Cell Line Authentication Service

STR Profiling Report

Sample From: iCell Bioscience Inc

Sample Type: Cell Line

Testing Method: STR Genotyping

Report Time: 2021/06/18

COMPANY STATEMENT

1. THIS REPORT IS ONLY RESPONSIBLE FOR THE SAMPLES ANALYZED.
2. THE TESTING RESULTS AND THE ORGANIZATION NAME WILL NOT BE USED FOR ADVERTISEMENT, COMMERCIAL EXHIBITIONS, COMMERCIAL PERFORMANCE AND OTHER COMMERCIAL ACTIVITIES.
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Cell Line Authentication – STR Profiling Report

Sample code

Table 1. Sample Code

Customer's code	**Company Code**
neuro-2a	20210611-01

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 ten STRs including one human locus were amplified by 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, mouse cell line authentication cytotechnology. 2014;66:133-147.

1. Result

Table 2. Matching information on the cell lines

Sample Code	**Multi-allele**	**Cell line matched**	**Cell Bank**	**Cross contamination**	**EV**
20210611-01	No	Neuro-2a	Control	No	1.0

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

2. Sample Description

The sample profile is Mus musculus (Mouse), but not a match for any profile in the EXPASY.

No multiple alleles and no cross contamination was found in the cell line.

As the STR database of **Neuro-2a** was not logged in, the matching result can't be displayed, The sample is exact match with the control cell line **Neuro-2a**. If the paper was to publish, these data could be submitted to the magazine.

3. Genotyping Result

Table 3. STR and Amelogenin Genotyping Results of Cell line

Loci	**Sample information**			**Cell Bank information**		
	Sample name：neuro-2a			Cell line name：Neuro-2a		
	Allele1	**Allele2**	**Allele3**	**Allele1**	**Allele2**	**Allele3**
4-2	241.59【21.3】	245.58【22.3】		241.83【21.3】	245.81【22.3】	
5-5	339.67【15】	347.65【17】		339.66【15】	347.81【17】	
6-4	299.89【18】	307.77【19】		300.1【18】	307.97【19】	
6-7	334.1【15】			334.44【15】		
9-2	221.06【15】	225.48【16】		221.26【15】	225.44【16】	
12-1	225.3【16】			225.85【16】		
15-3	197.02【21.3】	200.15【22.3】	205.17【23.3】	196.94【21.3】	200.29【22.3】	204.99【23.3
18-3	176.13【22】			176.52【22】		
X-1	404.29【26】	409.33【27】		405.08【26】	409.15【27】	
D4S2408	-	-				

Others:

1. Genotyping Strategy and Site Distribution

Attached Table. Experimental Strategy and Sites

	Panel1	Panel2
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)

The allele match algorithm compares the 9 core loci plus amelogenin only.

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. D4S2408 is a human locus, which is used to detect whether the cells are contaminated by human.

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