Cell Line Authentication Report

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1. Sample information:

Sample No.: “LNCaP clone FGC”

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	10	12			10	12	
D7S820	9.1	10.3			9.1	10.3	
D16S539	11	11			11	11	
VWA	16	18			16	18	
TH01	9	9			9	9	
AMEL	X	Y			X	Y	
TPOX	8	9			8	9	
CSF1PO	10	11			10	11	
D12S391	21	22					
FGA	19	20	21				
D2S1338	16	16					
D21S11	29	32.2					
D18S51	10	11	12				
D8S1179	12	14					
D3S1358	16	16					
D6S1043	11	18					
PENTAE	12	16					
D19S433	13.2	15					
PENTAD	12	12.3					
D1S1656	15	16					

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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 **LNCaP clone FGC.**

EV	Cell No.	Cell name	Locus names								
			D5S818	D13S317	D7S820	D16S539	VWA	TH01	AM	TPOX	CSF1PO
	Query (Your Cell)		*11,12*	*10,12*	*9.1,10.3*	*11,11*	*16,18*	*9,9*	*x,y*	*8,9*	*10,11*
1.00(36/36)	CRL-1740	LNCaP clone FGC	11,12	10,12	9.1,10.3	11,11	16,18	9,9	X,Y	8,9	10,11

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".

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