

### HuH-7 cells STR report

**Method:** An appropriate amount of HuH-7 cells (Cell number PC156,1×106) was used to extract DNA, 20 STR loci and gender identification loci were amplified by 21 CELLID System, PCR product detection was performed by ABI3130x1 genetic analyzer, detection results were analyzed by GeneMapper IDX software (Applied Biosystems), and compared with ATCC, DSMZ, JCRB, Cellosaurus and other databases.

#### **Experimental result:**

- 1. The results of negative and positive control were correct.
- 2. The genotyping results of STR locus of HuH-7 cell line are shown in the following table.

#### Conclusion:

- 1. The genomic DNA of HuH-7 cell line is clear and the result of genotyping is good.
- 2. The results of STR typing showed that no cross contamination of mouse cells and human cells was found in the cell line of HuH-7 cell line.
- 3. The DNA typing of the cell line was 98.18% matched with the cell type in the cell bank, and the cell line name was HuH-7.



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## Appendix I: The genotyping results of STR locus of HuH-7 cell line

| STR Loci   | Sample: PC156 | Database: HuH-7                       |
|------------|---------------|---------------------------------------|
| Amelogenin | X             | X                                     |
| CSF1PO     | 11            | 11                                    |
| D2S1338    | 19            | 19                                    |
| D3S1358    | 15            | 15                                    |
| D5S818     | 12            | 12                                    |
| D7S820     | 11            | 11                                    |
| D8S1179    | 14,15         | 14,15                                 |
| D13S317    | 10,11         | 10,11                                 |
| D16S539    | 10            | 10                                    |
| D18S51     | 15            | 15                                    |
| D19S433    | 13,14         | 13,14                                 |
| D21S11     | 30            | 30                                    |
| FGA        | 22            | 22,23                                 |
| PentaD     | 12            | 12                                    |
| PentaE     | 11            | 11                                    |
| TH01       | 7             | 7                                     |
| TPOX       | 8,11          | 8,11                                  |
| vWA        | 16,18         | 16,18                                 |
| D1S1656    | 16            |                                       |
| D6S1043    | 13,15         |                                       |
| D12S391    | 20,21         | * * * * * * * * * * * * * * * * * * * |
| D2S411     |               |                                       |

The Cellosaurus database has a matching rate of 98.18%, The number of matched bits is 20 (https://web.expasy.org/cellosaurus-str-search/)

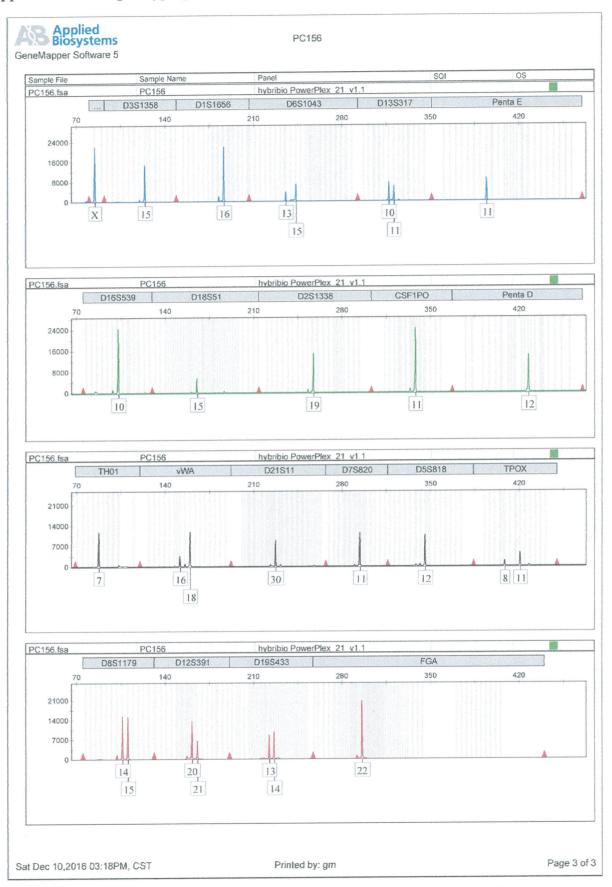
#### Note:

1. According to the cell STR identification standard established by the International Cell Line Authentication Committee (ICLAC), when the matching degree of cell lines is  $\geq 80\%$ , they are considered to be correlated, that is, derived from common ancestral cells; The matching degree is between 55% and 80%, and the correlation needs to be further verified. Less than 55% indicates no correlation between the two.

2. The effective peak of the map was the real PCR band; Small peaks and nonspecific bands were ignored in the calculation.

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# Appendix III: The genotyping results of STR locus of HuH-7 cell line



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