Short Tandem Repeat

Requestor: Rhiannon Darling, Boston University
Sample Receipt Date: 07Aug24
STR Amplification Date: 15Aug24

Sample Name	**BU3 NKX2.1 GFP P37**
WiCell CTR No.[1]	103368
FGA	20, 24
TPOX	11, 11
D8S1179	14, 14
vWA	16, 18
Amelogenin	X, Y
Penta_D	12, 12
CSF1PO	10, 11
D16S539	9, 13
D7S820	9, 11
D13S317	12, 12
D5S818	10, 11
Penta_E	12, 14
D18S51	15, 16
D21S11	29, 32
TH01	7, 9.3
D3S1358	14, 15
Allelic Polymorphisms	26
Matches[2]	See Results
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.

Form SOP-89.01
Version 13.0

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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 26 allelic polymorphisms across the 15 STR loci analyzed. Sample 103368 is a 100% match to 102698, 97328, 96370, 96367, 95034, 95033, 92643, 86268, 85081, 82830 and additional profiles. Additional matches can be provided upon request.

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%.

8/19/2024	8/19/2024	8/19/2024
X Amber Kuhn	X Kaylie Petersen	X Hunter Hefti
Tech #1 Characterization Signed by: Kuhn, Amber	Tech #2 Characterization Signed by: Petersen, Kaylie	QA Review Quality Assurance Signed by: Hefti, Hunter