

Cell line Authentication Report

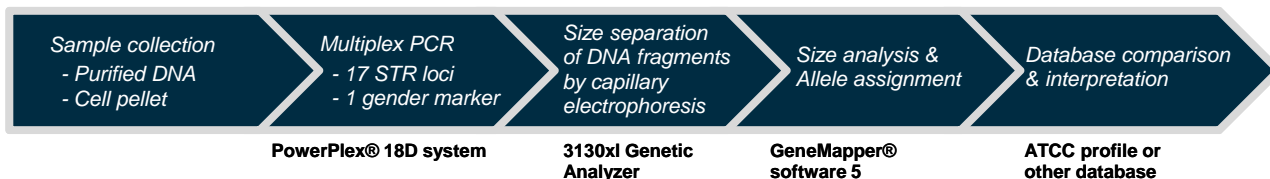
Customer Information

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Sample Information

Sample No.	Sample name	Sample type	Reference profile
1	ARPE-19	Cell pellet	CRL-2302
2			
3			
4			
5			
6			
7			
8			
9			
10			

STR Profiling Workflow



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 Reid et al., Authentication of Human Cell Lines by STR DNA Profiling Analysis. Assay Guidance Manual [Internet], 2013 May 1 published by NCBI. The match criterion is based on an algorithm that compares the number of shared alleles between the reference and sample profile.

$$\% \text{ Match} = \frac{\text{Number of shared alleles}}{\text{Total number of alleles in the reference database profile}}$$

* Homozygous alleles are counted as one allele

Lowest % Match	Result interpretation
≥ 80%	This result is consistent with the two samples being related (same donor)
56-79%	This result is indeterminant and may need further testing
≤ 55%	This result is consistent with the two samples being unrelated (different donors)

Sample No. 1

Match Analysis

Locus	Reference Database Profile		Sample Profile		Shared alleles #
	Database : ARPE-19 (ATCC CRL-2302)		Sample Name : ARPE-19		
D5S818	13		13		1
D13S317	11	12	11	12	2
D7S820	9	11	9	11	2
D16S539	9	11	9	11	2
vWA	16	19	16	19	2
TH01	6	9.3	6	9.3	2
TPOX	9	11	9	11	2
CSF1PO	11		11		1
AMEL	X	Y	X	Y	2
D3S1358			14	15	-
D21S11			28	29	-
D18S51			12	16	-
D8S1179			13		-
FGA			23		-
D2S1338			19		-
D19S433			12	13	-
Penta D			11	13	-
Penta E			7	11	-
<i>Number of shared alleles</i>					16
<i>Total number of alleles in the reference database profile</i>					16
<i>% match</i>					100.0%
Result interpretation					Related

Sample No. 1
Electropherogram

Applied Biosystems
GeneMapper Software 5

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