

Cell Line Authentication Service

STR Profiling Report

Sample From: the First Affiliated Hospital of
Zhengzhou University

Sample Type: Cell Line

Testing Method: STR Genotyping

Report Time: 3/30/2020

COMPANY STATEMENT

1. THIS REPORT IS ONLY RESPONSIBLE FOR THE SAMPLES ANALYZED.
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4. THE PAPER REPORT WITH CONTENT ALTERING, ADDING OR WITHOUT THE STAMPED SEAL OF THE COMPANY ARE INVALID.

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Cell Line Authentication – STR Profiling Report

Sample code

Table 1. Sample Code

Customer's code	Company Code
IHH-4	20200324-04

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 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. STR profile

Table 2. STR and Amelogenin Genotyping Results of Cell line.

Loci	Sample information			Cell Bank information		
	Sample name: IHH-4			Cell line name: IHH-4		
	Allele1	Allele2	Allele3	Allele1	Allele2	Allele3
D5S818	9	13		9	13	
D13S317	10	13		10	13	
D7S820	9	10		9	10	
D16S539	9	11		9	11	
VWA	16	18		16	18	
TH01	9	9		9	9	
AMEL	X	Y		X	Y	
TPOX	11	11		11	11	
CSF1PO	12	12		12	12	
FGA	23	24				
D21S11	30	31				
D18S51	13	15				
D8S1179	11	15				
D3S1358	16	16				

2. database annotation

Figure 1. STR matching analysis

Cell line name	IHH-4																												
Synonyms	IHH4																												
Accession	CVCL_2960																												
Resource Identification Initiative	To cite this cell line use: IHH-4 (RRID:CVCL_2960)																												
Comments	Part of: Cancer Cell Line Encyclopedia (CCLE) project. Part of: COSMIC cell lines project. Doubling time: 42 hours (PubMed=11686581). Microsatellite instability: Stable (MSS) (Sanger). Omics: Deep exome analysis. Omics: DNA methylation analysis. Omics: SNP array analysis. Omics: Transcriptome analysis.																												
Sequence variations	AKT1 p.Glu17Lys (c.49G>A) (PubMed=23833040; PubMed=30737244). BRAF p.Val600Glu (c.1799T>A) (PubMed=23833040; PubMed=30737244). CREBBP p.Trp592Ter (c.1776G>A) (PubMed=30737244). CRLF2 p.Trp255Ter (c.765G>A) (PubMed=30737244). EP300 p.Arg1312Ter (c.3934C>T) (PubMed=30737244). RAC1 p.Asp11Glu (c.33C>G) (PubMed=30737244). Heterozygous for TERT c.228C>T (-124C>T); in promoter (PubMed=23833040; PubMed=30737244).																												
Genome ancestry	Source: PubMed=30894373 <table border="1"> <thead> <tr> <th>Origin</th> <th>% genome</th> </tr> </thead> <tbody> <tr> <td>African</td> <td>1.71</td> </tr> <tr> <td>Native American</td> <td>0</td> </tr> <tr> <td>East Asian, North</td> <td>73.08</td> </tr> <tr> <td>East Asian, South</td> <td>21.44</td> </tr> <tr> <td>South Asian</td> <td>0</td> </tr> <tr> <td>European, North</td> <td>0.89</td> </tr> <tr> <td>European, South</td> <td>2.88</td> </tr> </tbody> </table>	Origin	% genome	African	1.71	Native American	0	East Asian, North	73.08	East Asian, South	21.44	South Asian	0	European, North	0.89	European, South	2.88												
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Disease	Thyroid gland papillary carcinoma (NCIt: C4035) Differentiated thyroid carcinoma (ORDO: Orphanet_146) Derived from metastatic site: Left cervical lymph node.																												
Species of origin	Homo sapiens (Human) (NCBI Taxonomy: 9606)																												
Hierarchy	Children: CVCL_3219 (TMH-1)																												
Sex of cell	Male																												
Age at sampling	75Y																												
Category	Cancer cell line																												
STR profile	Source(s): Cosmic-CLP; JCRB; PubMed=30737244 Markers: <table border="1"> <tbody> <tr> <td>Amelogenin</td> <td>X,Y</td> </tr> <tr> <td>CSF1PO</td> <td>12</td> </tr> <tr> <td>D3S1358</td> <td>16</td> </tr> <tr> <td>D5S818</td> <td>9,13</td> </tr> <tr> <td>D7S820</td> <td>9,10</td> </tr> <tr> <td>D8S1179</td> <td>11,15</td> </tr> <tr> <td>D13S317</td> <td>10,13</td> </tr> <tr> <td>D16S539</td> <td>9,11</td> </tr> <tr> <td>D18S51</td> <td>13,15</td> </tr> <tr> <td>D21S11</td> <td>30,31</td> </tr> <tr> <td>FGA</td> <td>23,24</td> </tr> <tr> <td>TH01</td> <td>9</td> </tr> <tr> <td>TPOX</td> <td>11</td> </tr> <tr> <td>YWA</td> <td>16,18</td> </tr> </tbody> </table>	Amelogenin	X,Y	CSF1PO	12	D3S1358	16	D5S818	9,13	D7S820	9,10	D8S1179	11,15	D13S317	10,13	D16S539	9,11	D18S51	13,15	D21S11	30,31	FGA	23,24	TH01	9	TPOX	11	YWA	16,18
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Note: The STR online match analysis of the test cell against EXPASY database, showing cell number (Cell No.) and cell name.

3. Authentication

The submitted sample profile is human, but not a match for any profile in the DSMZ STR database.

The submitted profile is an exact match for the following human cell line(s) in the EXPASY STR database (8 core loci plus Amelogenin): **IHH-4**.

The submitted profile is similar to the following DSMZ human cell line: /.

- **Note:** A cell line can be considered to be authenticated when 80% (exact match) of the alleles in its STR profile match profiles from tissue or other cell line samples from that donor or from database. Cell lines with between a 55% to 80% (similar) match require further profiling for investigation of relatedness.

Appendix:

1. Genotyping Strategy and Site Distribution

Table S1. Experimental Strategy and Sites

	Strategy 1	Strategy 2	Strategy 3	Strategy 4
1	D3S1358	D8S1179	D19S433	AMEL
2	VWA	D21S11	TH01	D1S1656
3	D7S820	D16S539	D13S317	D5S818
4	CSF1PO	D2S1338	TPOX	D12S391
5	PENTAE	PENTAD	D18S51	FGA
6	D6S1043			

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.

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Issued by: Yang Bai

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