Cell Line Authentication Report

Institution：Cobioer Biosciences CO.,LTD

Customer：Taohua Jiang

Tel：025-86880024

Email：jiangtaohua@cobioer.com

Vendor：Cobioer Biosciences CO.,LTD

Attention：Taohua Jiang

Tel：025-86880024

Email：jiangtaohua@cobioer.com

科伯生物Cobioer

1. Sample information:

Sample No.: “NCI-H2452”

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	12			11	12	
D13S317	12	12			12	12	
D7S820	9	11			9	11	
D16S539	11	13			11	13	
VWA	17	18			17	18	
TH01	6	9.3			6	9.3	
AMEL	X	Y			X	Y	
TPOX	8	11			8	11	
CSF1PO	11	12			11	12	
D12S391	17.3	21					
FGA	23	23					
D2S1338	20	20					
D21S11	28	32.2					
D18S51	15	15					
D8S1179	10	10					
D3S1358	17	17					
D6S1043	11	12					
PENTAE	12	15					
D19S433	13	13					
PENTAD	9	9					
D1S1656	12	17.3					

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 **NCI-H2452 [H2452].**

EV	Cell No.	Cell name	Locus names								
			D5S818	D13S317	D7S820	D16S539	VWA	TH01	AM	TPOX	CSF1PO
	Query (Your Cell)		11,12	12,12	9,11	11,13	17,18	6,9.3	X,Y	8,11	11,12
1.0(36/36)	CRL-5946	NCI-H2452 [H2452]	['11', '12']	['12', '12']	['9', '11']	['11', '13']	['17', '18']	['6', '9.3']	['X', 'Y']	['8', '11']	['11', '12']

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".

Operator：Xiaomei Liu, Qin Wang

Leader：Wei Zhou

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