

Cell Line Authentication Report

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1. Sample information:

Sample No.: “HCT116”

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
Amelogenin	X	Y			X	Y	
D5S818	10	11			10	11	
D13S317	10	12			10	12	
D7S820	11	12			11	12	
D16S539	11	13			11	13	
vWA	17	22			17	22	
TH01	8	9			8	9	
TPOX	8	8			8	8	
CSF1PO	7	10			7	10	
D19S433	12	13					
D21S11	29	30					
D18S51	16	17					
D6S1043	13	14					
D3S1358	12	17	18	19			
Penta D	9	13					
D2S441	11	12					
D8S1179	12	14					
Penta E	13	14					
D12S391	17	21	22				
D2S1338	16	16					
FGA	18	23					

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 **HCT 116**.

Similarity	Cell line	Source	Shared	D5S818	D7S820	D13S317	D16S539	vWA	TH01	TPOX	CSF1PO	Amelogenin
		Your query		10, 11	11, 12	10, 12	11, 13	17, 22	8, 9	8, 8	7, 10	X, Y
100 %	HCT 116	KCLB Korea 10247	9	10, 11	11, 12	10, 12	11, 13	17, 22	8, 9	8, 8	7, 10	X, Y

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”.

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