



Cell Line Authentication Service

STR Profile Report

Sample Submitted By: Dr. John Smith
State University
Main Street
City, State.
Zip Code, USA
jsmith@stateuniversity.edu

Email Address:

ATCC Sales Order: 0000111111

FTA Barcode: STR12345

Cell Line Designation: NCI-H358

Date Sample Received: Jan 1, 2014

Report Date: Jan 4, 2014

ATCC will provide a sales order number for the service. A barcode number is included with the sample collection card, which is used for tracking

Cell line designation from the customer

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.

Overview of kits, instruments and software used to generate the data.

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

How the data will be interpreted relative to the standards

ATCC 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. ATCC 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 ATCC 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 ATCC's option, refund of the fee paid for such service or repeat of the service.

The ATCC trademark and trade name, any and all ATCC catalog numbers are trademarks of the American Type Culture Collection. PowerPlex is a registered trademark of Promega Corporation. Applied Biosystems, ABI Prism and GeneMapper are registered trademarks of Life Technologies Corporation.

ATCC quality, disclaimer and trademark statements



Sample Profile

Profile for the ATCC reference cell line

Barcode: STR12345
Order: 0000111111

Test Results for Submitted Sample				ATCC Reference Database Profile			
Loci	Query Profile: NCI-H358			Database Profile: NCI-H358			
D3S1358	15	17					
TH01	8			6			
D21S11	29	30					
D18S51	12	17					
Penta_E	10	12					
D5S818	12			10	12		
D13S317	11	14		8	12		
D7S820	9			10	11		
D16S539	9			12	13		
CSF1PO	11	12		11	12		
Penta_D	9	15					
Amelogenin	X			X	Y		
vWA	16	17		17			
D8S1179	11	14					
TPOX	8	10		8	9		
FGA	23						
D19S433	13	14.2					
D2S1338	16	24					
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
<i>The allele match algorithm compares the 8 core loci plus amelogenin only, even though alleles from all loci will be reported when available.</i>							
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.							

How the standard was applied to the Sample profile data

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
- 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 (STR12345 (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 STR1234567.

e-Signature, Technician:	John 01/02/2014
e-Signature, Reviewer:	Bill 01/02/2014



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.

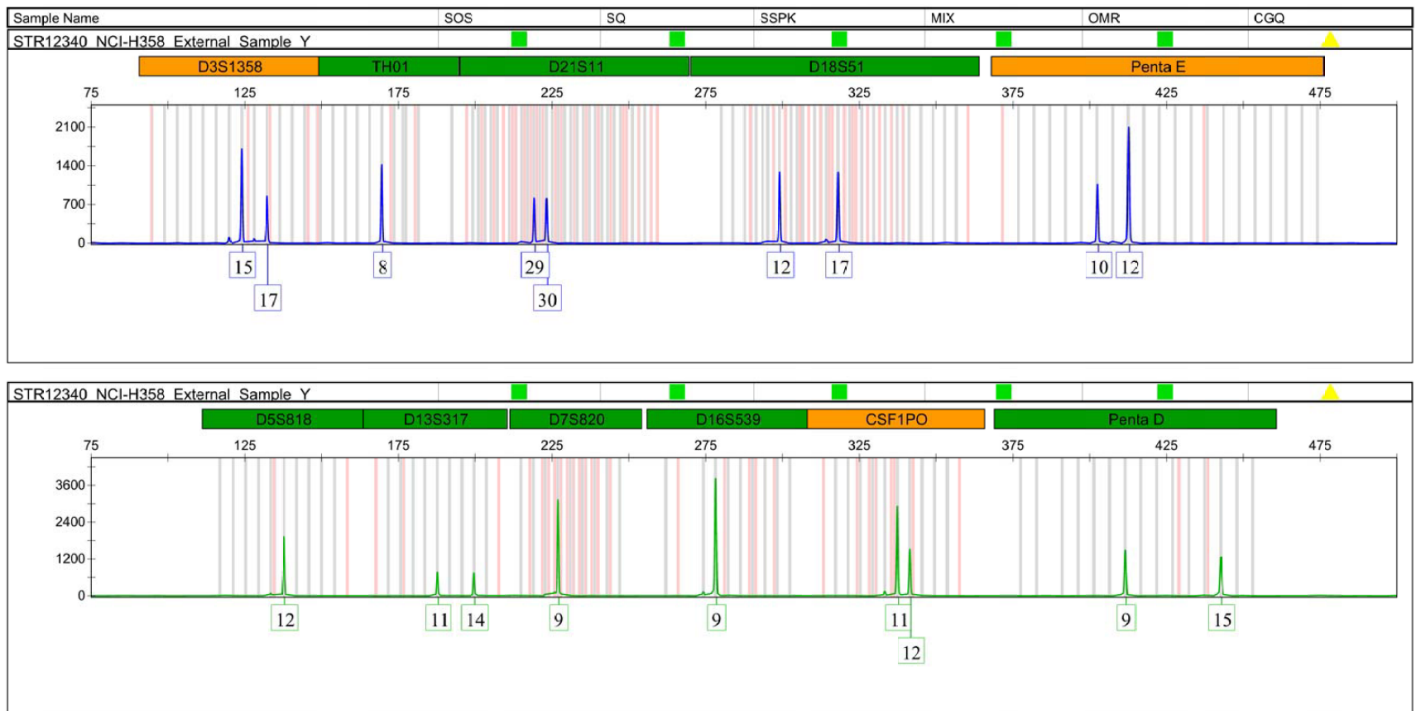


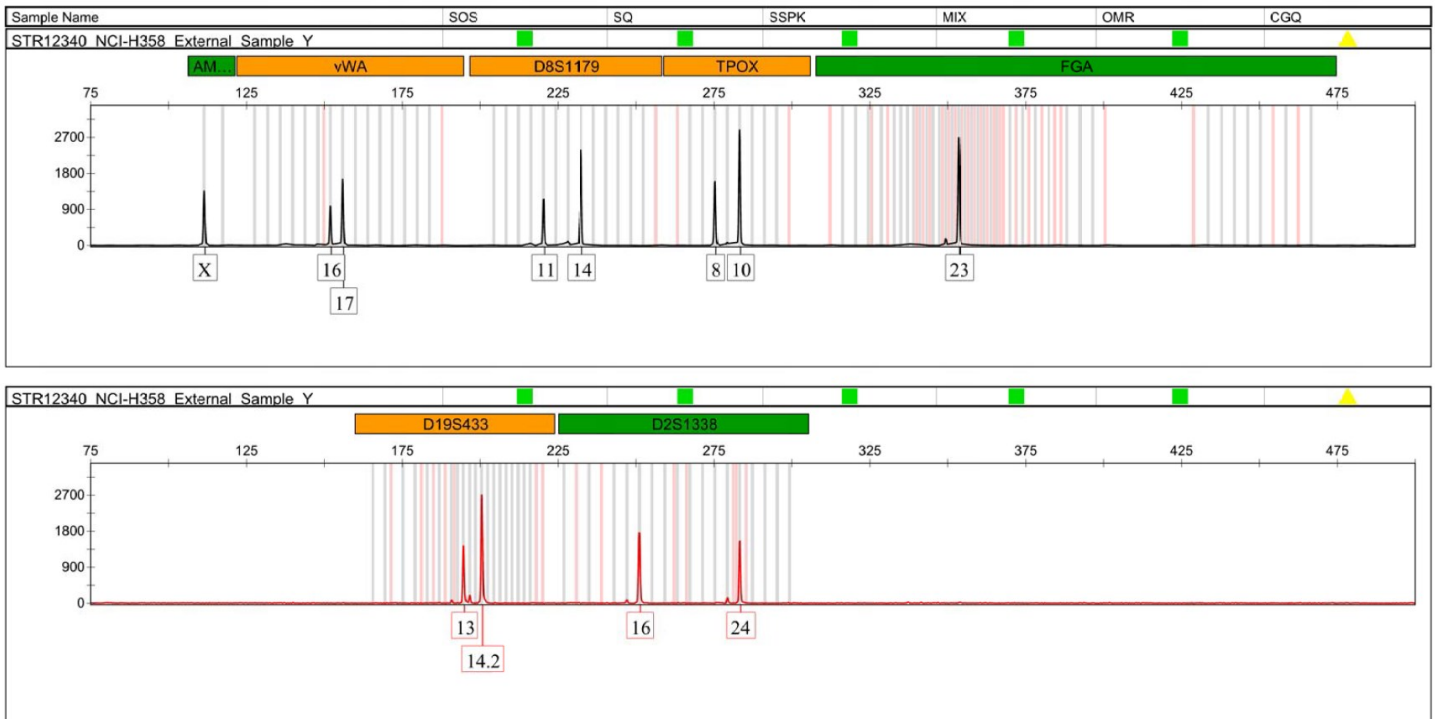
Addendum: Comparative Output from the ATCC STR Profile Database

% Match	ATCC® Cat. No.	Designation	D5S818	D13S317	D7S820	D16S539	vWA	THO1	AMEL	TPOX	CSF1PO
100	CRL-1872	A375.S2	12	11,14	9	9	16,17	8	X	8,10	11,12
100	CRL-1619	A-375	12	11,14	9	9	16,17	8	X	8,10	11,12
100	N/A	WSB-4	12	11,14	9	9	16,17	8	X	8,10	11,12
100	N/A	WSB-5	12	11,14	9	9	16,17	8	X	8,10	11,12
100	N/A	NCI-H358	12	11,14	9	9	16,17	8	X	8,10	11,12
38	CRL-5807	NCI-H358	10,12	8,12	10,11	12,13	17	6	X,Y	8,9	11,12

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:**

Terms and definitions which may be used within the 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.)