Cell Line Authentication Service

STR Profiling Report

Sample From: Guangdong Provincial People's Hospital

Sample Type: Cell Line

Testing Method: STR Genotyping

Report Time: 12/24/2021

COMPANY STATEMENT

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Cell Line Authentication – STR Profiling Report

Sample code

Table 1. Sample Code

Customer's code	**Company Code**
SiHa	20211224-01

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 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 asdescribed 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

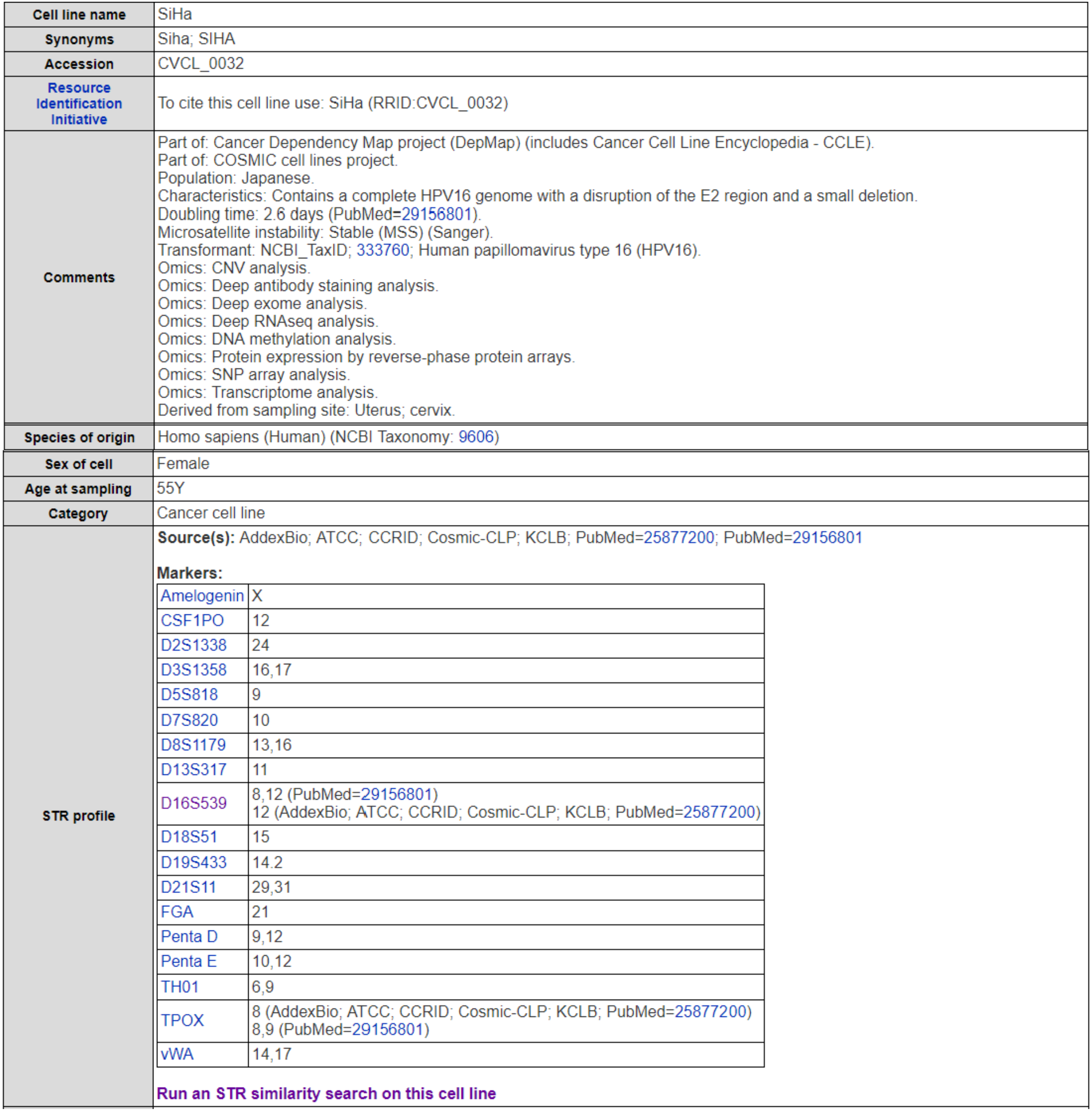
1. STR profile

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

Loci	**Sample information**			**Cell Bank information**		
	Sample name：SiHa			Cell line name：SiHa		
	Allele1	**Allele2**	**Allele3**	**Allele1**	**Allele2**	**Allele3**
D5S818	9			9		
D13S317	11			11		
D7S820	10			10		
D16S539	12			12		
VWA	14	17		14	17	
TH01	6	9		6	9	
AMEL	X			X		
TPOX	8			8		
CSF1PO	12			12		
FGA	21					
Penta E	10	12				
Penta D	9	12				
D21S11	29	31				
D18S51	15					
D8S1179	13	16				
D3S1358	16	17				
D19S433	14. 2					
D2S1338	24					

2. database annotation

Figure 1. STR matching analysis



Cell line name	SiHa
Synonyms	Siha; SIHA
Accession	CVCL_0032
Resource Identification Initiative	To cite this cell line use: SiHa (RRID:CVCL_0032)
Comments	Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE). Part of: COSMIC cell lines project. Population: Japanese. Characteristics: Contains a complete HPV16 genome with a disruption of the E2 region and a small deletion. Doubling time: 2.6 days (PubMed=29156801). Microsatellite instability: Stable (MSS) (Sanger). Transformant: NCBI_TaxID; 333760; Human papillomavirus type 16 (HPV16). Omics: CNV analysis. Omics: Deep antibody staining analysis. Omics: Deep exome analysis. Omics: Deep RNAseq analysis. Omics: DNA methylation analysis. Omics: Protein expression by reverse-phase protein arrays. Omics: SNP array analysis. Omics: Transcriptome analysis. Derived from sampling site: Uterus; cervix.
Species of origin	Homo sapiens (Human) (NCBI Taxonomy: 9606)
Sex of cell	Female
Age at sampling	55Y
Category	Cancer cell line
STR profile	**Source(s):** AddexBio; ATCC; CCRID; Cosmic-CLP; KCLB; PubMed=25877200; PubMed=29156801 **Markers:**

Amelogenin	X
CSF1PO	12
D2S1338	24
D3S1358	16,17
D5S818	9
D7S820	10
D8S1179	13,16
D13S317	11
D16S539	8,12 (PubMed=29156801) 12 (AddexBio; ATCC; CCRID; Cosmic-CLP; KCLB; PubMed=25877200)
D18S51	15
D19S433	14.2
D21S11	29,31
FGA	21
Penta D	9,12
Penta E	10,12
TH01	6,9
TPOX	8 (AddexBio; ATCC; CCRID; Cosmic-CLP; KCLB; PubMed=25877200) 8,9 (PubMed=29156801)
vWA	14,17

Run an STR similarity search on this cell line

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) **SiHa** .

☐ 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 lociwill 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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