

Cell Line Authentication Service

STR Profile Report

司法鉴定
检验检测专用章

The Query Sample ID: 2023-4014-HEK-293
Sample Submitted By: Xiaochen Wang
Institution: Zhejiang University
Cell Line Designation: HEK293(CVCL_0045)
Date Sample Received: Jul.12th, 2023
Report Date: Jul.18th, 2023

Methods:

Twenty one short tandem repeat (STR) loci plus the gender locus, Amelogenin, were amplified using the commercially available EX22 Kit from AGCU. The cell line sample was processed using the ABI Prism[®] 3500 Genetic Analyzer. Data were analyzed using GeneMapper[®] ID-X software v1.6 (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for the sample submitted. And the Query profile will be compared for match to STR reference profile from Cellosaurus.

Results:

STR Loci	Query Profile: 2023-4014-HEK-293 (Submitted by Wang)	Reference Profile: HEK293 (Cellosaurus CVCL_0045)
CSF1PO	12	11,12
D3S1358	15,17	15,17
D5S818	8	8,9
D7S820	11,12	11,12
D8S1179	12,14	12,14
D13S317	12,14	12,14
D16S539	9,13	9,13
D18S51	17,18	17,18
D21S11	28,30.2	28,30.2
FGA	23	23
TH01	7,9.3	7,9.3
TPOX	11	11
vWA	16,19	16,19
Analysis of STR data		
	2023-4014-HEK-293	HEK293
Total Number of Distinct Alleles	22	24
Number of Distinct Alleles Shared by Both Samples	22	
Match Algorithm	$[(22 \times 2) / (22 + 24)] \times 100\%$	
Percent Match	96%	

The allele match algorithm compares the 13 core loci only, even though alleles from all loci, including amelogenin locus, will be reported in the GeneMapper.

Note: These data and analysis are for research use only.

Explanation:

ANSI/ATCC ASN-0002 Revised 2021 Authentication Of Human Cell

Lines: Standardization of Short Tandem Repeat (STR) Profiling

recommends the use of a modified Tanabe Match algorithm:

$$\text{Tanabe \% Match} = \left[\frac{2 \times (\text{N}^\circ \text{ of STR alleles shared between Query and Reference Profiles})}{(\text{N}^\circ \text{ of STR alleles in Query Profile}) + (\text{N}^\circ \text{ of STR alleles in Reference Profile})} \right] \times 100\%$$

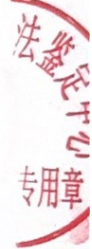
In this Standard, count single peaks once. Count only the alleles at shared STR loci. The alleles at the amelogenin loci are excluded from this calculation.

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.

Note: Percent matches of even 100% only indicate that the cell lines or tissue samples are derived from the same donor and do not mean the samples are genetically identical. STR analysis examines only a very small portion (< 0.0004%) of the entire genome.

Summary:

The Query STR profile: 2023-4014-HEK-293 (Submitted by Xiaochen Wang) and the Reference STR profile: HEK293 (Cellosaurus CVCL_0045) have a Percent Match score of 96% by using the Tanabe algorithm to compare, which indicates that the cell lines have very likely originated from the same donor.



Electrophoretogram:

