



Short Tandem Repeat

Requestor: Rhiannon Darling, Boston University

Sample Receipt Date: 02May24

STR Amplification Date: 06May24

Form SOP-89.01

Version 13.0

Sample Name	bBU1-CDX2G P19
WiCell CTR No. ¹	102005
FGA	20, 24
TPOX	8, 8
D8S1179	12, 13
vWA	16, 17
Amelogenin	X, Y
Penta_D	13, 13
CSF1PO	10, 12
D16S539	11, 12
D7S820	8, 13
D13S317	8, 8
D5S818	11, 13
Penta_E	5, 14
D18S51	13, 13
D21S11	28, 32.2
TH01	7, 9.3
D3S1358	14, 17
Allelic Polymorphisms	26
Matches ²	82829, 91261, 96368, 99833
Comments	

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 26 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

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