

Cell Line Authentication Report

Institution: Cobioer Biosciences CO.,LTD Vendor: Cobioer Biosciences CO.,LTD

Customer: Taohua Jiang

Attention: Taohua Jiang

Tel: 025-86880024

Tel: 025-86880024

Email: jiangtaohua@cobioer.com

Email: jiangtaohua@cobioer.com

1. Sample information:

Sample No.: “NB-1”

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 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	9	11			9	11	
D13S317	10	13			10	13	
D7S820	8	12			8	12	
D16S539	9	9			9	9	
VWA	16	19			16	19	
TH01	7	7			7	7	
AMEL	X	X			X	X	
TPOX	11	11			11	11	
CSF1PO	10	12			10	12	
D12S391	19	20					
FGA	19	22					
D2S1338	17	28					
D21S11	31	31.2					
D18S51	14	14					
D8S1179	12	16					
D3S1358	15	17					
D6S1043	14	19					
PENTAE	17	18					
D19S433	13.2	15.2					
PENTAD	8	9					

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 **NB-1**.

EV	Cell No.	Cell name	Locus names								
			D5S818	D13S317	D7S820	D16S539	VWA	TH01	AM	TPOX	CSF1PO
	Query (Your Cell)		9,11	10,13	8,12	9,9	16,19	7,7	X,X	11,11	10,12
1.00(36/36)	IFO50295	NB-1	9,11	10,13	8,12	9,9	16,19	7,7	X,X	11,11	10,12

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 $\geq 80\%$ but less than 100% match are considered to be “related”.

Operator: Xiaomei Liu, Qin Wang

Leader: Wei Zhou

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