

## 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. <sup>1</sup>	102005
FGA	20, 24
ΤΡΟΧ	8, 8
D8S1179	12, 13
vWA	16, 17
Amelogenin	Х, Ү
Penta_D	13, 13
CSF1PO	10, 12
D16S539	11, 12
D7\$820	8, 13
D13\$317	8, 8
D5\$818	11, 13
Penta_E	5, 14
D18S51	13, 13
D21S11	28, 32.2
TH01	7, 9.3
D3S1358	14, 17
Allelic Polymorphisms	26
Matches <sup>2</sup>	82829, 91261, 96368, 99833
Comments	

<sup>&</sup>lt;sup>1</sup> CTR No.: Characterization Test Request Number; also known as a laboratory accessioning number.

<sup>&</sup>lt;sup>2</sup> The STR profile of the sample(s) listed are a 100% match for the given sample unless otherwise specified.



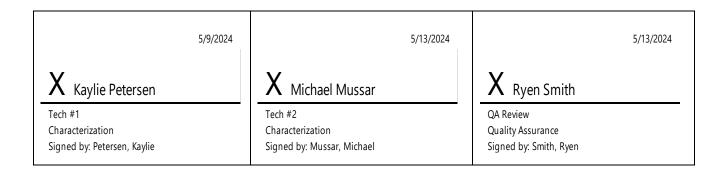
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<u>Assay Description</u>: Short Tandem Repeat (STR) analysis is performed using the PowerPlex<sup>®</sup> 16 HS System by Promega<sup>™</sup>. Results are reported as 13 CODIS STR markers, Amelogenin for sex determination and two low-stutter, highly discriminating pentanucleotide STR markers.

**<u>Results</u>**: 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%.



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