



Short Tandem Repeat

Requestor: Marianne James, Boston University

Samples Received: 07Dec22

STR Amplification Date: 12Dec22

Form SOP-89.01

Version 9.0

Sample Name	RC2 202-2Cr7 P22
WiCell CTR No. ¹	95035
FGA	22, 23
TPOX	8, 8
D8S1179	10, 11
vWA	14, 19
Amelogenin	X, Y
Penta_D	13, 13
CSF1PO	12, 14
D16S539	11, 13
D7S820	8, 9
D13S317	11, 14
D5S818	11, 12
Penta_E	12, 14
D18S51	14, 19
D21S11	28, 30.2
TH01	9.3, 9.3
D3S1358	15, 18
Allelic Polymorphisms	27
Matches*	95032
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 27 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 Comment, Client Request: This report has been updated to create individual report for sample 95035 at the request of the client on 20Jan23.

1/23/2023	1/24/2023	1/24/2023
<p>X Justin Hobson</p> <hr/> <p>Tech #1 Characterization Signed by: Hobson, Justin</p>	<p>X Amber Kuhn</p> <hr/> <p>Tech #2 Characterization Signed by: Kuhn, Amber</p>	<p>X Hunter Hefti</p> <hr/> <p>QA Review Quality Assurance Signed by: Hefti, Hunter</p>

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