

Short Tandem Repeat

Form SOP-89.01 Version 9.0

Requestor: Marianne James, Boston University Samples Received: 25May23 STR Amplification Date: 31May23

Sample Name	ATTR3-3 P14
WiCell CTR No.1	97324
FGA	22.2, 23
TPOX	8, 8
D8S1179	13, 14
vWA	16, 17
Amelogenin	X, Y
Penta_D	9, 14
CSF1PO	11, 12
D16S539	9, 11
D7S820	10, 11
D13S317	11, 12
D5S818	10, 11
Penta_E	10, 12
D18S51	13, 16
D21S11	27, 30.2
TH01	7, 9.3
D3S1358	14, 17
Allelic Polymorphisms	29
Matches*	
Comments	

*Note: The STR profile of the following sample is a 100% match for the given sample/samples unless otherwise specified.

¹ CTR No.: Characterization Test Request Number; also known as a laboratory accessioning number.



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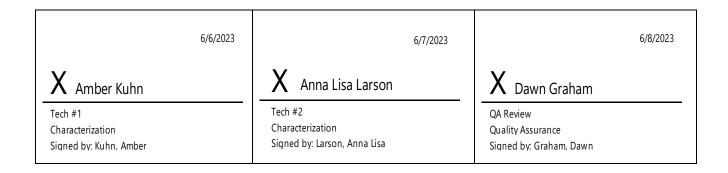
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<u>Assay Description:</u> STR analysis is performed using the PowerPlex 16 HS System by PromegaTM. Results are reported as 13 CODIS STR markers, Amelogenin for gender determination and two low-stutter, highly discriminating pentanucleotide STR markers.

Results: The genotypic profiles comprise a range of 29 allelic polymorphisms across the 15 STR loci analyzed.

<u>Interpretation:</u> The concentration of DNA required to achieve an acceptable STR genotype (signal/ noise) was equivalent to that required for the standard procedure (~1 ng/amplification reaction) from human genomic DNA. These results suggests that the cells submitted correspond to the cell lines as named and were not contaminated with any other human cells or a significant amount of mouse feeder layer cells.

<u>Sensitivity:</u> Sensitivity limits for detection of STR polymorphisms unique to either this or other human cell lines is ~2-4%.



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