



# Short Tandem Repeat

Requestor: Rhiannon Darling, Boston University

Sample Receipt Date: 07Aug24

STR Amplification Date: 15Aug24

Form SOP-89.01

Version 13.0

Sample Name	PiZZ1-1-Cr4-MM1 P61
WiCell CTR No. <sup>1</sup>	103369
FGA	21, 25
TPOX	8, 8
D8S1179	13, 13
vWA	15, 19
Amelogenin	X, Y
Penta_D	11, 13
CSF1PO	10, 12
D16S539	9, 10
D7S820	10, 10
D13S317	8, 13
D5S818	11, 11
Penta_E	10, 15
D18S51	14, 17
D21S11	30, 30
TH01	9, 9
D3S1358	14, 15
Allelic Polymorphisms	24
Matches <sup>2</sup>	80282
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 profiles comprise a range of 24 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%.

8/20/2024	8/20/2024	8/20/2024
<p><b>X</b> Amber Kuhn</p> <hr/> <p>Tech #1 Characterization Signed by: Kuhn, Amber</p>	<p><b>X</b> Kaylie Petersen</p> <hr/> <p>Tech #2 Characterization Signed by: Petersen, Kaylie</p>	<p><b>X</b> Ryen Smith</p> <hr/> <p>QA Review Quality Assurance Signed by: Smith, Ryen</p>

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