

For the data returned in response to Requirement 132, items 11, 12, 14, 15, an explanation of:

- a) **How a sample was included in the categories: blood, semen, saliva. For example, is it determined by a QPS or QHFSS administered presumptive test or by QPS attribution or all of the above or by some other means.**

The extract from bnda has the following criteria for blood:

- ExhibitBlood - either, Exhibit Category Swab Blood, Exhibit Description contains 'blood/combur/tmb', Exhibit Details ticked for Combur/TMB/HemaTrace
- These listed categories and/or descriptions are determined and entered by the QPS.

The extract from bdna has the following criteria for semen:

- ExhibitSemen - either, Exhibit Category SAIK/Condom, Exhibit Description contains 'semen/seminal fluid', Exhibit Details ticked for AP+ve/P30+ve
- These listed categories and/or descriptions are determined and entered by the QPS

The extract from bdna has the following criteria for saliva:

- ExhibitSaliva - either, Exhibit Category Swab Saliva, Exhibit Description contains 'saliva/sucking/bite/spit'
- These listed categories and/or descriptions are determined and entered by the QPS

The extract from bdna has the following criteria for saliva:

- ExhibitHighVaginalSwab - either, Exhibit Description contains 'high vaginal/hvs'
- This exhibit description is determined by Forensic DNA Analysis based on the physical labelling of the swab by the collecting doctor/nurse.

- b) **Whether a sample included in the category 'high vaginal swab' were limited to the male fraction only or included samples from both a male and female fraction.**

This data would include both spermatozoa and epithelial fractions which with "Exhibit Description contains 'high vaginal/hvs'" as per the bdna exhibit category breakdown. Please note, spermatozoa fractions are routinely submitted for DNA profiling, however epithelial fraction testing is sample specific (as determined using criteria including case circumstances and swab location). This means that not all epithelial fractions proceed beyond DNA extraction.

- c) **Whether a sample included in the category 'Uploaded to NCIDD' included only single source profiles, or also the major contributor of a mixture, or also more than one profile from a mixture.**

The samples included in the category 'Uploaded to NCIDD' would include all sample types with "final result lines that have NCIDD involvement" as per the bdna data extract. This would include single source profiles as well as one or more deconvoluted contributors to a mixed DNA profile.