

Cell Line Authentication Report

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1. Sample information:

Sample No.: “SK-N-SH”

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	11	11			11	11	
D7S820	7	10			7	10	
D16S539	8	13			8	13	
VWA	14	18			14	18	
TH01	7	10			7	10	
AMEL	X	X			X	X	
TPOX	8	11			8	11	
CSF1PO	11	11			11	11	
D12S391	18	22					
FGA	23.2	24					
D2S1338	17	19					
D21S11	31	31.2					
D18S51	13	16					
D8S1179	15	15					
D3S1358	15	16					
D6S1043	12	18					
PENTAE	7	11					
D19S433	13	14					
PENTAD	10	12					
D1S1656	12	12					

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 **SK-N-SH**.

EV	Cell No.	Cell name	Locus names								
			D5S818	D13S317	D7S820	D16S539	VWA	TH01	AM	TPOX	CSF1PO
		Query (Your Cell)	12,12	11,11	7,10	8,13	14,18	7,10	x,x	8,11	11,11
1.00(36/36)	RCB0426	SK-N-SH	12,12	11,11	7,10	8,13	14,18	7,10	X,X	8,11	11,11

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”.

Operator: Xiaomei Liu, Qin Wang

Leader: Wei Zhou

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