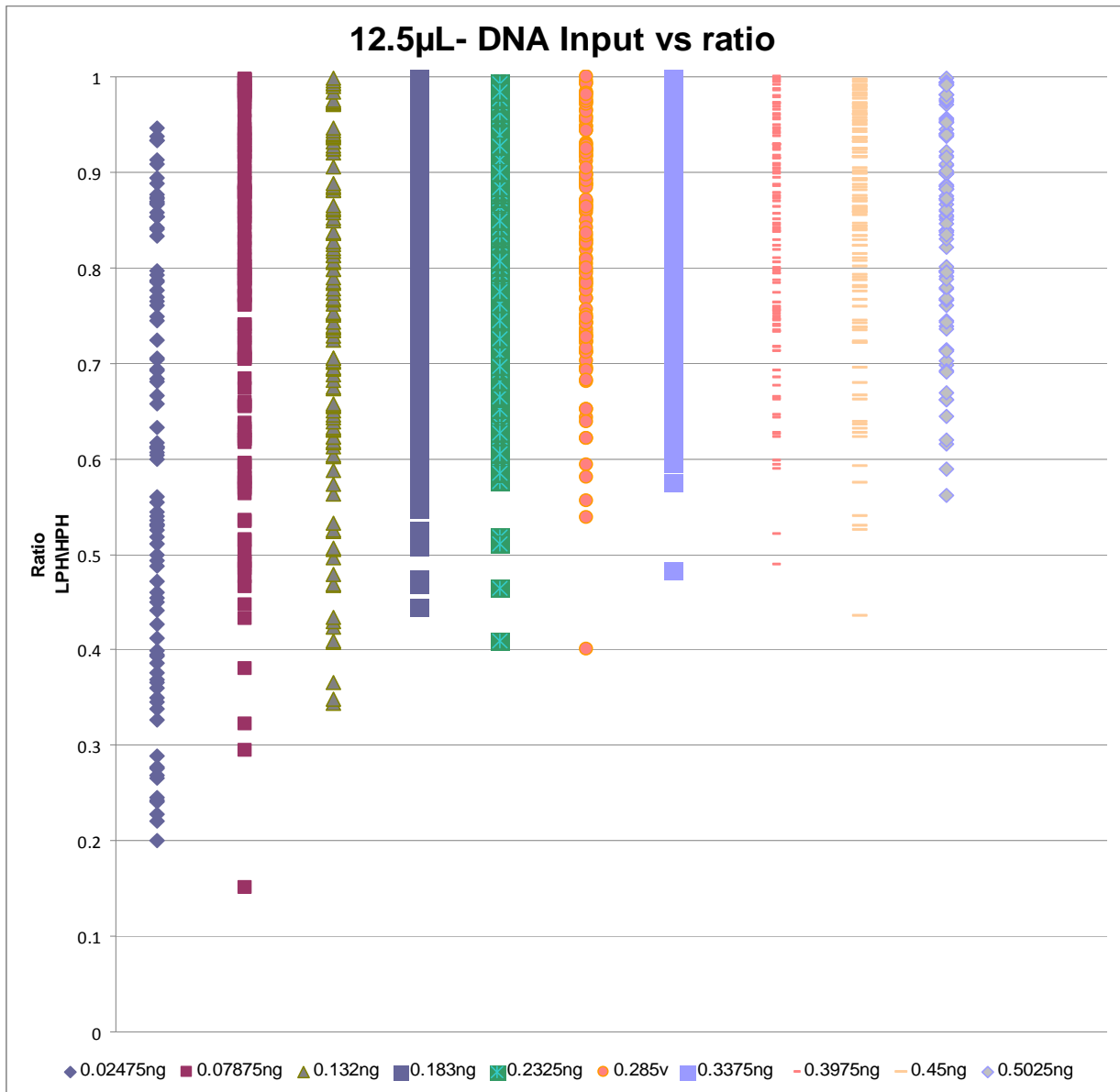


Figure 7 - 12.5µL Total PCR volume - Peak balance vs total input DNA.

Table 17 - Summary of calculated AI_{TH} .

| | 12.5µL | | | 25µL | | |
|-----------|----------|--------------|-------------|----------|--------------|-------------|
| | All Data | 0.132 - 0.50 | 0.183- 0.50 | All Data | 0.132 - 0.50 | 0.183- 0.50 |
| μ | 0.789 | 0.814 | 0.825 | 0.804 | 0.824 | 0.830 |
| σ | 0.160 | 0.134 | 0.124 | 0.140 | 0.123 | 0.119 |
| AI_{TH} | 0.311 | 0.414 | 0.452 | 0.386 | 0.455 | 0.472 |

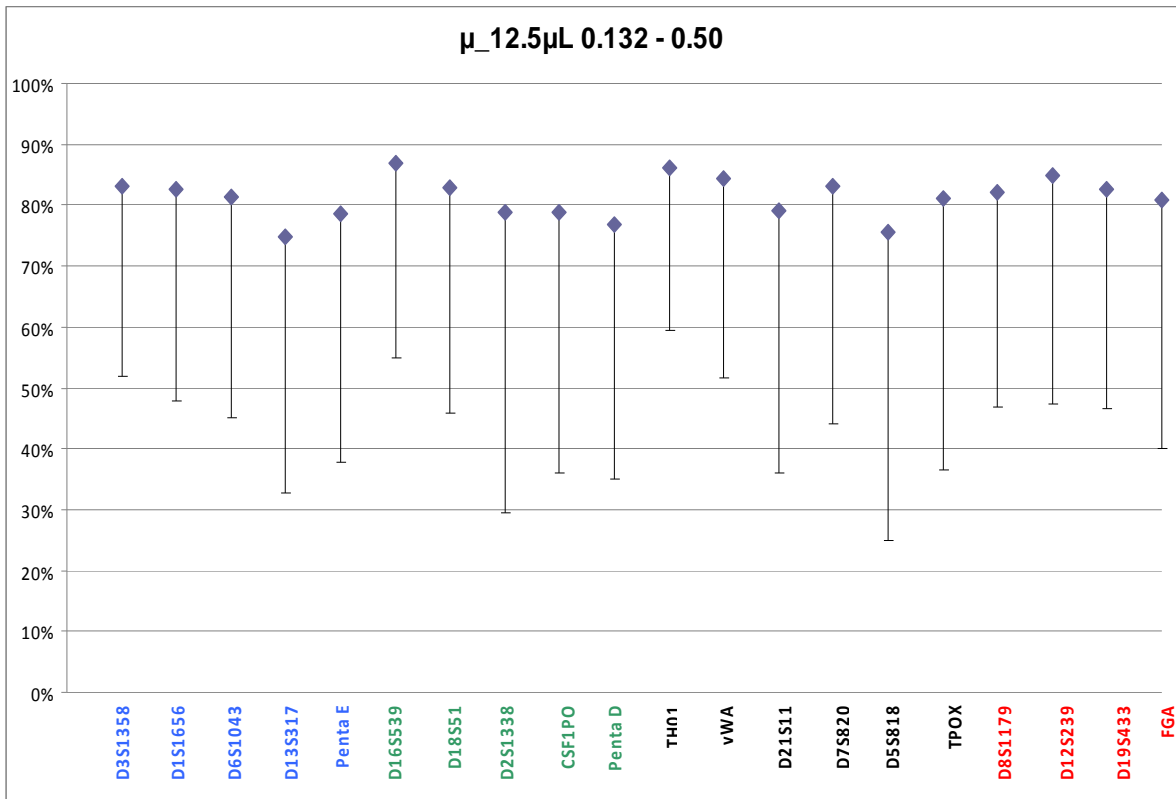


Figure 8 - 12.5µL total PCR volume µPHR per Loci

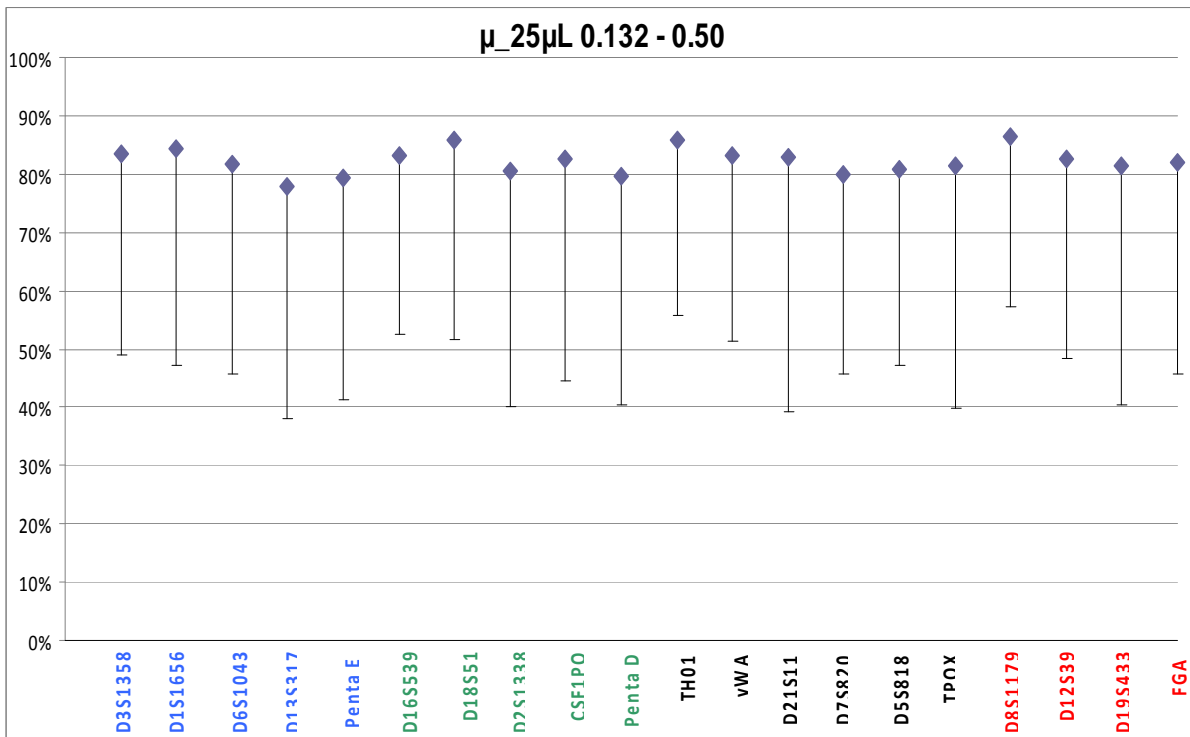


Figure 9 - 25µL total PCR volume µPHR per Loci

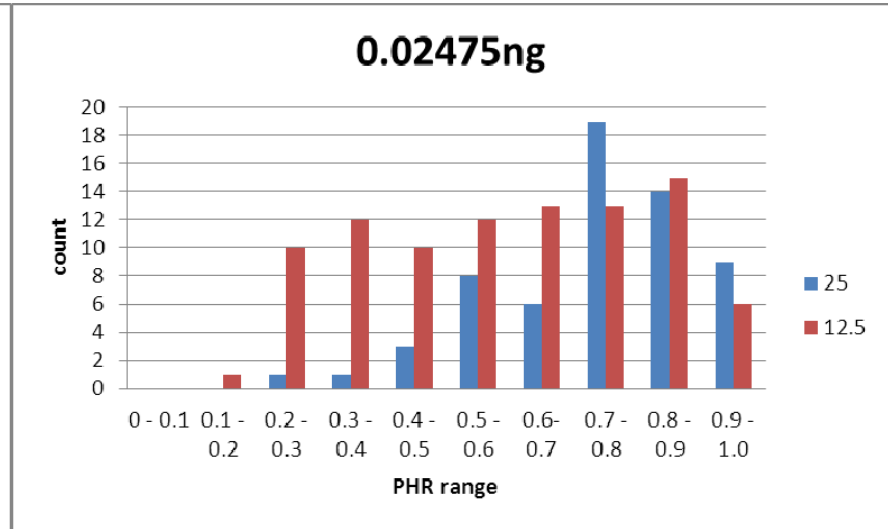
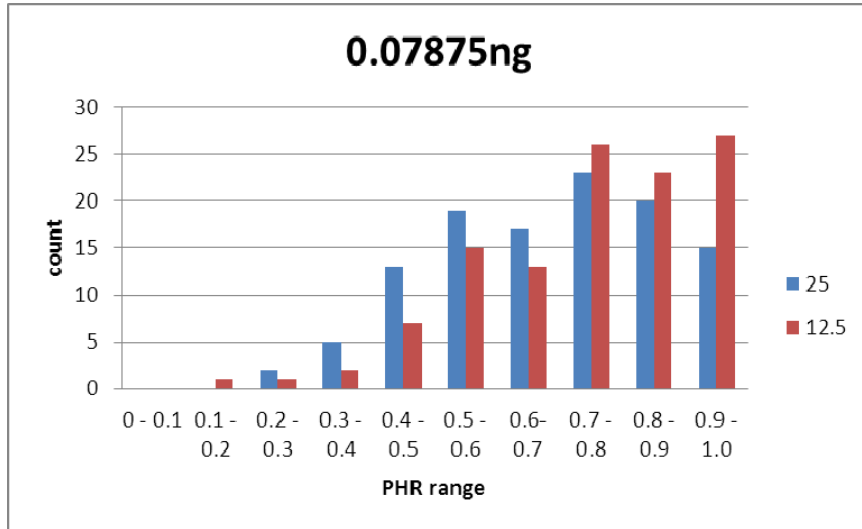


Figure 10 - The count of allele pairs per 0.1 PHR bin for 0.02475ng.

Figure 11 - The count of allele pairs per 0.1 PHR bin for 0.07875ng.

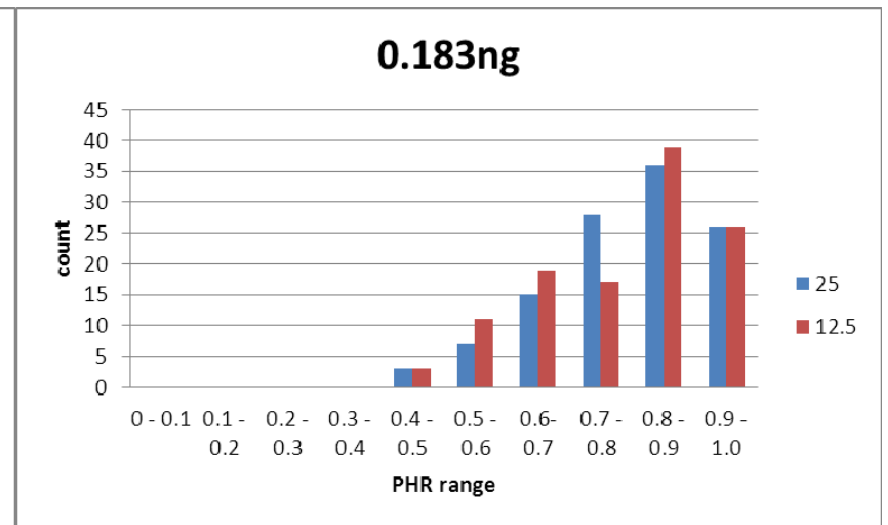
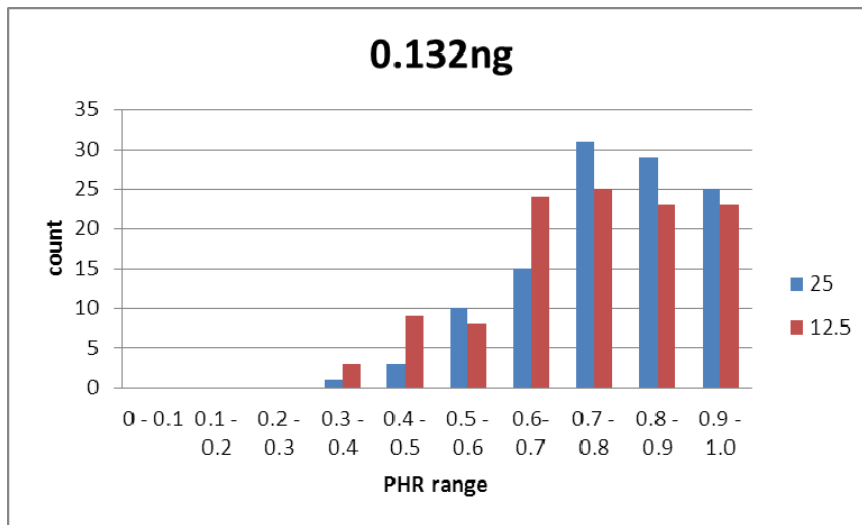


Figure 12 - The number of allele pairs per 0.1 PHR bin for 0.132ng.

Figure 13 - The count of allele pairs per 0.1 PHR bin for 0.183ng.

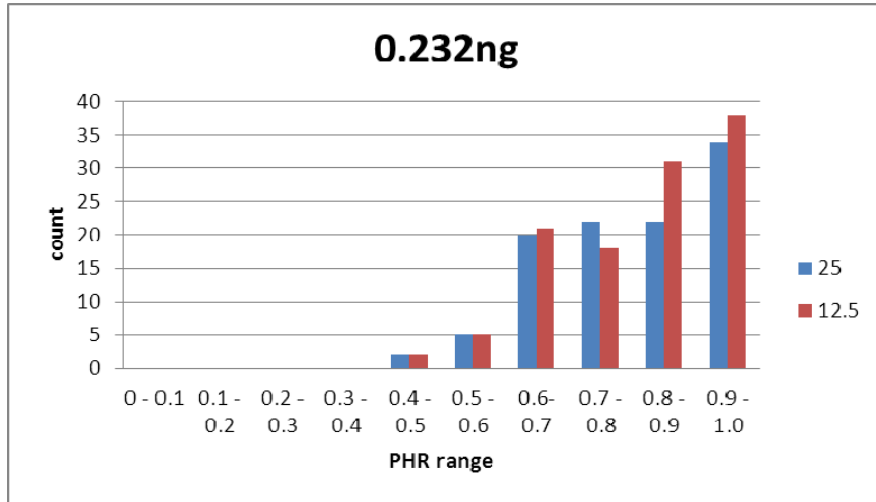


Figure 14 - The count of allele pairs per 0.1 PHR bin for 0.232ng.

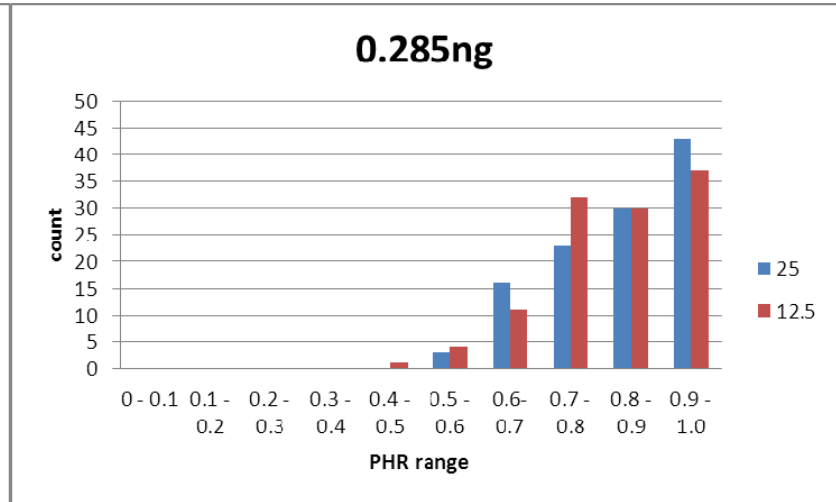


Figure 15 - The number of allele pairs per 0.1 PHR bin for 0.285ng.

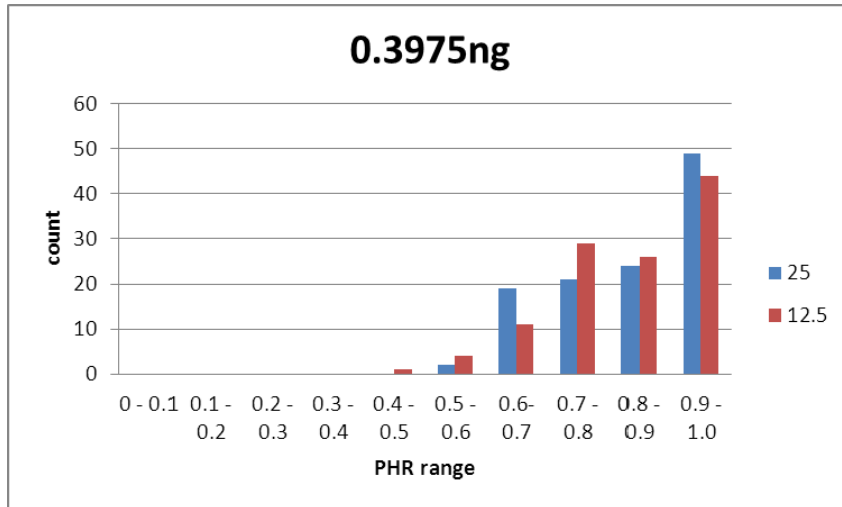


Figure 16 - The count of allele pairs per 0.1 PHR bin for 0.3375ng.

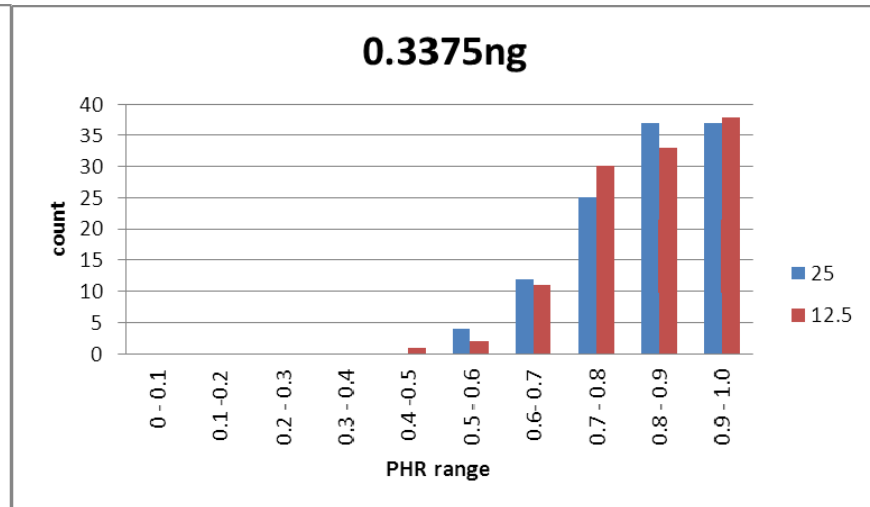


Figure 17 - The count of allele pairs per 0.1 PHR bin for 0.3975ng.

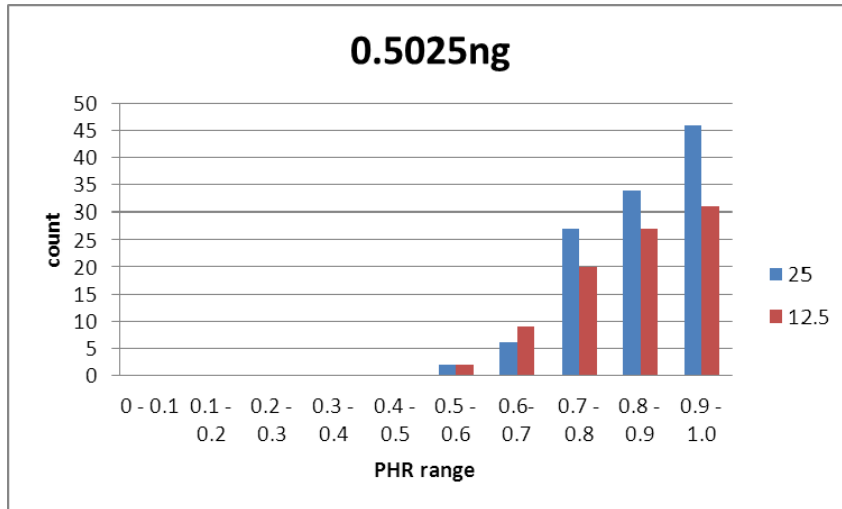


Figure 18 - The count of allele pairs per 0.1 PHR bin for 0.45ng.

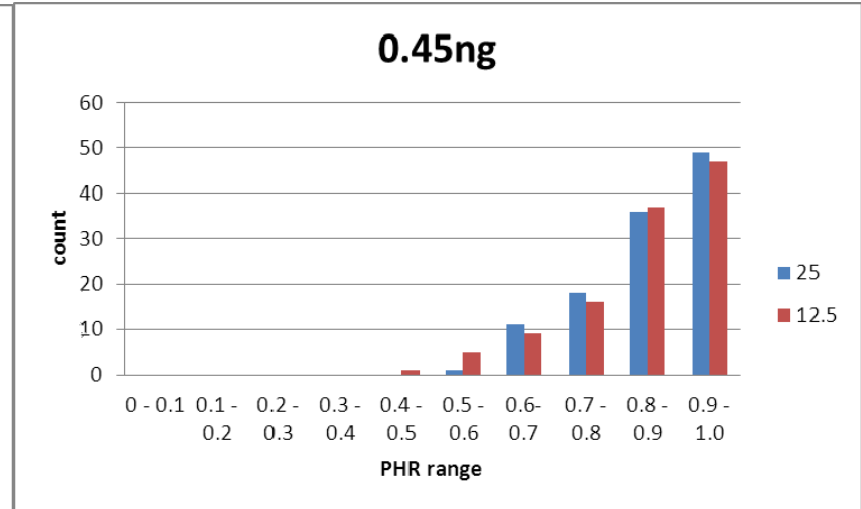


Figure 19 - The count of allele pairs per 0.1 PHR bin for 0.5025ng.

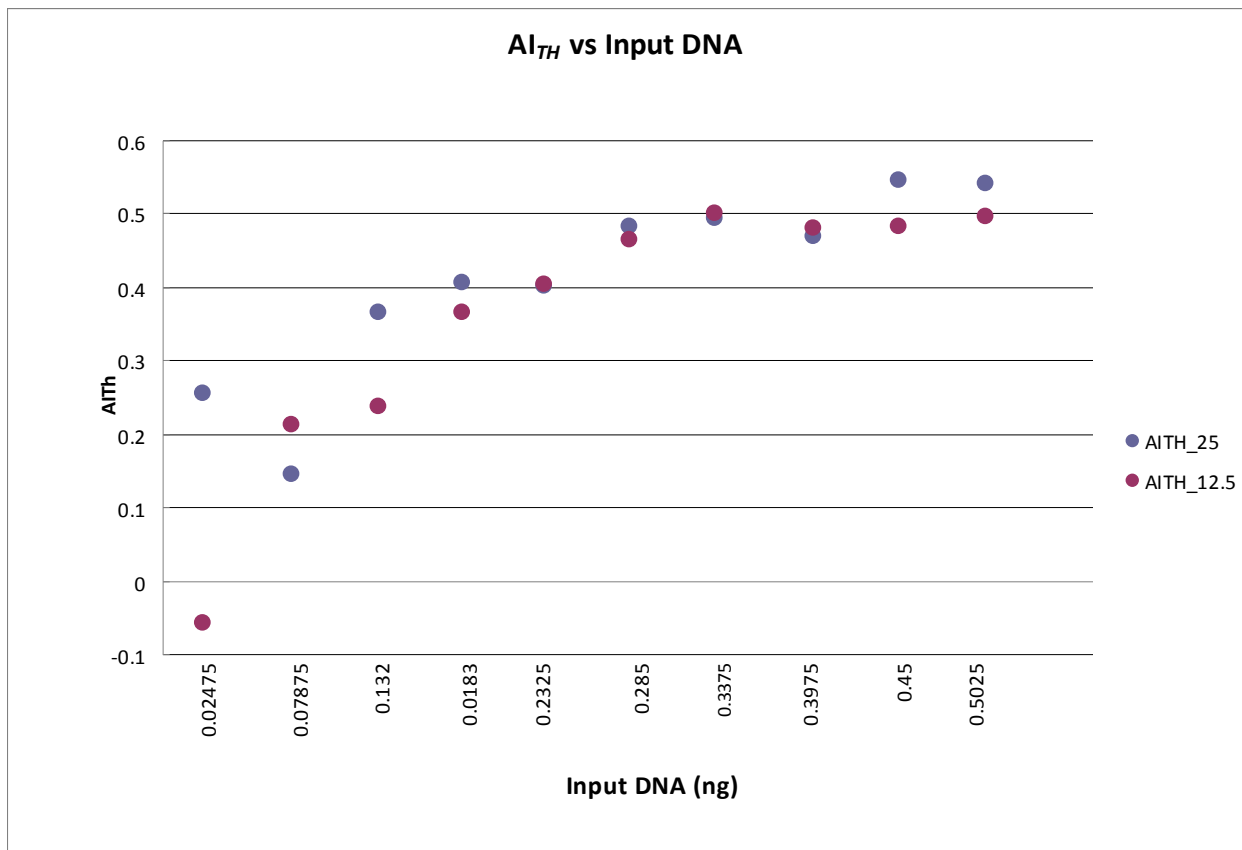


Figure 20 - Calculated AI_{TH} vs DNA template

6.7.2 Homozygote thresholds

The homozygote threshold is the threshold above which you can be confident that a heterozygote locus will not be incorrectly called as a homozygote locus.

Setting the homozygous threshold too high will result in excessive reworking of samples as a partial DNA profile would be called. Conversely, setting the threshold too low could result in false exclusions [1, 11, 23].

The method for determining the homozygote threshold varies in the literature. Traditionally, it had been arbitrarily designated at a particular level above the LOR. As already mentioned the risk of Type 1 and Type 2 errors should be balanced. Literature describes the setting of Th_{Hom} with respect to casework samples [21, 41, 42].

Previously in DNA Analysis, the Th_{Hom} was calculated as described in section 5.10 Equation 7. Using this method a figure of 176RFU for 25 μ L and 193RFU for 12.5 μ L was calculated. These thresholds have been calculated excluding data below 0.132ng DNA template.

Another method of determining the Th_{Hom} is described in the Promega Internal Validation of STR systems reference manual[15]. This plots the peak height ratio for heterozygous loci against the lower RFU peak. The

threshold is defined as the point at which peak height ratio drops off significantly. Figures 21 and 22 display the data, the average AI_{TH} calculated for the range 0.132ng-0.5ng in section 6.7.1 for 25 μ L and 12.5 μ L respectively. An RFU that encompasses the majority of the data that falls below the average AI_{TH} calculated.

Unlike data reported in other publications[21, 43] there is not a rapid drop off of peak height ratios observed in the PowerPlex® 21 system, most likely due to the exclusion of the lower template data that exhibits extreme allelic imbalance. We have observed that the PowerPlex® 21 system loci tend to completely drop out completely compared to partially dropping out.

As both methods used give similar results, it is recommended the homozygote threshold be set at 200RFU for 25 μ L and 250RFU for 12.5 μ L.

These methods are subjective but when considered with the observed drop out data in Figures 23-32, Th_{Hom} of 200RFU would result in no type 2 errors. Additionally the threshold is more than three times the LOR threshold so Type 1 errors would also be addressed.

The homozygote threshold calculated in this validation will be used for extracted reference samples as case work samples do not require a homozygote threshold for STRmix™ analysis.

To ensure all of the thresholds set for this validation are appropriate a post implementation review of the thresholds will be performed. If the thresholds are found to be too conservative and have resulted in additional processing the review will provide an opportunity to re-adjust the thresholds based on empirical data.

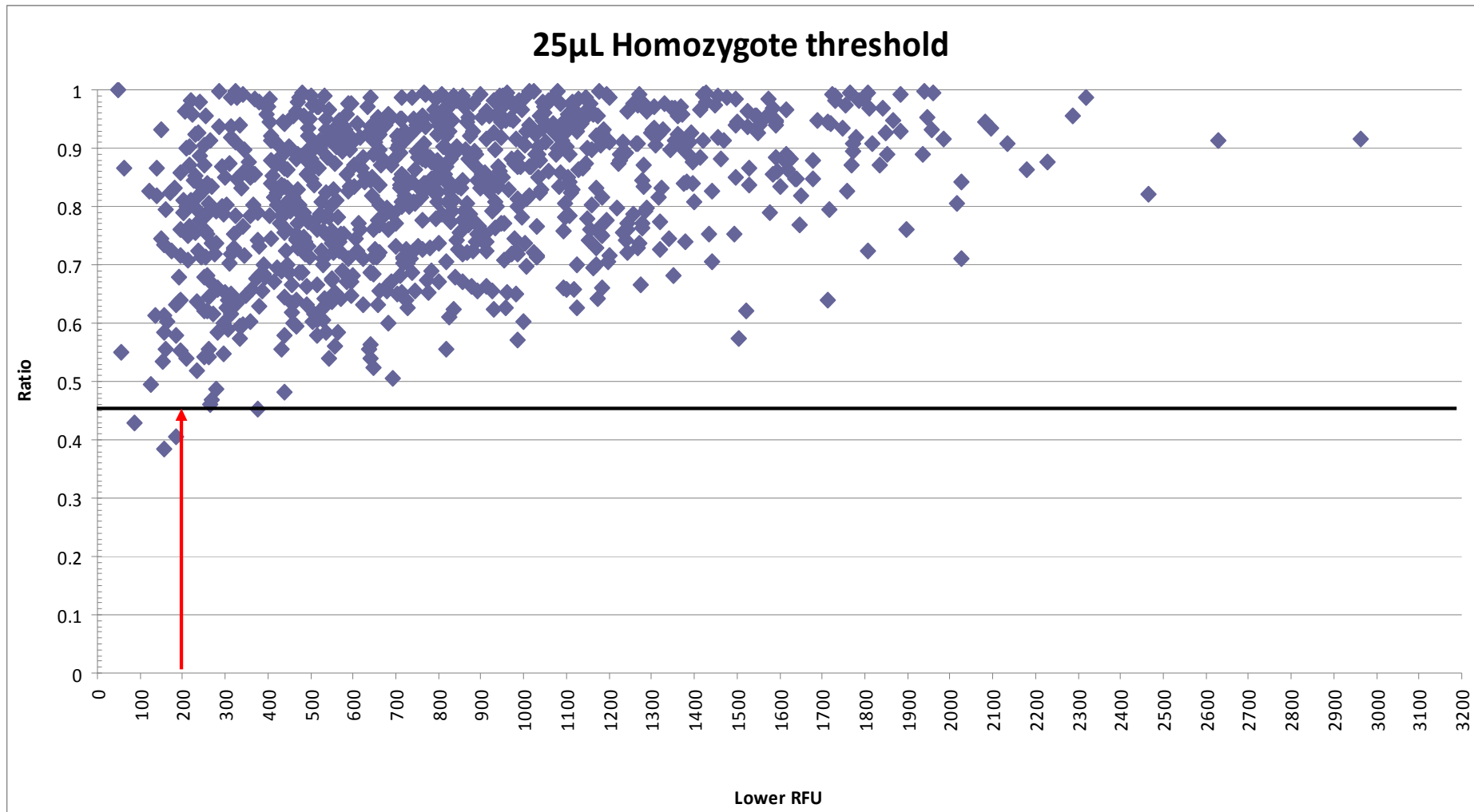


Figure 21 - Plot of the peak height ratio vs RFU of lower peak for 25µL. The black horizontal line is the AI_{TH} . The red vertical line is set to encompass the majority of points that fall below the AI_{TH} .

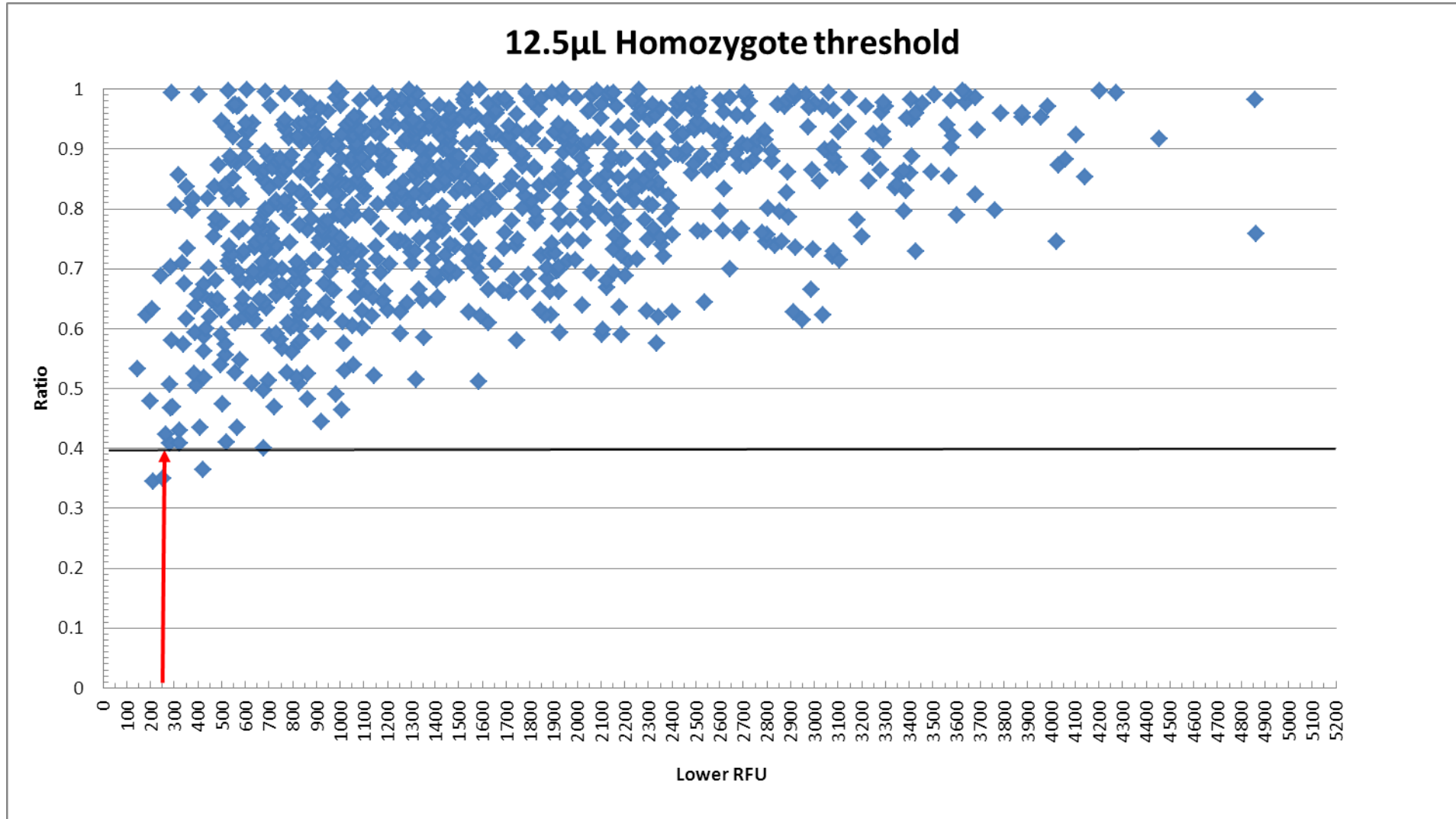


Figure 22 - Plot of the peak height ratio vs RFU of lower peak for 12.5µL. The black horizontal line is the AI_{TH} . The red vertical line is set to encompass the majority of points that fall below the AI_{TH}

6.8 Dropout Experiments

Allelic dropout is when one allele of a heterozygous pair has not appeared or has a very low peak height[44]. One cause of dropout is one allele of a heterozygous pair is preferentially amplified thus giving the false impression of a homozygous allele at a particular locus[31].

This experiment used sensitivity 1 data of the two donors from 1ng to 1pg the 4ng and 2ng data was excluded due to the excess nature of the profiles. The heat maps shown in figures 23, 24, 25 and 26 summarise the data to quickly compare the drop out events observed.

The data for the 25µL amplification shows 62 drop out events occurred across both donors from dilutions 0.001ng to 0.05ng. Figure 24 shows the highest peak height (RFU) where a heterozygous pair dropped out was at 160RFU for the 0.01ng dilution for donor 2 amplified at 25µL total PCR volume.

The data for the 12.5µL amplification shows 70 drop out events occurred across both donors from dilutions 0.001ng to 0.05ng. Figure 26 shows the highest peak height (RFU) where a heterozygous pair dropped out was at 399RFU for the 0.01ng dilution for donor 2.

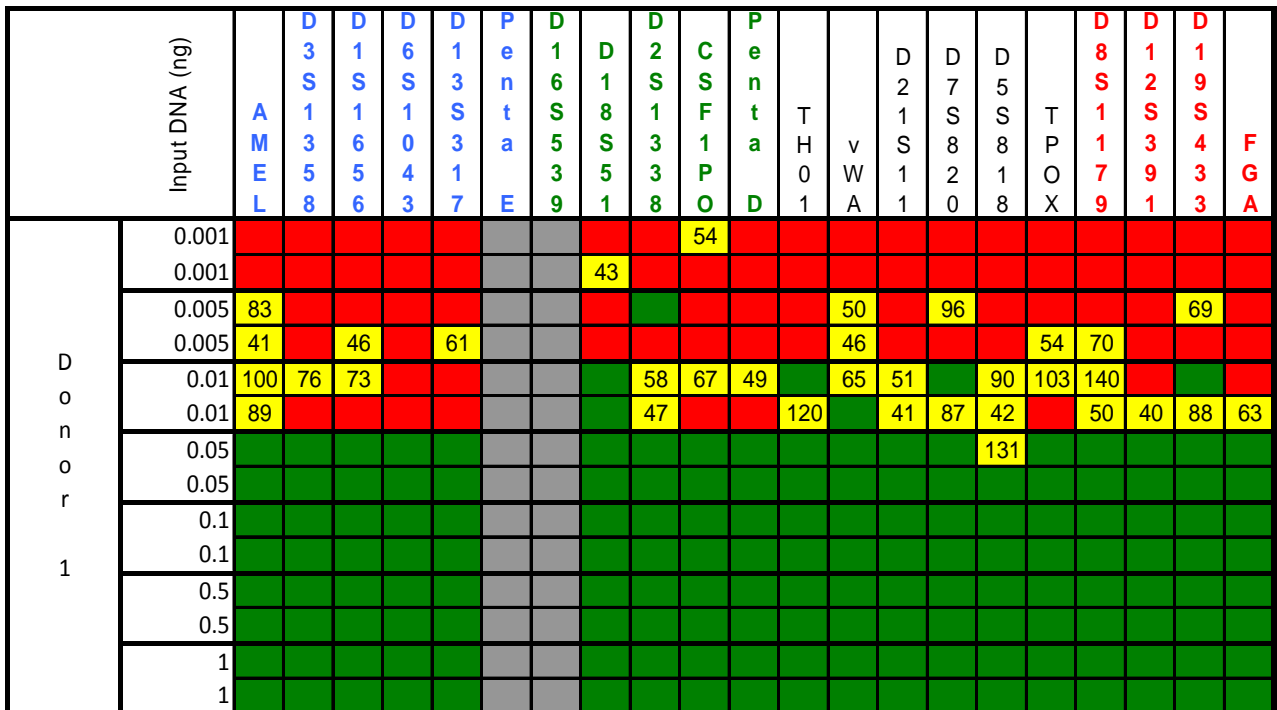
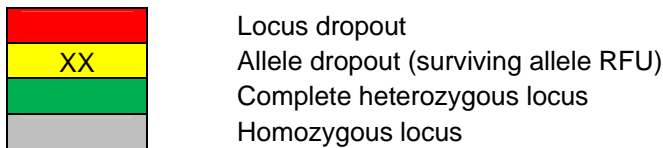


Figure 23 - Heat map - Donor 1 - 25µL total PCR volume

| Input DNA (ng) | | A | D3 | D1 | D6 | D1 | P | D1 | D2 | C | P | T | v | D2 | D7 | D5 | T | D8 | D1 | D1 | F |
|--------------------------------|-------|-----|----|----|----|-----|---|----|----|-----|-----|---|-----|----|----|----|---|----|----|----|---|
| | | M | S | S | S | S | e | 6 | 1 | S | S | H | W | 1 | S | S | P | S | 2 | S | S |
| | | L | 1 | 1 | 0 | 3 | n | 5 | 8 | 1 | 0 | A | 1 | 1 | 2 | 8 | O | 1 | 3 | 4 | A |
| | | 8 | 6 | 4 | 7 | a | 9 | 1 | 3 | P | D | 1 | 1 | 0 | 0 | 1 | X | 7 | 9 | 3 | 3 |
| D o n o r 2 | 0.001 | | 42 | 43 | | | | 60 | | | | | | | | | | | | | |
| | 0.001 | | | | | | | 40 | | 56 | | | | | | | | | | | |
| | 0.005 | | | | | | | | | 109 | | | | | 61 | | | | | | |
| | 0.005 | | | | | | | 73 | | | | | 66 | | | | | 84 | | 46 | |
| | 0.01 | 93 | | 70 | | 85 | | | | | 120 | | 160 | | 99 | | | | 54 | | |
| | 0.01 | 108 | 92 | 60 | 73 | 148 | | 63 | | | 83 | | 41 | | | 62 | | | 64 | | |
| | 0.05 | | | | | | | | | | | | | | | | | | | | |
| | 0.05 | | | | | | | | | | | | | | | | | | | | |
| | 0.1 | | | | | | | | | | | | | | | | | | | | |
| | 0.1 | | | | | | | | | | | | | | | | | | | | |
| | 0.5 | | | | | | | | | | | | | | | | | | | | |
| | 0.5 | | | | | | | | | | | | | | | | | | | | |
| 1 | | | | | | | | | | | | | | | | | | | | | |
| 1 | | | | | | | | | | | | | | | | | | | | | |

Figure 24 - Heat map - Donor 2 - 25µL total PCR volume

| Input DNA (ng) | | A | D3 | D1 | D6 | D1 | P | D1 | D2 | C | P | T | v | D2 | D7 | D5 | T | D8 | D1 | D1 | F |
|--------------------------------|-------|----|-----|----|----|----|---|----|-----|----|-----|-----|----|-----|----|-----|-----|----|----|----|-----|
| | | M | S | S | S | S | e | 6 | 1 | S | S | H | W | 1 | S | S | P | S | 2 | S | S |
| | | L | 1 | 1 | 0 | 3 | n | 5 | 8 | 1 | 0 | A | 1 | 1 | 2 | 8 | O | 1 | 3 | 4 | A |
| | | 8 | 6 | 4 | 7 | a | 9 | 1 | 3 | P | D | 1 | 1 | 0 | 0 | 1 | X | 7 | 9 | 3 | 3 |
| D o n o r 1 | 0.001 | | | 88 | | | | | 80 | | | | | | | | 50 | | 60 | | |
| | 0.001 | | | | | | | | | 44 | | | | | 61 | | | | | | |
| | 0.005 | 48 | | | | | | 43 | 115 | | | | 97 | 47 | | | | 60 | | | |
| | 0.005 | 79 | | 59 | | | | | 77 | | 183 | 48 | 89 | 44 | 40 | | | 47 | | | |
| | 0.01 | | 63 | | | 76 | | | | 99 | | 128 | | 119 | | 131 | | 45 | 95 | | 43 |
| | 0.01 | | 126 | | 49 | | | | | | 56 | | | 120 | 53 | 161 | 162 | 42 | | 52 | 80 |
| | 0.05 | | | | | | | | | | | | | | | | | | | | |
| | 0.05 | | | | | | | | | | | | | | | | | | | | 277 |
| | 0.1 | | | | | | | | | | | | | | | | | | | | |
| | 0.1 | | | | | | | | | | | | | | | | | | | | |
| | 0.5 | | | | | | | | | | | | | | | | | | | | |
| | 0.5 | | | | | | | | | | | | | | | | | | | | |
| 1 | | | | | | | | | | | | | | | | | | | | | |
| 1 | | | | | | | | | | | | | | | | | | | | | |

Figure 25 - Heat map - Donor 1 - 12.5µL total PCR volume

| Input DNA (ng) | | A | D3 | D1 | D6 | D13 | Penta | D16 | D18 | D21 | CSF1 | Penta | TH01 | vWA | D21S11 | D7S820 | D5S818 | TPOX | D8S1179 | D12S3391 | D19S4333 | FGA |
|----------------|-------|------|------|------|-------|------|-------|-----|-----|------|------|-------|------|-----|--------|--------|--------|------|---------|----------|----------|-----|
| | | MEL8 | S138 | S166 | S1043 | S317 | E | S59 | S51 | S338 | P10 | a | 1 | 1 | A | 1 | 2 | 1 | X | 9 | 1 | 3 |
| Donor 2 | 0.001 | | | | | | | | | | | | | | | | | | | | | |
| | 0.001 | | | | | | | | | | | | | | | | | | | | | |
| | 0.005 | 97 | | | 64 | | | | | | | 62 | | 53 | | | | | | | 47 | |
| | 0.005 | | 74 | 53 | | 42 | | | | | 103 | | | | | 77 | | | | 53 | | 47 |
| | 0.01 | | | 74 | | | | | | 89 | 124 | | 399 | | | 43 | | | | | 92 | 46 |
| | 0.01 | 230 | | 60 | | | | | | 154 | 298 | | 101 | | | 42 | 202 | | | | 54 | 44 |
| | 0.05 | | | | | | | | | | | | | | | | | | | | | |
| | 0.05 | | | | | | | | | | | | | | | | | | | | | |
| | 0.1 | | | | | | | | | | | | | | | | | | | | | |
| | 0.1 | | | | | | | | | | | | | | | | | | | | | |
| | 0.5 | | | | | | | | | | | | | | | | | | | | | |
| | 0.5 | | | | | | | | | | | | | | | | | | | | | |
| 1 | | | | | | | | | | | | | | | | | | | | | | |
| 1 | | | | | | | | | | | | | | | | | | | | | | |

Figure 26 - Heat Map – Donor 2 - 12.5µL total PCR volume

6.8.1 Drop out 2

Analysis for drop out 2 used the data obtain from the Aboriginal dataset, 10 x10 and both sensitivity experiments for 25µL total PCR volume and the 10 x10, both sensitivity experiments and concordance for 12.5µL total PCR volume. The dropout 2 results are displayed in figures 27 and 28. Figure 27 shows the dropout events for all samples amplified at 25µL total PCR volume. Figure 28 shows the dropout events for all samples amplified at 12.5µL total PCR volume.

For both 25µL and 12.5µL total PCR volume amplifications there are more drop out events of whole loci compared with a single allele drop out event

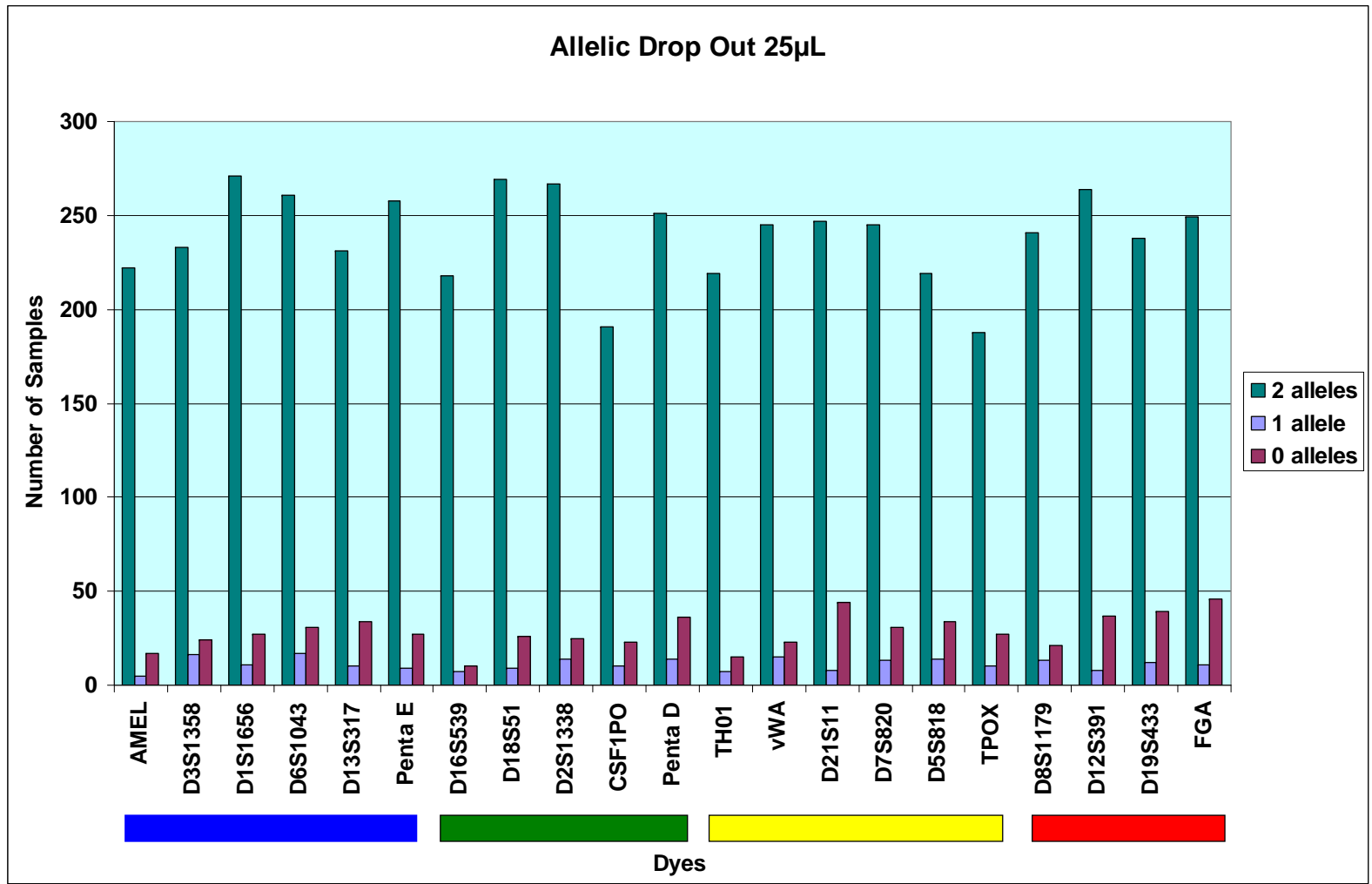


Figure 27 - Dropout events for samples amplified at 25µL

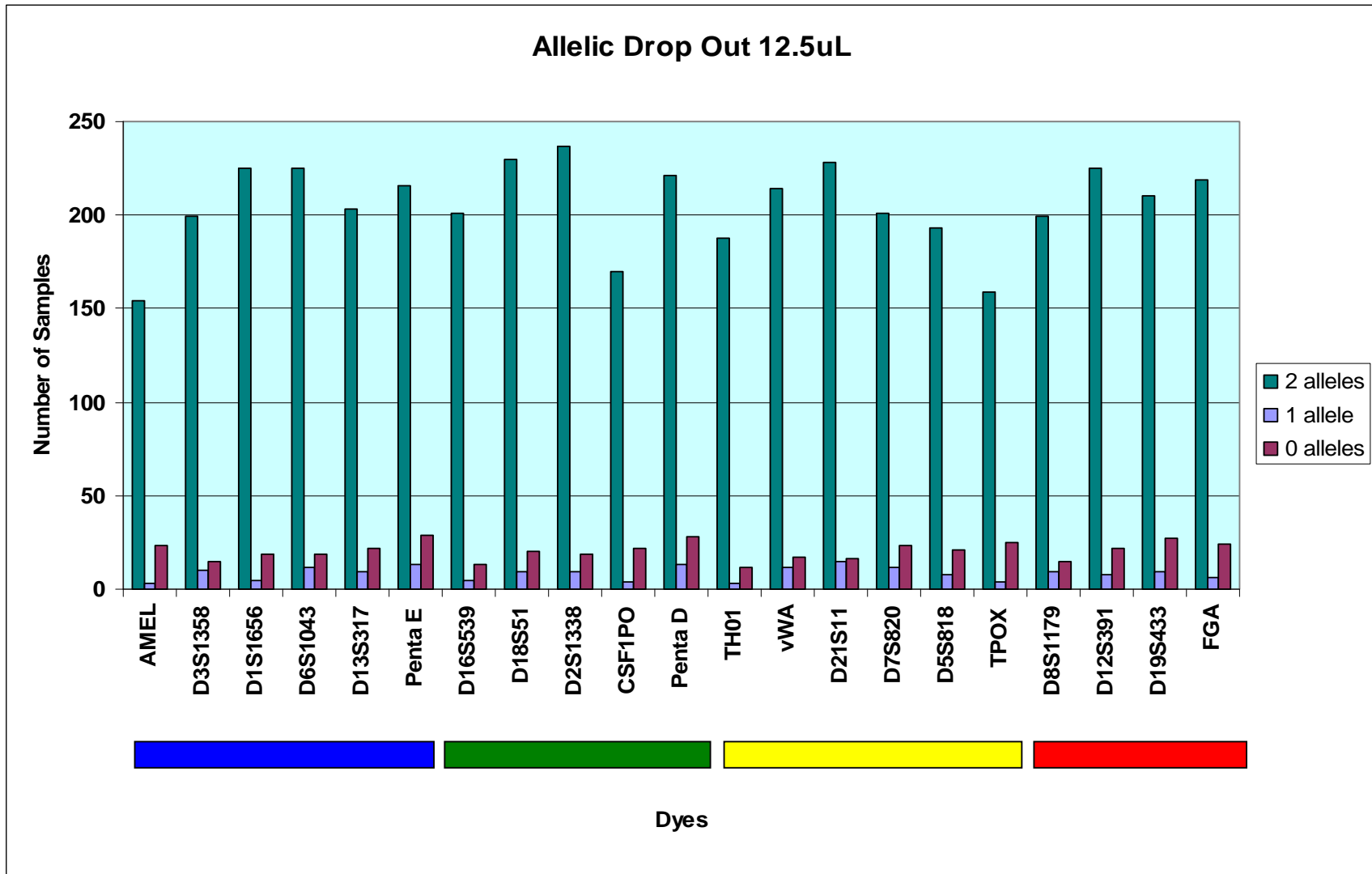


Figure 28 - Dropout events for samples amplified at 12.5µL

6.8.2 Drop out 3

Analysis for drop out 3 used the data from the baseline (10 x 10) and both sensitivity experiments at both 25 μ L and 12.5 μ L total PCR volume. There were 215 drop out events observed for the 25 μ L total PCR volume compared to 198 drop out events observed at 12.5 μ L total PCR volume. Figure 29 shows the number of drop out events for a range of peak heights. This shows the majority of drop out events occur below 150RFU for 25 μ L total PCR volume and below 180RFU for 12.5 μ L total PCR volume.

Figures 30, 31 and 32 show the peak heights where one of the heterozygote pairs has dropout at each DNA template. Figure 30 shows one dropout event occurred at 226RFU for the 12.5 μ L total PCR volume at a DNA template of 0.131ng whereas 17 dropout events occurred at 25 μ L total PCR volume at the same DNA template, however these dropout events occurred under 80RFU. The highest drop out seen for 12.5 μ L total PCR volume was at 234RFU at a DNA template of 0.025ng and for 25 μ L total PCR volume was at 106RFU. The total number of dropout events seen for the 10 x10 at 25 μ L total PCR volume was 68 and 30 at 12.5 μ L total PCR volume.

Figure 31 (Sensitivity 1) shows the highest drop out for 12.5 μ L total PCR volume was seen at 399RFU at a DNA template of 0.01ng and 160RFU at DNA template 0.01ng for the 25 μ L total PCR volume. The total number of dropout events seen for the sensitivity 1 experiment at 25 μ L total PCR volume was 58 and 66 at 12.5 μ L total PCR volume.

Figure 32 (Sensitivity 2) shows the highest drop out for 12.5 μ L total PCR volume was seen at 246RFU at a DNA template of 0.0094ng and 249RFU at a DNA template of 0.0375ng for the 25 μ L total PCR volume. The total number of dropout events seen for the sensitivity 2 experiment at 25 μ L total PCR volume was 89 and 102 at 12.5 μ L total PCR volume.

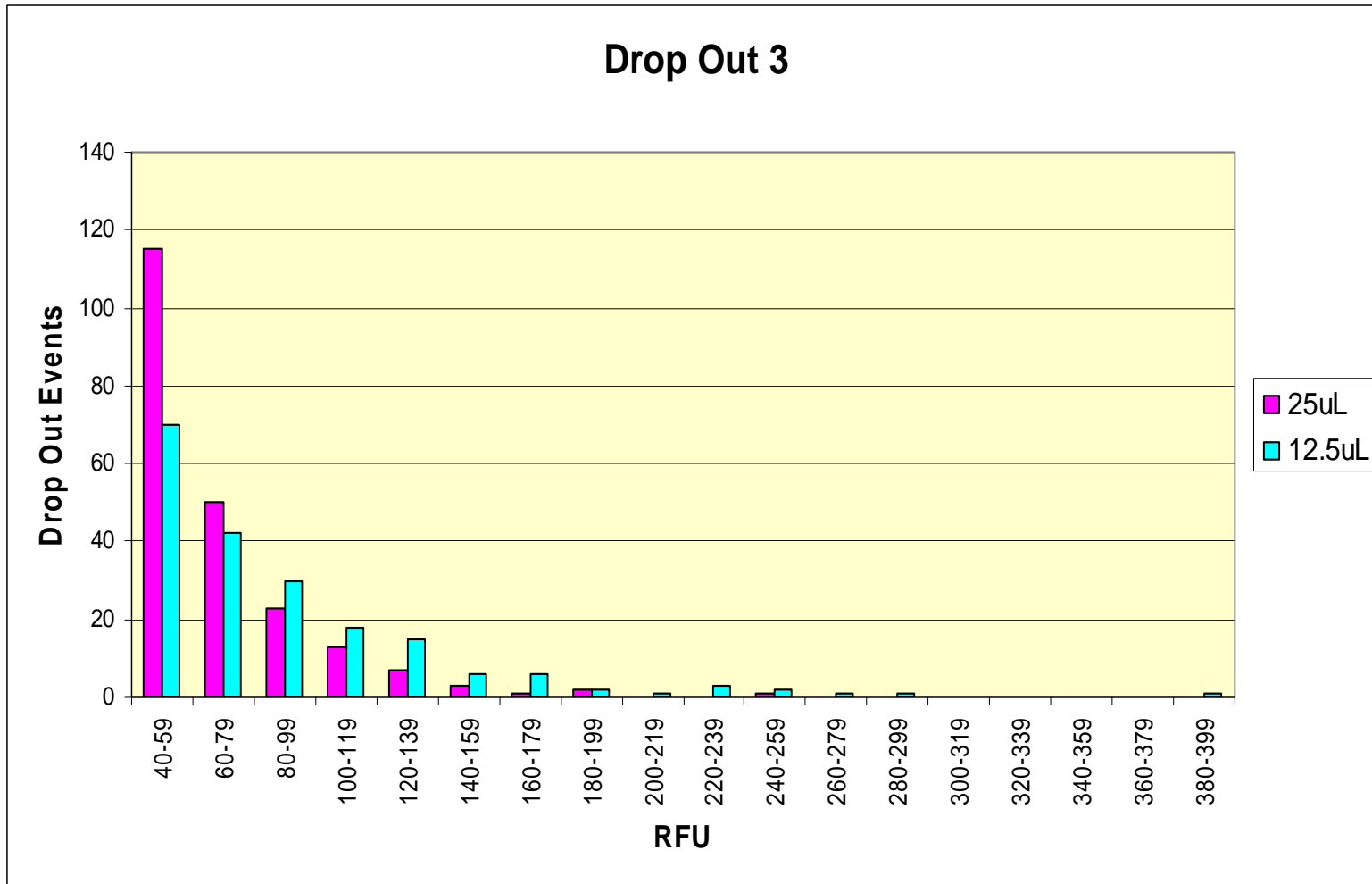


Figure 29 - Number of drop out events seen within peak height ranges at 25µL and 12.5µL amplifications

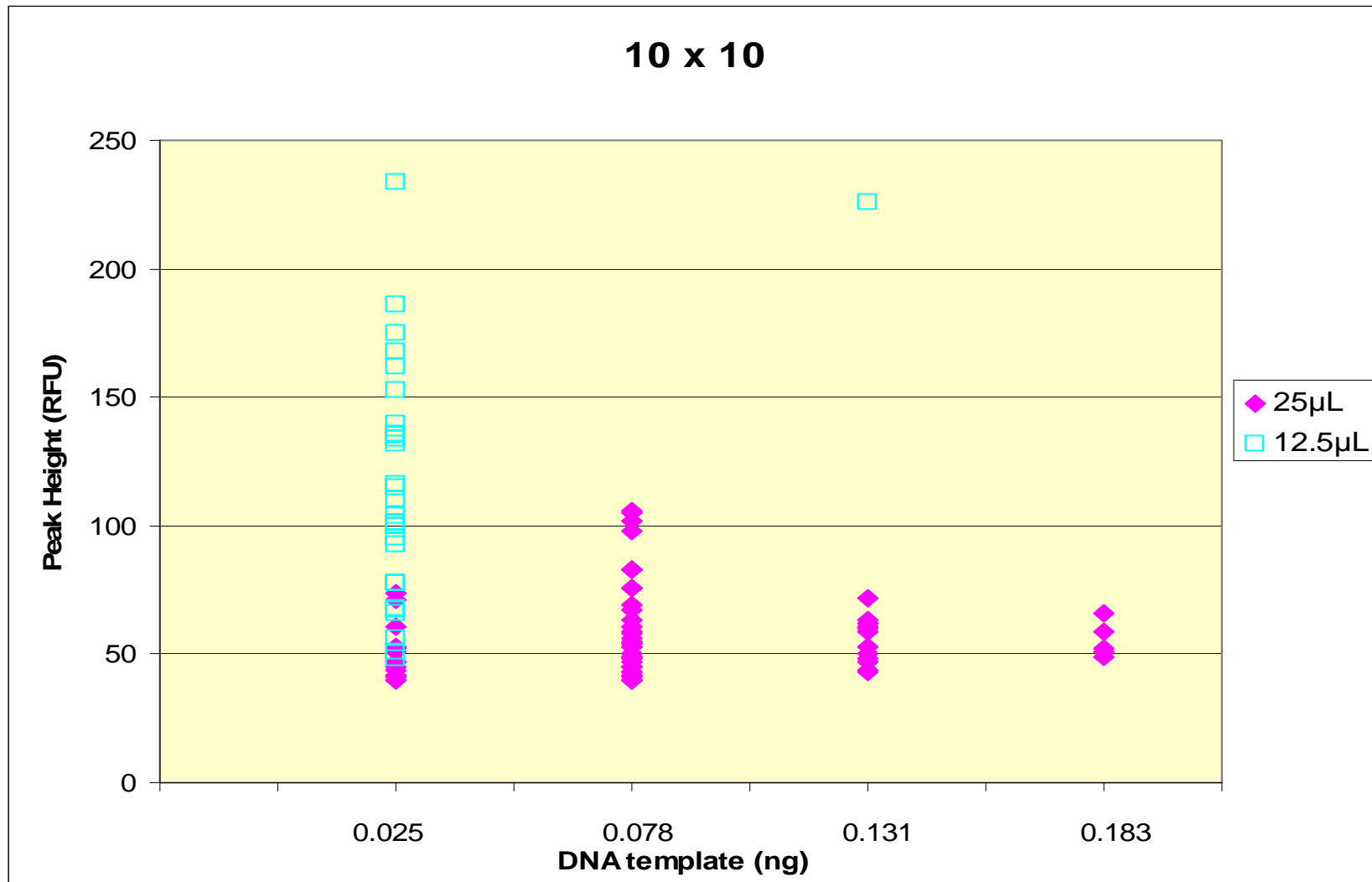


Figure 30 - Peak heights where the heterozygote pair has dropped out at different DNA templates for 12.5uL and 25uL using the baseline data (10 x10)

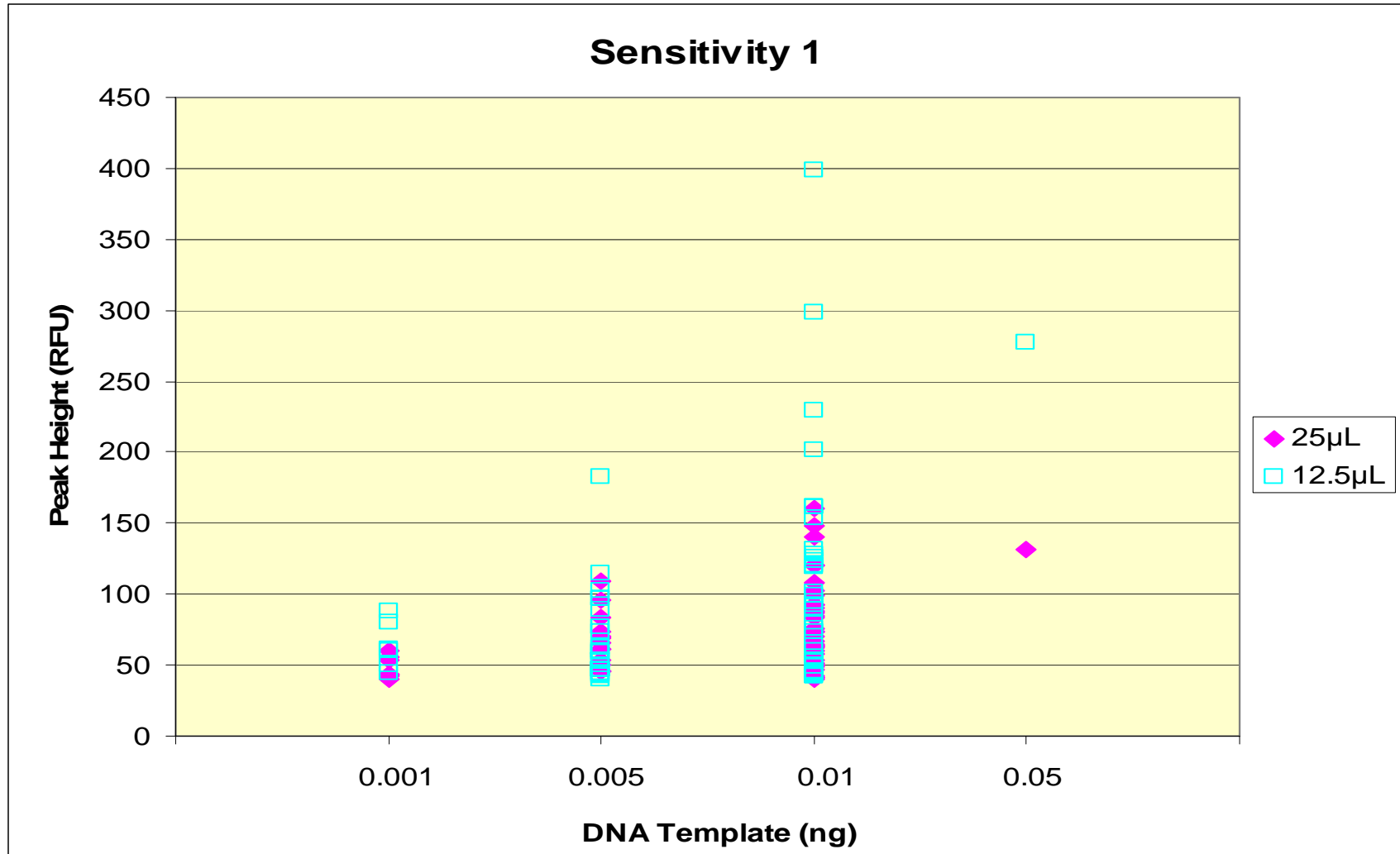


Figure 31 - Peak heights where the heterozygote pair has dropped out at different DNA templates for 12.5uL and 25uL using sensitivity 1 data

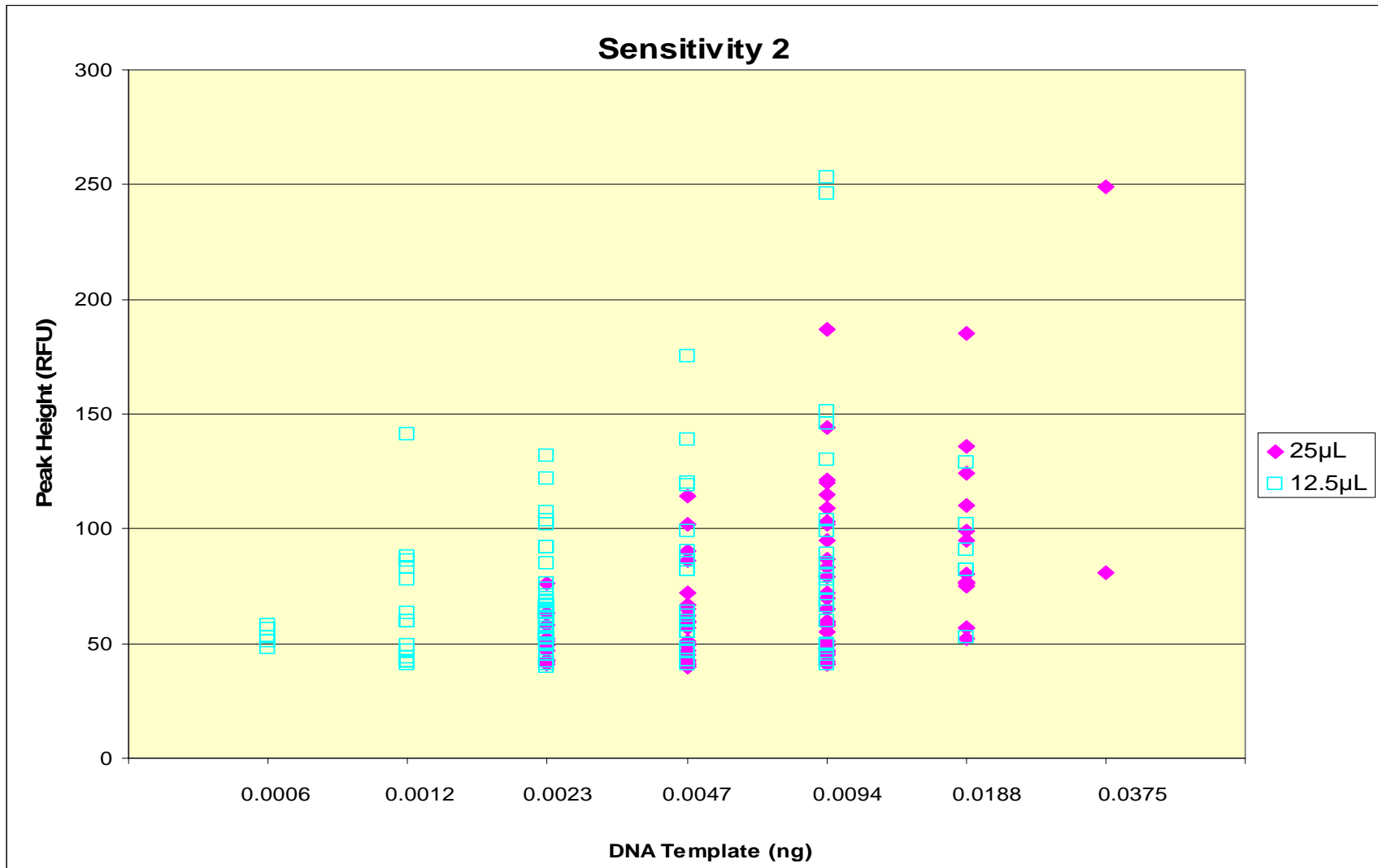


Figure 32 - Peak heights where the heterozygote pair has dropped out at different DNA templates for 12.5uL and 25uL using sensitivity 2 data

6.9 Mixture Studies

At a total input template of 0.5ng, for both 25 μ L and 12.5 μ L, all alleles were detected for the mixtures with ratios of 1:1, 2:1 and 5:1. Any allelic imbalance was observed at a level of greater than 40%.

When the template was decreased to 0.125ng for 5:1 mixtures, drop-out of the lower level contributor was observed for both 25 μ L and 12.5 μ L volumes. At this template level, allelic imbalance of down to 35% was observed for the lower level contributor at both 25 μ L and 12.5 μ L volumes, however, one of these peaks fell into the stutter position of the larger contributor.

When the template was decreased to 0.06ng for 2:1 mixtures, drop-out of the lower level contributor was observed for both 25 μ L and 12.5 μ L volume with the partner allele being as high as 562RFU. At this template level, allelic imbalance of down to 20% was observed for the lower level contributor and 23% for the higher level contributor.

For the remaining mixtures with ratios of 10:1, 20:1, 30:1 and 50:1 of varying template levels (maximum 0.5ng), the lower contributors exhibited, sometimes quite marked, stochastic variation. This included drop-out with peaks up to 392RFU and allelic imbalance as low as 20%.

The tables 16 and 17 show the approximate mixture ratio of the profile compared with the mixture ratio of the sample. For the 2 person mixtures this was averaged over all loci where there was no allele sharing between the two contributors and where the alleles did not fall into a stutter position. For the 3 person mixtures, the ratio was averaged over all loci where there was no allele sharing between the three contributors, however it was not possible to exclude loci where the alleles fell into stutter positions as there were no loci fulfilling this criteria. It was not possible to accurately calculate mixture ratios for the four person mixtures.

The data shows that the mixture ratio after DNA amplification is approximately equal to the mixture ratio of the initial sample for both 25 μ L and 12.5 μ L volumes at all ratios. The mixture ratio deviates more as the ratio increases most likely due to the stochastic effects of the lower contributor. The mixture ratios for the 25 μ L volume amp appear to be slightly lower than for the 12.5 μ L volume amp.

Although mixture ratios have not been calculated for the four person mixtures, the alleles obtained are consistent with expected profiles.

Table 18 - 12.5µL total PCR volume mixture studies

| Mixture Ratio of Sample | Total Input Template (ng) | Approximate Mixture Ratio of Profile |
|-------------------------|---------------------------|--------------------------------------|
| 2 Person Mixtures | | |
| 1:1 | 0.500 | 1.2:1 |
| 2:1 | 0.500 | 2.2:1 |
| | 0.060 | 2.9:1 |
| 5:1 | 0.500 | 6.1:1 |
| | 0.125 | 6.1:1 |
| 10:1 | 0.500 | 12:1 |
| | 0.125 | 11:1 |
| 20:1 | 0.500 | 24:1 |
| | 0.250 | 16:1 |
| | 0.125 | 19:1 |
| 30:1 | 0.500 | 21:1 |
| 50:1 | 0.500 | 35:1 |
| | 0.250 | 49:1 |
| | 0.125 | Unable to calculate |
| 3 Person Mixtures | | |
| 5:2:1 | 0.500 | 4.2:1.3:1 |
| | 0.125 | Unable to calculate |
| 10:5:1 | 0.500 | 13:9.1:1 |
| 20:10:1 | 0.500 | 10:5.7:1 |
| | 0.125 | Unable to calculate |
| 4 Person Mixtures | | |
| 5:3:2:1 | 0.500 | Unable to calculate |
| | 0.125 | Unable to calculate |

Table 19 - 25µL total PCR mixture studies

| Mixture Ratio of Sample | Total Input Template (ng) | Approximate Mixture Ratio of Profile |
|-------------------------|---------------------------|--------------------------------------|
| 2 Person Mixtures | | |
| 1:1 | 0.500 | 1.2:1 |
| 2:1 | 0.500 | 1.8:1 |
| | 0.060 | 1.7:1 |
| 5:1 | 0.500 | 4.1:1 |
| | 0.125 | 4.8:1 |
| 10:1 | 0.500 | 8.5:1 |
| | 0.125 | 6.3:1 |
| 20:1 | 0.500 | 22:1 |
| | 0.250 | 17:1 |
| | 0.125 | 10:1 |
| 30:1 | 0.500 | 15:1 |
| 50:1 | 0.500 | 26:1 |
| | 0.250 | 9.2:1 |
| | 0.125 | 6.7:1 |
| 3 Person Mixtures | | |
| 5:2:1 | 0.500 | 2.9:1.5:1 |
| | 0.125 | 2.7:1.1:1 |
| 10:5:1 | 0.500 | 7.4:5.4:1 |
| 20:10:1 | 0.500 | 10:6.4:1 |
| | 0.125 | 10:4.7:1 |
| 4 Person Mixtures | | |
| 5:3:2:1 | 0.500 | Unable to calculate |
| | 0.125 | Unable to calculate |

7 Conclusion

The results from this validation support that Promega's PowerPlex®21 System is suitable for analysis of STRs.

Despite slight differences observed between the two 3130xl analysers, the use of single LOD and LOR of 16RFU and 40RFU is more practical for use in DNA Analysis.

The PowerPlex21® System displays full concordance with all alleles observed in testing being concordant.

The three national population datasets (Caucasian, Aboriginal and SE Asian) created collaboratively within Australia, have been externally validated and will be implemented in conjunction with STRmix™ for statistical interpretation.

12.5µL total PCR volumes gave higher peak heights than their 25µL counterparts at the same DNA template.

The PowerPlex®21 system is a very sensitive amplification kit when used at either the standard amplification volume (25µL) or reduced volume amplification (12.5µL); however the increased sensitivity does not necessarily result in more reliable information.

The two sensitivity experiments explored the range on DNA template inputs from very large inputs (4ng) to very small inputs (0.00059ng). Within this validation complete PowerPlex® 21 DNA profiles were obtained with as little as 0.01875ng of template DNA. However, the PHR data indicate that as the amount of template DNA decreases the μ_{PHR} decreases and σ_{PHR} increases. The risk of type 2 errors is greatly increased from template DNA amounts of less than 0.132ng for both 25µL and 12.5µL total PCR volumes, which is supported by the experimental drop out data.

The data presented within this report indicates that input templates less than 0.132ng total DNA (concentrations 0.0176ng/µL if using 12.5µL total PCR volume or 0.0088ng/µL for 25µL total PCR volume) may result in increased stochastic effects.

As previously documented in DNA Analysis[45, 46], the Quantifiler™ Human DNA Quantification kit gives an estimate of the DNA concentration. Careful consideration of the DNA profile is required before reporting because the precision within a quantification method and between different quantification methods may vary.

For the range of DNA templates specified above, significant differences between 12.5µL and 25µL total PCR volumes was not observed. The use of 12.5µL total amplification volume as the default protocol with DNA Analysis is indicated. The disadvantage of the 12.5µL total PCR volume are the physical constraints of the process i.e. a maximum of 7.5µL of sample can be used compared with 15µL for the 25µL total PCR volume. However, higher peak heights and the cost savings associated with reduced volume amplifications even with additional processes to increase the sample concentration, mitigate the disadvantage.

The implementation of PowerPlex® 21 for amplification of DNA extracts will coincide with the implementation of STRmix™. The combination of the two processes will apply a continuous biological model rather than a binary model to DNA interpretation. STRmix™ models stutter, drop out, heterozygote balance and homozygote threshold for case work samples.

The rate of drop in events has been calculated for both total PCR volumes and will be implemented in conjunction with STRmix™.

At a total input template of 0.5ng, for 25µL and 12.5µL total PCR volumes, all alleles were detected for the mixtures with ratios of 1:1, 2:1 and 5:1.

For the remaining mixtures with ratios of 10:1, 20:1, 30:1 and 50:1 of varying template levels (maximum 0.5ng), the lower contributors exhibited, sometimes quite marked, stochastic variation.

Mixture interpretation is beyond the scope of this validation and will be dealt with in the STRmix™ validation report.

8 Recommendations

1. A common LOD/LOR (16RFU/40RFU) will be used for both 3130xl instruments as outline in section 6.4.
2. The default total PCR volume will be 12.5µL. Samples can also be amplified at 25µL total PCR volume.
3. Initially samples with concentrations below 0.01ng/µL will not be routinely processed in the first instance. If necessary, these samples may undergo post extraction concentration via centrifugal filter concentration procedure to increase the concentration or re-amplify at 25µL total PCR volume.
4. Initially samples with concentrations between 0.01ng/µL and 0.0176ng/µL will not be routinely amplified. These samples are considered as candidates for post extraction concentration via centrifugal filter concentration procedure to increase the concentration to the point that stochastic effects are minimized.
5. Initially samples with concentrations between 0.0176ng/µL and 0.0244ng/µL will be amplified and assessed for stochastic effects during case management to ensure the suitability of these DNA profiles for reporting.
6. Samples with concentrations above 0.0244ng/µL will be routinely amplified.
7. Al_{TH} to be set at 40% and Hom_{TH} 250RFU for extracted reference, environmental and quality control samples amplified at 12.5µL total PCR volume.
8. Al_{TH} to be set at 45% and Hom_{TH} 200RFU for extracted reference, environmental and quality control samples amplified at 25µL total PCR volume.

9. Adoption of the national Caucasian, Asian and Aboriginal sub-population datasets that DNA Analysis contributed to as part of this validation for use within statistical calculations.
10. Adoption of the locus specific stutter filter as per results section.
11. Thresholds listed in 7 and 8 are to be used as a guidelines when assessing the number of contributors in a mixture.
12. A post implementation review should be performed to review the appropriateness of points 3 – 8. The review will at minimum examine the outcomes of samples amplified within 0.0176ng/μL and 0.0244ng/μL concentration range. Similarly, all of the extracted reference samples will be reviewed with regards to the AI_{TH} and homozygote threshold.

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From: Josie Entwistle <[REDACTED]>
Sent: Friday, 4 December 2015 10:36 AM
To: Cathie Allen; Justin Howes; Kylie Rika; Amanda Reeves; Sharon Johnstone; Luke Ryan; Megan Mathieson; Kirsten Scott; Allan McNevin
Attachments: Assessment of results obtained from 'automatic-microcon' samples_v.2report.doc

Hi all,

Please find attached a copy of the proposed final draft of the Auto-mic assessment project report. If you could have a read over this and vote on one of the four proposed options, that would be appreciated. Please bear in mind that the general recommendation is to accept option 4. If this is the majority accepted option, then there will be no further changes and a hard copy will be issued for signing. If you have any additional feedback, please e-mail me.

Regards

Josie

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Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon[®] Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

January 2018

Justin Howes and Cathie Allen

Project Proposal #184 Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

Published by the State of Queensland (Queensland Health), November 2017



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Version history

| Version | Date | Changed by | Description |
|---------|------------|--------------|--------------------------|
| 1.0 | 30/11/2017 | Justin Howes | Document Created. |
| 2.0 | 09/01/2018 | Justin Howes | Post Management feedback |
| | | | |

Document sign off

This document has been **approved** by:

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1. Abstract

All samples that underwent a Microcon® process were evaluated and categorised into whether there was meaningful information obtained or not. This evaluation primarily focussed on samples that underwent an 'auto-microcon' process in 2016. The results suggest there to be arguably minimal value in performing the 'auto-microcon' process due to the limited meaningful DNA Intelligence obtained from these samples. Given this, further streamlining of workflow processes could be implemented that would provide significant efficiencies such that these efforts could be better placed in processing higher DNA-yielding samples.

2. Definitions

DNA Profile Intelligence: DNA profile information available for interpretation by Forensic DNA practitioners that is able to be provided to clients.

Fail: In this report, this is DNA profile information that was not suitable for comparing to reference DNA profiles. This word was used to filter the data into two possible outcomes (fail/success).

NCIDD: National Criminal Investigation DNA Database.

QPS: Queensland Police Service.

Success: In this report, this is DNA profile information that was obtained that was suitable for comparing to reference DNA profiles. This word was used to filter the data into two possible outcomes (fail/success).

3. Introduction

Microcon® Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane^[1].

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of extract from approximately 100uL to ≤20µL for amplification with AmpF!STR® Profiler Plus®, and to ≤35µL for amplification with PowerPlex® 21 system (PP21).

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of

<0.132ng were found to exhibit marked stochastic effects after amplification [2]. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process).

Anecdotally, the suitability to provide QPS with DNA profile Intelligence from extracts that have been concentrated has been noted to be limited. Furthermore, extracts that are of low quant value that have been automatically concentrated have been observed to rarely yield DNA information for QPS.

NB. Project #163 – *Assessment of results obtained from 'automatic-microcon' samples* [3] was conducted to evaluate the results of samples that were processed with the 'auto-microcon' process. A recommendation of this project was to re-evaluate after the introduction of the Forensic Register in conjunction with the use of Quantifiler® Trio DNA Quantification Kit.

This recommendation was based on the perceived ease of retrieving data from the FR as opposed to AUSLAB, and with the thought that the FR would soon be implemented. For the purposes of this project, it is not considered essential to have the FR implemented if the data can be retrieved from AUSLAB. However, it is considered important that the data be spanning a sufficient period of processing, and be based on the same Quantification system namely the Quantifiler® Trio DNA Quantification Kit.

The purpose of this project is to evaluate the suitability for interpretation of DNA profiles that may be obtained after the post-extraction concentration step using the Microcon® centrifugal filter devices. This evaluation includes an assessment of those samples that underwent the 'auto-microcon' process. This evaluation is based on a data mine of extracts in the year 2016 that were concentrated with Microcon® centrifugal filter devices, and assesses the 'suitability' of PP21 profile outcomes as a function of quant values obtained from using the Quantifiler® Trio DNA Quantification Kit.

This evaluation looks at two data sets as a function of the Quantification value:

1. PP21 DNA profile outcomes from extracts that were processed through the 'auto-microcon' process;
2. PP21 DNA profile outcomes from all extracts that were concentrated with the Microcon® filter devices.

4. Resources

The following resources were required for this validation/project:

Forensic DNA Analysis staff and computer time to retrieve data from AUSLAB and to use Microsoft Excel.

5. Methods

5.1. Data retrieval from AUSLAB (LIMS)

Data was retrieved from AUSLAB using Extended Enquiries. Data was searched for samples that had a testcode of 'XPLEX' and 'MCONC1' ordered in the year 2016 in Forensic DNA Analysis. These were High Priority (P2) samples.

The data was output with the corresponding Quantification value and the reported DNA profile interpretation (Exhibit Report Line in the Exhibit Report (EXH)) for that particular barcode. If the barcode was a sub-sample, the corresponding EXH line for the sub-sample was output.

For ease of data interrogation, the RAW data (I:\Change Management\Proposal#184 - Evaluation of the efficacy of Microcons\Data\RAW Data from AUSLAB) had a column added to describe whether the sample underwent the 'auto-microcon' process ('AUTO' = $0.001\text{ng}/\mu\text{L} < \text{Quant} < 0.0088\text{ng}/\mu\text{L}$) or not ('MANUAL' = $\text{Quant} > 0.0088\text{ng}/\mu\text{L}$). Another column was added to describe whether there was a Quantification value returned in the data collation ('TRUE' = Quant value obtained), or not ('FALSE' = no Quant value obtained (ie. $0\text{ ng}/\mu\text{L}$)).

The data excluded samples that had not returned a DNA profile result, Quality samples (including environmental monitoring samples), have no quant value in the data export, or have quality issues noted.

5.2. Data interrogation

The data was interrogated by assessing the DNA profile outcome results reported as Exhibit Report lines as a function of the Quantification value.

The Exhibit lines were interrogated and grouped into two interpretation outcomes as follows:

1. 'Fail': DNA profile interpretation outcomes of 'Complex unsuitable for interpretation', 'No DNA profile', 'Partial unsuitable for interpretation', 'No DNA Detected';
2. 'Success': All other DNA profile outcomes including single source DNA profiles matching assumed known contributors or different reference DNA profiles, mixtures that were suitable for comparison to reference DNA profiles, DNA profiles that were suitable for loading to NCIDD.

NB. These descriptions were used to filter the data. A 'fail' does not mean there was a Quality failure in the process; a 'success' does not necessarily mean a DNA match.

6. Experimental Design

6.1. Experiment 1: Assessment of 'auto-microcon' results

Intent

Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.

Data Analysis

The samples applicable to this experiment had Quantification values in the range 0.001ng/μL to 0.0088ng/μL, and a total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value. A percentage of samples that fell into these categories was determined.

The 'auto-microcon' data could be expressed as a function of Quantification value.

The percentage of samples that had an 'auto-microcon' process and led to an NCIDD upload was obtained. This data could be filtered further into the outcome from the NCIDD load, at the time of data collection.

Data on the DNA profile outcomes for various suspected biological types was obtained. Furthermore, data on the profile outcomes for various substrate types was obtained.

6.2. Experiment 2: Assessment of all DNA profile results from extracts that have had a concentration step.

Intent

Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 and underwent a post-extraction concentration step using Microcon[®] centrifugal filter devices.

Data Analysis

The samples that were applicable to this experiment had Quantification values above 0.001ng/ μ L, and underwent the Microcon[®] process. This included the 'auto-microcon' samples, and those that had a Microcon[®] rework performed (termed 'manual'). This combination of data was termed 'combined data'.

A total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value.

The percentage of samples that fell into these categories ('manual' and 'combined') was determined. 'Manual' referred to the samples beyond the 'auto-microcon' range that were reworked with the Microcon[®] process, and 'combined' referred to all samples ('auto-microcon' and 'manual').

There was a point where the number of 'success' samples was approximately the same as the number of 'fail' samples when the Microcon[®] process was performed. This appeared to be approximately Quant = 0.02ng/uL. Therefore, the data was interrogated further at a Quantification value lower than this mark to determine what percentage of samples in certain ranges led to DNA profile interpretation outcomes of 'success'.

From this data, a sub-section of samples was interrogated further to evaluate the effect on DNA Intelligence that was obtained. A range of samples with Quantification range up to 0.015ng/uL was chosen and a total number of samples was determined. This Quantification value was chosen as it was the approximate value where all samples below this value that underwent a Microcon[®] process, led to an approximate, round figure of 85% 'failure'.

The percentage of samples that were in this Quantification range and led to an NCIDD upload was determined. This data could be filtered further into the outcome from the NCIDD load. This data could then be used to evaluate the

potential for samples to not provide meaningful DNA Intelligence to QPS if the Microcon[®] process was re-defined in some way. By 'meaningful DNA Intelligence', this means DNA profile information that can be provided to the client that could lead to an identification of a person potentially associated to the alleged matter.

6.3. Experiment 3: Datamine of the difference in pre- and post-Microcon[®] Quantification values

Intent

Evaluate the difference between the values obtained from the Quantification process in samples that have had a Microcon[®] concentration step applied.

As this is purely a datamining experiment, only the samples that have yielded a result of 'success' was examined.

Data Analysis

The samples applicable to this experiment had Quantification values above 0.001ng/ μ L where the final result was 'success'.

The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/ μ L and 0.015ng/ μ L were examined.

This range was considered by the author to be able to provide a sufficient demonstration of the trend of the data.

7. Results and Discussion

7.1 Assessment of 'auto-microcon' results

For samples in the 'auto-microcon' Quantification range, the total number of samples that were processed this way (excluding certain samples as per Section 5.1) was N= 1449 samples.

The percentage of samples that resulted in a determination of 'fail' was 89.4% (Fig 1). As expected, the number of 'fails' increased when the Quantification decreased and approached the Limit of Detection of Quantification ie. 0.001ng/ μ L (Fig 2). This was considered to be due to there being less DNA detected in the extract, and therefore less DNA to concentrate.

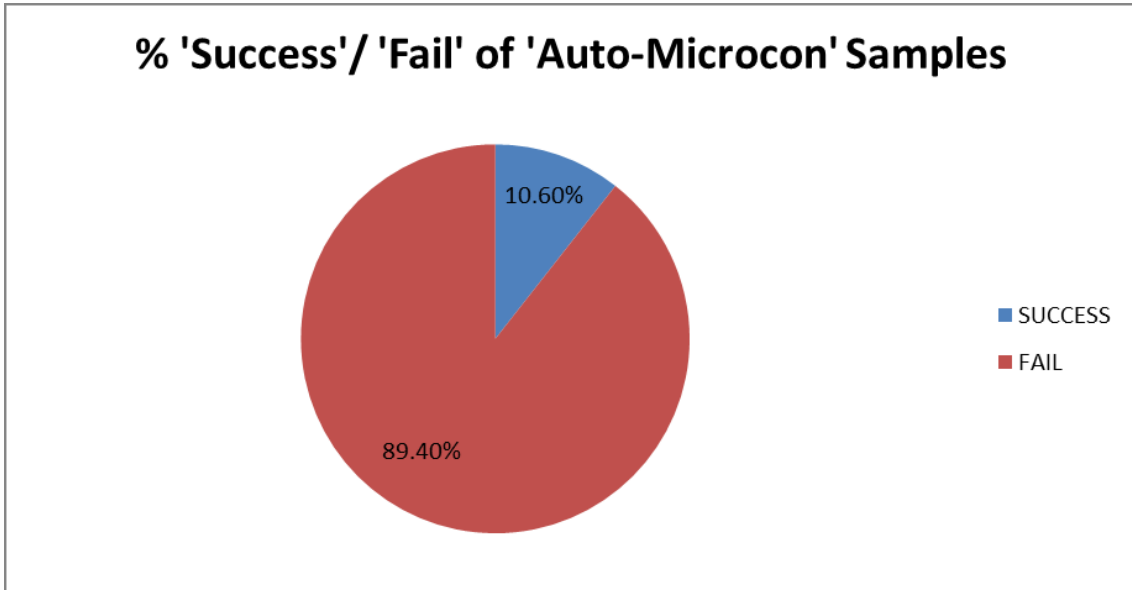


Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

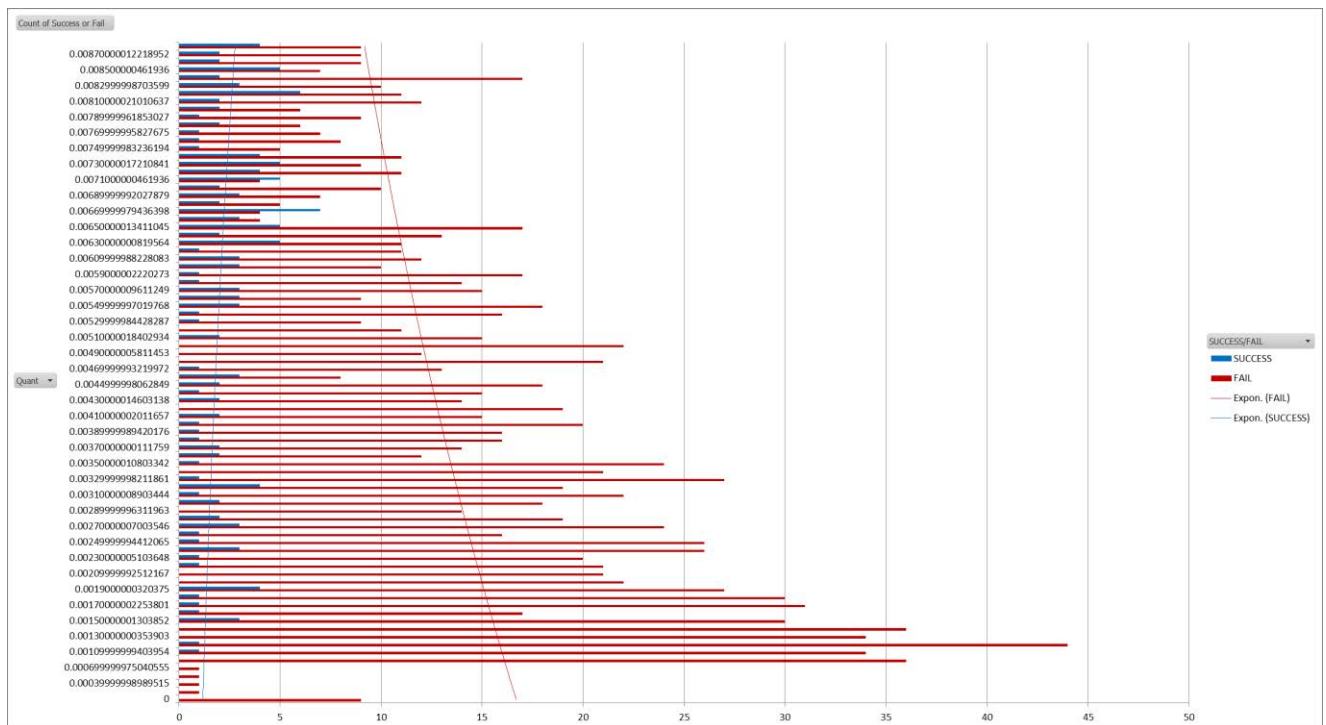


Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

If samples were not processed through the 'auto-microcon' process, what DNA Intelligence would the client miss out on? To evaluate this, the 'success' data was drilled down to the samples that had some NCIDD interaction and in particular, where they were the only samples in the case that were NCIDD-suitable for that particular profile (Fig 3). This represented 1.86% of all 'auto-microcon' samples. In looking at samples that provide *new* Intelligence, that is

DNA information available for future linking, or has provided a cold-link, this equated to 1.45% of all 'auto-microcon' samples.

This 1.45% of samples would be the pertinent value for the client to consider if the 'auto-microcon' process was not performed. In considering this, it would be important to evaluate the time and cost for processing, and the opportunity to concentrate efforts on other higher yielding samples. In saying this, with the ease of communication through the Forensic Register, these samples could process if the client has no other Forensic Intelligence assisting the matter, or if the item is considered to be of critical priority.

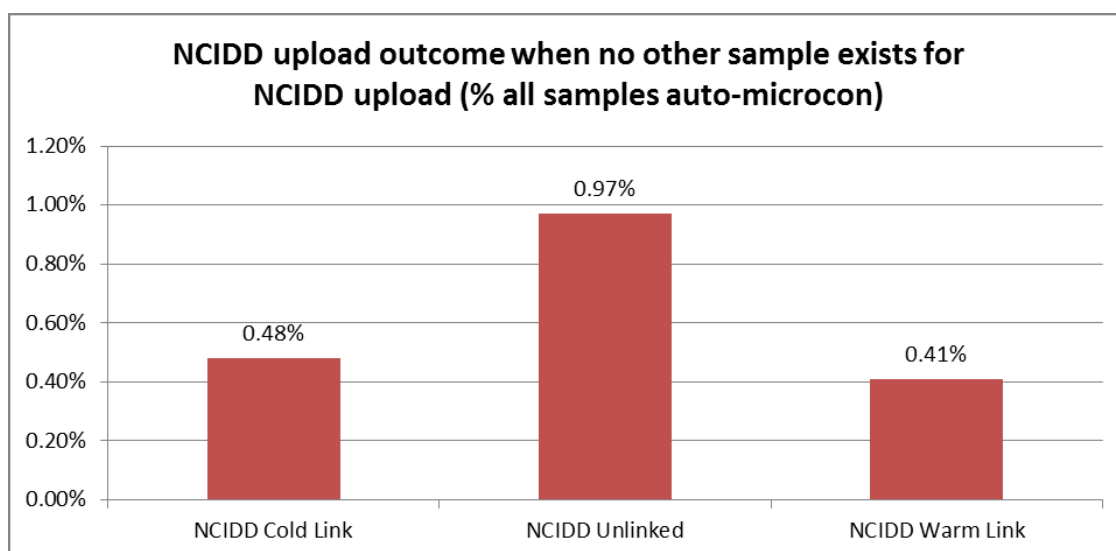


Figure 3: NCIDD outcome for samples that were loaded to NCIDD

The 'success' data was further evaluated to see if any particular substrate type or possible biological source, was more likely to lead to meaningful interpretations after an 'auto-microcon'. The data set for this evaluation was N=154 samples. These samples were broken down into three general interpretation outcomes:

- Profiles matching assumed known contributors. These were either single source DNA profiles, or mixed DNA profiles where the profile was conditioned with no information available for comparison in the remaining contribution (ie. peaks visible sub-threshold or the profile has allelic imbalance suggesting a mixture);
- Single source. These were DNA profiles that were attributed to unknowns, or matched reference DNA profiles, or were from items where ownership could not be confirmed; and,
- Mixtures where no statistical interpretation (NSIP) was performed or were suitable for comparison to reference DNA profiles for Likelihood Ratio (LR) purposes.

Figure 4 displays the DNA profile outcome as a function of the possible biological type, and Figure 5 displays the DNA profile outcome as a function of the substrate.

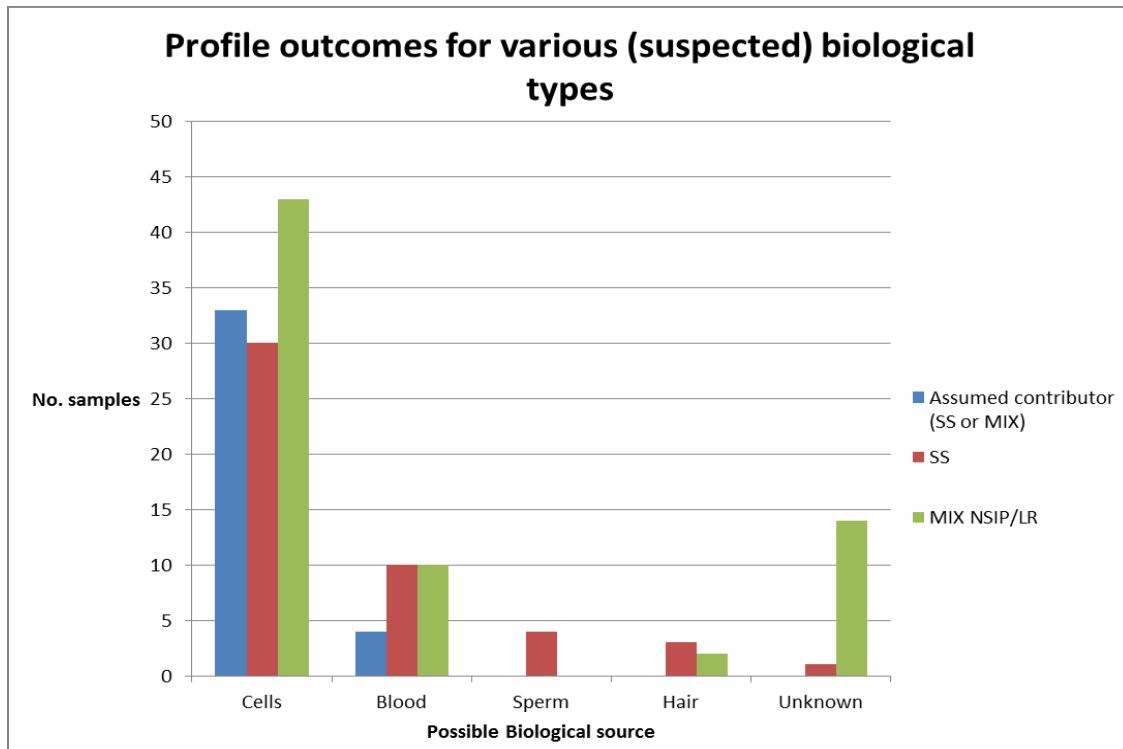


Figure 4: Profile outcomes for various (suspected) biological types

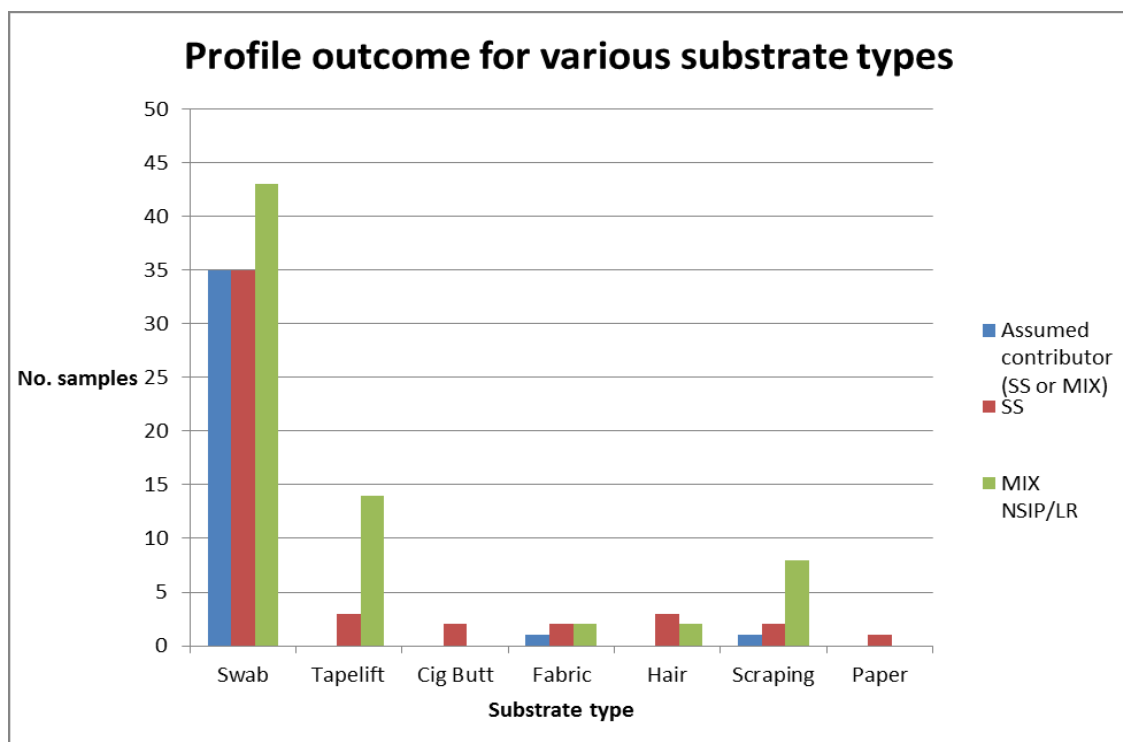


Figure 5: Profile outcome for various substrate types

Figures 4 and 5 show that there do not appear to be any obvious trends in the data. It is not unexpected to have a variety of DNA profile outcomes for different biological source types, and not unexpected for a variety of DNA profile outcomes for different substrate types. Interestingly, the number of 'assumed known contributors' is almost one-third of DNA profile outcomes for the most numerous suspected biological type (cells), and substrate type (swab). It could be argued that this DNA profile outcome is not meaningful to the client as the results are not unexpected.

What this means is that if the client requested a Microcon® process on a particular sample that was initially in the 'auto-microcon' Quantification range, there does not appear to be a predictive element to the likely success of the microcon rework for a particular biological source type, nor substrate type.

Ultimately, for approximately 90% of samples that underwent an 'auto-microcon' process, there is arguably negligible DNA profile Intelligence for the client. If the 'auto-microcon' was not applied as a streamlining strategy, there would be the following advantages, including but not limited to:

- the potential to make available at least 1449 processing positions for other samples including further available positions that would have been used for reworks. It must be noted that it is not unusual for low-quantification samples to be reworked further before determining if the profile is suitable for comparison to reference DNA profiles.

- the lack of a need for the considerable efforts required to prepare and process Microcon® (and further rework) batches for this number of samples,

- consumable and labour savings in the end-to-end processing of these samples, and

- time and effort could be redirected in the laboratory workflow to other activities including service extensions like Y-STR profiling.

7.2 Assessment of all DNA profile results from extracts that have had a concentration step.

All samples from 2016 that had a Microcon® process were determined. The total number of samples was N= 2201 samples, excluding certain samples as per Section 5.1.

The percentage of samples that resulted in a determination of 'fail' was 78.5% (see Fig 6). As expected, in looking at the spread of the 'combined' data, the number of 'successes' increased when the Quantification increased (Fig 7).

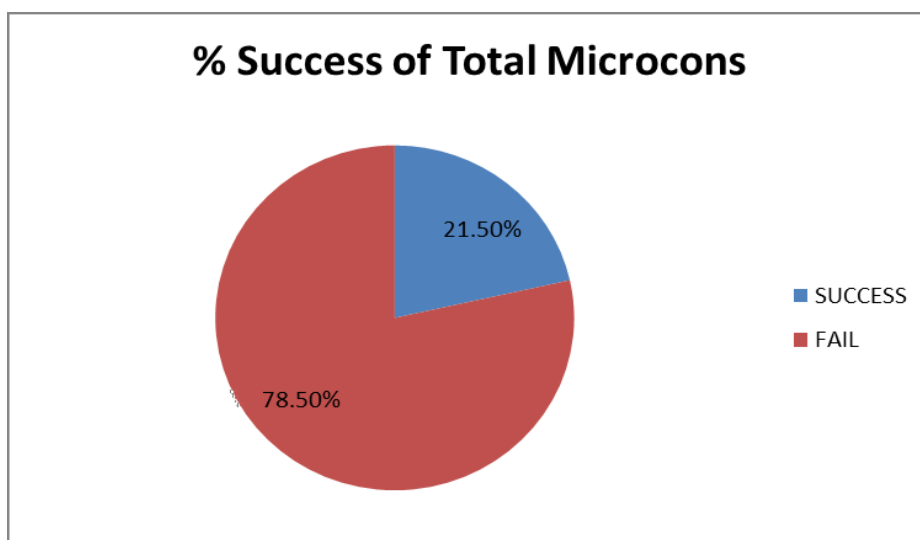


Figure 6: Percentage 'Success'/ 'Fail' of all Microcon® samples ('combined' data).

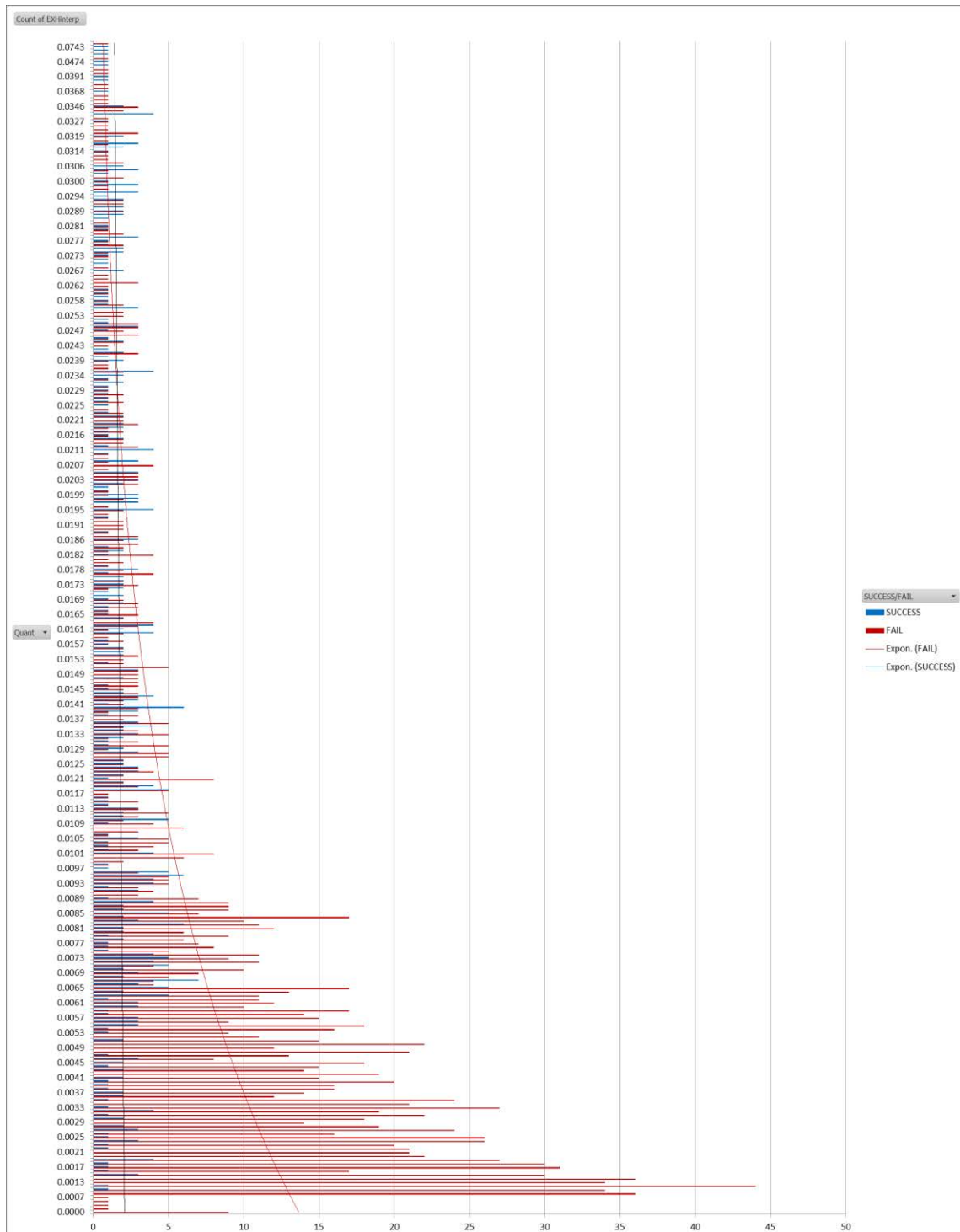


Figure 7: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

As mentioned in Section 5.2, the Quantification value where there was roughly the same number of ‘success’ and ‘fail’ samples was approximately 0.02ng/uL. It must be noted that this is a rough estimate *at this* particular Quantification value, and it is based on limited samples that returned that Quantification value. It can be argued that taking a range of Quantification values to look at the overall success/fail percentages could provide the client with approximate likelihoods of obtaining meaningful DNA Intelligence.

A number of ranges were looked at to determine the percentage 'success' of samples with Quantification values in various ranges (Fig 8). The ranges were established up to the highest Quantification value of 0.02ng/uL. As expected, the percentage 'success' increased as the Quantification increased due to the higher amount of DNA in the extract available to be concentrated.

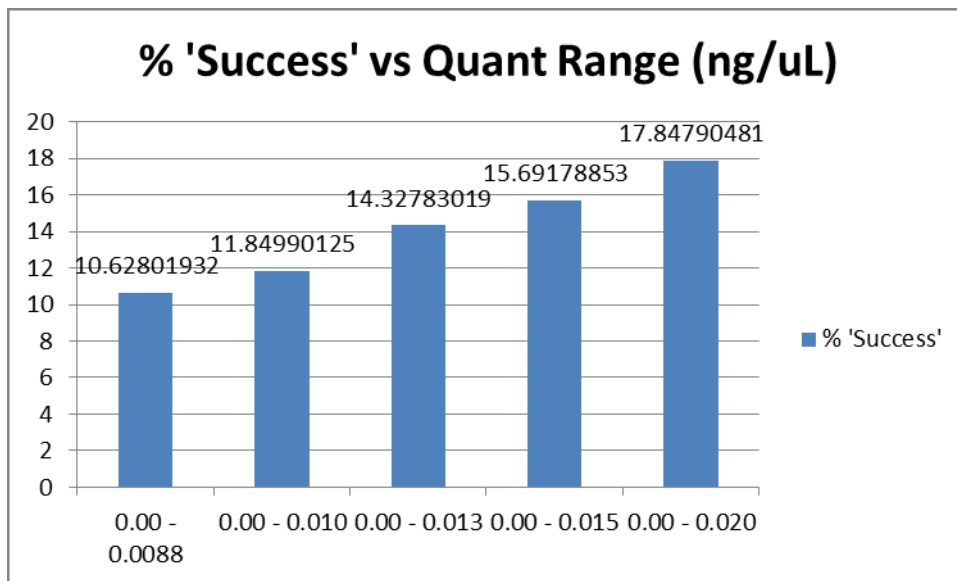


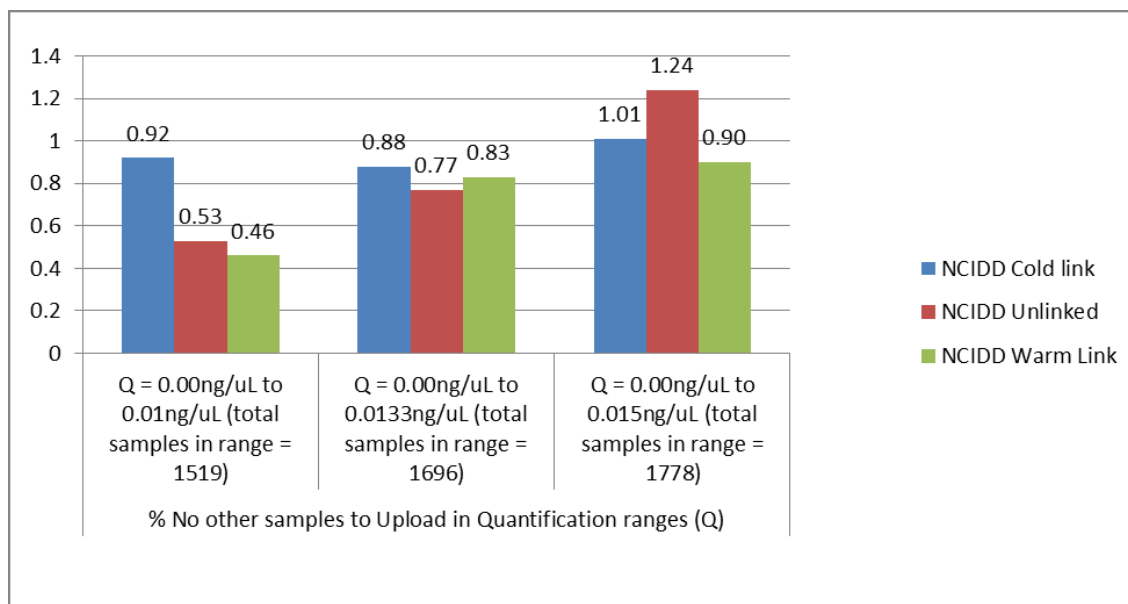
Figure 8: Percentage 'success' for samples that underwent a Microcon® process

In viewing the data in Fig 8, a limitation is that all samples that fell in the 'auto-microcon' range, had a Microcon® process performed, whereas there are samples that are in higher Quantification ranges that might not have required a Microcon® concentration rework step to yield useful DNA profiles. These samples were not evaluated.

A lower Quantification value to where the number of 'successes' roughly equalled the 'failures' was chosen to be the upper end of data ranges that were evaluated further. The value chosen was 0.015ng/uL. Table 1 and Figure 9 describe the risk to NCIDD upload for samples in these ranges if Microcon® concentration steps were not performed.

Table 1: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

| | % No other samples to Upload in Quantification ranges (Q) | | |
|-----------------|--|--|---|
| | Q = 0.00ng/uL to 0.01ng/uL (total samples in range = 1519) | Q = 0.00ng/uL to 0.0133ng/uL (total samples in range = 1696) | Q = 0.00ng/uL to 0.015ng/uL (total samples in range = 1778) |
| NCIDD Cold link | 0.92 | 0.88 | 1.01 |
| NCIDD Unlinked | 0.53 | 0.77 | 1.24 |
| NCIDD Warm Link | 0.46 | 0.83 | 0.90 |

**Figure 9:** NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

Approximately 1.45% of samples in the Quantification range up to 0.01ng/uL resulted in 'new' DNA Intelligence. This percentage is the same as that found in the 'auto-microcon' range. This percentage increased to 1.65% and 2.25% for the Quantification ranges up to 0.0133ng/uL and 0.015ng/uL respectively.

7.3 Datamine of the difference in pre- and post- Microcon® Quantification values

The samples applicable to this experiment had Quantification values above 0.001ng/ μ L where the final result was 'success'. The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/ μ L and 0.015ng/ μ L were examined.

As the Microcon® process concentrates the DNA extract from approximately 100uL to approximately 35uL, in theory it would be a reasonable expectation to obtain approximately two to three-fold increases in DNA Quantification after

concentration. Figure 10 shows the plot of the differences found for samples that resulted in 'success'.

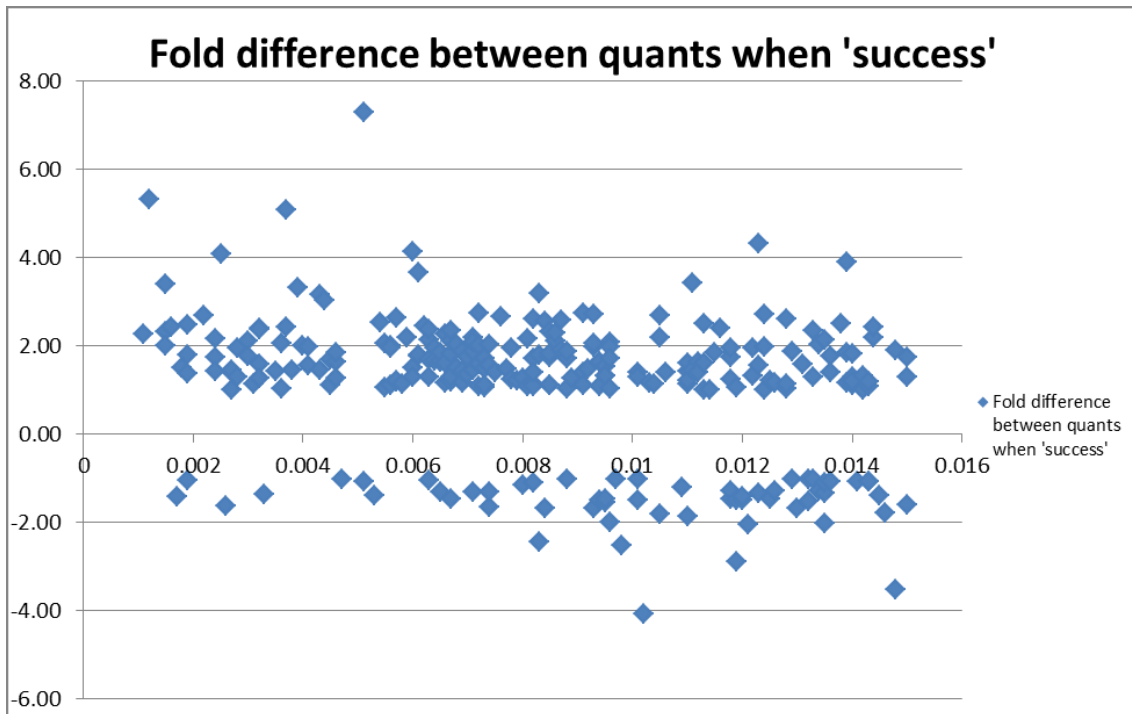


Figure 10: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results. Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 10 where the Quantification values decreased after concentration. Variability in results could be attributed to a number of things, including but not limited to the slight differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

8. Conclusion and Recommendations

The data analysis demonstrated that there was arguably minimal value in performing the 'auto-microcon' concentration step. This opinion was formed by analysing the data from 2016 where it was found that for all samples that underwent the 'auto-microcon' step, 89% did not yield results suitable for meaningful interpretation (or 'success' in this report).

It was found that in considering *all* samples that underwent a Microcon® step at some stage in 2016, 78.5% did not yield results suitable for meaningful interpretation. As expected, when the Quantification value increased, the percentage of meaningful results increased. However, it was also demonstrated in the data analysis that the Quantification values did not always improve after Microcon®, but where they did, the magnitude of change was roughly equivalent to the change in volume (from neat to concentrated sample).

Based on the data analysis, the following recommendations are offered:

1. Cease 'auto-microcon' (Quant range: 0.001ng/uL to 0.0088ng/uL) processing for all samples with the following exceptions:
 - a. Priority 1 samples (Critical Priority); and
 - b. Coronial/DVI samples where profiles are mostly single-source. Quite often incomplete profiles may be enough to provide Intelligence on possible identity.
2. Automatically send result information via the Forensic Register to QPS at Quantification stage for samples in the Quant range: 0.001ng/uL to 0.0088ng/uL. This result information is recommended to be the exhibit result line of 'DNA Insufficient for Further Processing'. This recommendation is an extension to the current 'No DNA Detected' process, which looks at Priority 2 samples yielding Quantification results of less than the Limit of Detection (0.001ng/uL).
3. After a six month period of processing, re-analyse samples that have had a Microcon® process performed and were in the initial Quantification range greater than 0.0088ng/uL, to evaluate whether the range from Recommendation 1 can be extended.
4. Communicate the change in process to QPS and ensure that QPS are aware that for samples in the range mentioned in Recommendations 1, that they could be requested for Microcon® concentration steps at any point in time. This request can be made via the Forensic Register after they have received the 'DNA insufficient...' result line.

9. References

- [1] QIS 19544v11 – Concentration of DNA Extracts Using Microcon Centrifugal Filter Devices
- [2] PowerPlex® 21– Amplification of Extracted DNA Validation. Megan Mathieson, Thomas Nurthen, Cathie Allen. December 2012. Forensic DNA Analysis.
- [3] Project #163 - Assessment of results obtained from ‘automatic-microcon’ samples. Josie Entwistle, Allison Lloyd, Kylie Rika, Thomas Nurthen, Cathie Allen. August 2015. Forensic DNA Analysis.

| Quant | EXHinterp | SUCCESS | EXH | Qant after MCONC | Fold difference between quants | XAMP1 | XAMP2 | INTERP for NCIDD upload - was there another sample that could have been uploaded? | Link - warm (w), cold (c), unlinked (u) | | | | |
|--------|-----------|---------|---|------------------|--------------------------------|-------|-------|---|---|--|--|--|--|
| 0.0056 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion | 0.0113 | 2.02 | y | | y | c | | | | |
| 0.0063 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion | 0.0082 | 1.30 | y | | y | c | | | | |
| 0.0067 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution | 0.0122 | 1.82 | y | | y | c | | | | |
| 0.0085 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0148 | 1.74 | y | | y | c | | | | |
| 0.0093 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0185 | 1.99 | n | | y | c | | | | |
| 0.0111 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.038 | 3.42 | n | | y | c | | | | |
| 0.0057 | SUCCESS | 1 | Two person mixed DNA profile 2 person mixed profile - conditioned on | 0.0068 | 1.19 | y | | y | u | | | | |
| 0.0068 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile DNA profile removed from NCIDD | 0.0102 | 1.50 | y | | y | u | | | | |
| 0.015 | SUCCESS | 1 | Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 Single evidence sample excluded | 0.0262 | 1.75 | y | | y | u | | | | |
| 0.0015 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile DNA profile removed from NCIDD | 0.0035 | 2.33 | y | | y | w | | | | |
| 0.0024 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded Excluded from mixed DNA profile | 0.0042 | 1.75 | y | | y | w | | | | |
| 0.0035 | SUCCESS | 1 | Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.005 | 1.43 | y | | y | w | | | | |
| 0.0039 | SUCCESS | 1 | Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion | 0.013 | 3.33 | y | | y | w | | | | |
| 0.0064 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile | 0.0125 | 1.95 | y | | y | w | | | | |
| 0.0066 | SUCCESS | 1 | Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile | 0.0077 | 1.17 | n | | y | w | | | | |
| 0.0072 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0115 | 1.60 | y | | y | w | | | | |
| 0.0082 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Micro positive for sperm. Submitted-Results pending | 0.0089 | 1.09 | y | | y | w | | | | |

| | | | | | | | | | | | | | | |
|--------|---------|---|---|--------|------|---|--|--|---|---|--|--|-----------|----|
| 0.0091 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution | 0.025 | 2.75 | n | | | y | w | | | | |
| 0.0091 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information NCIDD upload single source DNA profile | 0.0101 | 1.11 | n | | | y | w | | | | |
| 0.0093 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion | 0.0254 | 2.73 | n | | | y | w | | | | |
| 0.0095 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion | 0.0061 | 0.64 | n | | | y | w | | | | |
| 0.0105 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0058 | 0.55 | n | | | y | w | | | | |
| 0.0111 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile | 0.016 | 1.44 | y | | | y | w | | | SS Assume | 22 |
| 0.0112 | SUCCESS | 1 | Submitted as cells Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile Possible sub-threshold information | 0.0184 | 1.64 | n | | | y | w | | | | |
| 0.0133 | SUCCESS | 1 | Submitted-results pending. Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile Possible sub-threshold information | 0.0313 | 2.35 | n | | | y | w | | | | |
| 0.0019 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0018 | 0.95 | y | | | n | c | | | | |
| 0.0032 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution | 0.0041 | 1.28 | y | | | n | c | | | | |
| 0.0038 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0055 | 1.45 | y | | | n | c | | | | |
| 0.0056 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0063 | 1.13 | y | | | n | c | | | | |
| 0.0067 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile SS DNA profile 9 loci and above LR > 100 billion | 0.008 | 1.19 | y | | | n | c | | | | |
| 0.0068 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0138 | 2.03 | y | | | n | c | | | | |
| 0.0072 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0145 | 2.01 | y | | | n | c | | | | |
| 0.0097 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded | 0.0095 | 0.98 | y | | | n | c | | | | |
| 0.0106 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0149 | 1.41 | n | | | n | c | | | | |
| 0.0113 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0181 | 1.60 | n | | | n | c | | | | |
| 0.0113 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information | 0.0115 | 1.02 | n | | | n | c | | | | |
| 0.0123 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution | 0.0092 | 0.75 | n | | | n | c | | | | |

| | | | | | | | | | | | | | | | |
|--------|---------|---|--|--------|------|---|---------|-------|--|---|---|--|--|--|--|
| 0.0129 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile | 0.0127 | 0.98 | n | | | | n | c | | | | |
| 0.0134 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion | 0.0104 | 0.78 | n | | | | n | c | | | | |
| 0.0134 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0274 | 2.04 | y | | | | n | c | | | | |
| 0.0142 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information | 0.0144 | 1.01 | n | | | | n | c | | | | |
| 0.0143 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded Possible sub-threshold information | 0.0132 | 0.92 | n | | | | n | c | | | | |
| 0.0145 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0104 | 0.72 | y | | | | n | c | | | | |
| 0.0019 | SUCCESS | 1 | Hair located. Submitted-results pending Single source DNA profile NCIDD upload single source DNA profile | 0.0034 | 1.79 | y | | | | n | u | | | | |
| 0.0028 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0055 | 1.96 | y | | | | n | u | | | | |
| 0.0041 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0064 | 1.56 | y | | | | n | u | | | | |
| 0.0043 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0062 | 1.44 | y | | | | n | u | | | | |
| 0.0046 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile | 0.0075 | 1.63 | y | | | | n | u | | | | |
| 0.0051 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0372 | 7.29 | n | | | | n | u | | | | |
| 0.0051 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0048 | 0.94 | y | | | | n | u | | | | |
| 0.0055 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution Excluded from mixed DNA profile | 0.124 | | y | 2154.55 | 22.55 | | n | u | | | | |
| 0.0063 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Mixture-low support for contrib or supports non contrib | 0.006 | 0.95 | y | | | | n | u | | | | |
| 0.0065 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed DNA - inconclusive Excluded from mixed DNA profile 3 person mix - supports non contribution 3 person mix - supports non contribution | 0.0109 | 1.68 | y | | | | n | u | | | | |
| 0.0067 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0086 | 1.28 | y | | | | n | u | | | | |

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|--------|---------|---|--|--------|------|---|---|--|--|---|---|--|--|--|--|
| 0.0069 | SUCCESS | 1 | Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Two person mixed DNA profile Excluded from mixed DNA profile Intel report required for further interpretation 2 person mix profile - support for contrib > 100 billion | 0.008 | 1.16 | y | | | | n | u | | | | |
| 0.0074 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0151 | 2.04 | y | | | | n | u | | | | |
| 0.0086 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0182 | 2.12 | y | y | | | n | u | | | | |
| 0.0129 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information | 0.0241 | 1.87 | n | | | | n | u | | | | |
| 0.0135 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile | 0.0101 | 0.75 | n | | | | n | u | | | | |
| 0.0135 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0123 | 0.91 | y | | | | n | u | | | | |
| 0.0135 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Single evidence sample excluded | 0.0067 | 0.50 | y | | | | n | u | | | | |
| 0.0139 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile NCIDD upload - mixed DNA profile Excluded from mixed DNA profile | 0.0541 | 3.89 | y | | | | n | u | | | | |
| 0.0142 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Suspect check inconclusive - mixed DNA profile Suspect check - supports non contribution | 0.0148 | 1.04 | n | | | | n | u | | | | |
| 0.0146 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0082 | 0.56 | n | | | | n | u | | | | |
| 0.015 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0194 | 1.29 | y | | | | n | u | | | | |
| 0.0032 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0051 | 1.59 | n | | | | n | w | | | | |
| 0.0063 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0134 | 2.13 | n | | | | n | w | | | | |
| 0.0067 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending presump Saliva test positive Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion | 0.0082 | 1.22 | y | | | | n | w | | | | |
| 0.0082 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0093 | 1.13 | y | | | | n | w | | | | |
| 0.0088 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0151 | 1.72 | y | | | | n | w | | | | |
| 0.0088 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0086 | 0.98 | y | | | | n | w | | | | |
| 0.0096 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile | 0.0048 | 0.50 | y | | | | n | w | | | | |

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|--------|---------|---|--|--------|------|---|--|--|---|---|--|--|--|--|
| 0.0104 | SUCCESS | 1 | Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0118 | 1.13 | y | | | n | w | | | | |
| 0.0118 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0081 | 0.69 | n | | | n | w | | | | |
| 0.0121 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0059 | 0.49 | y | | | n | w | | | | |
| 0.0122 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0161 | 1.32 | y | | | n | w | | | | |
| 0.0124 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0246 | 1.98 | n | | | n | w | | | | |
| 0.0126 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded | 0.0099 | 0.79 | n | | | n | w | | | | |
| 0.0126 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion | 0.0147 | 1.17 | n | | | n | w | | | | |
| 0.014 | SUCCESS | 1 | Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information | 0.0183 | 1.31 | n | | | n | w | | | | |
| 0.0148 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution | 0.0042 | 0.28 | n | | | n | w | | | | |
| 0.0011 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.0025 | 2.27 | n | | | | | | | | |
| 0.0012 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.0064 | 5.33 | n | | | | | | | | |
| 0.0015 | SUCCESS | 1 | Submitted as cells Single Source DNA profile - assumed known contributor | 0.0051 | 3.40 | y | | | | | | | | |
| 0.0015 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Semen not detected Single source DNA profile Single source DNA profile < 9 loci LR 1000 - 10 000 | 0.003 | 2.00 | n | | | | | | | | |
| 0.0016 | SUCCESS | 1 | Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Two person mixed DNA profile No statistical interpretation performed | 0.0039 | 2.44 | y | | | | | | | | |
| 0.0017 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Single source DNA profile < NCIDD matching stringency Single Source DNA profile - assumed known contributor | 0.0012 | 0.71 | y | | | | | | | | |
| 0.0018 | SUCCESS | 1 | Hair located. Submitted-results pending Interim result - sample undergoing rework Two person mixed DNA profile 2 person mix - supports non contribution 2 person mix profile - support for contrib > 100 billion | 0.0027 | 1.50 | y | | | | | | | | |
| 0.0019 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending Presump Saliva test negative Single Source DNA profile - assumed known contributor | 0.0047 | 2.47 | n | | | | | | | | |
| 0.0019 | SUCCESS | 1 | Presumptive blood test pos. Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor | 0.0026 | 1.37 | n | | | | | | | | |
| 0.0022 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Single Source DNA profile - assumed known contributor | 0.0059 | 2.68 | n | | | | | | | | |

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|--------|---------|---|---|--------|------|---|---------|-------|--|--|--|--|--|--|
| 0.0023 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion | 0.0795 | | y | 3356.52 | 34.57 | | | | | | |
| 0.0024 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib | 0.0052 | 2.17 | y | | | | | | | | |
| 0.0024 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix - support for contrib 1 million - 1 billion | 0.0034 | 1.42 | n | | | | | | | | |
| 0.0025 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.0102 | 4.08 | y | | | | | | | | |
| 0.0026 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending presump Saliva test positive SS | 0.0016 | 0.62 | n | | | | | | | | |
| 0.0027 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor Possible sub-threshold information | 0.0038 | 1.41 | y | | | | | | | | |
| 0.0027 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion | 0.0027 | 1.00 | y | | | | | | | | |
| 0.0027 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.0039 | 1.44 | n | | | | | | | | |
| 0.0028 | SUCCESS | 1 | Hair located. Submitted-results pending Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - supports non contribution | 0.0036 | 1.29 | y | | | | | | | | |
| 0.003 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information | 0.0063 | 2.10 | n | | | | | | | | |
| 0.003 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion | 0.0053 | 1.77 | y | | | | | | | | |
| 0.0031 | SUCCESS | 1 | SS DNA profile 9 loci and above LR > 100 billion | 0.0035 | 1.13 | n | | | | | | | | |
| 0.0032 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile | 0.0077 | 2.41 | y | | | | | | | | |
| 0.0032 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile | 0.0076 | 2.38 | y | | | | | | | | |
| 0.0033 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Single Source DNA profile - assumed known contributor | 0.0024 | 0.73 | n | | | | | | | | |
| 0.0036 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Single source 20 loci DNA profile LR > 100 billion | 0.0074 | 2.06 | n | | | | | | | | |
| 0.0036 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor | 0.0037 | 1.03 | y | | | | | | | | |
| 0.0037 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Single evidence sample excluded | 0.0188 | 5.08 | y | | | | | | | | |
| 0.0037 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile 2 person mix profile - support for contrib > 100 billion | 0.009 | 2.43 | y | | | | | | | | |
| 0.004 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile 2 person mix profile - support for contrib > 100 billion | 0.008 | 2.00 | y | | | | | | | | |

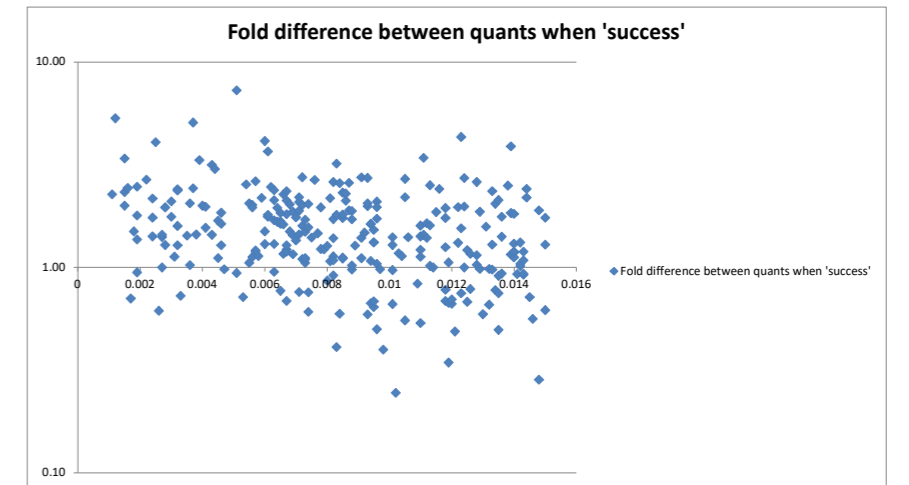
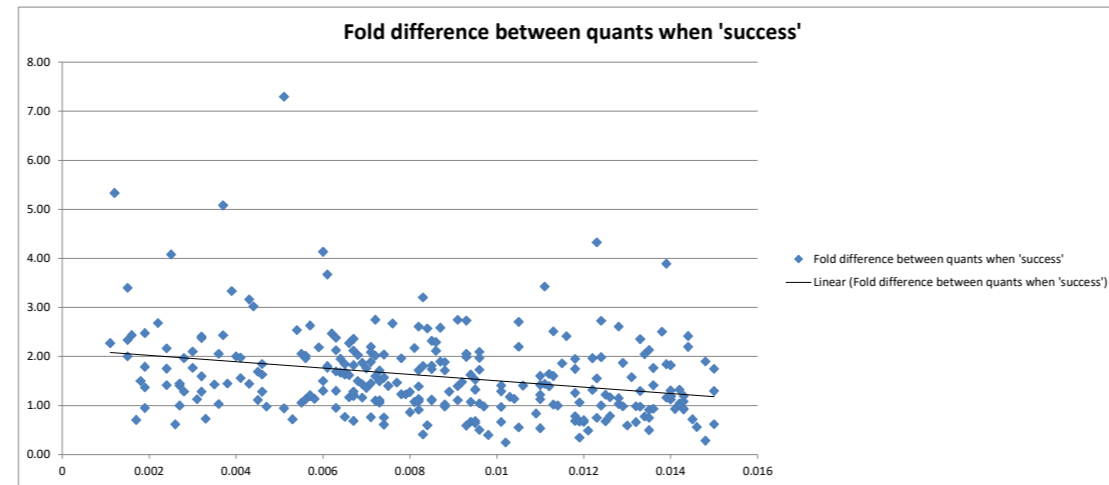
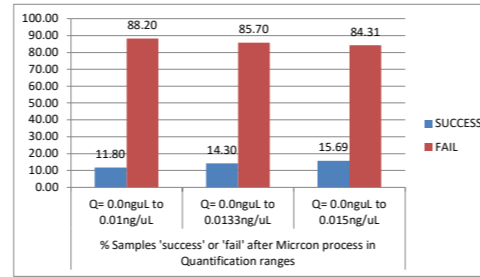
| | | | | | | | | | | | | | | |
|--------|---------|---|--|--------|------|---|---|--|--|--|--|--|--|--|
| 0.0041 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor | 0.0081 | 1.98 | n | | | | | | | | |
| 0.0043 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Single evidence sample excluded | 0.0136 | 3.16 | y | | | | | | | | |
| 0.0044 | SUCCESS | 1 | Submitted as cells Single source DNA profile | 0.0133 | 3.02 | y | | | | | | | | |
| 0.0045 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile 2 person mix - supports non contribution | 0.0076 | 1.69 | y | y | | | | | | | |
| 0.0045 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed | 0.005 | 1.11 | y | | | | | | | | |
| 0.0046 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending Presump Saliva test negative Three person mixed DNA profile 3 person mixed profile - conditioned on No statistical interpretation performed 3 person mix remaining - low support for contrib Single evidence sample excluded | 0.0085 | 1.85 | y | | | | | | | | |
| 0.0046 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on No statistical interpretation performed 3 person mix remaining - supports non contribution | 0.0059 | 1.28 | y | | | | | | | | |
| 0.0047 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion | 0.0046 | 0.98 | y | | | | | | | | |
| 0.0053 | SUCCESS | 1 | Submitted-results pending. Single Source DNA profile - assumed known contributor | 0.0038 | 0.72 | n | | | | | | | | |
| 0.0054 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile | 0.0137 | 2.54 | y | | | | | | | | |
| 0.0055 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion | 0.0058 | 1.05 | n | | | | | | | | |
| 0.0055 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Single source DNA profile NCIDD upload single source DNA profile SS DNA profile 9 loci and above LR > 100 billion DNA profile removed from NCIDD | 0.0113 | 2.05 | n | | | | | | | | |
| 0.0056 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.011 | 1.96 | n | | | | | | | | |
| 0.0057 | SUCCESS | 1 | Submitted-results pending. Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Possible sub-threshold information 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution | 0.0069 | 1.21 | y | | | | | | | | |
| 0.0057 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile | 0.015 | 2.63 | y | | | | | | | | |
| 0.0058 | SUCCESS | 1 | Submitted as cells Single source DNA profile Possible sub-threshold information | 0.0066 | 1.14 | n | | | | | | | | |
| 0.0059 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion | 0.0129 | 2.19 | n | | | | | | | | |

| | | | | | | | | | | | | | | |
|--------|---------|---|---|--------|------|---|---|--|--|--|--|--|--|--|
| 0.0069 | SUCCESS | 1 | Presumptive blood test pos. Submitted-results pending. Single Source DNA profile - assumed known contributor | 0.0129 | 1.87 | y | | | | | | | | |
| 0.0069 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information | 0.0099 | 1.43 | y | | | | | | | | |
| 0.007 | SUCCESS | 1 | Submitted-results pending. Single Source DNA profile - assumed known contributor | 0.0095 | 1.36 | n | | | | | | | | |
| 0.007 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded | 0.0123 | 1.76 | y | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Single Source DNA profile - assumed known contributor | 0.0156 | 2.20 | n | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information | 0.0134 | 1.89 | n | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - low support for contribution Excluded from mixed DNA profile | 0.0148 | 2.08 | y | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion | 0.0103 | 1.45 | n | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Presumptive blood test pos. Submitted-results pending. Single source DNA profile | 0.0054 | 0.76 | y | y | | | | | | | |
| 0.0072 | SUCCESS | 1 | Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person rem- support for contrib 1 million to 1 billion | 0.0079 | 1.10 | y | | | | | | | | |
| 0.0072 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed | 0.0198 | 2.75 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib | 0.0125 | 1.71 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile | 0.008 | 1.10 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed | 0.0077 | 1.05 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion | 0.0081 | 1.11 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending SS DNA profile 9 loci and above LR > 100 billion | 0.0109 | 1.49 | n | | | | | | | | |
| 0.0074 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion | 0.0045 | 0.61 | y | | | | | | | | |
| 0.0074 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed | 0.0056 | 0.76 | n | | | | | | | | |
| 0.0074 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib | 0.0116 | 1.57 | y | | | | | | | | |
| 0.0075 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending presump Saliva test positive Three person mixed DNA profile No statistical interpretation performed | 0.0105 | 1.40 | y | | | | | | | | |

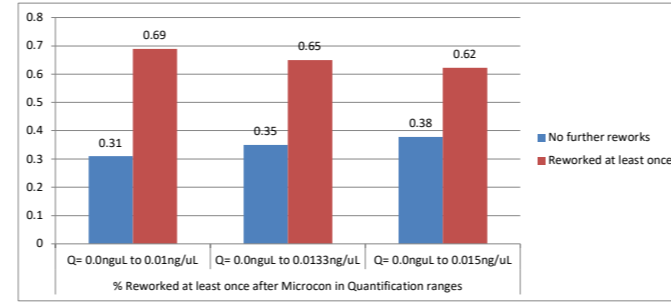
| | | | | | | | | | | | | | | |
|--------|---------|---|--|--------|------|---|--|--|--|--|--|--|--|--|
| 0.0085 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information | 0.0094 | 1.11 | y | | | | | | | | |
| 0.0085 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution | 0.0154 | 1.81 | y | | | | | | | | |
| 0.0085 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - support for contrib 100 000 to 1 million 2 person mix - supports non contribution Single evidence sample excluded | 0.0095 | 1.12 | y | | | | | | | | |
| 0.0086 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix - low support for contribution 3 person mixed DNA - inconclusive | 0.0197 | 2.29 | y | | | | | | | | |
| 0.0087 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution | 0.0225 | 2.59 | y | | | | | | | | |
| 0.0087 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded | 0.0165 | 1.90 | y | | | | | | | | |
| 0.0088 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion | 0.009 | 1.02 | y | | | | | | | | |
| 0.0088 | SUCCESS | 1 | Submitted-results pending. Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Single evidence sample excluded | 0.0166 | 1.89 | y | | | | | | | | |
| 0.0089 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed | 0.0114 | 1.28 | n | | | | | | | | |
| 0.0091 | SUCCESS | 1 | consistent elsewhere | 0.0127 | 1.40 | n | | | | | | | | |
| 0.0092 | SUCCESS | 1 | P SS | 0.0136 | 1.48 | n | | | | | | | | |
| 0.0093 | SUCCESS | 1 | P SS | 0.0055 | 0.59 | y | | | | | | | | |
| 0.0093 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0191 | 2.05 | n | | | | | | | | |
| 0.0094 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 1 million - 1 billion 3 person mix - support for contribution 100 to 1000 | 0.0063 | 0.67 | y | | | | | | | | |
| 0.0094 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion 3 person mix remaining - supports non contribution | 0.0153 | 1.63 | n | | | | | | | | |
| 0.0094 | SUCCESS | 1 | 3p | 0.0101 | 1.07 | y | | | | | | | | |
| 0.0094 | SUCCESS | 1 | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution 3 person mix - supports non contribution | 0.0153 | 1.63 | n | | | | | | | | |
| 0.0095 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution | 0.0145 | 1.53 | y | | | | | | | | |

| | | | | | | | | | | | | | | |
|--------|---------|---|---|--------|------|---|--|--|--|--|--|--|--|--|
| 0.0128 | SUCCESS | 1 | Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 100 000 to 1 million | 0.0334 | 2.61 | y | | | | | | | | |
| 0.0128 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information | 0.0132 | 1.03 | n | | | | | | | | |
| 0.0128 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion | 0.0147 | 1.15 | n | | | | | | | | |
| 0.013 | SUCCESS | 1 | Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information | 0.0077 | 0.59 | n | | | | | | | | |
| 0.0131 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion | 0.0207 | 1.58 | y | | | | | | | | |
| 0.0132 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution | 0.013 | 0.98 | y | | | | | | | | |
| 0.0132 | SUCCESS | 1 | mix | 0.0087 | 0.66 | y | | | | | | | | |
| 0.0133 | SUCCESS | 1 | Submitted-results pending. Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information | 0.013 | 0.98 | y | | | | | | | | |
| 0.0133 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution | 0.0172 | 1.29 | y | | | | | | | | |
| 0.0135 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution Mixture-low support for contrib or supports non contrib 3 person mix - low support for contribution | 0.0288 | 2.13 | y | | | | | | | | |
| 0.0136 | SUCCESS | 1 | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 100 000 to 1 million Mixture-low support for contrib or supports non contrib Excluded from mixed DNA profile | 0.0127 | 0.93 | y | | | | | | | | |
| 0.0136 | SUCCESS | 1 | Submitted as cells Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile | 0.024 | 1.76 | n | | | | | | | | |
| 0.0136 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed | 0.0192 | 1.41 | y | | | | | | | | |
| 0.0138 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded | 0.0346 | 2.51 | y | | | | | | | | |
| 0.0139 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile SS DNA profile 9 loci and above LR > 100 billion | 0.0256 | 1.84 | n | | | | | | | | |
| 0.0139 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution | 0.0161 | 1.16 | y | | | | | | | | |
| 0.014 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion | 0.0166 | 1.19 | n | | | | | | | | |

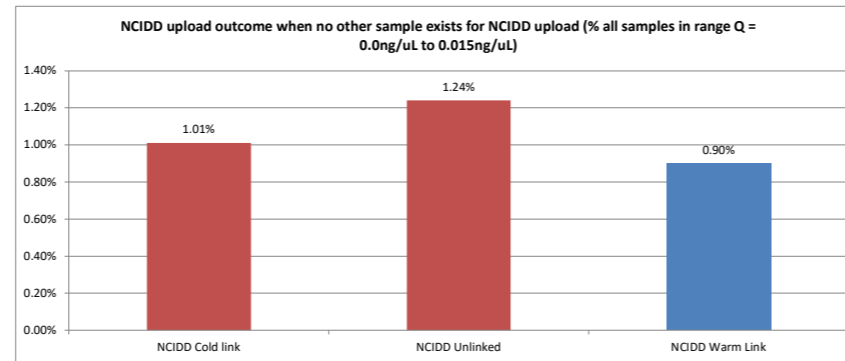
| % Samples 'success' or 'fail' after Micron process in Quantification ranges | | |
|---|----------------------------|---------------------------|
| Q= 0.0ng/uL to 0.01ng/uL | Q= 0.0ng/uL to 0.0133ng/uL | Q= 0.0ng/uL to 0.015ng/uL |
| 11.80 | 14.30 | 15.69 |
| 88.20 | 85.70 | 84.31 |



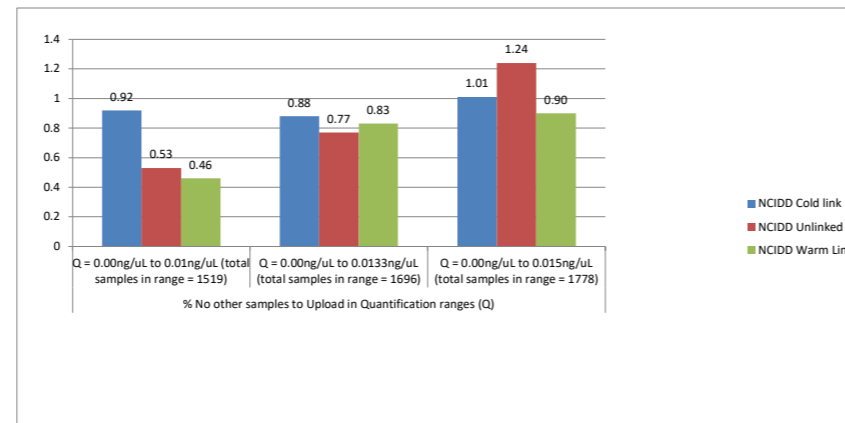
| | % Reworked at least once after Microcon in Quantification ranges | | |
|------------------------|--|----------------------------|---------------------------|
| | Q= 0.0ng/uL to 0.01ng/uL | Q= 0.0ng/uL to 0.0133ng/uL | Q= 0.0ng/uL to 0.015ng/uL |
| Further reworks | 0.31 | 0.35 | 0.38 |
| Reworked at least once | 0.69 | 0.65 | 0.62 |



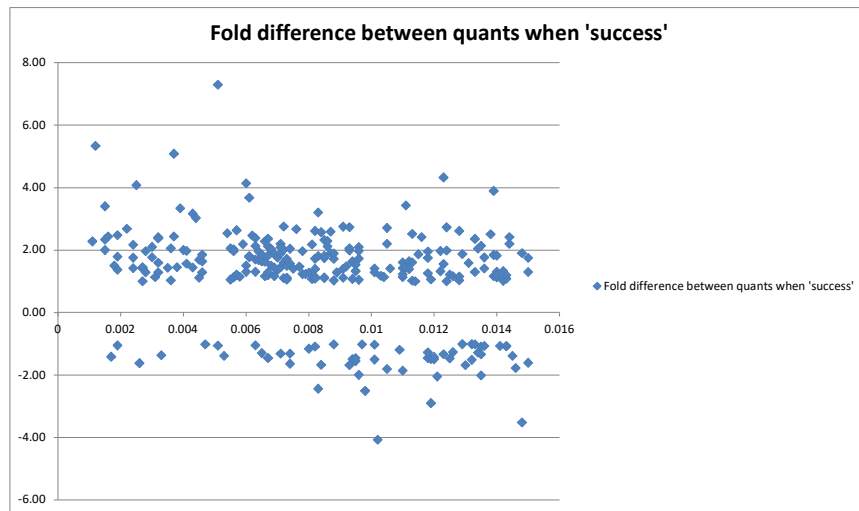
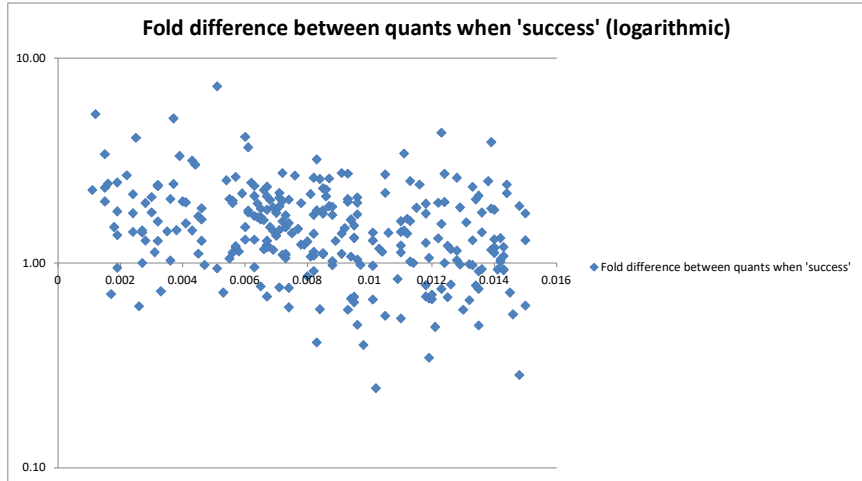
| | | Number of samples (where no other sample could be uploaded) | |
|--|-------------------------|---|----|
| % No other samples to Upload from the range = 56 | | | |
| es in range = 1778 | 0.00ng/uL to 0.015ng/uL | | |
| link | | 1.01% | 18 |
| ked | | 1.24% | 22 |
| n Link | | 0.90% | 16 |



| | % No other samples to Upload in Quantification ranges (Q) | | |
|--------------|--|--|---|
| | Q = 0.00ng/uL to 0.01ng/uL (total samples in range = 1519) | Q = 0.00ng/uL to 0.0133ng/uL (total samples in range = 1696) | Q = 0.00ng/uL to 0.015ng/uL (total samples in range = 1778) |
| DD Cold link | 0.92 | 0.88 | 1.01 |
| DD Unlinked | 0.53 | 0.77 | 1.24 |
| D Warm Link | 0.46 | 0.83 | 0.90 |



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| Fold difference between quants when 'success' |
| 2.27 |
| 5.33 |
| 2.33 |
| 3.40 |
| 2.00 |
| 2.44 |
| 1.41667 |
| 1.50 |
| 1.79 |
| -1.05556 |
| 2.47 |
| 1.37 |
| 2.68 |
| 1.75 |
| 2.17 |
| 1.42 |
| 4.08 |
| -1.625 |
| 1.41 |
| 1.00 |
| 1.44 |
| 1.96 |
| 1.29 |
| 2.10 |
| 1.77 |
| 1.13 |
| 1.59 |
| 1.28 |
| 2.41 |
| 2.38 |
| -1.375 |
| 1.43 |
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| 1.56 |
| 1.98 |
| 1.44 |
| 3.16 |
| 3.02 |
| 1.69 |
| 1.11 |
| 1.63 |
| 1.85 |
| 1.28 |
| -1.02174 |
| 7.29 |
| -1.0625 |
| -1.39474 |
| 2.54 |
| 1.05 |
| 2.05 |
| 1.13 |
| 2.02 |
| 1.96 |
| 1.19 |
| 1.21 |
| 2.63 |
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| 1.80 |
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| 1.67 |
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| 1.65 |
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| 1.62 |
| 2.27 |
| 1.22 |
| 1.19 |
| 1.28 |
| 1.82 |
| 1.45652 |
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| 2.36 |
| 2.03 |
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| 1.87 |
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| 1.36 |
| 1.76 |
| 2.20 |
| 1.89 |
| 2.08 |
| 1.45 |
| -1.31481 |
| 2.01 |
| 1.60 |
| 1.10 |
| 2.75 |
| 1.71 |
| 1.10 |
| 1.05 |
| 1.11 |
| 1.49 |
| 2.04 |
| -1.64444 |
| -1.32143 |
| 1.57 |
| 1.40 |
| 2.67 |
| 1.47 |
| 1.96 |
| 1.23 |
| 1.23 |
| 1.27 |
| -1.15942 |
| 1.07 |
| 2.17 |
| 1.13 |
| 1.09 |
| 1.72 |
| 2.61 |
| -1.09333 |
| 1.39 |
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| -1.68 |
| 1.74 |
| 2.32 |
| 1.11 |
| 1.81 |
| 1.12 |
| 2.12 |
| 2.29 |
| 2.59 |
| 1.90 |
| 1.72 |
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| 1.02 |
| 1.89 |
| 1.28 |
| 1.40 |
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| 1.11 |
| 1.48 |
| 1.99 |
| 2.73 |
| -1.69091 |
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| -1.49206 |
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| 1.07 |
| 1.63 |
| -1.55738 |
| 1.53 |
| 1.33 |
| 1.33 |
| 1.46154 |
| -2 |
| 2.09 |
| 1.04 |

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| | 1.97 | | |
| | 1.73 | | |
| | -1.02105 | | |
| | -2.51282 | | |
| | -1.03061 | | |
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| | 1.17 | | |
| | 1.13 | | |
| | 2.20 | | |
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| | -1.81034 | | |
| | 1.41 | | |
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| | 1.44 | | |
| | 1.64 | | |
| | 1.39 | | |
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| | 1.86 | | |
| | 2.41 | | |
| | -1.45679 | | |
| | 1.25 | | |
| | 1.75 | | |
| | 1.95 | | |
| | -1.28261 | | |
| | 0.02 | -46.2963 | |
| | -1.4875 | | |
| | 1.06 | | |
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| | -1.42857 | | |
| | -2.05085 | | |
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| | 4.33 | | |
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| | 1.33696 | | |
| | 1.00 | | |
| | 2.73 | | |
| | 1.98 | | |
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| | -1.27273 | | |
| | 1.17 | | |
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| | 1.03 | | |
| | 1.15 | | |
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| | -1.09756 | | |
| | 2.13 | | |
| | -2.01493 | | |
| | -1.07087 | | |
| | 1.76 | | |
| | 1.41 | | |
| | 2.51 | | |
| | 1.84 | | |
| | 1.16 | | |
| | 3.89 | | |
| | 1.19 | | |
| | 1.82 | | |
| | 1.19 | | |
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| | 1.04 | | |
| | 1.01 | | |
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| | 1.08 | | |
| | -1.07519 | | |
| | 1.20 | | |
| | 2.19 | | |
| | 2.42 | | |
| | -1.39423 | | |
| | -1.78049 | | |
| | 1.90 | | |
| | -3.52381 | | |
| | 1.29 | | |
| | 1.75 | | |
| | -1.6129 | | |

| Quant | EXHinterp | SUCCESS | EXH | Qant after MCONC | Fold difference between quants | XAMP1 | XAMP2 | INTERP for NCIDD upload - was there another sample that could have been uploaded? | Link - warm (w), cold (c), unlinked (u) | | | | | |
|--------|-----------|---------|---|------------------|--------------------------------|-------|-------|---|---|--|--|--|--|--|
| 0.0056 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion | 0.0113 | 2.02 | y | | y | c | | | | | |
| 0.0063 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion | 0.0082 | 1.30 | y | | y | c | | | | | |
| 0.0067 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution | 0.0122 | 1.82 | y | | y | c | | | | | |
| 0.0085 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0148 | 1.74 | y | | y | c | | | | | |
| 0.0093 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0185 | 1.99 | n | | y | c | | | | | |
| 0.0111 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.038 | 3.42 | n | | y | c | | | | | |
| 0.0057 | SUCCESS | 1 | Two person mixed DNA profile 2 person mixed profile - conditioned on | 0.0068 | 1.19 | y | | y | u | | | | | |
| 0.0068 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile DNA profile removed from NCIDD | 0.0102 | 1.50 | y | | y | u | | | | | |
| 0.015 | SUCCESS | 1 | Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 Single evidence sample excluded | 0.0262 | 1.75 | y | | y | u | | | | | |
| 0.0015 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile DNA profile removed from NCIDD | 0.0035 | 2.33 | y | | y | w | | | | | |
| 0.0024 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded Excluded from mixed DNA profile | 0.0042 | 1.75 | y | | y | w | | | | | |
| 0.0035 | SUCCESS | 1 | Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.005 | 1.43 | y | | y | w | | | | | |
| 0.0039 | SUCCESS | 1 | Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion | 0.013 | 3.33 | y | | y | w | | | | | |
| 0.0064 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile | 0.0125 | 1.95 | y | | y | w | | | | | |
| 0.0066 | SUCCESS | 1 | Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile | 0.0077 | 1.17 | n | | y | w | | | | | |
| 0.0072 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0115 | 1.60 | y | | y | w | | | | | |
| 0.0082 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Micro positive for sperm. Submitted-Results pending | 0.0089 | 1.09 | y | | y | w | | | | | |

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|--------|---------|---|---|--------|------|---|--|--|---|---|--|--|------------|----|--|
| 0.0091 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution | 0.025 | 2.75 | n | | | y | w | | | | | |
| 0.0091 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information NCIDD upload single source DNA profile | 0.0101 | 1.11 | n | | | y | w | | | | | |
| 0.0093 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion | 0.0254 | 2.73 | n | | | y | w | | | | | |
| 0.0095 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion | 0.0061 | 0.64 | n | | | y | w | | | | | |
| 0.0105 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0058 | 0.55 | n | | | y | w | | | | | |
| 0.0111 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile | 0.016 | 1.44 | y | | | y | w | | | SS Assumed | 22 | |
| 0.0112 | SUCCESS | 1 | Submitted as cells Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile Possible sub-threshold information | 0.0184 | 1.64 | n | | | y | w | | | | | |
| 0.0133 | SUCCESS | 1 | Submitted-results pending. Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile Possible sub-threshold information | 0.0313 | 2.35 | n | | | y | w | | | | | |
| 0.0019 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0018 | 0.95 | y | | | n | c | | | | | |
| 0.0032 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution | 0.0041 | 1.28 | y | | | n | c | | | | | |
| 0.0038 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0055 | 1.45 | y | | | n | c | | | | | |
| 0.0056 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0063 | 1.13 | y | | | n | c | | | | | |
| 0.0067 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile SS DNA profile 9 loci and above LR > 100 billion | 0.008 | 1.19 | y | | | n | c | | | | | |
| 0.0068 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0138 | 2.03 | y | | | n | c | | | | | |
| 0.0072 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0145 | 2.01 | y | | | n | c | | | | | |
| 0.0097 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded | 0.0095 | 0.98 | y | | | n | c | | | | | |
| 0.0106 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0149 | 1.41 | n | | | n | c | | | | | |
| 0.0113 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0181 | 1.60 | n | | | n | c | | | | | |
| 0.0113 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information | 0.0115 | 1.02 | n | | | n | c | | | | | |
| 0.0123 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution | 0.0092 | 0.75 | n | | | n | c | | | | | |

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|--------|---------|---|--|--------|------|---|---------|-------|--|---|---|--|--|--|--|
| 0.0129 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile | 0.0127 | 0.98 | n | | | | n | c | | | | |
| 0.0134 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion | 0.0104 | 0.78 | n | | | | n | c | | | | |
| 0.0134 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0274 | 2.04 | y | | | | n | c | | | | |
| 0.0142 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information | 0.0144 | 1.01 | n | | | | n | c | | | | |
| 0.0143 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded Possible sub-threshold information | 0.0132 | 0.92 | n | | | | n | c | | | | |
| 0.0145 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0104 | 0.72 | y | | | | n | c | | | | |
| 0.0019 | SUCCESS | 1 | Hair located. Submitted-results pending Single source DNA profile NCIDD upload single source DNA profile | 0.0034 | 1.79 | y | | | | n | u | | | | |
| 0.0028 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0055 | 1.96 | y | | | | n | u | | | | |
| 0.0041 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0064 | 1.56 | y | | | | n | u | | | | |
| 0.0043 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0062 | 1.44 | y | | | | n | u | | | | |
| 0.0046 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile | 0.0075 | 1.63 | y | | | | n | u | | | | |
| 0.0051 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0372 | 7.29 | n | | | | n | u | | | | |
| 0.0051 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0048 | 0.94 | y | | | | n | u | | | | |
| 0.0055 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix - supports non contribution Excluded from mixed DNA profile | 0.124 | | y | 2154.55 | 22.55 | | n | u | | | | |
| 0.0063 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Mixture-low support for contrib or supports non contrib | 0.006 | 0.95 | y | | | | n | u | | | | |
| 0.0065 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed DNA - inconclusive Excluded from mixed DNA profile 3 person mix - supports non contribution 3 person mix - supports non contribution | 0.0109 | 1.68 | y | | | | n | u | | | | |
| 0.0067 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0086 | 1.28 | y | | | | n | u | | | | |

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|--------|---------|---|--|--------|------|---|---|--|--|---|---|--|--|--|--|
| 0.0069 | SUCCESS | 1 | Submitted-results pending. Interim result- mixed profile obtained. Rework Reqd Two person mixed DNA profile Excluded from mixed DNA profile Intel report required for further interpretation 2 person mix profile - support for contrib > 100 billion | 0.008 | 1.16 | y | | | | n | u | | | | |
| 0.0074 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0151 | 2.04 | y | | | | n | u | | | | |
| 0.0086 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile | 0.0182 | 2.12 | y | y | | | n | u | | | | |
| 0.0129 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Possible sub-threshold information | 0.0241 | 1.87 | n | | | | n | u | | | | |
| 0.0135 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information NCIDD upload single source DNA profile | 0.0101 | 0.75 | n | | | | n | u | | | | |
| 0.0135 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0123 | 0.91 | y | | | | n | u | | | | |
| 0.0135 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Single evidence sample excluded | 0.0067 | 0.50 | y | | | | n | u | | | | |
| 0.0139 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile NCIDD upload - mixed DNA profile Excluded from mixed DNA profile | 0.0541 | 3.89 | y | | | | n | u | | | | |
| 0.0142 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Suspect check inconclusive - mixed DNA profile Suspect check - supports non contribution | 0.0148 | 1.04 | n | | | | n | u | | | | |
| 0.0146 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0082 | 0.56 | n | | | | n | u | | | | |
| 0.015 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile | 0.0194 | 1.29 | y | | | | n | u | | | | |
| 0.0032 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0051 | 1.59 | n | | | | n | w | | | | |
| 0.0063 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0134 | 2.13 | n | | | | n | w | | | | |
| 0.0067 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending presump Saliva test positive Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion | 0.0082 | 1.22 | y | | | | n | w | | | | |
| 0.0082 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0093 | 1.13 | y | | | | n | w | | | | |
| 0.0088 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0151 | 1.72 | y | | | | n | w | | | | |
| 0.0088 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0086 | 0.98 | y | | | | n | w | | | | |
| 0.0096 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile | 0.0048 | 0.50 | y | | | | n | w | | | | |

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|--------|---------|---|--|--------|------|---|--|--|---|---|--|--|--|--|
| 0.0104 | SUCCESS | 1 | Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0118 | 1.13 | y | | | n | w | | | | |
| 0.0118 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile Possible sub-threshold information | 0.0081 | 0.69 | n | | | n | w | | | | |
| 0.0121 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0059 | 0.49 | y | | | n | w | | | | |
| 0.0122 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0161 | 1.32 | y | | | n | w | | | | |
| 0.0124 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0246 | 1.98 | n | | | n | w | | | | |
| 0.0126 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Single evidence sample excluded | 0.0099 | 0.79 | n | | | n | w | | | | |
| 0.0126 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion | 0.0147 | 1.17 | n | | | n | w | | | | |
| 0.014 | SUCCESS | 1 | Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information | 0.0183 | 1.31 | n | | | n | w | | | | |
| 0.0148 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution | 0.0042 | 0.28 | n | | | n | w | | | | |
| 0.0011 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.0025 | 2.27 | n | | | | | | | | |
| 0.0012 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.0064 | 5.33 | n | | | | | | | | |
| 0.0015 | SUCCESS | 1 | Submitted as cells Single Source DNA profile - assumed known contributor | 0.0051 | 3.40 | y | | | | | | | | |
| 0.0015 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Semen not detected Single source DNA profile Single source DNA profile < 9 loci LR 1000 - 10 000 | 0.003 | 2.00 | n | | | | | | | | |
| 0.0016 | SUCCESS | 1 | Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Two person mixed DNA profile No statistical interpretation performed | 0.0039 | 2.44 | y | | | | | | | | |
| 0.0017 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Single source DNA profile < NCIDD matching stringency Single Source DNA profile - assumed known contributor | 0.0012 | 0.71 | y | | | | | | | | |
| 0.0018 | SUCCESS | 1 | Hair located. Submitted-results pending Interim result - sample undergoing rework Two person mixed DNA profile 2 person mix - supports non contribution 2 person mix profile - support for contrib > 100 billion | 0.0027 | 1.50 | y | | | | | | | | |
| 0.0019 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending Presump Saliva test negative Single Source DNA profile - assumed known contributor | 0.0047 | 2.47 | n | | | | | | | | |
| 0.0019 | SUCCESS | 1 | Presumptive blood test pos. Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor | 0.0026 | 1.37 | n | | | | | | | | |
| 0.0022 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Single Source DNA profile - assumed known contributor | 0.0059 | 2.68 | n | | | | | | | | |

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|--------|---------|---|---|--------|------|---|---------|-------|--|--|--|--|--|--|
| 0.0023 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix profile - support for contrib > 100 billion | 0.0795 | | y | 3356.52 | 34.57 | | | | | | |
| 0.0024 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib | 0.0052 | 2.17 | y | | | | | | | | |
| 0.0024 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix - support for contrib 1 million - 1 billion | 0.0034 | 1.42 | n | | | | | | | | |
| 0.0025 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.0102 | 4.08 | y | | | | | | | | |
| 0.0026 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending presump Saliva test positive SS | 0.0016 | 0.62 | n | | | | | | | | |
| 0.0027 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor Possible sub-threshold information | 0.0038 | 1.41 | y | | | | | | | | |
| 0.0027 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion | 0.0027 | 1.00 | y | | | | | | | | |
| 0.0027 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.0039 | 1.44 | n | | | | | | | | |
| 0.0028 | SUCCESS | 1 | Hair located. Submitted-results pending Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - supports non contribution | 0.0036 | 1.29 | y | | | | | | | | |
| 0.003 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information | 0.0063 | 2.10 | n | | | | | | | | |
| 0.003 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion | 0.0053 | 1.77 | y | | | | | | | | |
| 0.0031 | SUCCESS | 1 | SS DNA profile 9 loci and above LR > 100 billion | 0.0035 | 1.13 | n | | | | | | | | |
| 0.0032 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile | 0.0077 | 2.41 | y | | | | | | | | |
| 0.0032 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile | 0.0076 | 2.38 | y | | | | | | | | |
| 0.0033 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Single Source DNA profile - assumed known contributor | 0.0024 | 0.73 | n | | | | | | | | |
| 0.0036 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Single source 20 loci DNA profile LR > 100 billion | 0.0074 | 2.06 | n | | | | | | | | |
| 0.0036 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor | 0.0037 | 1.03 | y | | | | | | | | |
| 0.0037 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Single evidence sample excluded | 0.0188 | 5.08 | y | | | | | | | | |
| 0.0037 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile 2 person mix profile - support for contrib > 100 billion | 0.009 | 2.43 | y | | | | | | | | |
| 0.004 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile 2 person mix profile - support for contrib > 100 billion | 0.008 | 2.00 | y | | | | | | | | |

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|--------|---------|---|--|--------|------|---|---|--|--|--|--|--|--|--|
| 0.0041 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor | 0.0081 | 1.98 | n | | | | | | | | |
| 0.0043 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Single evidence sample excluded | 0.0136 | 3.16 | y | | | | | | | | |
| 0.0044 | SUCCESS | 1 | Submitted as cells Single source DNA profile | 0.0133 | 3.02 | y | | | | | | | | |
| 0.0045 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile 2 person mix - supports non contribution | 0.0076 | 1.69 | y | y | | | | | | | |
| 0.0045 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed | 0.005 | 1.11 | y | | | | | | | | |
| 0.0046 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending Presump Saliva test negative Three person mixed DNA profile 3 person mixed profile - conditioned on No statistical interpretation performed 3 person mix remaining - low support for contrib Single evidence sample excluded | 0.0085 | 1.85 | y | | | | | | | | |
| 0.0046 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on No statistical interpretation performed 3 person mix remaining - supports non contribution | 0.0059 | 1.28 | y | | | | | | | | |
| 0.0047 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix profile - support for contrib > 100 billion | 0.0046 | 0.98 | y | | | | | | | | |
| 0.0053 | SUCCESS | 1 | Submitted-results pending. Single Source DNA profile - assumed known contributor | 0.0038 | 0.72 | n | | | | | | | | |
| 0.0054 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile | 0.0137 | 2.54 | y | | | | | | | | |
| 0.0055 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion | 0.0058 | 1.05 | n | | | | | | | | |
| 0.0055 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Single source DNA profile NCIDD upload single source DNA profile SS DNA profile 9 loci and above LR > 100 billion DNA profile removed from NCIDD | 0.0113 | 2.05 | n | | | | | | | | |
| 0.0056 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor | 0.011 | 1.96 | n | | | | | | | | |
| 0.0057 | SUCCESS | 1 | Submitted-results pending. Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Possible sub-threshold information 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution | 0.0069 | 1.21 | y | | | | | | | | |
| 0.0057 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile | 0.015 | 2.63 | y | | | | | | | | |
| 0.0058 | SUCCESS | 1 | Submitted as cells Single source DNA profile Possible sub-threshold information | 0.0066 | 1.14 | n | | | | | | | | |
| 0.0059 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information Single source 20 loci DNA profile LR > 100 billion | 0.0129 | 2.19 | n | | | | | | | | |

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|--------|---------|---|---|--------|------|---|---|--|--|--|--|--|--|--|
| 0.0069 | SUCCESS | 1 | Presumptive blood test pos. Submitted-results pending. Single Source DNA profile - assumed known contributor | 0.0129 | 1.87 | y | | | | | | | | |
| 0.0069 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information | 0.0099 | 1.43 | y | | | | | | | | |
| 0.007 | SUCCESS | 1 | Submitted-results pending. Single Source DNA profile - assumed known contributor | 0.0095 | 1.36 | n | | | | | | | | |
| 0.007 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed profile - conditioned on Single evidence sample excluded | 0.0123 | 1.76 | y | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Single Source DNA profile - assumed known contributor | 0.0156 | 2.20 | n | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Submitted-results pending. Single Source DNA profile - assumed known contributor Possible sub-threshold information | 0.0134 | 1.89 | n | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - low support for contribution Excluded from mixed DNA profile | 0.0148 | 2.08 | y | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion | 0.0103 | 1.45 | n | | | | | | | | |
| 0.0071 | SUCCESS | 1 | Presumptive blood test pos. Submitted-results pending. Single source DNA profile | 0.0054 | 0.76 | y | y | | | | | | | |
| 0.0072 | SUCCESS | 1 | Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person rem- support for contrib 1 million to 1 billion | 0.0079 | 1.10 | y | | | | | | | | |
| 0.0072 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed | 0.0198 | 2.75 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib | 0.0125 | 1.71 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile | 0.008 | 1.10 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed | 0.0077 | 1.05 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion | 0.0081 | 1.11 | y | | | | | | | | |
| 0.0073 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending SS DNA profile 9 loci and above LR > 100 billion | 0.0109 | 1.49 | n | | | | | | | | |
| 0.0074 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion | 0.0045 | 0.61 | y | | | | | | | | |
| 0.0074 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed | 0.0056 | 0.76 | n | | | | | | | | |
| 0.0074 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib | 0.0116 | 1.57 | y | | | | | | | | |
| 0.0075 | SUCCESS | 1 | Submitted as cells, Presump saliva test pending presump Saliva test positive Three person mixed DNA profile No statistical interpretation performed | 0.0105 | 1.40 | y | | | | | | | | |

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|--------|---------|---|--|--------|------|---|--|--|--|--|--|--|--|--|
| 0.0085 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Possible sub-threshold information | 0.0094 | 1.11 | y | | | | | | | | |
| 0.0085 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution | 0.0154 | 1.81 | y | | | | | | | | |
| 0.0085 | SUCCESS | 1 | Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion 2 person mix - support for contrib 100 000 to 1 million 2 person mix - supports non contribution Single evidence sample excluded | 0.0095 | 1.12 | y | | | | | | | | |
| 0.0086 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix - low support for contribution 3 person mixed DNA - inconclusive | 0.0197 | 2.29 | y | | | | | | | | |
| 0.0087 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution | 0.0225 | 2.59 | y | | | | | | | | |
| 0.0087 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded | 0.0165 | 1.90 | y | | | | | | | | |
| 0.0088 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion | 0.009 | 1.02 | y | | | | | | | | |
| 0.0088 | SUCCESS | 1 | Submitted-results pending. Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion Single evidence sample excluded | 0.0166 | 1.89 | y | | | | | | | | |
| 0.0089 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile No statistical interpretation performed | 0.0114 | 1.28 | n | | | | | | | | |
| 0.0091 | SUCCESS | 1 | consistent elsewhere | 0.0127 | 1.40 | n | | | | | | | | |
| 0.0092 | SUCCESS | 1 | P SS | 0.0136 | 1.48 | n | | | | | | | | |
| 0.0093 | SUCCESS | 1 | P SS | 0.0055 | 0.59 | y | | | | | | | | |
| 0.0093 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.0191 | 2.05 | n | | | | | | | | |
| 0.0094 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile Mixture-low support for contrib or supports non contrib 3 person mix - support for contrib 1 million - 1 billion 3 person mix - support for contribution 100 to 1000 | 0.0063 | 0.67 | y | | | | | | | | |
| 0.0094 | SUCCESS | 1 | Three person mixed DNA profile 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion 3 person mix remaining - supports non contribution | 0.0153 | 1.63 | n | | | | | | | | |
| 0.0094 | SUCCESS | 1 | 3p | 0.0101 | 1.07 | y | | | | | | | | |
| 0.0094 | SUCCESS | 1 | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution 3 person mix - supports non contribution | 0.0153 | 1.63 | n | | | | | | | | |
| 0.0095 | SUCCESS | 1 | Micro positive for sperm. Submitted-Results pending Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion 3 person mix - supports non contribution | 0.0145 | 1.53 | y | | | | | | | | |

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|--------|------|----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| 0.0025 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0025 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0025 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0025 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Semen not detected Submitted as cells Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0026 | FAIL | -1 | Submitted-results pending. No DNA profile - possible sub-threshold peaks | | | | | | | | | | | | | | | | | |
| 0.0027 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0027 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0027 | FAIL | -1 | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes | | | | | | | | | | | | | | | | | |
| 0.0027 | FAIL | -1 | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes | | | | | | | | | | | | | | | | | |
| 0.0027 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0027 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0027 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0027 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0027 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0027 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0027 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |
| 0.0027 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | | |

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|--------|------|----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| 0.003 | FAIL | -1 | Submitted-results pending. Micro neg for sperm Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted for cells. Presumptive saliva test pending. presump Saliva test positive Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Partial DNA profile unsuitable for comparison purposes | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. No DNA profile Possible sub-threshold information | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0031 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0032 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0032 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0032 | FAIL | -1 | complex | | | | | | | | | | | | | | | | |
| 0.0032 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0032 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0032 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0032 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0032 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |

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|--------|------|----|---|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| 0.008 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.008 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.008 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0081 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0081 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0081 | FAIL | -1 | Submitted-results pending. Micro positive for sperm. Submitted-Results pending No DNA profile | | | | | | | | | | | | | | | | |
| 0.0081 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0081 | FAIL | -1 | Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0081 | FAIL | -1 | Submitted as cells Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0081 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0081 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0081 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0081 | FAIL | -1 | Submitted as cells Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0081 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0081 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0081 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0082 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0082 | FAIL | -1 | Presump. PSA test positive, no sperm found Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mix remaining - supports non contribution Mix remaining DNA contrib unsuitable for NCIDD searching | | | | | | | | | | | | | | | | |
| 0.0082 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0082 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0082 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0082 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0082 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0082 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0082 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0082 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0082 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0082 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0083 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0083 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0083 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0083 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |
| 0.0083 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | | |

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|--------|------|----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| 0.0098 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0099 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0099 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.01 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.01 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.01 | FAIL | -1 | cpu | | | | | | | | | | | | | | | |
| 0.01 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.01 | FAIL | -1 | cpu | | | | | | | | | | | | | | | |
| 0.01 | FAIL | -1 | cpu | | | | | | | | | | | | | | | |
| 0.0101 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0101 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0101 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0101 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0101 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0101 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0101 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0101 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0101 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0101 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0102 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0102 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0102 | FAIL | -1 | Submitted as cells Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0103 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0103 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0103 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0103 | FAIL | -1 | Submitted-results pending. Micro neg for sperm Two person mixed DNA profile 2 person mixed profile - conditioned on Mix remaining DNA contrib unsuitable for NCIDD searching | | | | | | | | | | | | | | | |
| 0.0104 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0104 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0104 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0104 | FAIL | -1 | Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0104 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0105 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |
| 0.0105 | FAIL | -1 | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison | | | | | | | | | | | | | | | |

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|--------|---------|---|--|--------|------|---|---|--|---|--|--|---|--|--|--|--|--|--|--|
| 0.0061 | SUCCESS | 1 | Single Source DNA profile - assumed known contributor Possible sub-threshold information | 0.0108 | 1.77 | n | | | | | | | | | | | | | |
| 0.0061 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Excluded from mixed DNA profile 2 person mix profile - support for contrib > 100 billion | 0.0224 | 3.67 | y | | | | | | | | | | | | | |
| 0.0061 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile No statistical interpretation performed | 0.011 | 1.80 | y | | | | | | | | | | | | | |
| 0.0062 | SUCCESS | 1 | Submitted-results pending. Micro neg for sperm Single Source DNA profile - assumed known contributor | 0.0153 | 2.47 | n | | | | | | | | | | | | | |
| 0.0063 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile Single source 20 loci DNA profile LR > 100 billion | 0.0082 | 1.30 | y | | | y | | | c | | | | | | | |
| 0.0063 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile Mixture-low support for contrib or supports non contrib | 0.006 | 0.95 | y | | | n | | | u | | | | | | | |
| 0.0063 | SUCCESS | 1 | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile | 0.0134 | 2.13 | n | | | n | | | w | | | | | | | |
| 0.0063 | SUCCESS | 1 | SS DNA profile 9 loci and above LR > 100 billion | 0.015 | 2.38 | y | | | | | | | | | | | | | |
| 0.0063 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Excluded from mixed DNA profile | 0.0107 | 1.70 | y | | | | | | | | | | | | | |
| 0.0064 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile | 0.0125 | 1.95 | y | | | y | | | w | | | | | | | |
| 0.0064 | SUCCESS | 1 | Two person mixed DNA profile Single evidence sample excluded Single evidence sample excluded | 0.0107 | 1.67 | y | y | | | | | | | | | | | | |
| 0.0065 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mixed DNA - inconclusive Excluded from mixed DNA profile 3 person mix - supports non contribution 3 person mix - supports non contribution | 0.0109 | 1.68 | y | | | n | | | u | | | | | | | |
| 0.0065 | SUCCESS | 1 | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion | 0.0106 | 1.63 | n | | | | | | | | | | | | | |
| 0.0065 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.005 | 0.77 | y | | | | | | | | | | | | | |
| 0.0065 | SUCCESS | 1 | Submitted-results pending. Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Mixture-low support for contrib or supports non contrib | 0.0107 | 1.65 | y | | | | | | | | | | | | | |
| 0.0065 | SUCCESS | 1 | Two person mixed DNA profile 2 person mixed profile - conditioned on Single evidence sample excluded 2 person mix remaining consistent with unknown Possible sub-threshold information 2 person mix rem - support for contribution > 100 billion Single evidence sample excluded | 0.012 | 1.85 | y | | | | | | | | | | | | | |
| 0.0066 | SUCCESS | 1 | Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile | 0.0077 | 1.17 | n | | | y | | | w | | | | | | | |
| 0.0066 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile Possible sub-threshold information | 0.0107 | 1.62 | y | | | | | | | | | | | | | |
| 0.0066 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion | 0.015 | 2.27 | y | | | | | | | | | | | | | |
| 0.0067 | SUCCESS | 1 | Submitted-results pending. Three person mixed DNA profile 3 person mix - supports non contribution | 0.0122 | 1.82 | y | | | y | | | c | | | | | | | |
| 0.0067 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile SS DNA profile 9 loci and above LR > 100 billion | 0.008 | 1.19 | y | | | n | | | c | | | | | | | |
| 0.0067 | SUCCESS | 1 | Submitted-results pending. Single source DNA profile NCIDD upload single source DNA profile | 0.0086 | 1.28 | y | | | n | | | u | | | | | | | |

| Barcode | HasQuant | Quant | Auto/Manual | EXHinterp | EXH |
|---------|----------|--------|-------------|-----------|---|
| | TRUE | 0.0028 | Auto | | Submitted-results pending. Submitted-results pending. |
| | TRUE | 0.0041 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0056 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.006 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0036 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile |
| | TRUE | 0.0024 | Auto | | 2 person mixed profile - conditioned on Submitted-results pending. |
| | TRUE | 0.0056 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0032 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0082 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0075 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0067 | Auto | | Single source 20 loci DNA profile LR > 100 billion Submitted-results pending. |
| | TRUE | 0.0061 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| | TRUE | 0.0038 | Auto | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| | TRUE | 0.0025 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0057 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0058 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0024 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0035 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| | TRUE | 0.0029 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0083 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0054 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0068 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison No DNA detected |
| | TRUE | 0 | Auto | FAIL | This sample has undergone further processing |
| | TRUE | 0.0036 | Auto | | Submitted as cells |
| | TRUE | 0.0065 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| | TRUE | 0.0026 | Auto | | Two person mixed DNA profile |
| | TRUE | 0.0081 | Auto | | 2 person mix - supports non contribution Submitted-results pending. |
| | TRUE | 0.0044 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0029 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0025 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0084 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| | TRUE | 0.0062 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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| TRUE | 0.0038 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0051 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0078 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0077 Auto | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0031 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0042 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0035 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0075 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0034 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0055 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0022 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0081 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0032 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0034 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0025 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0069 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0031 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0023 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0045 Auto | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.0064 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0038 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| TRUE | 0.0046 Auto | | QPS advised no further work required - results available Submitted as cells |
| TRUE | 0.0022 Auto | | QPS advised no further work required - results available Submitted-results pending. |
| TRUE | 0.0036 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0024 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0027 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0024 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0052 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0051 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0031 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0024 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Quality flag identified, on hold awaiting advice from QPS |
| TRUE | 0.0088 Auto | | Quality control failure, refer to QPS Three person mixed DNA profile |
| TRUE | 0.006 Auto | | No statistical interpretation performed |

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| TRUE | 0.0041 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0023 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0074 Auto | | QPS advised no further work required - results available Submitted-results pending. |
| TRUE | 0.0024 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.003 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.007 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0026 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0085 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0025 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| TRUE | 0.0044 Auto | | Single source DNA profile Submitted-results pending. |
| TRUE | 0.004 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.003 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| TRUE | 0.0081 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Presump Saliva test negative |
| TRUE | 0.006 Auto | | Two person mixed DNA profile Submitted-results pending. |
| TRUE | 0.0055 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0087 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0033 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes Single source DNA profile |
| TRUE | 0.003 Auto | | Possible sub-threshold information Submitted-results pending. |
| TRUE | 0.0043 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0084 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0029 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.008 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0051 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0066 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0063 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0034 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0025 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0033 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0083 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0023 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0027 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0064 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0067 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|------|---|
| TRUE | 0.0071 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0029 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0069 Auto | | Interim result- mixed profile obtained. Rework Reqd Two person mixed DNA profile |
| TRUE | 0.0044 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.008 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0027 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0065 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0031 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0084 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0023 Auto | FAIL | presump Saliva test positive Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0072 Auto | FAIL | Submitted as cells Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0022 Auto | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0058 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0051 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0028 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0088 Auto | | |
| TRUE | 0.0028 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0037 Auto | | |
| TRUE | 0.0071 Auto | | |
| TRUE | 0.0052 Auto | | |
| TRUE | 0.0042 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0027 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.003 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0059 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.004 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0049 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0054 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0063 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0059 Auto | | Single source DNA profile Possible sub-threshold information |
| TRUE | 0.0025 Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0023 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0044 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|------|--|
| TRUE | 0.0026 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0034 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.007 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0022 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0024 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0039 Auto | | 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion |
| TRUE | 0.0064 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0029 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0086 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0061 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0059 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0031 Auto | | Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS |
| TRUE | 0.0046 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0037 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0025 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0086 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.007 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0074 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0081 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0064 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0063 Auto | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0032 Auto | | Two person mixed DNA profile 2 person mix - supports non contribution |
| TRUE | 0.0031 Auto | | Submitted-results pending. QPS advised no further work required - results available |
| TRUE | 0.0022 Auto | FAIL | presump Saliva test positive Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0036 Auto | | |
| TRUE | 0.0074 Auto | | |
| TRUE | 0.0037 Auto | | |
| TRUE | 0.0027 Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0041 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0031 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0048 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0035 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0035 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|------|--|
| TRUE | 0.006 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0053 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0035 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0034 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single Source DNA profile - assumed known contributor Possible sub-threshold information Submitted-results pending. |
| TRUE | 0.0071 Auto | | |
| TRUE | 0.0028 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0045 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0088 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0066 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0086 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0076 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Quality flag identified, on hold awaiting advice from QPS |
| TRUE | 0.0055 Auto | | Quality control failure, refer to QPS |
| TRUE | 0.0073 Auto | | Submitted-results pending. |
| TRUE | 0.0029 Auto | | Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS |
| TRUE | 0.0026 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0084 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0056 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0027 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0028 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile Submitted-results pending. |
| TRUE | 0.0082 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0087 Auto | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.0045 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0039 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0024 Auto | | ENVM - Complex mixed DNA profile Submitted-results pending. |
| TRUE | 0.0056 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0046 Auto | | Two person mixed DNA profile Excluded from mixed DNA profile Submitted-results pending. |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0044 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0082 Auto | | Two person mixed DNA profile 2 person mixed profile - conditioned on Submitted-results pending. |
| TRUE | 0.0046 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0052 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0073 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0083 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|------|---|
| TRUE | 0.0087 Auto | | Submitted for cells. Presumptive saliva test pending. Presump Saliva test negative |
| TRUE | 0.0035 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0073 Auto | | Submitted-results pending. |
| TRUE | 0.0029 Auto | | Submitted-results pending. |
| TRUE | 0.0041 Auto | | |
| TRUE | 0.0043 Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0028 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0038 Auto | | |
| TRUE | 0.0023 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0072 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0054 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0028 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0047 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0036 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0087 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0027 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0032 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0076 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0037 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.005 Auto | | |
| TRUE | 0.0067 Auto | | |
| TRUE | 0.0054 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0057 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0084 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0045 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0022 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0024 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0079 Auto | | Three person mixed DNA profile Mixture-low support for contrib or supports non contrib |
| TRUE | 0.0055 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0032 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0039 Auto | | |
| TRUE | 0.0068 Auto | | |

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|------|-------------|------|--|
| TRUE | 0.0087 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0037 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0087 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0049 Auto | | |
| TRUE | 0.0065 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0032 Auto | | |
| TRUE | 0.0054 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0063 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0063 Auto | | SS DNA profile 9 loci and above LR > 100 billion |
| TRUE | 0.0078 Auto | | |
| TRUE | 0.0029 Auto | | |
| TRUE | 0.0038 Auto | | |
| TRUE | 0.0022 Auto | | |
| TRUE | 0.0074 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0032 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0073 Auto | | |
| TRUE | 0.0074 Auto | FAIL | Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0031 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0029 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0024 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0064 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0085 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0034 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0085 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0055 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0032 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0056 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0086 Auto | | Two person mixed DNA profile Submitted-results pending. |
| TRUE | 0.0038 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.005 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0088 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0071 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0035 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|---------|---|
| TRUE | 0.0043 Auto | SUCCESS | SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile |
| TRUE | 0.0061 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0023 Auto | | |
| TRUE | 0.0082 Auto | FAIL | Two person mixed DNA profile 2 person mixed profile - conditioned on |
| TRUE | 0.0073 Auto | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0042 Auto | FAIL | Submitted as cells Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0073 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0024 Auto | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0051 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0032 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0041 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0024 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0026 Auto | FAIL | Submitted as cells Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0029 Auto | | |
| TRUE | 0.0071 Auto | | |
| TRUE | 0.0049 Auto | | |
| TRUE | 0.0033 Auto | | |
| TRUE | 0.0058 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.006 Auto | FAIL | Presump. PSA test positive, no sperm found Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0044 Auto | | |
| TRUE | 0.004 Auto | | Two person mixed DNA profile Excluded from mixed DNA profile |
| TRUE | 0.0026 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0058 Auto | | Single source DNA profile Possible sub-threshold information |
| TRUE | 0.0054 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0073 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.006 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0045 Auto | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.004 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0055 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0078 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0051 Auto | | |
| TRUE | 0.003 Auto | | |
| TRUE | 0.0033 Auto | | Presump. PSA test positive, no sperm found Single Source DNA profile - assumed known contributor |

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|------|-------------|---------|--|
| TRUE | 0.0028 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0029 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0077 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0053 Auto | FAIL | Interim result - sample undergoing rework Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | | |
| TRUE | 0.0022 Auto | | |
| TRUE | 0.0066 Auto | | |
| TRUE | 0.0059 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0086 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0046 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0073 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0042 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0067 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0077 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0036 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0042 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0025 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0081 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0059 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0065 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0088 Auto | SUCCESS | SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile |
| TRUE | 0.0055 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0077 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0079 Auto | FAIL | presump Saliva test positive Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0034 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0079 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0031 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0072 Auto | | 2 person mixed profile - conditioned on 2 person rem- support for contrib 1 million to 1 billion |
| TRUE | 0.0086 Auto | | 3 person mixed profile - conditioned on 3 person mix - low support for contribution |
| TRUE | 0.0052 Auto | | Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS |
| TRUE | 0.0025 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0032 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0023 Auto | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |

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| TRUE | 0.0032 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0072 Auto | | Two person mixed DNA profile |
| TRUE | 0.0066 Auto | | |
| TRUE | 0.0034 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0084 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0052 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0058 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0022 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0029 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single source 20 loci DNA profile LR > 100 billion |
| TRUE | 0.0064 Auto | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0027 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes Single source DNA profile |
| TRUE | 0.0036 Auto | | Single source 20 loci DNA profile LR > 100 billion Submitted-results pending. |
| TRUE | 0.0047 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0047 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0074 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| TRUE | 0.0024 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0049 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0042 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0065 Auto | | 3 person mixed DNA - inconclusive Submitted-results pending. |
| TRUE | 0.0041 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0034 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0074 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0063 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0042 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0033 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0072 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0066 Auto | | |
| TRUE | 0.0044 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison This sample has undergone further processing Submitted-results pending. |
| TRUE | 0.0041 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0057 Auto | | Single source DNA profile Submitted-results pending. |
| TRUE | 0.0072 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0034 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0044 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|------|--|
| TRUE | 0.0055 Auto | | Two person mixed DNA profile 2 person mix - supports non contribution |
| TRUE | 0.0059 Auto | FAIL | presump Saliva test positive Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0026 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0059 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0047 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0057 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0066 Auto | | Submitted-results pending. |
| TRUE | 0.0071 Auto | | Presump. PSA test positive, no sperm found Single Source DNA profile - assumed known contributor Submitted-results pending. |
| TRUE | 0.0083 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0034 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0043 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0068 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0045 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.004 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0059 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0046 Auto | | |
| TRUE | 0.0074 Auto | | |
| TRUE | 0.0053 Auto | | |
| TRUE | 0.0086 Auto | | |
| TRUE | 0.0043 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0053 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0035 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0022 Auto | | Quality control failure - results not reportable Submitted-results pending. |
| TRUE | 0.0043 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0085 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0039 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0033 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0025 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0026 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0066 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0062 Auto | FAIL | Interim result- mixed profile obtained. Rework Reqd Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0029 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|---------|--|
| TRUE | 0.0044 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0035 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0023 Auto | | |
| TRUE | 0.0038 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0024 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0073 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.003 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0058 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0045 Auto | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.0055 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| TRUE | 0.0023 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0024 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0056 Auto | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0055 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0068 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0041 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.003 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0022 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0027 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0028 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0061 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0054 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0039 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0042 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.003 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0057 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0024 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0024 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0082 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0026 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0042 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes |

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|------|-------------|------|--|
| TRUE | 0.0025 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0031 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0045 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes This sample has undergone further processing |
| TRUE | 0.0073 Auto | | Three person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.0036 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0028 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0058 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0085 Auto | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0078 Auto | | |
| TRUE | 0.0022 Auto | FAIL | Presump. PSA test positive, no sperm found Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0032 Auto | | |
| TRUE | 0.0066 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0031 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0042 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0066 Auto | | |
| TRUE | 0.0057 Auto | | |
| TRUE | 0.0065 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0084 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0065 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0056 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.004 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile |
| TRUE | 0.0037 Auto | | Excluded from mixed DNA profile Two person mixed DNA profile |
| TRUE | 0.0061 Auto | | Excluded from mixed DNA profile |
| TRUE | 0.0085 Auto | | |
| TRUE | 0.0054 Auto | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0047 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | | |
| TRUE | 0.0043 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0054 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0078 Auto | | Single source 20 loci DNA profile LR > 100 billion 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0085 Auto | | Single evidence sample excluded presump Saliva test positive |
| TRUE | 0.0084 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0066 Auto | | 3 person mix profile - support for contrib > 100 billion |

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|------|-------------|---------|--|
| TRUE | 0.0067 Auto | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.0044 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0033 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0046 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0024 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0057 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0079 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0038 Auto | | Submitted-results pending. |
| TRUE | 0.0055 Auto | | Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion |
| TRUE | 0.0088 Auto | | Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion |
| TRUE | 0.008 Auto | | Submitted-results pending. |
| TRUE | 0.0048 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0083 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0032 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0048 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0043 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0036 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0049 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0038 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0067 Auto | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0061 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0041 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.003 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0057 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.004 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0026 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0075 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0086 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0034 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0068 Auto | SUCCESS | NCIDD upload single source DNA profile Presump Saliva test negative |
| TRUE | 0.0052 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Presump Saliva test negative |
| TRUE | 0.0033 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|------|---|
| TRUE | 0.0082 Auto | | Presump Saliva test negative Three person mixed DNA profile Submitted-results pending. |
| TRUE | 0.0028 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile Submitted-results pending. |
| TRUE | 0.0065 Auto | | 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.0058 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0039 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0033 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0028 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0033 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0022 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0022 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.007 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0036 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0057 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0042 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Presump Saliva test negative Three person mixed DNA profile |
| TRUE | 0.0046 Auto | | presump Saliva test positive |
| TRUE | 0.0058 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison 3 person mixed profile - conditioned on |
| TRUE | 0.0046 Auto | | No statistical interpretation performed |
| TRUE | 0.0072 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0039 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0087 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0074 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.006 Auto | | Quality flag identified, on hold awaiting advice from QPS Three person mixed DNA profile |
| TRUE | 0.0084 Auto | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.0072 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0061 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.003 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0027 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0029 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.008 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0041 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0037 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0056 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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| TRUE | 0.0023 Auto | | Submitted-results pending. No DNA profile - possible sub-threshold peaks Submitted as cells |
| TRUE | 0.0056 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0036 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0052 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.006 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0027 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0051 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0063 Auto | SUCCESS | NCIDD upload single source DNA profile |
| TRUE | 0.0088 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0044 Auto | | |
| TRUE | 0.0075 Auto | | presump Saliva test positive Three person mixed DNA profile Submitted-results pending. |
| TRUE | 0.0065 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0081 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0032 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison No DNA profile |
| TRUE | 0.0031 Auto | | Possible sub-threshold information Submitted-results pending. |
| TRUE | 0.0048 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0031 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes Three person mixed DNA profile |
| TRUE | 0.0087 Auto | FAIL | 3 person mixed profile - conditioned on Submitted-results pending. |
| TRUE | 0.0074 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0038 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0028 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0049 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0069 Auto | | Possible sub-threshold information Single source DNA profile |
| TRUE | 0.0081 Auto | | Possible sub-threshold information Submitted-results pending. |
| TRUE | 0.0028 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0057 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0028 Auto | | |
| TRUE | 0.0032 Auto | SUCCESS | SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0022 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0064 Auto | | |
| TRUE | 0.0027 Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0048 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0069 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes |

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| TRUE | 0.0047 Auto | | Submitted-results pending. |
| TRUE | 0.0024 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0079 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0048 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0084 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0037 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0065 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0036 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0058 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0026 Auto | | |
| TRUE | 0.0022 Auto | | |
| TRUE | 0.0053 Auto | | Submitted-results pending. Single Source DNA profile - assumed known contributor |
| TRUE | 0.0028 Auto | | |
| TRUE | 0.0059 Auto | | |
| TRUE | 0.0053 Auto | | |
| TRUE | 0.0038 Auto | | |
| TRUE | 0.0024 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0027 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0026 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0061 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0054 Auto | | |
| TRUE | 0.005 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0047 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0064 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0081 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0027 Auto | | |
| TRUE | 0.0024 Auto | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.0064 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0033 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0086 Auto | | |
| TRUE | 0.0025 Auto | | |
| TRUE | 0.0024 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0059 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|------|---|
| TRUE | 0.0047 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0065 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0058 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0025 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0054 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0048 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0072 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0087 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0043 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0031 Auto | | SS DNA profile 9 loci and above LR > 100 billion |
| TRUE | 0.0057 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0076 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0036 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0067 Auto | | presump Saliva test positive Two person mixed DNA profile |
| TRUE | 0.0042 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0045 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0024 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0017 Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0027 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0051 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.007 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0057 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0038 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0064 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0036 Auto | | |
| TRUE | 0.0052 Auto | | |
| TRUE | 0.0025 Auto | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0033 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.003 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0024 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0088 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0082 Auto | | Presump Saliva test negative Two person mixed DNA profile |
| TRUE | 0.008 Auto | | |

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|------|-------------|---------|--|
| TRUE | 0.008 Auto | | 2 person mixed profile - conditioned on |
| TRUE | 0.0052 Auto | FAIL | Single evidence sample excluded |
| TRUE | 0.0032 Auto | | |
| TRUE | 0.0024 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0055 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0048 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0064 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0065 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0057 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0075 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0025 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0051 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0027 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0033 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0081 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0042 Auto | FAIL | Three person mixed DNA profile 3 person mixed profile - conditioned on Submitted-results pending. |
| TRUE | 0.0065 Auto | | Single source 20 loci DNA profile LR > 100 billion Submitted-results pending. |
| TRUE | 0.0048 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| TRUE | 0.0068 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0039 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0032 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0065 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0038 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0061 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0052 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0041 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0032 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0059 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0037 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0029 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0049 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0041 Auto | SUCCESS | SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0049 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|---------|--|
| TRUE | 0.0044 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.007 Auto | | Three person mixed DNA profile 3 person mixed profile - conditioned on |
| TRUE | 0.004 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0059 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.003 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0088 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0026 Auto | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0051 Auto | FAIL | Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0054 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0063 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0026 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0088 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single evidence sample excluded |
| TRUE | 0.0064 Auto | | Single evidence sample excluded |
| TRUE | 0.0039 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.005 Auto | | |
| TRUE | 0.0034 Auto | | Submitted-results pending. |
| TRUE | 0.0077 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0049 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0045 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0043 Auto | | Three person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.0037 Auto | | Three person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.0051 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0072 Auto | SUCCESS | Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile |
| TRUE | 0.0072 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0051 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0072 Auto | | Two person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.004 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.007 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0083 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0022 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0084 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0079 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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| TRUE | 0.0062 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0026 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0047 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0033 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0047 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.004 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0062 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0039 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0063 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0042 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0023 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.004 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0035 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.004 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.006 Auto | | Single source DNA profile Submitted-results pending. |
| TRUE | 0.0027 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile |
| TRUE | 0.0065 Auto | | 2 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.0072 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0076 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0051 Auto | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0069 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.008 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0053 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0063 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0084 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0023 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Presump Saliva test negative |
| TRUE | 0.0035 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison presump Saliva test positive |
| TRUE | 0.0087 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0062 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0084 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0041 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0041 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|------|---|
| TRUE | 0.0033 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0082 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0023 Auto | FAIL | Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0031 Auto | FAIL | presump Saliva test positive Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0038 Auto | FAIL | presump Saliva test positive Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.008 Auto | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.004 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0067 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0023 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0053 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0038 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0078 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0055 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.003 Auto | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.0044 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.007 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0039 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0025 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.006 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0035 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0025 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0032 Auto | | Single source DNA profile Submitted-results pending. |
| TRUE | 0.0084 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0085 Auto | | 3 person mix - supports non contribution Submitted-results pending. |
| TRUE | 0.0079 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0074 Auto | | 3 person mix profile - support for contrib > 100 billion Micro positive for sperm. Submitted-Results pending |
| TRUE | 0.0057 Auto | | Three person mixed DNA profile |
| TRUE | 0.0068 Auto | | |
| TRUE | 0.0083 Auto | | 2 person mixed profile - conditioned on Single evidence sample excluded Submitted-results pending. |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0083 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|---------|--|
| TRUE | 0.0035 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending Submitted-results pending. |
| TRUE | 0.0043 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0081 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0034 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison presump Saliva test positive |
| TRUE | 0.0071 Auto | | Two person mixed DNA profile |
| TRUE | 0.0031 Auto | | |
| TRUE | 0.0031 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0046 Auto | | Micro neg for sperm |
| TRUE | 0.0031 Auto | | |
| TRUE | 0.0025 Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0062 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.004 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0062 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0064 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.003 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0064 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0028 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0068 Auto | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0086 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0045 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0032 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0039 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0034 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0042 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0059 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.006 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0074 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0049 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0037 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0042 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0045 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0053 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|------|---|
| TRUE | 0.0022 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0045 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0056 Auto | | Submitted-results pending. Two person mixed DNA profile |
| TRUE | 0.007 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0029 Auto | | |
| TRUE | 0.0074 Auto | | Two person mixed DNA profile No statistical interpretation performed presump Saliva test positive |
| TRUE | 0.0022 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0044 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0054 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0061 Auto | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.0069 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0045 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0034 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0062 Auto | | |
| TRUE | 0.0088 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0038 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0047 Auto | | Mixture-low support for contrib or supports non contrib Submitted-results pending. |
| TRUE | 0.0035 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.004 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0027 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile |
| TRUE | 0.0063 Auto | | Mixture-low support for contrib or supports non contrib Submitted-results pending. |
| TRUE | 0.0048 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0048 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0072 Auto | FAIL | Mixture-low support for contrib or supports non contrib Submitted-results pending. |
| TRUE | 0.0068 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0056 Auto | | |
| TRUE | 0.0054 Auto | | |
| TRUE | 0.0026 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0045 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.005 Auto | | |
| TRUE | 0.0072 Auto | | |
| TRUE | 0.0023 Auto | | |
| TRUE | 0.0045 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|---------|--|
| TRUE | 0.0084 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0035 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0043 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0036 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0047 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0073 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0027 Auto | FAIL | Micro neg for sperm Single Source DNA profile - assumed known contributor |
| TRUE | 0.0082 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0074 Auto | FAIL | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion |
| TRUE | 0.0061 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0035 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0082 Auto | FAIL | Two person mixed DNA profile Single evidence sample excluded |
| TRUE | 0.0025 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0065 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0027 Auto | FAIL | 3 person mixed profile - conditioned on 3 person mix rem - support for contribution > 100 billion |
| TRUE | 0.0071 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0078 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0036 Auto | FAIL | Micro neg for sperm Single Source DNA profile - assumed known contributor |
| TRUE | 0.0057 Auto | FAIL | Submitted-results pending. Two person mixed DNA profile |
| TRUE | 0.0073 Auto | FAIL | 2 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.0055 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.007 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0079 Auto | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0049 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0076 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0041 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0025 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0029 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0046 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0038 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0081 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison SS DNA profile 9 loci and above LR > 100 billion |
| TRUE | 0.0063 Auto | SUCCESS | NCIDD upload single source DNA profile |

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|------|-------------|------|---|
| TRUE | 0.0037 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0027 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0035 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0075 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0073 Auto | | Single source 20 loci DNA profile LR > 100 billion |
| TRUE | 0.0028 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0066 Auto | | Submitted-results pending. |
| TRUE | 0.0065 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0078 Auto | | Two person mixed DNA profile Single evidence sample excluded |
| TRUE | 0.005 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.003 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0057 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0084 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0082 Auto | | |
| TRUE | 0.0025 Auto | | |
| TRUE | 0.0029 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0048 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0049 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.005 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0023 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.003 Auto | FAIL | presump Saliva test positive Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0061 Auto | FAIL | Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0022 Auto | | Submitted-results pending. Micro neg for sperm |
| TRUE | 0.0045 Auto | | |
| TRUE | 0.0046 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0045 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0054 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0051 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0072 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0069 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0035 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.004 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0065 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|---------|--|
| TRUE | 0.0043 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0085 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0084 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0075 Auto | | |
| TRUE | 0.007 Auto | | Submitted-results pending. Single Source DNA profile - assumed known contributor |
| TRUE | 0.0047 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0078 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0051 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0023 Auto | | Presump Saliva test negative Micro neg for sperm |
| TRUE | 0.003 Auto | FAIL | Micro neg for sperm Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0081 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0071 Auto | | |
| TRUE | 0.0023 Auto | | |
| TRUE | 0.0065 Auto | | |
| TRUE | 0.0066 Auto | SUCCESS | Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile |
| TRUE | 0.0048 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0027 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0071 Auto | | Presumptive blood test pos. Submitted-results pending. Single source DNA profile |
| TRUE | 0.0088 Auto | | Micro positive for sperm. Submitted-Results pending Two person mixed DNA profile |
| TRUE | 0.0055 Auto | | |
| TRUE | 0.0074 Auto | | |
| TRUE | 0.0083 Auto | | Single source 20 loci DNA profile LR > 100 billion Submitted-results pending. |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0076 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0044 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0031 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0033 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0032 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0031 Auto | | Sample processed and final results under Submitted-results pending. |
| TRUE | 0.0039 Auto | | Sample processed and final results under Submitted-results pending. |
| TRUE | 0.0027 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0031 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.003 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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| TRUE | 0.0059 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0083 Auto | | Micro neg for sperm Single Source DNA profile - assumed known contributor |
| TRUE | 0.0023 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0042 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0023 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0025 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0076 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0059 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0049 Auto | | |
| TRUE | 0.0031 Auto | | |
| TRUE | 0.0026 Auto | | Submitted as cells, Presump saliva test pending presump Saliva test positive |
| TRUE | 0.0037 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0073 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.006 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0024 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0023 Auto | | Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS |
| TRUE | 0.0061 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0022 Auto | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0045 Auto | | |
| TRUE | 0.0057 Auto | | |
| TRUE | 0.0085 Auto | | |
| TRUE | 0.0038 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0023 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0052 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0065 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0088 Auto | | |
| TRUE | 0.0057 Auto | FAIL | presump Saliva test positive Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.005 Auto | | |
| TRUE | 0.0077 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0073 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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| TRUE | 0.006 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0039 Auto | | |
| TRUE | 0.0042 Auto | | |
| TRUE | 0.0062 Auto | | Micro neg for sperm Single Source DNA profile - assumed known contributor |
| TRUE | 0.003 Auto | | |
| TRUE | 0.0034 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0032 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0031 Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0082 Auto | SUCCESS | Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile |
| TRUE | 0.0088 Auto | SUCCESS | SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile |
| TRUE | 0.0054 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0055 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0044 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.005 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0055 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0025 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0053 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0026 Auto | FAIL | Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0086 Auto | FAIL | Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0027 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0062 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0055 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0051 Auto | FAIL | Interim result- mixed profile obtained. Rework Reqd Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0051 Auto | | Submitted-results pending. Three person mixed DNA profile |
| TRUE | 0.007 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0034 Auto | | Micro positive for sperm. Submitted-Results pending No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0073 Auto | | Micro positive for sperm. Submitted-Results pending SS DNA profile 9 loci and above LR > 100 billion |
| TRUE | 0.0025 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0081 Auto | | Micro positive for sperm. Submitted-Results pending No DNA profile |
| TRUE | 0.0069 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0082 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0073 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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| TRUE | 0.0034 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0038 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0059 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0031 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0058 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0022 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0063 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0023 Auto | FAIL | Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0085 Auto | FAIL | Submitted-results pending. Two person mixed DNA profile |
| TRUE | 0.0074 Auto | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.0034 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0074 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0034 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0058 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0035 Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0038 Auto | | |
| TRUE | 0.0035 Auto | SUCCESS | NCIDD upload single source DNA profile Possible sub-threshold information |
| TRUE | 0.0028 Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0044 Auto | | |
| TRUE | 0.0052 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0048 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0039 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0043 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0082 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0082 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0055 Auto | | Submitted-results pending. No DNA detected |
| TRUE | 0.0027 Auto | | Single Source DNA profile - assumed known contributor |
| TRUE | 0.003 Auto | | |
| TRUE | 0.0028 Auto | | |
| TRUE | 0.0037 Auto | | |
| TRUE | 0.0066 Auto | | |
| TRUE | 0.0033 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0035 Auto | FAIL | Interim result - sample undergoing rework Complex mixed profile unsuitable for interp or comparison |

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| TRUE | 0.0027 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0057 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0081 Auto | | |
| TRUE | 0.0069 Auto | | Presumptive blood test pos. Submitted-results pending. Single Source DNA profile - assumed known contributor |
| TRUE | 0.0033 Auto | | |
| TRUE | 0.0087 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.003 Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0074 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0083 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0028 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0053 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0035 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0035 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0043 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0048 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0043 Auto | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.0023 Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0028 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0022 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0071 Auto | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0032 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0047 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0022 Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0057 Auto | | Two person mixed DNA profile 2 person mixed profile - conditioned on |
| TRUE | 0.0027 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0071 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0067 Auto | | |
| TRUE | 0.004 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0035 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0035 Auto | | |
| TRUE | 0.0025 Auto | | Single Source DNA profile - assumed known contributor Submitted-results pending. |
| TRUE | 0.0052 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0059 Auto | | Submitted-results pending. |

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| TRUE | 0.0048 Auto | FAIL | Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | | |
| TRUE | 0.0065 Auto | | 2 person mixed profile - conditioned on Single evidence sample excluded |
| TRUE | 0.0086 Auto | FAIL | Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0064 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0079 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.006 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0023 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0076 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0052 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0044 Auto | | |
| TRUE | 0.0076 Auto | | 3 person mixed profile - conditioned on 3 person mix remaining - supports non contribution |
| TRUE | 0.0044 Auto | | Micro positive for sperm. Submitted-Results pending |
| TRUE | 0.005 Auto | | |
| TRUE | 0.0039 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0032 Auto | | Single source DNA profile presump Saliva test positive |
| TRUE | 0.0031 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single Source DNA profile - assumed known contributor Possible sub-threshold information |
| TRUE | 0.0061 Auto | | |
| TRUE | 0.0029 Auto | | |
| TRUE | 0.006 Auto | | |
| TRUE | 0.0022 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0078 Auto | | |
| TRUE | 0.0039 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0042 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0078 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0064 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0063 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0044 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0037 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0069 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0031 Auto | | ENVM -Partial DNA profile |
| TRUE | 0.0023 Auto | | ENVM -Partial DNA profile Submitted-results pending. |
| TRUE | 0.0063 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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| TRUE | 0.0037 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0087 Auto | | Two person mixed DNA profile 2 person mixed profile - conditioned on |
| TRUE | 0.0048 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0049 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0083 Auto | | |
| TRUE | 0.003 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0086 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0067 Auto | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.0055 Auto | SUCCESS | Micro neg for sperm Single source DNA profile |
| TRUE | 0.0045 Auto | | |
| TRUE | 0.0054 Auto | | Micro neg for sperm Single Source DNA profile - assumed known contributor |
| TRUE | 0.0025 Auto | | |
| TRUE | 0.0054 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0037 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending |
| TRUE | 0.0047 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0051 Auto | | |
| TRUE | 0.0039 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0056 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0067 Auto | | 2 person mixed profile - conditioned on 2 person rem- support for contrib 1 million to 1 billion |
| TRUE | 0.008 Auto | | |
| TRUE | 0.0085 Auto | | Two person mixed DNA profile 2 person mixed profile - conditioned on |
| TRUE | 0.005 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0024 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.004 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.008 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0083 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0044 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0079 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0048 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0037 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0055 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0074 Auto | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.0074 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |

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| TRUE | 0.0055 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0084 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0043 Auto | | |
| TRUE | 0.007 Auto | | presump Saliva test positive |
| TRUE | 0.0036 Auto | | |
| TRUE | 0.0031 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes Presumptive blood test pos. Submitted-results pending. |
| TRUE | 0.0045 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0083 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0059 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0034 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0077 Auto | | |
| TRUE | 0.0025 Auto | | |
| TRUE | 0.0022 Auto | | Micro positive for sperm. Submitted-Results pending Single Source DNA profile - assumed known contributor |
| TRUE | 0.0029 Auto | | |
| TRUE | 0.0033 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0088 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0062 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0045 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0027 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | | |
| TRUE | 0.004 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0058 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Presumptive blood test pos. Submitted-results pending. |
| TRUE | 0.0025 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| TRUE | 0.003 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| TRUE | 0.0077 Auto | | Single source DNA profile Submitted-results pending. |
| TRUE | 0.0062 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0058 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0039 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0062 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0028 Auto | | |
| TRUE | 0.0025 Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0029 Auto | FAIL | Partial DNA profile unsuitable for comparison purposes |

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| TRUE | 0.0038 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0085 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0055 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0039 Auto | | |
| TRUE | 0.0035 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0067 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.005 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0022 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0025 Auto | | Hair located. Submitted-results pending |
| TRUE | 0.0053 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0059 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0043 Auto | | |
| TRUE | 0.0067 Auto | | |
| TRUE | 0.0025 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0057 Auto | | SS DNA profile 9 loci and above LR > 100 billion |
| TRUE | 0.0034 Auto | | |
| TRUE | 0.0039 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0031 Auto | | |
| TRUE | 0.0031 Auto | | |
| TRUE | 0.0026 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0033 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.003 Auto | | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion |
| TRUE | 0.0085 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.005 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0081 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.004 Auto | | |
| TRUE | 0.0022 Auto | FAIL | Presump. PSA test positive, no sperm found Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0056 Auto | | Single Source DNA profile - assumed known contributor |
| TRUE | 0.0063 Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0041 Auto | | |
| TRUE | 0.0041 Auto | | Micro neg for sperm Single Source DNA profile - assumed known contributor |
| TRUE | 0.0026 Auto | | |

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|------|--------|------|------|---|
| TRUE | 0.0054 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0057 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0038 | Auto | | |
| TRUE | 0.0037 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0045 | Auto | | Submitted-results pending. |
| TRUE | 0.0082 | Auto | | Hair located. Submitted-results pending Single source 20 loci DNA profile LR > 100 billion |
| TRUE | 0.0042 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0046 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0031 | Auto | | |
| TRUE | 0.0044 | Auto | | |
| TRUE | 0.0079 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0045 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0059 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0065 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0036 | Auto | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0041 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0041 | Auto | FAIL | Submitted as cells Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0028 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0038 | Auto | | Submitted-results pending. Sample processed and final results under |
| TRUE | 0.0031 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0048 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0067 | Auto | | Three person mixed DNA profile 3 person mix - supports non contribution |
| TRUE | 0.0077 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0088 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0055 | Auto | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.0082 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single source 20 loci DNA profile LR > 100 billion |
| TRUE | 0.0084 | Auto | | Possible sub-threshold information |
| TRUE | 0.0024 | Auto | | Two person mixed DNA profile 2 person mix - support for contrib 1 million - 1 billion |
| TRUE | 0.0041 | Auto | | |
| TRUE | 0.0088 | Auto | | |
| TRUE | 0.0066 | Auto | | Single source DNA profile Possible sub-threshold information |
| TRUE | 0.0051 | Auto | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.008 | Auto | | Micro positive for sperm. Submitted-Results pending Single Source DNA profile - assumed known contributor |

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|------|-------------|---------|--|
| TRUE | 0.0024 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0048 Auto | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0062 Auto | | Submitted-results pending. Micro neg for sperm |
| TRUE | 0.0037 Auto | | |
| TRUE | 0.0032 Auto | FAIL | Single source DNA profile- unsuitable for NCIDD searching |
| TRUE | 0.0049 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0024 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0046 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.004 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0028 Auto | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0033 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0065 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0038 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0034 Auto | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.0025 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0082 Auto | | Submitted-results pending. |
| TRUE | 0.0054 Auto | | Submitted-results pending. |
| TRUE | 0.0044 Auto | | Submitted-results pending. |
| TRUE | 0.0023 Auto | | Submitted-results pending. |
| TRUE | 0.0063 Auto | | |
| TRUE | 0.0086 Auto | | Submitted-results pending. |
| TRUE | 0.0045 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0048 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Quality flag identified, on hold awaiting advice from QPS |
| TRUE | 0.007 Auto | | Quality control failure, refer to QPS Submitted-results pending. |
| TRUE | 0.008 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0028 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.005 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0055 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0061 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0031 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0031 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.004 Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0042 Auto | | Submitted-results pending. |

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|------|-------------|--------|---------|--|
| TRUE | 0.0082 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0023 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0037 | Auto | | Submitted-results pending. |
| TRUE | 0.0054 | Auto | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0063 | Auto | | |
| TRUE | 0.0067 | Auto | | Submitted-results pending. |
| TRUE | 0.0016 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0089 | Manual | | Two person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.0019 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.001 | Manual | | Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.028899999 | Manual | FAIL | Interim result- mixed profile obtained. Rework Reqd Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0 | Manual | FAIL | No DNA detected This sample has undergone further processing |
| TRUE | 0.0017 | Manual | | Single source DNA profile < NCIDD matching stringency |
| TRUE | 0.0013 | Manual | | Single Source DNA profile - assumed known contributor Submitted-results pending. |
| TRUE | 0.0189 | Manual | FAIL | No DNA profile Submitted-results pending. |
| TRUE | 0.038400002 | Manual | | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0 | Manual | FAIL | Three person mixed DNA profile 3 person mixed profile - conditioned on No DNA detected |
| TRUE | 0.0015 | Manual | FAIL | This sample has undergone further processing Submitted-results pending. |
| TRUE | 0.022500001 | Manual | | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0125 | Manual | FAIL | Three person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.015900001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0298 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.030099999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0207 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0207 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.024800001 | Manual | SUCCESS | Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information |
| TRUE | 0.028999999 | Manual | | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion |

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|------|-------------|--------|---------|---|
| TRUE | 0.0134 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | | |
| TRUE | 0.0013 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0155 | Manual | | Three person mixed DNA profile Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0021 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.002 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.001 | Manual | | No DNA profile - possible sub-threshold peaks Submitted-results pending. |
| TRUE | 0.002 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0208 | Manual | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0263 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0121 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0209 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0003 | Manual | FAIL | ENVM- Complex mixture unsuitable for interp or comparison |
| TRUE | 0.0004 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0187 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0211 | Manual | | 3 person mixed profile - conditioned on Three person mixed DNA profile |
| TRUE | 0.025599999 | Manual | | 3 person mix profile - support for contrib > 100 billion Three person mixed DNA profile |
| TRUE | 0.023499999 | Manual | | 3 person mix - support for contrib 10 000 - 100 000 Submitted-results pending. |
| TRUE | 0.0011 | Manual | | No DNA profile Submitted-results pending. |
| TRUE | 0.0019 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.028100001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.032099999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile |
| TRUE | 0.0198 | Manual | | 2 person mixed profile - conditioned on Submitted-results pending. |
| TRUE | 0.0136 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0018 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | | Submitted-results pending. |
| TRUE | 0.014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|------|--|
| TRUE | 0.0156 | Manual | | Three person mixed DNA profile Excluded from mixed DNA profile |
| TRUE | 0.0173 | Manual | | Three person mixed DNA profile 3 person mix - supports non contribution |
| TRUE | 0.016799999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0089 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0003 | Manual | | Submitted-results pending. No DNA detected |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0319 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.029999999 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.034600001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0091 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on |
| TRUE | 0.033 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0219 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on |
| TRUE | 0.0142 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0166 | Manual | | Three person mixed DNA profile Single evidence sample excluded |
| TRUE | 0.0019 | Manual | | Submitted-results pending. |
| TRUE | 0.0144 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0 | Manual | | Submitted-results pending. |
| TRUE | 0.020199999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.021500001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|---------|--|
| TRUE | 0.0137 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0105 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.023600001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0185 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0094 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0021 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0016 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0019 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0154 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison presump Saliva test positive |
| TRUE | 0.0108 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.017000001 | Manual | | Submitted-results pending. |
| TRUE | 0.0016 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0021 | Manual | | |
| TRUE | 0.0016 | Manual | | |
| TRUE | 0.0105 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.027100001 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.015799999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.026000001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.020199999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.020500001 | Manual | | Three person mixed DNA profile Single evidence sample excluded Submitted as cells |
| TRUE | 0.0109 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| TRUE | 0.032699998 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| TRUE | 0.0128 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.016899999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0136 | Manual | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.0136 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0261 | Manual | | 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0018 | Manual | | Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS |
| TRUE | 0.0139 | Manual | | Single source DNA profile SS DNA profile 9 loci and above LR > 100 billion |

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|------|-------------|--------|---------|--|
| TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0151 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.021600001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.017899999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.018200001 | Manual | | Three person mixed DNA profile Submitted-results pending. |
| TRUE | 0.0277 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0163 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.020300001 | Manual | | No statistical interpretation performed Three person mixed DNA profile |
| TRUE | 0.0133 | Manual | | 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0019 | Manual | | |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0232 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.01 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0122 | Manual | | No statistical interpretation performed Three person mixed DNA profile |
| TRUE | 0.026699999 | Manual | | 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.023 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison 3 person mixed profile - conditioned on |
| TRUE | 0.014 | Manual | | 3 person mix rem - support for contribution > 100 billion Submitted-results pending. |
| TRUE | 0.0164 | Manual | | Three person mixed DNA profile Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0115 | Manual | | No statistical interpretation performed Single source DNA profile |
| TRUE | 0.0154 | Manual | SUCCESS | NCIDD upload single source DNA profile presump Saliva test positive |
| TRUE | 0.016799999 | Manual | | Two person mixed DNA profile Submitted-results pending. |
| TRUE | 0.0014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.020400001 | Manual | FAIL | 3 person mix profile - support for contrib > 100 billion |

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|------|-------------|--------|---------|---|
| TRUE | 0.017100001 | Manual | | Three person mixed DNA profile 3 person mix - support for contrib 10 000 - 100 000 Presump Saliva test negative |
| TRUE | 0.0147 | Manual | FAIL | Two person mixed DNA profile Submitted-results pending. |
| TRUE | 0.0149 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0007 | Manual | FAIL | ENVM- Complex mixture unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.018200001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0002 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes Three person mixed DNA profile |
| TRUE | 0.0143 | Manual | | 3 person mixed profile - conditioned on |
| TRUE | 0 | Manual | FAIL | ENVM- Complex mixture unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0144 | Manual | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0118 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0131 | Manual | | No statistical interpretation performed |
| TRUE | 0 | Manual | FAIL | ENVM- Complex mixture unsuitable for interp or comparison |
| TRUE | 0.0002 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0263 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0003 | Manual | | ENVM - No DNA profile Three person mixed DNA profile |
| TRUE | 0.015699999 | Manual | | 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0094 | Manual | | |
| TRUE | 0.0162 | Manual | | Three person mixed DNA profile 3 person mix - support for contribution 1000 to 10 000 |
| TRUE | 0.0178 | Manual | | |
| TRUE | 0.0253 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0104 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0186 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.018300001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.015799999 | Manual | | 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.0184 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.023499999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted as cells |
| TRUE | 0.0243 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0125 | Manual | | Mixture-low support for contrib or supports non contrib Three person mixed DNA profile |
| TRUE | 0.0195 | Manual | | 3 person mix profile - support for contrib > 100 billion |

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|------|-------------|--------|---------|--|
| TRUE | 0.017200001 | Manual | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0119 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0274 | Manual | | Submitted as cells Three person mixed DNA profile |
| TRUE | 0.016000001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.031800002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.020199999 | Manual | SUCCESS | Single source DNA profile NCIDD Intel upload - single source partial profile |
| TRUE | 0.0305 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0016 | Manual | | Submitted-results pending. |
| TRUE | 0.074299999 | Manual | | Single source 20 loci DNA profile LR > 100 billion |
| TRUE | 0.0017 | Manual | | Submitted-results pending. |
| TRUE | 0.009 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.025599999 | Manual | | Submitted-results pending. Three person mixed DNA profile |
| TRUE | 0.024499999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.022 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0261 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0128 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0096 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.017899999 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0112 | Manual | | Two person mixed DNA profile Mixture-low support for contrib or supports non contrib |
| TRUE | 0.0101 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|---------|---|
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.002 | Manual | | |
| TRUE | 0.0014 | Manual | | |
| TRUE | 0.0128 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0019 | Manual | | |
| TRUE | 0.023800001 | Manual | FAIL | Three person mixed DNA profile Mixture-low support for contrib or supports non contrib Submitted-results pending. |
| TRUE | 0.0014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0174 | Manual | SUCCESS | NCIDD upload single source DNA profile |
| TRUE | 0.0093 | Manual | | |
| TRUE | 0.0222 | Manual | | Submitted-results pending. Single source DNA profile |
| TRUE | 0.0131 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.001 | Manual | | |
| TRUE | 0.032099999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.021299999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.018200001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0253 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0167 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0124 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0187 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0121 | Manual | SUCCESS | SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0135 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Submitted as cells |
| TRUE | 0.036899999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison NCIDD upload single source DNA profile |
| TRUE | 0.0173 | Manual | SUCCESS | Single Source DNA profile - assumed known contributor |
| TRUE | 0.0092 | Manual | | |
| TRUE | 0.015 | Manual | | |
| TRUE | 0.0164 | Manual | | |

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|------|-------------|--------|---------|--|
| TRUE | 0.0106 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0091 | Manual | | presump Saliva test positive |
| TRUE | 0.0104 | Manual | | Three person mixed DNA profile |
| TRUE | 0.022 | Manual | | |
| TRUE | 0.020300001 | Manual | | Submitted-results pending. |
| TRUE | 0.0222 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.022 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.024700001 | Manual | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.0153 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile |
| TRUE | 0.025699999 | Manual | | 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0021 | Manual | FAIL | Presump. PSA test positive, no sperm found Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0018 | Manual | | No DNA profile - possible sub-threshold peaks |
| TRUE | 0.024700001 | Manual | | Submitted-results pending. Two person mixed DNA profile |
| TRUE | 0.022 | Manual | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.0108 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0008 | Manual | | |
| TRUE | 0.0007 | Manual | FAIL | No DNA detected This sample has undergone further processing |
| TRUE | 0.0002 | Manual | FAIL | ENVM- Complex mixture unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0109 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0208 | Manual | | 2 person mix profile - support for contrib > 100 billion 2 person mix profile - support for contrib > 100 billion Submitted as cells |
| TRUE | 0.0174 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0131 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | | |
| TRUE | 0.001 | Manual | | |
| TRUE | 0.0287 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on |
| TRUE | 0.0018 | Manual | | |
| TRUE | 0.019200001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.034600001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.024800001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0018 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes |

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|------|-------------|--------|---------|---|
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0136 | Manual | | 3 person mix profile - support for contrib > 100 billion 3 person mix - support for contrib 100 000 to 1 million |
| TRUE | 0.029200001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0098 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0277 | Manual | | presump Saliva test positive Two person mixed DNA profile |
| TRUE | 0.017999999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0152 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0274 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.061099999 | Manual | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0096 | Manual | | |
| TRUE | 0.0255 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0121 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | FAIL | Presump. PSA test positive, no sperm found Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0113 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.0287 | Manual | | Three person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.0162 | Manual | | Submitted as cells Two person mixed DNA profile |
| TRUE | 0.0104 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0165 | Manual | FAIL | Two person mixed DNA profile 2 person mixed profile - conditioned on |
| TRUE | 0.0011 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0132 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on |
| TRUE | 0.028899999 | Manual | | Two person mixed DNA profile 2 person mixed profile - conditioned on |
| TRUE | 0.0242 | Manual | | Submitted-results pending. Two person mixed DNA profile |
| TRUE | 0.0199 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.019300001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | FAIL | Interim result - sample undergoing rework Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0018 | Manual | | |
| TRUE | 0.0143 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | | |
| TRUE | 0.016000001 | Manual | | Interim result - sample undergoing rework Quality flag identified, on hold awaiting advice from QPS |
| TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.018999999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|------|---|
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0228 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.014 | Manual | | |
| TRUE | 0.024499999 | Manual | | |
| TRUE | 0.0155 | Manual | | Micro positive for sperm. Submitted-Results pending QPS advised no further work required - results available |
| TRUE | 0.0121 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0272 | Manual | | Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information |
| TRUE | 0 | Manual | FAIL | No DNA detected This sample has undergone further processing |
| TRUE | 0 | Manual | FAIL | No DNA detected This sample has undergone further processing |
| TRUE | 0.0016 | Manual | FAIL | Hair located. Submitted-results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.027899999 | Manual | FAIL | Submitted as cells Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0228 | Manual | | No statistical interpretation performed Sample undergone further work - conditioned |
| TRUE | 0.0143 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0152 | Manual | | Submitted-results pending. Two person mixed DNA profile |
| TRUE | 0.0113 | Manual | | Three person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0135 | Manual | | Submitted-results pending. Three person mixed DNA profile |
| TRUE | 0.0015 | Manual | | No DNA profile Possible sub-threshold information |
| TRUE | 0.0134 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0 | Manual | FAIL | ENVM- Complex mixture unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0013 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0199 | Manual | | Single evidence sample excluded Submitted-results pending. |
| TRUE | 0.0155 | Manual | | Two person mixed DNA profile Submitted as cells |
| TRUE | 0.0015 | Manual | | Single Source DNA profile - assumed known contributor Submitted-results pending. |
| TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0011 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|---------|--|
| TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0112 | Manual | SUCCESS | Single Source DNA profile - assumed known contributor NCIDD upload single source DNA profile |
| TRUE | 0.0138 | Manual | | 3 person mixed profile - conditioned on Single evidence sample excluded |
| TRUE | 0.0222 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0119 | Manual | | Single Source DNA profile - assumed known contributor Possible sub-threshold information |
| TRUE | 0.024800001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.011 | Manual | | |
| TRUE | 0.032900002 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.0197 | Manual | | Single source DNA profile Single source 20 loci DNA profile LR > 100 billion |
| TRUE | 0.033 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0143 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.021199999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.032900002 | Manual | | Three person mixed DNA profile Submitted-results pending. |
| TRUE | 0.013 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Presump Saliva test negative |
| TRUE | 0.0019 | Manual | | Single Source DNA profile - assumed known contributor Submitted-results pending. |
| TRUE | 0.0016 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.024599999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0018 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0102 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison 3 person mixed profile - conditioned on |
| TRUE | 0.028999999 | Manual | | 3 person mix rem - support for contribution > 100 billion Single source DNA profile |
| TRUE | 0.0129 | Manual | SUCCESS | Possible sub-threshold information |
| TRUE | 0.0125 | Manual | | |
| TRUE | 0.0184 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.0008 | Manual | FAIL | ENVM- Complex mixture unsuitable for interp or comparison |
| TRUE | 0.0003 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.021199999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0105 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0123 | Manual | | |

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|------|-------------|--------|---------|---|
| TRUE | 0.0124 | Manual | | |
| TRUE | 0.0004 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0095 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.019099999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0095 | Manual | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.022299999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.053300001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison presump Saliva test positive |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0165 | Manual | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0019 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0017 | Manual | | No DNA profile - possible sub-threshold peaks Submitted-results pending. |
| TRUE | 0.002 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0019 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0094 | Manual | | |
| TRUE | 0.0148 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on Submitted-results pending. |
| TRUE | 0.0014 | Manual | | No DNA profile Submitted-results pending. |
| TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.002 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0017 | Manual | | No DNA profile Submitted-results pending. |
| TRUE | 0.0013 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0011 | Manual | | No DNA profile - possible sub-threshold peaks Submitted as cells |
| TRUE | 0.0013 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.01 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.024900001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0002 | Manual | FAIL | ENVM- Complex mixture unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0208 | Manual | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.028000001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0141 | Manual | | 3 person mixed profile - conditioned on Three person mixed DNA profile |
| TRUE | 0.0197 | Manual | | Excluded from mixed DNA profile |
| TRUE | 0.023499999 | Manual | | |
| TRUE | 0.024800001 | Manual | | |

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|------|-------------|--------|---------|---|
| TRUE | 0.0118 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on Two person mixed DNA profile |
| TRUE | 0.016100001 | Manual | | 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0 | Manual | | |
| TRUE | 0.0015 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0118 | Manual | SUCCESS | Single source 20 loci DNA profile LR > 100 billion NCIDD upload single source DNA profile |
| TRUE | 0.0109 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.017200001 | Manual | | |
| TRUE | 0.016799999 | Manual | | |
| TRUE | 0.032099999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0126 | Manual | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.023399999 | Manual | | Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information |
| TRUE | 0.0178 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.0021 | Manual | | |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0128 | Manual | | Single source DNA profile Possible sub-threshold information |
| TRUE | 0.0185 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0095 | Manual | | |
| TRUE | 0.0133 | Manual | | |
| TRUE | 0.0012 | Manual | FAIL | Submitted as cells Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0319 | Manual | | Submitted-results pending. Three person mixed DNA profile |
| TRUE | 0.025800001 | Manual | | Submitted-results pending. Three person mixed DNA profile |
| TRUE | 0 | Manual | | |
| TRUE | 0 | Manual | | |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0093 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0092 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0096 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0134 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |

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|------|-------------|--------|---------|--|
| TRUE | 0.0099 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0123 | Manual | | |
| TRUE | 0.034600001 | Manual | | Presump Saliva test negative Three person mixed DNA profile Submitted-results pending. |
| TRUE | 0.0149 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.002 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.017000001 | Manual | SUCCESS | Possible sub-threshold information Submitted-results pending. |
| TRUE | 0.0121 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Interim result- mixed profile obtained. Rework Reqd |
| TRUE | 0.0107 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0095 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0207 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.002 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0141 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0221 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.027899999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0144 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0089 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0146 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.024800001 | Manual | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.002 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.026000001 | Manual | | Single source 20 loci DNA profile LR > 100 billion Submitted-results pending. |
| TRUE | 0.0119 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0276 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Presump. PSA test positive, no sperm found |
| TRUE | 0.0018 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.002 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.020500001 | Manual | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.020500001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0165 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.039700001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0011 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Micro positive for sperm. Submitted-Results pending |
| TRUE | 0.0013 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0019 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|---------|---|
| TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | FAIL | Micro positive for sperm. Submitted-Results pending Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.011 | Manual | | Three person mixed DNA profile |
| TRUE | 0.0094 | Manual | | 3 person mix profile - support for contrib > 100 billion 3 person mixed profile - conditioned on |
| TRUE | 0.029899999 | Manual | | 3 person mix rem - support for contribution > 100 billion Two person mixed DNA profile |
| TRUE | 0.0095 | Manual | | 2 person mixed profile - conditioned on Micro positive for sperm. Submitted-Results pending |
| TRUE | 0.031500001 | Manual | SUCCESS | Single source 20 loci DNA profile LR > 100 billion Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.0244 | Manual | | Submitted-results pending. Three person mixed DNA profile |
| TRUE | 0.0252 | Manual | | Submitted-results pending. Three person mixed DNA profile |
| TRUE | 0.0156 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0396 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0102 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0123 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0 | Manual | | |
| TRUE | 0.0218 | Manual | | Three person mixed DNA profile 3 person mix - supports non contribution |
| TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0141 | Manual | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.038199998 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0091 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.023499999 | Manual | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.031599998 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0141 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0113 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0121 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0126 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0138 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0019 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison SS DNA profile 9 loci and above LR > 100 billion |
| TRUE | 0.0276 | Manual | SUCCESS | NCIDD upload single source DNA profile |
| TRUE | 0.0094 | Manual | | |
| TRUE | 0.0222 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0231 | Manual | | Three person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.020199999 | Manual | | Submitted-results pending. Three person mixed DNA profile |
| TRUE | 0.0265 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|------|--|
| TRUE | 0.0244 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.021600001 | Manual | | Two person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.024700001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0145 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0119 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.019099999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0163 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0162 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | | No DNA profile Submitted-results pending. |
| TRUE | 0.0017 | Manual | | No DNA profile Submitted-results pending. |
| TRUE | 0.002 | Manual | | No DNA profile Possible sub-threshold information Submitted-results pending. |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.031599998 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.0266 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0184 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.020300001 | Manual | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0096 | Manual | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.090700001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.022700001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0101 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|---------|--|
| TRUE | 0.021 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on |
| TRUE | 0.0218 | Manual | FAIL | Two person mixed DNA profile 2 person mixed profile - conditioned on |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0006 | Manual | | ENVM -Partial DNA profile |
| TRUE | 0.0009 | Manual | | ENVM -Partial DNA profile Submitted-results pending. |
| TRUE | 0.0112 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0136 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0186 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on |
| TRUE | 0 | Manual | | |
| TRUE | 0.0105 | Manual | SUCCESS | SS DNA profile 9 loci and above LR > 100 billion NCIDD upload single source DNA profile |
| TRUE | 0.0014 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0 | Manual | | |
| TRUE | 0 | Manual | | |
| TRUE | 0.0163 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0011 | Manual | | No DNA profile Possible sub-threshold information |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0146 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.032699998 | Manual | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0102 | Manual | FAIL | Submitted as cells Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.034899998 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0 | Manual | | ENVM -Partial DNA profile |
| TRUE | 0 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes |
| TRUE | 0 | Manual | | ENVM - No DNA profile |
| TRUE | 0.0002 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0019 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.011 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|------|---|
| TRUE | 0.0111 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0016 | Manual | | |
| TRUE | 0.0011 | Manual | | |
| TRUE | 0.0122 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0016 | Manual | | |
| TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | | |
| TRUE | 0.0199 | Manual | FAIL | Submitted as cells Complex mixed profile unsuitable for interp or comparison presump Saliva test positive |
| TRUE | 0.0016 | Manual | | Two person mixed DNA profile |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | | |
| TRUE | 0.0124 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0176 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0017 | Manual | | Quality flag identified, on hold awaiting advice from QPS Quality control failure, refer to QPS |
| TRUE | 0.0004 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0019 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0229 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0228 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0119 | Manual | | |
| TRUE | 0.032499999 | Manual | FAIL | Submitted as cells Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0275 | Manual | | Submitted as cells Three person mixed DNA profile |
| TRUE | 0.0129 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0101 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0135 | Manual | FAIL | Two person mixed DNA profile 2 person mixed profile - conditioned on Submitted-results pending. |
| TRUE | 0.0114 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0012 | Manual | | No DNA profile - possible sub-threshold peaks |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|------|---|
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0017 | Manual | | |
| TRUE | 0.001 | Manual | | |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.024900001 | Manual | | |
| TRUE | 0.009 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | | |
| TRUE | 0.0011 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0021 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0011 | Manual | | No DNA profile SS DNA profile 9 loci and above LR > 100 billion |
| TRUE | 0.0096 | Manual | | Possible sub-threshold information |
| TRUE | 0.0133 | Manual | | |
| TRUE | 0.011 | Manual | | |
| TRUE | 0.0239 | Manual | | 3 person mixed profile - conditioned on Cond mix rem-low supp for contrib or supp non contrib |
| TRUE | 0.014 | Manual | | 2 person mixed profile - conditioned on Excluded from mixed DNA profile |
| TRUE | 0.001 | Manual | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.0173 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0127 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0319 | Manual | | 3 person mix- support for contrib 1 billion - 100 billion 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.022700001 | Manual | | 3 person mix - support for contribution 1000 to 10 000 |
| TRUE | 0.029300001 | Manual | | |
| TRUE | 0.026699999 | Manual | | Three person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.001 | Manual | | |
| TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0239 | Manual | | Intel report required for further interpretation Submitted-results pending. |
| TRUE | 0.0148 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0176 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0232 | Manual | | 3 person mix - support for contrib 1 million - 1 billion |
| TRUE | 0.011 | Manual | | |
| TRUE | 0.0101 | Manual | | Two person mixed DNA profile 2 person mixed profile - conditioned on 2 person mixed profile - conditioned on |
| TRUE | 0.0186 | Manual | | 2 person mix rem - support for contribution > 100 billion Submitted-results pending. |
| TRUE | 0.002 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|---------|---|
| TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0011 | Manual | FAIL | Submitted as cells Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0124 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0 | Manual | | Submitted-results pending. No DNA detected |
| TRUE | 0.0151 | Manual | | |
| TRUE | 0.0112 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0118 | Manual | | |
| TRUE | 0 | Manual | | No DNA detected This sample has undergone further processing |
| TRUE | 0 | Manual | | No DNA detected This sample has undergone further processing |
| TRUE | 0 | Manual | | No DNA detected This sample has undergone further processing |
| TRUE | 0 | Manual | | No DNA detected This sample has undergone further processing |
| TRUE | 0.013 | Manual | | Single Source DNA profile - assumed known contributor Possible sub-threshold information |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0011 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0 | Manual | | |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0095 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.016000001 | Manual | | Three person mixed DNA profile 3 person mix - supports non contribution |
| TRUE | 0.034600001 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0112 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.025599999 | Manual | | |
| TRUE | 0.0139 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on |
| TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.012 | Manual | | |
| TRUE | 0.0019 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0134 | Manual | | Three person mixed DNA profile Single source 20 loci DNA profile LR > 100 billion |
| TRUE | 0.0111 | Manual | SUCCESS | NCIDD upload single source DNA profile |

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|------|-------------|--------|---------|---|
| TRUE | 0.0296 | Manual | | Two person mixed DNA profile 2 person mixed profile - conditioned on Submitted-results pending. |
| TRUE | 0.0107 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0113 | Manual | | Three person mixed DNA profile Submitted-results pending. |
| TRUE | 0.0115 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0019 | Manual | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.002 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.023399999 | Manual | | |
| TRUE | 0.0294 | Manual | | Submitted-results pending. |
| TRUE | 0.0019 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0014 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0173 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0111 | Manual | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.020300001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0199 | Manual | | 3 person mix - low support for contribution SS DNA profile 9 loci and above LR > 100 billion |
| TRUE | 0.0015 | Manual | SUCCESS | NCIDD upload single source DNA profile Three person mixed DNA profile |
| TRUE | 0.031599998 | Manual | | 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.0105 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0328 | Manual | FAIL | 3 person mixed profile - conditioned on Submitted-results pending. |
| TRUE | 0.0091 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0147 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0005 | Manual | | ENVM -Partial DNA profile |
| TRUE | 0.0003 | Manual | | ENVM -Partial DNA profile |
| TRUE | 0.0013 | Manual | | ENVM -Partial DNA profile |
| TRUE | 0 | Manual | | |
| TRUE | 0.0195 | Manual | | Three person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.0148 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0123 | Manual | | Three person mixed DNA profile No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.0178 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|---------|--|
| TRUE | 0 | Manual | | |
| TRUE | 0.0255 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0099 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0133 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0128 | Manual | | Submitted-results pending. |
| TRUE | 0.0021 | Manual | FAIL | Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | FAIL | Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.018999999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0165 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.020300001 | Manual | FAIL | Three person mixed DNA profile Excluded from mixed DNA profile |
| TRUE | 0.0154 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0153 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.020099999 | Manual | | Three person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.0139 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0093 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.0241 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.0127 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0096 | Manual | | |
| TRUE | 0.0142 | Manual | | Two person mixed DNA profile 2 person mixed profile - conditioned on |
| TRUE | 0.0021 | Manual | FAIL | Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | FAIL | Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | FAIL | presump Saliva test positive Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.057700001 | Manual | | presump Saliva test positive Three person mixed DNA profile |
| TRUE | 0.0136 | Manual | FAIL | Submitted as cells Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0091 | Manual | SUCCESS | Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information |
| TRUE | 0.0094 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0101 | Manual | | Submitted-results pending. Single source DNA profile |
| TRUE | 0.0121 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.020500001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.015799999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0163 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0135 | Manual | | Two person mixed DNA profile Single evidence sample excluded |
| TRUE | 0.0115 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|------|---|
| TRUE | 0.001 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0151 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | | Submitted-results pending. |
| TRUE | 0.020400001 | Manual | FAIL | Three person mixed DNA profile 3 person mixed profile - conditioned on Two person mixed DNA profile |
| TRUE | 0.0142 | Manual | | Suspect check inconclusive - mixed DNA profile |
| TRUE | 0.014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.014 | Manual | | 2 person mixed profile - conditioned on |
| TRUE | 0.014 | Manual | | 2 person mix rem - support for contribution > 100 billion |
| TRUE | 0.021500001 | Manual | | |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | FAIL | Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.028899999 | Manual | FAIL | Submitted-results pending. |
| TRUE | 0.030099999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0116 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0121 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.025800001 | Manual | FAIL | Submitted-results pending. |
| TRUE | 0.016899999 | Manual | | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0115 | Manual | FAIL | 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.024599999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.020400001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.029300001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0093 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0015 | Manual | | |
| TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0012 | Manual | | |
| TRUE | 0.0142 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0128 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison This sample has undergone further processing |
| TRUE | 0.016799999 | Manual | | 2 person mixed profile - conditioned on 2 person mix rem - support for contribution > 100 billion |
| TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0101 | Manual | | Single source DNA profile Possible sub-threshold information |
| TRUE | 0.028899999 | Manual | | Submitted-results pending. SS DNA profile 9 loci and above LR > 100 billion |

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|------|-------------|--------|---------|--|
| TRUE | 0.016100001 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0093 | Manual | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0175 | Manual | | |
| TRUE | 0.018300001 | Manual | | |
| TRUE | 0.0116 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0178 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.020300001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0021 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.015699999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0143 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0132 | Manual | | |
| TRUE | 0.0133 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.02 | Manual | | Three person mixed DNA profile Suspect Check Actioned - No Match |
| TRUE | 0.0185 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.024599999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0145 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0101 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0 | Manual | | ENVM - No DNA profile |
| TRUE | 0 | Manual | | |
| TRUE | 0.0002 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes |
| TRUE | 0.0007 | Manual | | ENVM - No DNA profile |
| TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0103 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0002 | Manual | | |
| TRUE | 0.0002 | Manual | | |
| TRUE | 0 | Manual | | |
| TRUE | 0.0145 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0108 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0089 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.018300001 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |

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|------|-------------|--------|------|---|
| TRUE | 0.0125 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0105 | Manual | | |
| TRUE | 0.0098 | Manual | | Single Source DNA profile - assumed known contributor Possible sub-threshold information |
| TRUE | 0.0144 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | | |
| TRUE | 0.0016 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0019 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0122 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.014 | Manual | | Single source DNA profile Possible sub-threshold information |
| TRUE | 0.022399999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | | |
| TRUE | 0.0019 | Manual | | |
| TRUE | 0.0143 | Manual | | Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information |
| TRUE | 0.0013 | Manual | | |
| TRUE | 0.0154 | Manual | | Submitted-results pending. Three person mixed DNA profile |
| TRUE | 0.021199999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.023800001 | Manual | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.0104 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0111 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | | |
| TRUE | 0.001 | Manual | | |
| TRUE | 0.001 | Manual | | |
| TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0164 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0 | Manual | | Submitted-results pending. No DNA detected |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.016100001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0241 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|---------|---|
| TRUE | 0.0019 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0104 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.024 | Manual | | Cond mix rem-low supp for contrib or supp non contrib Three person mixed DNA profile |
| TRUE | 0.031599998 | Manual | | 3 person mixed profile - conditioned on Submitted-results pending. |
| TRUE | 0.0018 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0142 | Manual | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0011 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0013 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0019 | Manual | | |
| TRUE | 0.0016 | Manual | | |
| TRUE | 0.0103 | Manual | FAIL | Micro neg for sperm Two person mixed DNA profile |
| TRUE | 0.0176 | Manual | | |
| TRUE | 0.002 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.002 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0241 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.032200001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0263 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.027000001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0273 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0101 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0167 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0011 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0136 | Manual | | 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.0018 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Presump Saliva test negative |
| TRUE | 0.0018 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0005 | Manual | | Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0019 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0134 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0002 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes |

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|------|-------------|--------|---------|--|
| TRUE | 0.0003 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0244 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0016 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0127 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Hair located. Submitted-results pending |
| TRUE | 0.0015 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.001 | Manual | | Submitted-results pending. |
| TRUE | 0.0011 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0305 | Manual | | 3 person mix profile - support for contrib > 100 billion Micro positive for sperm. Submitted-Results pending |
| TRUE | 0.0112 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.029300001 | Manual | | Three person mixed DNA profile |
| TRUE | 0.024900001 | Manual | | Three person mixed DNA profile No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.0196 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0239 | Manual | | 3 person mix profile - support for contrib > 100 billion Three person mixed DNA profile |
| TRUE | 0.030400001 | Manual | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.025699999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0119 | Manual | | Submitted-results pending. Three person mixed DNA profile |
| TRUE | 0.021199999 | Manual | | 3 person mix profile - support for contrib > 100 billion Three person mixed DNA profile |
| TRUE | 0.0198 | Manual | | 3 person mix - support for contrib 10 000 - 100 000 Submitted-results pending. |
| TRUE | 0.0111 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | | Single Source DNA profile - assumed known contributor Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0019 | Manual | FAIL | Three person mixed DNA profile Two person mixed DNA profile |
| TRUE | 0.016000001 | Manual | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.0207 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0273 | Manual | SUCCESS | NCIDD upload single source DNA profile Single source DNA profile |
| TRUE | 0.0135 | Manual | SUCCESS | Possible sub-threshold information Two person mixed DNA profile |
| TRUE | 0.012 | Manual | | 2 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.021299999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0162 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.0095 | Manual | | 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0285 | Manual | | Two person mixed DNA profile |
| TRUE | 0.0211 | Manual | | 2 person mix - support for contrib 1 million - 1 billion Submitted-results pending. |
| TRUE | 0.0118 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0118 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|------|--|
| TRUE | 0.0186 | Manual | | Single source 20 loci DNA profile LR > 100 billion Possible sub-threshold information Submitted-results pending. |
| TRUE | 0.0128 | Manual | | Single source 20 loci DNA profile LR > 100 billion Submitted-results pending. |
| TRUE | 0.0101 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.009 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Presump Saliva test negative |
| TRUE | 0.0013 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Presump Saliva test negative |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Presump Saliva test negative |
| TRUE | 0.0019 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile |
| TRUE | 0.047400001 | Manual | | Single evidence sample excluded Single source DNA profile |
| TRUE | 0.0296 | Manual | | Possible sub-threshold information |
| TRUE | 0.016899999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Single source 20 loci DNA profile LR > 100 billion |
| TRUE | 0.028100001 | Manual | | Possible sub-threshold information Submitted-results pending. |
| TRUE | 0.022600001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison 3 person mixed profile - conditioned on |
| TRUE | 0.0274 | Manual | | Single evidence sample excluded Submitted-results pending. |
| TRUE | 0.0148 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.023499999 | Manual | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.029999999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0021 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0013 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.022299999 | Manual | | Single source 20 loci DNA profile LR > 100 billion |
| TRUE | 0.0011 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.021500001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Micro neg for sperm |
| TRUE | 0.016000001 | Manual | | Single Source DNA profile - assumed known contributor Submitted-results pending. |
| TRUE | 0.0127 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison No DNA profile |
| TRUE | 0.0013 | Manual | | Possible sub-threshold information Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0146 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | | Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.001 | Manual | | No DNA profile - possible sub-threshold peaks Submitted-results pending. |
| TRUE | 0.0148 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|------|---|
| TRUE | 0.001 | Manual | | Three person mixed DNA profile |
| TRUE | 0.0305 | Manual | | 3 person mix - support for contribution 1000 to 10 000 |
| TRUE | 0.0095 | Manual | | Single source DNA profile |
| TRUE | 0.0146 | Manual | FAIL | Possible sub-threshold information Submitted-results pending. |
| TRUE | 0.025699999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.013 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0002 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes |
| TRUE | 0.0005 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0103 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0115 | Manual | | Submitted-results pending. |
| TRUE | 0.001 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.019300001 | Manual | | |
| TRUE | 0.029300001 | Manual | | 2 person mixed profile - conditioned on Excluded from mixed DNA profile |
| TRUE | 0.0093 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0119 | Manual | | |
| TRUE | 0.0118 | Manual | | |
| TRUE | 0.0093 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0094 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0142 | Manual | | Submitted-results pending. |
| TRUE | 0.0121 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | | |
| TRUE | 0.001 | Manual | | |
| TRUE | 0.0011 | Manual | | |
| TRUE | 0.001 | Manual | | |
| TRUE | 0.039099999 | Manual | | Submitted-results pending. Three person mixed DNA profile |
| TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.011 | Manual | | Three person mixed DNA profile Single evidence sample excluded |
| TRUE | 0.0162 | Manual | | Three person mixed DNA profile 3 person mix- support for contrib 1 billion - 100 billion |
| TRUE | 0.0156 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0018 | Manual | | Interim result - sample undergoing rework Two person mixed DNA profile |
| TRUE | 0.0151 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0095 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0123 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|------|---|
| TRUE | 0.0113 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.031199999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.024900001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | | Single Source DNA profile - assumed known contributor |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0162 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | | |
| TRUE | 0.0296 | Manual | | Submitted-results pending. Three person mixed DNA profile |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0133 | Manual | | Micro positive for sperm. Submitted-Results pending Single source 20 loci DNA profile LR > 100 billion |
| TRUE | 0.022600001 | Manual | | 3 person mixed profile - conditioned on Remaining contribution - inconclusive |
| TRUE | 0.0119 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0124 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.031500001 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on |
| TRUE | 0.013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0103 | Manual | | Three person mixed DNA profile No statistical interpretation performed |
| TRUE | 0.0121 | Manual | | |
| TRUE | 0.0107 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.01 | Manual | | |
| TRUE | 0.0101 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0195 | Manual | | Submitted-results pending. Two person mixed DNA profile |
| TRUE | 0.0123 | Manual | | Two person mixed DNA profile 2 person mix - supports non contribution |
| TRUE | 0.001 | Manual | FAIL | Hair located. Submitted-results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | | No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0018 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|---------|---|
| TRUE | 0.025900001 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.036200002 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0152 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0095 | Manual | | |
| TRUE | 0.0306 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on |
| TRUE | 0.026799999 | Manual | | Submitted-results pending. |
| TRUE | 0.0101 | Manual | | |
| TRUE | 0.023 | Manual | | |
| TRUE | 0.0175 | Manual | | Single Source DNA profile - assumed known contributor Possible sub-threshold information Submitted-results pending. |
| TRUE | 0.0021 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0011 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.002 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Presump saliva positive. Submitted-results pending. |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0016 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | | |
| TRUE | 0.0007 | Manual | | ENVM -Partial DNA profile Submitted-results pending. |
| TRUE | 0.0018 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.001 | Manual | | No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0126 | Manual | | Three person mixed DNA profile Mixture-low support for contrib or supports non contrib Submitted-results pending. |
| TRUE | 0.018200001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0239 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0131 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | | Micro neg for sperm Semen not detected |
| TRUE | 0.0143 | Manual | SUCCESS | Two person mixed DNA profile Single source DNA profile |
| TRUE | 0.021500001 | Manual | | Submitted-results pending. |
| TRUE | 0.018100001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0195 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0114 | Manual | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0019 | Manual | | Micro positive for sperm. Submitted-Results pending Submitted-results pending. |
| TRUE | 0.0133 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|------|---|
| TRUE | 0.0089 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0091 | Manual | | |
| TRUE | 0.0089 | Manual | FAIL | Hair located. Submitted-results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.027799999 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on Presump Saliva test negative |
| TRUE | 0.0113 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0021 | Manual | | No DNA profile - possible sub-threshold peaks Submitted-results pending. |
| TRUE | 0.0138 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0106 | Manual | FAIL | ENVM- Complex mixture unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0173 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | | |
| TRUE | 0.001 | Manual | | |
| TRUE | 0.0021 | Manual | | Submitted-results pending. No DNA detected |
| TRUE | 0.0091 | Manual | | Submitted-results pending. |
| TRUE | 0.0128 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison 3 person mix - support for contribution 1000 to 10 000 |
| TRUE | 0.015 | Manual | | Single evidence sample excluded Submitted-results pending. |
| TRUE | 0.02 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0103 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Interim result- mixed profile obtained. Rework Reqd |
| TRUE | 0.0144 | Manual | | Three person mixed DNA profile Interim result- mixed profile obtained. Rework Reqd |
| TRUE | 0.0128 | Manual | | Three person mixed DNA profile Interim result- mixed profile obtained. Rework Reqd |
| TRUE | 0.032900002 | Manual | | Three person mixed DNA profile Submitted-results pending. |
| TRUE | 0.0014 | Manual | | No DNA profile - possible sub-threshold peaks Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0154 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile |
| TRUE | 0.029899999 | Manual | | No statistical interpretation performed Two person mixed DNA profile |
| TRUE | 0.0231 | Manual | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0015 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0093 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.029899999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0089 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.018200001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.024700001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |

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|------|-------------|--------|---------|---|
| TRUE | 0.0105 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | | Submitted-results pending. No DNA profile |
| TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0219 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.020199999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0118 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0211 | Manual | | Excluded from mixed DNA profile Micro neg for sperm |
| TRUE | 0.0011 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0102 | Manual | | |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0017 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0012 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0018 | Manual | | |
| TRUE | 0.0018 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.019400001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0198 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0096 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0167 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0091 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison This sample has undergone further processing |
| TRUE | 0.0129 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.0127 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0021 | Manual | | |
| TRUE | 0.002 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.019200001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0002 | Manual | | ENVM - No DNA profile |
| TRUE | 0.0004 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes Two person mixed DNA profile |
| TRUE | 0.0211 | Manual | | 2 person mix profile - support for contrib > 100 billion |

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|------|-------------|--------|---------|--|
| TRUE | 0.019099999 | Manual | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.021 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0151 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.020500001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Single Source DNA profile - assumed known contributor |
| TRUE | 0.031399999 | Manual | SUCCESS | Possible sub-threshold information Submitted-results pending. |
| TRUE | 0.0309 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile |
| TRUE | 0.020500001 | Manual | | No statistical interpretation performed Submitted-results pending. |
| TRUE | 0.022600001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.013 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0309 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.017200001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile |
| TRUE | 0.032900002 | Manual | | 2 person mix profile - support for contrib > 100 billion 3 person mixed profile - conditioned on |
| TRUE | 0.0097 | Manual | | Single evidence sample excluded Three person mixed DNA profile |
| TRUE | 0.027799999 | Manual | | 3 person mixed profile - conditioned on Submitted-results pending. |
| TRUE | 0.031399999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0221 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0176 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0011 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.023499999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Three person mixed DNA profile |
| TRUE | 0.027799999 | Manual | | Single evidence sample excluded Two person mixed DNA profile |
| TRUE | 0.0139 | Manual | SUCCESS | NCIDD upload - mixed DNA profile |
| TRUE | 0.0109 | Manual | | |
| TRUE | 0.0198 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0094 | Manual | | Three person mixed DNA profile Mixture-low support for contrib or supports non contrib |
| TRUE | 0.0195 | Manual | | Submitted-results pending. Three person mixed DNA profile |
| TRUE | 0.023 | Manual | | Three person mixed DNA profile 3 person mix - supports non contribution |
| TRUE | 0.016000001 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.0167 | Manual | | |
| TRUE | 0.0019 | Manual | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0021 | Manual | FAIL | Micro positive for sperm. Submitted-Results pending Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0109 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on |

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|------|-------------|--------|---------|---|
| TRUE | 0.01 | Manual | | |
| TRUE | 0.0174 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0118 | Manual | | |
| TRUE | 0.0244 | Manual | | Submitted-results pending. Single source DNA profile |
| TRUE | 0.0017 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0162 | Manual | SUCCESS | NCIDD upload single source DNA profile Submitted-results pending. |
| TRUE | 0.0108 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0018 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0089 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0139 | Manual | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.0147 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0015 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Micro positive for sperm. Submitted-Results pending |
| TRUE | 0.0013 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0021 | Manual | | |
| TRUE | 0.0011 | Manual | | Semen not detected No DNA profile - possible sub-threshold peaks Submitted-results pending. |
| TRUE | 0.001 | Manual | | No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0094 | Manual | | 3 person mix profile - support for contrib > 100 billion 3 person mix - low support for contribution |
| TRUE | 0.016799999 | Manual | | |
| TRUE | 0.0229 | Manual | | Two person mixed DNA profile 2 person mix - supports non contribution |
| TRUE | 0.028000001 | Manual | | |
| TRUE | 0.0122 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0093 | Manual | | Two person mixed DNA profile |
| TRUE | 0.029899999 | Manual | | |
| TRUE | 0.0015 | Manual | FAIL | Submitted-results pending. Partial DNA profile unsuitable for comparison purposes Submitted-results pending. |
| TRUE | 0.0016 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0013 | Manual | | No DNA profile - possible sub-threshold peaks Submitted-results pending. |
| TRUE | 0.036800001 | Manual | | Three person mixed DNA profile |
| TRUE | 0.0195 | Manual | | Submitted-results pending. Single source 20 loci DNA profile LR > 100 billion |
| TRUE | 0.0189 | Manual | | Possible sub-threshold information |
| TRUE | 0.0012 | Manual | FAIL | Presumptive blood test pos. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison Two person mixed DNA profile |
| TRUE | 0.0118 | Manual | | 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.001 | Manual | | |
| TRUE | 0.0014 | Manual | | |

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|------|--------|--------|------|--|
| TRUE | 0.0014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0021 | Manual | | |
| TRUE | 0.0013 | Manual | | |
| TRUE | 0.0011 | Manual | | |
| TRUE | 0.0016 | Manual | | |
| TRUE | 0.0014 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0018 | Manual | | Submitted-results pending. No DNA profile |
| TRUE | 0.014 | Manual | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.022 | Manual | | Two person mixed DNA profile 2 person mix profile - support for contrib > 100 billion |
| TRUE | 0.0146 | Manual | | Submitted-results pending. |
| TRUE | 0.0305 | Manual | | Submitted-results pending. |
| TRUE | 0.002 | Manual | | |
| TRUE | 0.0195 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0241 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.001 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.0018 | Manual | | |
| TRUE | 0.0187 | Manual | FAIL | Suspect Check Actioned - No Match Suspect Check Actioned - No Match |
| TRUE | 0.0305 | Manual | | Suspect check - supports non contribution Suspect check - supports non contribution |
| TRUE | 0.0306 | Manual | | |
| TRUE | 0.0005 | Manual | FAIL | Presump. PSA test positive, no sperm found Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0002 | Manual | | |
| TRUE | 0.0003 | Manual | | |
| TRUE | 0.0241 | Manual | | Three person mixed DNA profile 3 person mixed profile - conditioned on |
| TRUE | 0.0014 | Manual | | Micro positive for sperm. Submitted-Results pending Submitted-results pending. |
| TRUE | 0.0014 | Manual | | No DNA profile - possible sub-threshold peaks Submitted-results pending. |
| TRUE | 0.0138 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0176 | Manual | | |
| TRUE | 0.0013 | Manual | | Submitted-results pending. No DNA profile - possible sub-threshold peaks |
| TRUE | 0.01 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0149 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0156 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0197 | Manual | | Three person mixed DNA profile 3 person mix profile - support for contrib > 100 billion |

| | | | | |
|------|-------------|--------|---------|---|
| TRUE | 0.0104 | Manual | FAIL | Presump Saliva test negative Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0101 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.001 | Manual | | |
| TRUE | 0.0095 | Manual | | Three person mixed DNA profile Mixture-low support for contrib or supports non contrib |
| TRUE | 0.0143 | Manual | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.022299999 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0112 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0124 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0021 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Single source DNA profile |
| TRUE | 0.0219 | Manual | SUCCESS | Possible sub-threshold information Submitted-results pending. |
| TRUE | 0.0166 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0198 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.015 | Manual | | Three person mixed DNA profile Two person mixed DNA profile |
| TRUE | 0.0275 | Manual | | 2 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| TRUE | 0.0019 | Manual | | Micro neg for sperm |
| TRUE | 0.0019 | Manual | | Micro positive for sperm. Submitted-Results pending Single Source DNA profile - assumed known contributor |
| TRUE | 0.0133 | Manual | SUCCESS | NCIDD upload single source DNA profile Interim result- mixed profile obtained. Rework Reqd |
| TRUE | 0.0132 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0021 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0011 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.030400001 | Manual | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.0011 | Manual | | Sample processed and final results under Submitted-results pending. |
| TRUE | 0.0016 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0012 | Manual | FAIL | Partial DNA profile unsuitable for comparison purposes |
| TRUE | 0.0013 | Manual | | Submitted-results pending. |
| TRUE | 0.0013 | Manual | | No DNA profile - possible sub-threshold peaks Submitted-results pending. |
| TRUE | 0.0014 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0014 | Manual | | |
| TRUE | 0.0012 | Manual | | |
| TRUE | 0.0108 | Manual | | |
| TRUE | 0.0135 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

| | | | | |
|------|-------------|--------|---------|--|
| TRUE | 0.0126 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Micro neg for sperm |
| TRUE | 0.0019 | Manual | | Single Source DNA profile - assumed known contributor |
| TRUE | 0.0007 | Manual | FAIL | ENVM- Complex mixture unsuitable for interp or comparison |
| TRUE | 0.036400001 | Manual | | Micro neg for sperm |
| TRUE | 0.0013 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0009 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes |
| TRUE | 0.0006 | Manual | FAIL | ENVM - Partial profile unsuitable for comparison purposes presump Saliva test positive |
| TRUE | 0.0284 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0276 | Manual | | |
| TRUE | 0.01 | Manual | | |
| TRUE | 0.0164 | Manual | | |
| TRUE | 0.0123 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0012 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0013 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0174 | Manual | | Three person mixed DNA profile 3 person mix - support for contrib 1 million - 1 billion |
| TRUE | 0.0196 | Manual | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0015 | Manual | | |
| TRUE | 0.0117 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0016 | Manual | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.0178 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0017 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0021 | Manual | | Submitted-results pending. Submitted-results pending. |
| TRUE | 0.0012 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0018 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0017 | Manual | | |
| TRUE | 0.044599999 | Manual | SUCCESS | Single source DNA profile NCIDD upload single source DNA profile |
| TRUE | 0.0018 | Manual | FAIL | Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0011 | Manual | | |
| TRUE | 0.031099999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0136 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |

| | | | | |
|-------|-------------|--------|------|--|
| TRUE | 0.0092 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.011 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0218 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.017999999 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.0206 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.034600001 | Manual | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| TRUE | 0.024800001 | Manual | FAIL | Three person mixed DNA profile 3 person mixed profile - conditioned on Submitted-results pending. |
| TRUE | 0.0262 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0092 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0137 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0096 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.016000001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.029200001 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0186 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.018100001 | Manual | FAIL | Micro neg for sperm Submitted-results pending. |
| TRUE | 0.0165 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0108 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0105 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison Submitted-results pending. |
| TRUE | 0.0208 | Manual | FAIL | Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 | n/a | | |
| FALSE | 0 | n/a | | Submitted-results pending. |
| FALSE | 0 | n/a | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 | n/a | FAIL | Presump saliva positive. Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 | n/a | | Three person mixed DNA profile No statistical interpretation performed |
| FALSE | 0 | n/a | | Submitted-results pending. Three person mixed DNA profile |
| FALSE | 0 | n/a | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 | n/a | | Three person mixed DNA profile |
| FALSE | 0 | n/a | | 3 person mix profile - support for contrib > 100 billion Submitted-results pending. |
| FALSE | 0 | n/a | FAIL | Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 | n/a | | |
| FALSE | 0 | n/a | | Submitted-results pending. |
| FALSE | 0 | n/a | | Three person mixed DNA profile |
| FALSE | 0 | n/a | | Three person mixed DNA profile |
| FALSE | 0 | n/a | | No statistical interpretation performed |

| | | | |
|-------|-------|------|---|
| FALSE | 0 n/a | | Submitted as cells Submitted-results pending. |
| FALSE | 0 n/a | | QPS advised no further work required - results available |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 n/a | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 n/a | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | FAIL | ENVM - Partial profile unsuitable for comparison purposes |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | | 3 person mix - supports non contribution Sample undergone further work - conditioned |
| FALSE | 0 n/a | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 n/a | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 n/a | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 n/a | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | FAIL | Submitted-results pending. Complex mixed profile unsuitable for interp or comparison |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | | |
| FALSE | 0 n/a | | Three person mixed DNA profile 3 person mixed profile - conditioned on |
| FALSE | 0 n/a | | Three person mixed DNA profile No statistical interpretation performed |
| FALSE | 0 n/a | | Three person mixed DNA profile 3 person mixed profile - conditioned on |
| FALSE | 0 n/a | | |



QUEENSLAND POLICE SERVICE SUBMISSION TO THE WOMEN'S SAFETY AND JUSTICE TASKFORCE

Discussion Paper 3: Women and girls' experiences across the criminal justice system as victims-survivors of sexual violence and also as accused persons and offenders

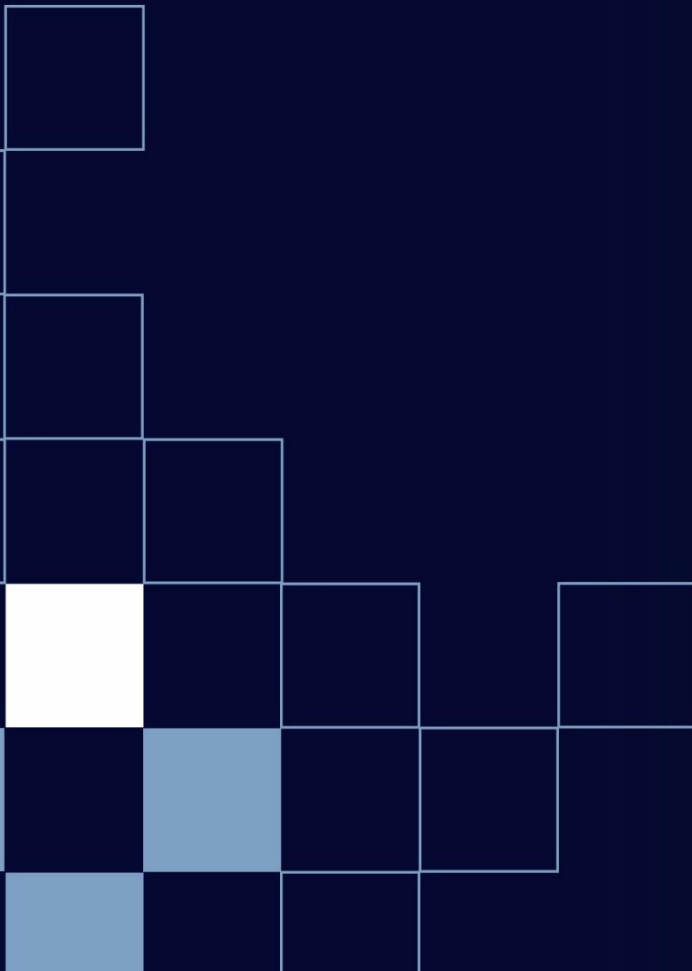


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BACKGROUND

The Queensland Police Service (QPS) welcomes the opportunity to provide this submission to the Women's Safety and Justice Taskforce (the Taskforce) with respect to Discussion Paper 3: *Women and girls' experiences across the criminal justice system as victims-survivors of sexual violence and also as accused persons and offenders* (Discussion Paper 3).

The QPS notes the content within its previous submissions to the Taskforce with respect to [Discussion Paper 1: Options for legislating against coercive control and the creation of a standalone domestic violence offence](#) and [Discussion Paper 2: Women and girls' experience of the criminal justice system \(proposed focus areas\)](#) (Discussion Paper 2). The QPS response to Discussion Paper 3 builds on the information provided in the two previous submissions and for the sake of brevity will not repeat the responses provided in those submissions, noting Discussion Paper 2 is particularly relevant to the issues raised in this discussion paper.

This submission will not address every question in the Discussion Paper but will focus on key elements that fall within the purview of the QPS. The QPS acknowledges and respects the views of people with lived experience of sexual violence and their support networks, and notes the terms victim, victim-survivor and victims-survivors are used throughout this document.

The Role of the QPS

The QPS is the primary law enforcement agency for the State of Queensland. Section 2.3 of the *Police Service Administration Act 1990* (PSAA) outlines the QPS functions which include the preservation of peace and good order, the prevention and detection of crime, and the protection of all communities in the State and all members of those communities. Officers predominantly exercise powers under the provisions of the *Police Powers and Responsibilities Act 2000* (PPRA) and are guided by policy contained in the [Operational Procedures Manual](#) (OPM). Officers also administer functions and exercise powers under a broad range of State and Commonwealth legislation.

The QPS delivers a 24 hour, seven days a week policing service including a first response to reported crime. This service has continued during a time of rapid population growth and unprecedented health and natural disasters which has increased demands for services and placed pressures on the allocation of available policing resources.

The policing environment in Queensland has entered a phase of significant transformation where traditional policing services are being challenged to meet the increasing complexity of policing demand. This transformation is driven by shifting community expectations and rapid technological innovation impacting policing and service delivery in a broader context¹. The growth of powers and obligations contained in the PPRA demonstrates the expanded legislative responsibilities placed on QPS members since the inception of the PPRA.

The QPS organisational chart (Appendix 1) reflects the depth and breadth of QPS responsibilities. There are seven (7) police regions and 15 police districts, supported by specialist commands including the Crime and Intelligence Command and the Domestic and Family Violence and Vulnerable Persons Command. Each command and region is led and managed by an Assistant Commissioner, to provide a decentralised law enforcement response across the State, to meet the demands of their local communities. [Chapter 1](#) of the OPM, particularly s1.4, details the structure of the Service and the responsibilities of key organisational leaders. As at 30 June 2021, the total number of full-time equivalent staff in the QPS was 15,953². This includes 12,139 sworn officers.

General duties police officers provide the first response to the community supported by specialist investigative resources including district Child Protection and Investigation Units (CPIU) and Criminal Investigation Branches (CIB), and Crime and Intelligence Command crime groups. There are a range of other specialist resources available to support policing responses to the community including Vulnerable Persons units, Domestic and Family Violence units, the First Nations and Multicultural Affairs unit, First

¹ QPS Annual Report 2020-21

² Report on Government Services 2022

Nations police liaison officers and cross-cultural liaison officers.

The Role of the CPIU

The CPIU format is unique in Australia and is staffed by highly trained, skilled and professional investigators. All police regions have CPIU officers who provide a specialist policing response, primarily focused on the investigation of criminal matters pertaining to child protection and youth justice issues. These dedicated officers provide an ongoing response to the safety of children within the community, where a situation has escalated to a point when police are required to respond.

The role of the QPS in the child protection system is principally the investigation of crimes committed against children (up to 16 years old). Generally, investigations fall into the broad categories of sexual abuse, physical abuse, and serious neglect where there is a suspected criminal offence. The CPIU is responsible, in some areas, for the investigation of criminal offences committed by children, including offences committed upon other children. The QPS' primary contribution to the child protection system is the provision of investigative expertise. Where there is no CPIU office available, the local CIB will assume responsibility for the investigation. If there is no CIB office, first response police will undertake the investigation (at least initially) with specialist assistance provided remotely.

The role and functions of the CPIU has grown over time to accommodate government and community expectations. The responsibilities have increased in response to legislative and policy change, responding directly to emerging social issues, and undertaking work on behalf of other agencies, particularly after hours and in rural and remote areas where those agencies have no physical presence.

The evolution of the policing role and function means CPIU investigators now assume responsibility for a wider variety of duties than ever before, including the following:

- Criminal investigations involving children as victims
- Forensic interviewing of child witnesses
- Investigation of general child protection notifications, particularly sexual and physical abuse
- School based investigations
- Child death investigations and internal child death and serious injury reviews
- Child exploitation investigations and other technologically facilitated crime
- Registration and ongoing monitoring of registered child sex offenders
- Suspected Child Abuse and Neglect (SCAN) team core member responsibilities
- Screening and investigation of domestic violence matters involving children
- Blue card services investigations and compliance activities
- Youth justice investigations, including conferences and diversions
- Missing child investigations including amber alerts
- Assistance to interstate counterparts for child protection investigations
- Information management and release of information to other agencies
- Delivery of training and education to internal and external stakeholders
- General policing roles as required, including major events and disaster management policing
- Establishing and maintaining local child protection and youth justice network relationships.

Suspected Child Abuse and Neglect (SCAN) teams

Chapter 5A, Part 3: 'The SCAN system' of the *Child Protection Act 1999* (CPA), establishes the SCAN team system, purpose, membership and core members and the responsibilities of its core members. The purpose of the SCAN team system is to enable a coordinated, multi-agency response to children where statutory intervention is required to assess and meet their protection needs. This is achieved by timely information sharing between SCAN team core members; planning and coordination of actions to assess and respond to the protection needs of children who have experienced harm or risk of harm; and holistic and culturally responsive assessments of children's protection needs.

The Service is a core member of the SCAN system. The criteria for a SCAN team referral is based on s.10: 'Who is a child in need of protection' of the CPA and relates to a child who has suffered harm, is suffering harm or is at unacceptable risk of suffering harm (per s9 CPA); concern that the child does not have a parent able and willing to protect the child from the harm; and a SCAN team core member believes

coordination of multi-agency actions and/or expert advice from more than one core member representative is required to effectively assess and respond to the protection needs of the child.

Technology facilitated crime

As well as a focus on child protection contact offending, CPIUs across the state, with the support of specialist investigators in Argos, also respond to online or technology facilitated child exploitation offences. This includes serial or organised paedophilia, proactive investigation of child sex offenders utilising the internet, possession, production and distribution of child exploitation material as well as self-produced child exploitation material.

Self-generated sexualised imagery, both pictures and videos, amongst teenagers continues to be a source and a concerning trend for CEM production. The most common age of offenders is between 13 and 15 years, predominantly shared via social media messaging applications (i.e. Snap Chat, Kik Messenger). The volume of self-generated CEM propagates the ongoing sexual exploitation of children and creates future vulnerabilities for children to be extorted and exploited.

Identifying the producers of CEM is an essential aspect of the work of the QPS unit dedicated to online child exploitation (Argos) as it most likely leads to rescuing a child from harm, which is the primary objective of that unit.

Significant numbers of images of children being sexually exploited continue to be seized on a regular basis during the course of police investigations into online sex offenders. QPS works with the Australian Centre to Counter Child Exploitation (ACCCE), national and international partners to process this material and analyse it for clues in relation to the identity of those child victims. The team is made up of international experts in the field of investigating online child sexual exploitation and digital media analysis and make the best use of available technology, intelligence and investigative resources to achieve their results. The team provides a response to requests for assistance in relation to child victim identification investigations. They also provide a high level of service, technical expertise and advice for service-wide victim identification strategies.

There are significant challenges faced in relation to technology facilitated sexual violence. The decentralised nature of the internet makes the control of online actions and content extremely difficult as no single governing body has ownership. Instead, each interconnected autonomous network is responsible for the enforcement of bespoke policies and rules based on internal company policies and jurisdictional legislation. With many communications providers based overseas, there are significant delays in seeking investigative information through conventional Mutual Assistance Request (MAR) protocols. With the recent signing of the 'Agreement between the Government of Australia and the government of the United States of America on access to electronic data for the purpose of countering serious crime', it is hoped these investigative delays will be greatly reduced when International Production Orders are introduced in late 2022 or early 2023.

Significant work has been undertaken across Australia in relation to the reporting of cybercrime related incidents. The Australian Signals Directorates (ASD) and the Australian Cyber Security Centre (ACSC) have been established to manage the operation and sustainment of existing cyber capabilities nationally.

The establishment of ReportCyber <https://www.cyber.gov.au/acsc/report> created a portal for members of the public to report cybercrime related incidents. The reporting of any threat or violence against women or children in any situation should be directed to a police officer for an immediate response, however, such reports can and have been reported through the ReportCyber portal including incidents of domestic violence, violence against women and vulnerable persons in general.

All matters reported via the ACSC ReportCyber portal are reviewed and triaged before being referred via the ReportCyber Application Platform to the respective state or territory for incident response. The ReportCyber Application Platform board continues to review and update the capabilities of the application platform to ensure it remains contemporary and responsive to the community needs.

The Financial and Cyber Crime Group within Crime and Intelligence Command is responsible for the receipt of information referred via the ReportCyber Application Platform. Officers attached to the Cyber Reporting Unit review all matters received via this platform with access to the system being available

from both their work and home environments.

All matters are triaged and prioritised against a risk assessment tool which provides a rating with Category 1 being the highest risk to community members.

| | |
|---|--|
| 1 | Any report (irrespective of category) with a Threat To Life (TTL) key word match OR victim is under 18 at time of report OR the report is a FKC (Financial Kill Chain) report. |
| 2 | Cyber stalking/harassment/bullying OR Online Image Abuse (OIA) |
| 3 | Fraud OR Identity Fraud + total loss > 250 000 |
| 4 | Fraud OR Identity Fraud |

Category 1 and 2 matters include matters which references any threats to life, suicide or domestic violence, including coercive control. These matters are dealt with as a matter of urgency and actioned within 12hrs.

The creation of the ReportCyber Application Platform has made it far easier for members of the public to report cyber related offences. The number cybercrime matters reported continues to increase, suggesting both an increase in cybercrime and the likelihood that there exists a greater level of awareness amongst the community to report.

Child Protection / Youth Justice

Traditionally CPIUs have played a major role in investigating and combating juvenile crime. This has been the preferred method of dealing with juvenile offenders, with CPIU staff being specifically trained and possessing a higher level of experience in enacting the provisions of the *Youth Justice Act 1992* (YJA) pertaining to restorative and diversionary justice measures. One of the key emerging issues for CPIU investigators includes the increased complexity and degree of offending by young people. Youth justice investigations have been traditionally conducted by CPIU officers, who consider diversionary options as a first response to a young person's offending behaviour. The investigation of crimes committed by young people requires additional safeguards and procedures to be utilised to ensure the youth justice principles in the YJA.

It is considered there is a significant overlap between children known to both the child protection and youth justice systems. CPIUs have historically tried to maintain a balance between youth justice and child protection work in order to provide a specialist response to all matters in which children have either committed offences or had offences committed against them. However, the time available for CPIUs to devote to youth justice investigations is decreasing as the volume of child protection matters increases. It is noted the implementation of legislative amendments to include 17 year olds in the youth justice system in February 2018 contributed to the increased demands on youth justice responses by the QPS.

The extraneous duties and escalation of CPIU workload as outlined above, means that CPIUs have less opportunity to attend to youth justice investigations and thus may not have the desired degree of interaction and engagement with children in the overlapping child protection and youth justice systems. Working with young people who are involved in both systems allows police to attempt to address deteriorating behaviours at an early stage. The inability to devote time to such matters also means that the 'overflow' of youth justice investigations the CPIU do not have capacity to deal with, are devolved to other police, primarily the CIB and district crime units.

The role of CIB

The CIB is responsible for delivering specialist investigation services across each QPS district in response to serious indictable/criminal offences. The range of offences includes homicide, robbery, arson, property and fraud offences, and personal and sexual violence committed against adults. Increasingly, CIB investigators are also involved in youth justice investigations, particularly when dealing with property offences such as burglary and unlawful use of motor vehicles, and offences of violence committed by young people and as members of criminal street gangs.

Crime and Intelligence Command

The Crime and Intelligence Command (CIC) commenced on 31 August 2020 as a result of the merging of State Crime Command and the intelligence component of the Intelligence and Covert Services Command. The merging of the specialist capabilities of crime and intelligence allows the Command to assist the frontline in protecting our community by delivering integrated and adaptable intelligence and investigative services to prevent, disrupt, respond and investigate crime.

The Command comprises of five (5) specialist crime groups (Child Abuse and Sexual Crime, Drug and Serious Crime, Financial and Cyber Crime, Homicide and Organised Crime Gangs groups) and two (2) intelligence groups (Intelligence Directorate and State Intelligence Group).

The members of CIC are responsible for state-wide provision of specialist crime and investigative expertise; coordination of state-wide and/or major criminal investigations, both within and outside the State; enhancing the Service's approach to intelligence to support serious, major and organised crime investigations and frontline policing operations; liaison with other law enforcement agencies; and representation of the Service both interstate and nationally on crime related matters.

Child Abuse and Sexual Crime Group

The Child Abuse and Sexual Crime Group (CASCG) aims to protect children and the community by identifying, responding to and preventing physical and sexual offending. The Group is led by a Detective Superintendent who is also the QPS Child Safety Director, and comprises of the following units:

- Argos, principally responsible for the investigation of organised paedophilia, child exploitation and computer facilitated child exploitation
- The Child Trauma Unit, which provides assistance in investigative and operational aspects on all sudden unexplained deaths of children (SUDI), suspicious child deaths and serious injury resulting from suspected child abuse and/or neglect
- The Sexual Crime Unit, which reviews unsolved adult rape investigations, investigates serious or complex cases of serial rape and sexual assault, and provides specialist investigative assistance to regional counterparts.
- The Child Protection Offender Registry (CPOR), which assists in the management and investigation of reportable offenders residing within the community. CPOR also includes a team of forensic behavioural analysts to support effective management of reportable offenders
- The Youth Justice Unit, which provides support to regions in relation to youth justice responses
- The Policy and Programs Unit, which fulfils a broad range of operational policy, training and corporate functions to support the Commissioner, the QPS Child Safety Director and regional Child Protection and Investigation Units.

In March 2021, the CASCG assumed responsibility for Service capability in relation to sexual crime, to ensure a coordinated, consistent and collaborative QPS response to sexual violence. The CASCG is responsible for leading the implementation of the QPS [Sexual Violence Response Strategy 2021-23](#).

Specialist Investigative Units Staffing

As of 28 February 2022, the QPS approved permanent positions for CPIU officers (including CPOR investigators) was 640, and substantive headcount^[1] was 608. This is comprised of specialist CPIU officers in each of the 15 QPS districts. Specialist investigators are also located within CIC, and there are 21 SCAN team representatives.

Likewise, the approved and actual strength of CIB units is 841 and 819 respectively. By gender, approximately 23% of CIB officers are female, compared to approximately 45% of CPIU investigators.

These figures are represented in the tables below:

| Allocation | Approved Permanent positions | Substantive Headcount |
|------------|------------------------------|-----------------------|
| CPIU | 640 | 608 |

^[1] Approved permanent positions relate to all permanent positions. The substantive person refers to substantive people occupying positions (some could be on leave, does not account for part-time arrangements).

| | | |
|-------------------------------|-------------|-------------|
| CASCG | 78 | 72 |
| SCAN | 22 | 21 |
| CIB | 841 | 819 |
| CIC (other than CASCG) | 405 | 390 |
| Total | 1986 | 1910 |

| Allocation | Female | Male |
|-------------------------------|------------------|-------------------|
| CPIU | 271 (45%) | 337 (55%) |
| CASCG | 31 (43%) | 41 (57%) |
| SCAN | 11 (53%) | 10 (47%) |
| CIB | 196 (23%) | 623 (77%) |
| CIC (Other than CASCG) | 72 (19%) | 318 (81%) |
| Total | 581 (30%) | 1182 (70%) |

When viewed in the context of the vast array of duties undertaken by investigators, these figures demonstrate the responsibility for completing this volume of work rests with a relatively small proportion (approximately 16%) of QPS sworn personnel. This workload presents significant challenges in terms of resource allocation, prioritisation, demand management and the ongoing psychological wellbeing of staff.

The Queensland Government committed to 2025 extra police personnel by the year 2025. The QPS is using part of this allocation to expand its capacity to respond to vulnerable person related crimes. By example, in the 2020/2021 Financial Year the existing 22 regional CPOR officer positions was supplemented by the allocation of an additional 19 permanent positions, increasing the dedicated regional capacity to 41 investigator positions. In 2022, the QPS will give consideration to the allocation of additional officers to other specialist units including CPIU, CIB and DFV VPU's to meet increasing demand.

Training

Training is a pivotal component of police work and is particularly relevant for CPIU and CIB officers due to the specialised nature of their duties. This in itself creates an issue in terms of allocating time to complete such training, maintaining mandatory training qualifications and completing specialised training as the need arises.

Officers selected to perform duty within the CPIU undertake a rigorous and meritorious selection process, including psychometric testing to assess their suitability for the role, and are subject to specialist training to perform the roles of a CPIU officer.

Unless already qualified, on appointment to a designated CPIU or CIB position, officers are required to complete the Detective Training Program as a qualification for appointment to Detective status. This program is mandatory for all staff being selected to undertake plain clothes, investigative roles within the QPS. Officers who successfully complete the program receive an Advanced Diploma of Public Safety (Police Investigations). The program requires an officer to attend three residential phases at the Queensland Police Academy in combination with workplace assessment and competency achievement. On average, a Detective appointment can take up to four years to attain.

In addition to compulsory training, specialist training to CPIU and CIB officers includes:

- Interviewing Children and Recording Evidence (ICARE) training (CPIU specific)
- Child Protection and Youth Justice Specialist Investigator's Course
- Investigative Interviewing
- Investigating Sexual Assault – Corroborating and Understanding Relationship Evidence (ISACURE)
- Fundamentals of Child Interviewing Skills (FoCIS)

- Child Sexual Abuse Fundamentals Education (CSAFE) Online Learning Product (OLP)
- CPOR OLP.

The People Capability Command (PCAP) Specialist Investigations Team (SIT) has six facilitators and one senior sergeant to deliver specialist training to plain clothes and detectives across the State in specialist and investigative course curriculum.

The SIT officers are also assisting the Domestic and Family Violence and Vulnerable Persons Command (DFVVPC) in the development of training products related to the trial of the use of video recorded evidence of victims of domestic and family violence (DFV). The online and face to face training will focus on trauma and investigative interviewing techniques, in addition to legislative requirements for the trial.

Also considered necessary for investigators are speciality workshops and training in the use of technology to assist investigations relating specifically to 'cyber' crime and technology enabled crime, including the Digital Field Triage Investigators Course (DFTIC) run by CIC, which skills officers to undertake digital evidence collection in-field.

Part 1 – Cross-Cutting Issues

- *Overrepresentation of Aboriginal and Torres Strait Islander women and girls in the criminal justice system as both victims and offenders*
- *Intersecting experiences of disadvantage*
- *Recognising and responding to trauma*
- *Protecting and promoting human rights*
- *Resourcing, investment and value for money*
- *Appropriate governance and accountability mechanisms*

The QPS recognises and acknowledges the significant impact of the cross-cutting issues identified in Discussion Paper 3, not only for women and girls in the criminal justice system, but also for the involved government, private and non-government stakeholders. Where relevant and appropriate, these issues will be addressed elsewhere in this submission. However, it is important to note in this section the legislation, policies and strategies the QPS is committed to ensure awareness of, and respect for, these issues.

Obligations under the *Human Rights Act 2019* (HRA) are embedded through policies, procedures and training products, including compulsory training for all QPS members. Training is also compulsory in relation to inclusion and diversity (relative to culture and gender), domestic and family violence and coercive control.

The QPS Operational Procedures Manual (OPM) provides guidance on application of legislation, policies and best practice policing responses to members of the community. The OPM addresses many of the cross-cutting issues identified in Discussion Paper 3. Relevant chapters of the OPM include:

- [Chapter 2 “Investigative Process”](#) provides direction in relation to specialist investigations including sexual offences. It is noted this section of the OPM is being updated and will be published in June 2022. The updates reflect the additional responsibilities of the Sexual Violence Liaison Officers, and updates current information to reflect the intent of the QPS, through the [Sexual Violence Response Strategy 2021-23](#) in responding to sexual violence. A copy of the revised draft OPM section is attached (Appendix 2)
- [Chapter 5 “Children”](#) outlines the extraordinary practice and procedures in place to respond to young offenders
- [Chapter 6 “Persons who are vulnerable, disabled, or have cultural needs”](#) provides direct links to relevant legislative provisions relating to identified vulnerabilities, and guidance on how to identify and respond to vulnerable members of the community
- [Chapter 7 “Child Harm”](#) relates to children at risk of harm or who have been harmed
- [Chapter 9 “Domestic Violence”](#) outlines policy and procedures for managing domestic violence incidents and providing assistance to members of the community who may be affected by domestic violence.

In addition to the OPM, specialist units and officers are available to assist investigators and first responders to identify and address vulnerability. The Communications, Culture and Engagement Division of the Service (Appendix 1 – Organisational Chart) includes the First Nations and Multicultural Affairs Unit (FNMAU), which aims to promote and maintain effective relationships with our diverse communities based on open communication, mutual understanding, respect, tolerance and trust. Included in this portfolio are Police Liaison Officers, First Nations and Multicultural Networks, and the Police Multicultural Advisory Group. The DFVVPC leads Vulnerable Persons Units across the State. The role of the DFVVPC and the Vulnerable Persons Units is outlined in QPS response to Discussion Paper 2. The CASC and District CPIUs consider intersecting and cross-cutting issues relating to children, and the QPS SCAN representatives are core members of the SCAN team system, which aims to provide a coordinated multi-agency response to the protection needs of children.

Police Liaison Officers (PLOs) are available to assist in supporting First Nations (FN) victims. In 2021 the Queensland Government committed to supporting growth of 65 new PLO positions. To date, 18 PLO growth positions have been provided to districts, with a staged rollout of the remaining positions throughout 2022/2023. Identification of districts to receive initial PLO growth positions was undertaken in consultation with districts and the Human Resources Unit as well as through community engagement and review of sentiment data.

The QPS launched the campaign “What’s your Story” during Harmony Week (21 to 27 March 2022), encouraging members of the Service to record their cultural background on the Human Resources system. While there is a requirement to meet the government aggregate target of 3%, the primary benefit of this information is that knowing where FN members are located throughout the state will assist in responding to critical or sensitive jobs involving FN issues/matters. These officers will also be able to assist in building relationships and connections with community.

Discrete community specific profiles were developed in 2021 and are able to be shared with regional police officers through engaging FNMAU. Following content review, the profiles will be made available to police through the FNMAU internal web pages.

Also under development is a First Nations Protocol. Following the establishment of a Police First Nations Advisory Group (PFNAG), the PFNAG will lead consultation with community to ensure community support prior to the endorsement and publication of the protocol.

All members of the QPS are obliged to complete the SBS Inclusion Program – Aboriginal and Torres Strait Islander Course, which was introduced on 1 February 2022. This course is designed to assist members in understanding the importance and advantages of Australian indigenous cultural diversity. The course is compulsory for all members of QPS with a due date of 30 June 2022.

The PCAP Recruitment Training unit is also conducting a review of recruit training and will take the opportunity to implement FN Cultural Intelligence training within the current recruitment training curriculum, in consultation with FNMAU and key stakeholders.

Supporting the steps being taken by the QPS, the [Australia New Zealand Policing Advisory Agency](#) (ANZPAA) recently released the *Australia and New Zealand Police Anti-Racism and Cultural Diversity Principles*, which reflect the commitment of all police commissioners to promote and advance anti-racism and cultural diversity.

The QPS recognises people of diverse genders, sexualities and sex characteristics, who are often referred to as lesbian, gay, bisexual, transgender, intersex, queer/questioning, and other identities represented by + in the acronym LGBTIQ+, are not a homogenous group; they have unique and distinct needs with diverse experiences and backgrounds. The QPS acknowledges that the relationship with LGBTIQ+ people, both from a historical and contemporary context, has not always been consistent with professional practice and community expectations. More broadly, people who are perceived to be different, including LGBTIQ+ people, are often subjected to violence, harassment, bullying and discrimination by those who are biased or ill-formed. The QPS is committed to strengthening relationships with the community to stop crime and make the community safer.

The QPS LGBTI Liaison Program began in 1997, to establish and maintain effective liaison between police and LGBTIQ+ communities. The program enables appropriate policies and strategies to be developed to ensure the delivery of an equitable service across the State. Integral to the Program is LGBTI liaison officers, who have completed specific LGBTIQ+ training and undertake their role in a

voluntary capacity in addition to their usual duties. LGBTI liaison officers are located across the State and can assist during investigations and other interactions with LGBTIQ+ people. An LGBTI liaison officer contact list is available for police and community members on the [QPS website](#).

Question 6: How are the impacts of trauma for women and girls understood and exercised at each point across the criminal justice system?

Question 7: How can the impacts of trauma be better recognised and responded to at each point across the criminal justice system?

The issues relating to impacts of trauma were explored in the Royal Commission into Institutional Responses to Child Sexual Abuse (the Royal Commission). The Royal Commission published its Criminal Justice report in August 2017, which included a number of recommendations to implement victim-centric, trauma informed responses to victims of child sexual abuse. These recommendations included training, alternative reporting options for vulnerable groups, and an intermediary scheme to support witnesses with communication difficulties to give their best evidence.

As mentioned in the QPS response to Discussion Paper 2, the QPS has commenced delivery of new and updated victim-centric and trauma-informed training products, to improve the QPS response to victims of sexual violence at all levels. This training package has been developed in partnership with the University of Queensland resultant from the Royal Commission and aligns with the ‘start by believing’ philosophy.

Some of the factors that may exacerbate trauma include lack of sentinel support for the victim throughout the course of the criminal justice process and beyond; the complexity of the system and the length of time taken to navigate and complete the process; navigation of forensic examination, including timeliness of the examination; and evidentiary requirements that may seem confronting (e.g. explaining the acts in detail, potentially on multiple occasions) and could be perceived as victim-blaming (e.g. what were you wearing, had you been drinking) but are required in order to prove or support elements of the offence and/or assist in the identification of evidence.

This submission will recommend the implementation of a process to electronically record a victim’s statement at the time of complaint, and to ensure the statement is a free narrative that provides a “whole story”, which can be used in any subsequent proceedings as evidence-in-chief of the witness.

The impacts of trauma can also be seen in children who are placed into care for their own safety, but is sometimes misidentified when the trauma is exhibited through extreme and challenging behaviours and police are called to respond. A recent Community Support and Services Committee [report](#) on the *Criminal Law (Raising the Age of Responsibility) Amendment Bill 2021* discussed concerns from stakeholders about the “criminalisation of the care system” when a child is placed into the care of the Department of Children, Youth Justice and Multicultural Affairs (DCYJMA), citing a stakeholder’s submission that “*there is evidence to suggest that for children in care there is a practice of relying on police and the justice system in lieu of adequate behavioural management*”. This issue is raised in this submission, noting that many children entering the care system have experienced trauma, and that a therapeutic response to behaviour borne of trauma is likely to result in better long-term outcomes for the child than a police response, thus preventing entry into the criminal justice system.

Question 8: How are the risks of vicarious trauma and compassion fatigue recognised and addressed by those working in Queensland’s criminal justice system? What works? What needs to be improved?

Primary (Preventative Interventions)

The inaugural QPS Wellbeing Strategy released in 2021 has identified several primary, secondary and tertiary interventions to support our people’s physical, social and psychological wellbeing. The Strategy identifies 24 initial recommendations that aim to provide education and awareness of wellbeing and psychological injuries such as vicarious trauma (VT) and compassion fatigue (CF). Further, there are several recommendations targeted at uplifting our internal health and wellbeing services to provide support for such psychological injuries. Whilst there are no specific recommendations regarding VT and CF, the overarching purpose of the Strategy is to increase awareness, reduce stigma and foster a supportive culture of comradery, where mental health and wellbeing is an organisational priority.

The QPS Psychological Assessment Unit conducts comprehensive, psychological assessments for all police officer applicants upon their entrance to the QPS; with the aim of screening individuals’ suitability

to policing and the inherent stressors in policing that can lead to outcomes such as VT and CF. Similarly, psychological assessments are also conducted as a mandatory requirement to work within identified high risk areas such as CPIU and CASCG.

The need for specific training regarding VT and CF has been recognised in a recent desktop review within the Recruit Training Program. Development of this content is currently underway with subject matter experts from within Safety & Wellbeing and Recruit Training Unit. Psychological injuries similar to VT and CF are explored within the 'Psychological Health and Fitness' OLP. Specifically, recognising the signs and symptoms in oneself and others, as well as help seeking and support options that our members can engage in themselves or via the extensive internal wellbeing support options.

The Senior Psychologists/Senior Social Workers within the QPS Employee Wellbeing unit also provide specific wellbeing workshops to plain clothes officers and detectives during their various training courses, which aim to provide insight into protecting wellbeing from such injuries. These workshops focus on foundationally understanding one's own wellbeing, preventing psychological injury and seeking help early.

The links between physical and mental health are well established in academic literature. The QPS has a team of exercise scientists and dietitians/nutritionists (HealthStart) who aim to provide preventative physical health interventions at a workplace and organisational level which invariably seeks to protect the mental health of our members.

Specialist high risk areas within the QPS including the CASCG and the Electronic Evidence Unit maintain staff wellbeing policies to minimise the risk of harm to its members. Since 2008, the CASCG has adhered to a policy to support the welfare of officers working within the Group, noting the variety of functions undertaken including viewing child exploitation material, direct contact with reportable offenders, investigating child death and serious injury, and investigating sexual offences (current, historical and serial or complex offences against adults). The policy includes a requirement to be psychologically assessed prior to commencement in the Group, and every six or twelve months thereafter; obligations on staff and supervisors to monitor themselves and colleagues and check in regularly; options to self-identify when psychological wellbeing is suffering and be supported to spend time away in another role; and to not view CEM within two hours of the end of their shift.

Secondary (Early Interventions)

The Psychological Assessment Unit also conducts annual Psychological Health Monitoring (PHM) with members of the CASCG, in accordance with the CASCG welfare policy. The intention of the annual PHM is to identify early, signs of poor wellbeing or mental injury in our high-risk areas and subsequently refer them to the appropriate internal and/or external services.

Our voluntary Peer Support Officer (PSO) network receive a comprehensive face-to-face training package which provides them with the tools to be a state-wide internal support option for all staff, but particularly those in high-risk roles. The PSOs can provide early intervention and support to our members and provide a referral to a professional internal wellbeing support option (i.e., Chaplain or Senior Psychologist/Senior Social Worker) or external wellbeing support such as a GP or community support group (i.e., Fortem Australia, LifeLine etc.).

Tertiary (Reactive Interventions)

Employed within the Safety and Wellbeing unit are a number of allied health professionals who are able to provide support to members who are experiencing a psychological illness, injury or significant distress. The QPS employs Senior Psychologists/Senior Social Workers and Chaplains who are able to provide professional, brief mental health intervention and subsequent referral to an appropriate external provider for long-term mental health intervention if required. Our support services have subject matter expertise in psychological illnesses such as VT and CF and can provide bespoke support to members experiencing such.

External support options provided by the QPS include the Early Intervention Treatment Program (EITP), 1800 ASSIST, 1800 4QPS DFV and 1800 Speak Safe. The QPS is also in the final stages of implementing an additional Self Refer program, whereby members can seek completely confidential treatment through external providers contracted to render treatment services, with expertise in first responder matters.

Question 9: What are your experiences or observations about how the rights of women and girls

who are involved in the criminal justice system as either victims-survivors of sexual violence or accused persons or offenders are protected and promoted?

As mentioned previously, the QPS obligations under the HRA are embedded in policies, procedures and training. Similarly, the QPS requires officers to adhere to the Charter of Victims' Rights enshrined in the *Victims of Crime Assistance Act 2009*. The Memorandum of Understanding between the QPS and the Office of the Director of Public Prosecutions (ODPP) respecting the communications between the ODPP and the QPS in sexual offence prosecutions also provides guidance in relation to responsibilities to victims when considering discontinuance of, or substantially reducing, charges against a person accused of sexual crime.

The QPS obligations to victims of crime are reflected throughout the OPM and reinforced in training to police. The training components include understanding sexual crimes, understanding trauma, how to communicate with people with known vulnerabilities including ensuring access to support persons and interpreters, and ensuring the victim understands the criminal justice process and is kept informed of all aspects of the investigation and prosecution.

There are numerous safeguards in legislation and policy to protect and promote the rights of offenders in Queensland. However, these rights and protections are considered gender neutral and apply equally to all offenders. Key safeguards can be found in the *Youth Justice Act 1992* and the *Police Powers and Responsibilities Act 2000*. These safeguards extend to provisions relating to the questioning and interviewing of offenders including special requirements for particular people including Aboriginal peoples and Torres Strait Islander peoples, children, persons with impaired capacity and intoxicated persons. Other safeguards address arrest and custody powers, search warrants, crime scene powers and obtaining personal particulars including DNA from offenders.

Question 10: What are the impacts and implications for women and girls who are victims-survivors of sexual assault if matters are delayed across the criminal justice system?

Evidence shows delays in the criminal justice process can be detrimental to victim-survivors. Anecdotally, there have been instances where victim-survivors have lost faith in the justice system and withdrawn their complaints. There have been instances where delays in investigations, particularly relating to historic and unsolved investigations, has led to the loss of evidence.

As mentioned previously (refer page 11), issues relating to the timeliness of forensic examinations has had a detrimental impact on victim-survivors. From an investigative perspective, the length of time taken to obtain the results of the forensic examination can impact on the time taken to complete an investigation and progress a matter to its conclusion. This can cause frustration for a victim, particularly if they do not have sentinel support to guide them through the criminal justice process. This submission will outline concerns regarding the capacity of the sexual assault support service sector to meet demand, and the impediments to providing consistent and sustained support to a victim from the initial decision whether to make a complaint to police to the conclusion of all proceedings and beyond.

Part 2 - Women and Girls' Experience as Victim-Survivors of Sexual Violence

Community understanding of sexual offending and barriers to reporting

The QPS response to Discussion Paper 2 highlighted the focus of cultural and attitudinal change in the Queensland Government's *Prevent. Support. Believe. Queensland's Framework to Address Sexual Violence* and the *Domestic and Family Violence Prevention Strategy 2016-2026*. The QPS [Sexual Violence Response Strategy 2021-23](#) (Strategy) also identifies the importance of engaging the Queensland community, to provide accessible information about sexual violence and the roles of each stakeholder in the criminal justice system.

The aims of the Strategy under the priority of "empower our community" are to:

- Increase community awareness of the QPS role as part of an integrated system response to sexual violence
- Support tailored strategic and evidence-informed prevention activities for diverse population

- groups in collaboration with government and nongovernment agency partners; and
- Increase awareness of identified and anonymous reporting avenues, and alternative justice options

To action these aims, the QPS has implemented a communication strategy (Appendix 3), which includes external media and communication, to provide information and resources to the community to:

- increase community awareness of sexual violence and its underreporting
- encourage more victims to come forward by highlighting the choices available to them, including the traditional and alternative reporting options available
- highlight how the QPS is taking meaningful action to better meet the needs of victims
- raise awareness of the QPS' role in responding to sexual violence, including how the QPS supports and assists victims and collaborates with partners.

Attitudes to consent including impacts of pornography

It is the QPS' position that the law in respect of rape and sexual assault must be unambiguous and readily enforceable. There must not be any unintended consequences arising from any reform to the current law that may undermine enforceability.

Investigators need to be able to assess the strength of a case based on the available evidence. Clarity in the law ensures there is certainty as to the evidentiary requirements to fulfil the elements of an offence to the required standard.

It is not uncommon for QPS investigators to encounter circumstances where there has been an absence of verbal or physical resistance (including a 'freeze' response) from the victim in a sexual violence case. A lack of resistance does not equate to consent, and the legislation could be clarified by providing explicit recognition of this.

Misinformation about sexual violence is considered a barrier to reporting sexual violence and effective public education campaigns to counter this would be beneficial.

QPS collaboration with Match Group (of which Tinder is a subsidiary) is discussed later in this submission (page 18) and highlights how the QPS is working with stakeholders to educate and better protect the public.

Question 25: Is the current approach in Queensland to the non-consensual sharing of intimate images striking the right balance between criminalising non-consensual behaviour and community education?

In February 2019, new offences relating to the distribution of intimate images came into effect. The sharing of intimate images, commonly referred to as 'sexting', is the act of taking sexually explicit images or videos and distributing the material to partners, friends or anyone else via mobile phone or any other communication method. Once an intimate image is transmitted, the owner of the image or anyone else depicted in the image loses control of it. This means that the recipient of the image, or a person who has accessed the image through other means such as computer hacking, could further distribute the image or upload it to a public forum without the owner's consent. In some cases, recipients of the image might use blackmail for further images or for money by threatening to post the already received image. This can happen to anyone, regardless of the relationship to the recipient.

In Queensland, it is a criminal offence if a person shares an intimate image of another person without their consent in a way that would reasonably cause them distress. It is also illegal if a person threatens to share an intimate image without the person's consent in a way that would cause them fear of the threat being carried out. This applies whether a person threatens the person depicted in the intimate image, or anyone else. This offence applies even if the image does not exist.

Information is provided on the Queensland Government website and on the QPS website for members of the community, with advice to contact the office of the E-Safety Commissioner and seek advice on techniques and strategies to remove the images.

During the development of the *Criminal Code (Non-consensual Sharing of Intimate Images) Amendment Bill 2018* (Intimate Images Bill), feedback indicated that the sufficiency of Queensland's response to CEM offending by children warranted further consideration.

The issue of concern for stakeholders was that Queensland law does not provide adequate protection for children who engage in sexting within their peer group which prima facie would constitute a CEM offence but lacks predatory-type conduct usually associated with these offences. A child convicted of a CEM offence might also be a reportable offender under the *Child Protection (Offender Reporting and Offender Prohibition Order) Act 2004*.

The QPS undertook to review the charging of children with CEM as part of its implementation of the Queensland Government Youth Justice Strategy, in consultation with the Department of Justice and Attorney-General (DJAG) and the then Department of Youth Justice.

Since the passage of the Intimate Images Bill on 13 February 2019, the QPS undertook significant steps to address those concerns including amending policies (refer section 7.11.3 OPM) in relation to sexting, adding similar policies in relation to intimate images offences and reinforcing the focus upon diversion in accordance with the *Youth Justice Act 1992*.

Between 1 July 2019 and 30 June 2021, a total of 738 children aged 10 to 17 inclusive came to the attention of the QPS for CEM offending. These offences included making, distributing, and possessing CEM under the Queensland Criminal Code and similar Commonwealth offences. Of these, approximately 726 children were dealt with including 44 through no further action, 577 diverted from the criminal justice system through cautioning, 30 receiving community conferencing or 75 via other action, with a focus on educative responses and encouraging children to accept responsibility for the impact of their actions.

A small number of children (11, or 1.5%) were charged with an offence, as they participated either in non-consensual behaviour, very serious offending, including violent offending, or consensual behaviour associated with other offending which led to formal charges.

Following identification of CEM charges relating to footage of assault and robbery (a schoolyard fight), advice was provided to QPS officers on the factors to be considered before charging a child with a CEM offence. These include whether there are more appropriate offence options, whether it is in the public interest to charge the child with CEM offences, the intent and spirit of the child exploitation legislation, and implications for the child including the potential to become a reportable offender if convicted on more than one CEM offence.

The QPS continues to reinforce messaging to specialist police regarding the importance of diversion and educative options for children being investigated for CEM offences and the matters to consider prior to charging children.

Question 26: How do pornography, sexting, dating apps or other emerging uses of technology influence community understanding of consent?

The size and popularity of online dating platforms has impacted dating trends altering, for many, their perceptions of and behaviours associated with these social interactions and relationships. An intelligence assessment examined the introduction of technology and its impact including changing views on sex and relationships. The assessment highlighted changing views as likely contributing to sexual assaults between online dating participants, as expectations of sex-on-demand increased and became reinforced.

The prevalence of online dating websites and apps is reported to be encouraging perceptions of a 'hook-up' culture and casualisation of sex. Research shows consumer behaviour in relation to online dating is different to in-person interactions with conversation on these apps turning sexual quickly, sometimes immediately and unwelcomed. The sexualisation of this communication likely reinforces expectations of sexual activity upon face to-face meetings, even if one of the users clearly articulates they do not want sexual activity.

The dissociated and/or anonymous nature of online dating likely extends opportunities for offenders to target previously out-of-reach victims – victims who, for various reasons, may not be comfortable in traditional dating or social behaviours. This anonymity also likely provides protection for offenders; particularly for sites that don't require identity verification. These platforms also extend offending

opportunities for offenders who have trouble in approaching potential victims in person and/or facilitates multiple approaches to potential victims.

A 2021 QPS intelligence assessment highlighted significant increases in reported internet-facilitated sexual offences between 2008 and 2020. A 2015 Australian Competition and Consumer Commission report indicated the Australian online dating industry was worth around \$113.3 million and recorded more than 4.6 million registrations. Research estimates up to 75% of 'millennials' (18 to 33 years) use online dating with online interactions now representing one of the most common ways of people meeting their partner. Tinder launched in the United States in 2012 before expanding internationally. In January 2020 Tinder recorded an estimated 3 million Australian users. The QPS intelligence assessment identified Tinder as the most prevalent platform (41%). Further information about the QPS collaboration with Tinder is on page 18 of this submission.

Barriers to reporting sexual violence

The QPS acknowledges reporting sexual violence can be a daunting prospect for many and notes that some of this reluctance is based on concerns that police will not believe them. The QPS also acknowledges the criticisms of some police in their handling of sexual violence investigations. There has been a long-standing public perception the police and the justice system are not uniformly meeting the needs of victims in every instance. This is supported by recent events indicating the QPS could further improve its response to victims of sexual violence. These include findings from the Royal Commission identifying inadequacies in the response to victims, such as lack of empathy; failing to adequately address victim needs in a trauma informed way; and victims feeling disempowered during investigation and prosecution processes. Although the report acknowledged police had taken steps to address such issues, negative perceptions remain, resulting in victims not reporting offences. The report recommended policing agencies undertake activities to encourage reporting.

The Queensland Sexual Violence Prevention Framework identified similar concerns, the ABC News published a report which was generally critical of the policing response to sexual assaults, and the Office of Health Ombudsman raised concerns about the quality of some police investigations of health practitioners accused of sexual offences.

In acknowledgement of these criticisms, the QPS is undertaking a range of strategies to improve its response to sexual assault investigations and vulnerable victims including the development and launch of the Sexual Violence Response Strategy with 25 actions, including the statewide rollout of SVLOs, and introduction of online reporting options. The Child Abuse and Sexual Crime Group was appointed as the capability owners for sexual violence, to ensure a consistent statewide response to sexual violence.

The QPS response to Discussion Paper 2 referenced the implementation of the online sexual assault reporting form in August 2020. The QPS implemented a digital solution to enable adult members of the public to report sexual violence online. The new form offers victims – including vulnerable members of the community – an alternative channel to reporting sexual assault.

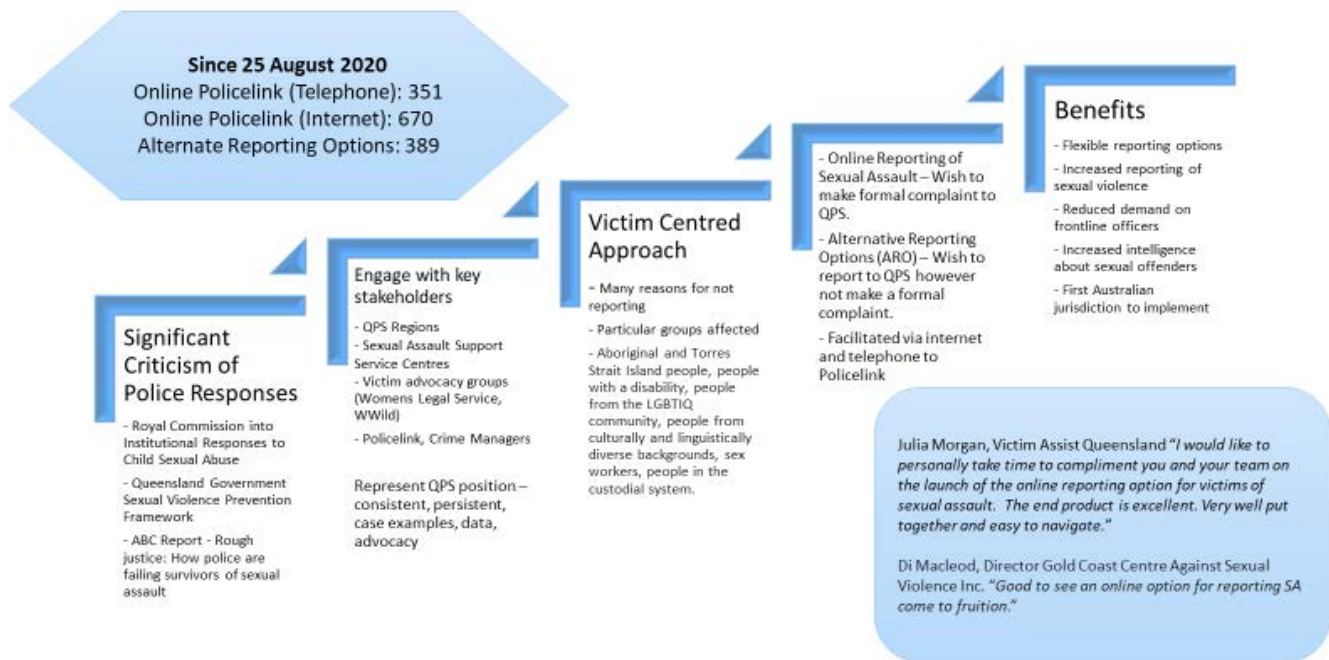
The project also saw the Alternative Reporting Options (ARO) form transition from print-and-complete to online functionality. Parallel consultation occurred to meet sexual assault victim needs and to ensure content and functionality alignment with the online sexual assault reporting form.

Additional to the online options, Policelink opted to expand its services and introduce telephone reporting for non-urgent sexual assault matters, providing a further channel for victims to report. This service enables victims to telephone Policelink and report a sexual assault. Policelink operators record the details, triage the reports, and send relevant tasks for investigation and response.

As part of the development and implementation of the online reporting process, the [QPS website](#) was updated in consultation with sexual assault support services, to ensure the accuracy and readability of the information about sexual violence reporting options. The QPS *Sexual Violence Response Strategy 2021-23* includes actions to increase awareness of reporting options and to direct members of the community and support services to the QPS website for further information.

The diagram below provides a snapshot of the online sexual assault reporting project, its scope, the products delivered, and the project benefits.

Snapshot: Online Reporting of Sexual Assault



'Disclaimer – these figures are not official Service statistics. Official Police Service statistics are released only through Research and Analytics, Organisational Capability Command after available data is collected, classified and collated in accordance with nationally accepted rules.'

Question 31: What can be done to reduce the feelings of shame and the stigma that surrounds sexual violence in our community?

Case Study – not for publication (currently before the courts)

Protracted operation, investigating a serial rape offender, active in Queensland between 2016-2020. The investigation resulted in the identification of 86 victims who wished to make a complaint. These consisted of 34 rape victims (24 of whom were drugged) and 52 victims of recordings in breach of privacy (recorded during sexual intercourse), with a total of 247 charges. There were close to 200 total victims.

Inquiries identified that the offender lured women to his home by catfishing them through the dating app Tinder. He was able to create multiple fake Tinder profiles by sourcing photos of models from elsewhere online and communicated via numerous messaging apps and using multiple phones and SIM cards. The women arrived with the expectation of meeting a male person of far different physical appearance to that of the offender. The offender would buzz them up to his unit before deploying a cover story both through his fake Tinder profile account (account of the person with whom the women believed they were meeting) and his own verbal communications with the women, implying the person they were there to meet was on his way back and wouldn't be too much longer.

The offender would offer them a drink of either alcohol, water or soft drink. The women reported nil recollection of events shortly after consuming the drink provided by the offender. Subsequent analysis of hair samples obtained from three women identified the presence of benzodiazepines in their system. The women further reported they had not consented to any sexual activity, nor recall engaging in sexual activity with the offender while at his residence. It should be noted some women were not drugged but felt pressured into sexual acts with the offender out of fear.

The matter was reported to police as a rape after one of the women who left his dwelling and crashed her car on the way home. She went to her GP for a blood/urine test which identified the presence of benzodiazepines. It was this fact that made her feel she had enough information to come to police and report the matter.

Benzodiazepines are a group of nervous system depressants commonly prescribed to treat stress, anxiety or insomnia. They are also known as 'minor tranquillisers' and sedatives. Common effects include relief from anxiety, muscle relaxation, sleepiness, a sense of being disconnected or detached from reality, dizziness, loss of inhibitions. It is noted that some of the women who had no recollection of events but where recordings of sexual activity were located appeared in the recordings to be lucid, active and willing participants.

One of the key learnings from this operation is that many of the women did not report their experiences to police. Most women recall some of the events and recall the situation being creepy/suspicious, however

they weren't reported for reasons including:

- *They were unaware of exactly what happened (owing to having been drugged)*
- *They were blocked on Tinder following the offence so lost all message history (evidence) to provide police*
- *They were communicating on Snapchat and other messaging apps which did not save the message threads*
- *They had been catfished on Tinder, so the profile details of the person they were meant to meet weren't real, so they had no information about the offender*
- *They felt partially to blame for having been tricked by the offender and so did not report the matter because they did not want to go through the court process. They did not realise they had been drugged and recorded. When they realised this, they felt empowered to make a complaint.*

This case study demonstrates the complexity of sexual violence reporting, and the variety of reasons for a person to resist reporting to police.

In November 2021, the Police Commissioner officially launched the QPS' joint safety campaign with Tinder. The campaign featured messaging to increase awareness of personal safety, offender behaviour, reporting and support options was the first of its kind, cobranded in partnership with Tinder.

The objectives of the campaign were to:

- promote awareness through messaging within the Tinder app, empowering but not alarming participants to take control of their safety.
- raise awareness among participants that the QPS prioritises the safety of the online community and is here to assist.
- reiterate that if something unwanted happens, individuals are not alone, with support and reporting options available.
- publicise to potential offenders that the QPS will move to protect safety within the online environment and that unwanted or criminal behaviour is not acceptable and will not be tolerated.
- reinforce that reporting sexual assault not only addresses an individual circumstance but can also
- assist police and Tinder in identifying offenders; preventing future occurrences; and supporting other victims.

The campaign culminated in messaging delivered to Queensland-based participants on the Tinder app, proactively promoting tailored safety messaging. The campaign reached 3 million people reached (1.8 million through media, 160,000 on QPS social media, 1 million on Tinder), with 30,000 visits to the campaign landing page on the Tinder app.

As referenced in the QPS response to Discussion Paper 2, the QPS advocated for the introduction of a Just in Case forensic examination process, to provide for collection of forensic evidence from a victim who has not yet determined whether to make a complaint to police. This process allows the victim to retain decision-making power in relation to her options, knowing that the collection of forensic material may assist police if she later chooses to report. In some areas of the state, however, it appears that once a victim attends a hospital for a Just in Case examination, some medical professionals are contacting police to attend and speak to the victim, causing angst for the victim and defeating the principle behind the Just in Case process.

Public reporting on sexual offending and domestic and family violence

The QPS notes the concerns raised at community forums regarding publication of names of victims and offenders include impacts for family members, particularly the children of the named people; the consequences for people in smaller communities; that many social media sites already name victims and offenders, and there does not appear to be many controls in this regard; and the options available to victims who consent to publication but subsequently change their mind as once details are published on the web it is extremely difficult to remove them.

The QPS acknowledges the views of victims are a significant consideration in the criminal justice process. It also acknowledges any community disclosure or reporting has the potential to cause negative consequences for victim survivors and offenders. It can lead to the re-traumatisation of victims, either at the time of publication or in the future. Ongoing and repeated publications by media and social media outlets can be detrimental to the coping and healing process for victims. Public reporting also provides

the ability to identify and target children of the victims and/or offenders, and can lead to the 'labelling' of a person as a victim or offender. Victims are not a homogeneous group. What may be restorative for one person may be detrimental to another. The potential to re-traumatise even one victim must be considered in policymaking.

Taking a conservative, victim-centric approach is particularly pertinent in the context of sex offence matters, as many victims are children, and most offending occurs within a complex intra-familial context³. Identifying victims (or fear of this occurring) through notification or disclosure processes may have significant psychological ramifications for victims and may disincentivise reporting of sexual abuse.

Research suggests that there is also a negative psychosocial impact on the children of identified offenders. In America, where sex offender register community notification schemes operate, a survey of 134 parents or caretakers of children whose other parent was registered sex offender, identified their children exhibited anger (80%), depression (77%), are ostracised by peers (65%) and are fearful (63%), with 13% exhibiting suicidal tendencies⁴.

This same research also identified other perverse impacts on family members of identified sex offenders, particularly those who reside with the sex offender, including the family member is more likely to experience social disadvantages and vigilantism themselves. 53% of family members experienced financial hardship due to the sex offender's loss of employment, 22% experienced housing problems, with 7% reporting being physically assaulted or injured, and 27% having property damaged due to their relationship with the identified sex offender.

Public identification of an offender can also potentially undermine protective risk factors such as stable housing, employment, and pro-social relationships.

The QPS notes and supports the limitations on publication of the names of young offenders, noting the principles of rehabilitation, similar to those in the *Criminal Law (Rehabilitation of Offenders) Act 1986*.

Reporting, investigating and charging of sexual offences

Police responses to reports of sexual violence

A key focus of the QPS *Sexual Violence Response Strategy 2021-23* is the delivery of victim-centric and trauma-informed responses to victims of sexual violence. The implementation of the Sexual Violence Liaison Officer (SVLO) responsibilities is a key driver of change in this regard. In January 2020, the QPS commenced a 12-month trial of dedicated SVLOs in response to the Queensland Government's *Prevent. Support. Believe. Queensland's Framework to address Sexual Violence*. Two trial sites were nominated: Logan District in South East Queensland, and Townsville District in Northern Queensland.

During the trial, the role of the SVLO was to ensure the QPS provides a victim-centric response to victims of sexual violence, liaise with local Sexual Assault Support Services to identify and address issues relating to victim experiences, and ensure accurate and consistent communication was provided to all victims of sexual violence who report to the QPS.

Following the trial, an evaluation identified positive outcomes including:

- Improved perceptions of the QPS response to victims
- Increased referrals offered to and accepted by victims
- Increased reports of sexual violence
- Increased number of distinct victims
- Decreased withdrawn offences
- Decreased unfounded outcomes

³ Lievore, D (2003). Non-reporting, and Hidden Recording of Sexual Assault: An International Literature Review, report. *Australian Institute of Criminology*. <https://www.aic.gov.au/publications/archive/archive-135>

⁴ Tewksbury, R., & Levenson, J. (2009). Stress experiences of family members of registered sex offenders. *Behavioral Sciences & the Law*, 27(4), 611-626. https://www.researchgate.net/publication/26269684_Stress_experiences_of_family_members_of_registered_sex_offenders.

The results from the evaluation were a driving factor in the decision to roll-out the SVLO role across the state and the expansion of the SVLO was incorporated as an action in the QPS' *Sexual Violence Response Strategy 2021-2023*.

SVLO responsibilities rest with the Officer in Charge (OIC) of each CPIU and CIB. The state-wide rollout commenced on 1 January 2022. The policy and procedure document (Instruction) that was utilised in the trial was revised in consultation with the SVLOs and forms the basis of the SVLO responsibilities. The Instruction (Appendix 4) will be incorporated into the OPM, due to be published in June 2022 (refer Appendix 2).

In addition to the direct communications with SVLOs, a communications pack was distributed to District Officers (senior leaders in the organisation) to help drive the key messages (Appendix 5) which include:

- Be aware of your own attitudes and biases
- Understand myths and misconceptions around sexual violence
- Understand trauma, how it can affect everyone differently and that a flexible and agile policing response is required
- Listen to the victim and ensure they feel supported
- Investigate the crime, not the victim.

Evidence gathering

As mentioned previously, the QPS response to children who have experienced sexual violence is primarily provided by CPIU investigators. Chapter 7 "Child Harm" of the OPM provides direction in relation to interviewing child victims and witnesses and investigating criminal offences against children. The commencement of the Queensland Intermediary Scheme Pilot Program in July 2021 provides further support and assistance to investigators to interview witnesses with communication difficulties when conducting child sexual offence investigations.

CPIU investigators record interviews with child witnesses and witnesses with an impairment of the mind, in accordance with s93A of the *Evidence Act 1977* (Evidence Act). The OPM states that "*statements in this format should be undertaken in accordance with the interviewing children and recording evidence (ICARE) interviewing model. The ICARE interviewing model encompasses an electronically recorded free narrative of the witnesses' recall of the event. The initial information obtained from a child is critical in the prosecution process. In instances of child abuse, sexual assault or where the witness suffers an intellectual disability, the matter is to be referred to the OIC of the district CPIU for their consideration, advice and where appropriate, the appointment of a suitably qualified officer to undertake an ICARE interview.*"⁵

Current legislative restrictions prevent the recording of evidence from adult witnesses who may be deemed to be special witnesses under s21A of the Evidence Act. Section 110A of the *Justices Act 1886* requires "written statements" to be tendered for the purposes of a committal proceeding. Section 21AF of the Evidence Act provides exceptions for the presentation of a "written statement" at committal for affected child witnesses, however there are no similar exceptions for any of the other special witnesses in s21A Evidence Act.

The effect of this legislation is that investigators must obtain a written statement from adult victims of sexual violence. This process is not victim-centric and can cause further trauma to the victim, noting that the time taken to sit with an investigator to type a statement is greater than the time taken to record a free narrative account. A free narrative account is considered best evidence as it allows the victim to describe the event in her own words. The taking of a typed statement can often unwittingly result in the words of the victim being altered by the investigator, recorded inaccurately, or otherwise forgotten in the telling and retelling of the account. This can often lead to questions in court about the credibility or recall of the victim.

Recommendation: *It is therefore recommended that consideration be given to more closely aligning the provisions of s93A and s21A of the Evidence Act to allow for the admission of electronically recorded evidence of all witnesses who would be deemed to be special witnesses.*

As outlined in the submission, an investigative tactic sometimes used by police is the use of pretext

⁵ Section 7.3 OPM

conversations. Pretext conversations are an investigative tool that can be utilised in a wide variety of investigations but are particularly effective in sexual assault matters. Conversations are recorded between victims/witnesses and a suspect to obtain voluntary admissions. Pretext conversations can be conducted either by phone or face to face with a suspect. There are clear guidelines for the conduct of pretext conversations to ensure compliance with evidentiary requirements and to establish appropriate safeguards for victims. Officers are required to consider the emotional impact the proposed conversation may have on the victim in reliving events with the suspect, the age of the victim and their suitability to participate in a pretext conversation as well as any safety issues for the victim arising from the conversation.

Forensic examinations

In 2018-19, the Queensland Audit Office (QAO) conducted an audit of forensic services in Queensland. The QPS contributed to the audit to highlight concerns from officers investigating sexual violence regarding inconsistent and untimely provision of forensic examinations, often referred to as Sexual Assault Investigation Kits (SAIK), by medical professionals. Case study examples were provided and discussions held with QAO officers to express concerns that medical responses were not victim centric, and in many ways caused further trauma to the victim. The issues included refusal to conduct the examination, requirement for a victim to travel up to ten hours to a hospital that would undertake the examination, waiting (often in the same clothes) for hours before being seen by a medical professional, all of which were likely to result in the victim deciding to not further proceed with the complaint.

The QPS engaged regularly with Queensland Health to seek resolution to the concerns raised, and to also discuss the implementation of a 'just in case' model for victims who were undecided about whether to report to police. The combined engagement and QAO report resulted in the implementation of the Just in Case process in 2019, and a commitment from Queensland Health to strengthen their forensic responses.

While improvements have been identified, there remains concerns across parts of Queensland that the forensic responses by medical professionals have not improved to any great extent. The QPS continues to engage with Queensland Health to identify issues as they arise in order to address issues early.

Reference DNA

In addition to the SAIK examination, reference DNA is required from the victim to compare against samples obtained during the SAIK examination. The Queensland Government Guidelines for Responding to Sexual Assault signed by a number of Government Agencies including Health and QPS in 2014, state that forensic medical examiners **should** take a DNA reference sample from a victim. It is considered this would reduce the trauma suffered by the victim in having a police officer (often male) take the reference sample at a later time.

Queensland Health practitioners stopped this practice, causing a delay in processing the analysis, and requiring police officers to revisit the victim to take the sample. The reason provided by Queensland Health is that the word 'should' is used in this statement regarding the taking of the reference sample, and thus is optional. On 31 March 2022, Queensland Health agreed in principle that replacing "should" with "shall" in the guidelines will remove doubt about the requirements to take a reference sample.

DNA Testing Threshold

There has been recent commentary in the media about DNA testing thresholds in Queensland compared to other states and territories in Australia. In February 2018 Queensland Health Forensic and Scientific Services (QHFSS) made a recommendation to QPS that testing of samples containing less than 0.008ng/uL of DNA should discontinue because the chance of obtaining meaningful evidence was low. Previously samples below this concentration underwent a process of micro-concentration to try and improve the likelihood of obtaining a useful profile. QHFSS advised that the overall success rate of micro-concentration was 10.6%. However, they advised that in most of these instances the process of micro-concentration did not provide any new evidence for the case due to the same profile already having been detected on other samples. They reported that the actual success rate of micro-concentration finding new evidence was 1.86%.

Based on the advice of QHFSS, QPS agreed that further testing of samples with less than 0.008ng/uL

of DNA should cease as a matter of routine. In these instances, the outcome of the testing would be reported to police as 'insufficient DNA for further processing' and investigators would be given the option to request testing (which involves micro-concentration) to continue if the sample was important for the case.

For the calendar year of 2021 the QPS gathered information to monitor the success rate of obtaining a usable profile when investigators requested testing to continue for samples initially reported as 'insufficient DNA for further processing'. The observed success rate of obtaining a profile from these low concentration samples was approximately 30%. This success rate includes samples collected in relation to all crime classes. Given the observed success rate was substantially higher than was forecast by QHFSS, in December 2021 the QPS requested that the process be reviewed by QHFSS including the threshold value used.

The success of further testing for samples collected in relation to sex offences was much higher which may be attributed to the sample type which are generally taken from intimate areas. During 2021, 583 samples relating to sex offences were initially reported as 'insufficient DNA for further processing'. Investigators requested for testing to continue for 47 of these samples. Upon the continuation of testing, 31 samples yielded a useable profile. This equates to a success rate of 66% when samples below the threshold progressed through the full testing process.

Support Persons

The QPS response to Discussion Paper 2 included detailed information about the Townsville Sexual Assault Response Team (SART), which is a multi-disciplinary, specialised team of stakeholders who are available 24/7 to engage directly with victims of sexual violence, and support victims throughout the criminal justice process. It is evident from research and stakeholder submissions that consistency of support from end to end helps victims to feel supported and to navigate the system, and that this function is best performed by sexual assault service workers, in collaboration with criminal justice stakeholders (QPS, Health, Justice and Courts).

The QPS response to Discussion Paper 2 discussed the evaluation of the SVLO trial. This evaluation identified the benefits of a SART model and noted a SART model will provide more benefit to victims than the SVLO model alone. The evaluation report noted concerns about the capacity of sexual assault support services to meet demand, particularly in rural and remote areas of the State, and recommended further funding be considered and acknowledged as a limitation in current support for victims. It is noted this recommendation is beyond the remit of the QPS, which does not fund these services, but it is an issue of concern for the QPS if there are limitations on the ability for police to refer victims for necessary support.

Through the SVLO role, it is anticipated stronger connections will be made between the QPS and sexual assault support services, however concerns about capacity of services to meet demand remain.

The QPS strongly favours a model of sentinel support, where specialist support services are available and able to be engaged from the time when a victim is considering her reporting options, throughout the course of the criminal justice process, and beyond. By way of example, the following communication from a victim-survivor was received by the investigating officer following conclusion of the appeal period: *"However difficult the trial was it was small beer to the aftershock. We have yet to find our new normal. ... Then there's the question of 'what next'? On that I'll have to get back to you – I'm still a bit lost there."*

Police Training

As mentioned in the QPS response to Discussion Paper 2, the QPS has commenced delivery of new and updated victim-centric and trauma-informed training products, to improve the QPS response to victims of sexual violence at all levels. This training package has been developed in partnership with the University of Queensland (UQ) and aligns with the 'start by believing' philosophy.

The CSAFE OLP, released on 31 January 2022, is the first in a series of products, mandatory for all police officers from the rank of Constable to Inspector, Policelink staff and Counter Service Officers, to address:

- Understanding institutional child sexual abuse
- Understanding trauma

- Survivors from diverse backgrounds (First Nations victims; Culturally and Linguistically Diverse victims, victims with disability)
- Child development
- Being effective communicators (how to take a disclosure).

This OLP is highly recommended for Superintendents to Assistant Commissioners as many manage investigative units across the State.

The second stage is an OLP scheduled for release in 2022 for generalist investigators to address:

- Biases and decision-making
- Myths and misperceptions of child sexual abuse, sexual violence, and domestic and family violence
- Trauma and complex trauma
- Vicarious trauma and self-care.

Additionally, the two-week Detective Training (Phase 2) curriculum includes training relating to understanding sex crimes. Members of the UQ team who partnered with QPS to develop trauma informed training were invited to observe this training in March 2022 and are currently working with PCAP to include trauma informed components to enhance investigative understanding and responsiveness to victims in this phase of training. The training will include a session on 'The Whole Story' to build the foundational understanding of trauma before they attend the ISACURE course.

The ISACURE course provides participants with the knowledge, skills and behaviours to effectively understand and support victims of sexual offences; and hone communication and investigation strategies to effectively prevent, disrupt and prosecute sex offences. Participants are challenged to critically examine their existing understanding of trauma; victim behaviour; 'sex offences' and 'sex offenders'; as well as their own investigative processes to see how they impact investigations. The course was developed in consultation with expert academics and external stakeholders with the aim of enabling investigators to provide an enhanced response to adult victims. Skills with which to work effectively within a multi-disciplinary team to achieve mutual outcomes are also emphasised.

As outlined in the QPS Discussion Paper 2 response, an evaluation of the ISACURE course identified that as a result of the training, it significantly changed investigators' knowledge and perceptions of their role and approach to victims of sexual assault, leading to improved investigative practices. Investigations undertaken by members who had completed the ISACURE course, compared to investigations by members who had not completed the course, achieved significantly greater proportions of solved sexual offences, significantly lower unfounded sexual offences and significantly reduced withdrawals (for rape and attempted rape).

In 2022, the Detective Training unit is facilitating 16 courses across all three phases to accommodate 520 students (4 of which are phase 2). There are 6 ISACURE courses to cater for 240 students.

The QPS Prevention Together Strategy aims to prevent harm, trauma and crime. Courses delivered at the Investigative Interviewing Training Unit (IITU) ensure the curriculum reflects this strategy, the QPS Sexual Violence Response Strategy, legislative and policy requirements in addition to addressing external recommendations such as Royal Commission, Inquiries or Coronial Inquests where required.

PCAP also provides face to face training for recruits and in-service police with respect to policing with influence and tactical communication. While not specific to sexual violence crime, the application of this training is designed to assist police to de-escalate violent situations and/or build rapport and actively listen to victims or community members in times of distress or crisis.

This training includes a focus on the following:

- de-escalation of incidents through effective communication skills; and specifically
- the use of the behavioural influence stairway model (BISM).

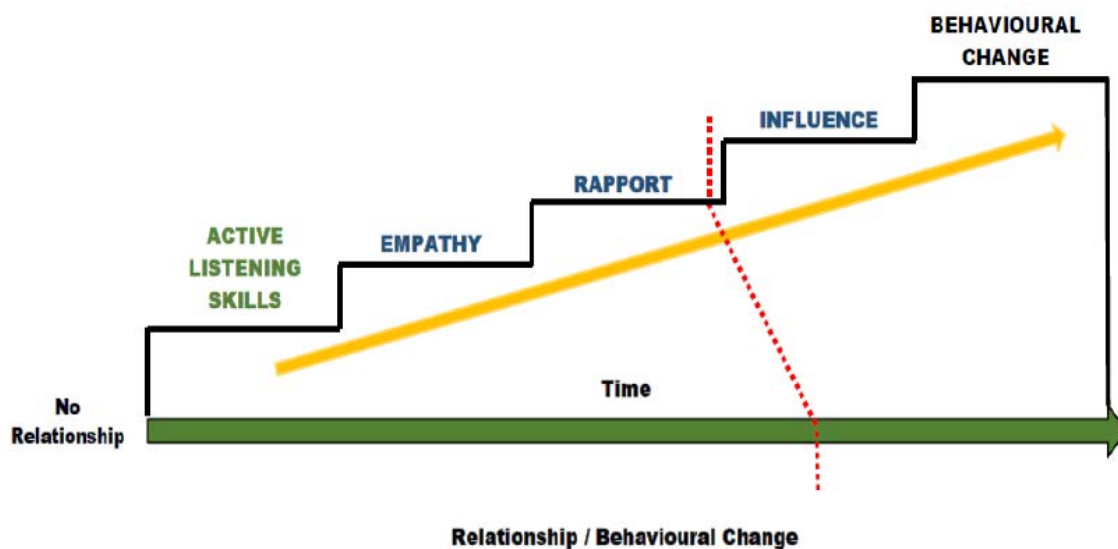
QPS Operational Skills and Training has included Statewide training to all police on the BISM model since 2018. The focus of this training is on communication techniques and specifically the ability to build relationships with people in crisis who are experiencing, or who have suffered traumatic events, including offenders, victims and witnesses alike. The BISM model is traditionally used by negotiators and has been included in general police training to educate all police on how to:

- use active listening skills
- empathise with the person they are speaking with
- build rapport
- influence behaviour
- change behaviours.

The techniques used in this model coincide with those used in high pressure police negotiations and investigative interviewing in general police work.

The skills, behaviours and principles incorporated in these training products are all transferrable to other aspects of policing activities outside of high risk or violent confrontations. For example, the model may be used by police generally to establish rapport, to assist persons experiencing a mental health related issue, victims of a crime or domestic & family violence; and witnesses of reportable incidents.

BEHAVIORAL INFLUENCE STAIRWAY MODEL (BISM)



Scenario based recruit training also includes policing with influence techniques (BISM) such as talking to aggrieved and respondent persons in domestic and family violence situations, non-compliant offenders and persons in distress due to mental health issues.

Legal and court processes for sexual offences

Adequacy of current sexual offences in Queensland

The QPS supports consideration of legal remedies to improve the experiences of victims through the prosecution process. We refer to the recommendation above in relation to electronic recording of victim and special witness evidence at investigation stage, and admissibility of the electronically recorded interview as the witness statement. As discussed previously, a free narrative account of the incident, with an ability to provide the Whole Story, will provide additional context around offender action and victim reaction⁶.

The QPS notes consideration of new offences relating to stealthing and acknowledges the submission from Respect Inc. about the lack of provision for charging a client of a sex worker with rape when they do not pay for services.

The QPS seeks consideration and possible review of judicial directions in sexual offence hearings, particularly in relation to the evidence of the victim, referred to as the "[Robinson](#)" direction. An alternate

⁶ Tidmarsh, P (2021) The Whole Story: Investigating Sexual Crime - Truth, Lies and the Path to Justice
Queensland Police Service

option to removal of the warning may be to allow expert evidence to explain to a jury and court participants such matters as the impact of trauma on memory, fight/flight/freeze responses, and offending behaviours.

Alternative justice responses

The QPS acknowledges that “justice” has different meaning for different victims. For example, some victims of child sexual abuse tell someone about the offending because they want the offending to stop. Other victims want their story to be heard, and to be believed. It is therefore considered appropriate that a variety of options be made available to victims to provide them with a sense of control over how they participate in the system.

A number of diversionary options are available to police when responding to young offenders, however there remains limited options for restorative justice beyond restorative justice conferences. There is no impediment to utilising these alternative responses with a young person who has committed a sexual offence.

Question 71: Should a special sexual violence court be trialled in Queensland? What would be the risks and benefits?

The benefits of a sexual violence court are unclear. The QPS notes the views of the Victorian Law Reform Commission as outlined in Discussion Paper 3. It is considered that greater benefits would be achieved universally with training in trauma-informed approaches to all criminal justice participants (police, prosecutors, defence, courts personnel), noting these skills can be applied when dealing with all victims, witnesses and defendants.

Part 3 - Women and Girls’ Experience of the Criminal Justice System as Accused People and Offenders

Why women and girls come into contact with the criminal justice system as accused persons and offenders

The PPRA provides the powers and safeguards when investigating offences and dealing with offenders. While there are no specific requirements in responding to women and girls, officers are required to comply with all safeguards and with requirements in the OPM when dealing with offenders, including Chapter 2 (Investigative process) and Chapter 6 (Persons who are Vulnerable, Disabled or have Cultural Needs).

The QPS acknowledges the stories of women with lived experience and the research which identifies that many women who commit offences have a history of trauma and disadvantage. The role of police in investigating crime is outlined in Chapters 2 and 3 of the OPM. Officers must act impartially in the discharge of their duties. Consideration must be given to whether there is sufficient evidence to charge someone with an offence, and to also consider whether it is in the public interest to do so. Section 3.1.1 of the OPM requires officers, when deciding what action in response to an offence is appropriate, to adopt the ‘PLAN’ approach (Proportionate, Lawful, Accountable, Necessary) to assess whether an action or decision is compatible with human rights, and to consider whether alternatives to charging would be more appropriate.

Children in Residential Care

Earlier in this submission, we discussed the criminalisation of the care system. Children who are removed from their homes for their own protection by DCYJMA can be placed in a range of care environments, including with other family members, foster carers, or residential care services. Residential care services accommodate children and young people with complex and/or extreme support needs. Some homes can house up to 4-6 children. There are currently over 450 residential care houses across Queensland.

Children placed in residential care homes are likely to have suffered significant trauma and may exhibit challenging behaviours which require a holistic, trauma-informed response.

Responding to calls for service from residential care consumes significant and disproportionate policing resources. Regular police attendance at these addresses leads to negative community perceptions, negative police interaction and greater exposure of children in residential care to the criminal justice system, resulting in poor long-term outcomes for these children.

In 2018, the Queensland Family and Child Commission (QFCC) led development of the *Joint Agency Protocol to reduce preventable police callouts to residential care services* (the Protocol), which was published in September 2018. The intent of the Protocol is to limit the exposure of children in residential care to police and the criminal justice system for actions that would be managed without police involvement in a family home.

An analysis of data relating to calls for service to residential care services for 2018 – 2019 was undertaken by the QPS and shared with Child Safety.

The key points include:

- 22,241 total calls for service for 2018/2019 calendar years
- 30 service providers are responsible for 370 juvenile care house addresses
- 60% of calls are in relation to 'absconders' incident group (absent from placement/missing persons)
- 70 addresses (18.9%) had over 100 calls for service (range 100-542) across the two year reporting period.

Ongoing engagement with stakeholders in intervening years has seen a significant and sustained reduction in the number of calls for service to residential care facilities. In that same timeframe, we have seen a significant increase in the number of residential care houses (from 299 in 2018 to 459 in 2021), and a similar significant increase in the number of children in residential care (814 to 1,374). The average number of calls per child has reduced from 12.5 to 4.9, however the risk remains that this cohort of children will be at greater risk of entering the criminal justice system.

In February 2022, Child Safety published Operational Guidelines to support the implementation of the Protocol. It is hoped the implementation of the Operational Guidelines will see further reductions in unnecessary police involvement with these children and a subsequent reduction in their involvement in the criminal justice system.

Engagement with police and the legal system

The Discussion Paper commentary in relation to gender-responsive policing is noted. In 2022, the QPS commenced working with the University of Queensland to trial a gendered policing model. It is noted a broader consideration of gendered responses across the criminal justice system may result from this current inquiry.

The QPS works closely with partner agencies to identify young people at risk of entering the criminal justice system and of the child protection system and to implement intervention strategies to divert them from that path. As previously discussed, the QPS is a core member of the SCAN team system which provides a multi-agency response to children at risk of significant harm.

One initiative currently supporting girls at risk of entering, or who have entered, the criminal justice system is the recent establishment of multi-agency collaborative panels in all police districts. These panels have been established to provide support and intensive case management for the serious repeat young offenders who are consistently entering/exiting detention. These panels include representatives from various Government agencies who collaborate to provide support and links to pathways to prevent re-offending and incarceration.

Youth co-responder teams (YCRT) consisting of QPS and DCYJMA (Youth Justice) employees operate in eight police districts throughout Queensland. These teams perform street and home visits to young girls who have entered or at risk of entering the criminal justice system. The teams provide links for the young person and their family to support services ensuring holistic support to the family unit.

The following examples identify the benefit of early engagement and access to support for girls at risk of entering the criminal justice system:

14 year old girl, commenced offending in August 2020 and escalated with 77 offences committed between January 2021 and October 2021. The girl was in care but living with kin. She has two older brothers, who were both involved in offending, which was the main influence of her behaviour. The offending related to property offences (unlawful use of motor vehicles (UUMV), fraud, stealing, shop stealing, and entering premises and committing offences). The YCRT commenced regular engagements in May 2021, checking in on the girl two or more times per week, providing support and referrals to the family. The YCRT also engaged with the girl's Child Safety officer. Since October 2021 the girl has only committed one offence, in March 2022. The YCRT still engage with the girl and her current carer, including recently assisting with transporting her to school which she commenced at the start of the year after being absent from schooling for two years.

14 year old girl, first came to QPS attention in June 2020 for assault matters, for which she was cautioned. Her offending escalated the following year from June to October 2021, charged with 22 property offences (UUMV, fraud and receiving tainted property). The YCRT commenced engagements in June 2021, with the girl and her mother, including attending the home address for bail checks, engagements and referrals offered. Peer influence was a big factor in the girl's offending behaviour, along with conflict with her mother. There were several barriers to overcome working with the girl due to the family conflict and disengagement from schooling. The YCRT also regularly engaged with the girl's mother and provided advice. The girl's last offence was in October 2021. QPS have not been called to the address this year due to any family conflict matters.

Diversion from the criminal justice system

The QPS notes the discussion about the use of diversion options for women and girls as offenders from the criminal justice system.

Girls have greater opportunity of being diverted from the criminal justice system than women due to the diversion options available to young people and the historic use of such diversion options. Police are well versed with the diversion options available under the *Youth Justice Act 1992* including taking no action, caution, restorative justice conference, drug diversion or the graffiti program. Some women may be provided the opportunity of an adult caution depending on the circumstances. Expansion of adult cautioning and the ability to provide restorative justice conferencing to adults would provide greater options for police when considering responses to offending. Any diversionary practice for women and girls which includes links with further support may provide greater long-term benefits.

In 2019, the QPS commenced a Protected Admission Scheme for young offenders. The Protected Admissions Scheme allows police (through a legal representative, parent or support person) and a young person to come to an agreement about the young person's eligibility for a court alternative such as a caution or youth justice conference and the use of any admission. The lawyers advising the young person can provide advice to the young person to admit the offence in the confidence that they are acting in the best interests of the young person.

The investigation of an offence by the young person does not change, nor does the cautioning or restorative justice conference schemes.

The Protected Admission Scheme only operates where the young person has declined to make an admission, but a caution or other diversionary option is appropriate. The scheme is designed to remove the potential blockage to the cautioning or restorative justice conference options. A protected admission interview allows the young person to make admissions during a police interview, but any admissions made are not admissible in court proceedings.

Conditions in prisons and watchhouses

Chapter 16 of the OPM outlines the requirements for the care and safety of people in police custody. The OPM states "*Holding cells at police stations are designed to hold prisoners in custody for a short time, whilst watchhouses are primarily designed to hold persons overnight or for 24 hours or longer. Never-the-less, both these facilities are for the temporary holding of prisoners before prisoners are released or transferred to a corrective services facility or detention centre. Therefore, prisoners are to be held in police custody for the minimum length of time necessary.*"

While the OPM is clear in relation to best practice, often circumstances and factors beyond the control of

the police result in the detention of prisoners for more than 24 hours. These circumstances include the inability to transport prisoners to and from remote locations within a timely and practical manner, which often require flights or long-distance driving, particularly if there are limited police resources available. Likewise, if there are no beds available at the correctional or detention centres, requests are made to police to keep the prisoners at the watchhouse for longer periods. Finally, if a court appearance is only a day or two ahead, prisoners are often kept in the watchhouse as a more logistically feasible option to ensure the prisoner is able to attend court, particularly in the northern and western parts of the State.

Section 5.9.4 in Chapter 5 of the OPM provides direction in relation to requirements when taking children into custody and further guidance is provided in s16.12.1 in relation to segregation of prisoners.

The QPS notes that watchhouses are not designed to respond specifically to the needs of women and girls.

Women's experience of reintegration into the community

A new statewide initiative called a "72-hour Release from Detention Plan" has been implemented in Queensland. It provides a dedicated plan for youth aged between 10-17 years in the first 72 hours post release from detention centre. The plans provide support to the young person including supervision and engagement opportunities to help prevent re-offending.

Consideration could be given to establishing a similar model for women exiting prison, to ensure appropriate supports are available to her to re-establish her connections in the community.

The QPS supports all programs which support successful reintegration into the community. Not only will this reduce demand on QPS resources, but more importantly it will reduce recidivism rates for women and girls.

Conclusion

The QPS is committed to the safety of the community now and into the future. Whilst there are many and varied activities developed and ongoing to support women and girls in the criminal justice system, we recognise that the more Government and non-Government agencies work together to support our community, the better the outcomes will be. As the primary law enforcement agency for the State of Queensland our 24 hour, seven days a week policing service is increasingly met with high levels of demand, shifting community expectations and rapid technological innovation. These factors, coupled with our access in all parts of the State including remote areas, where other support agencies are not available, ensure policing is often the only point of call for community members across a wide range of policing and non-policing issues.

ACRONYMS AND ABBREVIATIONS

| | |
|-----------------------------------|--|
| ARO | Alternative Reporting Options |
| CALD | Culturally and linguistically diverse people |
| CASCG | Child Abuse and Sexual Crime Group |
| CFMU | Clinical Forensic Medicine Unit |
| CIB | Criminal Investigation Branch |
| CPIU | Child Protection and Investigation Unit |
| CPYJ | Child Protection and Youth Justice |
| CSAFE | Child Sexual Abuse Fundamentals Education |
| DFV | Domestic and Family Violence |
| FoCIS | Fundamentals of Child Interviewing Skills |
| HHS | Hospital and Health Service |
| ICARE | Interviewing Children and Recording Evidence |
| ISACURE | Investigating Sexual Assault – Corroborating and Understanding Relationship Evidence |
| JIC | Just in Case Examination |
| LGBTQIA+ | Lesbian, gay, bisexual, transgender, queer, intersex and asexual |
| MOU | Memorandum of understanding |
| ODPP | Office of the Director of Public Prosecutions |
| OIC | Officer in Charge |
| OPM | Operational Procedures Manual |
| QH | Queensland Health |
| QPS | Queensland Police Service |
| SART | Sexual Assault Response Team |
| SASS | Sexual assault support service |
| SCAN | Suspected Child Abuse and Neglect |
| SCU | Sexual Crime Unit |
| Sexual Violence Framework | <i>Prevent. Support. Believe. Queensland's Framework to address Sexual Violence</i> |
| Sexual Violence Response Strategy | <u>QPS Sexual Violence Response Strategy 2021-2023</u> |
| SVLO | Sexual Violence Liaison Officer |
| Taskforce | Women's Safety and Justice Taskforce |

Appendices

1. QPS Organisational Chart
2. Chapter 2 OPM amendments (to be published in June 2022)
3. Sexual Violence Response Strategy – Communication Strategy
4. Sexual Violence Liaison Officer Instruction
5. District Officers Communication Pack
6. Sexual Violence Liaison Officer Trial Evaluation Report – not for publication
7. Sexual Assault Response Team Evaluation Report – not for publication

[end]

Paula Brisotto

From: Brock.AdrianC[OSC] <[REDACTED]>
Sent: Wednesday, 13 February 2019 4:47 PM
To: Justin Howes; Simpfendorfer.GerardM[OSC]
Cc: Hoffman.CarolynP[OSC]; Neville.DavidH[OSC]; Colloppen.RubenB[OSC]; Paula Brisotto; Birchall.ShelleyA[OSC]
Subject: [REDACTED]

Justin,

Thanks for the prompt advice. Let's look at reactivating the intimate samples you have there which have current insufficient DNA, if we have no success, I will look at sending the extra samples down for testing.

Do we know the pending result for the perianal sample. If this is linked to the suspect/offender then may all be a mute point. In saying that I have pressured the I/O to ensure a reference sample is obtained regarding the victim.

If we concentrate on samples already at FSS this way we are completely ruling out the all avenues from the SAIK prior to sending anything further.

Again, thanks for your advice on the sampling to date.

Gerard,

I believe below are the items with insufficient DNA at present which require reactivation

[REDACTED] - HIGH VAGINAL EXHIBIT A - VICTIM SAIK [REDACTED]
[REDACTED] - HIGH VAGINAL EXHIBIT A - VICTIM SAIK [REDACTED]
[REDACTED] - LOW VAGINAL EXHIBIT A - VICTIM SAIK [REDACTED]

Regards

Adrian

Senior Sergeant Adrian Brock

Forensic Coordinator

Central Forensic Area

c/- Rockhampton Police Complex

[REDACTED]
[REDACTED]

From: Justin Howes <[REDACTED]>
Sent: Wednesday, February 13, 2019 4:33 pm
To: Brock.AdrianC[OSC]; Simpfendorfer.GerardM[OSC]
Cc: Hoffman.CarolynP[OSC]; Neville.DavidH[OSC]; Colloopen.RubenB[OSC]; Paula Brisotto
Subject: [REDACTED]

Hi Adrian,

In my opinion, these samples are here and available to be requested for reactivation. Therefore, I would focus on the 'DNA insufficient' samples first given they are intimate swabs, but we will process whatever samples you or delegate decide to request.

Regards

Justin



Justin Howes

Team Leader - Forensic Reporting and Intelligence Team
Forensic DNA Analysis, Forensic & Scientific Services
Health Support Queensland, Queensland Health

[REDACTED]
[REDACTED]
[REDACTED]



Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

From: Brock.AdrianC[OSC] [mailto:[REDACTED]]
Sent: Wednesday, 13 February 2019 4:26 PM
To: Justin Howes <[REDACTED]> Simpfendorfer.GerardM[OSC]
<[REDACTED]>
Cc: Hoffman.CarolynP[OSC] <[REDACTED]> Neville.DavidH[OSC]
<[REDACTED]> Colloopen.RubenB[OSC] <[REDACTED]> Paula Brisotto
<[REDACTED]>
Subject: Re: [REDACTED]

Justin or Gerard,

Considering this is it more advantageous to send the AP positive items from the underwear down for testing, rather than wasting more time on these for little to possibly no result?

cheers

Adrian

Senior Sergeant Adrian Brock

Forensic Coordinator

Central Forensic Area

c/- Rockhampton Police Complex

From: Justin Howes <[REDACTED]>

Sent: Wednesday, February 13, 2019 4:13 pm

To: Simpfendorfer.GerardM[OSC]

Cc: Hoffman.CarolynP[OSC]; Brock.AdrianC[OSC]; Neville.DavidH[OSC]; Collophen.RubenB[OSC]; Paula Brisotto

Subject: RE: [REDACTED]

Hi Gerard

I have had a look at the screening results and the quant values obtained. The findings are not unexpected in my opinion.

There was no unknown female profile because no samples proceeded to be profiled after the quantification stage; they were either 'No DNA Detected' or 'DNA Insufficient...'. This means the samples did not proceed to amplification and then to profile; therefore, no male or female profiles. Please note one sample has proceeded to profiling and has not finished as yet – this was an epithelial fraction from the Perianal swab.

Background that may assist:

When possible semen samples are submitted for DNA extraction, they undergo a Differential Lysis procedure which aims to separate male and female DNA. Extract is separated into a 'spermatozoa fraction' and an 'epithelial fraction'. It is standard procedure to not profile the epithelial fraction of the process for SAIK samples; we haven't profiled these epithelial fractions for SAIK swabs for a number of years due to the high likelihood of there being female DNA matching the donor of the swab. There are some case circumstances where they are profiled however eg. Child complainants, external swabs (eg perianal, vulval).

The spermatozoa fractions for the samples you provided yielded either no semen being detected, or very low numbers of sperm were detected. Consequently, it is not unexpected to return the results that you have.

It is possible to rework any result such as these that have been sent to DNA Mgt. The expanded comment mentions this for DNA Insufficient samples, so please specify the sample/s you wish to be reactivated for DNA profiling through the normal request/task process.

Thanks for organising the victim reference sample as these are always important in sexual assault matters especially.

Regards

Justin



Justin Howes

Team Leader - Forensic Reporting and Intelligence Team
Forensic DNA Analysis, Forensic & Scientific Services
Health Support Queensland, Queensland Health

[Redacted]
[Redacted]
[Redacted]



Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

From: [Redacted] [\[mailto:\[Redacted\]\]](#)

Sent: Wednesday, 13 February 2019 1:27 PM

To: Justin Howes <[Redacted]>

Cc:

[Redacted] [Collopen.](#)

[Redacted]

Subject: [Redacted]

Good afternoon Justin,

We have been approached to provide advice as to why the SAIK from the victim in relation to this case has failed to return any profiles, not even an Unknown Female profile (which would presumably be the victim's) on the High Vaginal swab.

Could you please provide any insight in to why the high vaginal, low vaginal and perianal swabs all failed to return a profile, even the victim's profile?

Was there potentially a problem with the sampling process or the kit?

Is it possible to rework these samples to try to obtain a profile?

We have requested a victim reference sample be obtained to assist with any unresolved profiles or mixtures.

Exhibit List

1 - 18 / 18 Entries

| Barcode | Category | Date | Property Tag FilmNo | Employee | Location |
|--|---------------------|------------|---------------------|------------|-------------------------|
| ██████████3 | Epithelial Fraction | 06/02/2019 | | ██████████ | PSD 728119194 G12 |
| PERIANAL SWAB EXHIBIT A - VICTIM SAIK ██████████ - NCE | | | | | |
| ██████████ | Swab | 04/02/2019 | D3709057 | ██████████ | ██████████728118231 C06 |
| 1 HIGH VAGINAL EXHIBIT A - VICTIM SAIK ██████████ - Forensic and Scientific Services | | | | | |

QHSS POS ██████████ PRESUMP. AP TEST POSITIVE, SUBMITTED - RESULTS PENDING

QHSS POS ██████████ MICRO POSITIVE FOR SPERM. SUBMITTED-RESULTS PENDING

QHSS POS ██████████ DNA INSUFFICIENT FOR FURTHER PROCESSING

| | | | | | |
|--|------|------------|----------|------------|-------------------|
| ██████████ | Swab | 04/02/2019 | D3709057 | ██████████ | PSD 728118132 H05 |
| 2 HIGH VAGINAL EXHIBIT A - VICTIM SAIK ██████████ - Forensic and Scientific Services | | | | | |

QHSS POS ██████████. PSA TEST POSITIVE, SUBMITTED - RESULTS PENDING

QHSS POS ██████████ PRESUMP. AP TEST POSITIVE, SUBMITTED - RESULTS PENDING

QHSS POS ██████████ MICRO POSITIVE FOR SPERM. SUBMITTED-RESULTS PENDING

QHSS POS [REDACTED] DNA INSUFFICIENT FOR FURTHER PROCESSING

| | | | | | |
|------------|------|------------|----------|------------|-------------------|
| [REDACTED] | Swab | 04/02/2019 | D3709057 | [REDACTED] | PSD 728118121 E06 |
|------------|------|------------|----------|------------|-------------------|

LOW VAGINAL EXHIBIT A - VICTIM SAIK [REDACTED] - Forensic and Scientific Services

QHSS POS [REDACTED] PRESUMP. AP TEST POSITIVE, SUBMITTED - RESULTS PENDING

QHSS POS [REDACTED] MICRO NEG FOR SPERM

QHSS POS [REDACTED] SEMEN NOT DETECTED

QHSS POS [REDACTED] DNA INSUFFICIENT FOR FURTHER PROCESSING

| | | | | | |
|------------|------|------------|----------|------------|-------------------|
| [REDACTED] | Swab | 04/02/2019 | D3709057 | [REDACTED] | PSD 728118060 G10 |
|------------|------|------------|----------|------------|-------------------|

PERIANAL EXHIBIT A - VICTIM SAIK [REDACTED] - Forensic and Scientific Services

QHSS POS [REDACTED] MICRO NEG FOR SPERM

QHSS POS [REDACTED] SEMEN NOT DETECTED

QHSS POS [REDACTED] NO DNA DETECTED

| | | | | | |
|------------|-------|------------|----------|------------|-----|
| [REDACTED] | Paper | 04/02/2019 | D3709057 | [REDACTED] | PSD |
|------------|-------|------------|----------|------------|-----|

DROPSHEET EXHIBIT A - VICTIM SAIK [REDACTED] - Forensic and Scientific Services

| | | | | | |
|------------|------|------------|------------|------------|-------------------|
| [REDACTED] | Hair | 04/02/2019 | [REDACTED] | [REDACTED] | PSD 728119263 G02 |
|------------|------|------------|------------|------------|-------------------|

FROM DROPSHEET VICTIM SAIK [REDACTED] - NCE

QHSS POS [REDACTED] NO DNA DETECTED

Kind regards

Gerard

Gerard Simpfendorfer
Senior Sergeant 4009415
DNA Management Section, Forensic Services Group

Operations Support Command, Queensland Police Service

[Redacted text block]



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Kylie Rika

From: Kylie Rika
Sent: Wednesday, 8 July 2015 4:43 PM
To: Justin Howes
Subject: CONFIDENTIAL FW: Project plan Proposal #163 Auto Mic

When I was last acting for you, Paula and I discussed a data dump to look at this. It was never classified as a formal project. Then it was put on hold as per your advice. Then the green light came from you and Cathie (re reducing TATs) to go ahead with the "m'con project". So I did. I already had the green light from you and Cathie - it wasn't like a project plan was going to stop the work from happening if the other mgmt team members didn't like it.

There was also a bit of pressure to have some results for your QPS meeting - so what first - the work or the plan - what would QPS have appreciated more?

I can never get an email from her without some little dig in it...

I know, I know....suck it up.....

Kylie Rika BSc. PGDip (Forensic Science)
Senior Scientist - Forensic DNA Analysis
Police Services Stream | Forensic & Scientific Services | Health Support Queensland
Department of Health | Queensland Government

[REDACTED]

[REDACTED]



From: Cathie Allen
Sent: Wednesday, 8 July 2015 4:06 PM
To: Kylie Rika
Subject: RE: Project plan Proposal #163 Auto Mic

Hi Kylie

I would recommend that an Acceptance Criteria is included in the project proposal. Something like 'Recommendation to be put forward to the Decision Making Group if there is a clear trend which highlights a different quant value to use which may achieve a DNA profile after Microcon'. I'm sure you'll have better wording, but was thinking that some type of qualifier would be of value.

For future projects, could the project proposal be circulated and signed off prior to the commencement of the work.

Cheers
Cathie

From: Kylie Rika
Sent: Tuesday, 23 June 2015 4:18 PM
To: Justin Howes; Kirsten Scott; Amanda Reeves; Allison Lloyd; Luke Ryan; Allan McNevin; Emma Caunt; Cathie Allen
Subject: Project plan Proposal #163 Auto Mic

Hello

Please find attached the project plan for proposal # 163.

Your feedback ASAP would be appreciated.

thanks

Cathie Allen

From: Cathie Allen
Sent: Thursday, 9 July 2015 2:35 PM
To: Kylie Rika
Subject: RE: Project plan Proposal #163 Auto Mic

Hi Kylie

I don't have any other feedback for the plan.

Cheers
Cathie

From: Kylie Rika
Sent: Thursday, 9 July 2015 1:47 PM
To: Cathie Allen; Justin Howes; Sharon Johnstone; Amanda Reeves; Emma Caunt; Allan McNevin; Luke Ryan; Kirsten Scott
Subject: Project plan Proposal #163 Auto Mic

Hello

Please find attached an updated version of the project proposal with feedback incorporated. If there is no further feedback I will send around a hardcopy for signing.

thanks



HealthSupport
Queensland

Assessment of results obtained from ‘automatic- microcon’ samples

**Josie Entwistle, Allison Lloyd,
Kylie Rika, Thomas Nurthen,
Cathie Allen**

August 2015

Assessment of results obtained from 'automatic-microcon' samples

Published by the State of Queensland (Queensland Health), July 2015



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For more information contact:

Forensic DNA Analysis, Department of Health, GPO Box 48, Brisbane QLD 4001

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Document details

Contact for enquiries and proposed changes

If you have any questions regarding this document or if you have a suggestion for improvements, please contact:

Contact officer: Josie Entwistle
 Title: Scientist – Forensic Intelligence & Reporting
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 Email: [REDACTED]

Version history

| Version | Date | Changed by | Description |
|---------|------------|-----------------|--------------|
| 0.1 | 11/11/2015 | Josie Entwistle | First Draft |
| 0.2 | 04/12/2015 | Josie Entwistle | Second Draft |

Document sign off

This document has been **approved** by:

| Name | Position | Signature | Date |
|--------------|--------------------|-----------|------|
| Cathie Allen | Managing Scientist | | |

This document has been **endorsed** by:

| Name | Position | Signature | Date |
|------------------|-------------------------------|-----------|------|
| Justin Howes | Team Leader FRIT | | |
| Luke Ryan | A/Team Leader ER & Q | | |
| Sharon Johnstone | Senior Scientist Intel Team | | |
| Kirsten Scott | Senior Scientist Q & P | | |
| Allan McNevin | Senior Scientist ER | | |
| Megan Matheison | A/Senior Scientist Analytical | | |
| Amanda Reeves | Senior Scientist Reporting 1 | | |
| Kylie Rika | Senior Scientist Reporting 2 | | |

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1. Abstract

Since December 2012, casework samples with the parameters of PowerPlex priority 1 or 2, and have yielded a quantification value between 0.00214 ng/μL and 0.0088 ng/μL have been automatically processed with a Microcon Centrifugal Filter Device concentration step.

An assessment of results from these samples has been conducted.

Relevant data was extracted from AUSLAB, sorted, reconciled and interrogated. Broad categories of informative results and non-informative results were used based on result types that the Queensland Police Service consider informative (including single source and interpretable 2 and 3 person mixtures) and non-informative (complex profiles, no DNA detected, no DNA profile obtained).

From 1001 assessable samples, 184 yielded an informative result, with 79 samples being uploaded to NCIDD.

2. Introduction

Currently (and since 19/12/12), any priority 1 or 2 PowerPlex® 21 (PP21) casework samples that produce DNA extracts with a quantification value of between 0.00214 ng/μL and 0.0088 ng/μL are sent automatically for a concentration step using a Microcon® Centrifugal Filter Device. This concentration step was introduced as part of PP21 implementation in an effort to minimise the stochastic effects observed at these lower quantification values and improve the overall quality of the profile.

It has been observed anecdotally within the laboratory, that samples which have been sent automatically for concentration (quantification between 0.00214 ng/μL and 0.0088 ng/μL) often yield a DNA profile result which is unsuitable for interpretation or comparison (deemed 'non-informative'). In addition, the timeframe (from quantification to result release) can be seen to be lengthy, in comparison to other samples types, particularly if the sample has required further amplification/s to enhance or confirm the profile result.

As part of the laboratory's commitment to ongoing quality assessment, and improvement of processes and results released, an assessment of samples processed by automatic-microcon has been conducted. This assessment includes observations of the number of samples processed by automatic-microcon that are deemed 'informative' by QPS and the number of samples that have been nominated for uploading to NCIDD. This assessment also outlines possible process alternatives, including risks and benefits, and taking into consideration the opportunity to improve turn around times, laboratory expenditure, the ability to incorporate the recently

introduced Number of Contributors Guidelines to a broader range of suitable samples, and improvement of the quality of profiles and results issued.

3. Materials and Methods

3.1 Materials

The following resources have been required for this data mining project:

Staff

Computers (including applications such as Excel and AUSLAB)

PP21 case work samples that have already been processed within the laboratory via the automatic microcon concentration step

3.2 Methods

Extended enquiries functionality in AUSLAB was used to extract data pertaining to all samples with MCONC1 test codes with received dates from 2012 – March 2015 that have a 'parent' EXH (i.e. not sub-samples). This data dump included the following fields:

Sample ID

QP number

Result type (based on EXH lines released)

NCIDD upload

Original quantification value

Additional quantification values

Additional test codes

Sample type

Case type

A worksheet in Excel was created, containing the data from the data dump. This data was further sorted into columns and refined/filtered to produce only concentrated samples within the laboratory's 'automatic-microcon' quantification range.

Samples with 'no further work required' requests were removed from the data set as these samples couldn't be assessed and would otherwise skew the data.

The data was then interrogated in an attempt to observe any trends that may have suggested proposing changes to current laboratory processing rules and workflow.

4. Results and Discussion

Results

A data set of 1136 samples that had been concentrated via an automated microcon process was obtained. This was reduced to a data pool of 1001 assessable samples (designated as the assessable data pool), once samples with 'no further work required' requests were excluded.

From this data pool, 817 samples yielded a result that was considered non-informative (complex unsuitable, no DNA profile, no DNA detected). This represents ~82% of the assessable data pool.

184 samples yielded a result that was considered informative (single source, 2 person mixed DNA profile, 3 person mixed DNA profile). This represents ~18% of the assessable data pool.

Of the informative results, 127 samples yielded 2 or 3 person mixed DNA profiles and 57 samples yielded single source DNA profiles. Therefore the mixed DNA profile result samples represented ~12% of the assessable data pool, and ~69% of the informative result pool. The single source DNA profile result samples represented ~5% of the assessable data pool, and ~30% of the informative result pool.

79 samples from the assessable data pool obtained profiles that were uploaded to NCIDD. This represents ~8% of the assessable data pool and ~42% of the informative result pool. Some of the profiles uploaded to NCIDD were from sole samples within a case, and some of these NCIDD uploads resulted in 'cold links'.

| | Total from assessable pool | Percentage of total | Percentage of informative |
|---------------------------------------|-----------------------------------|----------------------------|----------------------------------|
| Total assessable results | 1001 | 100% | N/A |
| Informative | 184 | 18% | N/A |
| Non-informative | 817 | 82% | N/A |
| NCIDD | 79 | 8% | 42% |
| Single source DNA profiles | 57 | 5% | 30% |
| Informative mixed DNA profiles | 127 | 12% | 69% |

Table 1 Automatic-microcon category data

Observations can be made from the assessment of the categories of samples against quantification values.

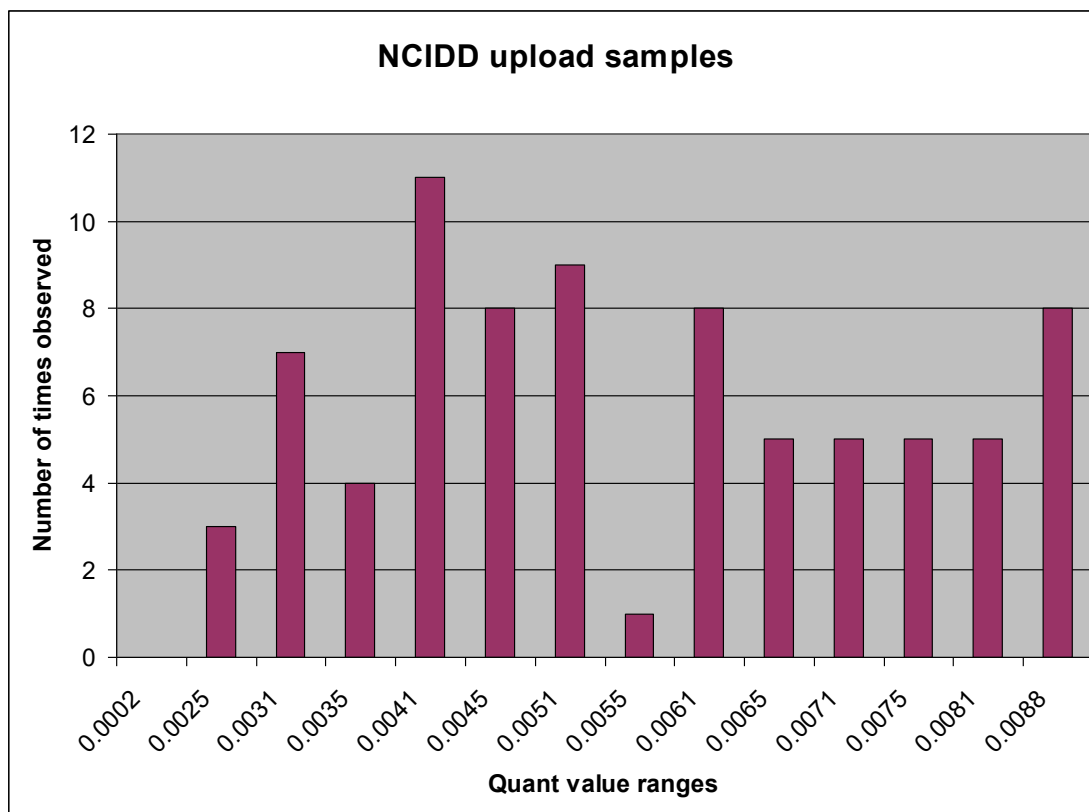


Figure 1 NCIDD upload samples

Automatic-microcon samples uploaded to NCIDD can be observed (see Figure 1) at each of the quant value ranges, with the exception of the range between 0.002 ng/ μ L and 0.0025 ng/ μ L and the single NCIDD upload at the quant value range of 0.0055 ng/ μ L to 0.0061 ng/ μ L.

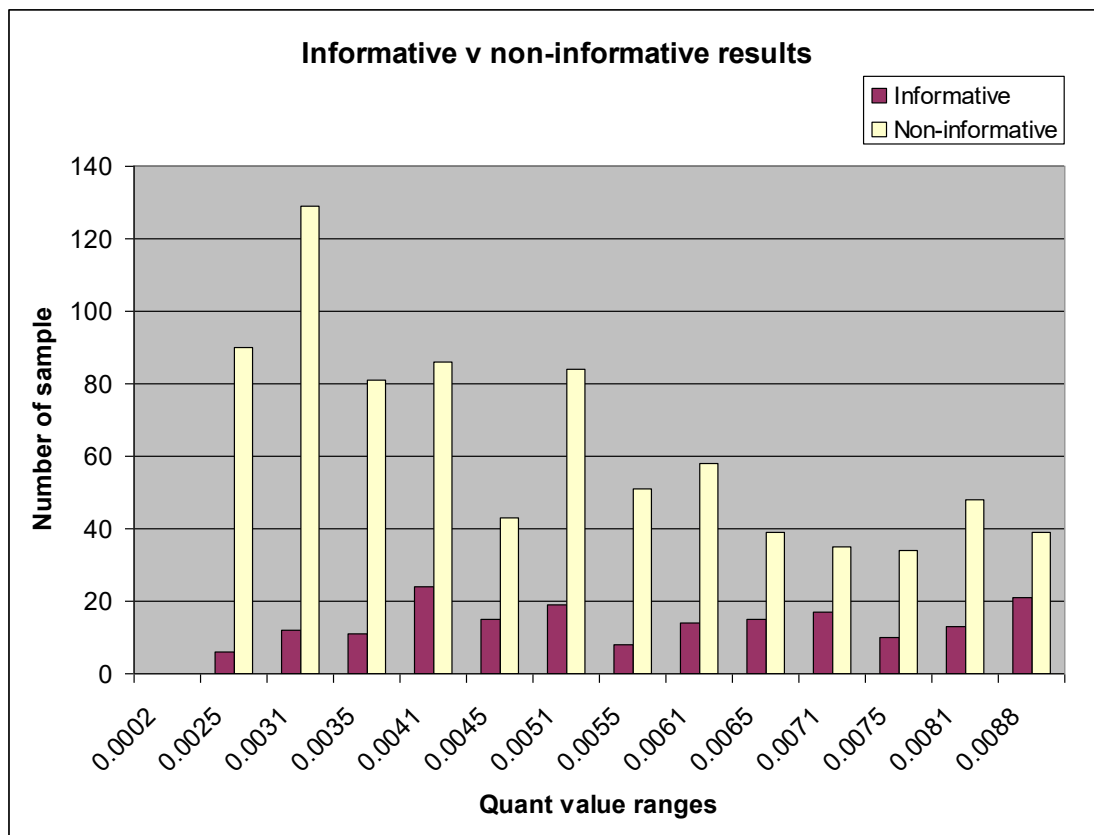


Figure 2 Informative v non-informative results

The number of non-informative results can be observed (see Figure 2) to decrease beyond the quantification value of 0.0035 ng/ μ L and become closer in occurrence with the numbers observed for informative results.

The number of informative results can be observed to be less than those of non-informative results for the majority of the quantification value ranges and remain fairly consistent across the quantification value ranges.

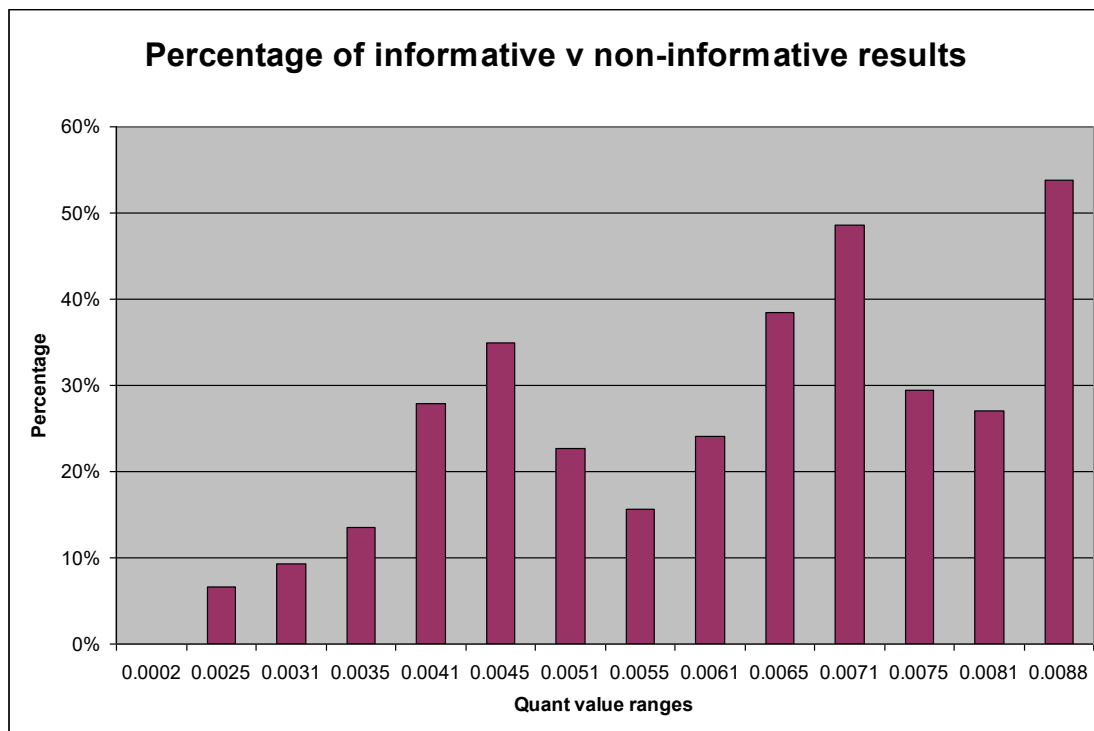


Figure 3 Percentage of informative v non-informative results

The percentage of informative v non-informative results can be observed (see Figure 3) to increase on the whole, with some fluctuation across the quantification value ranges. The lowest percentage of informative v non-informative occurs at the lowest quantification value range and the highest percentage occurs at the highest quantification value range.

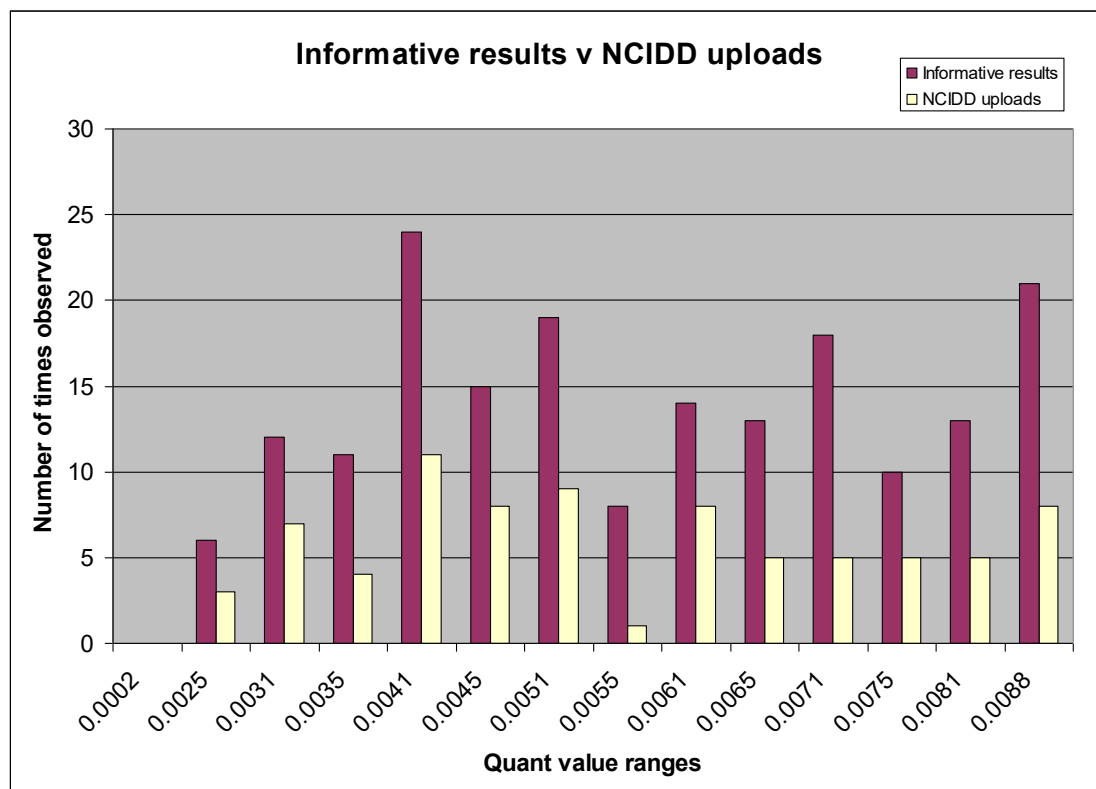


Figure 4 Informative results v NCIDD uploads

The number of samples uploaded to NCIDD can be observed (see Figure 4) to be generally consistent with the informative results and approximately half for each quantification value range. The number of samples uploaded to NCIDD is observed to be highest at the quantification value range of 0.0041 and lowest at the quantification value range of 0.0055 ng/ μ L.

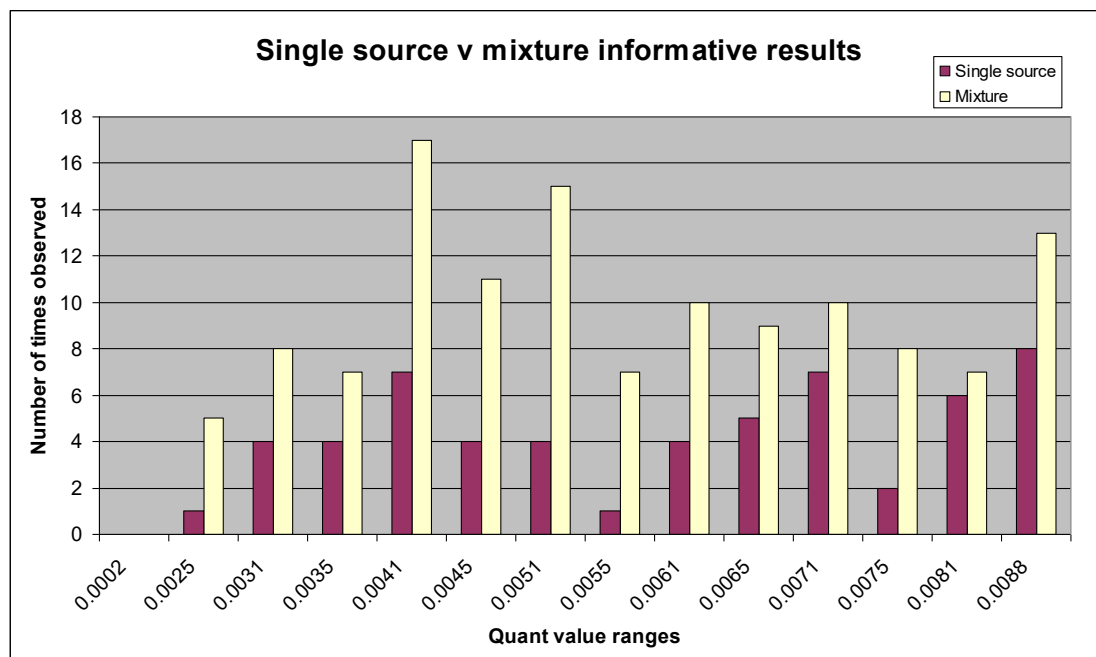


Figure 5 Single source v mixture informative results

The number of mixed DNA profile informative results can be observed (see Figure 5) to be higher than that of single source results. The highest number of informative mixture results can be observed at the quantification value range of 0.0041 ng/ μ L, and it appears that the bulk of the informative mixed DNA results occur beyond this quantification value range.

The single source informative results can be observed at each of the quantification value ranges and appears to fluctuate across the quantification value ranges.

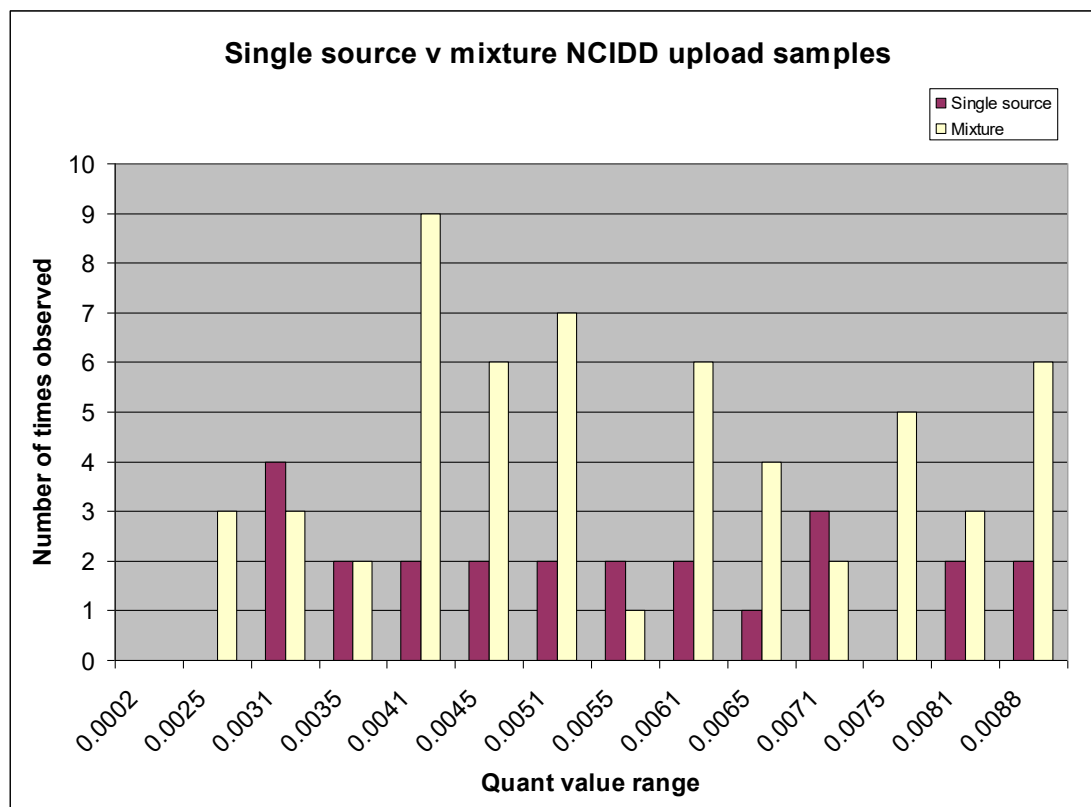


Figure 6 Single source v mixture NCIDD upload samples

The number of mixed DNA profiles uploaded to NCIDD can be observed (see Figure 6) to be highest at the quantification value range of 0.0041 ng/ μ L and lowest at the quantification value range of 0.0055. It appears that the bulk of uploads from mixed DNA profiles occurs beyond the quantification value range of 0.0041 ng/ μ L.

The number of NCIDD uploads from single source profiles can be observed to be less than that from mixed DNA profiles and with the exception of no uploads within the quantification value ranges of 0.0025 ng/ μ L and 0.0081 ng/ μ L, appears to be fairly consistent within the quantification value ranges.

Discussion

This data assessment has not been an in-depth study and more detailed statistical analyses was outside the scope, however the data obtained has shown that informative results were obtained across the quantification value ranges within the automatic-microcon process parameters as well as samples uploaded to NCIDD, even at the lowest quantification value ranges.

No real trend was observed for the number of informative results obtained, other than there being informative results and NCIDD uploads across the automatic-microcon quantification range. It appears that across the quantification value ranges, the number of samples loaded for NCIDD was approximately half of the number of informative

results obtained and this was generally consistent across the quantification value ranges.

A decline in non-informative results was observed as the quantification value increased. Given the observations in the PP21 validation of greater stochastic effects at lower quantification ranges, this observation is not unexpected.

It was observed that interpretable mixed DNA profiles were obtained and were greater in number than single source results, indicating that not all interpretable results from the automatic-microcon process are single source and that not all mixed DNA profile obtained are non-informative. Additionally, it can be seen that NCIDD uploads were obtained from both single source and mixed DNA results and a higher number of the NCIDD uploads were from mixed DNA profiles than from single source. These observations were consistent across the quantification value ranges.

An important point to note is that there are numerous other variables involved in whether a sample is nominated to upload to NCIDD and therefore, it is difficult to capture the true number of samples suitable for NCIDD uploading from the data pool.

Additionally, there may be a higher significance placed on some of these samples nominated for NCIDD upload, such as a sample being the only sample within the case, the priority and/or case type, and the potential (and actuality) for “cold links” arising from these uploads.

We don't have data from a similar assessment of informative vs non-informative results from samples processed outside the automatic-microcon quantification range to make a comparison. It is possible that what is observed here is similar for all quantification values and therefore these results shouldn't be overstated.

New instruments and processes are soon to be introduced into the laboratory and possibly in the future (Quant Trio, QIASymphony and Yfiler, for example). These instruments and process may introduce variations to the data observed here and may indicate changes to the processes, irrespective of any possible changes made at this point.

5. Conclusions and Recommendations

This assessment has indicated that there has been value in the automatic-microcon process, with informative results and NCIDD uploads obtained across the quantification value range, including the lowest value ranges, albeit with a high number of non-informative results, which declined as the quantification value increased.

A higher number of informative mixed results were obtained, which also represented the bulk of samples nominated for NCIDD.

NCIDD uploads were obtained across the quantification value ranges and were obtained from both mixed and single source samples and importantly, some of these uploads led to 'cold links' and some were from sole samples within a case.

It is possible that these observations are similar to observations that could be made for samples processed outside of the automatic-microcon process.

Automatic-microcon process changes, along with introduction of new laboratory instruments may assist in changing the balance of informative to non-informative results.

Based on the analysis of the data, an assessment of current practices and the risks and benefits, two process change options can be considered.

Process change consideration 1

One possible change to current process could be to submit all samples within the current automatic-microcon quantification range to a half microcon instead of full. Processing as half microcon would provide additional remaining volume to allow for additional amplification runs to enable reproducibility assessments.

Samples falling within this range could be directed to this process step automatically within the Forensic Register.

These samples could then be directed (again by the FR) to a separate CM list, bearing in mind that a large number of these samples may be mixtures and possibly non-informative at first run.

Any samples that can be initially interpreted with a final result could be assessed at this stage, much in the same way that the complex and single source case management lists operate currently.

Profiles that are assessed as requiring additional runs for reproducibility assessments could join the normal CM processing stream after the reworks have been requested.

Benefits

This option seeks to improve upon the already implemented automatic-microcon process, which has shown some success with obtaining informative results and NCIDD uploads from samples within higher stochastic quantification value ranges.

This option presents the least risk with regards to loss of informative results and loss of NCIDD uploads (including cold links).

All samples are given an opportunity for additional processing which may improve the initial result and/or possibly give more confidence with regards to number of contributors present and allowing for interpretation of an informative result.

Additionally, this allows for the use of the newly introduced Number of Contributors Guidelines, being a more consistent approach as with other PP21 samples, as currently the automatic-microcon samples cannot be case managed in this way as there is insufficient remaining volume.

A separate work list for these sample types may result in reduced turn around times for result reporting as some profiles can be reported with final results, with others having their additional runs ordered concurrently at the time of assessment, all from a smaller work list than the general categories in current use.

No additional time awaiting results would be experienced for samples requiring additional runs as both additional runs (XAMP1 and XAMP2) could be requested at the same time as they are likely to be required at full amplification volume.

Risks and disadvantages

The number of samples processed within this category will not be reduced and may in fact, increase with additional runs being requested for reproducibility assessments. The possible additional run (XAMP2) would increase the cost to the laboratory in terms of consumables, staff and time spent on task, including interpretation. This may also increase the turn around time for release of results with the interpretation of an additional profile with a reproducibility calculation.

Additional runs would increase the cost to the laboratory, in terms of staff, consumables and time spent on task (as opposed to other samples).

Process change consideration 2

An alternative to the above recommendation is to hold all samples within the current automatic-microcon range of 0.002 ng/ μ L and 0.0088 ng/ μ L. This would exclude all samples within the automatic-microcon quantification range from processing and case management, with the exception of samples within agreed parameters.

Priority 1 samples and sole samples within a case would be an exception from the hold process and could proceed to a half microcon.

Additionally, there may be an option for held samples to be reactivated if the remainder of samples within the case have yielded non-informative results.

A result line similar to “low DNA” would be sent and either at the discretion of QPS or Forensic DNA Analysis, these samples could be reactivated and proceed to a half microcon with further reworks as required and join the existing case management process.

Benefits

This option would reduce the amount of samples requiring processing (approximately 35 samples per month) and therefore provides the most benefit with regards to turn around times and cost, in terms of consumables, staff and time spent on task.

Risks and disadvantages

Turn around times would increase for reactivated samples, more so than for those requiring additional runs as in Option 1 due to the lag time of reactivation once the initial results have been released and actioned.

This option represents the highest risk for loss of informative results and NCIDD uploads from samples that are not reactivated.

This option gives less of an opportunity for possible improvement of the number of informative results released and uploads to NCIDD as the number of samples being processed by half microcon and with additional runs for reproducibility calculations would be reduced.

Despite the exclusion of Priority 1 samples and sole samples within a case, there remains a risk of possible informative results and NCIDD uploads being lost, with the potential for different informative results and NCIDD uploads not being processed.

Reporting of statements may be affected if reactivation of samples is desired after statement request as there may be limited time for processing and interpretation of samples.

This option represents a higher potential CM burden for analytical staff, with an increased amount of samples requiring validation of “low DNA” results.

Process change consideration 3

No change to existing process.

Benefits

Samples continue to have an opportunity to have improved results from concentration.

Number of samples requiring this process would not be increased.

No additional cost to the laboratory in terms of staff, time, consumables or funds.

Risks and disadvantages

Number of samples requiring this process wouldn't decrease.

No change in cost to the laboratory in terms of staff, time, consumables or funds.

No opportunity to improve the results for low quant samples.

Process change consideration 4

Finalise this project at this time, using the concept of this project for an assessment of this process six months post-implementation of the Forensic Register, in conjunction with QuantTrio.

Benefits

More effective and efficient use of data with the Forensic Register, with ability to capture additional parameters provided by QuantTrio and the Forensic Register including interpretation and Degradation Index.

Data reflective of procedures, instruments and LIMS in use at the time of data capture.

Better opportunity to suggest process improvements conducive to the technology, workflow and LIMS in use at that time.

Risks and disadvantages

Number of samples requiring this process wouldn't decrease for the short-term at least.

No change in cost to the laboratory in terms of staff, time, consumables or funds in the short-term.

No opportunity to improve the results for low quant samples in the short-term.

General recommendations and considerations

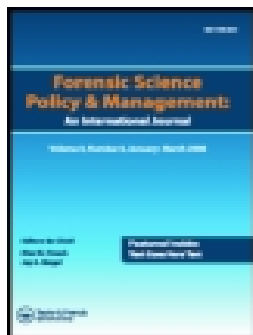
It is recommended that this project be finalised at this point and a new project commence approximately six months after the introduction of the Forensic Register; in conjunction with the use of QuantTrio. The concept of this project would be used to guide the new project in terms of a starting point for data mining and parameters of interest.

6. Abbreviations

| | |
|-------|--|
| CM | Case management |
| DNA | Deoxyribonucleic Acid |
| NCIDD | National Criminal Investigation DNA Database |
| QPS | Queensland Police Service |
| FR | Forensic Register |

7. References

- 1 Nurthen, T, Mathieson, M and Allen, C, *PowerPlex 21 – Amplification of Extracted DNA Validation v2.0*. Forensic DNA Analysis, Forensic & Scientific Serves, 2013



Forensic Science Policy & Management: An International Journal

ISSN: 1940-9044 (Print) 1940-9036 (Online) Journal homepage: <http://www.tandfonline.com/loi/ufpm20>

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To cite this article: Naftaly Einot, Moshe Shpitzen, Lev Voskoboinik, Jonathan Roth, Ilan Feine & Ron Gafny (2017): Reducing the Workload: Analysis of DNA Profiling Efficiency of Case Work Items, Forensic Science Policy & Management: An International Journal, DOI: [10.1080/19409044.2017.1332117](https://doi.org/10.1080/19409044.2017.1332117)

To link to this article: <http://dx.doi.org/10.1080/19409044.2017.1332117>



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Reducing the Workload: Analysis of DNA Profiling Efficiency of Case Work Items

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ABSTRACT

Due to the increased sensitivity of genotyping kits developed in recent years, laboratories were able to recover more usable information from smaller amounts of DNA on items of evidence (e.g., touch evidence). This led to increased submission of touch or trace DNA items, which in turn increased the overall workload (van Oorschot, Ballantyne, and Mitchell 2010).

In this work, the data collected from approximately 650 cases and 2,000 evidence items was analyzed in order to study the work efficiency, to optimize evidence items processing and to give guidelines for reducing the workload. We examined three aspects: the DNA profiling efficiency for each item type; the number of samples required to obtain a DNA profile from an item; the number of items needed to be examined to obtain a database eligible profile for each case.

To examine DNA profiling efficiency of various items, the productivity Index (PI) grade was calculated on a scale of 0–10 which measures the success rate and the amount of work required for DNA profiling. To the best of our knowledge, this is the first study that measures the combination of DNA profiling success rate and the work required to obtain it.

Body fluids items (blood and saliva) were the most efficient biological sources for DNA profiling (PI 6) while clothing items were less efficient (PI 2.6). Touch items were the least efficient (PI 1.6).

The successful recovery rate of a single source or a major DNA profile increased when items were sampled twice rather than once. No significant increase was obtained when items were sampled more than twice.

Four to five items per case was found to be the optimal number of items to be tested in a case in order to reduce the workload and increase the number of DNA profiles included in the DNA database.

ARTICLE HISTORY

Received 30 January 2017
Accepted 15 May 2017

KEYWORDS

Forensic science; DNA success rates; laboratory workload; forensic process

Introduction

In the past, the main sources of DNA on case items were body fluid stains such as blood, semen, and saliva (Walsh, Metzger, Higuchi 1991; Walsh et al. 1992). Such stains are easy to detect visually or by using a variety of presumptive tests, usually contain high DNA concentrations and rarely require mixture analysis. In recent years there were technological advances in collection, amplification and interpretation of trace DNA evidence from case-work items such as clothing and touched items (van Oorschot, Ballantyne, and Mitchell 2010). This type of biological material cannot be attributed to a specific body fluid or tissue and is deposited by direct or secondary transfer (Feine, Shpitzen, Roth, and Gafny 2016). Consequently, the workload in DNA casework laboratories increased for three different reasons. First, due to the increase in the

recovery potential of items to provide sufficient DNA for amplification, more items are collected at a crime scene and sent to the lab. Second, the number of samples per item increased since the location of trace DNA on an item is unknown. Finally, interpretation of results became more complex due to an increase in the frequency of mixed DNA profiles. The increasing workload in our lab, as in other forensic labs (National Institute of Justice 2006; Peterson, Crim, and Hickman 2005; Nelson 2011; Maguire, Houck, Williams, and Speaker 2012) has caused a significant backlog in case processing.

Several studies examined the DNA yield from different case items, different sampling techniques, the percentage of DNA profile database inclusion and the percentage of cold hits in DNA databases (Castella

and Mangin 2008; Bond and Hammond 2008; Mapes, Kloosterman, van Marion, and dePoot 2016). However, the data examined in these studies lack an analysis of the amount of work invested in DNA profile recovery. In addition, they did not address the overall success per case.

The aim of this work was to examine ways to manage the increasing workload. Three aspects were examined: (1) DNA profiling efficiency for each evidence item type; (2) number of samples required to obtain a DNA profile from an item; and (3) number of items needed to be examined in each case to obtain a database eligible profile.

To address these aspects, a method was created to calculate the efficiency of DNA profile recovery by estimating the work invested in processing the item in relation to the percentage of successful DNA profile recovery.

Materials and methods

DNA profiling

Case items were sampled by swabbing, cutting or tape lifting according to the lab S.O.Ps. Presumptive tests such as Kastle-Meyer, BlueStar[®] and Phadebas[®] (Tobe, Watson, and David 2007; Virkler and Lednev 2009) were performed prior to sampling, when required.

Samples were processed using the following kits and instruments: DNA extraction: AutoMate Express[™] Forensic DNA Extraction System combined with PrepFiler Express[™] or PrepFiler Express BTA[™] chemistries (Applied Biosystems[®], CA). Quantification: Quantifiler Duo DNA Quantification Kit (Applied Biosystems[®], CA) and GeneAmp PCR System 9700 (Applied Biosystems[®], CA). DNA amplification: Powerplex[®] ESI 16 kit (Promega, WI) in a GeneAmp[®] PCR System 9700 Thermal Cycler (Applied Biosystems[®], CA). Capillary electrophoresis was performed by the 3500xl Genetic Analyzer or 3130xl Genetic Analyzer (Applied Biosystems[®], CA).

Data collection

The data consists of 644 cases and 2016 items processed in our laboratory during the first half of 2013.

Sexual assault, high volume crime, and murder cases have specific considerations in item sampling in our lab, thus can bias results of this work. The

laboratory policy in high volume crime cases (burglary and motor vehicle theft) is to limit the item type to blood and saliva only (blood stains, cigarette butts, drinking and food items) and to perform only one attempt with each item to obtain a DNA profile. The processing policy of homicide and sexual assault cases is independent of workload considerations and thus not affected by the results of the present study. Therefore, they were excluded from this dataset. The dataset included crime types such as non-sexual assault, arson, robbery, terrorism, car accidents, drugs, and weapons. These cases mount up to approximately 50% of the total number of cases processed in our laboratory.

Data collected about the processing of case items was summarized and included the following:

- **Type of evidence items:**

The type and number of case items received per case and the number of samples taken from each item. Case items were grouped by type into three categories: body fluids, clothing and touch items (see Table 1).

- **Presumptive tests:** such as Kastle-Meyer (KM), BlueStar, Phadebas (if performed).

- **DNA profile interpretation:**

Table 1. Case-Items Categories

| Item category | Items type | Number of items | Number of samples |
|----------------|---|-----------------|-------------------|
| Body fluids | Total: | 683 (34%) | 837 (25%) |
| | • Cigarettes | 152 (22%) | 158 (19%) |
| | • Blood stains | 374 (55%) | 491 (59%) |
| | • Saliva items (chewing gum and other Phadebas positive items) | 38 (6%) | 60 (7%) |
| | • Drinking items (bottle necks, drinking cans. Not tested for saliva) | 119 (17%) | 128 (15%) |
| Clothing items | Total: | 268 (13%) | 607 (18%) |
| | • Clothing | 85 (32%) | 200 (33%) |
| | • Gloves | 95 (35%) | 192 (32%) |
| | • Head covering items (ski masks, helmets, scarfs, etc.) | 88 (33%) | 215 (35%) |
| Touch items | Total: | 1065 (53%) | 1845 (56%) |
| | • Cellphone | 33 (3%) | 37 (2%) |
| | • Cable tie | 32 (13%) | 35 (2%) |
| | • Weapons | 141 (10%) | 469 (25%) |
| | • Working tools | 103 (9%) | 150 (8%) |
| | • Packaging cloth items (bags, socks, and cloth) | 93 (14%) | 158 (9%) |
| | • Other (explosive device components, ropes, plastic bags, handles, lighters, etc.) | 145 (40%) | 301 (16%) |
| | • Adhesive tapes | 422 (5%) | 538 (29%) |
| | • Papers | 57 (4%) | 115 (6%) |
| | • Wires | 39 (22%) | 42 (2%) |
| | Total | | 2016 |

Data obtained from each case item was designated into three categories. (1) A single source or major profile: The number of DNA profiles suitable for DNA database inclusion (a single source or a major profile that has at least 8 STR loci). (2) A mixture: the number of samples that contain a complex mixture profile, which can be used for suspect exclusion only. (3) A negative result: Samples that had insufficient DNA for amplification (less than 250pg) or failed to amplify.

In addition, the total number of profiles submitted to the DNA database for each item and case were counted.

A detailed workflow diagram is presented in Figure 1.

To study the marginal benefit of multiple sampling an effort was made to focus on items with numerous samples. Since the analyzed dataset did not contain an adequate number of items sampled 5 times or more, a second dataset was collected composed of 100 items

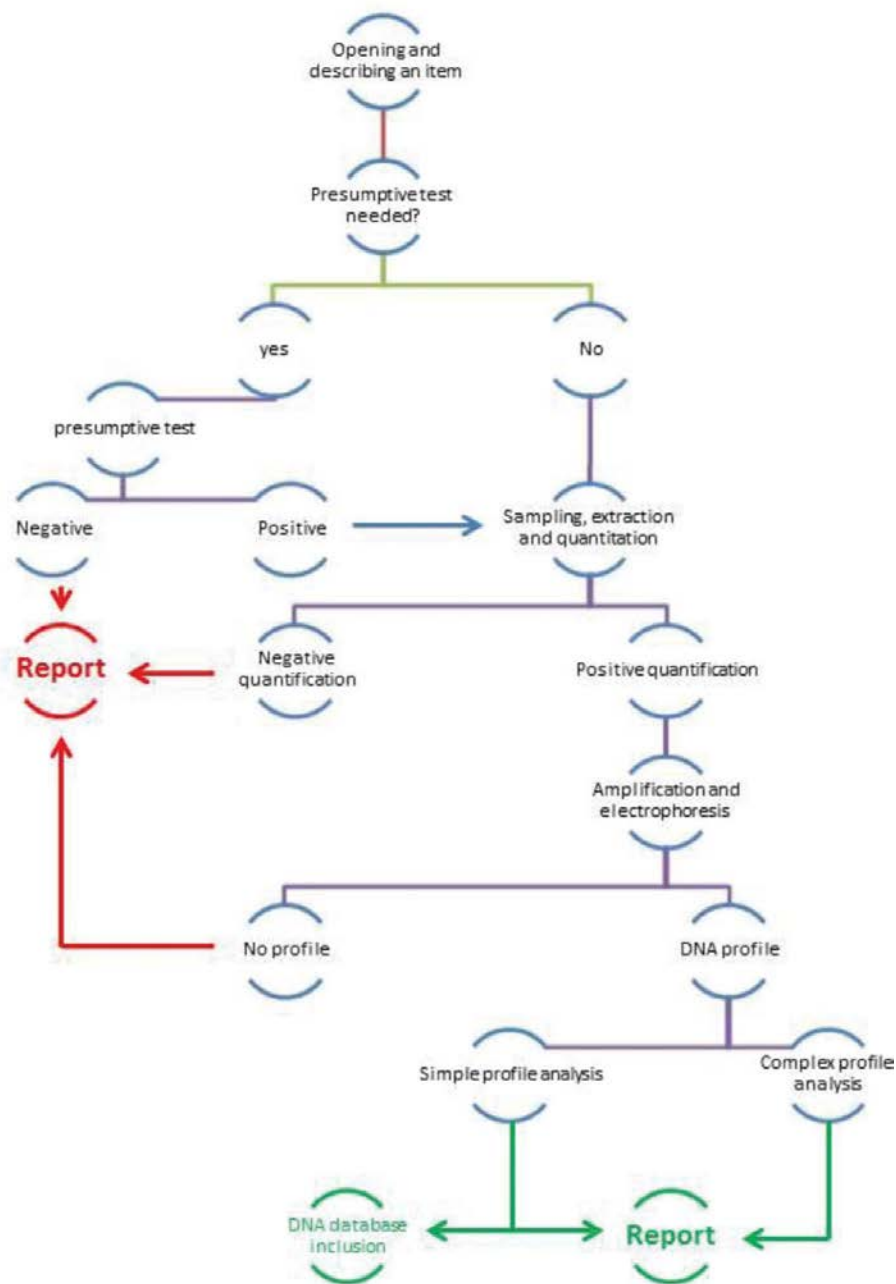


Figure 1. A detailed workflow diagram describing sample processing.

that have been sampled at least 5 times (upon first sampling session).

Productivity index (PI)

To evaluate the DNA profiling efficiency for each item type the DNA forensic testing was approached as a cost benefit system (Speaker 2009), where the benefit is the success rate of an item and the cost is the amount of work invested in testing the item (presumptive tests, sampling, and profile analysis). Success was defined as an item with at least one DNA profile suitable for DNA database inclusion, according to the Israel Police National DNA Database guidelines (a single or major DNA profile with at least 8 STR loci). All profiles included in the database were counted, regardless to whom they belonged. Success rate for each item type was calculated as:

$$\text{Success rate} = \frac{\text{(number of successful items)}}{\text{(total number of case items)}}$$

To calculate a normalized amount of work invested in each item, the actual amount of work on a specific item was calculated relative to the work that needed to be invested in an ideal item. An ideal item is considered an item which was sampled once with 100% success rate providing a DNA profile and without performing any presumptive tests.

The amount of work spent on a specific item was estimated by using an assigned work unit (AWU) scale. To this end, a survey was conducted among 10 analysts in our laboratory. They were asked to evaluate the amount of work required for each step of the DNA

Table 2. The AWU (Assigned Work Unit) Index.

| Work steps | AWU | Multiplication |
|------------------------------------|-----|---|
| Opening and describing an item | 5 | |
| Blood presumptive test | 1 | |
| Saliva presumptive test | 5 | |
| Sample extraction and quantitation | 3 | The number of samples taken |
| Amplification and electrophoresis | 3 | The number of samples with DNA |
| Simple profile analysis | 5 | The number of samples with single or major DNA profiles |
| Complex profile analysis | 10 | Samples with mixed profiles |

Notes: for each step of DNA profiling process AWU was defined. In order to calculate the total AWU for each item the AWU for each step multiplied with the multiplication column as described. A cigarette butt for example has 5 AWU for opening plus 3 AWU for sampling extracting and quantitating plus 3 AWU for replicating and electrophoresis and additional 5 AWU for single DNA profile analysis resulting in 16 AWU.

profiling process. The results of this survey served as a basis for AWU scale (shown in Table 2).

The relative work unit (RWU) is defined as the total AWU calculated for each item divided by 16, the amount of AWU of the most efficient item, which is sampled once with no presumptive tests and provides a profile suitable for DNA database inclusion. For a calculation of a cigarette butt, see notes in Table 2).

As mentioned above, the efficiency for DNA profiling of an item type is the success rate divided by the work invested. Hence, the productivity Index (PI) of an item type was calculated as its success rate divided by the average RWU. To present the data in a scale of 0–10 we multiplied the fraction result by 10, providing the PI (success over work) grade:

$$PI = \frac{\text{success rate}}{\text{average RWU}} \times 10$$

In this study only the steps described in Table 2 were considered. These steps are commonly used in forensic labs worldwide. Other aspects influencing the amount of work invested can vary between labs and therefore can significantly influence the PI grade. In order to create a common basis for evaluating the items efficiency between labs, several aspects such as financial costs, report writing and Q.A were excluded.

Results and discussion

The results in this study cover three different aspects: first, the effectiveness of recovering DNA profiles from different case items by assigning a 0–10 PI grade. Second, the effect of number of samples per item on the probability of recovering a DNA profile and finally the optimal number of items sent to the lab per case for efficient DNA profiling.

Productivity index (PI)

Item type success rate

Among items examined in this study, 34% were from the body fluids category, 13% were clothing and 53% were touch items (Table 1).

Table 3 summarizes the success rate for each category; body fluids, clothing and touch item, and for each item type. The low success rate obtained from drinking items (35%) compared to other saliva items such as cigarettes (89%) can be explained by other

Table 3. Summary of DNA profiling results for different items.

| Item category | Items type | Samples per item | Negative quantification | Distribution of Amplified Samples | | | Item Success rate | Relative Work Units | Productivity Index |
|----------------|-------------------------|------------------|-------------------------|-----------------------------------|---------|------------|-------------------|---------------------|--------------------|
| | | | | DNA profile | Mixture | No profile | | | |
| Body fluids | Total: | 1.23 | 16% | 93% | 5% | 2% | 80% | 1.28 | 6.2 |
| | • Cigarettes | 1.04 | 9% | 97% | 1% | 1% | 89% | 1.03 | 8.6 |
| | • Blood stains | 1.31 | 8% | 96% | 2% | 2% | 90% | 1.36 | 6.7 |
| | • Saliva items | 1.58 | 23% | 85% | 13% | 2% | 79% | 1.83 | 4.3 |
| | • Drinking items | 1.08 | 53% | 68% | 21% | 10% | 35% | 1.21 | 2.9 |
| Clothing items | Total: | 2.26 | 32% | 50% | 38% | 13% | 48% | 1.79 | 2.7 |
| | • Clothing | 2.35 | 34% | 60% | 30% | 10% | 54% | 1.76 | 3.1 |
| | • Gloves | 2.02 | 45% | 45% | 37% | 18% | 39% | 1.45 | 2.7 |
| | • Head covering items | 2.44 | 20% | 45% | 44% | 11% | 51% | 2.18 | 2.3 |
| Touch items | Total: | 1.73 | 64% | 34% | 36% | 29% | 17% | 1.06 | 1.6 |
| | • Cellphone | 1.12 | 38% | 62% | 24% | 14% | 39% | 1.00 | 3.9 |
| | • Cable tie | 1.09 | 57% | 53% | 33% | 13% | 25% | 0.86 | 2.9 |
| | • Weapons | 3.33 | 71% | 31% | 30% | 38% | 18% | 1.09 | 1.6 |
| | • Working tools | 1.46 | 79% | 52% | 31% | 17% | 14% | 0.87 | 1.6 |
| | • Packaging cloth items | 1.70 | 54% | 33% | 35% | 32% | 18% | 1.24 | 1.5 |
| | • Other | 2.08 | 52% | 25% | 46% | 30% | 19% | 1.39 | 1.4 |
| | • Adhesive tapes | 1.27 | 64% | 36% | 39% | 23% | 12% | 1.00 | 1.2 |
| | • Papers | 2.02 | 73% | 28% | 16% | 56% | 12% | 1.10 | 1.1 |
| | • Wire | 1.08 | 83% | 43% | 29% | 29% | 8% | 0.72 | 1.1 |

Notes: Sample per items: the average number of samples taken per item. Distribution of Amplified Samples – out of total amplified samples (beyond quantification threshold). Item success rate - the percentage of items from which at least one DNA profile suitable for DNA database inclusion was obtained.

means of use rather than direct contact with the mouth. Thus, some of these items may not actually contain biological material.

Success rate correlated to sample location

As shown in Table 3 the body fluids category has a considerably higher success rate (80%) compared to clothing (48%) and touch items (17%). Similar success rates were reported in a work published by Mapes et al. (2016). There are several explanations for this gap: first, when sampling an item containing body fluids, the location of the biological material is usually known owing to presumptive tests or visual identification of the stain. Second, body fluids are a good source for a single DNA profile compared to the properties of touch DNA (trace amounts and possible multiple donors) (van Oorschot, Ballantyne, and Mitchell 2010; Meakin and Jamieson 2013).

To examine whether prior knowledge of the biological material location on the item influences the success rate, the items were grouped into three categories: known location, assumed location, and unknown location of the biological material.

Figure 2 shows the correlation between the success rate of an item and the prior knowledge of the biological material location. The most successful items were

those containing known location of body fluids (90%), i.e., cigarettes butts. With items where the location was assumed (bottle necks for example) the success rate was reduced by more than a half (from 90% to 40%).

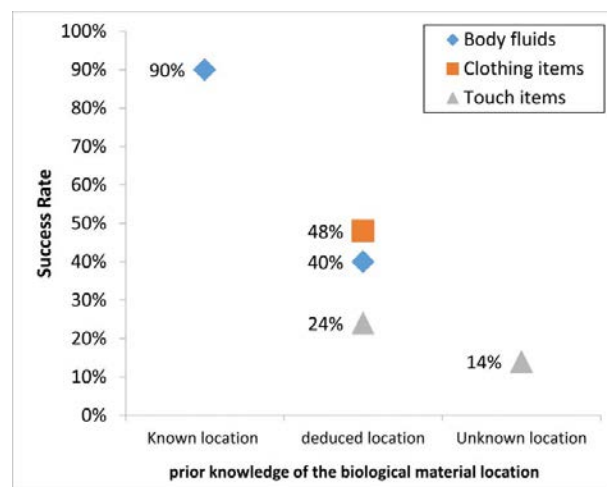


Figure 2. The success rate with body fluids, clothing items and touch items, in relation to the confidence of the biological material location on an item. Known location: the location of the biological material is identified visually or by presumptive tests. Assumed location: the location of the biological material is unknown but can be deduced according to the common use of the item (bottle neck or shirt for example). Unknown location: the location of the biological material is unknown and the sampling area was selected randomly (towels or paper sheets for example).

For touch items for which the biological material location was assumed (tools or weapons), the success rate was 24% but in cases where the location was unknown (cloth, towels, etc.) the items were sampled randomly and the success rate was reduced to 14%.

For clothing items, the location of the biological material is always deduced based on the examiner's experience and common sense (van Oorschot, Ballantyne, and Mitchell 2010). The success rate differences in the assumed category between body fluids (40%) clothing items (48%) and touch items (24%) might be explained by the DNA quantity deposited on those items.

Factors impacting the amount of work invested

When examining the efficiency of DNA profiling per item type, the success rate is not enough. One should also consider the work required to receive a meaningful result. In order to quantify the work invested in an item, the AWU and RWU measures were calculated, as detailed in the Materials and methods section and Table 2.

Several steps of DNA profiling have similar AWU score for all items (i.e., opening and describing an item) and therefore have no significant effect on their RWU score. Two of the steps have a major impact on the RWU score. First, the number of samples taken from each item varies according to the items properties. The more samples taken, the higher is the AWU score and consequently the RWU score increases. Second, the profile complexity influences the work invested during the expert analysis. For example, the analysis of complex mixtures requires more work than a single profile as reflected by the AWU score; the more complex mixtures obtained the higher the RWU score is.

The average number of samples per item

The average number of samples per item type is shown in Table 3. Several factors influence the number of samples taken from an item. The morphology and size of an item dictates the number of potential samples; some items such as a button can be sampled only once and others such as shirts can potentially be sampled multiple times from different locations. Prior knowledge of the biological material location can also affect the number of samples. Cigarettes have a well-defined location of the biological material and

therefore have an average of one sample per item. Weapons on the other hand, are sampled on average more than three times since the location of the biological material is uncertain.

Beyond the considerations mentioned above, other factors may influence the number of samples taken from each item category. For instance, the forensic circumstances; the number of individuals suspected of touching an item and other evidence, such as security camera video, pointing to a specific location on the item where the suspect's DNA might be found. In addition, the number of samples taken from an item is dependent on the expert's experience and judgment.

Sample quantification and genotyping

Body fluids stains usually originate from a single DNA donor, which explains the low mixture percentage (5%; see Table 3). Touch items on the other hand, are often used by multiple individuals and contain a higher percentage of complex mixtures (36%).

Negative quantification results prevent the downstream DNA profiling processing steps (see Table 3), thus reducing the RWU score of an item. Adhesive tapes and blood stains had a similar number of samples per item (1.27 and 1.31, respectively) and a mixture percentage of 39% and 2%, respectively. The difference between the RWU score for those items (1 and 1.36, respectively) can be explained by the significant difference of their negative quantification results (64% and 8% respectively), which lead to many adhesive tape samples not being amplified, thus requiring less work.

The efficiency of DNA recovery from case items (PI)

As discussed above, the PI grade takes into account the success rate and the amount of work invested (RWU) and reflects the cost benefit ratio, thus providing an assessment tool of items efficiency. Considering the success rate as the only parameter for assessing efficiency of items can be misleading. As shown in our results (Table 3), the success rate alone does not explain the variation of the PI score.

As expected, body fluids which have a high success rate were the most efficient items (6.2 PI) while clothing and touch items were less efficient (2.7 and 1.6, respectively).

Cigarettes, which have a high success rate (89%) and a 1.03 RWU (1 sample per item in average, 1%

mixtures, and do not require presumptive tests), are the most efficient items with 8.6 PI. Blood stains which had the highest success rate (90%) had a lower PI (6.7), due to an average of 1.3 samples per item and the need for presumptive tests which increase the amount of RWU invested.

Drinking items (i.e., bottle necks and drinking cans) have a low PI grade (2.9) as a result of their low success rate (35%) and a 1.21 RWU score. Saliva items (i.e., chewing gum and other Phadebas positive items), on the other hand, have a high success rate (79%) yet their PI grade is only 4.3 due to a relative high RWU score (1.83). This score stems from the need of saliva presumptive test (Phadebas) and other factors detailed in Table 3.

Clothing category which has a 48% success rate had only 2.7 PI grade. These items are routinely sampled more than twice (2.3 in average) since the biological material location is deduced. The mixture percentage of these items is substantially higher compared to body fluids (38% and 5%, respectively) since they can be used by multiple individuals. As a result, the RWU increases to 1.8, decreasing the PI.

Touch items have a high percentage of negative quantification results (64%) as reflected by a relatively low RWU (1.06). Combined with a low success rate (17%) their PI grade (1.6) is the lowest among all items type categories.

Cellphones and cable ties have different usage characteristics than other touch items. Cellphones are repeatedly used and may contain saliva traces. Cable ties are often used to restrain a victim thus increasing the probability of obtaining a DNA profile. Therefore, their PI grade (3.9 and 2.9, respectively) stand out compared to grades among other touch item category (1.1–1.6). However, it should be noted that in the majority of cases involving cable ties, the victim profile would be the evidentiary significant profile.

Number of samples per case item

When sampling case items, the examiner has to decide how many times to sample each case item. Here the marginal benefit of each additional sample to the probability of obtaining at least one DNA profile suitable for DNA database inclusion was examined.

To this end, a dataset of 100 case-items which were sampled at least five times (Figure 3) was analyzed. A single sample from a case-item results in a success rate

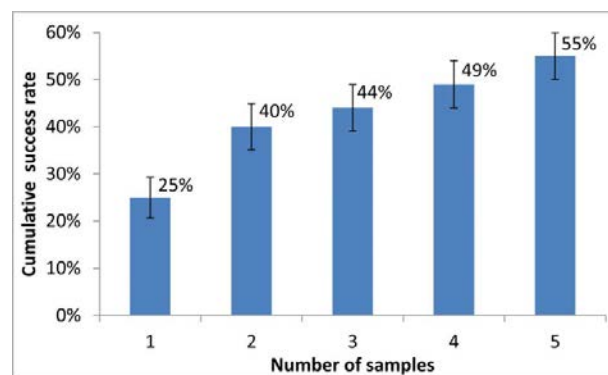


Figure 3. The cumulative rate of recovery of at least one DNA profile suitable for DNA database inclusion as a function of the number of samples taken from a case-item ($n = 100$ in each group). The error bars represents a 0.9 a confidence interval for the estimate of success proportion.

of 25%. The addition of a second sample increased the success rate by 15%. Adding a third, fourth, or fifth sample moderately increased the success rate (by approximately 5% each).

The decrease in the marginal benefit beyond two samples indicates that additional samples beyond two have a low chance of producing a profile. This may be explained by the distribution pattern of DNA on different case items. If sufficient DNA is present throughout a case item, success is expected within first few samples. On the other hand, items with minute amounts of DNA or with DNA concentrated in small, unknown locations are not expected to produce a successful profile even after numerous samples. These results are applicable only when a single DNA contributor is sought after. When DNA of more than one individual is expected on the item (according to the case information), more samples are required to increase chances of obtaining two or more different DNA profiles.

Obviously, each additional sample requires additional work to process and analyze so as the marginal contribution to success of each additional sample decreases, the efficiency (as reflected by the PI grade) decreases as well.

Number of items per case

The previous sections dealt with efficiency per case-item. Ultimately, the aim of the forensic examination is to produce sufficient evidence in each case as a whole. Therefore, in this section a success of a case is defined by the number of different profiles submitted to the DNA database.

To reduce the overall workload, it is important to examine the efficiency of case processing. The number of items sent to the DNA laboratory varies greatly between cases. In our dataset, 35.4% of the cases had 1 item, 32.1% had between 2–3 items, 12.1% had between 4–5 items, 11.5% had between 6–9 items, 7.3% had between 10–20 items, and 1.6% had more than 21 items. As the number of items rises, the number of different profiles added to the database (NDP – number of different profiles) increases moderately while the rise in the RWU is more significant (Figure 4). The RWU increase is constant since each additional item adds a similar amount of work. As more items are examined, the possibility of receiving at least one profile increases while the second profile has a higher probability to be identical to the first one. Therefore, the probability of obtaining different profiles increases with the number of tested items until reaching a plateau at the 6–7 item group.

In order to reduce the overall workload in our lab the optimal number of items for examination per case was searched by calculating the ratio between the NDP and the RWU. This ratio represents the cost benefit between the total amount of work invested in a case (RWU) and the number of different profiles added to the database (NDP). The ratio increases until reaching a peak at the 4–5 item group and then declines with the addition of items.

Our results indicate that testing more than 5 items per case is unproductive and increases the overall workload and thus should be limited. This limitation

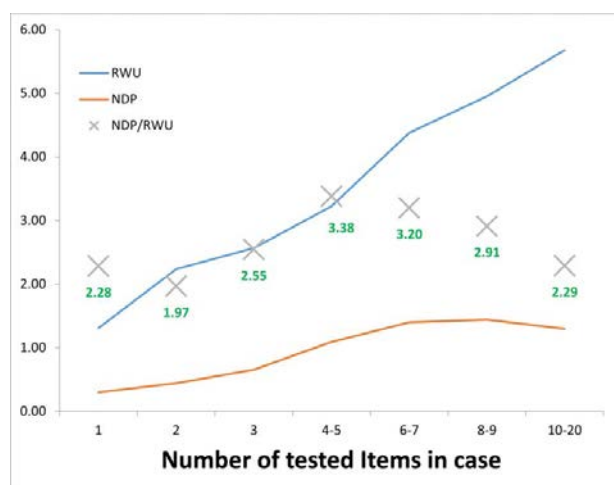


Figure 4. RWU and NDP as a function of the number of tested items per case. RWU – relative working units. NDP – Number of Different Profiles submitted to the database. The dataset consists of 463 profiles obtained from 644 cases.

will encourage the case investigators to prioritize the items submitted to the laboratory according to their relevance and success potential as previously suggested (Mapes et al. 2016). As a result, the laboratory workload will decrease and resources will be freed to handle more cases. In a situation where the investigators are not limited to a certain number of items per case, irrelevant case-items are submitted but returned without examination (17% of all received items in the dataset analyzed in this work, data not shown).

Conclusions

In order to reduce the workload in forensic DNA labs we recommend the following guidelines:

1. Prioritizing items based on efficiency criteria, such as the PI proposed here. This criterion takes both the work investment and the success rate into consideration.
2. Limiting the number of samples per item. In general, the benefit from additional samples beyond two samples per items is fairly low.
3. Limiting the number of items sent per case. Our results indicate that limiting the number of items to 4–5 does not substantially reduce the number of profiles included in the DNA database. Investigative units should be encouraged to send the items based on their relevance and efficiency (PI).

In each case the investigator should consider not only these recommendations but also the unique circumstances of the case such as the number of suspects and the relevance of each item to the forensic question, as well as the severity of the investigated crime.

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Allan McNevin

From: Justin Howes
Sent: Thursday, 27 July 2017 12:56 PM
To: Megan Mathieson; Allan McNevin; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Matthew Hunt; Paula Brisotto; Sharon Johnstone; Wendy Harmer
Subject: FW: paper of interest [SEC=UNCLASSIFIED]
Attachments: Reducing the Workload Analysis of DNA Profiling Efficiency of Case Work Items.pdf

Hi all, article FYI.

I had a quick scan and of interest is a call that 'DNA insufficient for processing' was given to 250pg and less.... Stay tuned for Project #184 proposal...

jah

**Justin Howes**

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
 Health Support Queensland, **Department of Health**

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From: Eva Bruenisholz [mailto: [REDACTED]]
Sent: Thursday, 27 July 2017 9:59 AM
To: SAG - Biology
Subject: paper of interest [SEC=UNCLASSIFIED]

UNCLASSIFIED

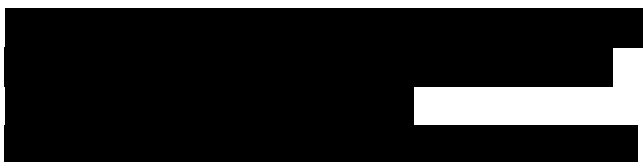
Happy reading,

Kind regards

Eva

Eva Bruenisholz

Senior Forensic Project Officer - Mon, Wed, Thu & Fri
 National Institute of Forensic Science



ANZPAA
Australia New Zealand
Policing Advisory Agency



IAFS 2020 Sydney Bid - The Australian and New Zealand Forensic Sciences community has partnered with Business Events Sydney (BESydney) and the NSW Government to bid to host the 22nd triennial meeting of the International Association of Forensic Sciences in Sydney, Australia in 2020. The conference will be at the new International Convention Centre (ICC Sydney). The whole oceanic region sees this as an opportunity to promote the advancement of the Forensic Science and Medicine work in our region and to collaborate internationally. We look forward to your support when we present our bid at the next IAFS 2017 in Toronto, Canada in August 2017.

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Message protected by MailGuard: e-mail anti-virus, anti-spam and content filtering.

| Funding Source (if applicable) | | |
|--------------------------------|------------------|-------------------------------------|
| Funding Source | Amount Requested | Approved |
| FSS Internal Fund | | NO <input type="button" value="▼"/> |
| Partner Contribution | | NO <input type="button" value="▼"/> |
| External Fund | | NO <input type="button" value="▼"/> |
| Total | 0 | |

| Expenditure Type | Monthly | For duration of project - Months: <u> 1 </u> |
|---|---------|---|
| <u>Labour</u> | | |
| DNA Analysis Personnel (Salaries and on-costs - for this email Business Management Information (BMI) Team for a salary forecast). | 5085 | |
| Other: | | |
| <u>Subtotal Labour:</u> | 5085 | 0 |
| <u>Non- Labour</u> | | |
| Equipment | 0 | |
| Consumables | 0 | |
| Travel | 0 | |
| Publication Costs | 0 | |
| Other: | 0 | |
| <u>Subtotal Non-labour:</u> | 0 | 0 |
| <u>Total:</u> | 5085 | 0 |

Justification of Funding (Non-Labour Costs)

Justify in terms of need and cost, each budget item in previous table. Please attach quotes where necessary

Total of 2 weeks work time for the Project Manager (HP6), including data interrogation and administration.

Justification of Funding (Labour Costs)

If project includes an appointment to assist or backfill, please provide details in the table below and submit to the BMI team for a detailed quote.

| | |
|---------------------------|---|
| Status | <input checked="" type="checkbox"/> Permanent |
| | <input type="checkbox"/> Part-Time |
| | <input type="checkbox"/> Temporary (<12mths) |
| | <input type="checkbox"/> Casual |
| Classification | <input type="checkbox"/> Administrative |
| | <input type="checkbox"/> Operational Officer |
| | <input checked="" type="checkbox"/> Health Practitioner |
| Time Period | 2 weeks |
| Position Title | Team Leader |
| Qualification Required | Nil |
| Budget Required - Salary: | 5085 |
| On-Costs: | |
| Total: | 5085 |
| Cost Centre | 787164 |

Any other information that you think maybe relevant please explain below:

YES
NO

2
2
2

Paula Brisotto

From: Cathie Allen
Sent: Monday, 31 July 2017 11:01 AM
To: Allan McNevin; Justin Howes; Kirsten Scott; Kylie Rika; Matthew Hunt; Paula Brisotto; Sharon Johnstone; Megan Mathieson; Saan Orion
Cc: Luke Ryan; Wendy Harmer
Subject: FW: Proposal #184
Attachments: Project Proposal_Evaluation of the efficacy of Microcons_July2017.doc; Budget_July2017.xls; Project Plan_Evaluation of the efficacy of Microcons_July2017.doc

Follow Up Flag: Follow up
Due By: Thursday, 10 August 2017 12:00 PM
Flag Status: Completed

Hi Everyone

Please find attached a Project Proposal, Project Plan and Budget for Project #184 – Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

These documents are held in I:\Change Management\Proposal#184 - Evaluation of the efficacy of Microcons

ACTION: Please consider the documents, undertake a risk assessment for your team and add this to the Project Plan and provide feedback to Justin Howes by Thursday, 17th of August 2017.

Cheers
Cathie

**Cathie Allen**

Managing Scientist – Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

[Redacted contact information]

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From: [Kirsten Scott](#)
To: [Justin Howes](#)
Subject: Feedback KDS Proposal #184
Date: Wednesday, 2 August 2017 1:19:00 PM

Justin,

Risk assessment completed.

Feedback as follows:

- Is there a reason you would assess all 2016 data, rather than including AUSLAB 2017 data?
- In comparing data sets microcons from 0.001-0.0088 will be compared with microcons from >0.0088. For best equivalency should it be compared with microcons from 0.088-0.0166 (same range of quant values – range of 0.0078). This will be a fairer comparison of result outcomes than an open ended, higher value range.

Kirsten

From: Cathie Allen
Sent: Monday, 31 July 2017 11:01 AM
To: Allan McNevin; Justin Howes; Kirsten Scott; Kylie Rika; Matthew Hunt; Paula Brisotto; Sharon Johnstone; Megan Mathieson; Saan Orion
Cc: Luke Ryan; Wendy Harmer
Subject: FW: Proposal #184

Hi Everyone

Please find attached a Project Proposal, Project Plan and Budget for Project #184 – Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

These documents are held in I:\Change Management\Proposal#184 - Evaluation of the efficacy of Microcons

ACTION: Please consider the documents, undertake a risk assessment for your team and add this to the Project Plan and provide feedback to Justin Howes by Thursday, 17th of August 2017.

Cheers
Cathie



Cathie Allen

Managing Scientist – Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**





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Paula Brisotto

From: Justin Howes
Sent: Wednesday, 30 August 2017 12:09 PM
To: Allan McNevin; Kylie Rika; Matthew Hunt; Sharon Johnstone; Kerry-Anne Lancaster; Kirsten Scott; Paula Brisotto; Megan Mathieson
Subject: Prop #184

Hi all

Thankyou for the feedback on this project. Kerry-Anne, thanks for feedback but no need for signature.

I have added all feedback and kept in a .xls in project folder.

I have added a datamine expnt to the proposal, but given this does not need much detail in the proposal document, I will still print for signing tomorrow.

If you feel inclined to read it before printing, please go to the project folder.

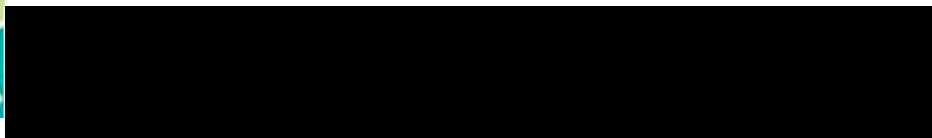
Thanks

JAH

**Justin Howes**

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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| Feedback due 20/12/2017 | | | |
|-------------------------|---------------|---|--|
| Staff member | Feedback date | Feedback | Response |
| LBR | 1/12/2017 | <p>Hi Justin Looks good to me. Just a few minor formatting comments:</p> <p>Figure 2 – maybe reduce to 4 decimal places?, also add X and Y axis labels Figure 6 – add X and Y axis labels Figure 7 – reduce decimals in labels Figure 10 – re-format legend so that graph has more room Throughout – sometimes the * is superscript and sometimes not (sorry that's very picky)</p> <p>Thanks Luke</p> | Fig 2 - the pivot table uses the raw data from the Quant file. Unable to change here. Fig 6 and Fig 2 - changes the image type in the doc so now have the labels. Fig 10 fixed. Fixed superscript. |
| KDS | 1/12/2017 | <p>Justin</p> <p>Feedback as follows:</p> <p>Abstract: A little disjointed to read – can the sentences/ideas be linked.</p> <p>Section 4:2 (and throughout)– I don't really like the use of the work "Fail" it indicates we did something wrong, or that there is a quality issue - which is not the case. We have processed them correctly, but the outcome from the biological submission is not informative. Can we use another term "Nil result" or "Nil Intel" or similar?</p> <p>Section 7: Could we/should we suggest case managers review cases on finalisation? If they think there is not much useful information in the case, and where they believe that the available profiles maybe useful (using their discretion) that they may consider manual Microcon reworks? While success rates are low, there are still potential successes.</p> <p>Kirsten</p> | Abstract being re-written. |
| ARM | 5/12/2017 | <p>G'day,</p> <p>Just a few things:</p> <p>Abstract Suggest reword "Given this, further workflow streamlining processes could be implemented that would provide significant processing efficiencies, and cost and time savings such that these efforts could be better placed in processing higher DNA-yielding samples" to "Given this, further streamlining of workflow processes could be implemented that would provide significant efficiencies such that these efforts could be better placed in processing higher DNA-yielding samples" or "Given this, further workflow process streamlining could be implemented that would provide significant processing efficiencies in order for resources to be better utilised processing higher DNA-yielding samples"</p> <p>5.2 "A total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection."</p> <p>I'm trying to work out why there are so many samples without quant as the whole point of m'con to 35 was so that they were quanted after microcon and they should have a pre-microcon quant as well – is there are a problem with the data export?</p> <p>Figure 1 </p> <p>Figure 2 </p> <p>Recommendations</p> <p>Recommendation 2 – I'd support up to 0.02ng/uL (template of 300ng) as this is the "cross-over" point and I'd also support implementing for both P2 and P3 samples, as recommendation 3 and 5 still give the QPS an option to ask for more work on the sample, it's easy for them to do & it's an extension of the triaging process</p> <p>Cheers Al</p> | Abstract being re-written, and suggested wording used. Note support for higher Q value, but will go with auto-mic range for implementation and check post-implementation. |

| | | | |
|-----|------------|---|--|
| KAL | 7/12/2017 | <p>Hi Justin</p> <p>I've had a look through the report (just in case it isn't signed off by the time Kirsten goes on holiday)..</p> <p>And with the recommendations – we will need to change the quant results upload programming in the FR to fit in line with the new values. I'm not sure how much work that would be for Troy etc. We would also then need to test the functionality works...</p> <p>This would include:</p> <ul style="list-style-type: none"> - P1 and Coronial samples only to go to auto-microcon - P2 samples at the auto-microcon value range to go to "DNA Insufficient" (we would have to make sure this works for samples, currently it only works for QPS envm samples) - P3 samples – would we keep the undetermined ones as "No DNA", then those up to 0.0133ng/uL make "DNA Insufficient"? - I think that's all... <p>Just some things to keep in mind.</p> <p>Thanks Kerry-Anne</p> | |
| PMB | 19/12/2017 | <p>Hi Justin,</p> <p>I've reviewed and happy with the theory and recommendations.</p> <p>I asked Lisa to have a look in the FR training site to see how the process for P3 samples would work once they move to PP21. I will forward you the email summarising this.</p> <p>Once a decision is reached on the range for quant values, we will need to submit enhancements to VSTS and create/write manual procedures for P3 samples both through Analytical and reporting. These manual processes will be in place until the enhancements are in FR.</p> <p>Thanks, Paula</p> | |
| KDR | 3/01/2018 | via track changes on doc in parent folder. | |
| AJR | 5/01/2018 | via track changes on doc in parent folder. | |
| | | | |
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| | | | |

Justin Howes

From: Luke Ryan
Sent: Friday, 1 December 2017 8:50 AM
To: Justin Howes
Subject: RE: Project #184 for review

Hi Justin

Looks good to me. Just a few minor formatting comments:

Figure 2 – maybe reduce to 4 decimal places?, also add X and Y axis labels

Figure 6 – add X and Y axis labels

Figure 7 – reduce decimals in labels

Figure 10 – re-format legend so that graph has more room

Throughout – sometimes the [®] is superscript and sometimes not (sorry that's very picky)

Thanks

Luke

From: Justin Howes
Sent: Thursday, 30 November 2017 12:50 PM
To: Allan McNevin; Amanda Reeves; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer
Subject: Project #184 for review

Hi all

Please find attached a report for Project #184 – Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon[®] Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

This has a due date of **Wednesday 20 December** for feedback. Please be mindful of this due-date and schedule time to review.

Thanks

Justin



Justin Howes

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
 Health Support Queensland, **Department of Health**



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Justin Howes

From: Kirsten Scott
Sent: Friday, 1 December 2017 2:46 PM
To: Justin Howes
Subject: RE: Project #184 for review

Justin

Feedback as follows:

Abstract: A little disjointed to read – can the sentences/ideas be linked.

Section 4:2 (and throughout)– I don't really like the use of the word "Fail" it indicates we did something wrong, or that there is a quality issue - which is not the case. We have processed them correctly, but the outcome from the biological submission is not informative. Can we use another term "Nil result" or "Nil Intel" or similar?

Section 7: Could we/should we suggest case managers review cases on finalisation? If they think there is not much useful information in the case, and where they believe that the available profiles maybe useful (using their discretion) that they may consider manual Microcon reworks? While success rates are low, there are still potential successes.

Kirsten

From: Justin Howes
Sent: Thursday, 30 November 2017 12:50 PM
To: Allan McNevin; Amanda Reeves; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer
Subject: Project #184 for review

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Allan McNevin

From: Allan McNevin
Sent: Tuesday, 5 December 2017 12:53 PM
To: Justin Howes
Subject: RE: Project #184 for review

G'day,

Just a few things:

Abstract

Suggest reword

“Given this, further workflow streamlining processes could be implemented that would provide significant processing efficiencies, and cost and time savings such that these efforts could be better placed in processing higher DNA-yielding samples”

to

“Given this, further streamlining of workflow processes could be implemented that would provide significant efficiencies such that these efforts could be better placed in processing higher DNA-yielding samples”

or

“Given this, further workflow process streamlining could be implemented that would provide significant processing efficiencies in order for resources to be better utilised processing higher DNA-yielding samples”

5.2

“A total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.”

I'm trying to work out why there are so many samples without quant as the whole point of m'con to 35 was so that they were quanted after microcon and they should have a pre-microcon quant as well – is there are a problem with the data export?

Figure 1 ☹

Figure 2 ☺

Recommendations

Recommendation 2 – I'd support up to 0.02ng/uL (template of 300ng) as this is the “cross-over” point and I'd also support implementing for both P2 and P3 samples, as recommendation 3 and 5 still give the QPS an option to ask for more work on the sample, it's easy for them to do & it's an extension of the triaging process

Cheers

AI

From: Justin Howes
Sent: Thursday, 30 November 2017 12:50 PM
To: Allan McNevin; Amanda Reeves; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer
Subject: Project #184 for review

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Justin



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Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

[Redacted contact information]

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Paula Brisotto

From: Paula Brisotto
Sent: Tuesday, 19 December 2017 11:20 AM
To: Justin Howes
Subject: RE: Project #184 for review

Hi Justin,

I've reviewed and happy with the theory and recommendations.

I asked Lisa to have a look in the FR training site to see how the process for P3 samples would work once they move to PP21. I will forward you the email summarising this.

Once a decision is reached on the range for quant values, we will need to submit enhancements to VSTS and create/write manual procedures for P3 samples both through Analytical and reporting. These manual processes will be in place until the enhancements are in FR.

Thanks,
 Paula

From: Justin Howes
Sent: Thursday, 30 November 2017 12:50 PM
To: Allan McNevin; Amanda Reeves; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer
Subject: Project #184 for review

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Thanks
 Justin

**Justin Howes**

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Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon[®] Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

November 2017

Justin Howes and Cathie Allen

Project Proposal #184 Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

Published by the State of Queensland (Queensland Health), November 2017



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Forensic DNA Analysis, Forensic and Scientific Services, Department of Health, GPO Box 48, Brisbane QLD 4001.

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Project Proposal #184 – Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

Document Details

Contact for enquiries and proposed changes

If you have any questions regarding this document or if you have a suggestion for improvements, please contact:

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Version history

| Version | Date | Changed by | Description |
|---------|------------|--------------|-------------------|
| 1.0 | 30/11/2017 | Justin Howes | Document Created. |
| | | | |
| | | | |

Document sign off

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Project Proposal #184 – Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon[®] Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

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1. Abstract

All samples that underwent a Microcon® process were evaluated and categorised into whether there was meaningful information obtained or not. This evaluation focussed primarily on samples processed in 2016 that underwent an 'auto-microcon' process. Arguably minimal value in proceeding (define value? For whom/what? If simply looking at success rates from a numbers perspective only, agree minimal value for us and the client. If looking at value from a sample/case perspective, then the 10% successes could potentially be very valuable to the client?) with this automatic processing step was found. Given this, further workflow streamlining processes could be implemented that would provide significant processing efficiencies, and cost and time savings such that these efforts could be better placed in processing higher DNA-yielding samples.

3.2. Introduction

Microcon® Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane^[1].

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of extract from approximately 100uL to ≤20µL for amplification with AmpF!STR® Profiler Plus®, and to ≤35µL for amplification with PowerPlex® 21 system (PP21).

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of <0.132ng were found to exhibit marked stochastic effects after amplification^[2]. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process).

Anecdotally, the suitability to provide the Queensland Police Service (QPS) with DNA profile Intelligence from extracts that have been concentrated has been noted to be limited. Furthermore, extracts that are of low quant value that have been automatically concentrated have been observed to rarely yield DNA information for QPS.

NB. Project #163 – *Assessment of results obtained from 'automatic-microcon' samples*^[3] was conducted to evaluate the results of samples that were processed with the 'auto-microcon' process. A recommendation of this project

Project Proposal #184 – Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

was to re-evaluate after the introduction of the Forensic Register in conjunction with the use of Quantifiler® Trio DNA Quantification Kit.

This recommendation was based on the perceived ease of retrieving data from the FR as opposed to AUSLAB, and with the thought that the FR would soon be implemented. For the purposes of this project, it is not considered essential to have the FR implemented if the data can be retrieved from AUSLAB. However, it is considered important that the data be spanning a sufficient period of processing, and be based on the same Quantification system namely the Quantifiler® Trio DNA Quantification Kit.

The purpose of this project is to evaluate the suitability for interpretation (this is your measure of success, then?) of DNA profiles that may be obtained after the post-extraction concentration step using the Microcon® centrifugal filter devices. This evaluation includes an assessment of those samples that underwent the 'auto-microcon' process. This evaluation is based on a data mine of extracts in the year 2016 that were concentrated with Microcon® centrifugal filter devices, and assesses the 'suitability' of PP21 profile outcomes as a function of quant values obtained from using the Quantifiler® Trio DNA Quantification Kit.

Formatted: Underline

This evaluation looks at two data sets as a function of the Quantification value:

1. PP21 DNA profile outcomes from extracts that were processed through the 'auto-microcon' process;
2. PP21 DNA profile outcomes from all extracts that were concentrated with the Microcon® filter devices.

4.3. Resources

The following resources were required for this validation/project:

Forensic DNA Analysis staff and computer time to retrieve data from AUSLAB and to use Microsoft Excel.

5.4. Methods

5.1.4.1. Data retrieval from AUSLAB (LIMS)

Data was retrieved from AUSLAB using Extended Enquiries. Data was searched for samples that had a testcode of 'XPLEX' and 'MCONC1' ordered in the year 2016 in Forensic DNA Analysis. Samples with the XPLEX (both testcodes?) testcode were High Priority (P2) samples.

Project Proposal #184 – Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

The data was output with the corresponding Quantification value and the reported DNA profile interpretation (Exhibit Report Line in the Exhibit Report (EXH)) for that particular barcode. If the barcode was a sub-sample, the corresponding EXH line for the sub-sample was output.

For ease of data interrogation, the RAW data (I:\Change Management\Proposal#184 - Evaluation of the efficacy of Microcons\Data\RAW Data from AUSLAB) had a column added to describe whether the sample underwent the 'auto-microcon' process ('AUTO' = $0.001\text{ng}/\mu\text{L} < \text{Quant} < 0.0088\text{ng}/\mu\text{L}$) or not ('MANUAL' = $\text{Quant} > 0.0088\text{ng}/\mu\text{L}$). Another column was added to describe whether there was a Quantification value returned in the data collation ('TRUE' = Quant value obtained), or not ('FALSE' = no Quant value obtained (ie. $0\text{ ng}/\mu\text{L}$)).

The data excluded samples that had not returned a DNA profile result, Quality samples (including environmental monitoring samples), have no quant value in the data export, or have quality issues noted.

5.2.4.2. Data interrogation

The data was interrogated by assessing the DNA profile outcome results reported as Exhibit Report lines as a function of the Quantification value.

The Exhibit lines were interrogated and grouped into two interpretation outcomes as follows:

1. 'Fail': DNA profile interpretation outcomes of 'Complex unsuitable for interpretation', 'No DNA profile', 'Partial unsuitable for interpretation', 'No DNA Detected';
2. 'Success': All other DNA profile outcomes. I think you need to be specific here, especially if you are going to go on to make further decisions with respect to 'value' of these success – ie NCIDD load

Perhaps accept and reject rather than success and fail for the first stage, where you are simply deciding which data to include?

Then perhaps redefine 'success' for each progressive section

6.5. Experimental Design

6.1.5.1. Experiment 1: Assessment of 'auto-microcon' results

Intent

Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.

Data Analysis

The samples applicable to this experiment had Quantification values in the range 0.001ng/ μ L to 0.0088ng/ μ L, and a total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value. A percentage of samples that fell into these categories was determined.

The 'auto-microcon' data could be expressed as a function of Quantification value.

Of the DNA profile interpretation outcomes of 'success', the data was broken down further to determine the percentage of samples that were reworked prior to the DNA profile outcome of 'success'.

The percentage of samples that had an 'auto-microcon' process and led to an NCIDD upload was obtained. This data could be filtered further into the outcome from the NCIDD load, at the time of data collection.

6.2.5.2. Experiment 2: Assessment of all DNA profile results from extracts that have had a concentration step.

Intent

Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 and underwent a post-extraction concentration step using Microcon[®] centrifugal filter devices.

Data Analysis

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The samples that were applicable to this experiment had Quantification values above 0.001ng/μL, and underwent the Microcon® process. This included the 'auto-microcon' samples, and those that had a Microcon® rework performed (termed 'manual'). This combination of data was termed 'combined data'.

A total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value.

The percentage of samples that fell into these categories ('manual' and 'combined') was determined. 'Manual' referred to the samples beyond the 'auto-microcon' range that were reworked with the Microcon® process, and 'combined' referred to all samples ('auto-microcon' and 'manual').

There was a point where the number of 'success' samples was approximately the same as the number of 'fail' samples when the Microcon® process was performed. This appeared to be approximately Quant = 0.02ng/uL. Therefore, the data was interrogated further at a Quantification value lower than this mark to determine what percentage of samples in certain ranges led to DNA profile interpretation outcomes of 'success'.

From this data, a sub-section of samples was interrogated further to evaluate the effect on DNA Intelligence ([is this defined somewhere?](#)) that was obtained. A range of samples with Quantification range up to 0.015ng/uL was chosen and a total number of samples was determined. This Quantification value was chosen as it was the approximate value where all samples below this value that underwent a Microcon® process, led to an approximate, round figure of 85% 'failure'.

With this Quantification value chosen, the data was interrogated further. The percentage of samples in this range that were determined to be a 'success' and were reworked further was determined.

The percentage of samples that were in this Quantification range and led to an NCIDD upload was determined. This data could be filtered further into the outcome from the NCIDD load. [Changing or developing 'success/value'](#) This data could then be used to evaluate the potential for samples to not provide meaningful DNA Intelligence [what is meaningful DNA intelligence?](#) to QPS if the Microcon® process was re-defined in some way.

5.3. Experiment 3: Datamine of the difference in pre- and post-Microcon® Quantification values

Intent

Evaluate the difference between the values obtained from the Quantification process in samples that have had a Microcon® concentration step applied.

As this is purely a datamining experiment, only the samples that have yielded a result of 'success' was examined. [Is 'success' in experiment the updated version? ie NCIDD upload/outcome](#)

Data Analysis

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'.

The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/μL and 0.015ng/μL were examined.

This range was considered by the author to be able to provide a sufficient demonstration of the trend of the data.

7.6. Results and Discussion

6.1 Assessment of 'auto-microcon' results

For samples in the 'auto-microcon' Quantification range, the total number of samples that were processed this way (excluding certain samples as per Section 5.1) was N= 1449 samples.

The percentage of samples that resulted in a determination of 'fail' was 89.4% (Fig 1). As expected, the number of 'fails' increased when the Quantification decreased and approached the Limit of Detection of Quantification ie. 0.001ng/uL (Fig 2). This was considered to be due to there being less DNA detected in the extract, and therefore less DNA to concentrate.

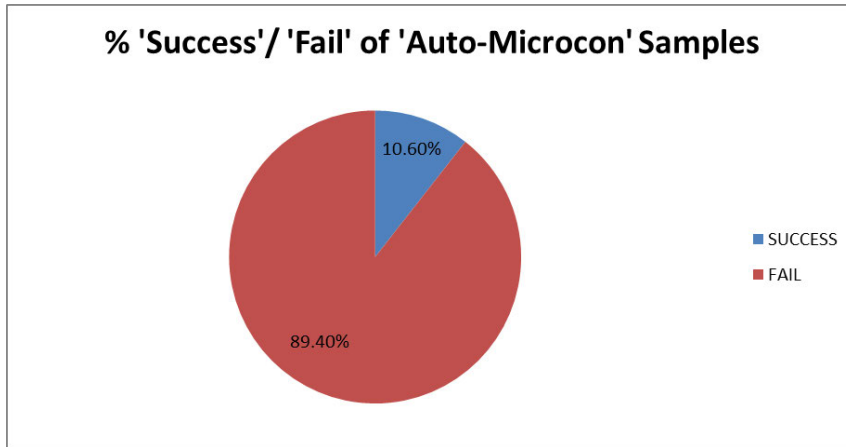


Figure 1: Percentage 'Success/ Fail' of 'Auto-Microcon' samples.

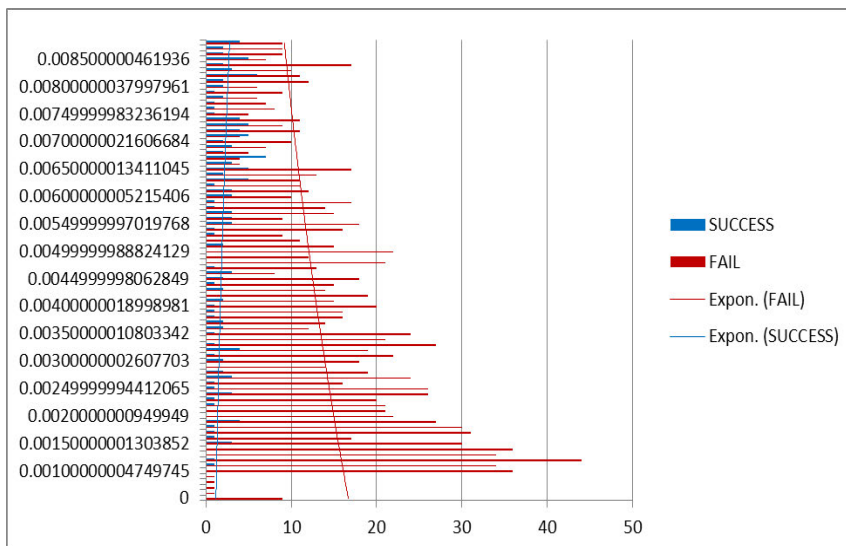


Figure 2: Spread of data and categorised as 'Success/ Fail' for 'Auto-Microcon' samples.

In order to reach a DNA profile interpretation outcome of 'success', it was found that 74.7% of samples had an additional rework to the Microcon® process (Fig 3). Is this because of number of contributors, considering these samples are all P2? (so might not necessarily reflect profile quality or lack thereof, per se) How relevant is this?

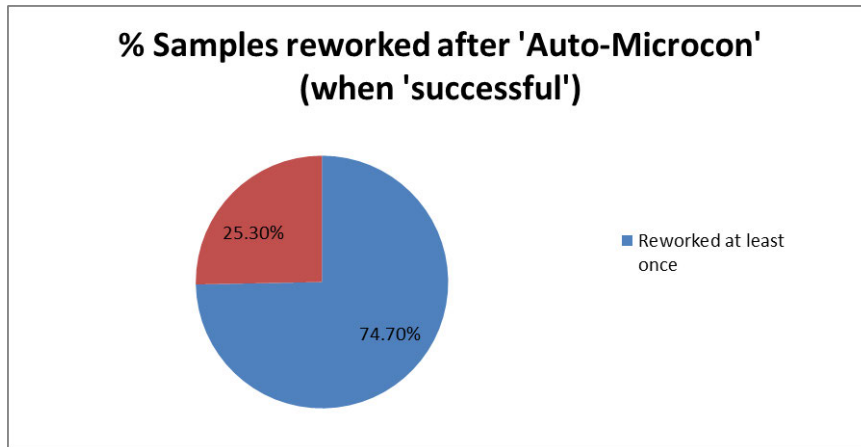


Figure 3: Percentage of 'Auto-Microcon' Samples that were reworked at least once and led to a 'successful' DNA profile outcome.

In putting the data behind Figures 2 and 3 together, if an 'auto-microcon' process was not conducted and was subsequently requested by the client for samples in this Quantification range, there would be approximately a 10% chance of obtaining a 'successful' DNA profile interpretation. Furthermore, in order to achieve that outcome, approximately 75% of these 'successful' samples would have needed a further rework. This means, for these samples, there would be a turnaround time factor for the client to consider, and in a potential fee-for-service model with requesting clients, being prepared to have increased processing costs associated with these low-quant samples would be a client consideration. I am not sure you can put these together in this way? Remember, you are using P2 samples (that require repro for STRmix)

If samples were not processed through the 'auto-microcon' process, what DNA Intelligence would the client miss out on? To evaluate this, the 'success' data was drilled down to the samples that had some NCIDD interaction and in particular, where they were the only samples in the case that were NCIDD-suitable for that particular profile (Fig 4). This is a bit too vague for me. This represented 1.86% of all 'auto-microcon' samples. In looking at samples that provide *new* Intelligence, that is DNA information available for future linking, or has provided a cold-link, this equated to 1.45% of all 'auto-microcon' samples.

This 1.45% of samples would be the pertinent value for the client to consider if the 'auto-microcon' process was not performed – this samples are our RISK if

we decide to remove this process – in removing this process we are also removing 1.45% of samples that do provide our client with ‘success’. In considering this, it would be important to evaluate the time and cost for processing, and the opportunity to concentrate efforts on other higher yielding samples. In saying this, with the ease of communication through the Forensic Register, these samples could be processed if the client has no other forensic Intelligence assisting the matter, or if the item is considered to be of critical priority.

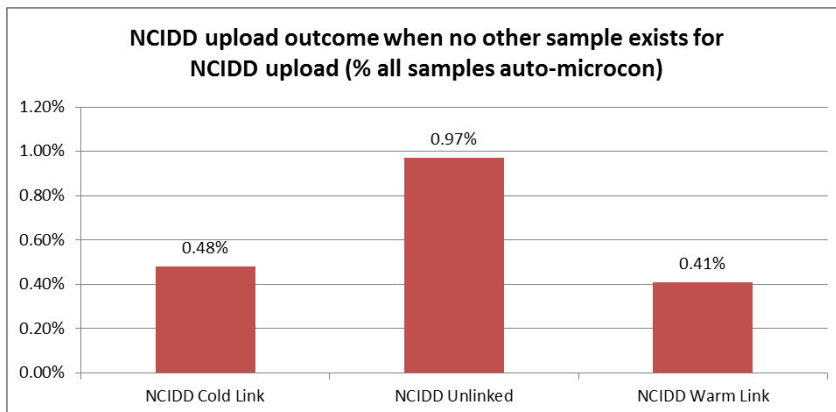


Figure 4: NCIDD outcome for samples that were loaded to NCIDD

Ultimately, this data means that for approximately 90% of samples that underwent an ‘auto-microcon’ process, there is arguably negligible DNA profile Intelligence for the client. If the ‘auto-microcon’ was not applied, there would be the following advantages, including but not limited to:

- the potential to make available at least 1449 processing positions for other samples including further available positions that would have been used for reworks,

- the lack of a need for the considerable efforts required to prepare and process Microcon® (and further rework) batches for this number of samples,

- consumable and labour savings in the end-to-end processing of these samples, and

- time and effort could be redirected in the laboratory workflow to other activities including service extensions like Y-STR profiling.

This is good, but for the argument to be presented in a balanced and transparent fashion perhaps you should include the perceived risks and impacts too? Maybe a table? This is particularly important for the ‘success’ samples – if you are going to remove a process that gives any ‘success’ then you need to

know what the impact will be and perhaps offer a mitigation strategy. For example, examine the 1.45% identified risk for QPS to see if there are any trends that predict success (ie sample type, substrate, collection location) that could be used to provide advice to QPS about which samples to request m'con on?

6.2 Assessment of all DNA profile results from extracts that have had a concentration step.

All samples from 2016 that had a Microcon® process were determined. The total number of samples was N= 2201 samples, excluding certain samples as per Section 5.1.

The percentage of samples that resulted in a determination of 'fail' was 78.5% (see Fig 5). As expected, in looking at the spread of the 'combined' data, the number of 'successes' increased when the Quantification increased (Fig 6).

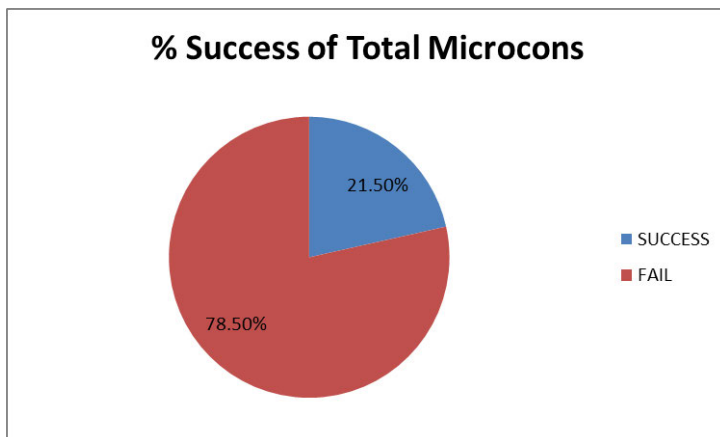


Figure 5: Percentage 'Success'/'Fail' of all Microcon® samples ('combined' data).

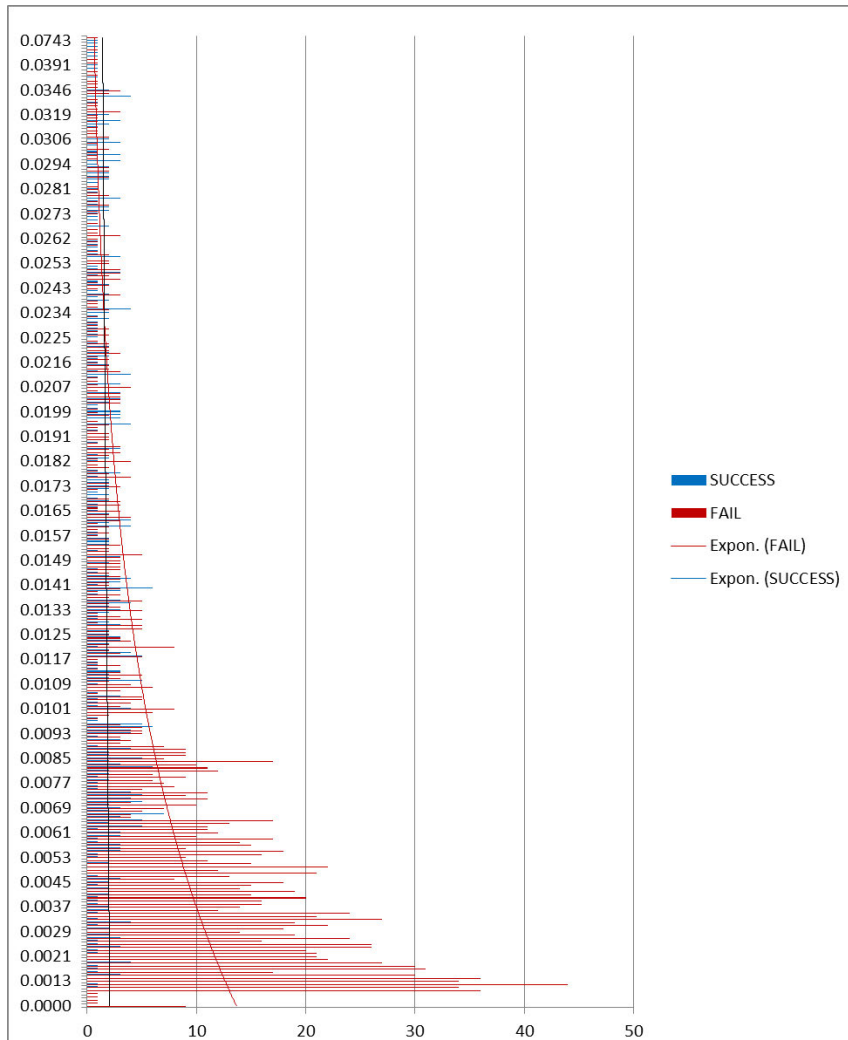


Figure 6: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

As mentioned in Section 5.2, the Quantification value where there was roughly the same number of 'success' and 'fail' samples was approximately 0.02ng/uL. It must be noted that this is a rough estimate *at this* particular Quantification value, and it is based on limited samples that returned that Quantification value. It can be argued that taking a range of Quantification values to look at the overall success/fail percentages could provide the client with approximate likelihoods of obtaining meaningful DNA Intelligence.

A number of ranges were looked at to determine the percentage 'success' of samples with Quantification values in various ranges (Fig 7). The ranges were established up to the highest Quantification value of 0.02ng/uL. As expected, the percentage 'success' increased as the Quantification increased due to the higher amount of DNA in the extract available to be concentrated.

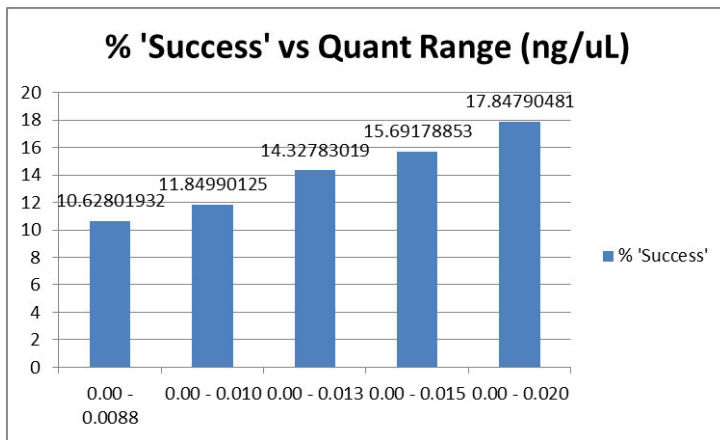


Figure 7: Percentage 'success' for samples that underwent a Microcon® process

In viewing the data in Fig 7, a limitation is that all samples that fell in the 'auto-microcon' range, had a Microcon® process performed, whereas there are samples that are in higher Quantification ranges that might not have required a Microcon® concentration rework step to yield useful DNA profiles. These samples were not evaluated.

A lower Quantification value to where the number of 'successes' roughly equalled the 'failures' was chosen to be the upper end of data ranges that were evaluated further. The value chosen was 0.015ng/uL. Table 1 and Figure 8 describe the risk to NCIDD upload for samples in these ranges if Microcon® concentration steps were not performed.

Table 1: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

| | % No other samples to Upload in Quantification ranges (Q) | | |
|-----------------|--|--|---|
| | Q = 0.00ng/uL to 0.01ng/uL (total samples in range = 1519) | Q = 0.00ng/uL to 0.0133ng/uL (total samples in range = 1696) | Q = 0.00ng/uL to 0.015ng/uL (total samples in range = 1778) |
| NCIDD Cold link | 0.92 | 0.88 | 1.01 |
| NCIDD Unlinked | 0.53 | 0.77 | 1.24 |
| NCIDD Warm Link | 0.46 | 0.83 | 0.90 |

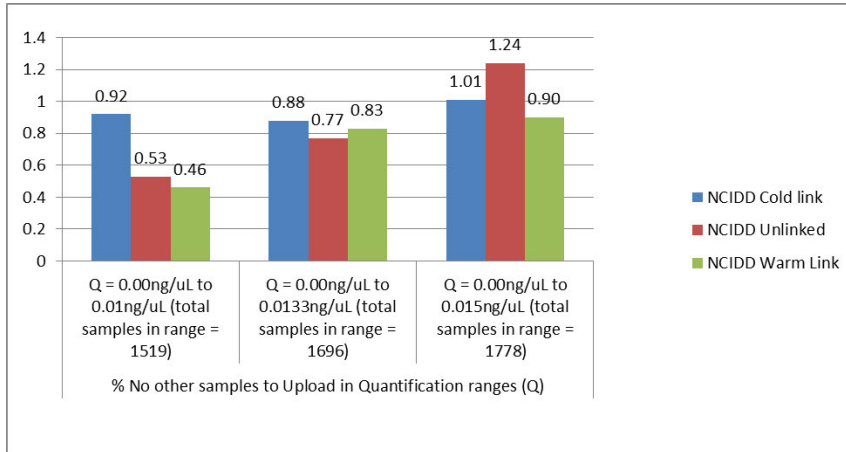


Figure 8: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

Approximately 1.45% of samples in the Quantification range up to 0.01ng/uL resulted in 'new' DNA Intelligence. This percentage is the same as that found in the 'auto-microcon' range. This percentage increased to 1.65% and 2.25% for the Quantification ranges up to 0.0133ng/uL and 0.015ng/uL respectively.

The number of further reworks required to obtain 'success' outcomes decreased as the Quantification increased. This is not unexpected given higher DNA yields detected would not necessarily require as many reworks in order to yield DNA profiles.

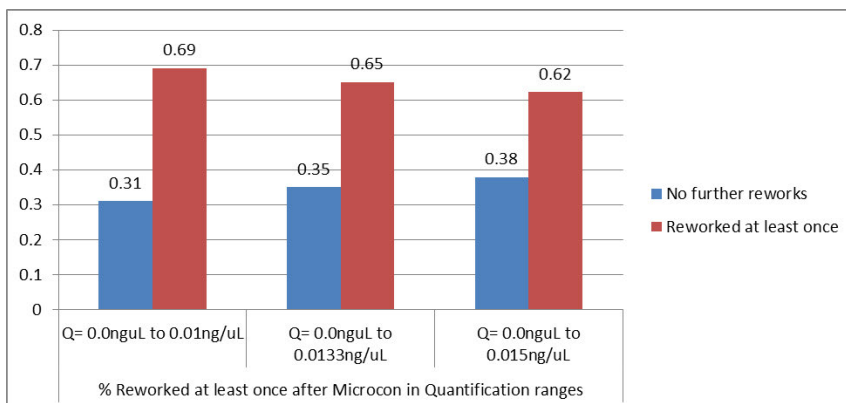


Figure 9: Percentage of samples reworked (in addition to a Microcon® process) in various Quantification ranges.

6.3 Datamine of the difference in pre- and post- Microcon® Quantification values

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'. The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/μL and 0.015ng/μL were examined.

As the Microcon® process concentrates the DNA extract from approximately 100uL to approximately 35uL, in theory it would be a reasonable expectation to obtain approximately two to three-fold increases in DNA Quantification after concentration. Figure 10 shows the plot of the differences found for samples that resulted in 'success'.

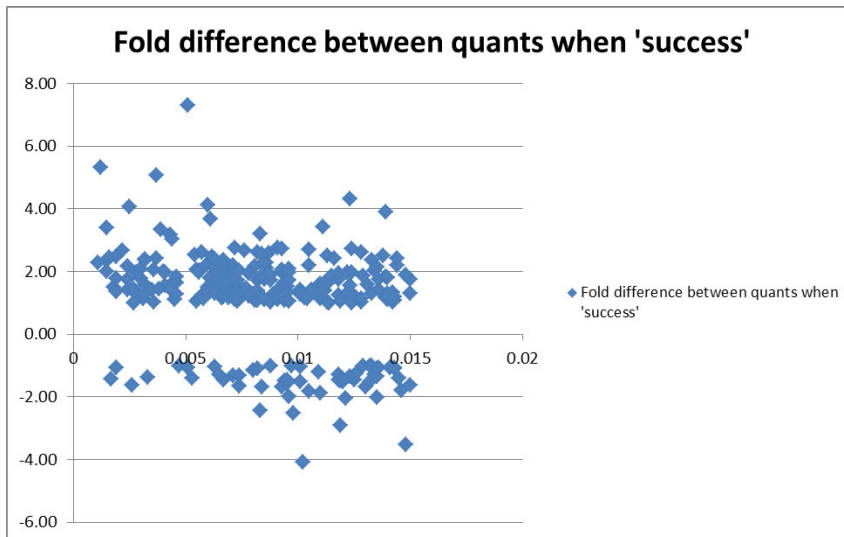


Figure 10: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results – [we know that quant step itself has inherent variability](#). Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 10 where the Quantification values decreased after concentration. Variability in results could be attributed to a number of things, including but not limited to the slight differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

8.7. Conclusion and Recommendations

The data analysis demonstrated that there was arguably minimal value in performing the 'auto-microcon' concentration step. This opinion was formed by analysing the data from 2016 where it was found that for all samples that underwent the 'auto-microcon' step, 89% did not yield meaningful results.

It was found that in considering all samples that underwent a Microcon® step at some stage in 2016, 78.5% did not yield meaningful results ([what does this mean? They are fails? Or they didn't give new intel?](#)). As expected, when the Quantification value increased, the percentage of meaningful results increased. However, it was also demonstrated in the data analysis that the Quantification values did not always improve after Microcon®, but where they did, the magnitude of change was roughly equivalent to the change in volume (from neat to concentrated sample).

Based on the data analysis, the following recommendations are offered:

1. Cease 'auto-microcon' processing with the following exceptions:
 - a. Priority 1 samples (Critical Priority); and
 - b. Coronial/DVI samples where profiles are mostly single-source and quite often incomplete profiles may be enough to provide Intelligence on possible identity.
2. Cease processing all Priority 3 samples up to the Quantification value of 0.0133ng/uL (template of 200ng). [Maybe this, and reworks, could form a part B to this project?](#)
3. For samples in the range described in Recommendation 2, automatically send result information via the Forensic Register to QPS at Quantification stage. This result information is recommended to be the exhibit result line of 'DNA Insufficient for Further Processing'. This recommendation is an extension to the current 'No DNA Detected' process, which looks at Priority 2 samples yielding Quantification results of less than the Limit of Detection.
4. Re-analyse Priority 2 samples in the range 0.0088ng/uL to 0.0133ng/uL after a six month period of processing to evaluate whether Recommendation 2 can be extended to Priority 2 samples.

5. Communicate the change in process to QPS and ensure that QPS are aware that for samples in the ranges mentioned in Recommendations 1 and 2, that they could be requested for Microcon® concentration steps at any point in time. This request can be made via the Forensic Register after they have received the 'DNA insufficient...' result line.

7.8. References

Formatted: Bullets and Numbering

- [1] QIS 19544v11 – Concentration of DNA Extracts Using Microcon Centrifugal Filter Devices
- [2] PowerPlex® 21– Amplification of Extracted DNA Validation. Megan Mathieson, Thomas Nurthen, Cathie Allen. December 2012. Forensic DNA Analysis.
- [3] Project #163 - Assessment of results obtained from 'automatic-microcon' samples. Josie Entwistle, Allison Lloyd, Kylie Rika, Thomas Nurthen, Cathie Allen. August 2015. Forensic DNA Analysis.

Justin Howes

From: Amanda Reeves
Sent: Friday, 5 January 2018 4:06 PM
To: Justin Howes
Subject: feedback 184
Attachments: AJR_Report_Evaluation of the efficacy of Microcons_v1.doc



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Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon[®] Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

November 2017

Justin Howes and Cathie Allen

Project Proposal #184 Evaluation of the Efficacy of a Post-Extraction Concentration Step Using the Microcon® Centrifugal Filter Devices in Yielding DNA Profile Intelligence.

Published by the State of Queensland (Queensland Health), November 2017



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Version history

| Version | Date | Changed by | Description |
|---------|------------|--------------|-------------------|
| 1.0 | 30/11/2017 | Justin Howes | Document Created. |
| | | | |
| | | | |

Document sign off

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1. Abstract

All samples that underwent a Microcon® process were evaluated and categorised into whether there was meaningful information obtained or not. This evaluation focussed primarily on samples processed in 2016 that underwent an 'auto-microcon' process. Arguably minimal value in proceeding (define value? For whom/what? If simply looking at success rates from a numbers perspective only, agree minimal value for us and the client. If looking at value from a sample/case perspective, then the 10% successes could potentially be very valuable to the client?)_ with this automatic processing step was found. Given this, further workflow streamlining processes could be implemented that would provide significant processing efficiencies, and cost and time savings such that these efforts could be better placed in processing higher DNA-yielding samples.

2. Abstract to be re-written.Introduction

Microcon® Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane [1].

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of extract from approximately 100uL to $\leq 20\mu\text{L}$ for amplification with AmpF!STR® Profiler Plus®, and to $\leq 35\mu\text{L}$ for amplification with PowerPlex® 21 system (PP21).

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of $<0.132\text{ng}$ were found to exhibit marked stochastic effects after amplification [2]. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process).

Anecdotally, the suitability to provide the Queensland Police Service (QPS) with DNA profile Intelligence from extracts that have been concentrated has been noted to be limited. Furthermore, extracts that are of low quant value that have been automatically concentrated have been observed to rarely yield DNA information for QPS.

NB. Project #163 – *Assessment of results obtained from 'automatic-microcon' samples* [3] was conducted to evaluate the results of samples that were processed with the 'auto-microcon' process. A recommendation of this project was to re-evaluate after the introduction of the Forensic Register in conjunction with the use of Quantifiler® Trio DNA Quantification Kit.

This recommendation was based on the perceived ease of retrieving data from the FR as opposed to AUSLAB, and with the thought that the FR would soon be implemented. For the purposes of this project, it is not considered essential to have the FR implemented if the data can be retrieved from AUSLAB. However, it is considered important that the data be spanning a sufficient period of processing, and be based on the same Quantification system namely the Quantifiler® Trio DNA Quantification Kit.

The purpose of this project is to evaluate the suitability for interpretation (this is your measure of success, then?) Definitions to be added of DNA profiles that may be obtained after the post-extraction concentration step using the Microcon® centrifugal filter devices. This evaluation includes an assessment of those samples that underwent the 'auto-microcon' process. This evaluation is based on a data mine of extracts in the year 2016 that were concentrated with Microcon® centrifugal filter devices, and assesses the 'suitability' of PP21 profile outcomes as a function of quant values obtained from using the Quantifiler® Trio DNA Quantification Kit.

This evaluation looks at two data sets as a function of the Quantification value:

1. PP21 DNA profile outcomes from extracts that were processed through the 'auto-microcon' process;
2. PP21 DNA profile outcomes from all extracts that were concentrated with the Microcon® filter devices.

3. Resources

The following resources were required for this validation/project:

Forensic DNA Analysis staff and computer time to retrieve data from AUSLAB and to use Microsoft Excel.

4. Methods

4.1. Data retrieval from AUSLAB (LIMS)

Data was retrieved from AUSLAB using Extended Enquiries. Data was searched for samples that had a testcode of 'XPLEX' and 'MCONC1' ordered in the year 2016 in Forensic DNA Analysis. Samples with the XPLEX (both testcodes?) Clarified in v2. testcode were High Priority (P2) samples.

The data was output with the corresponding Quantification value and the reported DNA profile interpretation (Exhibit Report Line in the Exhibit Report (EXH)) for that particular barcode. If the barcode was a sub-sample, the corresponding EXH line for the sub-sample was output.

For ease of data interrogation, the RAW data (I:\Change Management\Proposal#184 - Evaluation of the efficacy of Microcons\Data\RAW Data from AUSLAB) had a column added to describe whether the sample underwent the 'auto-microcon' process ('AUTO' = $0.001\text{ng}/\mu\text{L} < \text{Quant} < 0.0088\text{ng}/\mu\text{L}$) or not ('MANUAL' = $\text{Quant} > 0.0088\text{ng}/\mu\text{L}$). Another column was added to describe whether there was a Quantification value returned in the data collation ('TRUE' = Quant value obtained), or not ('FALSE' = no Quant value obtained (ie. $0\text{ ng}/\mu\text{L}$)).

The data excluded samples that had not returned a DNA profile result, Quality samples (including environmental monitoring samples), have no quant value in the data export, or have quality issues noted.

4.2. Data interrogation

The data was interrogated by assessing the DNA profile outcome results reported as Exhibit Report lines as a function of the Quantification value.

The Exhibit lines were interrogated and grouped into two interpretation outcomes as follows:

1. 'Fail': DNA profile interpretation outcomes of 'Complex unsuitable for interpretation', 'No DNA profile', 'Partial unsuitable for interpretation', 'No DNA Detected';
2. 'Success': All other DNA profile outcomes. I think you need to be specific here, especially if you are going to go on to make further decisions with respect to 'value' of these success – ie NCIDD load

Perhaps accept and reject rather than success and fail for the first stage, where you are simply deciding which data to include?

Then perhaps redefine 'success' for each progressive section
Definitions to be added.

5. Experimental Design

5.1. Experiment 1: Assessment of 'auto-microcon' results

Intent

Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.

Data Analysis

The samples applicable to this experiment had Quantification values in the range 0.001ng/ μ L to 0.0088ng/ μ L, and a total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value. A percentage of samples that fell into these categories was determined.

The 'auto-microcon' data could be expressed as a function of Quantification value.

Of the DNA profile interpretation outcomes of 'success', the data was broken down further to determine the percentage of samples that were reworked prior to the DNA profile outcome of 'success'.

The percentage of samples that had an 'auto-microcon' process and led to an NCIDD upload was obtained. This data could be filtered further into the outcome from the NCIDD load, at the time of data collection.

5.2. Experiment 2: Assessment of all DNA profile results from extracts that have had a concentration step.

Intent

Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 and underwent a post-extraction concentration step using Microcon[®] centrifugal filter devices.

Data Analysis

The samples that were applicable to this experiment had Quantification values above 0.001ng/ μ L, and underwent the Microcon[®] process. This included the

'auto-microcon' samples, and those that had a Microcon® rework performed (termed 'manual'). This combination of data was termed 'combined data'.

A total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value.

The percentage of samples that fell into these categories ('manual' and 'combined') was determined. 'Manual' referred to the samples beyond the 'auto-microcon' range that were reworked with the Microcon® process, and 'combined' referred to all samples ('auto-microcon' and 'manual').

There was a point where the number of 'success' samples was approximately the same as the number of 'fail' samples when the Microcon® process was performed. This appeared to be approximately Quant = 0.02ng/uL. Therefore, the data was interrogated further at a Quantification value lower than this mark to determine what percentage of samples in certain ranges led to DNA profile interpretation outcomes of 'success'.

From this data, a sub-section of samples was interrogated further to evaluate the effect on DNA Intelligence (is this defined somewhere?) Definitions to be added that was obtained. A range of samples with Quantification range up to 0.015ng/uL was chosen and a total number of samples was determined. This Quantification value was chosen as it was the approximate value where all samples below this value that underwent a Microcon® process, led to an approximate, round figure of 85% 'failure'.

With this Quantification value chosen, the data was interrogated further. The percentage of samples in this range that were determined to be a 'success' and were reworked further was determined.

The percentage of samples that were in this Quantification range and led to an NCIDD upload was determined. This data could be filtered further into the outcome from the NCIDD load. Changing or developing 'success/value' Definitions to be added This data could then be used to evaluate the potential for samples to not provide meaningful DNA Intelligence what is meaningful DNA intelligence? Definitions to be added to QPS if the Microcon® process was re-defined in some way.

5.3. Experiment 3: Datamine of the difference in pre- and post-Microcon[®] Quantification values

Intent

Evaluate the difference between the values obtained from the Quantification process in samples that have had a Microcon[®] concentration step applied.

As this is purely a datamining experiment, only the samples that have yielded a result of 'success' was examined. Is 'success' in experiment the updated version? ie NCIDD upload/outcome to be clarified.

Data Analysis

The samples applicable to this experiment had Quantification values above 0.001ng/ μ L where the final result was 'success'.

The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/ μ L and 0.015ng/ μ L were examined.

This range was considered by the author to be able to provide a sufficient demonstration of the trend of the data.

6. Results and Discussion

6.1 Assessment of 'auto-microcon' results

For samples in the 'auto-microcon' Quantification range, the total number of samples that were processed this way (excluding certain samples as per Section 5.1) was N= 1449 samples.

The percentage of samples that resulted in a determination of 'fail' was 89.4% (Fig 1). As expected, the number of 'fails' increased when the Quantification decreased and approached the Limit of Detection of Quantification ie. 0.001ng/ μ L (Fig 2). This was considered to be due to there being less DNA detected in the extract, and therefore less DNA to concentrate.

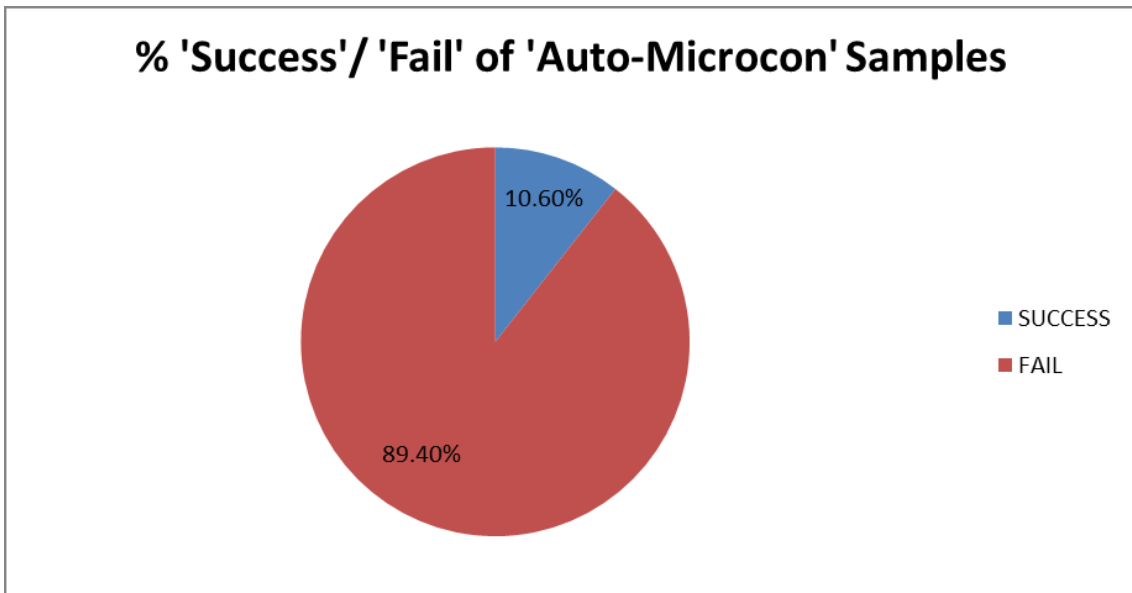


Figure 1: Percentage 'Success'/ 'Fail' of 'Auto-Microcon' samples.

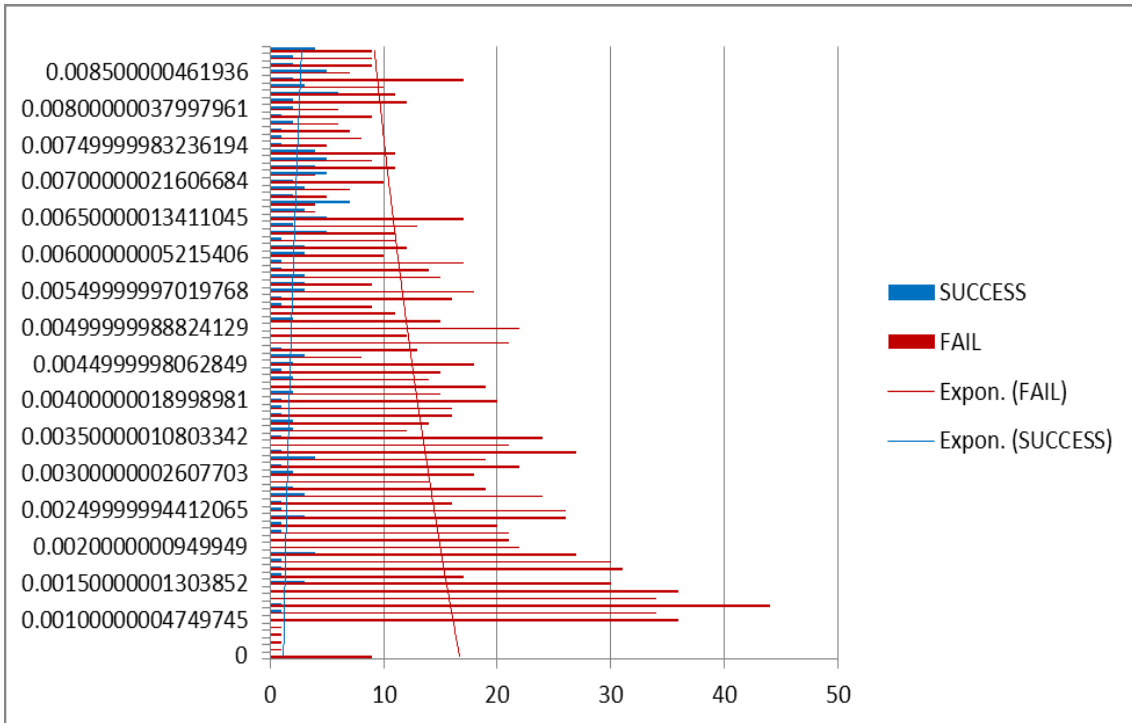


Figure 2: Spread of data and categorised as 'Success'/ 'Fail' for 'Auto-Microcon' samples.

In order to reach a DNA profile interpretation outcome of 'success', it was found that 74.7% of samples had an additional rework to the Microcon® process (Fig 3). Is this because of number of contributors, considering these samples are all P2? (so might not necessarily reflect profile quality or lack thereof, per se) How relevant is this? Reworks to be removed. No. contributs guidelines don't work for auto-mic sample.

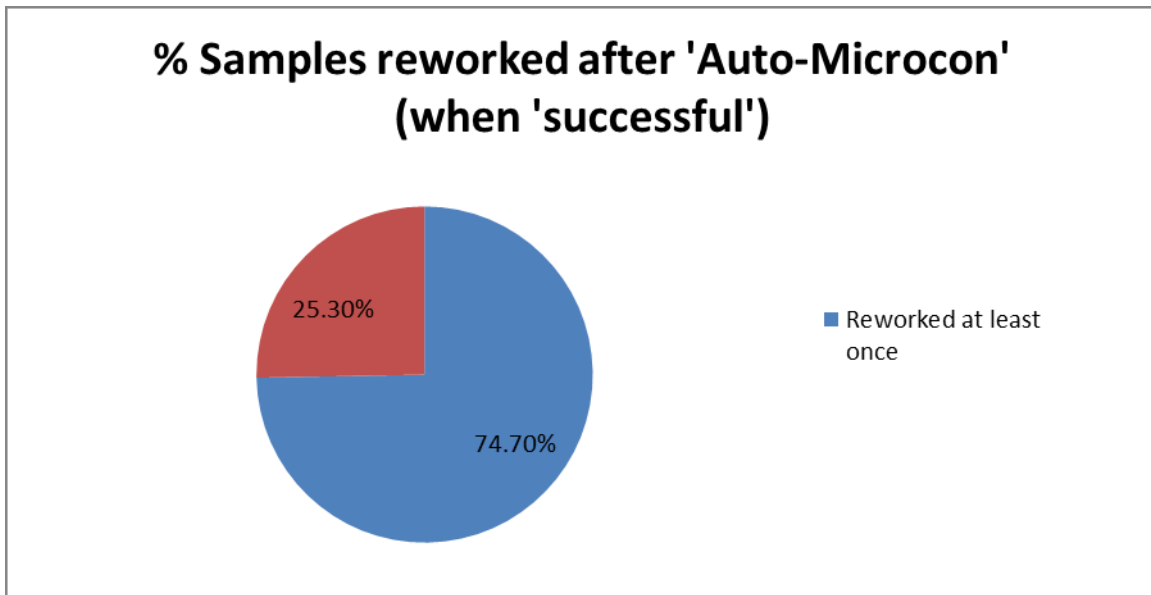


Figure 3: Percentage of 'Auto-Microcon' Samples that were reworked at least once and led to a 'successful' DNA profile outcome.

In putting the data behind Figures 2 and 3 together, if an 'auto-microcon' process was not conducted and was subsequently requested by the client for samples in this Quantification range, there would be approximately a 10% chance of obtaining a 'successful' DNA profile interpretation. Furthermore, in order to achieve that outcome, approximately 75% of these 'successful' samples would have needed a further rework. This means, for these samples, there would be a turnaround time factor for the client to consider, and in a potential fee-for-service model with requesting clients, being prepared to have increased processing costs associated with these low-quant samples would be a client consideration. I am not sure you can put these together in this way? Remember, you are using P2 samples (that require repro for STRmix) Repro/no contr doesn't work for auto-mics, but reworking discussion point to be removed anyway.

If samples were not processed through the 'auto-microcon' process, what DNA Intelligence would the client miss out on? To evaluate this, the 'success' data was drilled down to the samples that had some NCIDD interaction and in particular, where they were the only samples in the case that were NCIDD-suitable for that particular profile (Fig 4). This is a bit too vague for me This represented 1.86% of all 'auto-microcon' samples. In looking at samples that provide *new* Intelligence, that is DNA information available for future linking, or has provided a cold-link, this equated to 1.45% of all 'auto-microcon' samples.

This 1.45% of samples would be the pertinent value for the client to consider if the 'auto-microcon' process was not performed – this samples are our RISK if we decide to remove this process – in removing this process we are also removing 1.45% of samples that do provide our client with 'success'. Yes. In considering this, it would be important to evaluate the time and cost for processing, and the opportunity to concentrate efforts on other higher yielding samples. In saying this, with the ease of communication through the Forensic Register, these samples could processed if the client has no other forensic Intelligence assisting the matter, or if the item is considered to be of critical priority.

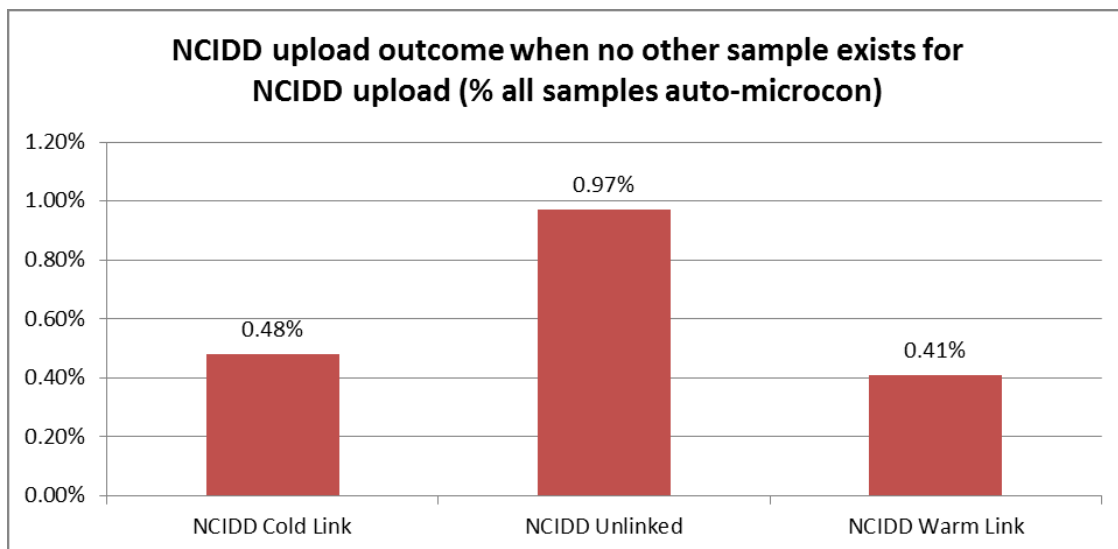


Figure 4: NCIDD outcome for samples that were loaded to NCIDD

Ultimately, this data means that for approximately 90% of samples that underwent an 'auto-microcon' process, there is arguably negligible DNA profile Intelligence for the client. If the 'auto-microcon' was not applied, there would be the following advantages, including but not limited to:

- the potential to make available at least 1449 processing positions for other samples including further available positions that would have been used for reworks,
- the lack of a need for the considerable efforts required to prepare and process Microcon® (and further rework) batches for this number of samples,
- consumable and labour savings in the end-to-end processing of these samples, and
- time and effort could be redirected in the laboratory workflow to other activities including service extensions like Y-STR profiling.

This is good, but for the argument to be presented in a balanced and transparent fashion perhaps you should include the perceived risks and impacts

too? Maybe a table? This is particularly important for the 'success' samples – if you are going to remove a process that gives any 'success' then you need to know what the impact will be and perhaps offer a mitigation strategy. For example, examine the 1.45% identified risk for QPS to see if there are any trends that predict success (ie sample type, substrate, collection location) that could be used to provide advice to QPS about which samples to request m'con on? These are all samples that were low quant first time round (hence the auto-mic), and all samples are available for QPS to request rework on. Can add some details from items in this 'success' category.

6.2 Assessment of all DNA profile results from extracts that have had a concentration step.

All samples from 2016 that had a Microcon® process were determined. The total number of samples was N= 2201 samples, excluding certain samples as per Section 5.1.

The percentage of samples that resulted in a determination of 'fail' was 78.5% (see Fig 5). As expected, in looking at the spread of the 'combined' data, the number of 'successes' increased when the Quantification increased (Fig 6).

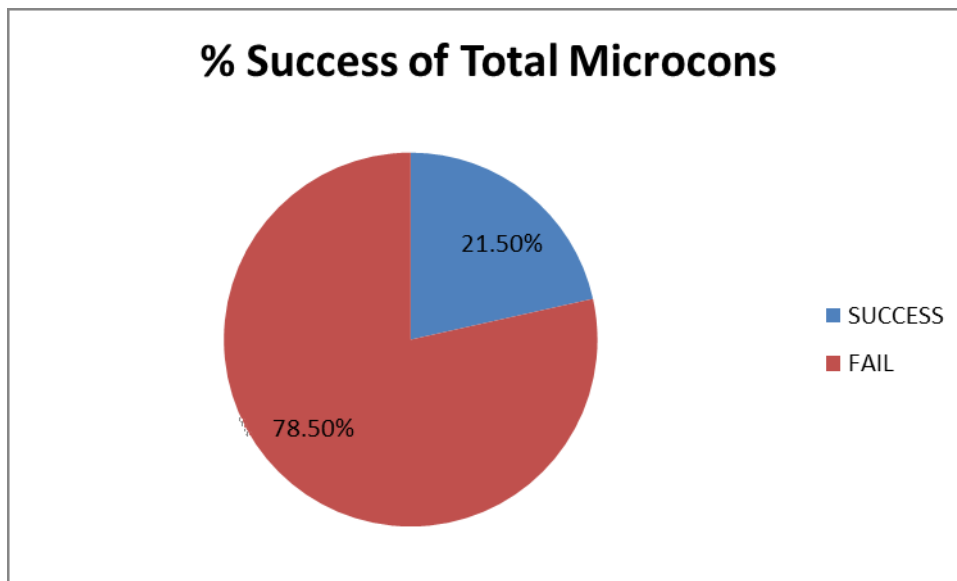


Figure 5: Percentage 'Success'/'Fail' of all Microcon® samples ('combined' data).

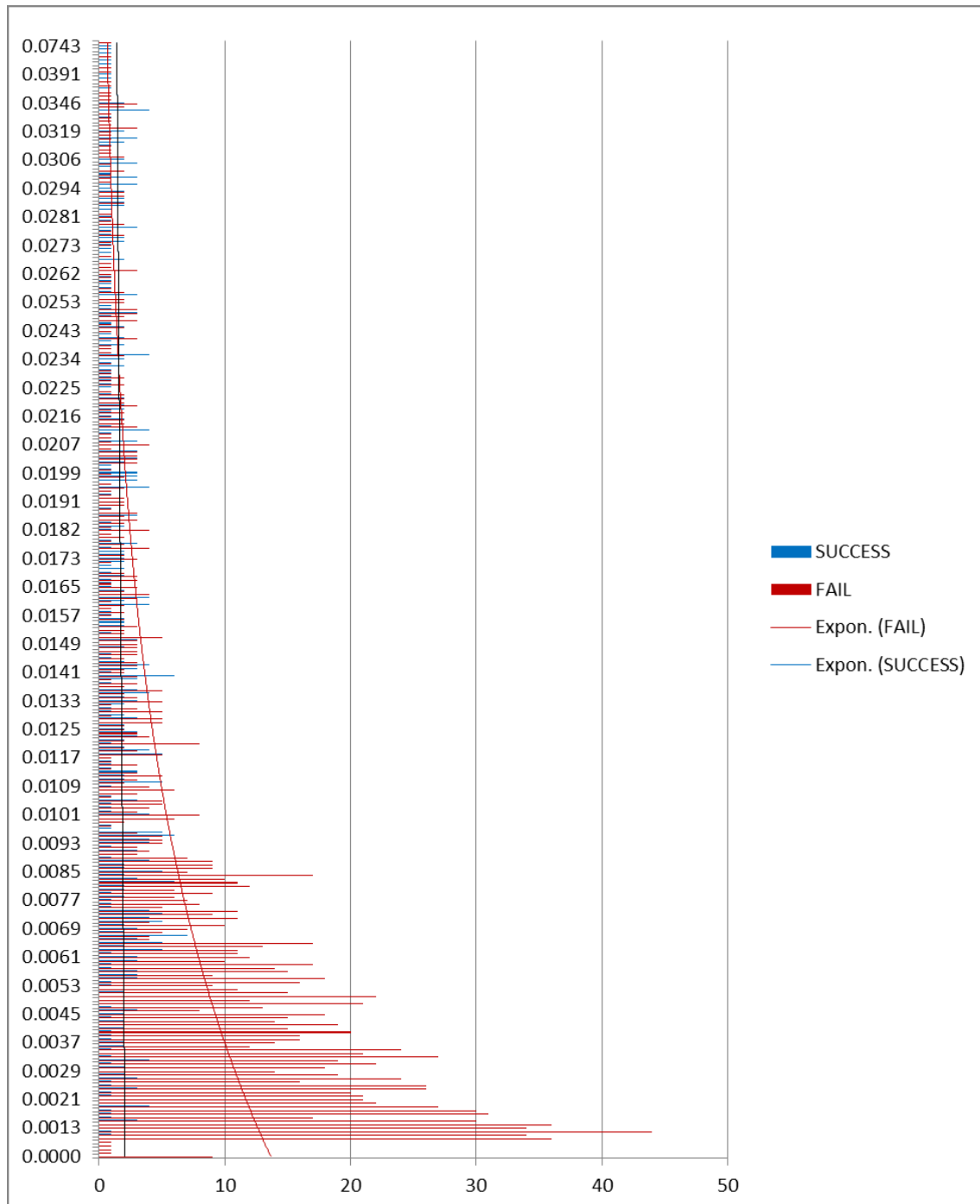


Figure 6: Combined data for samples that underwent the Microcon® process as a function of Quantification value.

As mentioned in Section 5.2, the Quantification value where there was roughly the same number of ‘success’ and ‘fail’ samples was approximately 0.02ng/uL. It must be noted that this is a rough estimate *at this* particular Quantification value, and it is based on limited samples that returned that Quantification value. It can be argued that taking a range of Quantification values to look at the overall success/fail percentages could provide the client with approximate likelihoods of obtaining meaningful DNA Intelligence.

A number of ranges were looked at to determine the percentage 'success' of samples with Quantification values in various ranges (Fig 7). The ranges were established up to the highest Quantification value of 0.02ng/uL. As expected, the percentage 'success' increased as the Quantification increased due to the higher amount of DNA in the extract available to be concentrated.

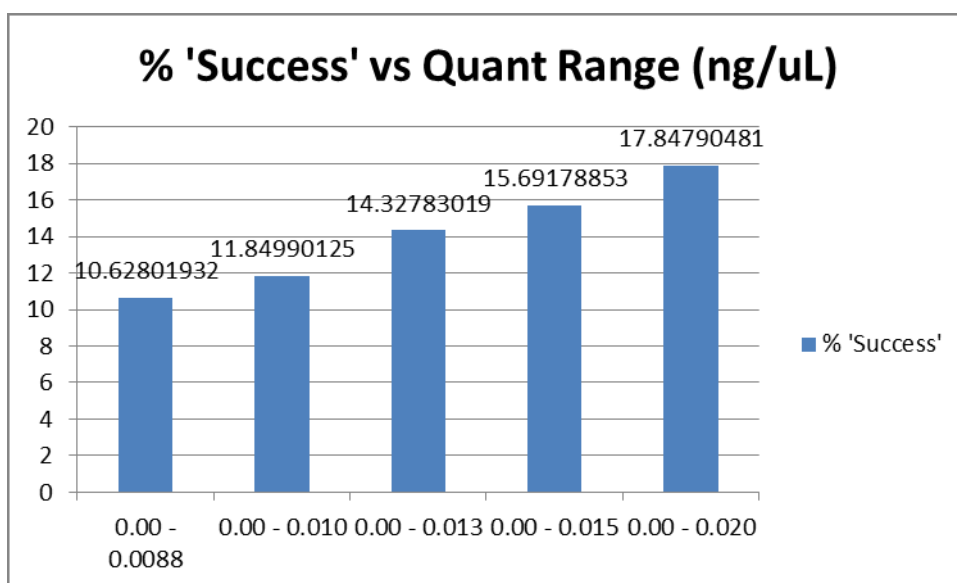


Figure 7: Percentage 'success' for samples that underwent a Microcon® process

In viewing the data in Fig 7, a limitation is that all samples that fell in the 'auto-microcon' range, had a Microcon® process performed, whereas there are samples that are in higher Quantification ranges that might not have required a Microcon® concentration rework step to yield useful DNA profiles. These samples were not evaluated.

A lower Quantification value to where the number of 'successes' roughly equalled the 'failures' was chosen to be the upper end of data ranges that were evaluated further. The value chosen was 0.015ng/uL. Table 1 and Figure 8 describe the risk to NCIDD upload for samples in these ranges if Microcon® concentration steps were not performed.

Table 1: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

| | % No other samples to Upload in Quantification ranges (Q) | | |
|-----------------|--|--|---|
| | Q = 0.00ng/uL to 0.01ng/uL (total samples in range = 1519) | Q = 0.00ng/uL to 0.0133ng/uL (total samples in range = 1696) | Q = 0.00ng/uL to 0.015ng/uL (total samples in range = 1778) |
| NCIDD Cold link | 0.92 | 0.88 | 1.01 |
| NCIDD Unlinked | 0.53 | 0.77 | 1.24 |
| NCIDD Warm Link | 0.46 | 0.83 | 0.90 |

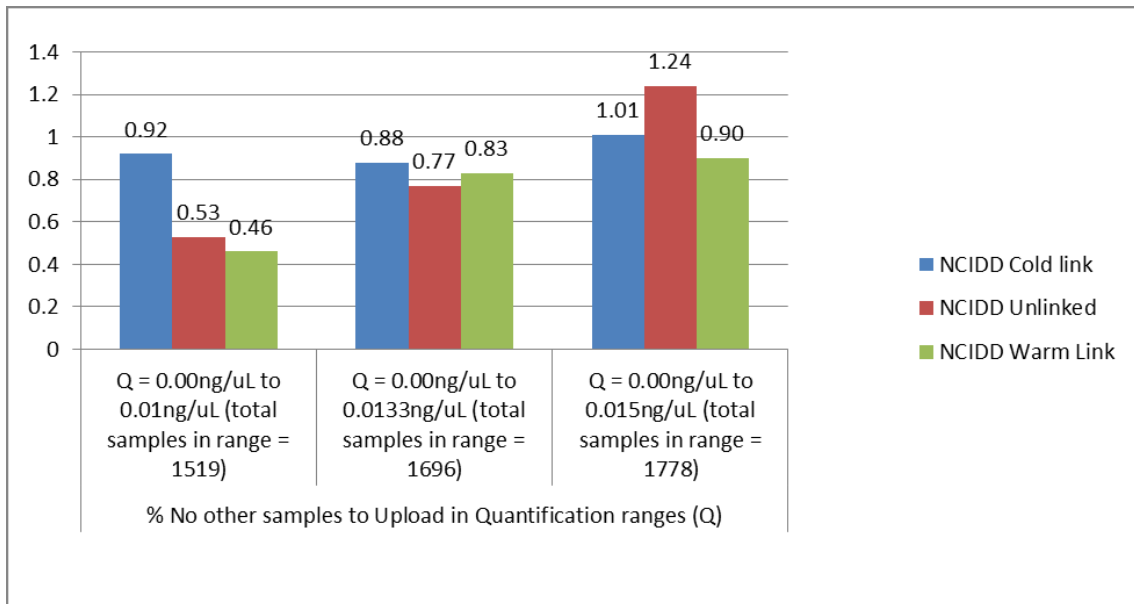


Figure 8: NCIDD outcome for samples that were loaded to NCIDD in various Quant ranges

Approximately 1.45% of samples in the Quantification range up to 0.01ng/uL resulted in ‘new’ DNA Intelligence. This percentage is the same as that found in the ‘auto-microcon’ range. This percentage increased to 1.65% and 2.25% for the Quantification ranges up to 0.0133ng/uL and 0.015ng/uL respectively.

The number of further reworks required to obtain ‘success’ outcomes decreased as the Quantification increased. This is not unexpected given higher DNA yields detected would not necessarily require as many reworks in order to yield DNA profiles.

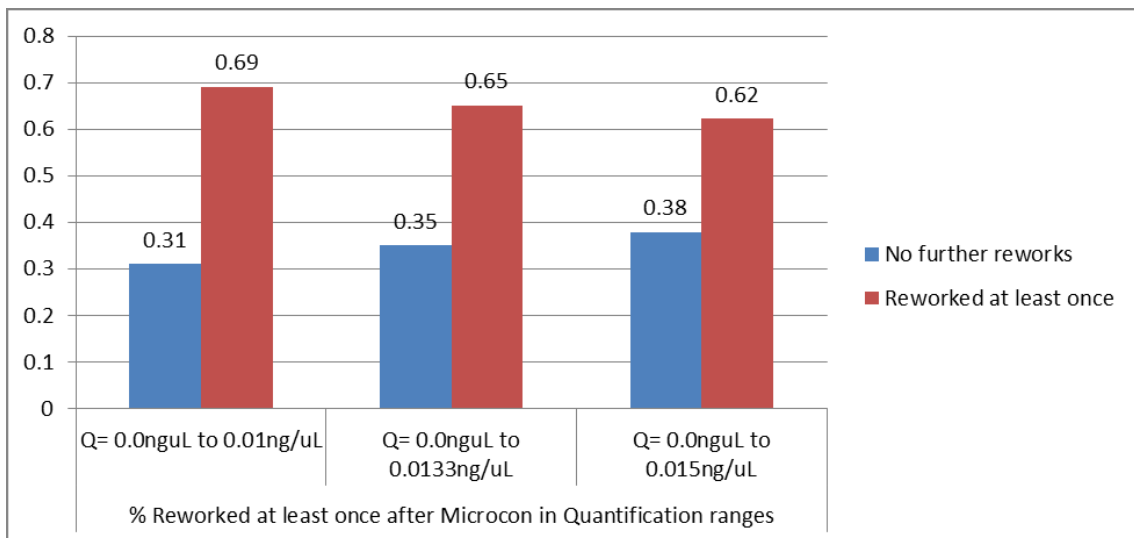


Figure 9: Percentage of samples reworked (in addition to a Microcon® process) in various Quantification ranges.

6.3 Datamine of the difference in pre- and post- Microcon® Quantification values

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'. The range was further refined as per Section 5.2, such that samples that had Quantification values between 0.001ng/μL and 0.015ng/μL were examined.

As the Microcon® process concentrates the DNA extract from approximately 100uL to approximately 35uL, in theory it would be a reasonable expectation to obtain approximately two to three-fold increases in DNA Quantification after concentration. Figure 10 shows the plot of the differences found for samples that resulted in 'success'.

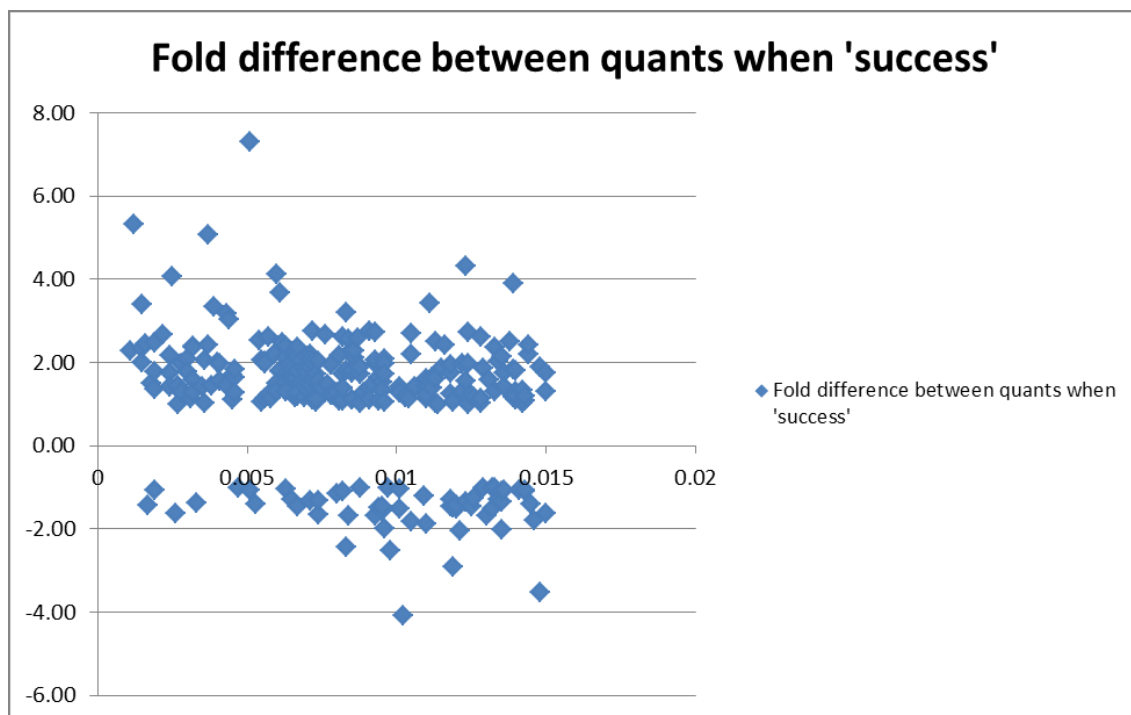


Figure 10: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results – we know that quant step itself has inherent variability. Can add more words around this as variability in all steps. Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 10 where the Quantification values decreased after concentration. Variability in results could be attributed to a number of things, including but not limited to the slight differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

7. Conclusion and Recommendations

The data analysis demonstrated that there was arguably minimal value in performing the 'auto-microcon' concentration step. This opinion was formed by analysing the data from 2016 where it was found that for all samples that underwent the 'auto-microcon' step, 89% did not yield meaningful results.

It was found that in considering all samples that underwent a Microcon® step at some stage in 2016, 78.5% did not yield meaningful results (what does this mean? They are fails? Or they didn't give new intel?). Definitions to be added. As expected, when the Quantification value increased, the percentage of meaningful results increased. However, it was also demonstrated in the data analysis that the Quantification values did not always improve after Microcon®, but where they did, the magnitude of change was roughly equivalent to the change in volume (from neat to concentrated sample).

Based on the data analysis, the following recommendations are offered: Recommendations to be revised as will keep simple/sample values for implementation, and revise further on as samples may get reworked where Q value is greater than 0.0088ng/uL.

1. Cease 'auto-microcon' processing with the following exceptions:
 - a. Priority 1 samples (Critical Priority); and
 - b. Coronial/DVI samples where profiles are mostly single-source and quite often incomplete profiles may be enough to provide Intelligence on possible identity.
2. Cease processing all Priority 3 samples up to the Quantification value of 0.0133ng/uL (template of 200ng). Maybe this, and reworks, could form a part B to this project?
3. For samples in the range described in Recommendation 2, automatically send result information via the Forensic Register to QPS at Quantification stage. This result information is recommended to be the exhibit result line of 'DNA Insufficient for Further Processing'. This recommendation is an extension to the current 'No DNA Detected' process, which looks at Priority 2 samples yielding Quantification results of less than the Limit of Detection.
4. Re-analyse Priority 2 samples in the range 0.0088ng/uL to 0.0133ng/uL after a six month period of processing to evaluate whether Recommendation 2 can be extended to Priority 2 samples.

5. Communicate the change in process to QPS and ensure that QPS are aware that for samples in the ranges mentioned in Recommendations 1 and 2, that they could be requested for Microcon® concentration steps at any point in time. This request can be made via the Forensic Register after they have received the 'DNA insufficient...' result line.

8. References

- [1] QIS 19544v11 – Concentration of DNA Extracts Using Microcon Centrifugal Filter Devices
- [2] PowerPlex® 21– Amplification of Extracted DNA Validation. Megan Mathieson, Thomas Nurthen, Cathie Allen. December 2012. Forensic DNA Analysis.
- [3] Project #163 - Assessment of results obtained from 'automatic-microcon' samples. Josie Entwistle, Allison Lloyd, Kylie Rika, Thomas Nurthen, Cathie Allen. August 2015. Forensic DNA Analysis.

Paula Brisotto

From: Justin Howes
Sent: Monday, 8 January 2018 9:04 AM
To: Kerry-Anne Lancaster; Allan McNevin; Amanda Reeves; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer
Cc: Allison Lloyd
Subject: Project #184

Hi all

I will have my door shut for most of today now that I have all feedback on v1 of the report.

I intend on sending v2 out today for urgent review by you all by 11am tomorrow. I don't think I am stepping on Paula's toes (for ERQ reviewers) by asking for this to be your No. 1 Priority as you all know how urgent this is now.

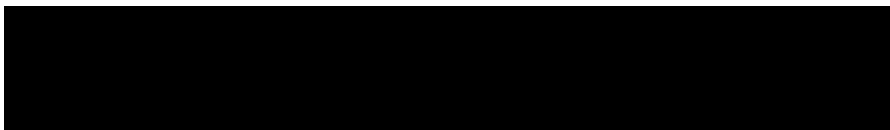
There will be some additions and removals as usual with reports.

Thanks
Justin

**Justin Howes**

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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Paula Brisotto

From: Justin Howes
Sent: Monday, 8 January 2018 4:47 PM
To: Kerry-Anne Lancaster; Allan McNevin; Amanda Reeves; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer
Subject: #184 report v2
Attachments: Report_Evaluation of the efficacy of Microcons_v2.doc

Hi all

I am after your swift review please by **1pm Tues 9 January**. This is to allow any further adjustments, hopefully by the end of the day.

I have made some changes:

- Removed the data and discussion on reworks
- Added evaluation of the 'success' samples – looked at profile outcome vs substrate type, and poss biological origin
- Revised the ranges to keep simple for both priority types – just the auto-mic range. All manual mics to be assessed again at a future date.
- Added some definitions
- Tried to fix labelling of graphs, but alas I couldn't for everything due to my use of pivot tables.

Thanks
Justin

**Justin Howes**

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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Justin Howes

From: Luke Ryan
Sent: Tuesday, 9 January 2018 8:31 AM
To: Justin Howes
Subject: RE: #184 report v2

Hi Justin

Looks great, I assume the recommendations apply to P3 samples amped in PP21? I'm ready to sign.

Thanks

Luke

From: Justin Howes
Sent: Monday, 8 January 2018 4:47 PM
To: Kerry-Anne Lancaster; Allan McNevin; Amanda Reeves; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer
Subject: #184 report v2

Hi all

I am after your swift review please by **1pm Tues 9 January**. This is to allow any further adjustments, hopefully by the end of the day.

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- Added some definitions
- Tried to fix labelling of graphs, but alas I couldn't for everything due to my use of pivot tables.

Thanks

Justin



Justin Howes

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
 Health Support Queensland, **Department of Health**



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Figures 4 and 5 show that there do not appear to be any obvious trends in the data. It is not unexpected to have a variety of DNA profile outcomes for different biological source types, and not unexpected for a variety of DNA profile outcomes for different substrate types. Interestingly, the number of 'assumed known contributors' is almost one-third of DNA profile outcomes for the most numerous suspected biological type (cells), and substrate type (swab). It could be argued that this DNA profile outcome is not meaningful to the client as the results are not unexpected.

What this means is that if the client requested a Microcon® process on a particular sample that was initially in the 'auto-microcon' Quantification range, there does not appear to be a predictive element to the likely success of the microcon rework for a particular biological source type, nor substrate type.

Ultimately, for approximately 90% of samples that underwent an 'auto-microcon' process, there is arguably negligible DNA profile Intelligence for the client. If the 'auto-microcon' was not applied as a streamlining strategy, there would be the following advantages, including but not limited to:

-the potential to make available at least 1449 processing positions for other samples including further available positions that would have been used for reworks. It must be noted that it is not unusual for low-quantification samples to be reworked further before determining if the profile is suitable for comparison to reference DNA profiles.

-the lack of a need for the considerable efforts required to prepare and process Microcon® (and further rework) batches for this number of samples,

-consumable and labour savings in the end-to-end processing of these samples, and

-time and effort could be redirected in the laboratory workflow to other activities including service extensions like ~~Y~~-STR profiling.

worth putting of a % of samples rework?

be } post mic these samples are often reworked further to enable interpretation
↑
is this what you are trying to say?
it causes even more work

? needed

-benefit.
reported profiles have better reproducibility?
as mic samples have low repro?

concentration. Figure 10 shows the plot of the differences found for samples that resulted in 'success'.

*increases/decreases of Q value
post
mic*

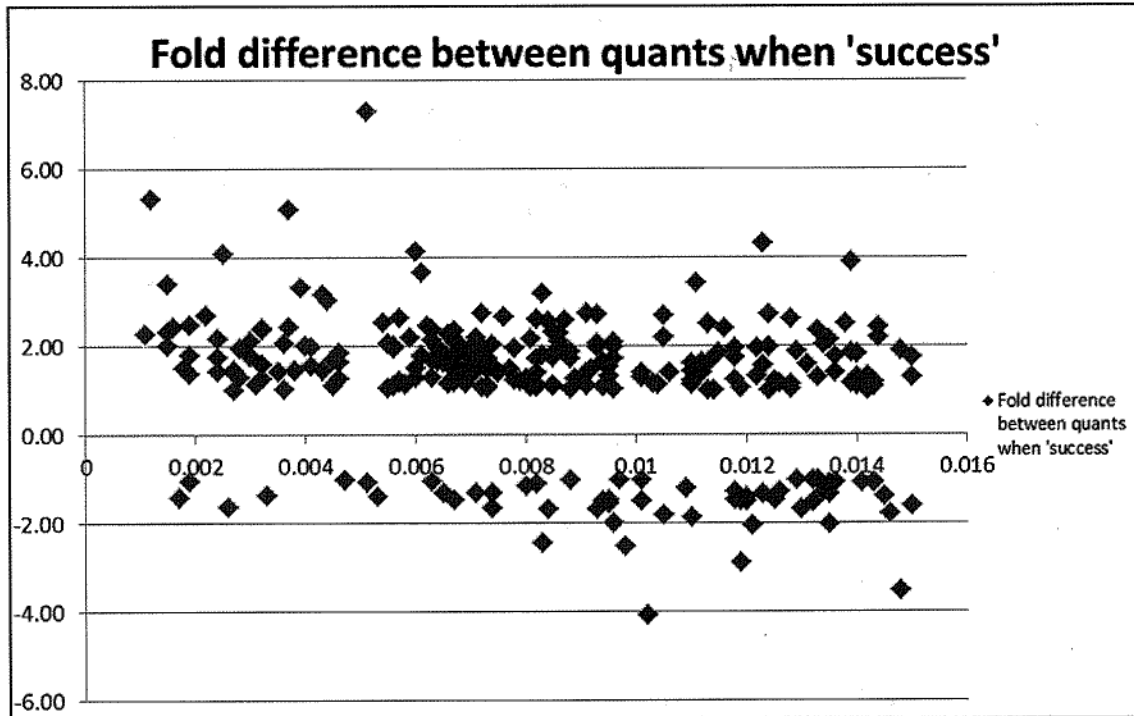


Figure 10: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results. Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 10 where the Quantification values decreased after concentration. Variability in results could be attributed to a number of things, including but not limited to the slight differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

8. Conclusion and Recommendations

The data analysis demonstrated that there was arguably minimal value in performing the 'auto-microcon' concentration step. This opinion was formed by analysing the data from 2016 where it was found that for all samples that underwent the 'auto-microcon' step, 89% did not yield results suitable for meaningful interpretation (or 'success' in this report).

It was found that in considering *all* samples that underwent a Microcon[®] step at some stage in 2016, 78.5% did not yield results suitable for meaningful interpretation. As expected, when the Quantification value increased, the percentage of meaningful results increased. However, it was also demonstrated in the data analysis that the Quantification values did not always improve after Microcon[®], but where they did, the magnitude of change was roughly equivalent to the change in volume (from neat to concentrated sample).

Based on the data analysis, the following recommendations are offered:

1. Cease 'auto-microcon' (Quant range: 0.001ng/uL to 0.0088ng/uL) processing for all samples with the following exceptions:

- a. Priority 1 samples (Critical Priority); and

- b. Coronial/DVI samples where profiles are mostly single-source. Quite often incomplete profiles may be enough to provide Intelligence on possible identity.

*⇒ how do you make this exception happen in the FR?
 ⇒ pl upgrade haphazard?
 Recommendation manual
 m/c*

2. Automatically send result information via the Forensic Register to QPS at Quantification stage for samples in the Quant range: 0.001ng/uL to 0.0088ng/uL. This result information is recommended to be the exhibit result line of 'DNA Insufficient for Further Processing'. This recommendation is an extension to the current 'No DNA Detected' process, which looks at Priority 2 samples yielding Quantification results of less than the Limit of Detection (0.001ng/uL).
3. After a six month period of processing, re-analyse samples that have had a Microcon[®] process performed and were in the initial Quantification range greater than 0.0088ng/uL, to evaluate whether the range from Recommendation 1 can be extended.
4. Communicate the change in process to QPS and ensure that QPS are aware that for samples in the range mentioned in Recommendations 1, that they could be requested for Microcon[®] concentration steps at any point in time. This request can be made via the Forensic Register after they have received the 'DNA insufficient...' result line.

Justin Howes

From: Luke Ryan
Sent: Tuesday, 9 January 2018 9:10 AM
To: Justin Howes
Subject: RE: #184 report v2

Excellent good one

From: Justin Howes
Sent: Tuesday, 9 January 2018 8:50 AM
To: Luke Ryan
Subject: RE: #184 report v2

Hey, added to R1:

1. Cease 'auto-microcon' (Quant range: 0.001ng/uL to 0.0088ng/uL) processing for all samples of Priority 2 and 3 requested to be amplified with PowerPlex 21, with the following exceptions:

jah



Justin Howes

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 Health Support Queensland, **Department of Health**



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From: Luke Ryan
Sent: Tuesday, 9 January 2018 8:41 AM
To: Justin Howes
Subject: RE: #184 report v2

Ok excellent. Might be worth specifying. I would either add a Scope section at the start (and say that recommendations apply to all P2 and P3 samples processed with PP21, or just specify in the Conclusion and Recommendations section – perhaps at start of recommendation 2? i.e. "For all Priority 2 and 3 samples processed with PP21, automatically....."

From: Justin Howes
Sent: Tuesday, 9 January 2018 8:35 AM
To: Luke Ryan
Subject: RE: #184 report v2

Hey, yes all samples. Do you think I should just expand this a bit?

jah



Justin Howes

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Health Support Queensland, **Department of Health**



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From: Luke Ryan
Sent: Tuesday, 9 January 2018 8:31 AM
To: Justin Howes
Subject: RE: #184 report v2

Hi Justin

Looks great, I assume the recommendations apply to P3 samples amped in PP21? I'm ready to sign.

Thanks
Luke

From: Justin Howes
Sent: Monday, 8 January 2018 4:47 PM
To: Kerry-Anne Lancaster; Allan McNevin; Amanda Reeves; Cathie Allen; Kirsten Scott; Kylie Rika; Luke Ryan; Paula Brisotto; Sharon Johnstone; Wendy Harmer
Subject: #184 report v2

Hi all

I am after your swift review please by **1pm Tues 9 January**. This is to allow any further adjustments, hopefully by the end of the day.

I have made some changes:

- Removed the data and discussion on reworks
- Added evaluation of the 'success' samples – looked at profile outcome vs substrate type, and poss biological origin
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- Added some definitions
- Tried to fix labelling of graphs, but alas I couldn't for everything due to my use of pivot tables.

Thanks
Justin



Justin Howes

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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RJP – Response to Project #184 proposal

- I will leave issues of what constitutes “meaningful information” and the issue of NCIDD “interaction” to others, though it think the former it needs to be specifically stated in the abstract (even a single peak can be informative if it excludes) and the rationale for the latter as a criterion needs to be stated more clearly in the introduction.
- It is good that source and substrate data have been added, though it would have been ideal to also gather sample source (blood/semen etc), substrate (swab/tapelift etc) for all samples as this could have been factored into the analysis using standard linear modelling techniques.
- It should be “n” not “N” for a sample size (“N” refers to a population size)
- Pg 14. It is unclear if the n=2201 is before or after the exclusion of unsuitable samples.
- My main concern with this proposal is the use of percentages and non-normalized data to draw conclusions from the data that are not valid.
 - By not normalizing the very low quant (<0.0088ng/uL; n=1449) data which represents the bulk of the samples (n_{total}=1731), percentages derived from data combined with the above very low quant samples (eg. Figure 8 and figure 9) are artificially skewed by the large number of close-to-zero quant values. Thus, it would not be expected for there to be an insignificant increase in the percentage of successful microcons as presented in figures 8 & 9). Even if 100% of the microcons in the 0.015-0.020 range were successful (n=94), this would have little effect on the mean success rate of the n=1492 samples that have lower quants ($94/1492 = 6.4\%$) at maximum.
 - The data needs to be normalized by obtaining the probability for the mean quant using a frequency distribution for a range of quant values.
 - My own analysis of the data shows that the data can be best modelled by a third order regression of the success/fail probability against the quant. I developed the data as a frequency distribution based on divisions of 0.001 ng/uL. The probability of success was calculated based on the outcome of all samples within a single division, thus normalizing the data. This reduced the data to 33 points. The data was analysed as a binomial distribution as is appropriate with binomial data and the 95% confidence intervals calculated.
 - These outcomes are presented in graphical and tabular form in the attached pages suggests a very different set of conclusions.
 - As can be seen from the results there is a mean success rate of approximately 30% at 0.010ng/uL up to approximately 43% at 0.015ng/uL. This is at odds with the conclusions drawn in section 7.2 of the project and with the justification for the use of 0.015ng/uL in the introduction to Experiment 2 (pg 8).
- As such, I conclude that setting the cut-off for no processing at 0.0088ng/uL is probably too high.
- Additionally, conclusion drawn from percentage values derived from non-normalized data cannot be trusted as the data is clearly skewed towards very low-level quants.

Table 1. 95% confidence intervals for the microcon success probabilities for all quant ranges. (eg. Line 6 represents the probability of success for all samples with a quant between 0.0055 and 0.0064.)

| | Mean Quant for range | lower | Estimated Prob of Success | upper |
|----|-------------------------|-----------|------------------------------|-----------|
| 1 | 0.001 | 0.061921 | 1.984695 | 2.907470 |
| 2 | 0.002 | 2.111484 | 3.275817 | 4.440151 |
| 3 | 0.003 | 3.746543 | 5.116828 | 6.487114 |
| 4 | 0.004 | 6.038001 | 7.574229 | 9.110456 |
| 5 | 0.005 | 8.936327 | 10.645507 | 12.354687 |
| 6 | 0.006 | 12.277503 | 14.244627 | 16.211752 |
| 7 | 0.007 | 15.868023 | 18.210662 | 20.553300 |
| 8 | 0.008 | 19.552401 | 22.337853 | 25.123304 |
| 9 | 0.009 | 23.205051 | 26.415076 | 29.625101 |
| 10 | 0.010 | 26.709850 | 30.259965 | 33.810081 |
| 11 | 0.011 | 29.959510 | 33.738579 | 37.517648 |
| 12 | 0.012 | 32.862823 | 36.769795 | 40.676767 |
| 13 | 0.013 | 35.350065 | 39.319138 | 43.288211 |
| 14 | 0.014 | 37.375481 | 41.387961 | 45.400441 |
| 15 | 0.015 | 38.919212 | 43.002380 | 47.085547 |
| 16 | 0.016 | 39.989907 | 44.204209 | 48.418510 |
| 17 | 0.017 | 40.625908 | 45.044506 | 49.463105 |
| 18 | 0.018 | 40.891674 | 45.579421 | 50.267168 |
| 19 | 0.019 | 40.869451 | 45.867744 | 50.866037 |
| 20 | 0.020 | 40.649724 | 45.969556 | 51.289388 |
| 21 | 0.021 | 40.323576 | 45.945520 | 51.567465 |
| 22 | 0.022 | 39.977440 | 45.856505 | 51.735570 |
| 23 | 0.023 | 39.689097 | 45.763385 | 51.837673 |
| 24 | 0.024 | 39.523421 | 45.726976 | 51.930532 |
| 25 | 0.025 | 39.526412 | 45.808084 | 52.089757 |
| 26 | 0.026 | 39.716517 | 46.067684 | 52.418852 |
| 27 | 0.027 | 40.074323 | 46.567177 | 53.060032 |
| 28 | 0.028 | 40.538169 | 47.368584 | 54.198998 |
| 29 | 0.029 | 41.021312 | 48.534376 | 56.047440 |
| 30 | 0.030 | 41.456547 | 50.126451 | 58.796354 |
| 31 | 0.031 | 41.839757 | 52.203470 | 62.567183 |
| 32 | 0.032 | 42.240691 | 54.815589 | 67.390487 |
| 33 | 0.033 | 42.793029 | 57.995491 | 73.197953 |

Rhys Parry

From: Rhys Parry
Sent: Tuesday, 9 January 2018 11:53 AM
To: Amanda Reeves
Subject: Project 184
Attachments: Response to JAH final proposal Jan 2018.doc; Binomial Plot Probs.pdf



Rhys Parry

Reporting Scientist

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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Paula Brisotto

From: Justin Howes [REDACTED]
Sent: Friday, 12 January 2018 11:18 AM
To: Paula Brisotto

Hi, Sorry about today. Didn't actually close eyes last night and exhausted. Do you mind emailing the v2 of mic report for me to convert to options paper?

Thanks, Justin.

[Sent from Yahoo7 Mail on Android](#)

From: Taylor.EwenN[OSC]
Sent: Wed, 31 Jan 2018 08:05:28 +1100
To: Collophen.RubenB[OSC];Gee
Kee.KenN[OSC];Harris.LibbyA[OSC];McIntyre.OliviaM[OSC]
Subject: FSS Options paper
Attachments: Review of efficacy of Microcons_options for QPS.doc

Good morning,

For your advice please.

Cheers,



Ewen TAYLOR
Acting Inspector
DNA Management Unit | Forensic Services Group
Operations Support Command
QUEENSLAND POLICE SERVICE





HealthSupport Queensland

A review of the automatic concentration of DNA extracts using Microcon[®] Centrifugal Filter Devices: Options for QPS consideration.

January 2018

Justin Howes and Cathie Allen

A review of the automatic concentration of DNA extracts using Microcon® Centrifugal Filter Devices: Options for QPS consideration.

Published by the State of Queensland (Queensland Health), January 2018



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For more information contact:

Forensic DNA Analysis, Forensic and Scientific Services, Department of Health,
GPO Box 48, Brisbane QLD 4001.

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Document Details

Contact for enquiries and proposed changes

If you have any questions regarding this document or if you have a suggestion for improvements, please contact:

Contact officer: Justin Howes
 Title: Team Leader – Forensic Reporting and Intelligence Team
 Phone: [REDACTED]
 Email: [REDACTED]

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1. Abstract

All casework DNA extracts that underwent a concentration step using the Microcon® process were evaluated and categorised into whether there was meaningful information obtained or not. This evaluation primarily focussed on samples that underwent an 'auto-microcon' process in 2016.

The findings of this evaluation are presented for the Queensland Police Service to advise on whether they would prefer their Priority 2 samples to continue with the 'auto-microcon' process, or to cease this automatic step and notify the laboratory if particular samples are requested to be reworked.

These options relate to Priority 2 (Major Crime) samples only, as the process developed in 2012 for Priority 3 (Volume Crime) samples will be reinstated with the operationally-required move to process these samples using PowerPlex® 21 system (PP21).

2. Definitions

DNA Profile Intelligence: DNA profile information available for interpretation by Forensic DNA practitioners that is able to be provided to clients.

Fail: In this report, this is DNA profile information that was not suitable for comparing to reference DNA profiles and other casework samples. This word was used to filter the data into two possible outcomes (fail/success).

NCIDD: National Criminal Investigation DNA Database.

QPS: Queensland Police Service.

Success: In this report, this is DNA profile information that was obtained that was suitable for comparing to reference DNA profiles and other casework samples. This word was used to filter the data into two possible outcomes (fail/success).

3. Introduction

Microcon® Centrifugal Filter Devices desalt and concentrate macromolecular solutions such as DNA-containing solutions. They employ Amicon's low binding, anisotropic, hydrophilic regenerated cellulose membrane^[1].

The use of Microcon® filters to concentrate extract has been a standard post-extraction process within Forensic DNA Analysis to reduce the volume of

extract from approximately 100uL to $\leq 35\mu\text{L}$ for amplification with PowerPlex[®] 21 system.

Since the implementation of PP21 amplification kit within Forensic DNA Analysis for casework samples in December 2012, extracts with low Quantification values were recommended to be concentrated. Templates of $<0.132\text{ng}$ (Quantification $<0.0088\text{ng/uL}$) were found to exhibit marked stochastic effects after amplification [2]. Consequently, a workflow that directed extracts automatically to a concentration step based on Quantification value was implemented ('auto-microcon' process) for Priority 2 samples.

A workflow for Priority 3 samples remained within active Standard Operating Procedures to have the DNA extracts not amplified, nor automatically concentrated with Microcon[®] filters, but to be held after Quantification and QPS informed that low levels of DNA were obtained that were insufficient for further processing at that stage [3][4].

Anecdotally, the suitability to provide QPS with DNA profile Intelligence from extracts that have been concentrated has been noted to be limited, and added to scientist's time and availability to direct resources to samples with more DNA detected.

4. Data interrogation

The 'auto-microcon' data was interrogated by assessing the DNA profile outcome results reported as Exhibit Report lines as a function of the Quantification value.

The Exhibit lines were interrogated and grouped into two interpretation outcomes as follows:

1. 'Fail': DNA profile interpretation outcomes of 'Complex unsuitable for interpretation', 'No DNA profile', 'Partial unsuitable for interpretation', 'No DNA Detected';
2. 'Success': All other DNA profile outcomes including single source DNA profiles matching assumed known contributors or different reference DNA profiles, mixtures that were suitable for comparison to reference DNA profiles, DNA profiles that were suitable for loading to NCIDD.

NB. These descriptions were used to filter the data. A 'fail' does not mean there was a Quality failure in the process; a 'success' does not necessarily mean a DNA match.

5. Assessment of 'auto-microcon' results

Intent

Evaluate the 'success' or 'fail' outcomes for PP21 samples that were processed in 2016 through the 'auto-microcon' workflow.

Data Analysis

The samples applicable to this experiment had Quantification values in the range 0.001ng/ μ L to 0.0088ng/ μ L, and a total number of samples that were processed this way was determined. This total number excluded environmental samples, samples without Quantification values, samples not requested for further work, samples where quality flags were raised, and samples that had not returned results at the time of data collection.

DNA profile interpretation outcomes were grouped into either 'success' or 'fail' as a function of the Quantification value. A percentage of samples that fell into these categories was determined.

The 'auto-microcon' data could be expressed as a function of Quantification value.

The percentage of samples that had an 'auto-microcon' process and led to an NCIDD upload was obtained. This data could be filtered further into the outcome from the NCIDD load, at the time of data collection.

6. Datamine of the difference in pre- and post- Microcon® Quantification values

Intent

Evaluate the difference between the Quantification values obtained for samples prior to the 'auto-microcon' step, and then after the 'auto-microcon' process. This is to assess, through the Quantification data, the effectiveness of the Microcon® step in concentrating the DNA extract.

As this is purely a datamining experiment, only the samples that yielded a result of 'success' were examined.

Data Analysis

The samples applicable to this experiment had Quantification values above 0.001ng/ μ L and less than 0.015ng/ μ L where the final result was 'success'.

This range was considered by the author to be able to provide a sufficient demonstration of the trend of the data (N=278 samples).

7. Results and Discussion

7.1 Assessment of 'auto-microcon' results

There were N=1449 samples in the 'auto-microcon' Quantification range, excluding certain samples as per Section 5.

The percentage of samples that resulted in a determination of 'fail' was 89.4% (Fig 1). As expected, the number of 'fails' increased when the Quantification decreased and approached the Limit of Detection of Quantification ie. 0.001ng/ μ L (Fig 2). This was considered to be due to there being less DNA detected in the extract, and therefore less DNA to concentrate.

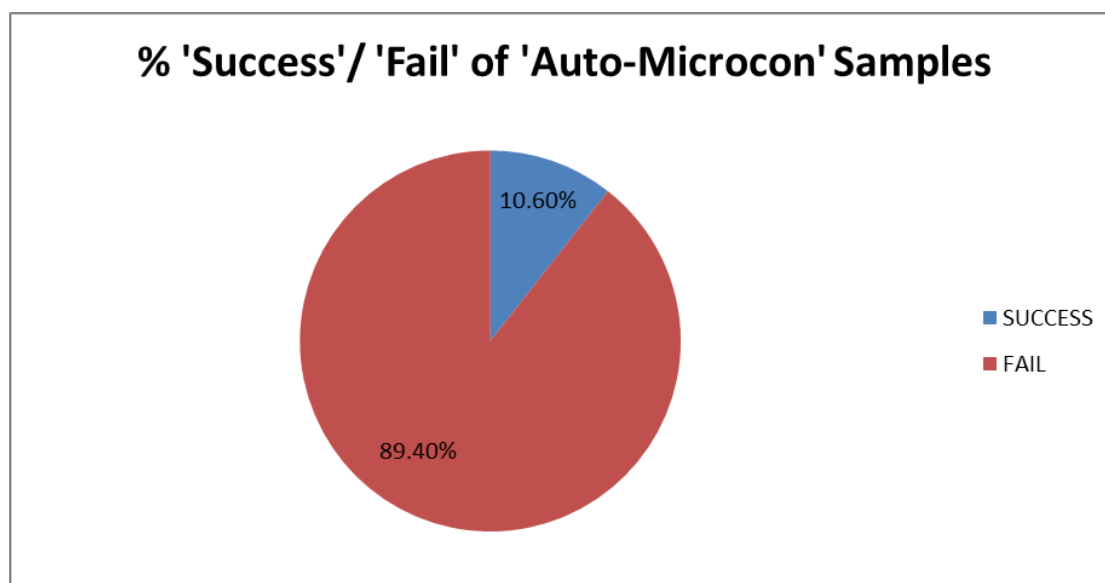


Figure 1: Percentage 'Success'/'Fail' of 'Auto-Microcon' samples.

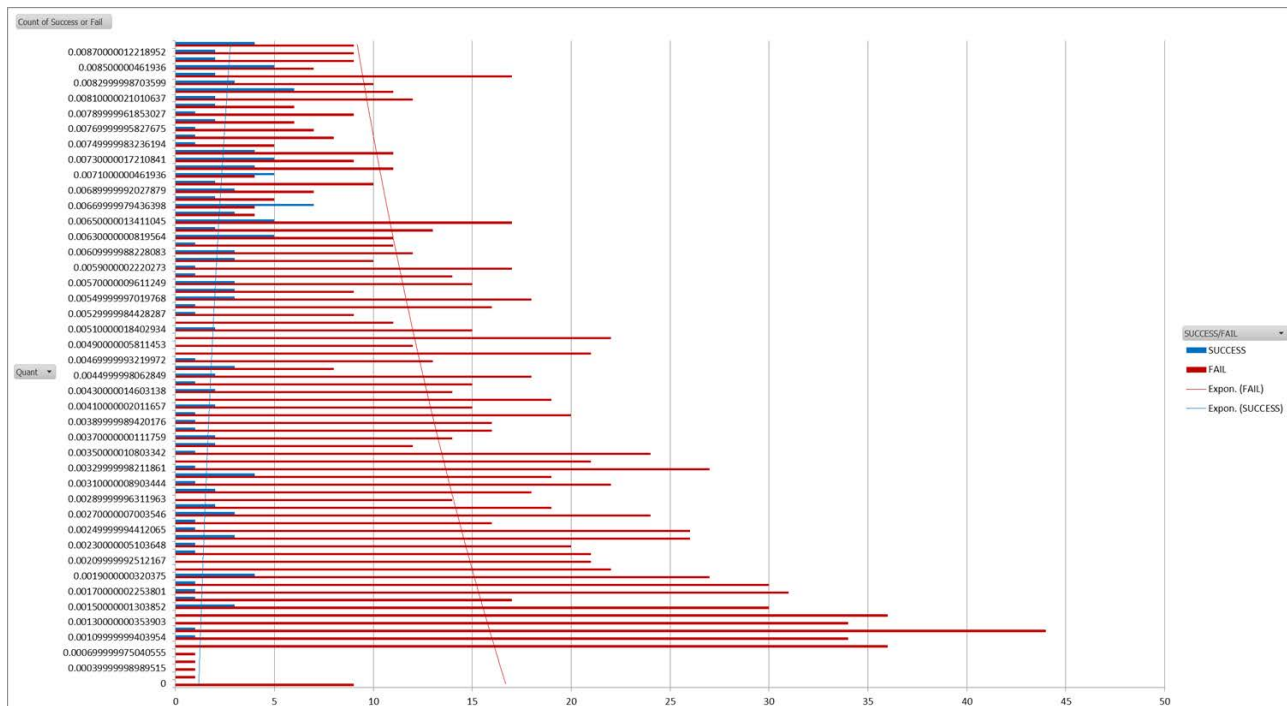


Figure 2: Spread of data and categorised as ‘Success’/ ‘Fail’ for ‘Auto-Microcon’ samples.

If samples were not processed through the ‘auto-microcon’ process, what DNA Intelligence would the client miss out on? To evaluate this, the ‘success’ data was drilled down to the samples that had some NCIDD interaction and in particular, where they were the only samples in the case that were NCIDD-suitable for that particular profile. This represented 1.86% of all ‘auto-microcon’ samples. In looking at samples that provide *new* Intelligence, that is DNA information available for future linking, or has provided a cold-link, this equated to 1.45% of all ‘auto-microcon’ samples (Fig 3)..

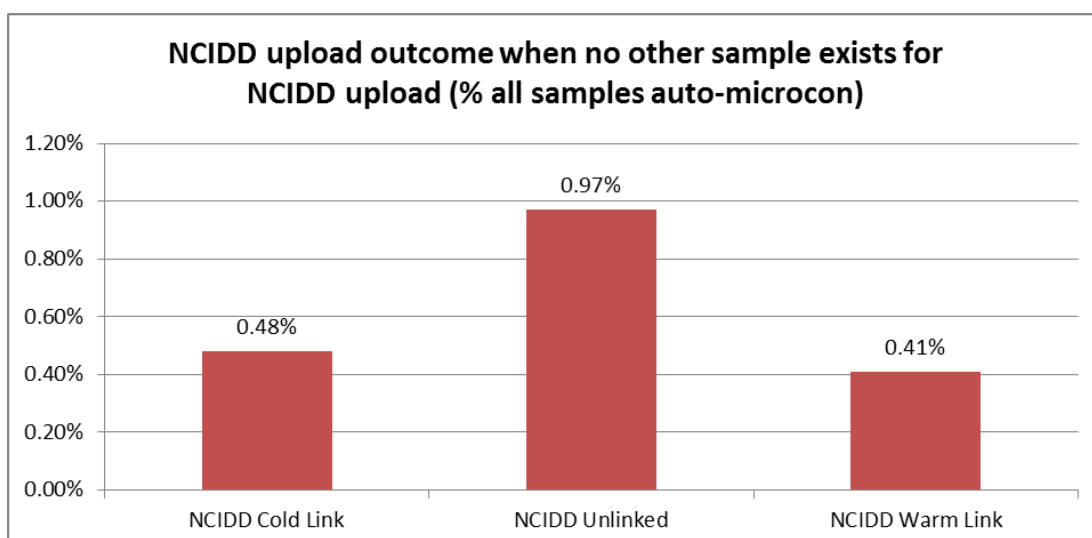


Figure 3: NCIDD outcome for samples that were loaded to NCIDD

This 1.45% of 'auto-microcon' samples is considered to be the pertinent value for the client to assess if the 'auto-microcon' process was not performed.

7.2 Datamine of the difference in pre- and post- Microcon® Quantification values

The samples applicable to this experiment had Quantification values above 0.001ng/μL where the final result was 'success'.

As the Microcon® process concentrates the DNA extract from approximately 100uL to approximately 35μL, in theory it would be a reasonable expectation to obtain approximately two to three-fold increases in DNA Quantification after concentration. Figure 4 shows the plot of the differences found for samples that resulted in 'success'.

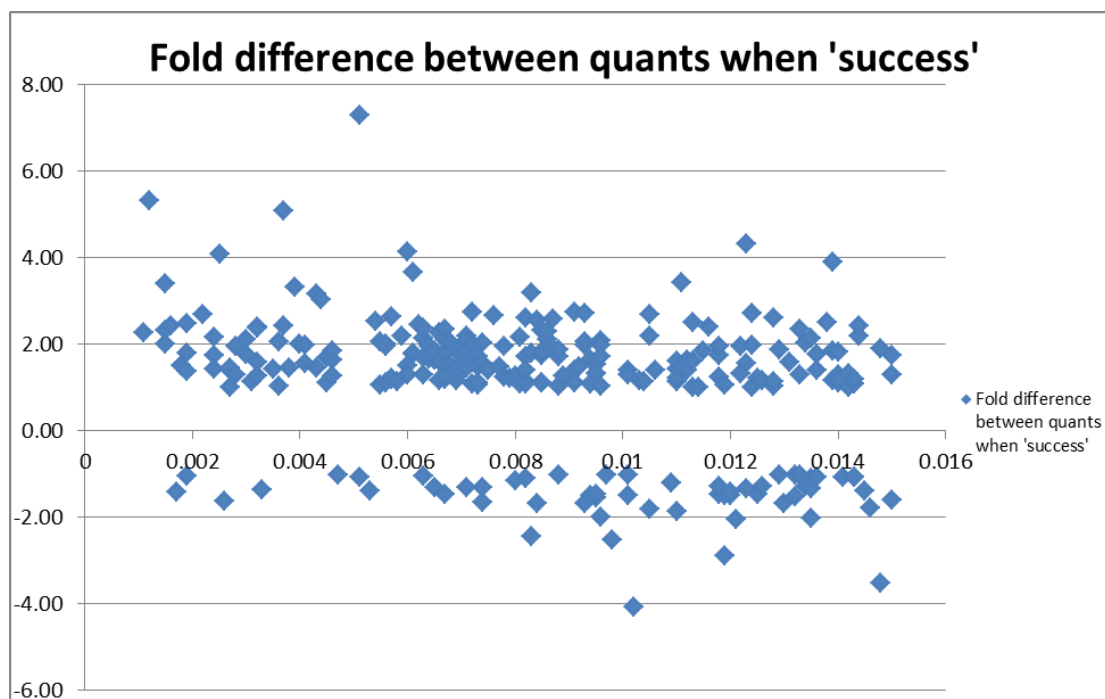


Figure 4: Quantification differences pre and post concentration

The findings are not unexpected as the scatter focusses mostly around two-fold increases in Quantification. It was also not unexpected to observe the variable results. Anecdotally, variability in success rates is found at profile management stage when assessing results of samples that have had this concentration step.

DNA can be lost in the process as seen in Fig 4 where the Quantification values decreased after concentration (below the horizontal axis). Variability in results could be attributed to a number of things, including but not limited to the slight

differences between operators and instrumentation, the differences in substrate type and level of degradation, and the variability in Quantification result.

8. Options for consideration

The options to consider are:

1. Continue with 'auto-microcon' process for Priority 2 (Major Crime) casework; or,
2. Cease the 'auto-microcon' process for Priority 2 (Major Crime) casework and report the exhibit result of 'DNA insufficient for further processing' based on Quantification result.
 - a. Priority 1 samples could proceed with the 'auto-microcon' process. If a DNA concentration rework is required, the Microcon® process can be ordered manually by the scientist.

In considering continuing or discontinuing the automatic concentration of DNA extracts for Priority 2 (Major Crime) samples, some key elements to consider include, but are not limited to:

- The opportunity to link DNA profiles on NCIDD would not be initially possible (without automatic concentration) for approximately 1.45% of samples that would qualify for this process. Of the 'auto-microcon' data set (N=1449 samples) evaluated, 1.45% equates to 21 samples;
- Time and cost for processing all samples in the 'auto-microcon' range, including batch preparation, Quality checking and control;
- Time and cost for processing these samples further with additional rework options, as one would expect with low levels of DNA detected initially;
- The ability to potentially reallocate staff time currently allocated to processing, interpreting and reporting 'auto-microcon' samples, to samples with higher DNA yield, thus improving the turnaround time for results on these samples;
- The opportunity to conserve DNA extract for further processing with other technologies should that be considered (eg. Y-STR analysis, Low Copy Number analysis);

- The improved ability to provide quick results to QPS (using the Forensic Register at Quantification stage) indicating low levels of DNA detected, thus enabling QPS to employ further strategies at their discretion (eg. further sampling of items, request the rework);
- The continued ability to process the DNA extract upon client request or depending on priority (eg Priority 1 – Critical Priority).

9. References

- [1] QIS 19544v11 – Concentration of DNA Extracts Using Microcon Centrifugal Filter Devices
- [2] PowerPlex® 21– Amplification of Extracted DNA Validation. Megan Mathieson, Thomas Nurthen, Cathie Allen. December 2012. Forensic DNA Analysis.
- [3] QIS 23008v15 – Explanation of EXR/EXH Results
- [4] QIS 24012v13 – Miscellaneous Analytical Section Tasks

From: Taylor.EwenN[OSC]
Sent: Wed, 31 Jan 2018 12:21:26 +1100
To: McIntyre.OliviaM[OSC]
Cc: Collophen.RubenB[OSC];Harris.LibbyA[OSC];Gee Kee.KenN[OSC]
Subject: RE: FSS Options paper

Thanks Olivia,

As discussed, I am in agreement. The 'auto-microcon' process would appear inefficient in this context, with time and resources appearing to be better spent in more worthwhile endeavours.

I am inclined to recommend your option 1, with an additional line added to the Q-prime update advising investigators of their option to request this additional process if required.

Does anyone have any further comment before I reply?

Cheers,



Ewen TAYLOR
Acting Inspector
DNA Management Unit | Forensic Services Group
Operations Support Command
QUEENSLAND POLICE SERVICE

[REDACTED]

From: McIntyre.OliviaM[OSC]
Sent: Wednesday, 31 January 2018 8:17 AM
To: Taylor.EwenN[OSC] <[REDACTED]>
Cc: Collophen.RubenB[OSC] <[REDACTED]> Harris.LibbyA[OSC]
<[REDACTED]> Gee Kee.KenN[OSC] <[REDACTED]>
Subject: RE: FSS Options paper

Good morning Ewen,

Further to our conversation, based on the statistics provided by FSS, it would appear it is not worthwhile continuing with the 'auto-microcon' process for Priority 2 samples.

If FSS ceases continuing with the 'auto-microcon' process for Priority 2 samples, I would imagine QPS can still request certain samples that are pertinent to an investigation be submitted through the 'auto-microcon' case, if it is required.

To identify these samples, I would imagine one of the following scenarios would apply:

1. If investigating police contact the DNA Management Section to inquire about testing, DMS staff can facilitate the 'auto-microcon' process on results that have been validated as "DNA insufficient for further processing', or
2. Results that are 'DNA insufficient for further processing', from unsolved occurrences are sent to a worklist for assessment by staff from DMS to determine whether further testing should be initiated.

Given the statistics provided by FSS, in relation to 'success' rates for these samples, I would imagine that Management may want to go with option 1.

Forwarded for your information.

Kind regards

[Olivia McIntyre](#) | DNA Management Officer | Profile Management Team | DNA Management Section
Forensic Services Group | Operations Support Command | Queensland Police Service
GPO Box 1440 | Brisbane QLD 4001 | Australia

[REDACTED]

From: Taylor.EwenN[OSC]

Sent: Wednesday, 31 January 2018 7:05 AM

To: Collophen.RubenB[OSC] <[REDACTED]> Gee Kee.KenN[OSC]

<[REDACTED]> Harris.LibbyA[OSC] <[REDACTED]>

McIntyre.OliviaM[OSC] <[REDACTED]>

Subject: FSS Options paper

Good morning,

For your advice please.

Cheers,



Ewen TAYLOR
Acting Inspector
DNA Management Unit | Forensic Services Group
Operations Support Command
QUEENSLAND POLICE SERVICE

[REDACTED]

From: Taylor.EwenN[OSC]
Sent: Wed, 31 Jan 2018 13:47:44 +1100
To: Harris.LibbyA[OSC]
Subject: RE: FSS Options paper

Cheers Lib



Ewen TAYLOR
 Acting Inspector
 DNA Management Unit | Forensic Services Group
 Operations Support Command
QUEENSLAND POLICE SERVICE

[REDACTED]

From: Harris.LibbyA[OSC]
Sent: Wednesday, 31 January 2018 12:08 PM
To: Taylor.EwenN[OSC] <[REDACTED]> McIntyre.OliviaM[OSC]
 <[REDACTED]>
Cc: Collophen.RubenB[OSC] <[REDACTED]> Gee Kee.KenN[OSC]
 <[REDACTED]>
Subject: RE: FSS Options paper

Yes I would agree with Olivia - Adding a comment would be more appropriate.

Lib

From: Taylor.EwenN[OSC]
Sent: Wednesday, 31 January 2018 11:21 AM
To: McIntyre.OliviaM[OSC] <[REDACTED]>
Cc: Collophen.RubenB[OSC] <[REDACTED]> Harris.LibbyA[OSC]
 <[REDACTED]> Gee Kee.KenN[OSC] <[REDACTED]>
Subject: RE: FSS Options paper

Thanks Olivia,

As discussed, I am in agreement. The 'auto-microcon' process would appear inefficient in this context, with time and resources appearing to be better spent in more worthwhile endeavours.

I am inclined to recommend your option 1, with an additional line added to the Q-prime update advising investigators of their option to request this additional process if required.

Does anyone have any further comment before I reply?

Cheers,



Ewen TAYLOR
 Acting Inspector
 DNA Management Unit | Forensic Services Group
 Operations Support Command
QUEENSLAND POLICE SERVICE

[REDACTED]

From: McIntyre.OliviaM[OSC]
Sent: Wednesday, 31 January 2018 8:17 AM
To: Taylor.EwenN[OSC] <[REDACTED]>
Cc: Collophen.RubenB[OSC] <[REDACTED]> Harris.LibbyA[OSC]
 <[REDACTED]> Gee Kee.KenN[OSC] <[REDACTED]>
Subject: RE: FSS Options paper

Good morning Ewen,

Further to our conversation, based on the statistics provided by FSS, it would appear it is not worthwhile continuing with the 'auto-microcon' process for Priority 2 samples.

If FSS ceases continuing with the 'auto-microcon' process for Priority 2 samples, I would imagine QPS can still request certain samples that are pertinent to an investigation be submitted through the 'auto-microcon' case, if it is required.

To identify these samples, I would imagine one of the following scenarios would apply:

1. If investigating police contact the DNA Management Section to inquire about testing, DMS staff can facilitate the 'auto-microcon' process on results that have been validated as "DNA insufficient for further processing', or
2. Results that are 'DNA insufficient for further processing', from unsolved occurrences are sent to a worklist for assessment by staff from DMS to determine whether further testing should be initiated.

Given the statistics provided by FSS, in relation to 'success' rates for these samples, I would imagine that Management may want to go with option 1.

Forwarded for your information.

Kind regards

[Olivia McIntyre | DNA Management Officer | Profile Management Team | DNA Management Section Forensic Services Group| Operations Support Command | Queensland Police Service](#)

[REDACTED]

From: Taylor.EwenN[OSC]
Sent: Wednesday, 31 January 2018 7:05 AM

To: Collopen.RubenB[OSC] <[REDACTED]> Gee Kee.KenN[OSC]
<[REDACTED]> Harris.LibbyA[OSC] <[REDACTED]>
McIntyre.OliviaM[OSC] <[REDACTED]>
Subject: FSS Options paper

Good morning,

For your advice please.

Cheers,



Ewen TAYLOR
Acting Inspector
DNA Management Unit | Forensic Services Group
Operations Support Command
QUEENSLAND POLICE SERVICE

[REDACTED]

From: Taylor.EwenN[OSC]
Sent: Wed, 8 Jun 2022 15:28:07 +1000
To: Taylor.EwenN[OSC]
Subject: FW: Options Paper for consideration



Ewen TAYLOR
Senior Sergeant, Officer in Charge
Hendra Scenes of Crime | Forensic Services Group
Operations Support Command
QUEENSLAND POLICE SERVICE



From: Taylor.EwenN[OSC]
Sent: Wednesday, 31 January 2018 13:41
To: Frieberg.DaleJ[OSC] <[REDACTED]>
Subject: RE: Options Paper for consideration

Good afternoon Dale,

I trust you had a pleasant trip to Toowoomba!

I have reviewed the attached document and conferred with senior staff within the DNA Unit (mainly Olivia) and Forensic Register Tech - Troy O'Malley.

From our perspective, we are in agreement that:

- There is clear data that it is not an efficient use of time and resources to continue with the 'auto-microcon' process for Priority 2 (*Major Crime*) samples.
- Option 2. "Cease the 'auto-microcon' process for Priority 2 casework..." Would appear to be a more productive & efficient choice.
- Scientists time and resources would be better spent working samples with a higher DNA yield and more potential.
- It would be beneficial to amend the Forensic Register to provide an automated Q-Prime update advising the Investigators of the option to request further 'Auto-microcon' processing for those samples for unsolved crime, which may prove worthwhile.
- DNA staff can request this additional processing if/when a request is received from the investigators.

We will no doubt discuss this further on Friday.

Kind Regards,



Ewen TAYLOR
 Acting Inspector
 DNA Management Unit | Forensic Services Group
 Operations Support Command
QUEENSLAND POLICE SERVICE

Phone [REDACTED]

From: Frieberg.DaleJ[OSC]
Sent: Tuesday, 30 January 2018 9:37 PM
To: Taylor.EwenN[OSC] <[REDACTED]>
Cc: Support Officer FSG <[REDACTED]>
Subject: FW: Options Paper for consideration

Ewen,

Can you please take a look and provide advice.

D

Dale Frieberg
 Superintendent
 Operations Commander
 Forensic Services Group
 Operations Support Command
 Queensland Police Service



From: Cathie Allen [[mailto:\[REDACTED\]](#)]
Sent: Tuesday, 30 January 2018 4:56 PM
To: Frieberg.DaleJ[OSC] <[REDACTED]> O'Malley.TroyS[OSC]
 <[REDACTED]> Taylor.EwenN[OSC] <[REDACTED]>
Cc: Paul Csoban <[REDACTED]>
Subject: Options Paper for consideration

Hi Dale

Please find attached an Options paper regarding concentration of major crime samples that we have prepared for your consideration. I'd like to discuss this on Friday with you.

Cheers
Cathie



Cathie Allen

Managing Scientist – Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



HSQ's vision | Delivering the best health support services and solutions for a safer and healthier Queensland.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and future.

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32 - 333 Week 5

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FSS Meeting - Carie Allen / Justin Howe / Paula BRISOTTO.

12 - 1300h FSS - CR102 - Conference Room.

✓ Morgue Contamination Issue - [Redacted]

✓ Familial Searching - FSS - Capability.

✓ PP21 - Volume Crime - impact / Solutions.

• Staff Issues - ZZ Staff - Z-T before May
DNA Unit - Structure - Reshuffle desks - New -
Processes. Phone Numbers

✓ Suspect Checks [Redacted]

- Imprints Check - [Redacted]

- Statement A NORTON, ✓

- Intelligence team email Sharon JOHNSTONE - Justin

- PP21 Upgrade case assessed - Justin

- PZ + Additional exhibit request Justin, Carie, Paula.

✓ Allen McNEVIN - Request tasks
- Stats affected

- Future Cases similar to Terrorism - Single Purpos samples
data-base for familial searching

- SAIK kits - OPM's amended - Further training.
- Person kit with SAIK's?

- Consideration for SOC to check for reference sample prior
to barcoding SAIK.

- Comm Games Impact to Unit,

- Additional submission of exhibits volume crime

- Meeting if need. -

5 weeks Comm - Limited leave embargo
- Sexual Assault - [Redacted]

- Coopers Plans
- High Profile.

| July | | | | | | | August | | | | | | | September | | | | | | | October | | | | | | | November | | | | | | | December | | | | | | |
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| 9 | 10 | 11 | 12 | 13 | 14 | 15 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
| 16 | 17 | 18 | 19 | 20 | 21 | 22 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 17 | 18 | 19 | 20 | 21 | 22 | 23 |
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February 2018

2
Friday

33 - 332 Week 5

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Meeting with Supt + FSS - Paul + Cathie.

2p - 3p - Supt. Conference Room.

Advised by Supt - Dan HURST not to take up 2nd relieving opportunity with Amanda BROWN HILL. Advised Les BULMURST. Don't to return or look for another contract

Communications - 3 main -
Cold Cases - Paula, Justin, Cathy.
MEETING

[Redacted] -6571 - RKM - 26/12/17 [Redacted]

No Person kit with SAIR.
2002 - Forensic under the Microscope.
QPrime - Prompt.
Kit won't be looked at till - Referre sample.

| January | | | | | | | February | | | | | March | | | | | April | | | | | May | | | | | June | | | | | | | | | | | | | | | | | | | | | | |
|---------|----|----|----|----|----|----|----------|----|----|----|----|-------|----|----|----|----|-------|----|----|----|----|-----|----|----|----|----|------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|---|
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| 15 | 16 | 17 | 18 | 19 | 20 | 21 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | |
| 22 | 23 | 24 | 25 | 26 | 27 | 28 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | |
| 29 | 30 | 31 | | | | | 26 | 27 | 28 | | | | | 26 | 27 | 28 | 29 | 30 | 31 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 28 | 29 | 30 | 31 | | | | 25 | 26 | 27 | 28 | 29 | 30 | | 29 | 30 | 31 | | | | | | |

February 2018

4

Sunday

35 - 330 Week 5

7.30 DNA FSS Meeting. Paul CSOBAN, Cathie ALLEN
7.45 Supt FRIEBERG, Insp O'MALLEY.

8.00 90% Doent Improve

8.15
8.30 1.5% Results. of remaining 10% provide a result.

8.45
9.00 Decided to invest Time + Resources into exhibit with
9.15 higher DNA Yield.

9.30
9.45 Supt to Forward Email advice to Cathie approxy
10.00 Option 2.

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| January | | | | | | | February | | | | | | | March | | | | | | | April | | | | | | | May | | | | | | | June | | | | | | | | | | | | | | | |
|---------|----|----|----|----|----|----|----------|----|----|----|----|----|----|-------|----|----|----|----|----|----|-------|----|----|----|----|----|----|-----|----|----|----|----|----|----|------|----|----|----|----|----|----|--|--|--|--|--|--|--|--|--|
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| 15 | 16 | 17 | 18 | 19 | 20 | 21 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | | | | | | | | | |
| 22 | 23 | 24 | 25 | 26 | 27 | 28 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | | | | | | | | | |
| 29 | 30 | 31 | 26 | 27 | 28 | 26 | 27 | 28 | 29 | 30 | 31 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 28 | 29 | 30 | 31 | 25 | 26 | 27 | 28 | 29 | 30 | | | | | | | | | | | | | | | | | | | | | | |

February 2018

19
Monday

50 - 315 Week 8

7.30

7.45

Trial 1 -

8.00

8.15

8.30

8.45

Detective Ben WEARE -

9.00

No longer on expected witness list.

9.15

9.30

9.45

Decrease boxes on Exhibit information.

10.00

10.15

Phone Conference FSS - 10.30 - 11.30 @MS.

10.30

10.45

11.00

11.15

11.30

11.45

12.00

12.15

12.30

12.45

1.00

1.15

1.30

1.45

2.00

2.15

2.30

2.45

3.00

FSS - Conference.

3.30

KEATINGE, Jamie + Rachelle COOK, Anne FEWSON -

4.00

FSS - Justin HOWES, Allan McNEVIN, Paula BRISOTTO.

4.15

Exhibit Screen. Exhibit - Record.

4.45

Description field - Blood. - Put into DNA Statement. *
Descriptions between 'Category' - 'Description'.

5.15

5.30

Blood, size, shape, colour, wet/dry. - Not needed by FSS.

6.00

Uniform Descriptions in Exhibit.

6.30

Surfaces no longer inhibit - Samples (Improved DNA Extraction Process Improved).

6.45

7.00

| July | | | | | | | August | | | | | | | September | | | | | | | October | | | | | | | November | | | | | | | December | | | | | | |
|------|----|----|----|----|----|----|--------|----|----|----|----|----|----|-----------|----|----|----|----|----|----|---------|----|----|----|----|----|----|----------|----|----|----|----|----|----|----------|----|----|----|----|----|----|
| M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S |
| 30 | 31 | | | | | 1 | 1 | 2 | 3 | 4 | 5 | | 1 | 2 | | | | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 1 | 2 | 3 | 4 | | | | 31 | | | | | | 1 | 2 | |
| 2 | 3 | 4 | 5 | 6 | 7 | 8 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
| 9 | 10 | 11 | 12 | 13 | 14 | 15 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
| 16 | 17 | 18 | 19 | 20 | 21 | 22 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 17 | 18 | 19 | 20 | 21 | 22 | 23 |
| 23 | 24 | 25 | 26 | 27 | 28 | 29 | 27 | 28 | 29 | 30 | 31 | | | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 29 | 30 | 31 | | | | | 26 | 27 | 28 | 29 | 30 | | | 24 | 25 | 26 | 27 | 28 | 29 | 30 |

February 2018

20

Tuesday FSS - Meeting

51 - 314 Week 8

7.30

7.45

image - Trace, no longer required. soco. Exam summary.

8.00

8.15

located / Owner -

8.30

- When ownership is known

8.45

(Shirt taken off suspect) - Not shirt by anyone

9.00

Unknown if not possible

9.15

9.30

Unknown new box in 'Relationship' folder

9.45

10.00

Washed + Diluted useful

10.15

10.30

10.45

X

✓

11.00

Leather Down Jacket

Washed Diluted

11.30

11.45

Oil, Grease, Vegetal

Finger Print

12.00

12.15

Seminal

12.30

12.45

Saliva

1.00

1.15

Other

1.30

1.45

Sample in tube stem - disregard

2.00

2.15

2.30

2.45

Quebec Markup

3.00

3.15

3.30

3.45

4.00

4.15

4.30

4.45

5.00

5.15

5.30

488116

5.45

6.00

Paula - 2007

6.15

2008 - Result not reported

6.30

6.45

7.00

| January | | | | | | | February | | | | | | | March | | | | | | | April | | | | | | | May | | | | | | | June | | | | | | | |
|---------|----|----|----|----|----|----|----------|----|----|----|----|----|----|-------|----|----|----|----|----|----|-------|----|----|----|----|----|----|-----|----|----|----|----|----|----|------|----|----|----|----|----|----|---|
| M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S | |
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | | | 1 | 2 | 3 | 4 | | | 1 | 2 | 3 | 4 | 30 | | | | | | 1 | | | 1 | 2 | 3 | 4 | 5 | 6 | | | | | | | 1 | 2 | 3 |
| 8 | 9 | 10 | 11 | 12 | 13 | 14 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | |
| 15 | 16 | 17 | 18 | 19 | 20 | 21 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | |
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| 29 | 30 | 31 | 26 | 27 | 28 | 26 | 27 | 28 | 29 | 30 | 31 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 28 | 29 | 30 | 31 | 25 | 26 | 27 | 28 | 29 | 30 | | | | | | | | | | | | | | |

March 2018

13
Tuesday

72 - 293 Week 11

7.30 1pm Meeting Justin HOWES / Sharon JOHNSTONE

7.45

8.00

8.15

8.30

8.45 Person - Multiple samples - FR

9.00 -FR unique.

9.15

9.30

9.45

10.00 Profoto within FR - 3 years worth FR. - if required

10.15

10.30

10.45

11.00

11.15

11.30

11.45 I N S - Outline of a work cover claim to make further investigation.

12.00

12.15

12.30

12.45

1.00

1.15

1.30

1.45

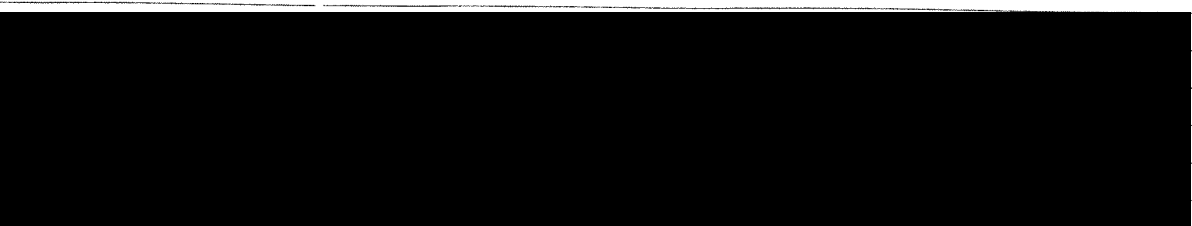
2.00

2.15

2.30

2.45

leave with no pay.



| July | | | | | August | | | | | September | | | | | October | | | | | November | | | | | December | | | | | | | | | |
|------|----|----|----|----|--------|----|----|----|----|-----------|----|----|----|----|---------|----|----|----|----|----------|----|----|----|----|----------|----|----|----|----|----|----|----|----|----|
| M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S |
| 30 | 31 | | | | 1 | | 1 | 2 | 3 | 4 | 5 | | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 |
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| 9 | 10 | 11 | 12 | 13 | 14 | 15 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |
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| 23 | 24 | 25 | 26 | 27 | 28 | 29 | 27 | 28 | 29 | 30 | 31 | | | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 29 | 30 | 31 | | | | | 26 | 27 | 28 | 29 | 30 | | |

June 2018

13

Wednesday

Shannon.

164 - 201 Week 24

7.30 FSS Tour

7.45

8.00

8.15 Group 1

Group 2

8.30

8.45 Ruben

Carolyn M

9.00 Rebecca

Olivier

9.15 ~~Angela~~ Kelly.

Libby

9.30 Lize

Megan

9.45 Steve

Belinda Jen

10.00 Sharon

Alan

10.15 Belinda

Stella

10.30 Kellie

10.45

11.00

Kelly if anyone pulls out.

Carolyn P if anyone pulls out.

11.15

11.30 Lize attending appointment.

11.45

12.00

12.15

12.30

12.45

1.00

1.15

1.30

1.45

2.00

2.15

2.30

2.45

3.00

3.15

3.30

3.45

4.00

4.15

4.30

4.45

5.00

5.15

5.30

5.45

6.00

6.15

6.30

6.45

7.00

80 days -

17-18 PD cycle.

Taxi.

| July | | | | | | | August | | | | | | | September | | | | | | | October | | | | | | | November | | | | | | | December | | | | | | |
|------|----|----|----|----|----|----|--------|----|----|----|----|----|----|-----------|----|----|----|----|----|----|---------|----|----|----|----|----|----|----------|----|----|----|----|----|----|----------|----|----|----|----|----|----|
| M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S | M | T | W | T | F | S | S |
| 30 | 31 | | | | 1 | | 1 | 2 | 3 | 4 | 5 | | | 1 | 2 | | | | | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 1 | 2 | 3 | 4 | | | | 31 | | | | | | |
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| 9 | 10 | 11 | 12 | 13 | 14 | 15 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
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| 23 | 24 | 25 | 26 | 27 | 28 | 29 | 27 | 28 | 29 | 30 | 31 | | | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 29 | 30 | 31 | | | | | 26 | 27 | 28 | 29 | 30 | | | 24 | 25 | 26 | 27 | 28 | 29 | 30 |

Date:

Page:

Forensic DNA Analysis & the QPS 01.02.2018

- Monthly meeting with Agenda.
 - Insp Dave Neville - on another project but is the substantive for DNA Insp.
 - Even in the role until June 2018.
 - Comm Games - challenged - North Bris req's Even back during Comm Games.
 - Ruben & Ken involved in Comm Games
 - Even is HECT.
 - Possible desktop DVI in FR Training site.
 - ↓ 38 to 22 staff members.
 - 2 areas combined into 1.
 - Struggling with results man → means OT.
 - new Sgt Steve Foxaer - starting, detective but not a long lot of forensic experience
 - Angela Green - in S/Con position - starts April
 - 4 vacant AD2 positions
 - Streamline after Options Paper
- Range - DNA insufficient range.
 ↳ would be applied for both May & Vol if ops agrees to the Options Paper.
- omm's.
- Contamⁿ between child & deceased - Mortuary.
 - Ref Samples for SAKs - Even has amended OPMⁿ but will be in next one. - then education program
 - Feb 14th management meeting @ QPS HQ

Cathie Allen

From: Frieberg,DaleJ[OSC] <[REDACTED]>
Sent: Friday, 2 February 2018 3:38 PM
To: Cathie Allen; O'Malley.TroyS[OSC]; Taylor.EwenN[OSC]
Cc: Paul Csoban
Subject: RE: Options Paper for consideration

Hi Cathie and Paul,

Thank you for your time this afternoon and for discussion around this options paper. Thank you also to both Troy and Ewen with your assistance and expertise/advice around the paper.

As discussed, I am in agreement that:

- There is clear data that it is not an efficient use of time and resources to continue with the 'auto-microcon' process for Priority 2 (*Major Crime*) samples.
- Option 2. "Cease the 'auto-microcon' process for Priority 2 casework..." Would appear to be a more productive & efficient choice.
- Scientists time and resources would be better spent working samples with a higher DNA yield and more potential.
- It would be beneficial to amend the Forensic Register to provide an automated Q-Prime update advising the Investigators of the option to request further 'Auto-microcon' processing for those samples for unsolved crime, which may prove worthwhile.
- DNA staff can request this additional processing if/when a request is received from the investigators.

I trust this is of assistance.

Kind regards,

Dale.

Dale Frieberg
Superintendent
Operations Commander
Forensic Services Group
Operations Support Command
Queensland Police Service



From: Cathie Allen [mailto: [REDACTED]]
Sent: Tuesday, 30 January 2018 4:56 PM
To: Frieberg.DaleJ[OSC] < [REDACTED] > O'Malley.TroyS[OSC]
< [REDACTED] > Taylor.EwenN[OSC] < [REDACTED] >
Cc: Paul Csoban < [REDACTED] >
Subject: Options Paper for consideration

Hi Dale

Please find attached an Options paper regarding concentration of major crime samples that we have prepared for your consideration. I'd like to discuss this on Friday with you.

Cheers
Cathie



Cathie Allen
Managing Scientist – Police Services Stream
Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

[REDACTED]
[REDACTED]

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Paula Brisotto

From: Cathie Allen
Sent: Friday, 2 February 2018 4:00 PM
To: Justin Howes; Paula Brisotto
Subject: FW: Options Paper for consideration

Sensitivity: Confidential

Hi Paula and Justin

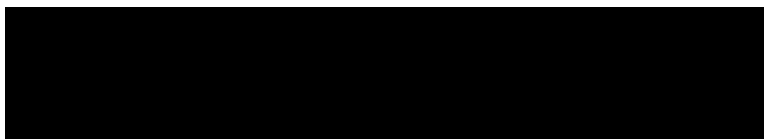
The QPS have agreed with Option 2, so we can proceed with that option. I will send out further information to management team but I will not be sending the below email. This is just for your information only at this stage.

Cheers
 Cathie

**Cathie Allen**

Managing Scientist – Police Services Stream

Forensic & Scientific Services,
 Health Support Queensland, **Department of Health**



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Operations Commander
Forensic Services Group
Operations Support Command
Queensland Police Service



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Cathie Allen

Managing Scientist – Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

[Redacted contact information]

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Paula Brisotto

From: Cathie Allen
Sent: Monday, 5 February 2018 9:31 AM
To: Paula Brisotto; Justin Howes
Subject: Options Paper

Hi Paula and Justin

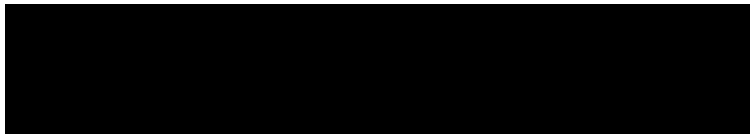
Regarding the Options Paper, my intention was to email management team letting them know that the Options Paper was presented to the QPS and that they have elected Option 2 for us moving forward. And I was going to attach the Options Paper. Do you see any issues with this?

Cheers
Cathie

**Cathie Allen**

Managing Scientist – Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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Paula Brisotto

From: Paula Brisotto
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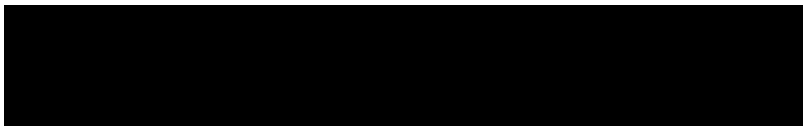
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**Cathie Allen**

Managing Scientist – Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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Paula Brisotto

From: Justin Howes
Sent: Monday, 5 February 2018 9:40 AM
To: Paula Brisotto; Cathie Allen
Subject: RE: Options Paper

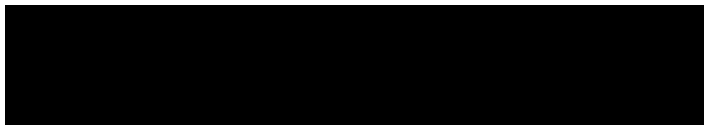
Hi, yes agree – happy for sending out. I haven't saved it to #184, but when you send out, I will save that copy and watermark the other reports that they have been superseded.

Thanks
Justin

**Justin Howes**

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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Cheers

Cathie



Cathie Allen

Managing Scientist – Police Services Stream

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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Justin Howes

From: Justin Howes
Sent: Wednesday, 7 February 2018 4:14 PM
To: Emma Caunt
Cc: Kylie Rika
Subject: RE: Auto-microcons

Hi, yes I will be changing the expanded comment as I know it is not exactly what we mean. The wording will be similar to the statement wording and making it clear that requests can be actioned.

QPS will have their processes expanded to enable this as well as including how to request further work. The expanded comment change will be added to the current SOP as a comment.

JAH



Justin Howes

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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From: Emma Caunt
Sent: Wednesday, 7 February 2018 4:07 PM
To: Justin Howes
Cc: Kylie Rika
Subject: RE: Auto-microcons

Hi Justin

I've had a look at the reports for this and, NCIDD aside, it shows that 10% of samples that went through the auto-microcon gave interpretable results.

The expanded comment for the 'DNA Insufficient for further processing' line states the following:

This item/sample was submitted for DNA analysis; however the amount of DNA detected at the quantitation stage indicated the sample was insufficient for further processing (due to the limitations of current analytical and interpretational techniques). No further processing was conducted on this item. Please contact Forensic DNA Analysis if further information is required.

This indicates to scientific staff that there is nothing further that can be done with this sample, which is not the case for 10% of samples. It also does not give them the option to request for this sample to be processed further. Can I request that we update the expanded comment to be clear that there may be a chance of getting a usable profile and that they have the option of requesting this? We should probably bring this expanded comment in line with your suggested statement wording as they say different things.

Thanks

Emma

From: Justin Howes

Sent: Wednesday, 7 February 2018 3:18 PM

To: Adrian Pippia; Alicia Quartermain; Allison Lloyd; Amanda Reeves; Angela Adamson; Angelina Keller; Anne Finch; Cassandra James; Claire Gallagher; Deborah Nicoletti; Emma Caunt; Hannah Pattison; Helen Williams; Ingrid Moeller; Jacqui Wilson; Josie Entwistle; Justin Howes; Kylie Rika; Lisa Benstead; Matthew Hunt; Penelope Taylor; Rhys Parry; Sharon Johnstone; Susan Brady; Thomas Nurthen; Timothy Gardam

Subject: Auto-microcons

Hi all

On the back of case manager's anecdotal feedback and our lab's second round of datamining of samples that underwent the auto-microcon process, an Options Paper was presented to QPS Superintendent of Forensic Services Dale Frieberg on ways forward for QPS to consider – continue with auto-microcon process, or cease auto-microcons.

QPS have advised the laboratory that they do not wish for our efforts to be put to the auto-microcon process (including the efforts in interpretation) for Priority 1 or 2 samples.

This means samples in the range 0.001ng/uL (LOD) - 0.0088ng/uL will be reported at Quant stage as 'DNA Insufficient for Further Processing'. This is consistent with the process in place for P3 samples. The manual Microcon process may be performed upon QPS request.

To report in a statement, the following wording could be used:

Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.

This is slightly different to the wording written in 2012/13 for these samples (P3) but after some consultation, appears a good starting point.

An enhancement has been requested to enable this to occur from 12 February. Reactivating samples for further post-extraction processing, if requested from QPS, will be directed to Luke via an FR Request. If there are changes to the 12 February date, I will let you know. As usual, appropriate comments to SOPs will follow.

Regards

Justin



Justin Howes

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
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Justin Howes

From: Justin Howes
Sent: Friday, 23 February 2018 2:16 PM
To: Kylie Rika
Subject: RE: Auto-microcons

Hi Kylie,

I do want to catch you up on this, and will catch you when I return next Thurs. I have some urgent work that I am trying to complete before I go.

Thanks
Justin



Justin Howes

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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From: Kylie Rika
Sent: Friday, 23 February 2018 11:32 AM
To: Justin Howes
Subject: RE: Auto-microcons

Hi Justin

Just following up on your thoughts re below

thanks



Kylie Rika Dip Mgt BSc PGrad Dip (Forensic)

Senior Reporting Scientist – Forensic Reporting and Intelligence Team

Forensic DNA Analysis | Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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From: Kylie Rika
Sent: Friday, 9 February 2018 9:27 AM
To: Justin Howes
Subject: FW: Auto-microcons

Hi Justin

This is a concern.

I guess it's one thing for the QPS to understand this risk (if they do) but it's not full testing/disclosure for the case from our lab.

Perhaps the process needs to be re-assessed?

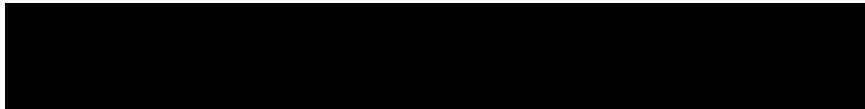
thanks



Kylie Rika Dip Mgt BSc PGrad Dip (Forensic)

Senior Reporting Scientist – Forensic Reporting and Intelligence Team

Forensic DNA Analysis | Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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From: Emma Caunt
Sent: Thursday, 8 February 2018 4:56 PM
To: Kylie Rika
Subject: RE: Auto-microcons

Hi Kylie

I understand from a conversation with Justin that the DNA Insuff process will continue as per the no DNA detected process so samples won't be assessed taking into account the circumstances of the case. I just want to pass on one example.

Rape case

Nothing on the SAIK

Underpants – EFRAC had auto microcon and gave 2 pers mixture of complainant and defendant
Only other sample in the case was defendant on a shoe found in a park

In this case the auto-microcon gave the only evidence to substantiate the claims of the complainant

Thanks

Emma

From: Emma Caunt
Sent: Thursday, 8 February 2018 9:37 AM
To: Justin Howes
Cc: Kylie Rika
Subject: RE: Auto-microcons

Hi Justin

I've been thinking about this a bit more. I want to say from the outset that I am not necessarily opposed to stopping the auto-microcon process, but I do think that there is a risk that we are able to manage.

I am assuming that the 'DNA insuff for processing' line will be added automatically and that it will be added to a list for validation. My question is, how will the validation process be managed?

My personal opinion is that the line should not be validated until the whole case has been assessed to see if processing of this sample would be of benefit, particularly as the quant value reaches the upper range. Obviously at the statement stage, the reporter can assess these samples, but the gap will be if no statement is requested. Since we case manage on a sample by sample basis the 'DNA insuff' results won't be monitored during the normal case management process.

Thanks

Emma

From: Justin Howes
Sent: Wednesday, 7 February 2018 4:14 PM
To: Emma Caunt
Cc: Kylie Rika
Subject: RE: Auto-microcons

Hi, yes I will be changing the expanded comment as I know it is not exactly what we mean. The wording will be similar to the statement wording and making it clear that requests can be actioned.

QPS will have their processes expanded to enable this as well as including how to request further work. The expanded comment change will be added to the current SOP as a comment.

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Justin Howes

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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This indicates to scientific staff that there is nothing further that can be done with this sample, which is not the case for 10% of samples. It also does not give them the option to request for this sample to be processed further. Can I request that we update the expanded comment to be clear that there may be a chance of getting a usable profile and that they have the option of requesting this? We should probably bring this expanded comment in line with your suggested statement wording as they say different things.

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Emma

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Subject: Auto-microcons

Hi all

On the back of case manager's anecdotal feedback and our lab's second round of datamining of samples that underwent the auto-microcon process, an Options Paper was presented to QPS Superintendent of Forensic Services Dale Frieberg on ways forward for QPS to consider – continue with auto-microcon process, or cease auto-microcons.

QPS have advised the laboratory that they do not wish for our efforts to be put to the auto-microcon process (including the efforts in interpretation) for Priority 1 or 2 samples.

This means samples in the range 0.001ng/uL (LOD) - 0.0088ng/uL will be reported at Quant stage as 'DNA Insufficient for Further Processing'. This is consistent with the process in place for P3 samples. The manual Microcon process may be performed upon QPS request.

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Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.

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Regards
Justin



Justin Howes

Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

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From: Neville.DavidH[OSC]
Sent: Wed, 14 Nov 2018 15:46:58 +1100
To: Cathie Allen
Cc: [REDACTED] McNab.BruceJ[OSC];Simpfendorfer.GerardM[OSC]
Subject: Removal of the microcon step from P1 workflow.
Attachments: Review of efficacy of Microcons_options for QPS.DOC
Importance: High

Dear Cathie

During the course of the investigation into [REDACTED] over 15 samples were submitted as Priority 1. On initial testing, four samples were reported as having insufficient DNA present for further testing. Upon receipt of that result my staff requested additional testing and each of those samples yielded a result as follows:

- [REDACTED] - SINGLE SOURCE 20 LOCI DNA PROFILE LR > 100 BILLION (Deceased match); and POSSIBLE SUB-THRESHOLD INFORMATION
- [REDACTED] - SINGLE SOURCE DNA PROFILE - ASSUMED KNOWN CONTRIBUTOR – (Deceased match)
- [REDACTED] SS DNA PROFILE 9 LOCI AND ABOVE LR > 100 BILLION (Deceased match)
- [REDACTED] - COMPLEX MIXED PROFILE UNSUITABLE FOR INTERP OR COMPARISON

Could you confirm if the profiles for the four samples listed above were obtained after micro-concentration was performed, please. Could you also confirm if the microcon step has been removed from the workflow as a matter of routine for P1 samples. My understanding as per the below was that this was only to occur for P2. If this process has been removed from the P1 workflow, could it please be reintroduced as it will stop delays in obtaining results that are considered urgent, please.



The removal of the microcon step in the process was agreed to on 2 February 2018 by Supt Frieberg based on the advice included in the attached paper. This paper estimates that there would be less than a 2% reduction in the number of useable results if the step was eliminated.

Based on the fact that 3 out of 4 samples for this case yielded a result when testing was continued, anecdotally it would seem that we may be missing out on more than 2% of results.

Since eliminating this step, has your laboratory undertaken any statistical analysis to determine if there has been a drop in the proportion of samples that give a useable profile, please.

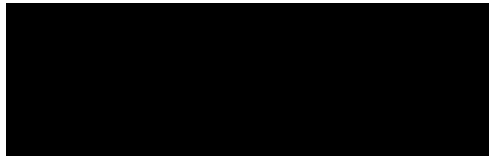
There are other serious matters including homicides where testing has stopped once advice was received that there is insufficient DNA for further testing. Based on the results for this case (75% success rate for the ones received back so far), would you recommend that these cases be re-examined please.

Could you please direct your response to Gerard and Bruce.



David Neville
Inspector
DNA Management Unit | Forensic Services Group
Operations Support Command
QUEENSLAND POLICE SERVICE

Phone
Email
Address



Paula Brisotto

From: Cathie Allen
Sent: Friday, 16 November 2018 3:04 PM
To: Angela Adamson; Josie Entwistle; Luke Ryan
Cc: Justin Howes; Paula Brisotto
Subject: FW: Concentrating of P1 samples [REDACTED]

Importance: High

Hi Everyone

Paula provided me with Quant results from the 10 Urgent items delivered yesterday. Given that 4 of them were DNA Insufficient, I phoned the Forensic Coordinator – Snr Sgt Greg Smith to ask how to proceed (given the below). Greg has requested that each of the 4 samples are concentrated – [REDACTED]

I've added a Case File Notation regarding the phone conversation.

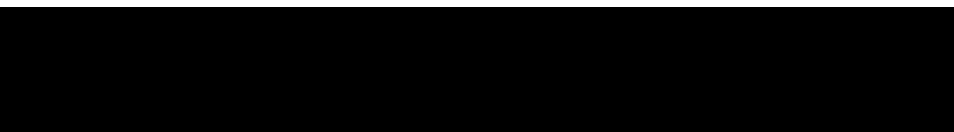
Cheers
Cathie



Cathie Allen

Managing Scientist

Police Services Stream, Forensic & Scientific Services
 Health Support Queensland, Queensland Health



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From: Cathie Allen
Sent: Friday, 16 November 2018 11:14 AM
To: 'Angela Adamson'; 'Luke Ryan'
Cc: 'Justin Howes'; 'Paula Brisotto'
Subject: FW: Concentrating of P1 samples [REDACTED]
Importance: High

Hi Angela & Luke

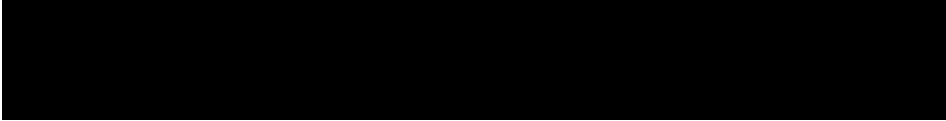
Please see advice below regarding [REDACTED] and use of Microcon on P1 samples. I've added a Case File Notation.

Cheers
Cathie



Cathie Allen
Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health



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From: Smith.GregS[OSC] [mailto:Smith.GregS@police.qld.gov.au]
Sent: Friday, 16 November 2018 10:26 AM
To: Cathie Allen; Simpfendorfer.GerardM[OSC]
Subject: Concentrating of P1 samples.

Hi Cathie

As discussed and thanks for the advice. if we could hold off the concentrating of P1 samples until we run out these further samples. Circumstances have changed and as suggested more prudent to hold off.

Many thanks.

Greg

Greg Smith
Senior Sergeant 5027
Operations Support Command | Queensland Police Service



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have received this electronic message in error, please
inform the sender or contact [REDACTED]

This footnote also confirms that this email message has
been checked for the presence of computer viruses.

Justin Howes

From: Justin Howes
Sent: Tuesday, 20 November 2018 12:44 PM
To: Penelope Taylor; Adrian Pippia
Subject: FW: reactivation of some samples

Hi both, I have sent tasks to Gerard re fact that Addendums will be required and will follow standard timeframes.

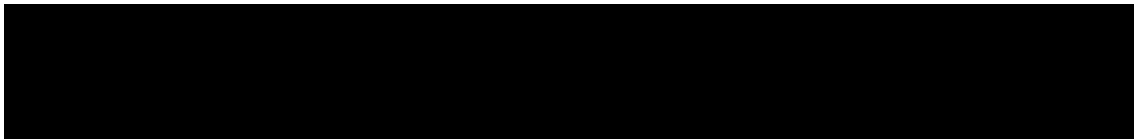
JAH



Justin Howes

Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services
 Health Support Queensland, Queensland Health



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From: Justin Howes
Sent: Tuesday, 20 November 2018 9:44 AM
To: Penelope Taylor <[redacted]> Adrian Pippia <[redacted]>
 Hannah Pattison <[redacted]> Deborah Nicoletti <[redacted]>
 Cassandra James <[redacted]> Jacqui Wilson <[redacted]> 'Rhys
 Parry' <[redacted]> Angela Adamson <[redacted]>
Cc: Paula Brisotto <[redacted]> Luke Ryan <[redacted]>
Subject: reactivation of some samples

Hi there

You were allocated some P1 jobs that had one or more samples reported as DNA Insufficient. These samples have been requested by QPS to be reworked.

As these cases were allocated, the sample rework decision is best with you and I have sent Casefile Notations to you for these cases. The decision is one of rework type: mic to full, half, 35uL, Nucl, spin etc etc.

I am finding out if the rework on these samples are to be P2 or P1 (they were originally P1 but the cases themselves in some situations are early 2018). Until notice comes, please change to P2 for this rework (order a Notation in the Exhibit Testing and change to P2) and we can always change back to P1 if that direction is received.

There are two cases where statements have been issued and I will be sending tasks to DNA Mgt that this will mean Addendum statement requests will need to be received, and standard timeframes apply. Adrian and Penny, these are the two that you have.

Thanks
 justin



Justin Howes

Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services

Health Support Queensland, Queensland Health



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Paula Brisotto

From: Cathie Allen
Sent: Thursday, 22 November 2018 4:01 PM
To: Paula Brisotto; Justin Howes
Subject: FW: Removal of the Microcon step - QPS advice

Another day, another email.....

Cheers
 Cathie



Cathie Allen
 Managing Scientist

Police Services Stream, Forensic & Scientific Services

[Redacted]

[Redacted]

[Redacted]

[Redacted]

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From: Simpfindorfer.GerardM[OSC] [mailto:[Redacted]]
Sent: Thursday, 22 November 2018 3:54 PM
To: Cathie Allen
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]; Collophen.RubenB[OSC]; Harris.LibbyA[OSC]
Subject: RE: Removal of the Microcon step - QPS advice

Hi Cathie,

That wasn't really what I was chasing as I am not questioning the code of conduct or the evidence that is given in Court by the Scientist as we have no issue with this and know you and your staff always act in good faith.

It could be how I phrased the question/issue, so I'll try again.

In your email you said the following:

There are a number of factors that would be taken into consideration regarding the balance between concentrating the sample vs preserving extract for other testing.

And then went on to describe a number of these factors in the rest of that paragraph. You also started the next paragraph with some 'key factors' and finished that paragraph with the following:

All of these factors are taken into consideration prior to requesting a Microcon. We have assessed a large amount of data to provide the best indication of how profiles have behaved and provide this advice to the QPS to assist.

My questions around the above 2 sentences are:

- At what point of the examination process are these factors taken in to consideration?
- How do you provide this advice to QPS to assist?

I thought the line "THIS SAMPLE HAS UNDERGONE FURTHER PROCESSING" meant that either the QPS or the Scientist had requested further processing of the sample which is the rework process and that the Microcon step had commenced.

I do not believe this line provides advice on the best indication for how profiles may behave or if another of the factors you have considered may be more beneficial in obtaining a usable profile for the investigation.

Is there another option to this line to provide the QPS with this advice around your best indication in these cases besides proceeding with Microcon considering the Microcon step will consume all the available extract?

We believe the risk of deciding whether or not to Micron should not be left to the QPS solely as we do not have the expertise or access to the data about the quality and quantity of DNA in the sample. What we are chasing is some sort of decision making tree so we know what should trigger us to request further processing. At the moment it seems to be a stab in the dark for us, if we don't request a rework we get no result. But, the chance of a result is better than nothing in certain circumstances.

So, it may be that the process stays as it is, but when we send the request through to Luke Ryan for further processing we request advice on proceeding with Microcon step or whether some other process or testing may have a better opportunity based on the factors that have been taken into consideration to produce a usable profile, what are your thoughts on this?

That way the investigating officer and the QPS can make an informed decision before authorising the consumption of all the extract.

I hope this is a little clearer.

Kind regards

Gerard

Gerard Simpfendorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service

000

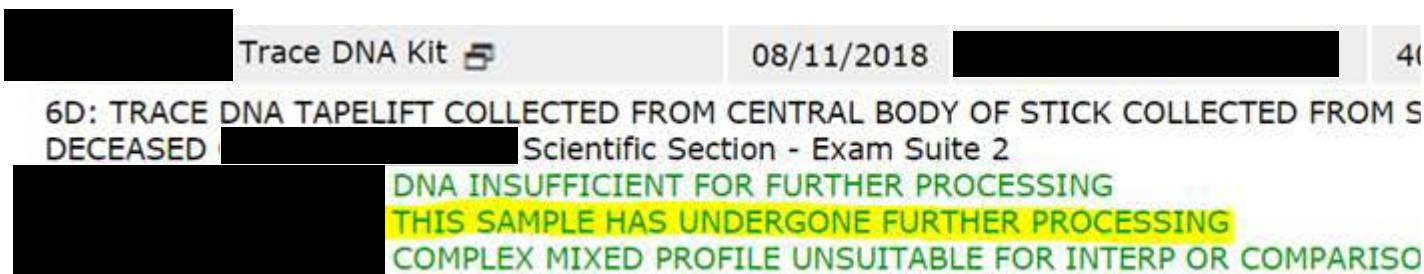


From: Cathie Allen <[REDACTED]>
Sent: Wednesday, 21 November 2018 12:14 PM
To: Simpfendorfer.GerardM[OSC] <[REDACTED]>
Cc: Craig Russell <[REDACTED]> Neville.DavidH[OSC] <[REDACTED]>
 McNab.BruceJ[OSC] <[REDACTED]> Collophen.RubenB[OSC]
 <[REDACTED]>
Subject: RE: Removal of the Microcon step - QPS advice

Hi Gerard

Scientists in Forensic DNA Analysis apply scientific principles to processing and reworking of all samples that they review, as they are bound by the Code of Conduct for the Queensland Public Service and are committed to ensuring the best possible outcome for the Queensland Community. Reporting scientists are questioned under oath about the scientific decisions that they have made and provide answers based on scientific principles.

If the sample is reworked after a result has been released to the QPS, the QPS is advised electronically by a result line advising that the sample has undergone further processing as per the example below:

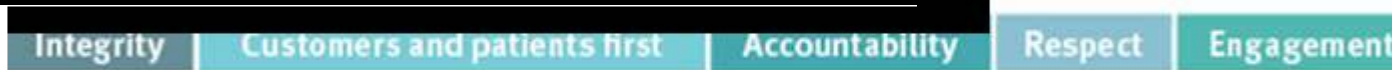
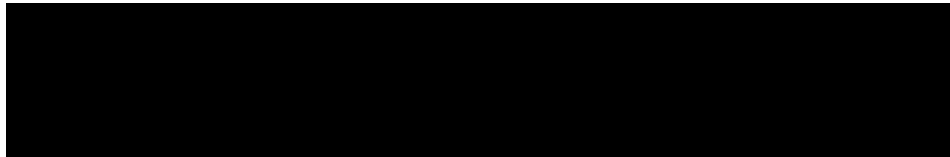


Cheers
Cathie



Cathie Allen
Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health



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From: Simpfordorfer.GerardM[OSC] [mailto:]
Sent: Tuesday, 20 November 2018 3:35 PM
To: Cathie Allen
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]; Colloppen.RubenB[OSC]
Subject: Removal of the Microcon step - QPS advice

Hi Cathie,

And thank you for your response.

You mention there are a number of factors that would be taken into consideration regarding the balance between concentrating the sample vs preserving extract for other testing and you gave some examples including assessing the quality and quantity of the DNA as a key factor to obtaining a DNA profile.

1. Do you take these factors into consideration only when sending through the DNA Insufficient result for:
 - All exhibits?
 - P1 and P2 only exhibits?
 - P1 only exhibits?

2. Or do you take these factors in to consideration only when the QPS requests further processing of the exhibit?


3. Or do you take these factors in to consideration only when the QPS requests advice on other testing options?

If it is option 1 or 2, how do you provide this advice to the QPS to assist investigators, especially if in the Scientists expert opinion requesting a Microcon step may not be the best for obtaining a possible DNA result due to this process consuming all the available extract.

Kind regards

Gerard

Gerard Simpfendorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service



We have more than 12,000 crimes with DNA evidence.
We just need the offender.
Always check/take offender's DNA.



From: Cathie Allen <[REDACTED]>
Sent: Friday, 16 November 2018 4:01 PM
To: Simpfendorfer.GerardM[OSC] <[REDACTED]>
Cc: Craig Russell <[REDACTED]> Neville.DavidH[OSC] <[REDACTED]>
McNab.BruceJ[OSC] <[REDACTED]>
Subject: RE: Removal of the microcon step from P1 workflow.

Hi Gerard

The quantification values between 0.001 and 0.008ng/uL is the range for the result line of DNA Insufficient – so this is the range that prior to Feb 2018 would have automatically proceeded for concentration.

There are a number of factors that would be taken into consideration regarding the balance between concentrating the sample vs preserving extract for other testing – some examples, but limited to, – the indication within the quantification of the Y chromosome, pooling of samples from a similar area prior to concentrating as this may have a better chance of concentrating the available DNA for a 'useable' profile, preserving 1 sample and concentrating another sample from similar areas (rather than doing both in the first instance), the quantification value and if it's likely to be a mixture, the sample type (ie tapelift from a particular exhibit vs swab from a more probative area) or targeting particular samples for concentration in the context of the case (rather than all priority 1 samples).

The quality and quantity of the DNA are the key factors in obtaining a DNA profile. For these samples, whilst there was a small amount of DNA, the quality of the DNA may have been quite good, which has meant that a DNA profile was able to be generated (I haven't looked into these samples, I'm providing information on a general basis). Whilst our processes provide a quantification value, indication of degradation and indication of Y chromosome, it's the generation of DNA profile that assists in highlighting the quality of the DNA that was available. The DNA in the sample may only just be above the acceptance criteria to be called an allele, and it may generate enough alleles to provide a Likelihood Ratio of >100 billion, however its viewing the DNA profile that can show the extent of the degradation or inhibition factors that may be associated. All of these factors are taken into consideration prior to

requesting a Microcon. We have assessed a large amount of data to provide the best indication of how profiles have behaved and provide this advice to the QPS to assist.

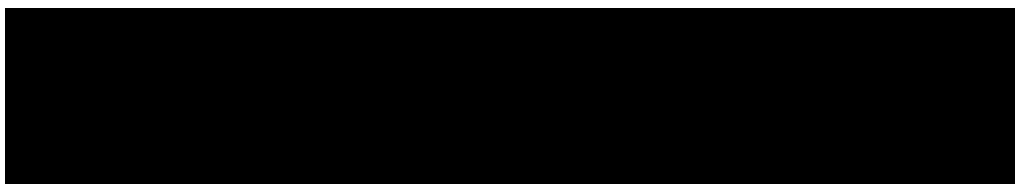
Please let me know if you have any further questions.

Cheers
Cathie



Cathie Allen
Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health



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From: Simpfindorfer.GerardM[OSC] [<mailto:> 
Sent: Thursday, 15 November 2018 3:24 PM
To: Cathie Allen
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]
Subject: RE: Removal of the microcon step from P1 workflow.

Hi Cathie,

Thank you for the below advice.

Could you advise is there a quant cut off where microcon would automatically occur?

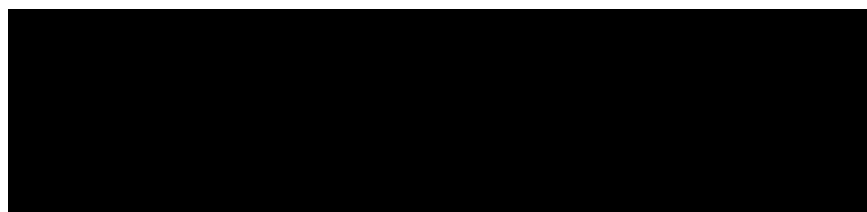
What would be the decision making advice around preserving the sample and also enhancing chances of getting a result?

Also, why did these samples yield a result and could the factors involved be used to determine future processes?

Kind regards

Gerard

Gerard Simpfindorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service



From: Cathie Allen <[REDACTED]>
Sent: Thursday, 15 November 2018 9:20 AM
To: Simpfindorfer.GerardM[OSC] <[REDACTED]> McNab.BruceJ[OSC]
<[REDACTED]>
Cc: Craig Russell <[REDACTED]> Neville.DavidH[OSC] <[REDACTED]>
Subject: FW: Removal of the microcon step from P1 workflow.
Importance: High

Hi Gerard and Bruce

I can confirm that the Microcon process has been applied to the below four sample as requested by the QPS on the dates listed below:

- Snr Sgt Simpfindorfer requested Microcon 29/10/2018
- Snr Sgt Simpfindorfer requested Microcon 06/11/2018
- Snr Sgt Simpfindorfer requested Microcon 06/11/2018
- Snr Sgt Simpfindorfer requested Microcon 06/11/2018

During a meeting on 1st of Feb 2018, Paul Csohan (previous Executive Director for FSS) and I met with Supt Dale Frieberg to discuss the Options Paper that had previously been provided to the QPS for decision. During this meeting, the Superintendent agreed that Option 2 was the preferred option, which was later confirmed via email (as per below). During the discussion, the second part of Option 2 (section a) was discussed, which related to Priority 1 samples and the Superintendent indicated that Priority 1 samples should be processed the same as Major crime (P2) and Volume crime samples (P3), which is not to be automatically progressed through the Microcon process. After the approval from the QPS in Feb 2018, all samples have not automatically progressed through the Microcon process. The QPS or a Forensic DNA Analysis staff member can request a Microcon process for a sample at any time.

Automatic progression of samples through the Microcon process means that all available DNA extract will be consumed, so no further testing can be conducted on these samples after this step. This means that if a sample could yield a profile by specific Y chromosome testing for example, there would be no extract available for that testing to be conducted. It also means that samples that are eligible to be pooled together, as they are from the same item or area, are not able to be as there is no DNA extract left to undertake pooling. Scientists or Forensic officers reviewing results in the context of a case are able to request a Microcon process for a sample or samples.

As the decision on the automatic Microcon process was made last financial year, the budget for this financial year has been adjusted for that consumable, so this will increase the cost.

If the QPS wishes for P1 samples to automatically be processed through the Microcon process, which leaves no available extract for other testing, this process can be re-introduced. Please confirm if the QPS requires the re-introduction of this step.

The Options Paper reviewed 1449 Major crime samples that had been progressed through the Microcon process over a one year period, as this was considered to be sufficient sample numbers to demonstrate a clear trend.

The laboratory is unable to search the FR to undertake any statistical analysis regarding 'useable' profile numbers – this was highlighted to FSS during development that large or medium scale interrogation of the FR could only be undertaken by the QPS, as they would need to construct the search and ensure the timing of the search was undertaken so as not to add extra burden to the FR during peak operational times. If the QPS were able to generate this data, the laboratory would undertake this analysis and provide feedback. The Microcon process was no longer automatically undertaken for P1 or P2 samples from the 12th of Feb 2018.

Whilst the Microcon process has not been automatically applied to Major crime samples (P2) since mid Feb, scientists have reviewed those results and requested a Microcon process if in the context of the case it could have been of potential benefit. If the QPS undertook a search of all 'DNA insufficient' results on P1 and P2 samples since the 12th of Feb, the laboratory could undertake an analysis of the cases to determine if additional testing through

the Microcon process is required. This would require resources and would reduce the number of results that are reviewed by the lab until this analysis was completed.

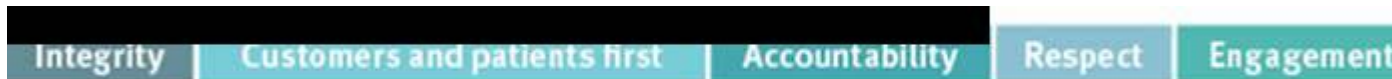
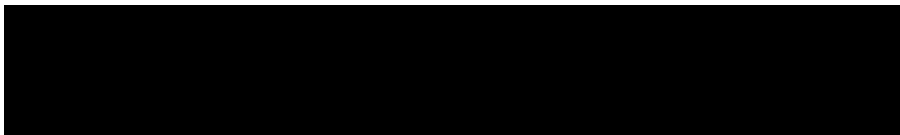
I await your advice regarding this. If you have any further questions, please let me know how I can assist.

Cheers
Cathie




Cathie Allen
Managing Scientist


Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health

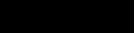


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From: Neville.DavidH[OSC] [<mailto:> 
Sent: Wednesday, 14 November 2018 2:47 PM
To: Cathie Allen
Cc: Craig Russell; McNab.BruceJ[OSC]; Simpfordorfer.GerardM[OSC]
Subject: Removal of the microcon step from P1 workflow.
Importance: High

Dear Cathie

During the course of the investigation into  over 15 samples were submitted as Priority 1. On initial testing, four samples were reported as having insufficient DNA present for further testing. Upon receipt of that result my staff requested additional testing and each of those samples yielded a result as follows:

 - SINGLE SOURCE 20 LOCI DNA PROFILE LR > 100 BILLION (Deceased match); and POSSIBLE SUB-THRESHOLD INFORMATION

 - SINGLE SOURCE DNA PROFILE - ASSUMED KNOWN CONTRIBUTOR – (Deceased match)

- SS DNA PROFILE 9 LOCI AND ABOVE LR > 100 BILLION (Deceased match)

- COMPLEX MIXED PROFILE UNSUITABLE FOR INTERP OR COMPARISON

Could you confirm if the profiles for the four samples listed above were obtained after micro-concentration was performed, please. Could you also confirm if the microcon step has been removed from the workflow as a matter of routine for P1 samples. My understanding as per the below was that this was only to occur for P2. If this process has been removed from the P1 workflow, could it please be reintroduced as it will stop delays in obtaining results that are considered urgent, please.

From: Frieberg.DaleJ[OSC]
Sent: Friday, 2 February 2018 3:38 PM
To: Cathie Allen [REDACTED]; O'Malley.TroyS[OSC]; [REDACTED]
Cc: Paul Csohan [REDACTED]
Subject: RE: Options Paper for consideration

Hi Cathie and Paul,

Thank you for your time this afternoon and for discussion around this options paper. Thank you also to

As discussed, I am in agreement that:

- There is clear data that it is not an efficient use of time and resources to continue with the 'auto-microcon' process for Priority 2 casework....
- Option 2. "Cease the 'auto-microcon' process for Priority 2 casework...." Would appear to be a better use of resources.
- Scientists time and resources would be better spent working samples with a higher DNA yield
- It would be beneficial to amend the Forensic Register to provide an automated Q-Prime update
- DNA staff can request this additional processing if/when a request is received from the investor

I trust this is of assistance.

Kind regards,

Dale.

Dale Frieberg
 Superintendent
 Operations Commander
 Forensic Services Group
 Operations Support Command
 Queensland Police Service

The removal of the microcon step in the process was agreed to on 2 February 2018 by Supt Frieberg based on the advice included in the attached paper. This paper estimates that there would be less than a 2% reduction in the number of useable results if the step was eliminated.

Based on the fact that 3 out of 4 samples for this case yielded a result when testing was continued, anecdotally it would seem that we may be missing out on more than 2% of results.

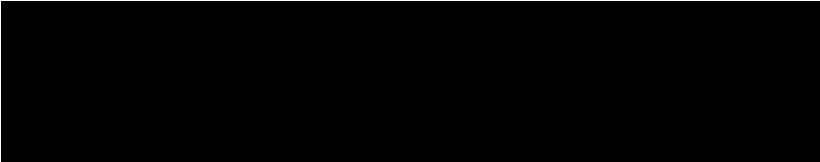
Since eliminating this step, has your laboratory undertaken any statistical analysis to determine if there has been a drop in the proportion of samples that give a useable profile, please.

There are other serious matters including homicides where testing has stopped once advice was received that there is insufficient DNA for further testing. Based on the results for this case (75% success rate for the ones received back so far), would you recommend that these cases be re-examined please.

Could you please direct your response to Gerard and Bruce.



David Neville
Inspector
DNA Management Unit | Forensic Services Group
Operations Support Command
QUEENSLAND POLICE SERVICE



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Paula Brisotto

From: Cathie Allen
Sent: Thursday, 6 December 2018 11:42 AM
To: Justin Howes; Paula Brisotto
Subject: FW: Removal of the Microcon step - QPS advice

FYI

From: Simpfendorfer.GerardM[OSC] [mailto: [REDACTED]]
Sent: Thursday, 6 December 2018 9:23 AM
To: Cathie Allen
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]; Collophen.RubenB[OSC]; Harris.LibbyA[OSC]
Subject: RE: Removal of the Microcon step - QPS advice

Thanks Cathie,

Yes that is correct, unless otherwise advised at P1 approval, all P1 samples are requested to go for automatic concentration that are "DNA Insufficient".

Kind regards

Gerard

Gerard Simpfendorfer
 Acting Inspector 4009415
 DNA Management Section, Forensic Services Group
 Operations Support Command, Queensland Police Service



From: Cathie Allen < [REDACTED] >
Sent: Thursday, 6 December 2018 9:07 AM
To: Simpfendorfer.GerardM[OSC] < [REDACTED] >
Cc: Craig Russell < [REDACTED] > Neville.DavidH[OSC] < [REDACTED] >
 McNab.BruceJ[OSC] < [REDACTED] > Collophen.RubenB[OSC]
 < [REDACTED] > Harris.LibbyA[OSC] < [REDACTED] >
Subject: RE: Removal of the Microcon step - QPS advice

Hi Gerard

Just to confirm - The reworking options and their visibility will be available for P2 and P3 samples, as it's my assumption that the QPS still wish to keep automatic concentration for P1 samples that are 'DNA Insufficient' – is this correct?

Cheers

Cathie



Cathie Allen

Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health

[Redacted]



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From: Simpfendorfer.GerardM[OSC] [mailto:[Redacted]]
Sent: Thursday, 6 December 2018 7:41 AM
To: Cathie Allen
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]; Colloopen.RubenB[OSC]; Harris.LibbyA[OSC]
Subject: RE: Removal of the Microcon step - QPS advice

Cathie,

Sounds like a good option, will wait and see how it looks when the first ones come through, but basically similar process to what we currently have but with Health providing the QPS more visibility around re-work options that are available before requesting any further processing which we still do via the current process.

Kind regards

Gerard

Gerard Simpfendorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service

[Redacted]

We have more than 12,000 crimes with DNA evidence.
We just need the offender.
Always check/take offender's DNA.

From: Cathie Allen <[Redacted]>
Sent: Wednesday, 5 December 2018 5:51 PM
To: Simpfendorfer.GerardM[OSC] <[Redacted]>
Cc: Craig Russell <[Redacted]> Neville.DavidH[OSC] <[Redacted]>

McNab.BruceJ[OSC] <[REDACTED]> Colloopen.RubenB[OSC]

<[REDACTED]> Harris.LibbyA[OSC] <[REDACTED]>

Subject: FW: Removal of the Microcon step - QPS advice

Hi Gerard

I've been working with the Team Leaders regarding this. We have devised wording within the expanded comments of the result lines to provide more visibility to the QPS regarding re-working options that are available. If re-working is required, the scientist would review the data available for the sample and select the most appropriate re-work option, after the QPS have advised re-work can go ahead. The process whereby the QPS send through a Request / Task to a Team Leader would be the best course of action for this.

Please let me know if you have any further queries.

Cheers

Cathie



Cathie Allen

Managing Scientist

Police Services Stream, Forensic & Scientific Services

Health Support Queensland, Queensland Health



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From: Cathie Allen

Sent: Friday, 30 November 2018 3:30 PM

To: 'Simpfendorfer.GerardM[OSC]'

Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]; Colloopen.RubenB[OSC]; Harris.LibbyA[OSC]

Subject: RE: Removal of the Microcon step - QPS advice

Hi Gerard

I'm currently working on this with the Team Leaders in Forensic DNA Analysis.

This week, both Forensic Chemistry and Forensic DNA Analysis have had NATA technical assessments, so I've had limited opportunity for this given my commitments with the assessments.

Cheers

Cathie



Cathie Allen

Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health

[REDACTED]
[REDACTED]
[REDACTED]

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From: Simpfendorfer.GerardM[OSC] [[mailto:\[REDACTED\]](mailto:[REDACTED])]
Sent: Friday, 30 November 2018 1:51 PM
To: Cathie Allen
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]; Collophen.RubenB[OSC]; Harris.LibbyA[OSC]
Subject: RE: Removal of the Microcon step - QPS advice

Hi Cathie,

Just wondering if you have had a chance to consider the below email?

In particular the suggestion: So, it may be that the process stays as it is, but when we send the request through to Luke Ryan (or Justin or Paula) for further processing we request advice on proceeding with Microcon step or whether some other process or testing may have a better opportunity based on the factors that have been taken into consideration to produce a usable profile, what are your thoughts on this?

I did this process recently with Justin Howes (via Luke Ryan) where I sent a request through for some assistance on options and Justin provide a good response allowing the QPS to make an informed decision. This was for a case where the investigating officer requested further processing, but when we reviewed the request we thought it better to get further advice from Health, which will hopefully prove beneficial in furthering this particular investigation.
[REDACTED] refers.

This week I also processed through 4 requests to Luke Ryan for further processing as a result of tasks from investigators where when we reviewed the request, the reason the investigator was requesting further processing and the case decided to proceed with the Microcon step without further advice from Health.

Hope you have a good weekend.

Kind regards

Gerard

Gerard Simpfendorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service

[REDACTED]
[REDACTED]
[REDACTED]
[REDACTED]



From: Simpfendorfer.GerardM[OSC]

Sent: Thursday, 22 November 2018 3:54 PM

To: Cathie Allen <[REDACTED]>

Cc: Craig Russell <[REDACTED]> Neville.DavidH[OSC] <[REDACTED]>
McNab.BruceJ[OSC] <[REDACTED]> Collophen.RubenB[OSC]

<[REDACTED]> Harris.LibbyA[OSC] <[REDACTED]>

Subject: RE: Removal of the Microcon step - QPS advice

Hi Cathie,

That wasn't really what I was chasing as I am not questioning the code of conduct or the evidence that is given in Court by the Scientist as we have no issue with this and know you and your staff always act in good faith.

It could be how I phrased the question/issue, so I'll try again.

In your email you said the following:

There are a number of factors that would be taken into consideration regarding the balance between concentrating the sample vs preserving extract for other testing.

And then went on to describe a number of these factors in the rest of that paragraph. You also started the next paragraph with some 'key factors' and finished that paragraph with the following:

All of these factors are taken into consideration prior to requesting a Microcon. We have assessed a large amount of data to provide the best indication of how profiles have behaved and provide this advice to the QPS to assist.

My questions around the above 2 sentences are:

- At what point of the examination process are these factors taken in to consideration?
- How do you provide this advice to QPS to assist?

I thought the line "THIS SAMPLE HAS UNDERGONE FURTHER PROCESSING" meant that either the QPS or the Scientist had requested further processing of the sample which is the rework process and that the Microcon step had commenced.

I do not believe this line provides advice on the best indication for how profiles may behave or if another of the factors you have considered may be more beneficial in obtaining a usable profile for the investigation.

Is there another option to this line to provide the QPS with this advice around your best indication in these cases besides proceeding with Microcon considering the Microcon step will consume all the available extract?

We believe the risk of deciding whether or not to Microcon should not be left to the QPS solely as we do not have the expertise or access to the data about the quality and quantity of DNA in the sample. What we are chasing is some sort of decision making tree so we know what should trigger us to request further processing. At the moment it seems to be a stab in the dark for us, if we don't request a rework we get no result. But, the chance of a result is better than nothing in certain circumstances.

So, it may be that the process stays as it is, but when we send the request through to Luke Ryan for further processing we request advice on proceeding with Microcon step or whether some other process or testing may have a better opportunity based on the factors that have been taken into consideration to produce a usable profile, what are your thoughts on this?

That way the investigating officer and the QPS can make an informed decision before authorising the consumption of all the extract.

I hope this is a little clearer.

Kind regards

Gerard

Gerard Simpfendorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service

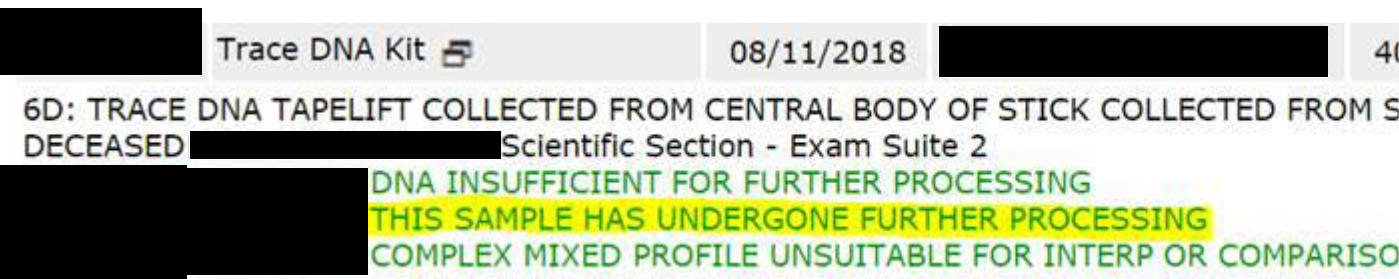


From: Cathie Allen <[REDACTED]>
Sent: Wednesday, 21 November 2018 12:14 PM
To: Simpfendorfer.GerardM[OSC] <[REDACTED]>
Cc: Craig Russell <[REDACTED]> Neville.DavidH[OSC] <[REDACTED]>
 McNab.BruceJ[OSC] <[REDACTED]> Colloopen.RubenB[OSC] <[REDACTED]>
Subject: RE: Removal of the Microcon step - QPS advice

Hi Gerard

Scientists in Forensic DNA Analysis apply scientific principles to processing and reworking of all samples that they review, as they are bound by the Code of Conduct for the Queensland Public Service and are committed to ensuring the best possible outcome for the Queensland Community. Reporting scientists are questioned under oath about the scientific decisions that they have made and provide answers based on scientific principles.

If the sample is reworked after a result has been released to the QPS, the QPS is advised electronically by a result line advising that the sample has undergone further processing as per the example below:



Cheers
Cathie

**Cathie Allen**

Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health

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From: Simpfendorfer.GerardM[OSC] [mailto: [REDACTED]]
Sent: Tuesday, 20 November 2018 3:35 PM
To: Cathie Allen
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]; Collophen.RubenB[OSC]
Subject: Removal of the Microcon step - QPS advice

Hi Cathie,

And thank you for your response.

You mention there are a number of factors that would be taken into consideration regarding the balance between concentrating the sample vs preserving extract for other testing and you gave some examples including assessing the quality and quantity of the DNA as a key factor to obtaining a DNA profile.

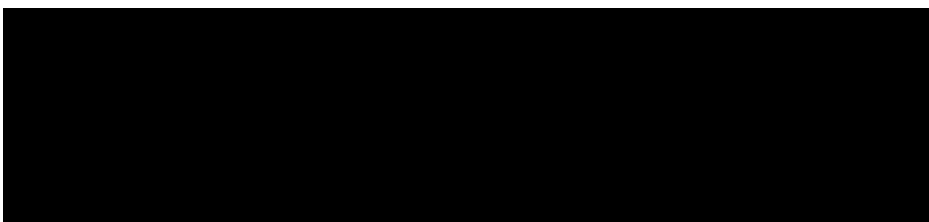
1. Do you take these factors into consideration only when sending through the DNA Insufficient result for:
 - All exhibits?
 - P1 and P2 only exhibits?
 - P1 only exhibits?
2. Or do you take these factors in to consideration only when the QPS requests further processing of the exhibit?
3. Or do you take these factors in to consideration only when the QPS requests advice on other testing options?

If it is option 1 or 2, how do you provide this advice to the QPS to assist investigators, especially if in the Scientists expert opinion requesting a Microcon step may not be the best for obtaining a possible DNA result due to this process consuming all the available extract.

Kind regards

Gerard

Gerard Simpfendorfer
Acting Inspector 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service





From: Cathie Allen <[REDACTED]>
Sent: Friday, 16 November 2018 4:01 PM
To: Simpfendorfer.GerardM[OSC] <[REDACTED]>
Cc: Craig Russell <[REDACTED]> Neville.DavidH[OSC] <[REDACTED]>
McNab.BruceJ[OSC] <[REDACTED]>
Subject: RE: Removal of the microcon step from P1 workflow.

Hi Gerard

The quantification values between 0.001 and 0.008ng/uL is the range for the result line of DNA Insufficient – so this is the range that prior to Feb 2018 would have automatically proceeded for concentration.

There are a number of factors that would be taken into consideration regarding the balance between concentrating the sample vs preserving extract for other testing – some examples, but limited to, – the indication within the quantification of the Y chromosome, pooling of samples from a similar area prior to concentrating as this may have a better chance of concentrating the available DNA for a 'useable' profile, preserving 1 sample and concentrating another sample from similar areas (rather than doing both in the first instance), the quantification value and if it's likely to be a mixture, the sample type (ie tapelift from a particular exhibit vs swab from a more probative area) or targeting particular samples for concentration in the context of the case (rather than all priority 1 samples).

The quality and quantity of the DNA are the key factors in obtaining a DNA profile. For these samples, whilst there was a small amount of DNA, the quality of the DNA may have been quite good, which has meant that a DNA profile was able to be generated (I haven't looked into these samples, I'm providing information on a general basis). Whilst our processes provide a quantification value, indication of degradation and indication of Y chromosome, it's the generation of DNA profile that assists in highlighting the quality of the DNA that was available. The DNA in the sample may only just be above the acceptance criteria to be called an allele, and it may generate enough alleles to provide a Likelihood Ratio of >100 billion, however its viewing the DNA profile that can show the extent of the degradation or inhibition factors that may be associated. All of these factors are taken into consideration prior to requesting a Microcon. We have assessed a large amount of data to provide the best indication of how profiles have behaved and provide this advice to the QPS to assist.

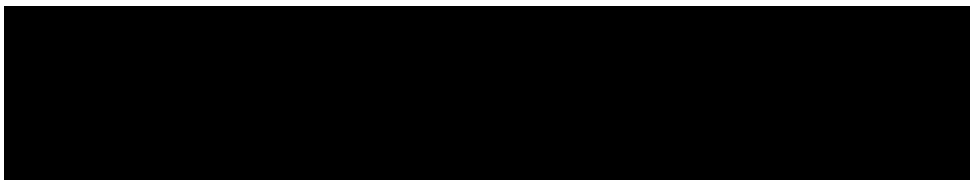
Please let me know if you have any further questions.

Cheers
Cathie



Cathie Allen
Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health



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From: Simpfendorfer.GerardM[OSC] [mailto: [REDACTED]]
Sent: Thursday, 15 November 2018 3:24 PM
To: Cathie Allen
Cc: Craig Russell; Neville.DavidH[OSC]; McNab.BruceJ[OSC]
Subject: RE: Removal of the microcon step from P1 workflow.

Hi Cathie,

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Also, why did these samples yield a result and could the factors involved be used to determine future processes?

Kind regards

Gerard

Gerard Simpfendorfer
 Acting Inspector 4009415
 DNA Management Section, Forensic Services Group
 Operations Support Command, Queensland Police Service

From: Cathie Allen < [REDACTED] >
Sent: Thursday, 15 November 2018 9:20 AM
To: Simpfendorfer.GerardM[OSC] < [REDACTED] > McNab.BruceJ[OSC]
 < [REDACTED] >
Cc: Craig Russell < [REDACTED] > Neville.DavidH[OSC] < [REDACTED] >
Subject: FW: Removal of the microcon step from P1 workflow.
Importance: High

Hi Gerard and Bruce

I can confirm that the Microcon process has been applied to the below four sample as requested by the QPS on the dates listed below:

[REDACTED] Snr Sgt Simpfendorfer requested Microcon 29/10/2018
 [REDACTED] Snr Sgt Simpfendorfer requested Microcon 06/11/2018
 [REDACTED] Snr Sgt Simpfendorfer requested Microcon 06/11/2018
 [REDACTED] Snr Sgt Simpfendorfer requested Microcon 06/11/2018

During a meeting on 1st of Feb 2018, Paul Csoban (previous Executive Director for FSS) and I met with Supt Dale Frieberg to discuss the Options Paper that had previously been provided to the QPS for decision. During this meeting, the Superintendent agreed that Option 2 was the preferred option, which was later confirmed via email (as per below). During the discussion, the second part of Option 2 (section a) was discussed, which related to Priority 1

samples and the Superintendent indicated that Priority 1 samples should be processed the same as Major crime (P2) and Volume crime samples (P3), which is not to be automatically progressed through the Microcon process. After the approval from the QPS in Feb 2018, all samples have not automatically progressed through the Microcon process. The QPS or a Forensic DNA Analysis staff member can request a Microcon process for a sample at any time.

Automatic progression of samples through the Microcon process means that all available DNA extract will be consumed, so no further testing can be conducted on these samples after this step. This means that if a sample could yield a profile by specific Y chromosome testing for example, there would be no extract available for that testing to be conducted. It also means that samples that are eligible to be pooled together, as they are from the same item or area, are not able to be as there is no DNA extract left to undertake pooling. Scientists or Forensic officers reviewing results in the context of a case are able to request a Microcon process for a sample or samples.

As the decision on the automatic Microcon process was made last financial year, the budget for this financial year has been adjusted for that consumable, so this will increase the cost.

If the QPS wishes for P1 samples to automatically be processed through the Microcon process, which leaves no available extract for other testing, this process can be re-introduced. Please confirm if the QPS requires the re-introduction of this step.

The Options Paper reviewed 1449 Major crime samples that had been progressed through the Microcon process over a one year period, as this was considered to be sufficient sample numbers to demonstrate a clear trend.

The laboratory is unable to search the FR to undertake any statistical analysis regarding 'useable' profile numbers – this was highlighted to FSS during development that large or medium scale interrogation of the FR could only be undertaken by the QPS, as they would need to construct the search and ensure the timing of the search was undertaken so as not to add extra burden to the FR during peak operational times. If the QPS were able to generate this data, the laboratory would undertake this analysis and provide feedback. The Microcon process was no longer automatically undertaken for P1 or P2 samples from the 12th of Feb 2018.

Whilst the Microcon process has not been automatically applied to Major crime samples (P2) since mid Feb, scientists have reviewed those results and requested a Microcon process if in the context of the case it could have been of potential benefit. If the QPS undertook a search of all 'DNA insufficient' results on P1 and P2 samples since the 12th of Feb, the laboratory could undertake an analysis of the cases to determine if additional testing through the Microcon process is required. This would require resources and would reduce the number of results that are reviewed by the lab until this analysis was completed.

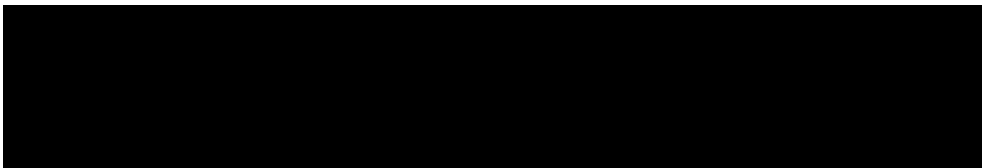
I await your advice regarding this. If you have any further questions, please let me know how I can assist.

Cheers
Cathie



Cathie Allen
Managing Scientist

Police Services Stream, Forensic & Scientific Services
Health Support Queensland, Queensland Health



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From: Neville.DavidH[OSC] [<mailto:> ██████████]
Sent: Wednesday, 14 November 2018 2:47 PM
To: Cathie Allen
Cc: Craig Russell; McNab.BruceJ[OSC]; Simpfendorfer.GerardM[OSC]
Subject: Removal of the microcon step from P1 workflow.
Importance: High

Dear Cathie

During the course of the investigation into ██████████ over 15 samples were submitted as Priority 1. On initial testing, four samples were reported as having insufficient DNA present for further testing. Upon receipt of that result my staff requested additional testing and each of those samples yielded a result as follows:

██████████ - SINGLE SOURCE 20 LOCI DNA PROFILE LR > 100 BILLION (Deceased match); and POSSIBLE SUB-THRESHOLD INFORMATION
 ██████████ - SINGLE SOURCE DNA PROFILE - ASSUMED KNOWN CONTRIBUTOR – (Deceased match)
 ██████████ - SS DNA PROFILE 9 LOCI AND ABOVE LR > 100 BILLION (Deceased match)
 ██████████ - COMPLEX MIXED PROFILE UNSUITABLE FOR INTERP OR COMPARISON

Could you confirm if the profiles for the four samples listed above were obtained after micro-concentration was performed, please. Could you also confirm if the microcon step has been removed from the workflow as a matter of routine for P1 samples. My understanding as per the below was that this was only to occur for P2. If this process has been removed from the P1 workflow, could it please be reintroduced as it will stop delays in obtaining results that are considered urgent, please.

From: Frieberg.DaleJ[OSC]
Sent: Friday, 2 February 2018 3:38 PM
To: Cathie Allen [REDACTED] O'Malley.TroyS[OSC] [REDACTED]
Cc: Paul Csoban [REDACTED]
Subject: RE: Options Paper for consideration

Hi Cathie and Paul,

Thank you for your time this afternoon and for discussion around this options paper. Thank you also to

As discussed, I am in agreement that:

- There is clear data that it is not an efficient use of time and resources to continue with the 'auto-microcon' process for Priority 2 casework....
- Option 2. "Cease the 'auto-microcon' process for Priority 2 casework...." Would appear to be a better use of resources.
- Scientists time and resources would be better spent working samples with a higher DNA yield
- It would be beneficial to amend the Forensic Register to provide an automated Q-Prime update
- DNA staff can request this additional processing if/when a request is received from the investor

I trust this is of assistance.

Kind regards,

Dale.

Dale Frieberg
 Superintendent
 Operations Commander
 Forensic Services Group
 Operations Support Command
 Queensland Police Service

The removal of the microcon step in the process was agreed to on 2 February 2018 by Supt Frieberg based on the advice included in the attached paper. This paper estimates that there would be less than a 2% reduction in the number of useable results if the step was eliminated.

Based on the fact that 3 out of 4 samples for this case yielded a result when testing was continued, anecdotally it would seem that we may be missing out on more than 2% of results.

Since eliminating this step, has your laboratory undertaken any statistical analysis to determine if there has been a drop in the proportion of samples that give a useable profile, please.

There are other serious matters including homicides where testing has stopped once advice was received that there is insufficient DNA for further testing. Based on the results for this case (75% success rate for the ones received back so far), would you recommend that these cases be re-examined please.

Could you please direct your response to Gerard and Bruce.



David Neville
Inspector
DNA Management Unit | Forensic Services Group
Operations Support Command
QUEENSLAND POLICE SERVICE

[REDACTED]

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Paula Brisotto

From: Justin Howes
Sent: Wednesday, 13 February 2019 4:32 PM
To: Brock.AdrianC[OSC]; Simpfendorfer.GerardM[OSC]
Cc: Hoffman.CarolynP[OSC]; Neville.DavidH[OSC]; Collophen.RubenB[OSC]; Paula Brisotto
Subject: RE: [REDACTED]

Hi Adrian,

In my opinion, these samples are here and available to be requested for reactivation. Therefore, I would focus on the 'DNA insufficient' samples first given they are intimate swabs, but we will process whatever samples you or delegate decide to request.

Regards
 Justin

**Justin Howes**

Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services

Health Support Queensland, Queensland Health



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From: Brock.AdrianC[OSC] [mailto:[REDACTED]]
Sent: Wednesday, 13 February 2019 4:26 PM
To: Justin Howes <[REDACTED]> Simpfendorfer.GerardM[OSC]
 <[REDACTED]>
Cc: Hoffman.CarolynP[OSC] <[REDACTED]> Neville.DavidH[OSC]
 <[REDACTED]> Collophen.RubenB[OSC] <[REDACTED]> Paula Brisotto
Subject: Re: [REDACTED]

Justin or Gerard,

Considering this is it more advantageous to send the AP positive items from the underwear down for testing, rather than wasting more time on these for little to possibly no result?

cheers

Adrian
 Senior Sergeant Adrian Brock
 Forensic Coordinator
 Central Forensic Area

[REDACTED]

From: Justin Howes <[REDACTED]>
Sent: Wednesday, February 13, 2019 4:13 pm
To: Simpfendorfer.GerardM[OSC]
Cc: Hoffman.CarolynP[OSC]; Brock.AdrianC[OSC]; Neville.DavidH[OSC]; Colloppen.RubenB[OSC]; Paula Brisotto
Subject: RE: [REDACTED]

Hi Gerard

I have had a look at the screening results and the quant values obtained. The findings are not unexpected in my opinion.

There was no unknown female profile because no samples proceeded to be profiled after the quantification stage; they were either 'No DNA Detected' or 'DNA Insufficient...'. This means the samples did not proceed to amplification and then to profile; therefore, no male or female profiles. Please note one sample has proceeded to profiling and has not finished as yet – this was an epithelial fraction from the Perianal swab.

Background that may assist:

When possible semen samples are submitted for DNA extraction, they undergo a Differential Lysis procedure which aims to separate male and female DNA. Extract is separated into a 'spermatozoa fraction' and an 'epithelial fraction'. It is standard procedure to not profile the epithelial fraction of the process for SAIK samples; we haven't profiled these epithelial fractions for SAIK swabs for a number of years due to the high likelihood of there being female DNA matching the donor of the swab. There are some case circumstances where they are profiled however eg. Child complainants, external swabs (eg perianal, vulval).

The spermatozoa fractions for the samples you provided yielded either no semen being detected, or very low numbers of sperm were detected. Consequently, it is not unexpected to return the results that you have.

It is possible to rework any result such as these that have been sent to DNA Mgt. The expanded comment mentions this for DNA Insufficient samples, so please specify the sample/s you wish to be reactivated for DNA profiling through the normal request/task process.

Thanks for organising the victim reference sample as these are always important in sexual assault matters especially.

Regards

Justin



Justin Howes

Team Leader - Forensic Reporting and Intelligence Team
Forensic DNA Analysis, Forensic & Scientific Services
Health Support Queensland, Queensland Health

[REDACTED]

[REDACTED]

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From: [REDACTED] [mailto:[REDACTED]]

Sent: Wednesday, 13 February 2019 1:27 PM

To: Justin Howes <[REDACTED]>

Cc: [REDACTED]

Subject: FR1798755 / QP1802307119

Good afternoon Justin,

We have been approached to provide advice as to why the SAIK from the victim in relation to this case has failed to return any profiles, not even an Unknown Female profile (which would presumably be the victim's) on the High Vaginal swab.

Could you please provide any insight in to why the high vaginal, low vaginal and perianal swabs all failed to return a profile, even the victim's profile?

Was there potentially a problem with the sampling process or the kit?

Is it possible to rework these samples to try to obtain a profile?

We have requested a victim reference sample be obtained to assist with any unresolved profiles or mixtures.

Exhibit List

1 - 18 / 18 Entries

| Barcode | Category | Date | Property Tag FilmNo | Employee | Location |
|---|---------------------|------------|---------------------|------------|-------------------|
| [REDACTED] | Epithelial Fraction | 06/02/2019 | | [REDACTED] | PSD 728119194 G12 |
| PERIANAL SWAB EXHIBIT A - VICTIM SAIK XEE-ANA HENAWAY - NCE | | | | | |
| [REDACTED] | Swab | 04/02/2019 | D3709057 | [REDACTED] | PSD 728118231 C06 |
| 1 HIGH VAGINAL EXHIBIT A - VICTIM SAIK XEE-ANA HENAWAY - Forensic and Scientific Services | | | | | |

QHSS POS [REDACTED] PRESUMP. AP TEST POSITIVE, SUBMITTED - RESULTS PENDING

QHSS POS [REDACTED] MICRO POSITIVE FOR SPERM. SUBMITTED-RESULTS PENDING

QHSS POS [REDACTED] DNA INSUFFICIENT FOR FURTHER PROCESSING

| | | | | | |
|---|------|------------|----------|------------|-------------------|
| [REDACTED] | Swab | 04/02/2019 | D3709057 | [REDACTED] | PSD 728118132 H05 |
| 2 HIGH VAGINAL EXHIBIT A - VICTIM SAIK XEE-ANA HENAWAY - Forensic and Scientific Services | | | | | |

QHSS POS [REDACTED] PRESUMP. PSA TEST POSITIVE, SUBMITTED - RESULTS PENDING

QHSS POS [REDACTED] . AP TEST POSITIVE, SUBMITTED - RESULTS PENDING

QHSS POS [REDACTED] MICRO POSITIVE FOR SPERM. SUBMITTED-RESULTS PENDING

QHSS POS [REDACTED] DNA INSUFFICIENT FOR FURTHER PROCESSING

| | | | | | |
|------------|------|------------|----------|------------|-------------------|
| [REDACTED] | Swab | 04/02/2019 | D3709057 | [REDACTED] | PSD 728118121 E06 |
|------------|------|------------|----------|------------|-------------------|

LOW VAGINAL EXHIBIT A - VICTIM SAIK XEE-ANA HENAWAY - Forensic and Scientific Services

QHSS POS [REDACTED] PRESUMP. AP TEST POSITIVE, SUBMITTED - RESULTS PENDING

QHSS POS [REDACTED] MICRO NEG FOR SPERM

QHSS POS [REDACTED] SEMEN NOT DETECTED

QHSS POS [REDACTED] DNA INSUFFICIENT FOR FURTHER PROCESSING

| | | | | | |
|------------|------|------------|----------|------------|-------------------|
| [REDACTED] | Swab | 04/02/2019 | D3709057 | [REDACTED] | PSD 728118060 G10 |
|------------|------|------------|----------|------------|-------------------|

PERIANAL EXHIBIT A - VICTIM SAIK XEE-ANA HENAWAY - Forensic and Scientific Services

QHSS POS [REDACTED] MICRO NEG FOR SPERM

QHSS POS [REDACTED] SEMEN NOT DETECTED

QHSS POS [REDACTED] NO DNA DETECTED

| | | | | | |
|------------|-------|------------|----------|------------|-----|
| [REDACTED] | Paper | 04/02/2019 | D3709057 | [REDACTED] | PSD |
|------------|-------|------------|----------|------------|-----|

DROPSHEET EXHIBIT A - VICTIM SAIK XEE-ANA HENAWAY - Forensic and Scientific Services

| | | | | | |
|------------|------|------------|------------|------------|-------------------|
| [REDACTED] | Hair | 04/02/2019 | [REDACTED] | [REDACTED] | PSD 728119263 G02 |
|------------|------|------------|------------|------------|-------------------|

FROM DROPSHEET VICTIM SAIK XEE-ANA HENAWAY - NCE

QHSS POS [REDACTED] NO DNA DETECTED

Kind regards

Gerard

Gerard Simpfendorfer
Senior Sergeant 4009415
DNA Management Section, Forensic Services Group
Operations Support Command, Queensland Police Service

[REDACTED]



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Paula Brisotto

From: Luke Ryan
Sent: Tuesday, 2 January 2018 12:28 PM
To: Allan McNevin; Amanda Reeves; Cathie Allen; Justin Howes; Kirsten Scott; Kylie Rika; Paula Brisotto; Sharon Johnstone; Kerry-Anne Lancaster
Subject: Profiler Plus

Afternoon All

FYI we have approximately 550 Profiler Plus reactions remaining (approx. 5-6 full amps depending on Taq usage). Expiry for these kits is 22/01/2018. Given there are 250 P3s on the received list, I anticipate we will use the last reactions by end next week.

Thanks

Luke

**Luke Ryan**

Senior Scientist – Analytical Team

Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



Minutes

Analytical Team Meeting

| | | | |
|-------------------------|---|-----------------------|---|
| Chairperson: | LBR | Date and Time: | 08/01/2018 10:00am |
| Venue: | FSS-CR-611 | Secretariat: | LBR |
| Meeting Purpose: | Weekly meeting | File Location: | G:\ForBio\DNA Analysis Team Meetings\Analytical\Minutes\2018 Meetings\08-01-2017.docm |
| Attendees: | SCN, BUA, GSL, MLM, TJD, CI, PA, LMF, LWL, AK, AKD, MJC | | |
| Guests: | | | |
| Apologies: | | | |
| Absent: | TLP, BM, AC | | |

| | |
|--|--|
| 1.0 | PREVIOUS MINUTES ENDORSED |
| Previous meeting held (18-12-2017) were accepted by GSL | |
| 2.0 | CONFLICTS OF INTEREST |
| Nil | |
| 3.0 | BUSINESS ARISING FROM PREVIOUS MINUTES |
| Refer "Action Table" for business arising from previous minutes – Page 2 | |
| 4.0 | STANDING AGENDA ITEMS |
| Item 4.1: | |
| Subject: | Rosters |
| Discussion: | Roster for upcoming month to reviewed in the meeting the last Monday of the preceding month. G:\ForBio\AAA Analytical Section\Analytical training & rosters\Roster 2016.xls G:\ForBio\AAA Administration\Timesheets and HR forms\Leave DNA Analysis 2016.xls |
| ACTION: | All staff to note |
| Responsibility: | All staff |
| Due Date/Status: | N/A |
| Item 4.2: | |
| Subject: | KPI Figures |
| Discussion: | G:\ForBio\AAA Analytical\Whiteboard figures\Combined Stats 2016.xls |
| ACTION: | All staff to note |
| Responsibility: | All staff |
| Due Date/Status: | N/A |
| Item 4.3: | |
| Subject: | Issues Logs / Registers |
| Discussion: | Analytical Issues log I:\AAA Analytical Section\Analytical Logs\Analytical Issues Log.xls Operational Issues log I:\AAA Operational Staff\Issues Log Minor Changes log I:\Change Management |
| ACTION: | All staff to note |
| Responsibility: | All staff |
| Due Date/Status: | N/A |
| Item 4.4: | |
| Subject: | Project Updates |
| Discussion: | |

Forensic and Scientific Services

1. QS5 – validation plan approved. Commence 2nd week Feb.
2. Hamilton C – Commenced. Approved for Bio-strategy to come up to us early next year.
3. Retain supernatant on Maxwell – Experimental design signed, can get started.
4. 9700 HTER – waiting on quotes. Nil difference from FRIT.
5. MPS Project – Revised plan approved, waiting on QPS input.
6. QIASymphony Bone/Teeth Extraction – Experimental design signed, not to start Feb.
7. Second QIASymphony – Experimental design signed off.
8. Verifiler Plus Trial

ACTION: All staff to note

Responsibility: All staff

Due Date/Status: N/A

Item 4.5:

Subject: OQIs

Discussion: Nil

ACTION: All staff to note

Responsibility: All staff

Due Date/Status: N/A

Item 4.6:

Subject: Instrument Updates

Discussion: Instrument: Pre PCR STARlets

Issue: Tube height being modified for master mix tubes, mainly on half volume amps. AKD and TJD to look at heights and tube dimensions. Check all samples are capped correctly by the decapper.

Instrument: QIASymphony

Issue: Waste drawer not closing properly due to the hook on the back the rubber waste chute.

08/01/2018 – this issue resolved by putting the rubber drip catcher on instrument with the grooves/chevrons towards the front/operator (closest to operator).

ACTION: All staff to note

Responsibility: All staff

Due Date/Status: N/A

5.0 NEW BUSINESS**Item 5.1:**

Subject: FR Update/Items

Discussion: Enhancements: workflow diary in FR, equipment maintenance in FR (daily, weekly etc), test quant and test amp templates in FR, batch can't be completed unless sequence check has been done.

Enhancement raised about reference dilutions, FR to blank on quant results, then add the parent to the reference dilution worklist, we will still need to add in a dilution factor.

08/01/2018 – Quant bug raised where results file was loaded as a PDF. This has been resolved.

ACTION:

Responsibility:

Due Date/Status:

Forensic and Scientific Services

| | |
|-------------------------|---|
| Item 5.2: | |
| Subject: | CEQ Check Notes |
| Discussion: | Please ensure that your notes are thorough. E.g. if there are extra pks, cross talk etc so that if samples are being reworked the reason is obvious. Also important for plate readers/CMs to know that you have noted it. Please don't just use the UD2 comments as this cannot be attributed to an operator. UD2 is only for plate readers. |
| ACTION: | All staff to do |
| Responsibility: | All staff |
| Due Date/Status: | |

| | |
|------------------|----------------------------------|
| 6.0 | NEW BUSINESS – FOR NOTING |
| Item 6.1: | |

| | |
|-------------------------|---|
| Subject: | Finalising Quants with P1s No DNAs |
| Discussion: | Please ensure that you notify someone so that the P1 Quant results can be reviewed ASAP |
| ACTION: | All staff to do |
| Responsibility: | All staff |
| Due Date/Status: | |

| | |
|------------------|--|
| Item 6.2: | |
|------------------|--|

| | |
|-------------------------|---|
| Subject: | P+ Finish |
| Discussion: | Please retain P+ matrix and size standard after we run out of P+ kits for re-CE All samples will be processed using PP21. Awaiting FRIT advice on P3 workflow (i.e. for quant transition). Without further advice we will process as per P2. |
| ACTION: | All staff to note |
| Responsibility: | All staff |
| Due Date/Status: | |

| | |
|------------------|--|
| Item 6.3: | |
|------------------|--|

| | |
|-------------------------|---|
| Subject: | CE |
| Discussion: | Please remember to complete batches and upload PDFs for CE batches. (i.e. when you put the amp on the TC). If you are creating a CE batch and see a batch is not completed please do it then. |
| ACTION: | All staff to do |
| Responsibility: | All staff |
| Due Date/Status: | |

| | |
|------------------|--|
| Item 6.4: | |
|------------------|--|

| | |
|-------------------------|---|
| Subject: | ENVM Sampling |
| Discussion: | Please print out the proper labels instead of using the labels from the rolls, because the roll labels rub off. |
| ACTION: | All staff to do |
| Responsibility: | All staff |
| Due Date/Status: | |

| | |
|------------------|--|
| Item 6.5: | |
|------------------|--|

| | |
|-----------------|--|
| Subject: | |
|-----------------|--|

Forensic and Scientific Services

| | |
|-------------------------|--|
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| Item 6.6: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| Item 6.7: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| Item 6.8: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| Item 6.9: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| Item 6.10: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| Item 6.11: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| | |
| | |

7.0 CLOSURE

Forensic and Scientific Services

Meeting Closed at: 10:30

8.0 NEXT MEETING

Date: 8/01/2018 Time: 10.00am

Venue: CR-611

Minutes

Analytical Team Meeting

| | | | |
|-------------------------|--|-----------------------|---|
| Chairperson: | LBR | Date and Time: | 15/01/2018 10:00am |
| Venue: | FSS-CR-611 | Secretariat: | LBR |
| Meeting Purpose: | Weekly meeting | File Location: | G:\ForBio\DNA Analysis Team Meetings\Analytical\Minutes\2018 Meetings\15-01-2017.docm |
| Attendees: | SCN, BUA, MLM, TJD, CI, PA, LMF, LWL, AKD, MJC, AC | | |
| Guests: | | | |
| Apologies: | GSL, AK | | |
| Absent: | TLP, BM | | |

| | |
|--|--|
| 1.0 | PREVIOUS MINUTES ENDORSED |
| Previous meeting held (08-01-2018) were accepted by BUA | |
| 2.0 | CONFLICTS OF INTEREST |
| Nil | |
| 3.0 | BUSINESS ARISING FROM PREVIOUS MINUTES |
| Refer "Action Table" for business arising from previous minutes – Page 2 | |
| 4.0 | STANDING AGENDA ITEMS |
| Item 4.1: | |
| Subject: | Rosters |
| Discussion: | Roster for upcoming month to reviewed in the meeting the last Monday of the preceding month. G:\ForBio\AAA Analytical Section\Analytical training & rosters\Roster 2016.xls G:\ForBio\AAA Administration\Timesheets and HR forms\Leave DNA Analysis 2016.xls |
| ACTION: | All staff to note |
| Responsibility: | All staff |
| Due Date/Status: | N/A |
| Item 4.2: | |
| Subject: | KPI Figures |
| Discussion: | G:\ForBio\AAA Analytical\Whiteboard figures\Combined Stats 2016.xls |
| ACTION: | All staff to note |
| Responsibility: | All staff |
| Due Date/Status: | N/A |
| Item 4.3: | |
| Subject: | Issues Logs / Registers |
| Discussion: | Analytical Issues log I:\AAA Analytical Section\Analytical Logs\Analytical Issues Log.xls Operational Issues log I:\AAA Operational Staff\Issues Log Minor Changes log I:\Change Management |
| ACTION: | All staff to note |
| Responsibility: | All staff |
| Due Date/Status: | N/A |
| Item 4.4: | |
| Subject: | Project Updates |
| Discussion: | |

Forensic and Scientific Services

1. QS5 – validation plan approved. Installation today.
2. Hamilton C – Commenced. CE programs are being written. Modules ordered.
3. Retain supernatant on Maxwell – Commenced. Exp 2 lab work done. Exp 1 to be started this week.
4. 9700 HTER – had demo of Proflex networking software.
5. MPS Project – Revised plan approved, waiting on QPS input.
6. QIAsymphony Bone/Teeth Extraction – Experimental design signed, not to start Feb.
7. Second QIAsymphony – Commenced – ARTEL of AS passed
8. Verifiler Plus Trial

ACTION: All staff to note

Responsibility: All staff

Due Date/Status: N/A

Item 4.5:

Subject: OQIs

Discussion: Nil

ACTION: All staff to note

Responsibility: All staff

Due Date/Status: N/A

Item 4.6:

Subject: Instrument Updates

Discussion: Instrument: Pre PCR STARlets

Issue: Issues with decappers on PrePCR STARlets capping/decapping. May be due to manufacturing differences with caps and tubes. When placing rack back on decapper stage sometimes not placing properly – may need adjusting – TJD to log issue with Bio Strategy for engineer to visit.

Instrument: QIAsymphony

Issue: Laura visited on Friday – will replace the Perspex panel between SP/AS on B. Also looked at scratches on cabinet and will compensate with kits/consumables. Crash on SP-A last week – refer to adverse event 432. Please ensure that you check the consumables before loading onto the SP/AS.

ACTION: All staff to note

Responsibility: All staff

Due Date/Status: N/A

5.0 NEW BUSINESS

Item 5.1:

Subject: FR Update/Items

Discussion: Enhancements: workflow diary in FR, equipment maintenance in FR (daily, weekly etc), test quant and test amp templates in FR, batch can't be completed unless sequence check has been done.

Enhancement raised about reference dilutions, FR to blank on quant results, then add the parent to the reference dilution worklist, we will still need to add in a dilution factor.

08/01/2018 – Quant bug raised where results file was loaded as a PDF. This has been resolved.

ACTION:

Responsibility:

Forensic and Scientific Services

| | |
|-------------------------|--|
| Due Date/Status: | |
| Item 5.2: | |
| Subject: | P+ Finish |
| Discussion: | P+ expires at end of this week, so please do P+ amps as a priority even if it is a small batch. JAH is working on modified P3 workflow which includes changes to the auto microcon rules. |
| ACTION: | All staff to note |
| Responsibility: | All staff |
| Due Date/Status: | |

| | |
|--------------------------------------|---|
| 6.0 NEW BUSINESS – FOR NOTING | |
| Item 6.1: | |
| Subject: | Ref Amps (EREFs) |
| Discussion: | Please keep these batches to half a plate, don't wait for a full batch. These are often difficult plates, with difficult samples and many reasons for re-CE etc. |
| ACTION: | All staff to note |
| Responsibility: | All staff |
| Due Date/Status: | |
| Item 6.2: | |
| Subject: | Insufficient Vols and Mcon duplicates |
| Discussion: | Please ensure that add a notation to the sample and allocate to PDA worklist (see LBR if unsure). If the samples don't go back onto the PDA worklist there will be a delay in the CM. |
| ACTION: | All staff to note |
| Responsibility: | All staff |
| Due Date/Status: | |
| Item 6.3: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| Item 6.4: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| Item 6.5: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |

Forensic and Scientific Services

| | |
|-------------------------|--|
| Item 6.6: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| Item 6.7: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| Item 6.8: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| Item 6.9: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| Item 6.10: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |
| Item 6.11: | |
| Subject: | |
| Discussion: | |
| ACTION: | |
| Responsibility: | |
| Due Date/Status: | |

7.0 CLOSURE

Meeting Closed at: 10:30

8.0 NEXT MEETING

Forensic and Scientific Services

Date: 8/01/2018 Time: 10.00am

Venue: CR-611

Vol in PP21

From: Paula Brisotto </o=queensland health/ou=exchange administrative group (fydibohf23spdl)/cn=recipients/cn=taylorpm">
To: Luke Ryan [REDACTED]
Cc: Justin Howes [REDACTED]
Date: Mon, 15 Jan 2018 17:30:53 +1100

Hi Luke,

I can confirm that we will commence processing Volume Crime samples in PP21 on Monday 22nd January, as the P+ kits expire at this time.

An official comm. will be dra. ed before then; however I am providing you with this for your informaon as w e discussed in earlier today.

If we run out of P+ before then, we will hold Volume crime processing over untl the 22nd, and commence processing P3 samples in PP21 on the Monday.

The processing of P3 samples at this time will follow the established processes in FR for NDNAD <0.001, and NIFP for >/= 0.001 to </= 0.0088.

Auto microcon of P2 samples will continue as is current process untl advised otherwise.

Let me know if you have any questions.

Thanks,
Paula



Paula Brisotto

Team Leader – Evidence Recovery and Quality Team, Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services,
Health Support Queensland, Department of Health



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Josie Entwistle

From: Kylie Rika
Sent: Wednesday, 17 January 2018 6:53 AM
To: Alicia Quartermain; Anne Finch; Claire Gallagher; Deborah Nicoletti; Emma Caunt; Hannah Pattison; Ingrid Moeller; Jacqui Wilson; Josie Entwistle; Penelope Taylor
Cc: Justin Howes; Amanda Reeves; Sharon Johnstone
Subject: FW: Volume crime processing in PP21

Hi RT2

Please see email below from Paula. Justin has asked Sharon and I to put together a plan for the CM of P3 samples in PP21 and what to do at statement stage. This information will be available shortly.

thanks

**Kylie Rika Dip Mgt BSc PGrad Dip (Forensic)**

Senior Reporting Scientist – Forensic Reporting and Intelligence Team

Forensic DNA Analysis | Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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From: Paula Brisotto
Sent: Tuesday, 16 January 2018 2:13 PM
To: Allan McNevin; Luke Ryan; Kerry-Anne Lancaster; Kirsten Scott; Cathie Allen; Amanda Reeves; Kylie Rika; Sharon Johnstone; Justin Howes
Subject: Volume crime processing in PP21

Hi all,

As advised in previous communications, the last of the Profiler Plus kits expire on the 22nd of January 2018.

As such, we will commence processing Volume Crime samples in PP21 on Monday 22nd January.

The processing of P3 samples at this time will follow the established process of No DNA Detected (NDNAD) for quant values <0.001ng/μL, and DNA insufficient for further processing (DIFP) for quant values in the range of >/= 0.001 to </= 0.0088ng/μL as per the current SOPs.

Can you please pass this information on to your teams.

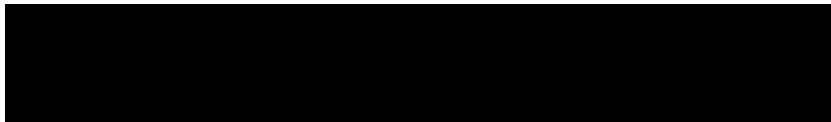
Let me know if you have any questions.

Thanks,
Paula



Paula Brisotto

Team Leader – Evidence Recovery and Quality Team, Forensic DNA Analysis, Police Services Stream
Forensic & Scientific Services,
Health Support Queensland, **Department of Health**



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Workflow for P3 samples in PP21

From: Kylie Rika <[REDACTED]>
 To: Matthew Hunt <[REDACTED]> Allison Lloyd <[REDACTED]>
 Adrian Pippia <[REDACTED]> Thomas Nurthen
 <[REDACTED]> Angela Adamson <[REDACTED]>
 Amanda Reeves <[REDACTED]> Angelina Keller
 <[REDACTED]> Rhys Parry <[REDACTED]> Cassandra James
 <[REDACTED]> Timothy Gardam <[REDACTED]> Susan
 Brady <[REDACTED]> Lisa Benstead <[REDACTED]> Helen
 Williams <[REDACTED]> Luke Ryan <[REDACTED]> Allan McNevin
 <[REDACTED]> Kerry-Anne Lancaster <[REDACTED]>
 Kirsten Scott <[REDACTED]> Paula Brisotto <[REDACTED]>
 Alicia Quartermain <[REDACTED]> Anne Finch
 <[REDACTED]> Claire Gallagher <[REDACTED]> Deborah
 Nicoletti <[REDACTED]> Emma Caunt <[REDACTED]>
 Hannah Pattison <[REDACTED]> Ingrid Moeller
 <[REDACTED]> Jacqui Wilson <[REDACTED]> Josie Entwistle
 <[REDACTED]> Penelope Taylor <[REDACTED]>
 Cc: Justin Howes <[REDACTED]> Sharon Johnstone
 <[REDACTED]>
 Date: Wed, 24 Jan 2018 14:53:17 +1100
 Attachments: Workflow for P3 samples in PP21.doc (30.72 kB)

Hi all

Please find attached a workflow for P3 samples in PP21 given that now all of our P3 samples are being run in PP21.

This workflow has had input from a couple of case managers from both the intel and reporting teams.

Our aim was to find a balance between all samples in the laboratory being done in PP21 with the continuous model and case managing the P3s with limited reworks given there has been no change to the agreement with P about limited reworks for P3s.

This is our first attempt at workflow and I'm sure it will get refined as we go but for now please use this when you come across a P3 sample to case manage that has been amplified in PP21.

mma, I will add this as a comment to the PDA P

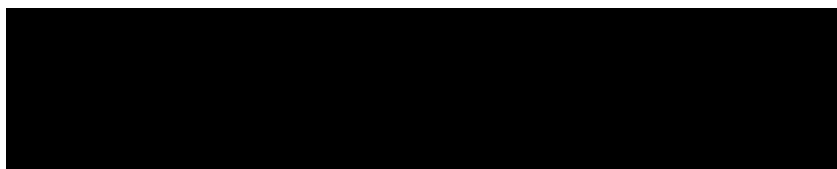
Many thanks



Kylie Rika Dip Mgt BSc PGrad Dip (Forensic)

Senior Reporting Scientist – Forensic Reporting and Intelligence Team

Forensic DNA Analysis | Forensic & Scientific Services,
 Health Support Queensland, Department of Health



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Workflow for P3 samples in PP21**4p or greater**

PDA page CX checked

Result CMPU

Profile review

Single source

If sub th peaks present but do not affect the interp report as below with extra Result line PSTI

If at any point the profile is ambiguous in the number of contributors, an assessment needs to be made if it is suitable for comparison or not. Also consider if 2p.

Single source <6 alleles

PDA page check 1p

No decon required

Result 1SSUND Single source DNA profile- unsuitable for NCIDD searching

Profile review

Single source >6 & <12 PP21 alleles

PDA page check 1p

No decon required

Result 1SSLND Single source DNA profile < NCIDD matching stringency

Profile review

Single source >12 PP21 alleles

PDA page check 1p

decon as 1p by PDA'er (as should be quick)

STRmix file imported

Unknown person assigned

Loaded to NCIDD if required

Profile review

Even mixture 2p or 3p no Ref Sample

PDA page 2 or 3p checked

Result # 2MX or 3MX and NSIP

Profile review

No decon required

Profile review

Major/ minor mixture expected would separate no Ref Sample

2p with ≤ 4 peaks in minor including sub threshold

decon as 2p by PDA'er (as should be quick)

PDA page 2p checked

STRmix file imported

Unknown persons assigned

Major loaded to NCIDD if required

Result 2MX

NCIDD upload line if required (intel or mix)

Profile review

2p with ≥ 4 peaks in minor including sub threshold/3p with 2 in the minor

Put on STRmix list to have decon done as 3p by HP2 (scientist does not assign the sample to themselves at this stage)

When returns to PDA list

Unknown persons assigned

Major loaded to NCIDD if required

Result 3MX

NCIDD upload line if required (intel or mix)

Profile review

Major/ minor mixture expected would separate, Ref sample in case

2p with ≤ 4 peaks in minor including sub threshold and ref sample matches major

(check to see if ownership of item can be ascertained and condition if necessary) decon as 2p by PDA'er (as should be quick)

Comparison to be made to ref sample in STRmix

PDA page 2p checked

STRmix file imported

Unknown persons assigned if any

Major loaded to NCIDD if required

Result 2MX

NCIDD upload line if required (intel or mix)

Matches to ref reported if required

Profile review

2p with > 4 peaks in minor including sub threshold/3p with 2 in minor and ref sample matches major

(check to see if ownership of item can be ascertained and condition if necessary) decon as 3p by HP2

Comparison to be made to ref sample in STRmix

PDA page 3p checked

STRmix file imported

Unknown persons assigned if any

Major loaded to NCIDD if required

Result 3MX

NCIDD upload line if required (intel or mix)

Matches to ref reported if required

Profile review

2p with > 4 peaks in minor including sub threshold and ref sample doesn't match major

Rework sample x 2 to calculate repro for number of contributors

Scientist assigns sample to themselves for future finalisation of case management

Put on STRmix list to have decon done by HP2 (decon as 2p)

When returns to PDA list

Unknown persons assigned

Minor loaded to NCIDD if required

Result 2MX

NCIDD upload line if required (intel or mix)

Profile review

Reference samples received after initial PDA (+Ref list)

See as for above with reference samples in case. Reworks must be considered at this stage if there is any doubt in the number of contributors. This removes the need to rework any samples at statement stage, which avoids the renegeing of results after being pursued to court by QPS.

kits

From: Kylie Rika <[REDACTED]>
 To: Alicia Quartermain <[REDACTED]> Anne Finch <[REDACTED]> Claire
 Gallagher <[REDACTED]> Deborah Nicoletti <[REDACTED]>
 Emma Caunt <[REDACTED]> Hannah Pattison <[REDACTED]> Ingrid
 Moeller <[REDACTED]> Jacqui Wilson <[REDACTED]> Josie Entwistle
 <[REDACTED]> Penelope Taylor <[REDACTED]>
 Cc: Justin Howes <[REDACTED]>
 Date: Mon, 28 May 2018 13:55:54 +1000

Hello

A few of you have asked me about the possibility of using a different kit.

A while ago, Justin put together an options paper outlining the options available to continue processing P3 samples a. er
 cessaon of P+ kit. This paper outlined the pros and cons of the different options and kits.

This paper was used to aid in discussions with QPS. QPS chose to use PP21 for P3 samples.

This would mean only one kit in use in the laboratory which is not ideal.

Since then mgmt. have been considering another kit in addition to PP21. There are many options, however it is preferred
 to use an additional kit from a company that is not Promega (as we already have PP21).

A few kits have been considered. Beatrice from AB sent us some information on Verifiler Plus – as it has some promising
 features. They asked us if we could do some beta testing for them. For the reasons listed below, we said yes:

(from Beatrice)

So here's the new kit--Verifiler Plus has the following Key facts:

- 1) Loci match PP21 (list below): database built up can still be used, stats still valid
- 2) 17.5 uL DNA sample volume input for improved sensitivity instead of 15ul
- 3) 2 Internal Quality Control (IQC) markers to help assess DNA quality
- 4) Faster PCR protocol (approximately 80 min): quicker TAT
- 5) 11 mini-STR (<250bp): higher chance to recover reportable information
- 6) 500pg, 29 cycles: increased sensitivity avoiding stochastic effects
- 7) Improved 6-dye chemistry : reduced baseline noise
- 8) Database/ref kit (Verifiler Express) has been validated down to 10ul total volume : huge cost savings

Verifiler Express (database) and Plus (casework) was specifically launched with the Pentas. VFP does not contain SE33.

The yellow dye has changed for this kit. Previously, we've changed the red channel to a less noisy dye (for Globalfiler)
 and on top of that, we've also changed NED to TED.

NED can be slightly noisy and have a lower relative intensity requiring potentially additional primers. TED is a better and
 cleaner dye. So with this change, we're hoping for a more balanced profile as well.

The main advantage to waiting to test other kits has been to be able to do an end to end beta testing (and also possibly
 validation – if it looks good) using our new thermal cyclers and 3500.

So the long and the short of it is that yes we will be having another kit validated – in terms of which one will be the routine
 kit and which one will be the back-up – not sure – depends on results as we need to use the best kit as our routine one.

Hope this information answers some questions some of you may have had.

thanks



Forensic & Scientific Services,
Health Support Queensland, Department of Health



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From: [Luke Ryan](#)
To: [Sharon Johnstone](#); [Paula Brisotto](#)
Subject: FW: Last 5 kits of Profiler Plus on the planet
Date: Wednesday, 6 July 2022 10:54:38 AM

Morning Sharon and Paula

This was the last order for P+ - we received the final 5 P+ kits manufactured. When our stocks were exhausted there were no more P+ kits globally.

We did enough stock (in addition to the 5 kits) to continue P+ processing until Jan 2018.

Thanks
Luke

From: Goh, Beatrice [REDACTED]
Sent: Monday, 17 July 2017 10:14 PM
To: Luke Ryan [REDACTED]
Subject: Last 5 kits of Profiler Plus on the planet

Hi Luke,

Good news of a sort.

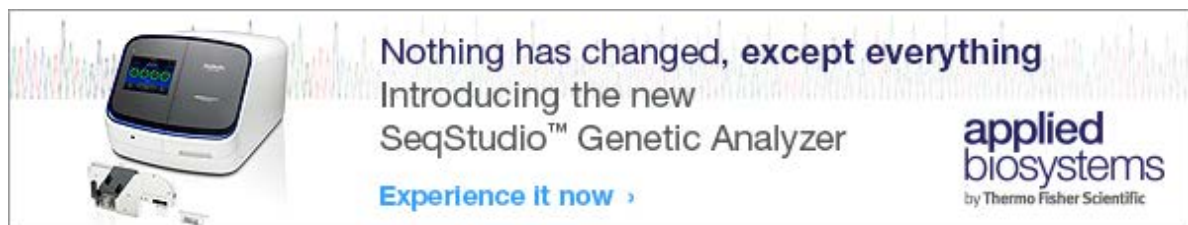
I have 5 x [REDACTED] in transit to AU01, this will arrive in AU this week.

The lot is [REDACTED], expiration date 22nd Jan2018.

Please let me know when you get a PO# and we can get them to you.

Thank you,
Bea

Beatrice Goh, PhD
HID Field Application Specialist Australasia
Account Lead - Queensland
Genetic Sciences Division



Nothing has changed, except everything
Introducing the new
SeqStudio™ Genetic Analyzer
Experience it now ›

applied
biosystems
by Thermo Fisher Scientific

The advertisement features a white SeqStudio Genetic Analyzer with a blue screen and a sample tray. The background is a light blue grid with a DNA sequence visualization. The text is in a clean, sans-serif font.

From: Neville.DavidH[OSC]
Sent: Thu, 16 Aug 2018 16:22:06 +1000
To: Neville.DavidH[OSC]
Subject: Elimination of auto-microcon step

Hi Cathie and Justin,

I was just reading the report that you both authored titled "A review of the automatic concentration of DNA extracts using Microcon Centrifugal Filer Devices: Options for QPS consideration".

Can I start with telling you how pleasing this report was. This is a great example of how LEAN philosophy can be applied within the laboratory setting. It seemed a great deal of effort for a measly 1.4% success rate.

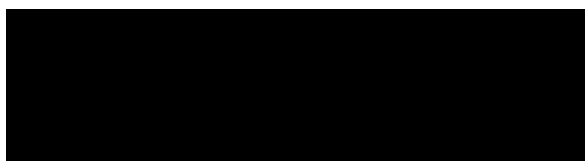
I understand that the QPS agreed to eliminate this step for priority 2 cases based on the advice. The paper indicated that this initiative will allow you to "...potentially reallocate staff time currently allocated to processing, interpreting and reporting 'auto-microcon' samples, to samples with higher DNA yield, thus improving the turnaround times for results of these samples." This would be a great outcome. Can I ask how this is progressing and if you are seeing the desired outcome, please?

The report also indicates a cost saving in the analysis. Are you able to give an indication of the actual saving please?

Again, this is a very good example of a QH initiative that if successful, helps us disrupt crime. So thank you both for initiating it and I look forward to hearing about its success.



David Neville
Inspector
DNA Management Unit | Forensic Services Group
Operations Support Command
QUEENSLAND POLICE SERVICE



STATEMENT OF ROBERT GRAHAM

I, Robert Graham, **Acting CFO Metro South Health, of Garden City Office Park Building 5 Level 1, 2404 Logan Road, Eight Mile Plains, QLD 4113**, do solemnly and sincerely declare that:

Background

Question 1 – List your qualifications. In your answer include the institution you obtained the qualification from and the year you obtained it.

1. **Bachelor of Accounting, Central Queensland University, 2008**

Question 2 – In brief, describe your work history. Attach a current CV.

2. **Two decades of business-facing management experience. Worked in various commercial roles in private and public healthcare and private practice, during which time involved in the support and enabling of business.**

No current CV available.

Question 3 – Identify your current position/role.

3. **Acting Chief Financial Officer, Metro South Health (Leave relief to 7/10/22)**

Question 4 – Describe any experience with forensic DNA testing or analysis prior to working as General Manager, Strategy, Community and Scientific Support.

4. **No prior experience with forensic DNA testing or analysis.**

Your role

Question 5 – Describe the position of General Manager, Strategy, Community and Scientific Support (General Manager), which you held for a period in about 2018. Include in your answer the responsibilities/duties of that position, who you reported, the units/departments which you had oversight of, and who reported to you.

Robert Graham

Louise Graham

5. **Lead and manage Strategy, Governance, the Health Contact Centre, Forensic and Scientific Support Services, Customer Experience, Communications, Engagement and Web service lines.**
6. **Lead the development and implementation of strategic and operational planning.**
7. **Lead and manage the effective governance and alignment of audit and risk, planning, legal coordination and other strategic initiatives.**

Question 6 – Include in your answer the date you commenced and the date you ceased working as General Manager.

8. **05/03/2018 to 04/05/2018 (10 weeks)**

Question 7 – As part of your onboarding/induction, what issues with respect to the DNA Laboratory were brought to your attention (if any)?

9. **No issues with respect to the DNA Laboratory were brought to my attention.**

Question 8 – Explain what type of contact and oversight of the DNA Laboratory you had. As part of your answer, identify:

- a. who you typically had contact with that worked in the DNA Laboratory;
10. **Paul Csoban, Executive Director, Forensic and Scientific Services QLD**
- b. what issues in the DNA laboratory were raised with you or you were aware of; and
11. **No issues in the DNA laboratory were raised with myself.**
- c. any actions taken to address those issues.
12. **Not applicable, per above.**

Question 9 – Who was the Executive Director at Forensic and Scientific Services (FSS) when you worked as General Manager?

13. **Paul Csoban**

The Options Paper

Question 10 – In about January 2018, a document titled A review of the automatic concentration of DNA extracts using Microcon Centrifugal Filter Devices: Options for QPS consideration (Options Paper) was presented to the Queensland Police Service (QPS). Attached is a copy of the Options Paper.

- a. What knowledge of the Options Paper did you have prior to its presentation to QPS in January 2018?
- 14. **No knowledge of the Option Paper, noting January 2018 was prior to my tenure.**
- b. Did you have any involvement in the decision to present the Options Paper to QPS?
- 15. **No I did not.**
- c. If you were not involved with the Options Paper, were you briefed about the paper or any changes in processes related to the paper when you commenced or worked as General Manager.
- 16. **No I was not.**

Question 11 – In your opinion:

- a. Should the Options Paper have been brought to the attention of the General Manager by staff at the DNA laboratory or the Executive Director of Forensic and Scientific Services? Why/why not?
- 17. **If it involved communication with external parties, changing service provision and or agreements/financial arrangements then yes the General Manager should be briefed in written form. Once briefed the matter is passed onto the Office of the Chief Executive for consideration.**
- b. If yes, should the decision to accept the recommendation in the Options Paper have been made by the General Manager, or should the General Manager at least have been involved in the making of such a decision? Why/why not?
- c. **The General Manager should be involved in matters leading to recommendation but is not the decision maker. They would seek endorsement from the delegate as set out in OH's Delegations Framework.**

Robert Graham

Louise Graham

18. Involved in the

- d. As part of your answers to (a) and (b), identify any policies, procedures, framework or committee terms of reference at Queensland Health that stipulated whether such matters and decisions should have been brought to the General Manager's attention or attention of some similar management position.

19. **No information available.**

Question 12 – If the Options Paper had been brought to the General Manager's attention, is it something that the General Manager would have raised with another person in Queensland Health that sits higher in the management hierarchy than the General Manager? Why or why not?

- a. If yes, identify who it should have been raised with, and in what way.

20. **Yes, the paper should be tabled and briefed for Chief Executive consideration.**

- b. As part of your answer, identify any policies, procedures, framework or committee terms of reference at Queensland Health that stipulated what level of management should have been made aware of the Options Paper/the decision it entailed.

21. **No information available.**

Question 13 – Attach to your statement any documents you identify in responding to question 11 (c) and 12(b), above. Attach the versions that were in place when you commenced as General Manager.

22. **Not applicable.**

Question 14 – If not already discussed in response to one of the above items, explain the role and function of the executive management committees in Queensland Health (such as the Safety and Risk Committee).

23. **The purpose of the executive committees are to advise and make recommendations to the Chief Executive about matters, within the scope of HSQ's functions.**

- a. If not already attached in response to item 13, attach the Terms of Reference of the Resource Committee, Strategic Governance Committee and Safety and Risk Committee (or similar). Attach the versions that were in place when you commenced as General Manager.

24. **I have no access to Executive Committee Term of Reference documents.**

Question 15 – Having read the Options Paper, what additional information would you require if you were the decision-maker and why?

25. **Needs analysis, risk assessment, project proposal, detailed costings, and brief seeking endorsement for the “Delegate” to exercise an appropriate delegation.**

Question 16 – What would you have expected the QPS to do, research or check once they were presented with the Options Paper? Why would you have expected that?

26. **I am unaware of QPS’s decision framework so cannot make comment on what would be expected.**

Question 17 – To your knowledge, at any point after the recommendation in the Options Paper was accepted and while you were General Manager, were any concerns raised by scientists at FSS about the changes brought about by the Options Paper? If so, explain these in detail.

27. **Not at any point in my tenure was I aware of the Options Paper or subsequent issues resulting from its recommendations.**

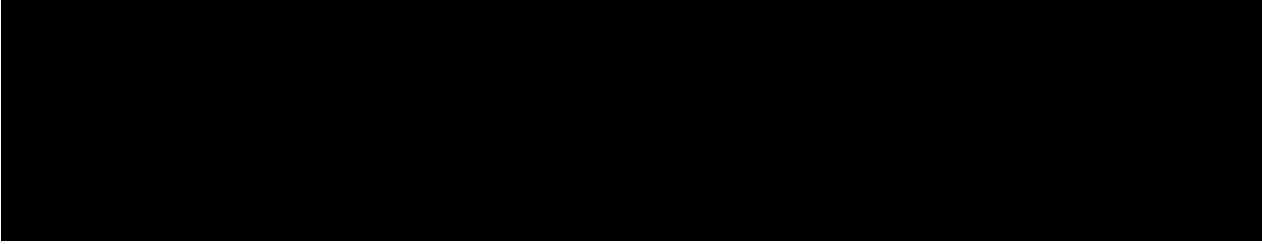
All the facts and circumstances declared in my statement, are within my own knowledge and belief, except for the facts and circumstances declared from information only, and where applicable, my means of knowledge and sources of information are contained in this statement.

I make this solemn declaration conscientiously believing the same to be true and by virtue of the provisions of the *Oaths Act 1867*.

Robert Graham

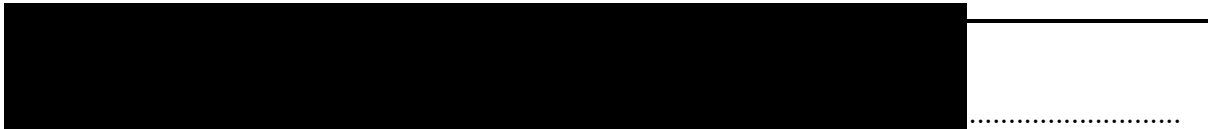
Louise Graham

TAKEN AND DECLARED before me at Mount Coolum in the State of Queensland this 16th day of September 2022



Robert Graham

Louise Graham



Robert Graham

Louise Graham