Professor Linzi Wilson-Wilde OAM PhD

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REPORT

Report to: Walter Sofronoff KC, Commissioner Commissioner of Inquiry into Forensic DNA Testing in Queensland Report Date: 24 November 2022 This report has been requested by the Commission of Inquiry into Forensic DNA **Request:** Testing in Queensland. The instructions to the expert provided by the Commission of Inquiry can be found at Appendix 1. The main purpose of this report is to comment on whether the DNA analysis and profile generation success rates obtained by Queensland Health Forensic Science Services (QHFSS) is within the range of what would be expected for a laboratory in Australia. Information The index of information provided and considered as part of the development of **Reviewed:** this report can be found at Appendix 2. Qualifications I commenced my career at Victoria Police in 1996 as a forensic biologist, attending crime scenes, with expertise in biological fluid identification and DNA analysis. In 2000 I joined New South Wales Police as a Forensic DNA Specialist working on legislative reform, policy development, the investigation of highprofile murder cases, cold case reviews and the highly publicised mass DNA screen in the town of Wee Waa, NSW. After moving to the Australian Federal Police (AFP) in 2002 as Team Leader of the Biology Team, I coordinated the DNA analysis of all samples involved in the disaster victim identification and criminal investigation of the Bali Bombing in October 2002 and advised on the associated legislative change. Whilst at the AFP I commenced my PhD at the University of Canberra in species identification of Diprotodontia for wildlife crime investigations, which I completed in 2011. I joined the National Institute of Forensic Science (NIFS) in 2008 and succeeded to Director NIFS in 2015. I am the Chair of Standards Australia committee CH041 and ISO committee TC272 – Forensic Sciences, developing forensic specific Australian and international Standards respectively. I am the current President of the International Forensic Strategic Alliance and represent them on the International Criminal Court Office of the Prosecutor Scientific Advisory Board. I am currently the Director of Forensic Science SA. My Curriculum Vitae has been previously provided to the Commission.

Comments and Opinions

Issue whether the data is within the range of what you might expect for a laboratory in Australia, or outside that range?

Introduction

- 1. DNA analysis success rates can be important to examine whether there are any issues with any aspect of the DNA analysis process.
- 2. Of the items received by a laboratory, not all may be analysed. Items identified for analysis may be sampled for testing. Of those that commence the DNA analysis process, not all samples may go through to DNA profile generation and interpretation. There are numerous reasons for this including the ability to obtain a result from the sample, the probative value of the sample, or laboratory processing thresholds aimed at managing the workflow and resources.
- 3. The success rate of the DNA analysis process refers to the ability to progress a sample through the DNA analysis process from DNA extraction, quantitation, amplification, and interpretation.
- 4. The percentage of samples that progress through each of the DNA analysis stages may be used to infer if the methodology is operating appropriately within expected ranges.
- 5. However, the success rate is a factor of policy thresholds aimed at managing workflows. For example, if the threshold after quantitation is set high (i.e. a high amount of DNA is required for progression to amplification) then it would be expected that the success rate of the amplification will also be high, as there is a greater quantity of DNA to target for amplification. Conversely, if the threshold after quantitation is set low, it would be expected that more samples will not result in a DNA profile as there is less DNA to target for amplification and so the success rate will decrease.
- 6. Care should be taken when comparing success rates between laboratories and to published literature, as sampling protocols, analysis criteria and thresholds, differences in DNA analysis methodology (including different sensitivity of various DNA amplification kits), training etc will impact on the ability of a laboratory to generate a DNA profile.

Success rates analysis

- Three spreadsheets, regarding four sets of data containing the number of samples that progressed through various stages of the DNA analysis process were reviewed. These datasets were:
 - Item 11 samples relating to those categorised as no DNA detected (NDNAD) after quantitation
 - Item 12 samples relating to those categorised as DNA insufficient for further processing (DIFP) after quantitation
 - Item 14 all samples received
 - Item 15 samples relating to biological material types: blood, semen, saliva and high vaginal swabs (HVS).
- 8. A summary of the analysis of each of the sets of data can be found in Appendix 3. Whilst NCIDD upload rates have been included in the summary analysis, commentary in this report relates to profile generation, as this represents the greatest potential value for a case investigation.
- 9. It should be noted that the details behind the numbers of samples progressing through each of the DNA analysis stages was difficult to determine from the information provided. The document listed as 4.9 in Appendix 2, contained a list of search criteria for samples that produced a DNA profile that can be used for comparison to a reference sample. The list was extensive, and it is not clear whether only one criterion from the list was chosen per sample, as

some criteria could apply to the same sample (such as "Mixed DNA profile. Major component" and "Mixed DNA profile. Minor Component"). Therefore, I note that I have interpreted the numbers provided as per sample numbers.

- The spreadsheet labelled item 14 provides a breakdown of all samples categorised by priority (1-3, 1 being high priority and 3 low priority) that progressed through the DNA analysis process by:
 - samples received,
 - cases received,
 - cases sampled,
 - samples tested,
 - samples contaminated by a Queensland Police Officer (QPOL) officer
 - samples that produced a profile, and
 - samples uploaded to the National Criminal Investigation DNA Database (NCIDD).
- 11. The results indicate that more serious cases (priority 1 and 2) have a higher success rate than volume cases (priority 3). These results are not surprising. This is because generally you would expect to receive a higher percentage of trace DNA samples associated with volume crime, which generally have a lower success rate than biological samples such as blood and semen.
- 12. It should be noted that it is not unexpected that in some instances contamination of samples may occur from first responders and police. Appendix 3f indicates the percentage of total samples tested that had a contamination event sourced to a police officer. The percentage as a total number of events was very low, ranging from 0.09%-0.21%. Pickrahn *et al.* 2017 found a police contamination rate of 0.75% over a 17-year period (2000-2016) in Austria (see reference 5.1 listed in Appendix 2), and Basset and Castella 2018 and Neuhuber *et al.* 2017 (see reference 5.2 and 5.3 listed in Appendix 2) found 709 contamination events over a four-year period, however this included police and laboratory agencies. Therefore, the results found in Queensland could be considered within an acceptable range.
- 13. When contaminated events are found, regardless of the origin, it is important that appropriate awareness raising protocols, with the person to whom the contamination originated from, are in place, which should be coupled to a retraining/additional program if required.
- 14. The spreadsheet labelled item 15 provides a breakdown of sample numbers for blood, semen, saliva and HVS samples that progressed through the DNA analysis process by:
 - samples received,
 - samples tested,
 - samples that produced a profile, and
 - samples uploaded to NCIDD.
- 15. There is a small fluctuation in success rates for the sample types, however overall, the percentage of profiles tested that produce a DNA profile are: blood 82% (n 19487), semen 81% (n 3743), saliva 67% (n 10001), HVS 74% (n 1829). These are within an expected range for these sample types, considering the quantitation threshold applied. In comparison, according to a study by Einot *et al.* 2017 (see reference 5.4 listed in Appendix 2), biological fluids had a success rate of 80%, clothing 48% and trace samples 17%.
- 16. The spreadsheet labelled item 12 provides a breakdown of samples that had been categorised as DIFP that had been progressed through DNA amplification and interpretation. For the biological material type breakdown, the numbers were too small by year to infer any meaningful interpretation regarding the success rates, therefore the total figures were reviewed by year and as a whole for each biological material type.

- 17. It is noted that a small percentage of DIFP samples progressed through to amplification (10-16%) and of these relatively good success rates were obtained (55-67%). The success rate of these low quantitation value samples is dependent on the biological material, as can be seen in the breakdown by biological material type. All semen samples progressed gave a DNA profile. Blood and HVS samples gave a DNA profile in 40% and 59% of samples respectively, whilst only 15% of saliva samples produced a DNA profile. This highlights the need for scientist discretion when determining whether a sample should proceed through to DNA analysis. These results are in the expected range for these sample types, considering the quantitation threshold applied.
- 18. The spreadsheet labelled item 11 provides a breakdown of samples that had been categorised as NDNAD that had been progressed through DNA amplification and interpretation. Looking at the overall figures by year, it is noted that the number of samples categorised as NDNAD that progress through to DNA analysis has reduced, whilst the success rate of those samples in producing a DNA profile has increased. This is expected. If samples are targeted for processing based of the ability to obtain a DNA profile (for example based on biological material type), it is expected that better results would be obtained than processing all samples.
- 19. It is assumed that the unlabelled samples (see end of relevant table in Appendix 3) represent all samples categorised as NDNAD and which were progressed through to DNA amplification. This represents 13% of total samples, of which 63% returned a DNA profile. These figures are higher than expected for this sample type, the cause of which cannot be deduced from the information provided.
- 20. Overall, the success rate figures could be considered within the scope expected by a forensic DNA laboratory. However, it should be noted that the thresholds used at various stages within the DNA analysis process will affect this.



Appendix 1 – Instructions to expert

Instructions to expert

19 November 2022

Professor Linzi Wilson-Wilde OAM

Overview of engagement

Professor Linzi Wilson-Wilde is engaged to review data and comment on whether the DNA analysis and profile generation success rates obtained by Queensland Health Forensic Science Services (QHFSS) is within the range of what would be expected for a laboratory in Australia.

Material provided

The Commission requested a number of categories of data from Queensland Health which have been provided in spreadsheets. The following data sets are provided in those spreadsheets:

- 1. samples relating to those categorised as no DNA detected after quantitation (item 11)
- 2. samples relating to those categorised as DNA insufficient for further processing after quantitation (item 12)
- 3. all samples received (item 14)
- 4. samples relating to biological material types: blood, semen, saliva and high vaginal swabs (item 15)

Instructions

Professor Linzi Wilson-Wilde is to advise the Commission:

- 1. whether that data is within the range of what you might expect for a laboratory in Australia, or outside that range;
- 2. if outside the range, what might be the cause of that difference, if it is possible to tell; and
- 3. if outside that range what should be done to identify if the data is representative of a problem in the laboratory.

No.	Document
1.	Letter to Expert
1.1	Email instructions to Linzi Wilson-Wilde
2.	Terms of Reference
2.1	Terms of Reference – Commission of Inquiry into DNA Testing in Queensland
4.	Data and Information
4.1	Explanation of data in Items 11, 12, 14 and 15
4.2	Updated explanation of data in Items 11, 12, 14 and 15
4.3	Explanation of data for Items 11 and 12 (No DNA and DIFP)
4.4	Spreadsheet- Items 11 and 12 (No DNA and DIFP)
4.5	Spreadsheet - Item 14 – data (all samples)
4.6	Item 14 – email information
4.7	Spreadsheet - Item 15 Original Data provided by QH
4.8	Spreadsheet - Item 15 QH Data annotated by COI
4.9	List of result lines included in data for "produced a DNA profile that can be used for
	comparison to a reference sample"
5.	References
5.1	Pickrahn, I., Kreindl, G., Müller, E., Dunkelmann, B., Zahrer, W., Cemper-Kiesslich, J. and Neuhuber, F., 2017. Contamination incidents in the pre-analytical phase of forensic DNA analysis in Austria—Statistics of 17 years. Forensic Science International: Genetics, 31, pp.12-18.
5.2	Basset, P. and Castella, V., 2019. Positive impact of DNA contamination minimization procedures taken within the laboratory. Forensic Science International: Genetics, 38, pp.232-235.
5.3	Neuhuber, F., Kreindl, G., Kastinger, T., Dunkelmann, B., Zahrer, W., Cemper-Kiesslich, J. and Grießner, I., 2017. Police officer's DNA on crime scene samples–indirect transfer as a source of contamination and its database-assisted detection in Austria. Forensic Science International: Genetics Supplement Series, 6, pp.e608-e609.
5.4	Einot, N., Shpitzen, M., Voskoboinik, L., Roth, J., Feine, I. and Gafny, R., 2017. Reducing the workload: analysis of DNA profiling efficiency of case work items. Forensic Science Policy & Management: An International Journal, 8(1-2), pp.13-21.

Appendix 2 – Index of information provided and considered

Appendix 3 – Summarised Data tables

Appendix 3a – Item 11 – No DNA Detected (NDNAD) results – by year

	Exhibit_ND NAD_Coun t Total	Exhibit_ND NAD_Coun t_FurtherP rocessing	% of total samples processed	Count_Sam pleProfiled _withSubs amples	% of processed samples that gave a profile	Count_Sam pleProfile UploadedT oNCIDD_wi thSubsamp les	% of samples processed that were uploaded to NCIDD
2018	3235	575	18%	316	55%	30	5%
2019	3067	401	13%	245	61%	27	7%
2020	2837	524	18%	303	58%	31	6%
2021	2401	205	9%	160	78%	24	12%
2022	2477	133	5%	129	97%	18	14%

Count SamplePr Exhibit_NDNAD Count_SamplePro ofileUploadedT Exhibit_NDNAD _Count_Further filed_withSubsam oNCIDD_withSu Fina ialYear FinancialHalf SampleCategory _Count_Total Processing ples bsample 1 Blood 2018 Half_1 104 Half 2 144 2018 1 Blood 2019 Half_1 1_Blood 161 9 1 2019 Half_2 1_Blood 115 4 2020 Half_1 1_Blood 126 2 2 2020 Half 2 1 Blood 128 8 4 2021 Half 1 1 Blood 79 2021 Half_2 1_Blood 132 14 2022 Half_1 1_Blood 119 6 2022 Half_2 1_Blood 131 1 1239 53 10 19% 4% 0% % samples % samples % samples tested tested uploaded received that gave profile to NCIDD processed 2018 Half_1 2_Semen 5 2 2018 Half_2 2_Semen 5 4 2019 Half_1 2_Semen 10 2019 Half 2 2_Semen 2 2 2020 Half 1 2 Semen 14 11 1 2020 Half_2 2 Semen 3 3 2021 Half_1 2_Semen 3 2021 Half 2 2_Semen 4 2 2 Half_1 Half_2 2022 2 Semen 1 1 2022 2 Semen 17 1 3 64 34 53% 26% 6% % samples % samples . received % samples tested tested uploaded that gave profile to NCIDD processed 2018 Half_1 3_Saliva 59 8 2018 Half 2 3_Saliva 107 6 2019 Half_1 3 Saliva 72 4 Half 2 2019 3 Saliva 82 3 Half_1 3_Saliva 2020 83 4 2020 Half_2 3_Saliva 68 2021 Half 1 3_Saliva 63 4 2021 Half 2 3 Saliva 70 5 2022 Half 1 3 Saliva 70 6 2022 Half_2 3_Saliva 78 3 752 46 6% % samples received processed 2018 Half_1 4_HighVaginalSwab 5 2018 Half_2 4_HighVaginalSwab 2 2 2019 Half 1 4_HighVaginalSwab 3 3 Half 2 2019 4 HighVaginalSwab 3 2 Half_1 2020 4_HighVaginalSwab 2 2 2020 Half_2 4_HighVaginalSwab 2 2 2021 Half 1 4_HighVaginalSwab 7 5 1 Half_1 4_HighVaginalSwab 2022 4 1 1 2022 Half_2 4_HighVaginalSwab 1 1 22 29 76% 27% % samples received % samples tested that gave profile process 2018 Half_1 1246 324 138 14 2018 Half_2 1989 251 178 16 2019 Half 1 1520 199 119 13 2019 Half 2 1547 202 126 14 14 17 Half 1 1288 141 2020 219 2020 Half_2 1549 305 162 2021 Half_1 1150 160 120 16 2021 Half 2 1251 45 40 2022 Half 1 1279 83 103 12 2022 Half_2 1198 50 26 14017 1838 1153 130 13% 63% 7% % samples % samples . received % samples tested tested uploaded processed that gave profile to NCIDD

Appendix 3b - Item 11 - No DNA Detected (NDNAD) results - by biological material type

	Exhibit_DIF P_Count_T otal	Exhibit_DIF P_Count_F urtherProc essing	% samples processed	Count_Sam pleProfiled _withSubs amples	% samples processed that gave profiles	Count_Sam pleProfile UploadedT oNCIDD_wi thSubsamp les	% samples processed uploaded to NCIDD
2018	2426	247	10%	154	62%	17	7%
2019	4294	546	13%	307	56%	28	5%
2020	4277	658	15%	392	60%	41	6%
2021	3647	478	13%	318	67%	52	11%
2022	3727	593	16%	327	55%	51	9%

Appendix 3c – Item 12 – DNA Insufficient for Further Processing (DIFP) results – by year

Appendix 3d – Item 12 – DNA Insufficient for Further Processing (DIFP) results – by biological material type

FinancialYear	FinancialHalf	SampleCategory	Exhibit_DIFP_C ount_Total	Exhibit_DIFP_ Count_Furthe rProcessing	Count_Sample Profiled_with Subsamples	Count_SampleP rofileUploaded ToNCIDD_withS ubsamples
2018	Half_1	1_Blood	6	1	•	•
2018	Half_2	1_Blood	119	15	8	1
2019	Half_1	1_Blood	143	9	3	1
2019	Half_2	1_Blood	75	8	4	1
2020	Half_1	1_Blood	91	5	3	
2020	Half_2	1_Blood	99	6	6	1
2021	Half_1	1_Blood	91	9	4	1
2021	Half_2	1_Blood	93	10	7	2
2022	Half_1	1_Blood	165	69	21	2
2022	Half_2	1_Blood	85	30	8	1
			967	162	64	10
				% samples received processed	40% % samples tested that gave profile	6% % samples tested uploaded to NCIDD
2018	Half_2	2_Semen	1			
2019	Half_1	2_Semen	4	3	3	
2019	Half_2	2_Semen	2	1	1	
2020	Half_1	2_Semen	3	3	1	
2020	Half_2	2_Semen	3	1	1	
2021	Half_1	2_Semen	3	2	3	
2021	Half_2	2_Semen	1	1		
2022	Half_1	2_Semen	2		2	
			19	11	11	0
				58% % samples received processed	100% % samples tested that gave profile	0% % samples tested uploaded to NCIDD
2018	Half_1	3_Saliva	4			
2018	Half_2	3_Saliva	161	10	1	1
2019	Half_1	3_Saliva	113	6		
2019	Half_2	3_Saliva	115	5	1	
2020	Half_1	3_Saliva	122	6	1	
2020	Half_2	3_Saliva	139	9		
2021	Half_1	3_Saliva	101	6		
2021	Half_2	3_Saliva	128	5		
2022	Half 1	3 Saliva	125	11	6	3
2022	Half 2	3 Saliva	87	3		
	_		1095	61	9	4
				6% % samples received processed	15% % samples tested that gave profile	7% % samples tested uploaded to NCIDD
2018	Half_2	4_HighVaginalSwab	20	11	5	
2019	Half_1	4_HighVaginalSwab	22	21	8	
2019	Half_2	4_HighVaginalSwab	29	26	9	2
2020	Half_1	4_HighVaginalSwab	28	25	9	1
2020	Half_2	4_HighVaginalSwab	20	18	8	
2021	Half_1	4_HighVaginalSwab	23	19	6	1
2021	Half_2	4_HighVaginalSwab	14	5	5	1
2022	Half_1	4_HighVaginalSwab	17	7	11	2
2022	Half_2	4_HighVaginalSwab	3	3	3	_
			176	135	64	7
				77% % samples received processed	47% % samples tested that gave profile	5% % samples tested uploaded to NCIDD
2018	Half_1		62	4	1	
2018	Half_2		2364	243	153	17
2019	Half_1		2187	299	135	14
2019	Half_2		2107	247	172	14
2020	Half_1		2081	336	194	21
2020	Half_2		2196	322	198	20
2021	Half_1		1795	311	208	38
2021	Half_2		1852	167	110	14
2022	Half_1		2062	302	175	28
2022	Half_2		1665	291	152	23
			18371	2522	1498	189
				14%	59%	7%
				% samples received processed	% samples tested that gave profile	% samples tested uploaded to NCIDD

										%
										samples
							% samples		%	received
						No.	received		samples	NDNAD
						NDNAD	NDNAD	No. DIFP	received	and DIFP
	Total	No.	% samples	No.	% samples	not	not	not	DIFP not	not
	samples	samples	received	samples	received	processed	processed	processed	processe	processe
Year	received	NDNAD	NDNAD	DIFP	DIFP	further	further	further	d further	d further
2018	25761	3235	12.6%	2426	9.4%	2660	10.3%	2179	8.5%	18.8%
2019	23852	3067	12.9%	4294	18.0%	2666	11.2%	3748	15.7%	26.9%
2020	25416	2837	11.2%	4277	16.8%	2313	9.1%	3619	14.2%	23.3%
2021	22702	2404	10.10/	2647	4 - 40/	24.00	0.20/	21.00	12 40/	22 60/
2021	. 23/02	2401	10.1%	3647	15.4%	2196	9.3%	3109	13.4%	22.0%

Appendix 3e – Item 11/12/14 – Samples by year NDNAD and FIFP not processed further

			% of samples tested		% of samples tested	
	Tested	Profile	that gave		to NCIDD	
2018	Testeu	Tionic	aprome			
1	279	112	40%	42	15%	
2	11281	6187	55%	2158	19%	
2	13783	5400	39%	4040	29%	
J Total	25343	11699	46%	6240	25%	
Total	25545	11055	-070	0240	2370	
2019						
1	214	106	50%	39	18%	
2	11776	6397	54%	2162	18%	
3	11608	4609	40%	3786	33%	
Total	23598	11112	47%	5987	25%	
2020						
1	99	66	67%	21	21%	
2	12339	7193	58%	2488	20%	
3	12687	5307	42%	4442	35%	
Total	25125	12566	50%	6951	28%	
2021						
1	98	52	53%	20	20%	
2	12715	7579	60%	2677	21%	
3	10725	4657	43%	3887	36%	
Total	23538	12288	52%	6584	28%	
2022						
1	154	99	64%	29	19%	
2	13415	8057	60%	2696	20%	
3	12703	5991	47%	4896	39%	
Total	26272	14147	54%	7621	29%	
Overall	123876	61812	50%	33383	54%	

Appendix 3f – Item 14 – All samples by priority by year

Year	No. samples QPS Contamination	Total samples tested	%police contamination of total samples tested
2018	52	25343	0.21%
2019	21	23598	0.09%
2020	32	25125	0.13%
2021	41	23538	0.17%
2022	27	26272	0.10%

Appendix 3g – Item 14 – All samples percentage police contamination events

						% of
				%		samples
				samples		tested
				tested		uploade
	Total			that gave		d to
	Count	Tested	Profiles	profiles	NCIDD	NCIDD
2018						
Blood	3754	3667	2968	80.94	1571	42.84
Semen	787	779	616	79.08	236	30.30
Saliva	2007	2001	1242	62.07	979	48.93
HVS	306	304	250	82.24	40	13.16
2019						
Blood	3863	3828	3089	80.69	1595	41.67
Semen	648	646	532	82.35	264	40.87
Saliva	1951	1949	1285	65.93	1041	53.41
HVS	332	329	268	81.46	60	18.24
2020						
Blood	3956	3892	3233	83.07	1679	43.14
Semen	713	712	586	82.30	281	39.47
Saliva	2117	2111	1396	66.13	1152	54.57
HVS	348	346	296	85.55	61	17.63
2021						
Blood	3953	3941	3382	85.82	1646	41.77
Semen	766	758	644	84.96	334	44.06
Saliva	1858	1858	1281	68.95	1053	56.67
HVS	356	355	250	70.42	67	18.87
2022						
Blood	4407	4159	3288	79.06	1535	36.91
Semen	885	848	668	78.77	340	40.09
Saliva	2148	2082	1502	72.14	1253	60.18
HVS	498	495	298	60.20	54	10.91

Appendix 3h – Item 15 –Samples by biological material type by year

FinancialY	Financial		Count_Tot	Count_Exh	Count_Sam	Count_Sam pleProfiled _withSubsa	% samples tested that gave	Count_Sam pleProfile UploadedT oNCIDD_wi thSubsamp	%samples tested uploaded
ear	Half	SampleCategory	al	ibitBlood	plesTested	mples	profile	les	to NCIDD
2018	Half_1	1_Blood	1930	1930	1843	1521		814	
2018	Half_2	1_Blood	1824	1824	1824	1447		757	
2019	Half_1	1_Blood	2068	2068	2057	1595		/68	
2019	Half_2	1_Blood	1/95	1/95	1//1	1494		827	
2020	Half_1	1_BIOOD	1930	1930	18/1	1557		821	
2020	Half_2	1_Blood	2026	2026	2021	16/6		858	
2021	Half_1	1_Blood	2041	2041	2036	1/69		894	
2021	Half_2	1_Blood	1912	1912	1905	1613		752	
2022	Half_1	1_Blood	2218	2218	2186	1///		/84	
2022	Half_2	1_BIOOD	2189	2189	1973	1511	0.20/	/51	410/
			19933	19933	19487	12900	82%	8026	41%
2018	Half_1	2_Semen	371	0	364	273		114	
2018	Half_2	2_Semen	416	0	415	343		122	
2019	Half_1	2_Semen	341	0	339	272		129	
2019	Half_2	2_Semen	307	0	307	260		135	
2020	Half_1	2_Semen	342	0	341	283		135	
2020	Half_2	2_Semen	371	0	371	303		146	
2021	Half_1	2_Semen	370	0	362	316		167	
2021	Half_2	2_Semen	396	0	396	328		167	
2022	Half_1	2_Semen	404	0	404	369		178	
2022	Half_2	2_Semen	481	0	444	299		162	
			3799	0	3743	3046	81%	1455	39%
2018	Half_1	3_Saliva	1055	0	1050	707		550	
2018	Half_2	3_Saliva	952	0	951	535		429	
2019	Half_1	3_Saliva	964	0	964	603		499	
2019	Half_2	3_Saliva	987	0	985	682		542	
2020	Half_1	3_Saliva	1025	0	1023	693		560	
2020	Half_2	3_Saliva	1092	0	1088	703		592	
2021	Half_1	3_Saliva	899	0	899	632		520	
2021	Half_2	3_Saliva	959	0	959	649		533	
2022	Half_1	3_Saliva	1034	0	1031	760		635	
2022	Half_2	3_Saliva	1114	0	1051	742	-	618	
			10081	0	10001	6706	67%	5478	55%
2018	Half 1	4 HighVaginalSwab	158	0	158	134		26	
2018	Half 2	4 HighVaginalSwab	148	0	146	116		14	
2019	Half_1	4_HighVaginalSwab	156	0	154	125		26	
2019	Half_2	4_HighVaginalSwab	176	0	175	143		34	
2020	Half_1	4_HighVaginalSwab	173	0	171	146		28	
2020	Half_2	4_HighVaginalSwab	175	0	175	150		33	
2021	Half_1	4_HighVaginalSwab	160	0	160	118		30	
2021	Half_2	4_HighVaginalSwab	196	0	195	132		37	
2022	Half_1	4_HighVaginalSwab	233	0	232	168		35	
2022	Half_2	4_HighVaginalSwab	265	0	263	130		19	
			1840	0	1829	1362	74%	282	15%
		Overall			35060	27074	77%	15241	56%

Appendix 3i – Item 15 –Samples by biological material type