

# Cell Line Authentication – STR Profiling Report

Sample Type: Cell Line Testing Type: STR

Sample code:

Table 1. Sample Code

Customer's code	Company Code
HT22	20220310-01

Sample Number:1

Sample Type: Cell line

Testing Type: STR

Sample From: Shanghai Zhong Qiao Xin Zhou Biotechnology Co.,Ltd.

# Testing Method:

DNA was extracted by a commercial kit from CORNING (AP-EMN-BL-GDNA-250G). Twenty short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, 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 as described 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.



#### Test Results:

#### 1. Result

Table 2. Matching information on the cell lines

Sample Code	Multi-allele	Cell line matched	Cross contamination	EV
20220310-01	YES	Mouse	/	/

• Multi-allele means some STR contain more than two loci.

#### 2. Sample Description

#### 20220310-01:

- A. The STR results showed that multiple alleles were found in this cell line, and no cross contamination of human cells was found in the cell line.
- B.The sample profile is Mus musculus (Mouse), No matching cell lines were found in the cell line retrieval. The matching results could not be displayed because relevant STR data information was not entered into the database.

## 3. Genotyping Result

	Sample information				Cell Bank information		
Loci	Sample name: HT-22			Cell line name: /			
	Allele1	Allele2	Allele3	Allele4	Allele1	Allele2	Allele3
	233.37	237.42			229.37	233.39	237.42
4-2	【19.3】	【20.3】			[18.3]	【19.3】	[20.3]



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5-5	335.28	347.6	351.62		331.27	335.35	339.33
	【14】	[17]	[18]		[13]	[14]	[15]
6-4	290.46	299.6			290.57		
0-4	<b>[</b> 16 <b>]</b>	[18]			[15.3]		
	334	338.02	346.07		334		
6-7	[12]	【13】	[15]		[12]		
	220.94	233.18			220.93	224.96	
9-2	【15】	[18]			【15.1】	<b>【</b> 16 <b>】</b>	
10.1	229.48	241.7			241.68	245.79	
12-1	[17]	【20】			[20]	<b>[</b> 21 <b>]</b>	
15.0	192.5	196.51	200.43	204.66	192.55		
15-3	【20.3】	[21.3]	【22.3】	【23.3】	[20.3]		
	151.66	159.82			155.62	163.73	
18-3	【16】	[18]			[17]	<b>【</b> 19 <b>】</b>	
X-1	408.19	412.18			400.13		_
	[27]	[28]			[25]		
D4S2408							

Table 3. STR and Amelogenin Genotyping Results of Cell line 20220310-01

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

# **Others:**



## 1.Genotyping Strategy and Site Distribution

Attached Table. Experimental Strategy and Sites

	Strategy 1	Strategy 2
1	18-3(FAM)	12-1(FAM)
2	4-2 (FAM)	5-5(FAM)
3	6-7(FAM)	X-1(FAM)
4	9-2(NED)	15-3(NED)
5		6-4(NED)
6		D4S2408(NED)

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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