



## Short Tandem Repeat

Requestor: Rhiannon Darling, Boston University

Sample Receipt Date: 06Feb25

STR Amplification Date: 10Feb25

Form SOP-89.01

Version 14.0

Sample Name	BU8- TetOn:NICD1 P32
WiCell CTR No. <sup>1</sup>	105798
FGA	20, 24
TPOX	9, 11
D8S1179	10, 10
vWA	15, 19
Amelogenin	X, X
Penta_D	9, 13
CSF1PO	10, 12
D16S539	11, 12
D7S820	8, 9
D13S317	11, 14
D5S818	12, 13
Penta_E	13, 16
D18S51	14, 16
D21S11	28, 30
TH01	7, 9.3
D3S1358	15, 17
Allelic Polymorphisms	29
Matches <sup>2</sup>	105800, 99832, 97325
Comments	

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

<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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**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 profile has 29 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%.

2/17/2025	2/17/2025	2/17/2025
<b>X</b> John Raff	<b>X</b> Amber Kuhn	<b>X</b> Dawn Graham
Tech #1 Characterization Signed by: Raff, John	Tech #2 Characterization Signed by: Kuhn, Amber	QA Review Quality Assurance Signed by: Graham, Dawn

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