



Short Tandem Repeat

Requestor: David Broderick, Boston University

Samples Received: 24Mar22

STR Amplification Date: 30Mar22

Form SOP-89.01

Version 8.0

Sample Name	BT1-1 P23
Label on tube	91262
FGA	22, 23
TPOX	8, 11
D8S1179	10, 13
vWA	14, 18
Amelogenin	X, X
Penta_D	9, 12
CSF1PO	11, 12
D16S539	11, 11
D7S820	11, 12
D13S317	8, 8
D5S818	10, 11
Penta_E	11, 14
D18S51	16, 17
D21S11	28, 29
TH01	8, 9
D3S1358	16, 18
Allelic Polymorphisms	28
Matches*	
Comments	

**Note: The STR profile of the following sample is an exact match for the given sample/samples.*



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Assay Description: STR analysis is performed using the PowerPlex 16 HS System by Promega™. 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 28 allelic polymorphisms across the 15 STR loci analyzed.

Interpretation: 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.

Sensitivity: Sensitivity limits for detection of STR polymorphisms unique to either this or other human cell lines is ~2-5%.

4/5/2022	4/5/2022	4/5/2022
X Molly Miles	X Amber Kuhn	X Dawn Graham
Tech #1 Characterization Signed by: Miles, Molly	Tech #2 Characterization Signed by: Kuhn, Amber	QA Review Quality Assurance Signed by: Graham, Dawn

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Raw data is available upon request.