Cell Line Authentication Report
STR Profiling

Sample Type: Cell Line

Sample from: ATCC, USA

Testing Method: STR Genotyping

Report Time: December 13, 2017

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.
3. OBJECTIONS SHOULD BE RAISED WITHIN FIFTEEN DAYS AFTER THE RECEIPT OF THIS REPORT.
4. THE PAPER REPORT WITH CONTENT ALTERING, ADDING OR WITHOUT THE STAMPED SEAL OF THE COMPANY ARE INVALID.

Cell Line Authentication – STR Profiling Report

Sample code

Table 1. Sample Code

Customer's code	Company Code
BV-2	20171205-01

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.

Test Results:

1. Result

Table 2. Matching information on the cell lines

Sample Code	Multi-allele	Cell line matched	Cross contamination	EV
20171205-01	No	Mouse cell line	No	1.00

- Multi-allele means some STR contain more than two loci.
- The test result of each cytotype is good.

2. Sample Description

A. The STR results showed that no multiple alleles were found in this cell line, and no cross contamination of human cells was found in the cell line.

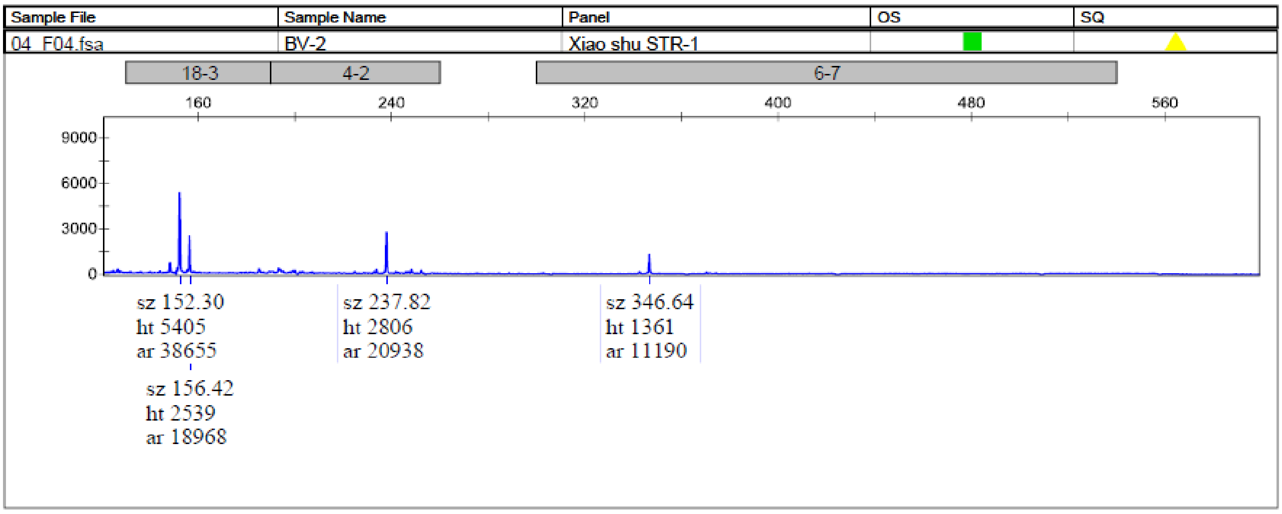
B. No cross contamination was found in the cell line, and the cell line was normal. As the STR database of EF021 was not logged in, the matching result could not be displayed. If the paper was to publish, these data could be submitted to the magazine.

3. Genotyping Result

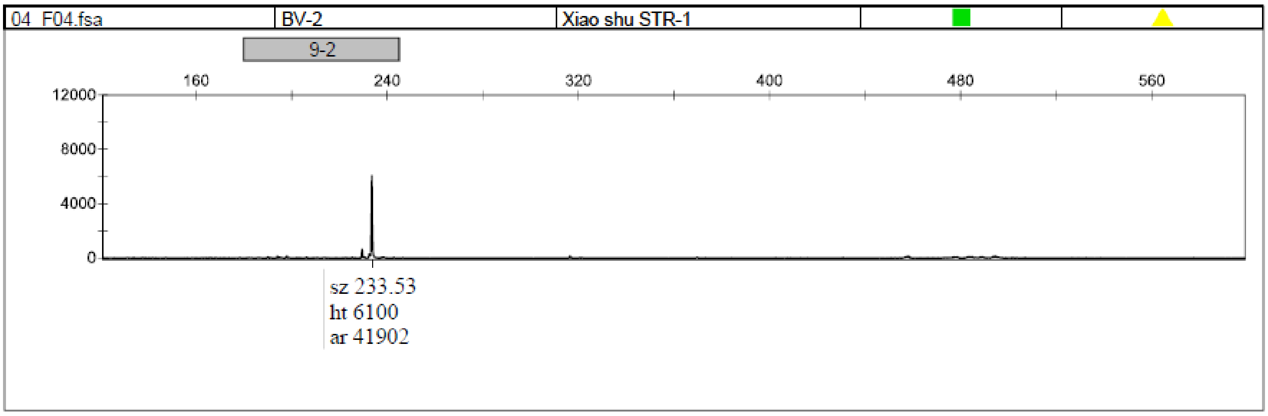
Table 3. STR and Amelogenin Genotyping Results of Cell line 20171127-01

Loci	**Sample information**			**Cell Bank information**		
	Sample name：BV-2			Cell line name：		
	Allele1	**Allele2**	**Allele3**	**Allele1**	**Allele2**	**Allele3**
4-2	237.82					
5-5	348.21					
6-4	300.1					
6-7	346.64					
9-2	233.53					
12-1	230.09					
15-3	201.16	205.14				
18-3	152.3	156.42				
X-1	408.42					
D4S2408						

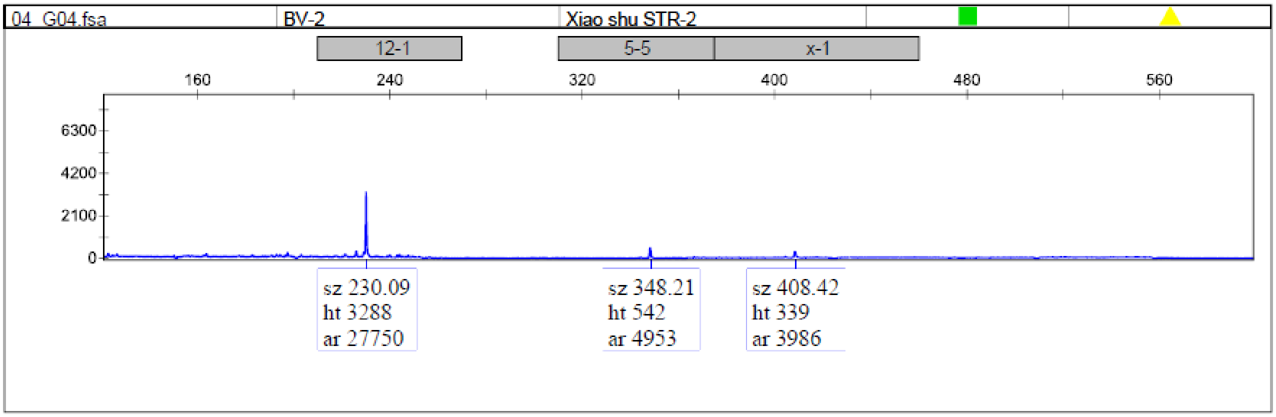
GeneMapper Analysis:



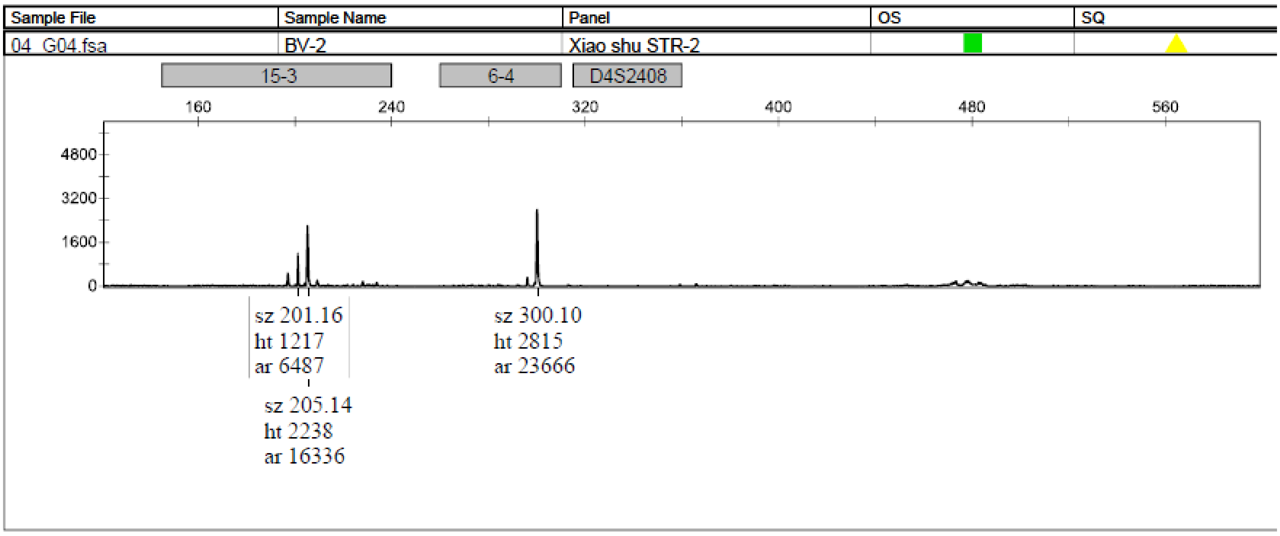
Sample File	Sample Name	Panel	OS	SQ
04_F04.fsa	BV-2	Xiao shu STR-1	🟩	▲



04_F04.fsa	BV-2	Xiao shu STR-1	🟩	▲



04_G04.fsa	BV-2	Xiao shu STR-2	🟩	▲



Sample File	Sample Name	Panel	OS	SQ
04_G04.fsa	BV-2	Xiao shu STR-2	🟩	▲

Others:

1. Genotyping Strategy and Site Distribution

Table 4. Experimental Strategy and Sites

	Plan1	**Plan2**
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 8 core loci plus amelogenin only, even though alleles from all loci will 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.

Issue date: December 13, 2017