

# Short Tandem Repeat Analysis

**Requestor:** WiCell Characterization

Boston University - Aine Russell

**Receive Date:** 02/10/20

**Report Sent:** 02/17/20

<b>Label on tube</b>	MA-012 p.0 D01 (80272)
<b>Label on Report</b>	MA-012 p.0 D01 (80272)
<b>conc (ng/μL)</b>	82.9
<b>A260/280</b>	1.68
<b>Assay Date</b>	2/11/2020
<b>File Name</b>	STR 200212 wmr
<b>FGA</b>	21,21
<b>TPOX</b>	8,11
<b>D8S1179</b>	11,13
<b>vWA</b>	18,18
<b>Amelogenin</b>	X,Y
<b>Penta_D</b>	9,14
<b>CSF1PO</b>	11,11
<b>D16S539</b>	9,12
<b>D7S820</b>	10,13
<b>D13S317</b>	11,12
<b>D5S818</b>	9,12
<b>Penta_E</b>	21,22
<b>D18S51</b>	15,15
<b>D21S11</b>	29,31
<b>TH01</b>	6,9
<b>D3S1358</b>	16,16
<b>Allelic Polymorphisms</b>	25
<b>Matches*</b>	
<b>Comments</b>	

## Short Tandem Repeat Analysis

**Results:** Based on the DNA submitted by WiCell Characterization Department for Boston University - Aine Russell dated and received on 02/10/20, these samples define the STR profiles of the human cell lines as indicated by name. The genotypic profiles comprise a range of 24-29 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 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 ~2-5%.

\* **Note:** The STR profile of the following sample is an exact match for the given sample/samples.

X *RMB*

Digitally Signed on 02/17/20

Rebecca M. Baus, BA

TRIP Laboratory, Molecular

X *WMR*

Digitally Signed on 02/17/20

William M. Rehrauer, PhD, Director / Co-Director

UWHC Molecular Diagnostics Laboratory / UW SMPH TRIP Laboratory

Testing was accomplished by analysis of human genetic polymorphisms at STR loci. This methodology has not yet been approved by the FDA and is for investigational use only.

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