

## Report of Human Cell Line Authentication

|                                      |                                        |
|--------------------------------------|----------------------------------------|
| <b>Sample Label:</b> PC-9            | <b>Sample Quantity:</b> 1 tube         |
| <b>Sample Number:</b> X3B0424-000707 | <b>Sample Type:</b> Cell precipitation |
| <b>Sample State:</b> Precipitation   | <b>ReceivingDate:</b> 2024-02-22       |
| <b>Sample Submitted By:</b> 赵威       | <b>TestDate:</b> 2024-02-22            |
| <b>Contact:</b> 13911063713          | <b>Report Date:</b> 2024-02-26         |
| <b>Client:</b> 北京市肿瘤防治研究所            |                                        |

**Data Interpretation** Method refer to “The Pharmacopoeia of the People's Republic of China, Volume III General Requirements, Requirements for Preparation and Control of Animal Cell Substrates Used for Production of Biologics”. The STR profile was compared with the ATCC, DSMZ and ExPASy databases for reference matching<sup>1,2</sup> and result interpretation were based on “ATCCASN-0002 revised 2021—Standardization of Short Tandem Repeat (STR) Profiling”.

**Methodology** **Sample DNA was extracted**, and PCR amplified with STR Multi-amplification Kit (Microreader™ 21 ID System). PCR products were assayed with ABI 3730xl DNA Analyzer (Applied Biosystems®). Appropriate positive and negative controls were run and confirmed for each sample submitted. Data of 20 STR loci plus the Amelogenin locus were analyzed and extracted using GeneMapperID-X software and designated as the STR profile of the test sample.

**Results** The results of the negative and positive control match expectations. The STR profiles of the test sample are clear, which are shown in the attached table and figure. Multiple Alleles<sup>3</sup> are shown following.

| #of Multiple Alleles | Locus |
|----------------------|-------|
| 0                    | ---   |

**Explanation of Test Results**

According to ATCC ASN-0002-2021, Cell lines with  $\geq 80\%$  match at 13 STR loci or  $\geq 90\%$  match at eight STR loci are considered to be related.

**PC-9:**

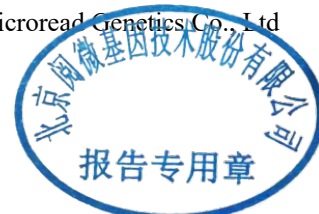
- 1、 The submitted sample profile is human.
- 2、 The submitted profile has no human Cell lines with  $\geq 56\%$  match in ATCC database.
- 3、 The submitted profile has a 100% match on 9 loci of the following human cell line(s) in DSMZ database: PC-9 (formerly known as PC-14).
- 4、 The submitted profile has a 96.77% match on 12-STR of the following human cell line(s) in ExPASy database: PC-14.
- 5、 The submitted profile has a 93.88% match on 19-STR of the following human cell line(s) in ExPASy database: PC-9.

Operator: *Xiaodie Li*

Auditor: *Linyu Wu*

Signatory: *Xuejia Sun*

Beijing Microread Genetics Co., Ltd



### Results of database comparison (the highest percent match to the query)

|            | ATCC | DSMZ    | ExPASy      |           |    | Sample         |
|------------|------|---------|-------------|-----------|----|----------------|
| Cell Name  | NA   | PC-9    | PC-9(PC-14) | PC-9      |    | PC-9           |
| Cell ID    | NA   | RCB0446 | CVCL_1640   | CVCL_B260 |    | X3B0424-000707 |
| Amelogenin | NA   | X, X    | X           | X         | X  | X              |
| D5S818     | NA   | 11, 11  | 11          | 11        | 11 | 11             |
| D13S317    | NA   | 8, 8    | 8           | 8         | 8  | 8              |
| D7S820     | NA   | 10, 11  | 10,11       | 10,11     | 10 | 11             |
| D16S539    | NA   | 9, 9    | 9           | 9         | 9  | 9              |
| vWA        | NA   | 17, 17  | 17          | 17        | 17 | 17             |
| TH01       | NA   | 7, 7    | 7           | 7         | 7  | 7              |
| TPOX       | NA   | 11, 11  | 11          | 11        | 11 | 11             |
| CSF1PO     | NA   | 11, 11  | 11          | 11        | 11 | 11             |
| D19S433    | /    | -       |             | 13, 15.2  | 13 | 15.2           |
| D21S11     | NA   | -       | 29,30       | 30        | 29 | 30             |
| D18S51     | NA   | -       | 15          | 15        | 15 | 15             |
| D6S1043    | /    | /       |             |           | 13 | 19             |
| D3S1358    | NA   | -       |             | 16        | 16 | 16             |
| Penta D    | /    | -       |             | 13        | 9  | 13             |
| D2S441     | /    | /       |             | 11        | 11 | 11             |
| D8S1179    | NA   | -       | 11,15       | 11,15     | 11 | 15             |
| Penta E    | /    | -       |             | 11        | 11 | 15             |
| D12S391    | /    | /       |             | 18        | 18 | 18             |
| D2S1338    | /    | -       |             | 19,20     | 19 | 20             |
| FGA        | NA   | -       | 23,25       | 23        | 23 | 23             |
| Shared STR | NA   | 9       | 12          | 19        |    |                |

|  | ATCC | DSMZ | ExPASy | Sample |
|--|------|------|--------|--------|
|--|------|------|--------|--------|

loci<sup>4</sup>

|                       |    |      |        |        |
|-----------------------|----|------|--------|--------|
| Matching <sup>5</sup> | NA | 100% | 96.77% | 93.88% |
|-----------------------|----|------|--------|--------|

|                             |   |                                   |                                   |  |
|-----------------------------|---|-----------------------------------|-----------------------------------|--|
| Interpretation <sup>6</sup> | — | Likely to be from the same donor. | Likely to be from the same donor. |  |
|-----------------------------|---|-----------------------------------|-----------------------------------|--|

## Remarks

1. The short tandem repeat (STR) profile is indicative only of the sample sent to Beijing Microread Genetics Co., Ltd at the time it was sent. Effective peaks are real PCR bands, small peaks and non-specific bands are ignored in calculation.
2. The STR genotyping profile of the submitted cell is compared with ATCC,DSMZ and ExPASy databases, in which STR genotypes of over 100,000 human cell lines from ATCC, DSMZ, JCRB, ECACC, Riken etc. were recorded.Cells that are not included in above databases could not be compared. For failed sample, it's genotyping and figure result would be shown as NA.
3. Both mixed cultures and MSIpositive cell lines can show additional STR alleles in one or more STR loci. In short, two fundamentally different causes can be the reason for multiple alleles at a locus: drifted alleles by MSI or some other DNA replication error or the presence of a mixed culture containing a contaminating second human cell line.
4. The number of STR loci shared by the submitted sample and the cells in database. Amelogenin does not belong to STR locus.
5. The matching score ofATCC,DSMZ and ExPASyis“Tanabe”—  $2 \times (\text{number of alleles matching}) / (\text{total number of alleles in database profile and query sample}) \times 100\%$ .
6. The interpretation is based on “ATCC ASN-0002-2021”.“Two samples are considered possibly related when their STR profiles match at 80-90% of alleles across the 13 core STR loci, as calculated using the matching algorithm. At matches of 90% or greater, the cell lines have very likely originated from the same donor. Samples between 60 and 79% match tend to be unrelated, but need may further investigation to confirm that they are unrelated. Two common causes of related cell lines scoring below 80% are (1) if the cell line has extra alleles due to it being MSI unstable, and (2) misidentification of the cell line's origin. Generally, cell lines are authentic (i.e., are derived from the same original tissue donor) when they show the expected percent match ( $\geq 80\%$  at 13 STR loci or  $> 90\%$  match at eight STR loci) to other results from that donor (tissue or other cell line samples within the database).”
7. The testingresults were calculated and generated by each cell database ONLINE tool.In some case, there may be differentprofiles of same cell line in each database and possibly lead to different matching results. In addition, limited by the algorithm of the calculation model (the

less the number of shared STR sites, the higher the probability of matching unrelated cells), non-cell line(s)human cells/sample(s) may also match to cell(s) in database. Inthese conditions, the comparison results in this report are for reference only.

8. Beijing Microread Genetics performs STR Profiling following ISO 9001:2015 and ISO 13485:2016 quality standards. The results are judged according to industry standards or consensus and can only be used for cell line inspection and authentication. We are NOT responsible for any purpose or interpretation other than the purpose specified.

Figure1: STR profiles ofPC-9cell line

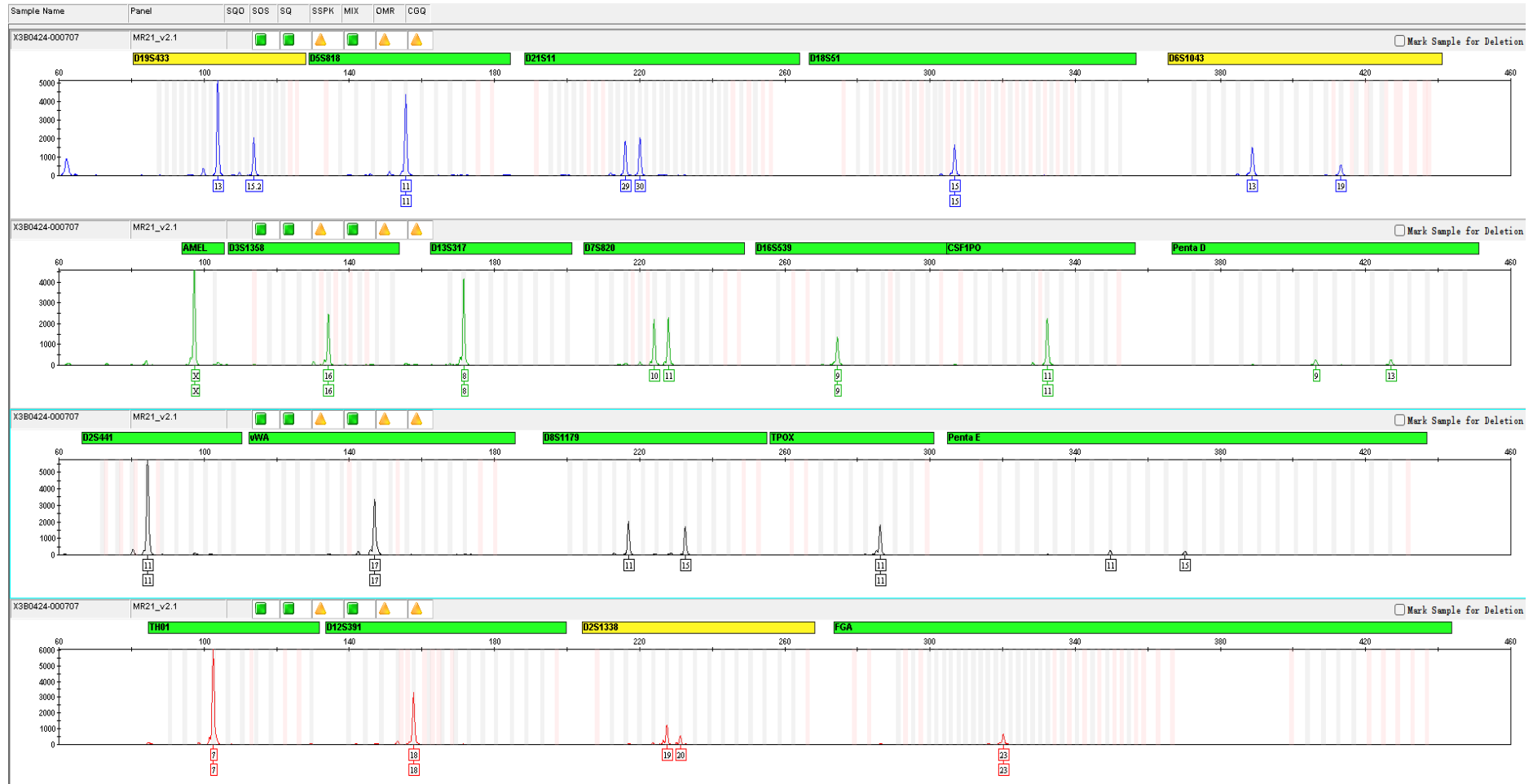


Figure2: Result of STR matching analysis in ATCC STR database Part 1



## Search the STR Database

As part of our continuing efforts to characterize and authenticate the cell lines in the Cell Biology collection, ATCC has developed a comprehensive database of short tandem repeat (STR) DNA profiles for all of our human cell lines. [Download our guide before starting.](#)

1. [STR Profiling Analysis](#)
2. [Matching Algorithm](#)
3. [Interrogating the Database](#)

**Disclaimer:**

Reference to this database and the data contained therein may be cited in publications, and ATCC encourages such citation or reference. While every reasonable effort has been made to assure the accuracy of these data, no warranty, express or implied, is made by ATCC as to their accuracy.

While ATCC has largely used the Promega PowerPlex® 1.2 System in the creation of these data and recommends that researchers wishing to produce data for comparison also use a Promega PowerPlex® System ATCC does not provide a general endorsement of this product or provide any warranty or representation regarding its quality or performance in the scientific community for the identification of human cell lines.

**Search by ATCC Number:**




OR

**Search by Amelogenin (AMEL) + at least 7 loci:**

There are two ways to fill in allele entries for search. You can either enter allele entries in below table or populate a file with the information and upload the file. Please separate each allele entry with a comma (e.g., CSF1PO = 11, 12). Note that currently only one single sample is supported.

Figure3: Result of STR matching analysis in ATCC STR database Part 2



## Search the STR Database

As part of our continuing efforts to characterize and authenticate the cell lines in the Cell Biology collection, ATCC has developed a comprehensive database of short tandem repeat (STR) DNA profiles for all of our human cell lines. [Download our guide before starting.](#)

1. [STR Profiling Analysis](#)
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### Search by ATCC Number:

SEARCH

CLEAR

OR

### Search by Amelogenin (AMEL) + at least 7 loci:

There are two ways to fill in allele entries for search. You can either enter allele entries in below table or populate a file with the information and upload the file. Please separate each allele entry with a comma (e.g., CSF1PO = 11, 12). Note that currently only one single sample is supported.



Figure4: Result of STR matching analysis in DSMZ STR database

STR Profile Search

The human STR profile database includes data sets of 2455 cell lines from ATCC, DSMZ, JCRB and RIKEN.

Refine search | Start new search

Your search uses the non-empty-based scoring mode.

| Similarity | Cell line           | Source   | Shared | D5S818 | D7S820 | D13S317   | D16S539 | vWA        | TH01 | TPOX   | CSF1PO | Amelogenin | D3S1358 | D21S11 | D18S51 | PentaE | PentaD | D8S1179 | FGA    | D19S433   | D251338 |
|------------|---------------------|----------|--------|--------|--------|-----------|---------|------------|------|--------|--------|------------|---------|--------|--------|--------|--------|---------|--------|-----------|---------|
|            | Your query          |          |        | 11, 11 | 10, 11 | 8, 8      | 9, 9    | 17, 17     | 7, 7 | 11, 11 | 11, 11 | X, X       | 16, 16  | 29, 30 | 15, 15 | 11, 15 | 9, 13  | 11, 15  | 23, 23 | 13, 15, 2 | 19, 20  |
| 100 %      | PC-14               | RCB0446  | 9      | 11, 11 | 10, 11 | 8, 8      | 9, 9    | 17, 17     | 7, 7 | 11, 11 | 11, 11 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 91.7 %     | PC-9 (formerly k... | HPACC    | 18     | 11, 11 | 10, 10 | 8, 8      | 9, 9    | 17, 17     | 7, 7 | 11, 11 | 11, 11 | X, X       | 16, 16  | 29, 30 | 15, 15 | 11, 11 | 9, 13  | 11, 15  | 23, 23 | 13, 16    | 19, 20  |
| 72.2 %     | SCH                 | JCRB0251 | 9      | 11, 11 | 10, 11 | 11, 12    | 9, 9    | 17, 17     | 6, 7 | 11, 11 | 10, 11 | X, Y       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 66.7 %     | Lu-143              | RCB1773  | 9      | 11, 11 | 10, 11 | 8, 8      | 9, 9    | 17, 20     | 6, 6 | 11, 11 | 12, 12 | X, Y       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 66.7 %     | HTOA                | RCB0692  | 9      | 11, 13 | 9, 10  | 8, 10     | 9, 13   | 17, 17     | 7, 7 | 11, 11 | 12, 13 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 66.7 %     | Hs 38,T             | CRL-7826 | 9      | 11, 11 | 9, 9   | 12, 12    | 9, 9    | 17, 17     | 9, 9 | 11, 11 | 11, 11 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 66.7 %     | Hs 281,T            | CRL-7227 | 9      | 9, 13  | 8, 10  | 8, 12     | 9, 10   | 17, 17     | 6, 7 | 11, 11 | 11, 11 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 61.1 %     | HE47                | RCB2263  | 9      | 11, 11 | 10, 12 | 11, 12    | 9, 11   | 17, 17     | 6, 9 | 11, 11 | 11, 12 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 61.1 %     | HE13                | RCB2234  | 9      | 10, 11 | 9, 11  | 8, 8      | 10, 11  | 17, 17     | 7, 7 | 8, 8   | 11, 13 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 61.1 %     | JHOC-8              | RCB1723  | 9      | 11, 11 | 8, 11  | 8, 8      | 9, 9    | 14, 17     | 7, 9 | 8, 9   | 14, 14 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 61.1 %     | JHUEM-3             | RCB1552  | 9      | 11, 11 | 9, 11  | 8, 13     | 9, 11   | 14, 19, 20 | 7, 7 | 8, 11  | 11, 12 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 61.1 %     | TOM-2               | RCB1125  | 9      | 11, 13 | 10, 11 | 8, 12     | 10, 14  | 17, 17     | 7, 7 | 8, 8   | 11, 12 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 61.1 %     | FCP-S2H             | RCB0784  | 9      | 11, 11 | 11, 11 | 8, 10     | 9, 10   | 17, 18     | 7, 9 | 11, 11 | 9, 10  | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 61.1 %     | HOKUG               | RCB0657  | 9      | 11, 11 | 8, 11  | 8, 11     | 9, 9    | 17, 18     | 6, 9 | 11, 11 | 10, 12 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 61.1 %     | SF8761              | RCB0589  | 9      | 11, 12 | 11, 12 | 8, 10, 11 | 9, 9    | 16, 19     | 7, 7 | 9, 11  | 11, 12 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 61.1 %     | Lu-134-B            | RCB0467  | 9      | 11, 11 | 11, 11 | 9, 9      | 9, 9    | 17, 17     | 9, 9 | 11, 11 | 12, 12 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 61.1 %     | Lu-134-A            | RCB0466  | 9      | 11, 11 | 11, 11 | 9, 9      | 9, 9    | 17, 17     | 9, 9 | 11, 11 | 12, 12 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 61.1 %     | TC-YIK              | RCB0443  | 9      | 10, 11 | 8, 11  | 8, 9      | 9, 11   | 17, 18     | 7, 9 | 11, 11 | 11, 12 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 61.1 %     | JHH-1               | NIHS0329 | 9      | 11, 13 | 9, 10  | 8, 10     | 9, 13   | 17, 17     | 7, 7 | 8, 11  | 12, 13 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |
| 61.1 %     | KYM-1               | JCRB0627 | 9      | 11, 14 | 11, 11 | 8, 8      | 9, 10   | 17, 17     | 7, 9 | 8, 11  | 12, 12 | X, X       | -       | -      | -      | -      | -      | -       | -      | -         | -       |

Download | Number of results: 20

Figure5: Result of STR matching analysis in ExpASy STR database

| Export table    |           |            |        |      |        |         |        |         |        |         |        |         |         |         |         |        |         |        |       |         |         |       |       |       |
|-----------------|-----------|------------|--------|------|--------|---------|--------|---------|--------|---------|--------|---------|---------|---------|---------|--------|---------|--------|-------|---------|---------|-------|-------|-------|
| Accession       | Name      | N° Markers | Score  | Amel | CSF1PO | D2S1338 | D2S441 | D3S1358 | D5S818 | D6S1043 | D7S820 | D8S1179 | D12S391 | D13S317 | D16S539 | D18S51 | D19S433 | D21S11 | FGA   | Penta D | Penta E | TH01  | TPO   | vWA   |
| NA              | Query     | NA         | NA     | X,X  | 11,11  | 19,20   | 11,11  | 16,16   | 11,11  | 13,19   | 10,11  | 11,15   | 18,18   | 8,8     | 9,9     | 15,15  | 13,15.2 | 29,30  | 23,23 | 9,13    | 11,15   | 7,7   | 11,11 | 17,17 |
| CVCL_1640 Best  | PC-14     | 12         | 96.77% | X    | 11     |         |        |         | 11     |         | 10,11  | 11,15   |         | 8       | 9       | 15     |         | 29,30  | 23,25 |         |         | 7     | 11    | 17    |
| CVCL_1640 Worst | PC-14     | 12         | 93.33% | X    | 11     |         |        |         | 11     |         | 10     | 11,15   |         | 8       | 9       | 15     |         | 29,30  | 23,25 |         |         | 7     | 11    | 17    |
| CVCL_B260       | PC-9      | 19         | 93.88% | X    | 11     | 19,20   | 11     | 16      | 11     |         | 10,11  | 11,15   | 18      | 8       | 9       | 15     | 13,15.2 | 30     | 23    | 13      | 11      | 7     | 11    | 17    |
| CVCL_A1VU       | 150057    | 8          | 78.26% | X    | 9,11   |         |        |         | 11     |         | 10,11  |         |         | 8,10    | 9,13    |        |         |        |       |         |         | 7,9   | 11    | 16,17 |
| CVCL_1687       | SCH       | 8          | 76.19% | X,Y  | 10,11  |         |        |         | 11     |         | 10,11  |         |         | 11,12   | 9       |        |         |        |       |         |         | 6,7   | 11    | 17    |
| CVCL_3348       | Lu-143    | 8          | 73.68% | X,Y  | 12     |         |        |         | 11     |         | 10,11  |         |         | 8       | 9       |        |         |        |       |         |         | 6     | 11    | 17,20 |
| CVCL_ZF96       | CLC35     | 8          | 72.73% | X    | 11,13  |         |        |         | 10,11  |         | 8,10   |         |         | 8       | 9       |        |         |        |       |         |         | 7     | 9,11  | 17,18 |
| CVCL_A9TA       | GSC#23P   | 8          | 70.00% | X,Y  | 11     |         |        |         | 11     |         | 10,11  |         |         | 12      | 9,11    |        |         |        |       |         |         | 7     | 8,9   | 17    |
| CVCL_F928       | IHGK      | 8          | 70.00% | X    | 11     |         |        |         | 11     |         | 11     |         |         | 8,9     | 9,12    |        |         |        |       |         |         | 7     | 9     | 17,20 |
| CVCL_LH21       | CG1680    | 8          | 69.57% | X    | 10,11  |         |        |         | 11     |         | 10,11  |         |         | 8       | 9,12    |        |         |        |       |         |         | 9,9.3 | 9,11  | 14,17 |
| CVCL_A158       | Ma-Mel-21 | 9          | 69.23% | X    | 10,11  |         |        | 16      | 11,12  |         | 9,11   |         |         | 8,11    |         |        |         |        | 23,24 |         |         | 7     | 11,12 | 17,18 |
| CVCL_JH16       | AP395     | 8          | 66.67% | X    | 11,12  |         |        |         | 11     |         | 10     |         |         | 12      | 9,11    |        |         |        |       |         |         | 6,7   | 11    | 14,17 |
| CVCL_4J79       | C-378     | 8          | 66.67% | X,Y  | 11     |         |        |         | 11     |         | 10     |         |         | 11      | 11      |        |         |        |       |         |         | 7     | 9,11  | 17    |
| CVCL_U332       | C-386     | 8          | 66.67% | X,Y  | 11     |         |        |         | 11     |         | 10     |         |         | 11      | 11      |        |         |        |       |         |         | 7     | 9,11  | 17    |

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## Report of Human Cell Line Authentication

|                                      |                                        |
|--------------------------------------|----------------------------------------|
| <b>Sample Label:</b> H-1650          | <b>Sample Quantity:</b> 1 tube         |
| <b>Sample Number:</b> X3B0424-000708 | <b>Sample Type:</b> Cell precipitation |
| <b>Sample State:</b> Precipitation   | <b>ReceivingDate:</b> 2024-02-22       |
| <b>Sample Submitted By:</b> 赵威       | <b>TestDate:</b> 2024-02-22            |
| <b>Contact:</b> 13911063713          | <b>Report Date:</b> 2024-02-25         |
| <b>Client:</b> 北京市肿瘤防治研究所            |                                        |

**Data Interpretation** Method refer to “The Pharmacopoeia of the People's Republic of China, Volume III General Requirements, Requirements for Preparation and Control of Animal Cell Substrates Used for Production of Biologics”. The STR profile was compared with the ATCC, DSMZ and ExPASy databases for reference matching<sup>1,2</sup> and result interpretation were based on “ATCCASN-0002 revised 2021—Standardization of Short Tandem Repeat (STR) Profiling”.

**Methodology** **Sample DNA was extracted**, and PCR amplified with STR Multi-amplification Kit (Microreader™ 21 ID System). PCR products were assayed with ABI 3730xl DNA Analyzer (Applied Biosystems®). Appropriate positive and negative controls were run and confirmed for each sample submitted. Data of 20 STR loci plus the Amelogenin locus were analyzed and extracted using GeneMapperID-X software and designated as the STR profile of the test sample.

**Results** The results of the negative and positive control match expectations. The STR profiles of the test sample are clear, which are shown in the attached table and figure. Multiple Alleles<sup>3</sup> are shown following.

| #of Multiple Alleles | Locus |
|----------------------|-------|
| 0                    | ---   |

### Explanation of Test Results

According to ATCC ASN-0002-2021, Cell lines with  $\geq 80\%$  match at 13 STR loci or  $\geq 90\%$  match at eight STR loci are considered to be related.

#### H-1650:

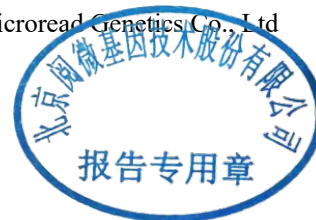
- 1、The submitted sample profile is human.
- 2、The submitted profile has a 100% match on 14 loci of the following ATCC human cell line(s) in ATCC STR database: NCI-H1650 (H1650) Bronchoalveolar carcinoma; Human.
- 3、The submitted profile has a 97.2% match on 18 loci of the following human cell line(s) in DSMZ database: NCI-H1650.
- 4、The submitted profile has a 100% match on 19 STR of the following human cell line(s) in ExPASy database: NCI-H1650.

Operator: *Xiaodie Li*

Auditor: *Linyu Wu*

Signatory: *Xuejia Sun*

Beijing Microread Genetics Co., Ltd



### Results of database comparison (the highest percent match to the query)

|            | ATCC                                                   | DSMZ      | ExPASy    | Sample         |     |
|------------|--------------------------------------------------------|-----------|-----------|----------------|-----|
| Cell Name  | NCI-H1650<br>(H1650)Bronchoalveolarcarcinoma;<br>Human | NCI-H1650 | NCI-H1650 | H-1650         |     |
| Cell ID    | CRL-5883                                               | CRL-5883  | CVCL_1483 | X3B0424-000708 |     |
| Amelogenin | X                                                      | X, X      | X         | X              | X   |
| D5S818     | 11                                                     | 11, 11    | 11        | 11             | 11  |
| D13S317    | 11                                                     | 11, 11    | 11        | 11             | 11  |
| D7S820     | 8,9                                                    | 8, 9      | 8,9       | 8              | 9   |
| D16S539    | 11,12                                                  | 11, 12    | 11,12     | 11             | 12  |
| vWA        | 18                                                     | 18, 18    | 18        | 18             | 18  |
| TH01       | 9.3                                                    | 9.3, 9.3  | 9.3       | 9.3            | 9.3 |
| TPOX       | 11                                                     | 11, 11    | 11        | 11             | 11  |
| CSF1PO     | 11                                                     | 11, 11    | 11        | 11             | 11  |
| D19S433    | /                                                      | 15, 15    | 15        | 15             | 15  |
| D21S11     | 30                                                     | 30, 30    | 30        | 30             | 30  |
| D18S51     | 10                                                     | 10, 10    | 10        | 10             | 10  |
| D6S1043    | /                                                      | /         |           | 13             | 13  |
| D3S1358    | 18                                                     | 18, 18    | 18        | 18             | 18  |
| Penta D    | /                                                      | 8, 8      | 8         | 8              | 8   |
| D2S441     | /                                                      | /         | 10        | 10             | 10  |
| D8S1179    | 12                                                     | 12, 12    | 12        | 12             | 12  |
| Penta E    | /                                                      | 12, 12    | 12        | 12             | 12  |
| D12S391    | /                                                      | /         | 22        | 22             | 22  |

|                             | ATCC                                          | DSMZ                                          | ExPASy                                        | Sample |    |
|-----------------------------|-----------------------------------------------|-----------------------------------------------|-----------------------------------------------|--------|----|
| D2S1338                     | /                                             | 19, 19                                        | 19                                            | 19     | 19 |
| FGA                         | 20                                            | 20,23.2                                       | 20                                            | 20     | 20 |
| Shared STR                  | 14                                            | 18                                            | 19                                            |        |    |
| loci <sup>4</sup>           |                                               |                                               |                                               |        |    |
| Matching <sup>5</sup>       | 100%                                          | 97.2%                                         | 100%                                          |        |    |
| Interpretation <sup>6</sup> | Most likely to originate from the same donor. | Most likely to originate from the same donor. | Most likely to originate from the same donor. |        |    |

## Remarks

1. The short tandem repeat (STR) profile is indicative only of the sample sent to Beijing Microread Genetics Co., Ltd at the time it was sent. Effective peaks are real PCR bands, small peaks and non-specific bands are ignored in calculation.
2. The STR genotyping profile of the submitted cell is compared with ATCC,DSMZ and ExPASy databases, in which STR genotypes of over 100,000 human cell lines from ATCC, DSMZ, JCRB, ECACC, Riken etc. were recorded.Cells that are not included in above databases could not be compared. For failed sample, it's genotyping and figure result would be shown as NA.
3. Both mixed cultures and MSIpositive cell lines can show additional STR alleles in one or more STR loci. In short, two fundamentally different causes can be the reason for multiple alleles at a locus: drifted alleles by MSI or some other DNA replication error or the presence of a mixed culture containing a contaminating second human cell line.
4. The number of STR loci shared by the submitted sample and the cells in database. Amelogenin does not belong to STR locus.
5. The matching score ofATCC,DSMZ and ExPASyis“Tanabe”—  $2 \times (\text{number of alleles matching}) / (\text{total number of alleles in database profile and query sample}) \times 100\%$ .
6. The interpretation is based on “ATCC ASN-0002-2021”.“Two samples are considered possibly related when their STR profiles match at 80-90% of alleles across the 13 core STR loci, as calculated using the matching algorithm. At matches of 90% or greater, the cell lines have very likely originated from the same donor. Samples between 60 and 79% match tend to be unrelated, but need may further investigation to confirm that they are unrelated. Two common causes of related cell lines scoring below 80% are (1) if the cell line has extra alleles due to it being MSI unstable, and (2) misidentification of the cell line’s origin. Generally, cell lines are authentic (i.e., are derived from the same original tissue donor) when they show the expected percent match ( $\geq 80\%$  at 13 STR loci or  $> 90\%$  match at eight STR loci) to other

results from that donor (tissue or other cell line samples within the database).”

7. The testing results were calculated and generated by each cell database ONLINE tool. In some case, there may be different profiles of same cell line in each database and possibly lead to different matching results. In addition, limited by the algorithm of the calculation model (the less the number of shared STR sites, the higher the probability of matching unrelated cells), non-cell line(s) human cells/sample(s) may also match to cell(s) in database. In these conditions, the comparison results in this report are for reference only.
8. Beijing Microread Genetics performs STR Profiling following ISO 9001:2015 and ISO 13485:2016 quality standards. The results are judged according to industry standards or consensus and can only be used for cell line inspection and authentication. We are NOT responsible for any purpose or interpretation other than the purpose specified.



Figure1: STR profiles ofH-1650cell line

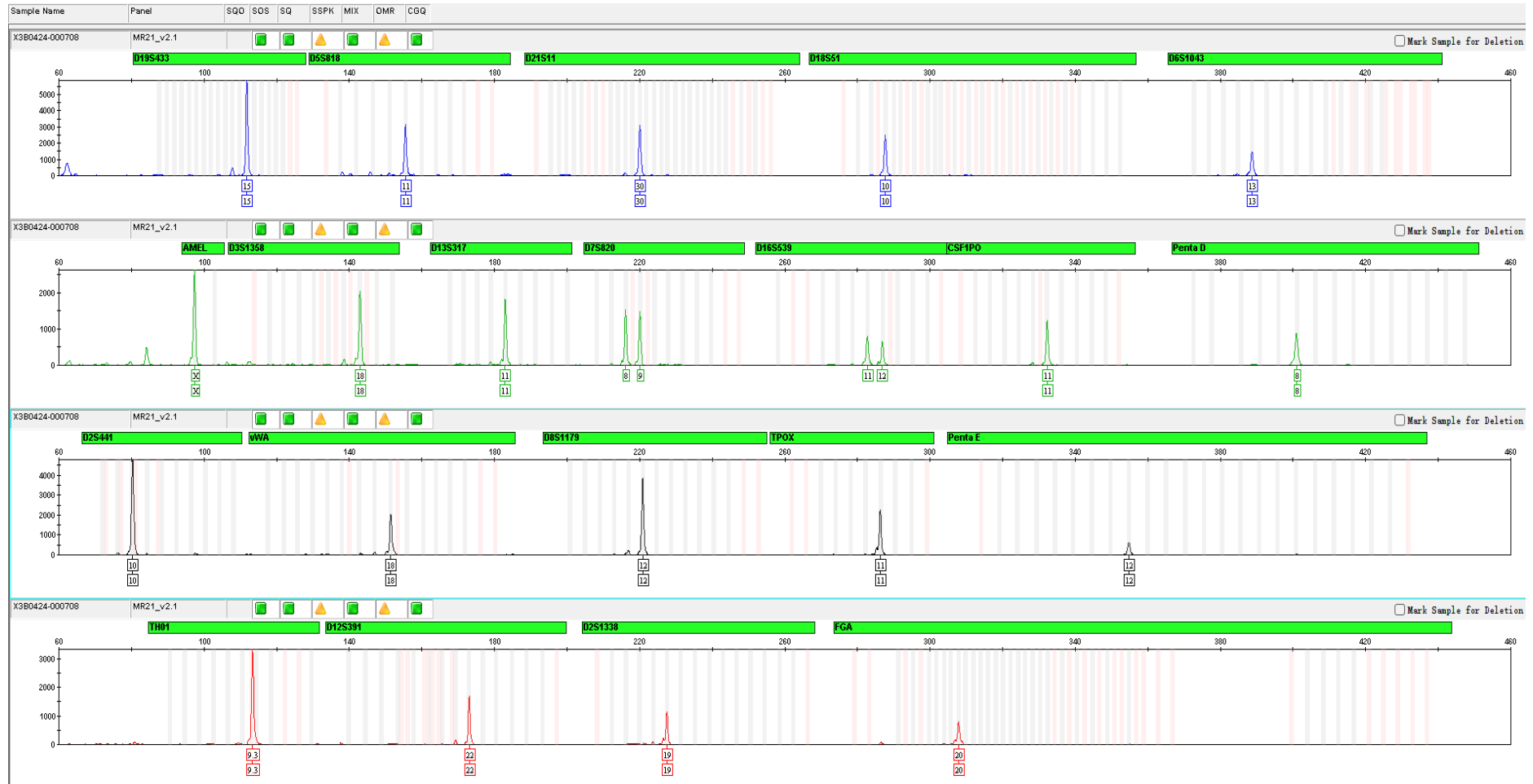


Figure2: Result of STR matching analysis in ATCC STR database Part 1

3. [Interrogating the Database](#)

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| Add to Cart | %Match | ATCC® Number | Designation                                            | D5S818 | D13S317 | D7S820 | D16S539 | vWA | TH01 | AMEL | TPOX | CSF1PO | D3S |
|-------------|--------|--------------|--------------------------------------------------------|--------|---------|--------|---------|-----|------|------|------|--------|-----|
|             | 100.0  | CRL-5883     | NCI-H1650<br>(H1650)Bronchoalveolarcarcinoma;<br>Human | 11     | 11      | 8,9    | 11,12   | 18  | 9.3  | X    | 11   | 11     |     |

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Disclaimer:

Reference to this database and the data contained therein may be cited in publications, and ATCC encourages such citation or reference. While every reasonable effort has been made to assure the accuracy of these data, no warranty, express or implied, is made by ATCC as to their accuracy.

While ATCC has largely used the Promega PowerPlex® 1.2 System in the creation of these data and recommends that researchers wishing to produce data for comparison also use a Promega PowerPlex® System ATCC does not provide a general endorsement of this product or provide any warranty or representation regarding its quality or performance in the scientific community for the identification of human cell lines.

Search by ATCC Number:


SEARCH CLEAR

Figure3: Result of STR matching analysis in ATCC STR database Part 2

3. [Interrogating the Database](#)

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| Match                           | D5S818 | D13S317 | D7S820 | D16S539 | vWA | TH01 | AMEL | TPOX | CSF1PO | D3S1358 | D21S11 | D18S51 | D8S1179 | FGA |
|---------------------------------|--------|---------|--------|---------|-----|------|------|------|--------|---------|--------|--------|---------|-----|
| H1650<br>Adenocarcinoma;<br>man | 11     | 11      | 8,9    | 11,12   | 18  | 9,3  | X    | 11   | 11     | 18      | 30     | 10     | 12      | 20  |

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While ATCC has largely used the Promega PowerPlex® 1.2 System in the creation of these data and recommends that researchers wishing to produce data for comparison also use a Promega PowerPlex® System ATCC does not provide a general endorsement of this product or provide any warranty or representation regarding its quality or performance in the scientific community for the identification of human cell lines.

Search by ATCC Number:


SEARCH CLEAR

Figure4: Result of STR matching analysis in DSMZ STR database

STR Profile Search

The human STR profile database includes data sets of 2455 cell lines from ATCC, DSMZ, JCRB and RIKEN.

Refine search | Start new search

Your search uses the non-empty-based scoring mode.

| Similarity | Cell line                | Source   | Shared | D5S818 | D7S820   | D13S317    | D16S539 | vWA    | TH01      | TPOX   | CSF1PO     | Amelogenin | D3S1358 | D21S11 | D18S51 | PentaE | PentaD | D8S1179 | FGA      | D19S433 | D2S1338 |
|------------|--------------------------|----------|--------|--------|----------|------------|---------|--------|-----------|--------|------------|------------|---------|--------|--------|--------|--------|---------|----------|---------|---------|
|            | Your query               |          |        | 11, 11 | 8, 9     | 11, 11     | 11, 12  | 18, 18 | 9.3, 9.3  | 11, 11 | 11, 11     | X, X       | 18, 18  | 30, 30 | 10, 10 | 12, 12 | 8, 8   | 12, 12  | 20, 20   | 15, 15  | 19, 19  |
| 97.2 %     | NCI-H1650 [H-L]          | CRL-5883 | 18     | 11, 11 | 8, 9     | 11, 11     | 11, 12  | 18, 18 | 9.3, 9.3  | 11, 11 | 11, 11     | X, X       | 18, 18  | 30, 30 | 10, 10 | 12, 12 | 8, 8   | 12, 12  | 20, 23.2 | 15, 15  | 19, 19  |
| 77.8 %     | 184B5                    | CRL-8799 | 9      | 11, 11 | 9, 11    | 11, 11     | 11, 12  | 18, 19 | 9.3, 9.3  | 11, 11 | 10, 10     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 77.8 %     | 184A1                    | CRL-8798 | 9      | 11, 13 | 9, 11    | 11, 11     | 11, 12  | 18, 19 | 9.3, 9.3  | 11, 11 | 10, 11     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 72.2 %     | Hs 571.T                 | CRL-7846 | 9      | 11, 11 | 8, 9     | 10, 11     | 11, 12  | 18, 18 | 6, 9.3    | 8, 11  | 10, 10     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 66.7 %     | EC-GI-10                 | RCB0774  | 9      | 11, 11 | 8, 11    | 11, 11     | 11, 12  | 16, 18 | 7, 9      | 11, 11 | 10, 11     | X, Y       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 66.7 %     | HEC-1-B                  | NIHS0480 | 9      | 11, 13 | 9, 11    | 11, 11     | 11, 12  | 18, 18 | 6, 7      | 11, 11 | 10, 12     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 66.7 %     | FTC-238                  | HPACC    | 9      | 11, 12 | 9, 10    | 11, 11     | 11, 12  | 15, 18 | 9.3, 9.3  | 9, 9   | 10, 11     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 66.7 %     | EA.hy926                 | CRL-2922 | 9      | 11, 11 | 8, 9, 10 | 11, 11     | 11, 12  | 14, 17 | 6, 8, 9.3 | 8, 9   | 10, 11, 12 | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 61.1 %     | ACJ Cells No. 27         | STRJ0011 | 9      | 11, 13 | 8, 10    | 8, 11      | 11, 12  | 18, 18 | 6, 10     | 11, 11 | 8, 10      | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 61.1 %     | 633                      | RCB2352  | 9      | 11, 11 | 8, 11    | 11, 11     | 11, 12  | 14, 14 | 8, 9.3    | 8, 11  | 10, 12     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 61.1 %     | PMF-ko14                 | RCB1426  | 9      | 11, 11 | 8, 8     | 13, 14, 15 | 11, 12  | 17, 18 | 9.3, 9.3  | 11, 12 | 10, 12     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 61.1 %     | HEC-1-B                  | NIHS0480 | 9      | 11, 13 | 9, 11    | 11, 11     | 11, 12  | 18, 18 | 6, 7      | 8, 11  | 10, 12     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 61.1 %     | HEC-1-B                  | JCRB1193 | 9      | 11, 13 | 9, 11    | 11, 11     | 11, 12  | 18, 18 | 6, 7      | 8, 11  | 10, 12     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 61.1 %     | HEC-1-B                  | JCRB1193 | 9      | 11, 13 | 9, 11    | 11, 11     | 11, 12  | 18, 18 | 6, 7      | 8, 11  | 10, 12     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 61.1 %     | HEC-1                    | JCRB0042 | 9      | 11, 13 | 11, 11   | 11, 11     | 11, 12  | 18, 18 | 6, 7      | 11, 11 | 10, 12     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 61.1 %     | HMT-3522 T4-2            | HPACC    | 9      | 9, 11  | 8, 9     | 11, 11     | 11, 13  | 14, 17 | 9, 9.3    | 8, 11  | 11, 12     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 61.1 %     | T 174                    | CRL-7726 | 9      | 11, 11 | 8, 12    | 13, 13     | 10, 11  | 18, 18 | 9.3, 9.3  | 9, 9   | 10, 11     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 61.1 %     | HE-SK                    | CRL-7718 | 9      | 11, 11 | 8, 11    | 9, 11      | 11, 12  | 17, 18 | 7, 9      | 9, 11  | 11, 13     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 61.1 %     | HE-LU(Rif <sup>r</sup> ) | CRL-7717 | 9      | 11, 11 | 8, 11    | 9, 11      | 11, 12  | 17, 18 | 7, 9      | 9, 11  | 11, 13     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |
| 61.1 %     | Hs 894(B).T              | CRL-7632 | 9      | 11, 11 | 8, 11    | 9, 11      | 11, 12  | 17, 18 | 7, 9      | 9, 11  | 11, 13     | X, X       | -       | -      | -      | -      | -      | -       | -        | -       | -       |

Download | Number of results: 20

Figure5: Result of STR matching analysis in ExpASy STR database

| Accession       | Name               | N° Markers | Score   | Amel | CSF1PO | D2S1338 | D2S441 | D3S1358 | D5S818 | D6S1043 | D7S820 | D8S1179 | D12S391 | D13S317 | D16S539 | D18S51 | D19S433 | D21S11  | FGA     | Penta D | Penta E | TH01    | TPOX  | vWA   |
|-----------------|--------------------|------------|---------|------|--------|---------|--------|---------|--------|---------|--------|---------|---------|---------|---------|--------|---------|---------|---------|---------|---------|---------|-------|-------|
| NA              | Query              | NA         | NA      | X,X  | 11,11  | 19,19   | 10,10  | 18,18   | 11,11  | 13,13   | 8,9    | 12,12   | 22,22   | 11,11   | 11,12   | 10,10  | 15,15   | 30,30   | 20,20   | 8,8     | 12,12   | 9,3,9,3 | 11,11 | 18,18 |
| CVCL_1483 Best  | NCI-H1650          | 19         | 100.00% | X    | 11     | 19      | 10     | 18      | 11     |         | 8,9    | 12      | 22      | 11      | 11,12   | 10     | 15      | 30      | 20      | 8       | 12      | 9.3     | 11    | 18    |
| CVCL_1483 Worst | NCI-H1650          | 19         | 97.67%  | X    | 11     | 19      | 10     | 18      | 11     |         | 8,9    | 12      | 22      | 11      | 11,12   | 10     | 15      | 30      | 20,23,2 | 8       | 12      | 9.3     | 11    | 18    |
| CVCL_C9CY       | NCI-H1650-GAS-Luc2 | 8          | 100.00% | X    | 11     |         |        |         | 11     |         | 8,9    |         |         | 11      | 11,12   |        |         |         |         |         |         | 9.3     | 11    | 18    |
| CVCL_4W95       | NCI-H1650-Luc      | 8          | 100.00% | X    | 11     |         |        |         | 11     |         | 8,9    |         |         | 11      | 11,12   |        |         |         |         |         |         | 9.3     | 11    | 18    |
| CVCL_0802       | Hs 571.T           | 8          | 78.26%  | X    | 10     |         |        |         | 11     |         | 8,9    |         |         | 10,11   | 11,12   |        |         |         |         |         |         | 6,9,3   | 8,11  | 18    |
| CVCL_3040       | 184A1              | 9          | 76.92%  | X    | 10,11  |         |        |         | 11,13  |         | 9,11   |         |         | 11      | 11,12   |        |         | 29,30   |         |         |         | 9.3     | 11    | 18,19 |
| CVCL_Y093       | H184B5F5/M10       | 8          | 76.19%  | X    | 10     |         |        |         | 11     |         | 9,11   |         |         | 11      | 11,12   |        |         |         |         |         |         | 9.3     | 11    | 18,19 |
| CVCL_VR72       | MDA-PATC66         | 8          | 72.00%  | X    | 11     |         |        |         | 11,12  |         | 8,11   |         |         | 11,12   | 11,12   |        |         |         |         |         |         | 6,9,3   | 8,11  | 16,18 |
| CVCL_C617 Best  | FM93/2             | 10         | 66.67%  | X    | 12,14  |         |        | 18      | 11,12  |         | 9      |         |         | 11      | 11,12   |        |         |         | 20      |         |         | 9,9,3   | 9     | 17,18 |
| CVCL_C617 Worst | FM93/2             | 10         | 61.54%  | X    | 12,14  |         |        | 18      | 11,12  |         | 9      |         |         | 11      | 11,12   |        |         |         | 20      |         |         | 9,9,3   | 9     | 17    |
| CVCL_DD59       | A6-IPSC            | 9          | 66.67%  | X    | 12     |         |        |         | 11     |         | 9,11   |         |         | 9,11    | 11,12   |        |         | 30,31,2 |         |         |         | 7,9,3   | 8,11  | 15,18 |
| CVCL_F204       | ND27760            | 9          | 66.67%  | X    | 12     |         |        |         | 11     |         | 9,11   |         |         | 9,11    | 11,12   |        |         | 30,31,2 |         |         |         | 7,9,3   | 8,11  | 15,18 |
| CVCL_LH10       | CG1634             | 8          | 66.67%  | X    | 12     |         |        |         | 11     |         | 8,9    |         |         | 10,11   | 12,13   |        |         |         |         |         |         | 9       | 11    | 18    |
| CVCL_2888       | Dempsey            | 8          | 66.67%  | X,Y  | 11,12  |         |        |         | 11,13  |         | 8,12   |         |         | 11      | 11,12   |        |         |         |         |         |         | 8,9,3   | 8     | 17,18 |

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