



# Short Tandem Repeat

Requestor: Aine Russell, Boston University

Samples Received: 09Sep20

STR Amplification Date: 16Sep20

Form SOP-89.01

Version 1.0

<b>Sample Name</b>	bBU1C2
<b>Label on tube</b>	82829
<b>FGA</b>	20, 24
<b>TPOX</b>	8, 8
<b>D8S1179</b>	12, 13
<b>vWA</b>	16, 17
<b>Amelogenin</b>	X, Y
<b>Penta_D</b>	13, 13
<b>CSF1PO</b>	10, 12
<b>D16S539</b>	11, 12
<b>D7S820</b>	8, 13
<b>D13S317</b>	8, 8
<b>D5S818</b>	11, 13
<b>Penta_E</b>	5, 14
<b>D18S51</b>	13, 13
<b>D21S11</b>	28, 32.2
<b>TH01</b>	7, 9.3
<b>D3S1358</b>	14, 17
<b>Allelic Polymorphisms</b>	26
<b>Matches*</b>	
<b>Comments</b>	

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



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**Results**The genotypic profiles comprise a range of \_\_26\_\_ 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%.

X

Tech #1  
Characterization

X

Tech #2  
Characterization

X

QA Review  
Quality Assurance

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*Raw data is available upon request.*