

Cell Line Authentication Report

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1. Sample information:

Sample No.: “SF763”

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
D5S818	12	12			12	12	
D13S317	10	12			10	12	
D7S820	11	12			11	12	
D16S539	10	10			10	10	
VWA	16	17			16	17	
TH01	9	9			9	9	
AMEL	X	X			X	X	
TPOX	10	11			10	11	
CSF1PO	9	9			9	9	
D12S391	17	18					
FGA	22	22					
D2S1338	19	19					
D21S11	27	30					
D18S51	16	16					
D8S1179	13	14					
D3S1358	15	15					
D6S1043	12	12					
PENTAE	5	13					
D19S433	13	15					
PENTAD	11	12					
D1S1656	14	15					

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 **SF763**.
- C. STR profile was published:CCRID=1101HUM-PUMC000050; PubMed=22570425.

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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