Additional File 1

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| Table 1: Mean depth, coverage at 10x depth across target region and VerifyBamID freemix values for each sample. **Sample ID** | **Mean depth** | **Coverage of target region at 10x (%)\*** | **VerifyBamID Freemix\*\*** |
| 39 | 89.6 | 91.2 | 0.0001 |
| 51 | 101.6 | 93.2 | 0.0004 |
| 60 | 178.3 | 94.7 | 0.0000 |
| 82 | 88.9 | 91.5 | 0.0019 |
| 89 | 53.9 | 87.7 | 0.0016 |
| 98 | 59.3 | 87.8 | 0.0002 |
| 128 | 47.7 | 86.6 | 0.0014 |
| 210 | 118.3 | 93.1 | 0.0003 |

\*10X coverage indicates the average times of sequencing occurred for each nucleotide in the exome.

\*\* Score of the level of contamination in the common SNPs