Cell Line Authentication Service

STR Profiling Report

Sample From: Department of Radiation Oncology, The First Affiliated Hospital of Nanjing Medical University, Nanjing, China.

Sample Type: Cell Line

Testing Method: STR Genotyping

Report Time: December 21, 2022

Add: Room 502, NO.1015 Longteng Rd , Songjiang District, Shanghai/ Tel:+86-18521538068 / E-mail: zhusn@biowing.com.cn

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Testing Company: Shanghai Biowing Applied Biotechnology Co. Ltd

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Sample code

Table 1. Sample Code

Customer's code	Company Code
CNE-2	20221219-02

Sample Number :1

Sample Type: Cell line

Testing Type: STR

Testing Method:

DNA was extracted by a commercial kit from CORNING (AP-EMN-BL-GDNA-250G). The twenty STRs including Amelogenin locus were amplified by six multiplex PCR and separated on ABI 3730XL Genetic Analyzer. The signals were then analyzed by the software GeneMapper.

Data Interpretation:

Cell lines were authenticated using Short Tandem Repeat (STR) analysis asdescribed in 2012 in ANSI Standard (ASN-0002) by the ATCC Standards Development Organization (SDO) and in Capes-Davis et al., Match criteria for human cell line authentication: Where do we draw the line? Int J Cancer.2013;132(11):2510-9.

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Test Results

1. STR profile

Table 2. STR and Amelogenin Genotyping Results of Cell line.

Loci	Sample information			Cell Bank information		
	Sample name：CNE-2			Cell line name：CNE-2		
	Allele1	**Allele2**	**Allele3**	**Allele1**	**Allele2**	**Allele3**
D5S818	11	12		11	12	
D13S317	10	12	13.3	10	12	13.3
D7S820	10	12		10	12	
D16S539	9	10		9	10	
VWA	14	16	17	14	16	
TH01	6	7	9	6	7	9
AMEL	X	X		X	X	
TPOX	8	9	12	8	9	12
CSF1PO	10	11		10	11	
D12S391	20	21				
FGA	18	21	22			
D2S1338	17	23				
D21S11	27	30				
D18S51	13	16				
D8S1179	12	12				
D3S1358	15	18				
D6S1043	11	14	18			
PENTAE	17	20				
D19S433	13	13				
PENTAD	9	12				
D1S1656	12	15				

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2. database annotation

Figure 1. STR matching analysis

EV	Cell No.	Cell name	Locus names							
			D5S818	D13S317	D7S820	D16S539	VWA	TH01	AM	TPOX	CSF1PO
	Query (Your Cell)		11,12,	10,12,13.3	10,12,	9,10,	14,16,17	6,7,9	X,X,	8,9,12	10,11,
0.98(35/36)	CVCL_6889	CNE-2	['11', '12']	['10', '12', '13.3']	['10', '12']	['9', '10']	['14', '16']	['6', '7', '9']	['X', 'X']	['8', '9', '12']	['10', '11']

Note: The STR online match analysis of the test cell against DSMZ/ATCC/EXPASY database, showing cell number (Cell No.) and cell name.

3. Authentication

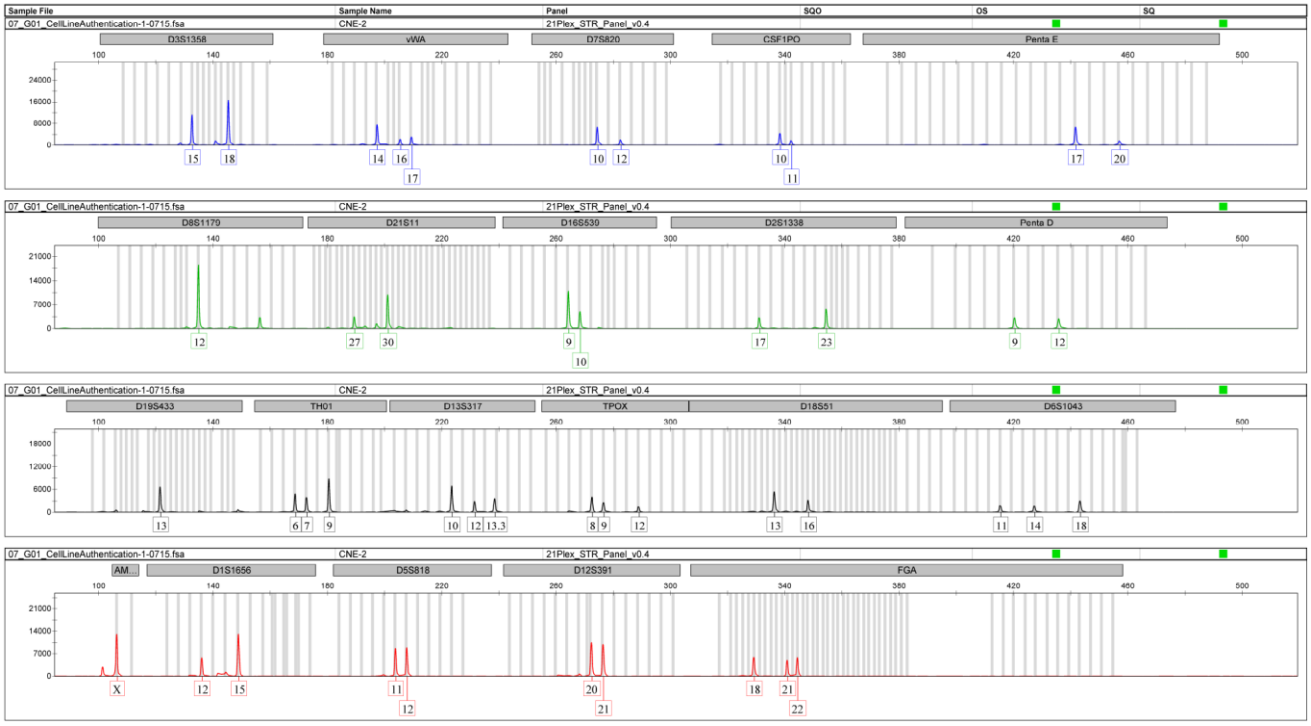
☐ The submitted sample profile is human, but not a match for any profile in the DSMZ STR database.

☑ The submitted profile is exact match for the following human cell line(s) in the DSMZ STR database (8 core loci plus Amelogenin): **CNE-2**.

☐ The submitted profile is similar to the following DSMZ human cell line: /.

- **Note:** A cell line are considered to be related, derived from a common ancestry, when 80% (exact match) of the alleles in its STR profile match profiles from tissue or other cell line samples from that donor or from database. Cell lines with between a 55% to 80% (similar) match require further profiling for investigation of relatedness.

Figure 2. STR profiles of sample cell line



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Appendix

1. Genotyping Strategy and Site Distribution

Table S1. Experimental Strategy and Sites

	Strategy 1	Strategy 2	Strategy 3	Strategy 4
1	D3S1358	D8S1179	D19S433	AMEL
2	VWA	D21S11	TH01	D1S1656
3	D7S820	D16S539	D13S317	D5S818
4	CSF1PO	D2S1338	TPOX	D12S391
5	PENTAE	PENTAD	D18S51	FGA
6			D6S1043	

The allele match algorithm compares the 8 core loci plus amelogenin only, even though alleles from all lociwill be reported when available.

2. DSMZ tools was used to carry on the cell line comparison, which contains 2455 cell lines STR data from ATCC, DSMZ, JCRB ,ECACC， GNE and RIKEN databases. If the cell is not included in the above cell library, users need to compared with other databases.

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