TYPE OF REPORT	INVESTIGATING AGENT	CASE NUMBER	DATE
Initial	Assistant Director Kellon Hassenstab	IIA-23-05	February 26, 2024

Known Error Types in Woods' Case Work, as of February 6, 2024:

Observation	Outcome	Impact	Issue	# of cases
Reagent blanks (RBs) without a quant value, but 'cycle threshold value' (Ct) is present. Or the opposite, a Ct value is missing but the quant value is present.	RBs can occasionally have a quant/Ct value indicating possible contamination present within the DNA batch. If this occurs procedures outline the proper processes to evaluate the source of contamination thoroughly and to document the occurrence. In these instances no documentation is present showing any troubleshooting into why these values were missing, instead the values appear to be manually deleted.	RBs were run in accordance to the procedure in all but 1 of these batches in spite of deleted data. This could indicate the RBs were tampered with. Batch 17ymw1 was not run per policy, but the policy was changed 2 days later and appears to be as a result of this batch and explains this batch.	1- Data deleted 2- Possible RBs tampering	153
Altered reagent blank quant data. Data present on the instrument is different than what is present in the case-associated DNA batch notes.	Possible contamination was present within the DNA batch which was not evaluated. The value was manipulated by multiple orders of magnitude or to "undetermined". This misrepresented the amount of DNA present in the RBs (also seen via quant calculations).	RBs appear to be tampered with, either with a dilution of the RB or replacement with a new RB. Quant values were deliberately reduced in RB so troubleshooting would not appear to be necessary by a technical reviewer.	1- Deliberate data change 2- Tampered with RBs	443
Requanting of DNA batch data in instances where quant values were present in reagent blanks in the first quant, but are now gone in the second quant.	Possible contamination was present within the DNA batch which was not evaluated. This misrepresented the amount of DNA present in the samples. A second run is permitted, however, it needs to be documented, TL needs to be notified and troubleshooting needs	Entire run was rerun. First data was ignored and not included in cases. RBs in 2nd run show lower to no quant values. RBs appear to be tampered with, either with a dilution or replacement of the sample	1- Deliberately ignored entire run of data and did not record it in case record 2- Tampered with RBs	24

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	to occur prior to continuing on.			
Male quant target value is missing when a Male Ct value is present (which cannot occur) or vice versa in female reference samples and in evidence samples collected from female victims	Samples were all amped appropriately and there was not any risk to analysis in the cases. It is unknown why these values are missing as they would not be if one or the other was present per the manufacturer.	Cases worked as expected	1- Deleted data	4
Male quant target value is missing when a Male Ct value is present (which cannot occur) or vice versa in female reference samples and in evidence samples collected from female victims	Troubleshooting of female references were not performed per the guidance in place at the time.	Failed to follow procedure, procedure later changed to allow this action.	1- Deleted data	9
Male quant target value is missing when a Male Ct value is present (which cannot occur) or vice versa in female reference samples and in evidence samples collected from female victims	Evidence samples could have been analyzed in YSTR if suspect buccals were submitted since male DNA was present. DNA results were reported inaccurately stating no male DNA present when there was an uninterpretable amount.	Cases were worked as expected, but reported inaccurately stating no male DNA. Could do more work with suspect buccal in the future. Amended report is needed.	1- Deleted data 2- Incorrectly reported No Male DNA, more analysis could be done with a future submission of suspect buccals	8
Male quant target value is missing when a Male Ct value is present (which cannot occur) or vice versa in female reference samples and in evidence samples	Possible contamination in female victim hair control. Troubleshooting should have been performed, but was not. Sample had SA and male quant values, so should have	Case was not worked as expected. Samples should be amped.	1- Deleted data 2- Additional analysis should have been performed and was not	2

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collected from	been amped in arson			
female victims	case.			
Entire male quant target row missing (which cannot occur) from evidence samples and male references which includes the both the quant and Ct values	Samples should have been analyzed with YSTR analysis if applicable per case circumstances and if suspect buccals had been submitted.	Cases worked as expected	1- Deleted data 2-more analysis could be done with a future submission of suspect buccals	4
Small/large autosomal target quant values and Ct values missing in evidence samples (either quant values present and no Ct values or vice versa)	Samples were all amped appropriately and there was not any risk to analysis in the cases. It is unknown why these values are missing as they would not be if one or the other was present per the manufacturer.	Cases worked as expected	1- Deleted data	6
Small/large autosomal target quant values and Ct values missing in evidence samples (quant values present and no Ct values)	No DNA profile obtained from item after two extractions which is odd given the quant value. Additional troubleshooting was necessary, but was not performed.	Additional troubleshooting was need for this item	1- Deleted data 2-Additional analysis should have been performed and was not	1
Quant data fields being manually manipulated to different values or to "undetermined".	Appears analyst may have added notes regarding M:F ratio to the wrong field of quant data resulting in the quant large autosomal target being "ratio" in one instance. Primarily we are seeing quant values manipulated so that the values appear smaller. Also saw quant values manipulated so the values appeared higher so that the M:F	Case worked as expected	1- Altered data	126

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	ratio went higher and samples no longer needed to be amplified.			
Undocumented additional work (additional extractions without documentation)	It appears the analyst went back to items of evidence to repeat extractions without any documentation in the worksheet nor reasoning behind this. In multiple instances the item was consumed without permission or appeared to have another item extracted in its place.	Additional evidence was consumed and is not available for further testing. There is no documentation as to why, and permission to consume was not obtained.	1-Deliberately ignoring data from one extraction/quant/amp/CE and cutting additional sample with no documentation/permission	4
	784=	Total number of cases per issue. Some cases had multipl issues that were found, if a case had two issues it will be marked here as two separate entries.		
	656=	Total number of cases with an identified issue. Some cases had multiple issues that were found, if a case had two issues it will be marked in this total as one entry.		had
	227=	Number of independent intentional actions to manipulate 7= change or delete data.		ulate,