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

1. Sample information:

Sample No.: “NCI-H446”

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 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				Database		
	Allele1	Allele2	Allele3	Allele4	Allele1	Allele2	Allele3
D5S818	11	11			11	11	
D13S317	8	8			8	8	
D7S820	10	11			10	11	
D16S539	12	12			12	12	
VWA	18	19			18	19	
TH01	8	9.3			8	9.3	
AMEL	X	Y			X	Y	
TPOX	9	11			9	11	
CSF1PO	13	14			13	14	
D12S391	17	18					
FGA	22	22					
D2S1338	18	20					
D21S11	28	28					
D18S51	12	13					
D8S1179	13	15					
D3S1358	17	17					
D6S1043	11	11					
PENTAE	9	10					
D19S433	13	14					
PENTAD	12.1	13.1					

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-H446.**

Similarity	Cell line	Source	Shared	D5S818	D7S820	D13S317	D16S539	vWA	TH01	TPOX	CSF1PO	Amelogenin
		Your query		11, 11	10, 11	8, 8	12, 12	18, 19	8, 9.3	9, 11	13, 14	X, Y
100 %	NCI-H446 [H446]	HTB-171	9	11, 11	10, 11	8, 8	12, 12	18, 19	8, 9.3	9, 11	13, 14	X, Y

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

Operator：Xiaomei Liu, Qin Wang

Leader：Wei Zhou

Date：2018-03-27