Form SOP-89.01
Version 13.0

Short Tandem Repeat

Requestor: Rhiannon Darling, Boston University
Sample Receipt Date: 02May24
STR Amplification Date: 06May24

Sample Name	**PiZZ6S-3-M2 P33**
WiCell CTR No.[1]	102002
FGA	22, 26
TPOX	11, 11
D8S1179	14, 15
vWA	17, 19
Amelogenin	X, X
Penta_D	10, 12
CSF1PO	7, 12
D16S539	13, 14
D7S820	10, 11
D13S317	11, 12
D5S818	10, 13
Penta_E	13, 17
D18S51	14, 15
D21S11	29, 29
TH01	7, 8
D3S1358	15, 17
Allelic Polymorphisms	28
Matches[2]	80276
Comments	

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

[2] The STR profile of the sample(s) listed are a 100% match for the given sample unless otherwise specified.

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Assay Description: Short Tandem Repeat (STR) analysis is performed using the PowerPlex® 16 HS System by Promega™. Results are reported as 13 CODIS STR markers, Amelogenin for sex 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 suggest 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 ~2-4%.

5/9/2024	5/13/2024	5/13/2024
X Kaylie Petersen	X Michael Mussar	X Ryen Smith
Tech #1 Characterization Signed by: Petersen, Kaylie	Tech #2 Characterization Signed by: Mussar, Michael	QA Review Quality Assurance Signed by: Smith, Ryen