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Cell Line Authentication Service

STR Profiling Report

Sample Type: Cell Line

Sample from: Department of General Surgery, Renji Hospital,
School of Medicine, Shanghai Jiao Tong University

Testing Method: STR Genotyping

Report Time: March 29, 2018



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Cell Line Authentication – STR Profiling Report

Sample code

Table 1. Sample Code

| Customer's code | Company Code |
|-----------------|--------------|
| SGC-7901 | 20180329-02 |

Sample Number:1

Sample Type: Cell line

Testing Type: STR

Sample From: Department of General Surgery, Renji Hospital, School of Medicine, Shanghai Jiao Tong University

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 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 | Cell Bank | EV | Percentage |
|-------------|--------------|-------------------|-----------|----|------------|
| 20180329-02 | No | SGC-7901 | CRC | 1 | 9/9 |

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

2. Sample Description



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20180329-02:

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. The DNA of the cell lines found to basic match the type of cell lines in a cell line retrieval, CRC database shows that cells called **SGC7901**, corresponding to the cell number _

3111C0001CCC000236 .

| 匹配结果表 | | | | | | | | | | | | | | | |
|-------|---------|---------|--------|--------|--------|---------|------|---------|---------|---------|---------|-------|------|--------|------------|
| ID | 细胞名 | D8S1179 | D21S11 | D7S820 | CSF1PO | D3S1358 | TH01 | D13S317 | D16S539 | D2S1338 | D19S433 | VWA | TPOX | D18S51 | Amelogenin |
| | 你的数据 | 12 | 27,28 | 8,12 | 9,10 | 15,18 | 7 | 12,13,3 | 9,10 | 17 | 13,14 | 16,18 | 8,12 | 16 | X |
| 64 | SGC7901 | 12 | 27,28 | 12 | 10 | 15,18 | 7 | 13,3 | 9,10 | 17 | 13 | 16,18 | 12 | 16 | X |

3. Genotyping Result

Table 3. STR and Amelogenin Genotyping Results of Cell line 20180329-02

| Loci | Sample information | | | Cell Bank information | | |
|---------|-----------------------|---------|---------|--------------------------|---------|---------|
| | Sample name : SGC7901 | | | Cell line name : SGC7901 | | |
| | Allele1 | Allele2 | Allele3 | Allele1 | Allele2 | Allele3 |
| D5S818 | 11 | 12 | | 11 | 12 | |
| D13S317 | 12 | 13.3 | | 12 | 13.3 | |
| D7S820 | 8 | 12 | | 8 | 12 | |
| D16S539 | 9 | 10 | | 9 | 10 | |
| VWA | 16 | 18 | | 16 | 18 | |
| TH01 | 7 | 7 | | 7 | 7 | |
| AMEL | X | X | | X | X | |
| TPOX | 8 | 12 | | 8 | 12 | |
| CSF1PO | 9 | 10 | | 9 | 10 | |
| D12S391 | 20 | 25 | | | | |
| FGA | 21 | 21 | | | | |
| D2S1338 | 17 | 17 | | | | |
| D21S11 | 27 | 28 | | | | |
| D18S51 | 16 | 16 | | | | |



| | | | |
|---------|----|----|--|
| D8S1179 | 12 | 13 | |
| D3S1358 | 15 | 18 | |
| D6S1043 | 18 | 19 | |
| PENTAE | 7 | 17 | |
| D19S433 | 13 | 14 | |
| PENTAD | 8 | 15 | |

Others:

1. Genotyping Strategy and Site Distribution

Attached Table. Experimental Strategy and Sites

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

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.

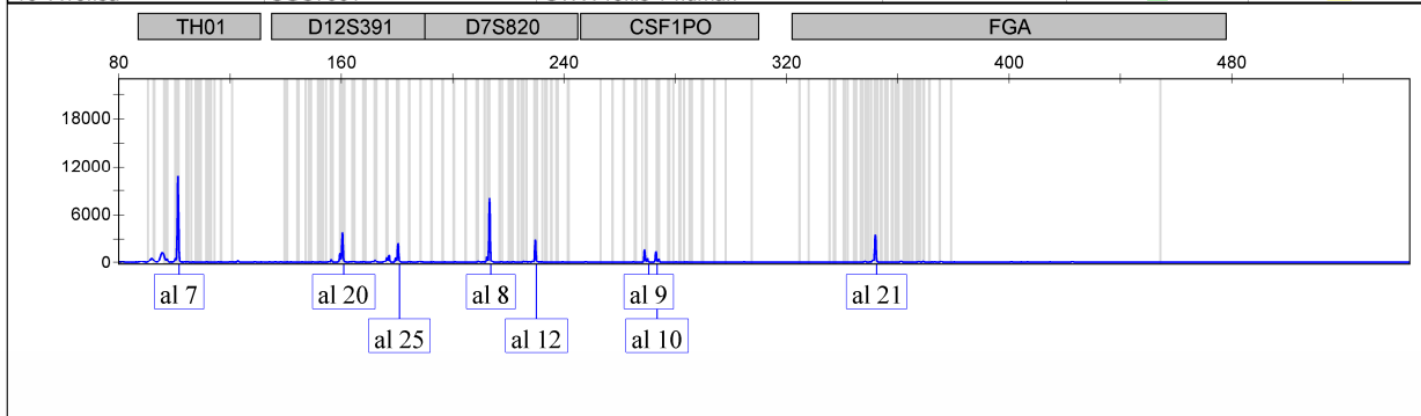
Technician: Menglu Shen

Check: Yang Bai

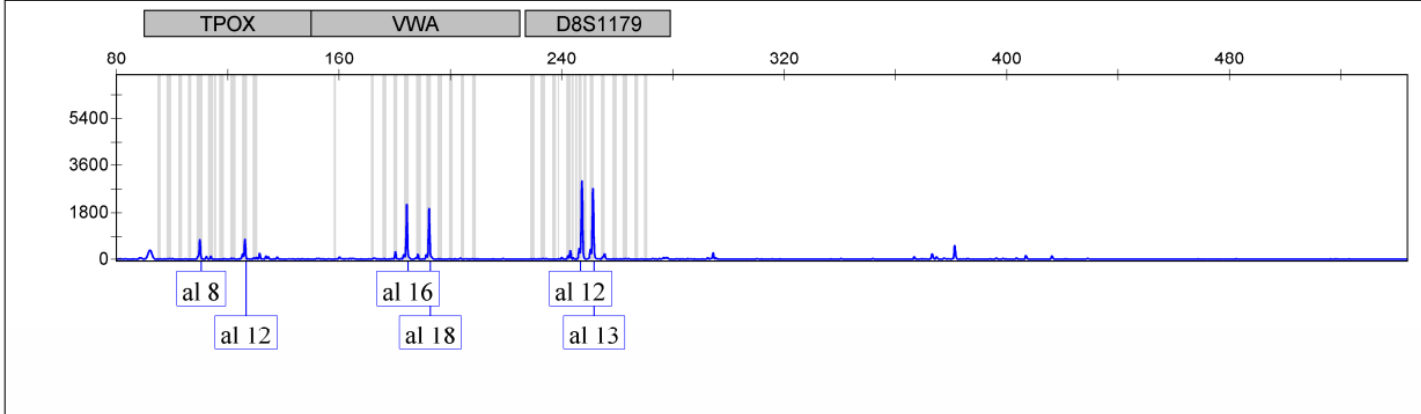
Person in Charge: Yiqun Chen

Issue date: March 29, 2018

| Sample File | Sample Name | Panel | SQI | OS | SQ |
|-------------|-------------|---------------------|-----|--------------------------------------|---------------------------------------|
| 10_A10.fsa | SGC7901 | STR Profile 1-human | | ■ | ▲ |



| Sample File | Sample Name | Panel | SQI | OS | SQ |
|-------------|-------------|---------------------|-----|--------------------------------------|---------------------------------------|
| 10_F10.fsa | SGC7901 | STR Profile 2-human | | ■ | ▲ |



| Sample File | Sample Name | Panel | SQI | OS | SQ |
|-------------|-------------|---------------------|-----|--------------------------------------|---------------------------------------|
| 11_C11.fsa | SGC7901 | STR Profile 3-human | | ■ | ▲ |

