Cell Line Authentication Service
STR Profile Report

Sample Submitted By:	Bioalternatives Guenin
Email Address:	s.guenin@bioalternatives.com
ATCC Sales Order:	SO0152500
FTA Barcode:	STRA7150
Cell Line Designation:	HCE-2_50.B1
Date Sample Received:	Wednesday, November 01, 2017
Report Date:	Monday, November 06, 2017

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) Authentication of Human Cell Lines: Standardization of STR Profiling 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: 10.1002/ijc.27931

ATCC performs STR Profiling following ISO 9001:2008 and ISO/IEC 17025:2005 quality standards.

Technical questions?

ATCC Technical Support
(800) 638-6597 / +1 703-365-2700
STRTechSupport@atcc.org

Ordering questions?

800-638-6597 or 703-365-2700
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Test Results for Submitted Sample					ATCC Reference Database Profile			
Locus	**Query Profile: HCE-2_50.B1**				**Database Profile: HCE-2 (50.B1); Corneal Epithelium; Human (Homo sapiens)**			
D3S1358	17							
TH01	6	9			6	9		
D21S11	30							
D18S51	15	17						
Penta_E	7	8						
D5S818	11	12			11	12		
D13S317	8	11			8	11		
D7S820	8	10			8	10		
D16S539	11				9	11		
CSF1PO	10	13			10	13		
Penta_D	10							
Amelogenin	X	Y			X	Y		
vWA	15	18			15	18		
D8S1179	11	15						
TPOX	10	11			10	11		
FGA	21	25						
D19S433	13	14						
D2S1338	19	22						

Number of shared alleles between query sample and database profile:	17
Total number of alleles in the database profile:	18
Percent match between the submitted sample and the database profile:	94

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.

☐ 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):

☒ The submitted profile is similar to the following ATCC human cell line(s): CRL-11135

☐ An STR profile could not be generated.

Additional Comments:

Submitted sample, STRA7150 (HCE-2_50.B1), is a similar match to ATCC cell line CRL-11135 (HCE-2).

e-Signature, Technician:	snicholson 11/6/2017
e-Signature, Reviewer:	gsykes 11/6/2017

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Addendum: Comparative Output from the ATCC STR Profile Database

% Match	ATCC® Cat. No.	Designation	D5S818	D13S317	D7S820	D16S539	vWA	THO1	AMEL	TPOX	CSF1PO
100	STRA7150	HCE-2_50.B1	11,12	8,11	8,10	11	15,18	6,9	X,Y	10,11	10,13
94	CRL-11135	HCE-2 (50.B1); Corneal Epithelium; Human (Homo sapiens)	11,12	8,11	8,10	9,11	15,18	6,9	X,Y	10,11	10,13

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.)

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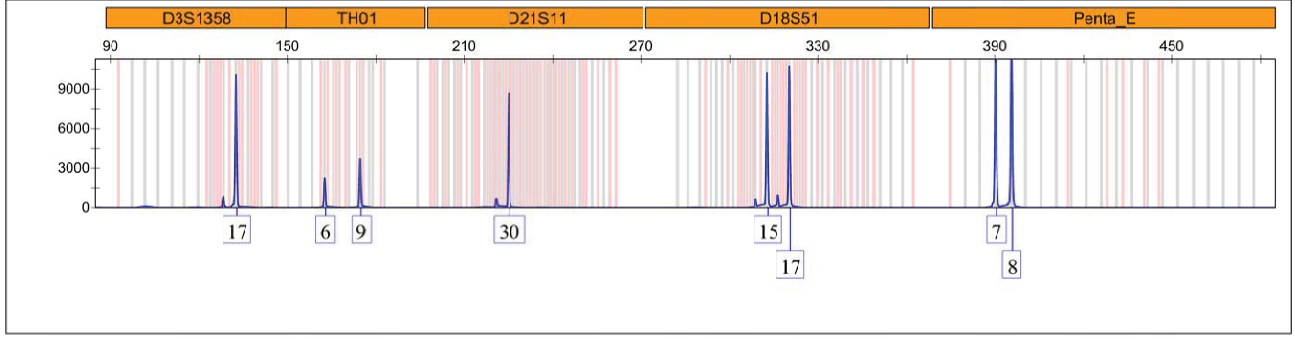
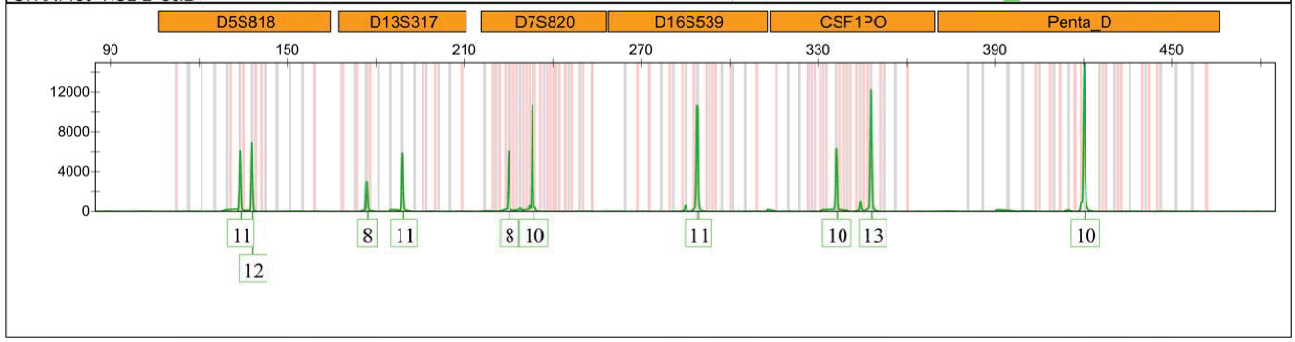
Applied Biosystems
GeneMapper® ID-X 1.2

Project: 20171102-SN-STR

Sample Name	SQ
STRA7150_HCE-2_50.B1	



STRA7150_HCE-2_50.B1



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