Cell Line Authentication Service
STR Profile Report

Sample Submitted By: Dr. John Smith
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ATCC Sales Order: 0000111111
FTA Barcode: STR12345
Cell Line Designation: NCI-H358
Date Sample Received: Jan 1, 2014
Report Date: Jan 4, 2014

Methodology:
Seventeen short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, were amplified using the commercially available PowerPlex® 18D Kit from Promega. The cell line sample was processed using the ABI Prism® 3500xl Genetic Analyzer. Data were analyzed using GeneMapper® ID-X v1.2 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. 2012 Nov 8. doi: 0.1002/ijc.27931

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Overview of kits, instruments and software used to generate the data.
How the data will be interpreted relative to the standards
ATCC quality, disclaimer and trademark statements
### Sample Profile

#### ATCC Reference Database Profile

<table>
<thead>
<tr>
<th>Loci</th>
<th>Query Profile: NCI-H358</th>
<th>ATCC Reference Database Profile</th>
</tr>
</thead>
<tbody>
<tr>
<td>D3S1358</td>
<td>15</td>
<td>17</td>
</tr>
<tr>
<td>TH01</td>
<td>8</td>
<td>6</td>
</tr>
<tr>
<td>D21S11</td>
<td>29</td>
<td>30</td>
</tr>
<tr>
<td>D18S51</td>
<td>12</td>
<td>17</td>
</tr>
<tr>
<td>Penta_E</td>
<td>10</td>
<td>12</td>
</tr>
<tr>
<td>D5S818</td>
<td>12</td>
<td>10</td>
</tr>
<tr>
<td>D13S317</td>
<td>11</td>
<td>14</td>
</tr>
<tr>
<td>D7S820</td>
<td>9</td>
<td>10</td>
</tr>
<tr>
<td>D16S539</td>
<td>9</td>
<td>12</td>
</tr>
<tr>
<td>CSF1PO</td>
<td>11</td>
<td>12</td>
</tr>
<tr>
<td>Penta_D</td>
<td>9</td>
<td>15</td>
</tr>
<tr>
<td>Amelogenin</td>
<td>X</td>
<td>Y</td>
</tr>
<tr>
<td>vWA</td>
<td>16</td>
<td>17</td>
</tr>
<tr>
<td>D8S1179</td>
<td>11</td>
<td>14</td>
</tr>
<tr>
<td>TPOX</td>
<td>8</td>
<td>10</td>
</tr>
<tr>
<td>FGA</td>
<td>23</td>
<td></td>
</tr>
<tr>
<td>D19S433</td>
<td>13</td>
<td>14.2</td>
</tr>
<tr>
<td>D2S1338</td>
<td>16</td>
<td>24</td>
</tr>
</tbody>
</table>

Number of shared alleles between query sample and database profile: 6
Total number of alleles in the database profile: 16
Percent match between the submitted sample and the database profile: 38%

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.

Electropherograms showing raw data are attached.

### 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 ATCC STR database
- [x] The submitted profile is an exact match for the following ATCC human cell line(s) in the ATCC STR database (8 core loci plus Amelogenin): CRL-1619 (A-375)
- [ ] The submitted profile is similar to the following ATCC human cell line(s):

### Additional Comments:

Submitted sample (STR123455 (NCI-H358)), shows a 38% match to ATCC cell line CRL-5807 (NCI-H358). Submitted sample is however, an exact match to ATCC cell lines CRL-1619 (A-375) and CRL-1872 (A375.S2). ATCC cell line CRL-1872, was derived from parental cell line CRL-1619. Submitted sample is an exact match to additional submitted samples STR123456 and STR123457.

<table>
<thead>
<tr>
<th>e-Signature, Technician:</th>
<th>John 01/02/2014</th>
</tr>
</thead>
<tbody>
<tr>
<td>e-Signature, Reviewer:</td>
<td>Bill 01/02/2014</td>
</tr>
</tbody>
</table>

Using the internal ATCC database, the closest matches to the sample profile are provided with an explanation and the signatures of the technician performing the assay and a data reviewer.
The highest matches to the sample profile in the database along with the standard loci for the cell line sample submitted by the customer.

Electropherogram for the customer’s sample, set 1 of 2.
Definitions of terms used in this report:

**Peak Area Difference (PAD):**
Refers to a heterozygous peak imbalance. Two alleles at a single locus should amplify in a similar manner; and therefore produce peaks of similar height and area. Peaks which are above threshold (50 rfu) but are not of similar area, within 50% of each other, are referred to as a PAD. Due to their nature cell lines do not amplify in the same manner as a sample taken from a fresh buccal swab. PAD is far more common in cell line samples.

**Stutter:**
A stutter peak is a small peak which occurs immediately before the true peak. It is defined as being a single repeat unit smaller than the true peak. The stutter peak should be less than 15% of the true peak. The stutter is caused by the polymerase.

**+4 Peak:**
A +4 is similar to a stutter but occurs immediately after the true peak. A stutter peak should be less than 5% for a homozygous and 10% for a heterozygous.

**Below Threshold Peak(s):**
Cell lines can produce unusual profiles and occasionally a peak will amplify poorly and be below threshold. Where we find a below threshold peak which we believe is valid we indicate it as a below threshold peak. Our cell line analysis criteria, Homozygous and Heterozygous peaks must be equal to or above the set height threshold for it to be considered a true peak.

**Ladder/ Off Ladder Peak(s):**
The allelic ladder consists of most or all known alleles in the population and allows for precise assignment of alleles. Those which do not align are termed ‘off ladder.’

**Artifact:**
A non-allelic product of the amplification process, an anomaly of the detection process, or a by-product of primer synthesis.

**Pull-up:**
A term used to describe when signal from one dye color channel produces artificial peaks in another, usually adjacent, color.

**Spike:**
An extraneous peak resulting from dust, dried polymer, an air bubble, or an electrical surge.

**Dye blob:**
Free dye not coupled to primer that can be injected into the capillary (A known and documented dye blob is often found at the D3S1358 locus.)