



Short Tandem Repeat

Requestor: Marianne James, Boston University

Samples Received: 22Mar23

STR Amplification Date: 27Mar23

Form SOP-89.01

Version 12.0

Sample Name	BU2 N1 P33
WiCell CTR No. ¹	96369
FGA	21, 22
TPOX	8, 8
D8S1179	14, 14
vWA	16, 19
Amelogenin	X, Y
Penta_D	12, 14
CSF1PO	12, 15
D16S539	12, 13
D7S820	10, 13
D13S317	11, 14
D5S818	11, 11
Penta_E	10, 12
D18S51	14, 14
D21S11	29, 30
TH01	7, 9.3
D3S1358	14, 14
Allelic Polymorphisms	25
Matches*	86270
Comments	

**Note: The STR profile of the following sample is a 100% match for the given sample/samples unless otherwise specified.*

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



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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 25 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 ~2-4%.

Amended Report: This report has been updated to create a separate report for sample 96369 at the request of the client on 25Mar24.

3/29/2024	3/29/2024	3/29/2024
<p>X Amber Kuhn</p> <hr/> <p>Tech #1 Characterization Signed by: Kuhn, Amber</p>	<p>X Anna Lisa Larson</p> <hr/> <p>Tech #2 Characterization Signed by: Larson, Anna Lisa</p>	<p>X Ryen Smith</p> <hr/> <p>QA Review Quality Assurance Signed by: Smith, Ryen</p>

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