

Cell Line Authentication Report

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1. Sample information:

Sample No.: “NCI-H460”

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 were analyzed using GeneMapper4.0 software and then compared with the ATCC, DSMZ or JCRB databases for reference matching.

3. Results:

STR profile

Marker	Sample				Cobioer Database		
	Allele1	Allele2	Allele3	Allele4	Allele1	Allele2	Allele3
D5S818	9	10			9	10	
D13S317	13	13			13	13	
D7S820	9	12			9	12	
D16S539	9	9			9	9	
VWA	17	17			17	17	
TH01	9.3	9.3			9.3	9.3	
AMEL	X	Y			X	Y	
TPOX	8	8			8	8	
CSF1PO	11	12			11	12	
D12S391	21	21					
FGA	21	23					
D2S1338	17	25					
D21S11	30	30					
D18S51	13	15					
D8S1179	12	12					
D3S1358	15	18					
D6S1043	11	14					
PENTAE	5	5					
D19S433	14	14					
PENTAD	11	13					

4. Conclusion

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

B. The percent match between the sample and the STR database profile is **100%**, the cell name is **NCI-H460**.

EV	Cell No.	Cell name	Locus names								
			D5S818	D13S317	D7S820	D16S539	VWA	TH01	AM	TPOX	CSF1PO
	Query (Your Cell)		9,10	13,13	9,12	9,9	17,17	9.3,9.3	X,Y	8,8	11,12
1.00(36/36)	737	NCI-H460	9,10	13,13	9,12	9,9	17,17	9.3,9.3	X,Y	8,8	11,12

Note:

1. The STR profile data were compared with the ATCC, DSMZ or JCRB databases, if the cell line was not included in the three institutions, the results were not correct. More information you provide 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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Leader: Wei Zhou

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