## **Short Tandem Repeat**



Requestor: David Broderick, Boston University
Samples Received: 09Sep21

ification Date: 13Sep21

| Sample Name           | PiZZ102-37B-<br>Cr2 Px+9(3) |
|-----------------------|-----------------------------|
| Label on tube         | 88321                       |
| FGA                   | 20, 25                      |
| ТРОХ                  | 8, 11                       |
| D8S1179               | 13, 13                      |
| vWA                   | 14, 16                      |
| Amelogenin            | X, X                        |
| Penta_D               | 10, 14                      |
| CSF1PO                | 12, 12                      |
| D16S539               | 12, 12                      |
| D7S820                | 10, 11                      |
| D13S317               | 10, 12                      |
| D5S818                | 11, 12                      |
| Penta_E               | 7, 15                       |
| D18S51                | 18, 19                      |
| D21S11                | 28, 28                      |
| TH01                  | 8, 9.3                      |
| D3S1358               | 14, 17                      |
| Allelic Polymorphisms | 26                          |
| Matches*              |                             |
| Comments              |                             |

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



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Form SOP-89.01 Version 7.0

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<u>Assay Description:</u> STR analysis is performed using the PowerPlex 16 HS System by Promega<sup>TM</sup>. 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 25-30 allelic polymorphisms across the 15 STR loci analyzed.

<u>Interpretation:</u> 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%.



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Raw data is available upon request.