

Cell Line Authentication Report

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1. Sample information:

Sample No.: “22RV.1”

2. Methods:

- Genomic DNA was extracted from the cell pellets provided by the customer.
- Samples, together with positive and negative control were amplified using GenePrint System (Promega).
- Amplified products were processed using the ABI3730xl Genetic Analyzer.
- Data was analyzed by GeneMapper4.0 software and then compared with the ATCC, DSMZ or JCRB databases for reference matching.

3. Results:

STR profile

Marker	Sample				Database			
	Allele1	Allele2	Allele3	Allele4	Allele1	Allele2	Allele3	Allele4
Amelogenin	X	Y			X	Y		
D5S818	11	13			11	13	12	
D13S317	9	12			9	12		
D7S820	9	10	11		9	10	11	
D16S539	12	12			12	12		
vWA	15	21			15	21		
TH01	6	9.3			6	9.3		
TPOX	8	8			8	8		
CSF1PO	10	11			10	11		
D19S433	13	14						
D21S11	30	30						
D18S51	13	14						
D6S1043	16	16						
D3S1358	15	15						
Penta D	9	12						
D2S441	11	12						
D8S1179	13	14						
Penta E	5	13						
D12S391	18	25						
D2S1338	17	18						
FGA	20	23						

4. Conclusion

A. The STR results show that there are no four alleles on the main nine locus, there is certainly no cross contamination of human cells in this cell line.

B. The match percent between the sample and the STR database profile is **100%**, the cell name is **22RV1**.

Similarity	Cell line	Source	Shared	D5S818	D7S820	D13S317	D16S539	vWA	TH01	TPOX	CSF1PO	Amelogenin
		Your query		11, 13	9, 10, 11	9, 12	12, 12	15, 21	6, 9, 3	8, 8	10, 11	X, Y
100 %	22RV1	CRL-2505	9	11, 12, 13	9, 10, 11	9, 12	12, 12	15, 21	6, 9, 3	8, 8	10, 11	X, Y

C. The D5S818 Loci with 11,13 was supported by the paper(CLS=305037; PubMed=25877200; PubMed=27271795).

Note:

1. The STR profile data was compared with the ATCC, DSMZ or JCRB databases, if the cell line is not included in the three institutions, the results are not correct. More information you provided would be useful for Cell Line Authentication.
2. Based on the ANSI Standard, cell lines with 100% match are considered to be “identical”; cell lines with $\geq 80\%$ but less than 100% match are considered to be “related”.

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