Supplementary Table 1. PCR Array results of nerve related genes in endometrial cancer (test) and para-cancer (control) tissues

| Symbol  | Well | AVG ΔCₜ  | 2^ΔCₜ  | Fold Change |
|---------|------|----------|--------|-------------|
|         |      | (Ct(GOI) - Ave Ct (HKG)) |         | Test Sample /Control Sample |
| **Test Sample** | **Control Sample** | **Test Sample** | **Control Sample** | **Test Sample /Control Sample** |
| ADRA1A  | 1    | 28.67    | 27.96  | 2.3E-09     | 3.8E-09     | 0.61         |
| ADRA1D  | 2    | 26.41    | 24.36  | 1.1E-08     | 4.6E-08     | 0.24         |
| ADRA2A  | 3    | 21.27    | 21.44  | 4.0E-07     | 3.5E-07     | 1.12         |
| ADRA1B  | 4    | 26.41    | 25.57  | 3.9E-08     | 2.0E-08     | 1.94         |
| ADRA2B  | 5    | 28.14    | 26.29  | 3.4E-09     | 1.2E-08     | 0.28         |
| ADRA2C  | 6    | 22.65    | 21.72  | 1.5E-07     | 2.9E-07     | 0.52         |
| ADRB1   | 7    | 25.97    | 25.47  | 1.5E-08     | 2.2E-08     | 0.70         |
| ADRB2   | 8    | 22.89    | 23.74  | 1.3E-07     | 7.1E-08     | 1.80         |
| ADRB3   | 9    | 27.38    | 27.81  | 5.7E-09     | 4.2E-09     | 1.35         |
| CHRM1   | 10   | 27.79    | 27.05  | 4.3E-09     | 7.2E-09     | 0.60         |
| CHRM4   | 11   | 27.48    | 27.64  | 5.4E-09     | 4.8E-09     | 1.12         |
| CHRM5   | 12   | 27.98    | 27.64  | 3.8E-09     | 4.8E-09     | 0.79         |
| CHRNA3  | 13   | 25.94    | 23.82  | 1.6E-08     | 6.7E-08     | 0.23         |
| CHRNA4  | 14   | 28.45    | 27.16  | 2.7E-09     | 6.7E-09     | 0.41         |
| CHRNA5  | 15   | 24.26    | 23.75  | 5.0E-08     | 7.1E-08     | 0.70         |
| CHRNA6  | 16   | 26.59    | 25.64  | 9.9E-09     | 1.9E-08     | 0.52         |
| CHRNA7  | 17   | 25.60    | 25.74  | 2.0E-08     | 1.8E-08     | 1.10         |
| CHRNE   | 18   | 26.63    | 25.42  | 9.7E-09     | 2.2E-08     | 0.43         |
| DRD1    | 19   | 28.92    | 27.80  | 2.0E-09     | 4.3E-09     | 0.46         |
| DRD2    | 20   | 24.01    | 25.84  | 5.9E-08     | 1.7E-08     | 3.54         |
| DRD3    | 21   | 25.99    | 26.00  | 1.5E-08     | 1.5E-08     | 1.01         |
| DRD4    | 22   | 23.28    | 22.51  | 9.8E-08     | 1.7E-07     | 0.59         |
| DRD5    | 23   | 24.52    | 24.68  | 4.2E-08     | 3.7E-08     | 1.12         |
| GABRA1  | 24   | 28.59    | 28.98  | 2.5E-09     | 1.9E-09     | 1.30         |
| GABRA2  | 25   | 26.64    | 25.36  | 9.6E-09     | 2.3E-08     | 0.41         |
| GABRA4  | 26   | 26.19    | 26.75  | 1.3E-08     | 8.9E-09     | 1.47         |
| GABRA5  | 27   | 30.62    | 27.42  | 6.1E-10     | 5.6E-09     | 0.11         |
| Gene   | Row | Column | Direction | z-value | p-value | p spearman | p pearson |
|--------|-----|--------|-----------|---------|---------|------------|-----------|
| GABRA6 | 28  | 27.05  | 2.7E-09   | 3.3E-08 | 0.22    |            |           |
| GABRB1 | 29  | 26.94  | 2.7E-09   | 1.1E-08 | 0.72    |            |           |
| GABRB3 | 30  | 26.18  | 1.3E-08   | 3.0E-08 | 0.44    |            |           |
| GABRD  | 31  | 30.80  | 1.3E-08   | 5.3E-10 | 0.36    |            |           |
| GABRE  | 32  | 26.49  | 1.1E-08   | 1.1E-08 | 1.00    |            |           |
| GABRG1 | 33  | 24.91  | 1.1E-08   | 3.0E-08 | 0.59    |            |           |
| GABRG2 | 34  | 27.42  | 1.1E-08   | 1.1E-08 | 1.00    |            |           |
| GABRG3 | 35  | 26.25  | 1.0E-07   | 9.9E-08 | 1.02    |            |           |
| GABRQ  | 36  | 18.82  | 2.2E-06   | 2.0E-07 | 10.58   |            |           |
| GABRR1 | 37  | 24.01  | 5.9E-08   | 6.7E-09 | 0.88    |            |           |
| GABRR2 | 38  | 27.48  | 5.3E-09   | 3.9E-09 | 1.39    |            |           |
| GRIA1  | 39  | 26.17  | 1.3E-08   | 2.5E-08 | 0.53    |            |           |
| GRIA2  | 40  | 18.82  | 2.2E-06   | 2.0E-07 | 10.58   |            |           |
| GRIA3  | 41  | 24.76  | 3.5E-08   | 8.3E-08 | 0.80    |            |           |
| GRIK1  | 42  | 26.17  | 1.3E-08   | 2.5E-08 | 0.53    |            |           |
| GRIK2  | 43  | 24.01  | 3.6E-08   | 6.7E-08 | 0.88    |            |           |
| GRIK4  | 44  | 27.48  | 5.3E-09   | 3.9E-09 | 1.39    |            |           |
| GRIK5  | 45  | 26.60  | 9.8E-09   | 7.2E-09 | 1.35    |            |           |
| GRIN1  | 46  | 29.10  | 9.5E-10   | 9.5E-10 | 1.82    |            |           |
| GRIN2A | 47  | 31.07  | 4.4E-10   | 4.1E-10 | 1.09    |            |           |
| GRIN2B | 48  | 31.37  | 3.6E-10   | 1.8E-10 | 2.01    |            |           |
| GRIN2C | 49  | 27.05  | 7.2E-09   | 3.9E-09 | 1.86    |            |           |
| GRM1   | 50  | 26.11  | 1.4E-08   | 1.1E-08 | 1.24    |            |           |
| GRM3   | 51  | 28.36  | 2.4E-09   | 1.3E-09 | 2.19    |            |           |
| GRM4   | 52  | 26.85  | 8.2E-09   | 8.7E-09 | 0.95    |            |           |
| GRM5   | 53  | 26.12  | 1.4E-08   | 7.3E-09 | 1.89    |            |           |
| GRM6   | 54  | 27.62  | 4.9E-09   | 3.4E-09 | 1.44    |            |           |
| GRM7   | 55  | 25.84  | 1.7E-08   | 4.2E-08 | 0.40    |            |           |
| GRM8   | 56  | 27.62  | 4.9E-09   | 3.4E-09 | 1.44    |            |           |
| HTR1A  | 57  | 27.32  | 6.0E-09   | 3.3E-09 | 1.83    |            |           |
| HTR1B  | 58  | 28.43  | 2.8E-09   | 2.9E-09 | 0.95    |            |           |
| HTR1D  | 59  | 26.65  | 9.5E-09   | 1.3E-08 | 0.71    |            |           |
| Gene   | Value1 | Value2 | Value3   | Value4   | Value5  |
|--------|--------|--------|----------|----------|---------|
| HTR1F  | 23.21  | 25.06  | 1.0E-07  | 2.9E-08  | 3.61    |
| HTR2A  | 25.79  | 25.91  | 1.7E-08  | 1.6E-08  | 1.09    |
| HTR2C  | 25.81  | 26.21  | 1.7E-08  | 1.3E-08  | 1.31    |
| HTR3A  | 26.00  | 25.82  | 1.5E-08  | 1.7E-08  | 0.88    |
| HTR4   | 26.59  | 26.13  | 9.9E-09  | 1.4E-08  | 0.73    |
| HTR7   | 25.76  | 25.83  | 1.8E-08  | 1.7E-08  | 1.05    |
| HTR1E  | 25.24  | 23.80  | 2.5E-08  | 6.9E-08  | 0.37    |
| HTR2B  | 21.10  | 19.67  | 4.5E-07  | 1.2E-06  | 0.37    |
| HTR3B  | 27.28  | 27.54  | 6.1E-09  | 5.1E-09  | 1.20    |
| HTR3C  | 28.20  | 27.87  | 3.2E-09  | 4.1E-09  | 0.79    |
| HTR3D  | 27.67  | 27.49  | 4.7E-09  | 5.3E-09  | 0.88    |
| HTR3E  | 29.47  | 26.81  | 1.3E-09  | 8.5E-09  | 0.16    |
| HTR5A  | 27.16  | 26.83  | 6.7E-09  | 8.4E-09  | 0.80    |
| HTR6   | 27.77  | 27.36  | 4.4E-09  | 5.8E-09  | 0.75    |
| NEFH   | 25.24  | 22.57  | 2.5E-08  | 1.6E-07  | 0.16    |
| NEFL   | 25.93  | 25.30  | 1.6E-08  | 2.4E-08  | 0.65    |
| NEFM   | 24.85  | 22.13  | 3.3E-08  | 2.2E-07  | 0.15    |
| AVPR1A | 23.12  | 21.71  | 1.1E-07  | 2.9E-07  | 0.37    |
| AVPR1B | 29.19  | 29.22  | 1.6E-09  | 1.6E-09  | 1.02    |
| HRH1   | 22.23  | 20.60  | 2.0E-07  | 6.3E-07  | 0.32    |
| HRH4   | 27.09  | 26.87  | 7.0E-09  | 8.1E-09  | 0.86    |
| NPY2R  | 27.11  | 27.97  | 6.9E-09  | 3.8E-09  | 1.81    |
| NPY5R  | 25.60  | 26.21  | 2.0E-08  | 1.3E-08  | 1.52    |
| SSTR1  | 24.35  | 26.34  | 4.7E-08  | 1.2E-08  | 3.97    |
| SSTR2  | 26.02  | 26.25  | 1.5E-08  | 1.3E-08  | 1.18    |
| SSTR4  | 28.64  | 31.56  | 2.4E-09  | 3.2E-10  | 7.54    |
| TACR1  | 25.80  | 27.18  | 1.7E-08  | 6.6E-09  | 2.60    |
| TACR2  | 26.99  | 26.76  | 7.5E-09  | 8.8E-09  | 0.85    |
| TACR3  | 26.91  | 27.20  | 7.9E-09  | 6.5E-09  | 1.22    |
| BRS3   | 27.86  | 27.97  | 4.1E-09  | 3.8E-09  | 1.08    |
| CCKBR  | 31.21  | 29.66  | 4.0E-10  | 1.2E-09  | 0.34    |
| CNR1   | 28.00  | 27.99  | 3.7E-09  | 3.8E-09  | 0.99    |
| GCGR   | 32.75  | 31.57  | 1.4E-10  | 3.1E-10  | 0.44    |
| GRPR   | 27.19  | 27.18  | 6.5E-09  | 6.6E-09  | 1.00    |
| Gene  | ID  | Mean1 | Mean2 | Std1   | Std2   | Fold |
|-------|-----|-------|-------|--------|--------|------|
| HCRTR2 | 96  | 29.52 | 28.38 | 1.3E-09| 2.9E-09| 0.45 |
| NTSR2  | 97  | 28.01 | 27.31 | 3.7E-09| 6.0E-09| 0.62 |
| OXTR   | 98  | 28.52 | 29.69 | 2.6E-09| 1.2E-09| 2.26 |
| PROKR2 | 99  | 29.52 | 28.77 | 1.3E-09| 2.2E-09| 0.60 |
| SCTR   | 100 | 30.87 | 32.55 | 5.1E-10| 1.6E-10| 3.22 |
| TSPO   | 101 | 21.59 | 20.54 | 3.2E-07| 6.6E-07| 0.48 |
| COMT   | 102 | 27.26 | 26.01 | 6.2E-09| 1.5E-08| 0.42 |
| DBH    | 103 | 28.59 | 27.98 | 2.5E-09| 3.8E-09| 0.65 |
| DDC    | 104 | 24.66 | 26.63 | 3.8E-08| 9.6E-09| 3.91 |
| EPHB1  | 105 | 27.46 | 26.56 | 5.4E-09| 1.0E-08| 0.53 |
| GDNF   | 106 | 26.93 | 26.46 | 7.8E-09| 1.1E-08| 0.72 |
| GFAP   | 107 | 28.25 | 28.79 | 3.1E-09| 2.2E-09| 1.45 |
| MAOA   | 108 | 21.09 | 21.09 | 4.5E-07| 4.5E-07| 1.00 |
| MAOB   | 109 | 19.81 | 19.31 | 1.1E-06| 1.5E-06| 0.70 |
| NR4A1  | 110 | 20.55 | 22.83 | 6.5E-07| 1.3E-07| 4.85 |
| NR4A3  | 111 | 25.00 | 26.78 | 3.0E-08| 8.7E-09| 3.45 |
| PDYN   | 112 | 28.98 | 29.31 | 1.9E-09| 1.5E-09| 1.26 |
| PTGS2  | 113 | 25.28 | 24.69 | 2.5E-08| 3.7E-08| 0.67 |
| SYN2   | 114 | 27.10 | 26.34 | 6.9E-09| 1.2E-09| 0.59 |
| SLC18A1| 115 | 28.83 | 28.33 | 2.1E-09| 3.0E-09| 0.71 |
| SLC18A2| 116 | 22.20 | 20.62 | 2.1E-07| 6.2E-07| 0.33 |
| SLC6A3 | 117 | 27.92 | 26.80 | 3.9E-09| 8.6E-09| 0.46 |
| SLC6A4 | 118 | 31.28 | 30.53 | 3.8E-10| 6.4E-10| 0.60 |
| TDO2   | 119 | 24.99 | 23.99 | 3.0E-08| 6.0E-08| 0.50 |
| TH     | 120 | 32.38 | 29.90 | 1.8E-10| 1.0E-09| 0.18 |
| TPH1   | 121 | 26.86 | 27.48 | 8.2E-09| 5.4E-09| 1.54 |
| TPH2   | 122 | 26.82 | 26.88 | 8.5E-09| 8.1E-09| 1.05 |
| CHAT   | 123 | 29.38 | 29.00 | 1.4E-09| 1.9E-09| 0.77 |
Cell Line Authentication Service
STR Profile Report

Sample Submitted By: Dr. Yudong Wang
International Peace Maternity and Child Health Hospital, Shanghai Jiao Tong University School of Medicine

Email Address: niting6688@126.com
Sales Order: 180124C
Cell Line Designation: HEC-1-A
Date Sample Received: Jan 24th, 2018
Report Date: Jan 25th, 2018

Methodology: Nineteen short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, were amplified using the commercially available EX20 Kit from AGCU. The cell line sample was processed using the ABI Prism® 3500 Genetic Analyzer. Data were analyzed using GeneMapper® ID-X v1.4 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

Data Interpretation: Cell lines were authenticated using Short Tandem Repeat (STR) analysis as described in 2012 in ANSI Standard (ASN-0002) by the ATCC Standards Development Organization (SDO) and in Capes-Davis et al., Match criteria for human cell line authentication: Where do we draw the line? Int J Cancer. 2013;132(11):2510-9.

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Jiangsu, P.R. China
| Loci       | Query Profile: HEC-1-A | DSMZ Reference Database Profile |
|------------|------------------------|---------------------------------|
| Amelogenin | X                      | X                               |
| D3S1358    | 15                     |                                 |
| D13S317    | 11                     | 11                              |
| D7S820     | 9                      | 11                              |
| D16S539    | 12                     | 12                              |
| Penta E    | 11                     |                                 |
| TPOX       | 8                      | 8                               |
| TH01       | 6                      | 6                               |
| D2S1338    | 18                     | 19                              |
| CSF1PO     | 10                     | 12                              |
| Penta D    | 9                      | 13                              |
| D19S433    | 13                     |                                 |
| vWA        | 18                     | 19                              |
| D2S11      | 30                     | 31                              |
| D18S51     | 16                     | 17                              |
| D6S1043    | 12                     | 18                              |
| D8S1179    | 13                     | 14                              |
| D5S818     | 11                     | 15                              |
| D12S391    | 19                     |                                 |
| FGA        | 21                     | 22                              |

The allele match algorithm compares the 8 core loci plus amelogenin only, even though alleles from all loci will be reported when available.

Note: Loci highlighted in grey (8 core STR loci plus Amelogenin) can be made public to verify cell identity. In order to protect the identity of the donor, please do not publish the allele calls from all the STR loci tested.

**Explanation of Test Results**

Cell lines with ≥80% match are considered to be related; i.e., derived from a common ancestry. Cell lines with between a 55% to 80% match require further profiling for authentication of relatedness.

- The submitted sample profile is human, but not a match for any profile in the DSMZ STR database.
- The submitted profile is an exact match for the following human cell line(s) in the DSMZ STR database (8 core loci plus Amelogenin):
  - The submitted profile is similar to the following DSMZ human cell line(s): HEC-1-A (89% match)

**Addendum:** Electropherogram/matching results for the customer’s sample set 1 of 1
Cell Line Authentication Service

STR Profile Report

Sample Name

HEC J A

| Sample Name | D3S1358 | D13513 | D7S820 | D16564 | Fetal B |
|-------------|---------|--------|--------|--------|---------|
|             | 105     | 175    | 245    | 315    | 365     | 455     |
|             | 15      | 11     | 9      | 11     |         |         |

HEC J A

| Sample Name | TH01    | D2S1338 | D3S1424 | CSF1PO | Fetal D |
|-------------|---------|---------|---------|--------|---------|
|             | 105     | 175     | 245     | 315    | 365     | 455     |
|             | 8       | 11      | 6       | 18     | 10      | 9       |
|             | 7       | 6       | 7       | 19     | 12      | 13      |

HEC J A

| Sample Name | D19S433 | D9S939 | P5A5 | D21S111 | TH01 | D8S1179 |
|-------------|---------|--------|------|---------|------|---------|
|             | 105     | 175    | 245  | 315     | 385  | 455     |
|             | 13      | 19     | 18   | 30      | 16   | 12      |
|             | 19      | 11     | 31   | 17      | 22   | 12      |

HEC J A

| Sample Name | D3S1358 | D5S818 | D2S388 | FGA    |
|-------------|---------|--------|--------|--------|
|             | 105     | 175    | 245    | 315    |
|             | 13      | 14     | 11     | 15     |
|             | 19      | 19     | 19     | 22     |

Thu Jan 25, 2018, 03:19PM, CST

Printed by: gmxdx
Sample Submitted By: Dr. Yudong Wang
International Peace Maternity and Child Health Hospital, Shanghai Jiao Tong University School of Medicine

Email Address: niting6688@126.com
Sales Order: 180124B
Cell Line Designation: ISHIKAWA
Date Sample Received: Jan 24th, 2018
Report Date: Jan 25th, 2018

Methodology: Nineteen short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, were amplified using the commercially available EX20 Kit from AGCU. The cell line sample was processed using the ABI Prism® 3500 Genetic Analyzer. Data were analyzed using GeneMapper® ID-X v1.4 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

Data Interpretation: Cell lines were authenticated using Short Tandem Repeat (STR) analysis as described in 2012 in ANSI Standard (ASN-0002) by the ATCC Standards Development Organization (SDO) and in Capes-Davis et al., Match criteria for human cell line authentication: Where do we draw the line? Int J Cancer. 2013;132(11):2510-9.

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### Test Results for Submitted Sample

| Loci       | Query Profile: ISHIKAWA | DSMZ Reference Database Profile |
|------------|--------------------------|---------------------------------|
| Amelogenin | X                        | X                               |
| D3S1358    | 15 16                    |                                 |
| D13S317    | 9 12                     | 9 12                            |
| D7S820     | 9 10                     | 9 10                            |
| D16S539    | 9                        |                                 |
| Penta E    | 11 19 21                 |                                 |
| TPOX       | 8                        | 8                               |
| TH01       | 9 10                     | 9 10                            |
| D2S1338    | 19 21                    |                                 |
| CSF1PO     | 11 12                    | 11 12                           |
| Penta D    | 10 11                    |                                 |
| D19S433    | 12.2 14 15               |                                 |
| vWA        | 14 17                    | 14 17                           |
| D21S11     | 28                       |                                 |
| D18S51     | 12 20 21                 |                                 |
| D6S1043    | 12 18                    |                                 |
| D8S1179    | 13 16                    |                                 |
| D5S818     | 10 11                    | 10 11                           |
| D12S391    | 18 20 21                 |                                 |
| FGA        | 21 22                    |                                 |

The allele match algorithm compares the 8 core loci plus amelogenin only, even though alleles from all loci will be reported when available.

Note: Loci highlighted in grey (8 core STR loci plus Amelogenin) can be made public to verify cell identity. In order to protect the identity of the donor, **please do not publish** the allele calls from all the STR loci tested.

### Explanation of Test Results

Cell lines with ≥80% match are considered to be related; i.e., derived from a common ancestry. Cell lines with between a 55% to 80% match require further profiling for authentication of relatedness.

- The submitted sample profile is human, but not a match for any profile in the DSMZ STR database.
- The submitted profile is an exact match for the following human cell line(s) in the DSMZ STR database (8 core loci plus Amelogenin): ISHIKAWA
- The submitted profile is similar to the following DSMZ human cell line(s):

---

Addendum: Electropherogram/matching results for the customer’s sample set 1 of 1
| Sample Name | DBS1179 | 31 | 12 | 245 | 141 | 318 | 365 | 485 |
|-------------|---------|----|----|-----|-----|-----|-----|-----|
|             | X       | 13 | 16 | 10  | 11  | 20  | 21  | 22  |

Date: Thu Jan 25, 2018 03:19PM, CST
Printed by: gmisx
Sample Submitted By: Dr. Yudong Wang  
International Peace Maternity and Child Health Hospital, Shanghai Jiao Tong University School of Medicine

Email Address: niting6688@126.com
Sales Order: 180211A
Cell Line Designation: KLE
Date Sample Received: Feb 11th, 2018
Report Date: Feb 12th, 2018

Methodology: Nineteen short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, were amplified using the commercially available EX20 Kit from AGCU. The cell line sample was processed using the ABI Prism® 3500 Genetic Analyzer. Data were analyzed using GeneMapper® ID-X v1.4 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

Data Interpretation: Cell lines were authenticated using Short Tandem Repeat (STR) analysis as described in 2012 in ANSI Standard (ASN-0002) by the ATCC Standards Development Organization (SDO) and in Capes-Davis et al., Match criteria for human cell line authentication: Where do we draw the line? Int J Cancer. 2013;132(11):2510-9.

GTB™ performs STR Profiling following ISO 9001:2008 and ISO/IEC 17025:2005 quality standards. There are no warranties with respect to the services or results supplied, express or implied, including, without limitation, any implied warranty of merchantability or fitness for a particular purpose. Genetic Testing Biotechnology (GTB) is not liable for any damages or injuries resulting from receipt and/or improper, inappropriate, negligent or other wrongful use of the test results supplied, and/or from misidentification, misrepresentation, or lack of accuracy of those results. Your exclusive remedy against GTB and those supplying materials used in the services for any losses or damage of any kind whatsoever, whether in contract, tort, or otherwise, shall be, at GTB's option, refund of the fee paid for such service or repeat of the service.

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Cell Line Authentication Service
STR Profile Report

Sales Order: 180211A

| Loci       | Query Profile: KLE | DSMZ Reference Database Profile |
|------------|--------------------|-------------------------------|
| Amelogenin | X                  | X                             |
| D3S1358    | 17                 |                               |
| D13S317    | 12                 | 12                            |
| D7S820     | 11 12              | 11 12                         |
| D16S539    | 11 12              | 11 12                         |
| Penta E    | 7                  |                               |
| TPOX       | 8 11               | 8 11                          |
| TH01       | 6 7                | 6 7                           |
| D2S1338    | 18 19              |                               |
| CSF1PO     | 13 14              | 13 14                         |
| Penta D    | 13                 |                               |
| D19S433    | 15                 |                               |
| vWA        | 16                 | 16                            |
| D21S11     | 28 30              |                               |
| D18S51     | 13 17              |                               |
| D6S1043    | 13 14              |                               |
| D8S1179    | 8 14               |                               |
| D5S818     | 9 12               | 9 12                          |
| D12S391    | 20 25              |                               |
| FGA        | 23 25              |                               |

The allele match algorithm compares the 8 core loci plus amelogenin only, even though alleles from all loci will be reported when available.

Note: Loci highlighted in grey (8 core STR loci plus Amelogenin) can be made public to verify cell identity. In order to protect the identity of the donor, please do not publish the allele calls from all the STR loci tested.

Explanation of Test Results

Cell lines with ≥80% match are considered to be related; i.e., derived from a common ancestry. Cell lines with between a 55% to 80% match require further profiling for authentication of relatedness.

- The submitted sample profile is human, but not a match for any profile in the DSMZ STR database.
- The submitted profile is an exact match for the following human cell line(s) in the DSMZ STR database (8 core loci plus Amelogenin): KLE
- The submitted profile is similar to the following DSMZ human cell line(s):

More information

Addendum: Electropherogram/matching results for the customer’s sample set 1 of 1
