Cell Line Authentication Report

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科佰生物Cobioer

1. Sample information:

Sample No.: “HARA”

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
Amelogenin	X	Y			X	Y	
D5S818	12	12			12	12	
D13S317	9	9			9	9	
D7S820	12	12			12	12	
D16S539	10	10			10	10	
vWA	16	17			16	17	
TH01	7	7			7	7	
TPOX	8	9			8	9	
CSF1PO	13	13			13	13	
D19S433	13	13					
D21S11	30	30					
D18S51	13	13					
D6S1043	11	14					
D3S1358	15	15					
Penta D	9	9					
D2S441	11	11					
D8S1179	10	12					
Penta E	11	11					
D12S391	18	19					
D2S1338	19	20					
FGA	20	20					

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 **HARA [Human squamous cell lung carcinoma].**

Accession	Name	N° Markers	Score	Amel	CSF1PO	D2S1338	D3S1358	D5S818	D7S820	D8S1179	D13S317	D16S539	D18S51	D19S433	D21S11	FGA	Penta D	Penta E	TH01	TPOX	vWA
NA	Query	NA	NA	x,y	13,13			12,12	12,12		9,9	10,10							7,7	8,9	16,17
CVCL_2914	HARA [Human squamous cell lung carcinoma]	8	100.00%	X,Y	13			12	12		9	10							7	8,9	16,17

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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