Cell Line Authentication Report

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1. Sample information:

Sample No.: “NOZ”

2. Methods:

a. Genomic DNA was extracted from the cell pellets provided by the customer.
b. Samples, together with positive and negative control were amplified using GenePrint System (Promega).
c. Amplified products were processed using the ABI3730xl Genetic Analyzer.
d. 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	11	13			11	13	
D13S317	8	12			8	12	
D7S820	10	11			10	11	
D16S539	9	11			9	11	
VWA	19	19			19	19	
TH01	7	9			7	9	
AMEL	X	X			X	X	
TPOX	8	11			8	11	
CSF1PO	11	13			11	13	
D12S391	19	19					
FGA	17	17					
D2S1338	20	24					
D21S11	30	31					
D18S51	12	12					
D8S1179	9	9					
D3S1358	15	17					
D6S1043	13	13					
PENTAE	12	17					
D19S433	14	14					
PENTAD	11	13					
D1S1656	11	11					

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 **NOZ.**

EV	Cell No.	Cell name	Locus names								
			D5S818	D13S317	D7S820	D16S539	VWA	TH01	AM	TPOX	CSF1PO
	Query (Your Cell)		11,13	8,12	10,11	9,11	19,19	7,9	X,X	8,11	11,13
1.0(36/36)	JCRB1033	NOZ	['11','13']	['8','12']	['10','11']	['9','11']	['19','19']	['7','9']	['X','X']	['8','11']	['11','13']

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 ≥80% but less than 100% match are considered to be "related".

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