Cell Line Authentication Report

Cell Line Authentication Report

Customer: Jundan Yu

Quotation Number: 80-980049557_R3

Completion Date: 07/29/2022

1. **Sample ID: HEK293T**

2. **Original Material: Cell pellet**

3. **Methods:**

    1).Genomic DNA was extracted from the cell pellets provided by the customer.

    2).Samples, together with positive and negative control were amplified using GenePrint 10 System (Promega).

    3). Amplified products were processed using the ABI3730xl Genetic Analyzer.

    4). Data were analyzed using GeneMapper4.0 software and then compared with the ATCC, DSMZ, JCRB and

RIKEN databases for reference matching.

4. **Results:**

    1) **10 Loci STR Profile：**

Genetic Site	Cell Bank information		Customer sample	
(Locus)	HEK293T		HEK293T	
Amelogenin	X	X	X	X
CSF1PO	11	12	11	12
D13S317	12	14	12	14
D16S539	9	13	9	13
D5S818	8	9	8	9
D7S820	11	11	11	11
THO1	7	9.3	7	9.3
TPOX	11	11	11	11
vWA	16	19	16	19
D21S11			28	30.2
Percent match between the sample and the database profile：100%				

Summary:

Your cell line is considered to be "identical" to the reference cell line in the Cell Bank STR database, as the STR

profile yields a 100% match.

Notes：

1. P=100% x (2xM)/N; M=18, N=36 P=100% x (2x18)/36=100%

M: number of the matching peaks;   N: number of all peaks

2. Based on the ANSI Standard, cell lines with ≥80% match are considered to be related; i.e., derived from a common ancestry. Cell lines with between a 55% to 80% match require further profiling for authentication of relatedness.

3. The short tandem repeat (STR) profile generated by Azenta is indicative only of the sample sent to Azenta at the time it was sent. This data and analysis are for research use only.

2) Electrophoretogram
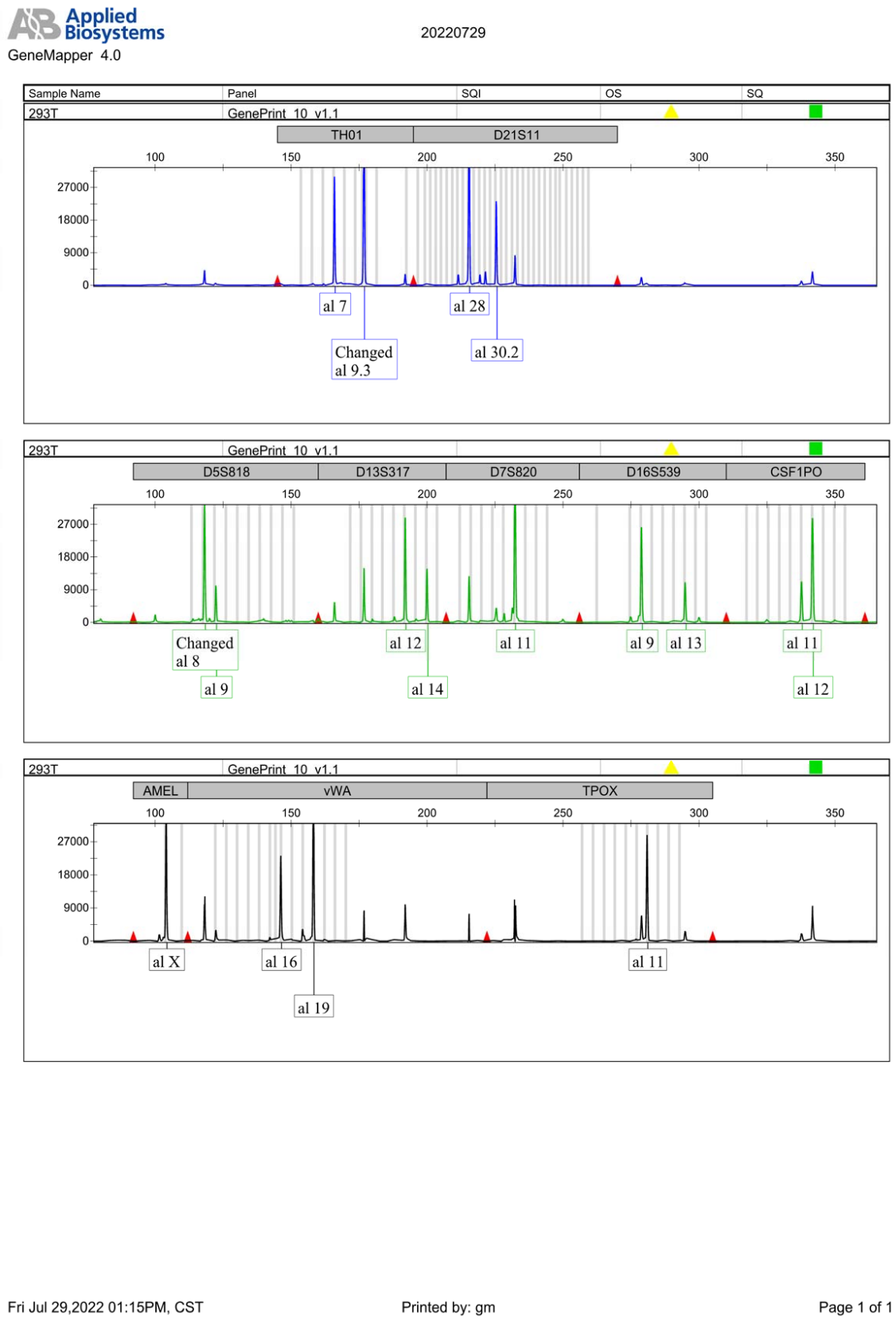
Note：Raw data in appendix

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Customer: Jundan Yu

Quotation Number: 80-980049557_R3

Completion Date: 07/29/2022

1. **Sample ID: GBC-SD**

2. **Original Material: Cell pellet**

3. **Methods:**

   1).Genomic DNA was extracted from the cell pellets provided by the customer.

   2).Samples, together with positive and negative control were amplified using GenePrint 10 System (Promega).

   3). Amplified products were processed using the ABI3730xl Genetic Analyzer.

   4). Data were analyzed using GeneMapper4.0 software and then compared with the ATCC, DSMZ, JCRB and RIKEN databases for reference matching.

4. **Results:**

   1) **10 Loci STR Profile：**

Genetic Site	Cell Bank information		Customer sample	
(Locus)	GBC-SD		GBC-SD	
Amelogenin	X	Y	X	Y
CSF1PO	13	13	11	11
D13S317	8	12	8	12
D16S539	11	13	11	13
D5S818	11	11	11	11
D7S820	11	12	11	12
THO1	7	10	7	10
TPOX	11	11	11	11
vWA	16	17	16	17
D21S11			30	31
Percent match between the sample and the database profile：88.89%				

Summary:

Your cell line is considered "related" to the reference cell line in the Cell Bank STR database, as the STR profile yields matches that are ≥ 80% but less than 100%.

Notes：
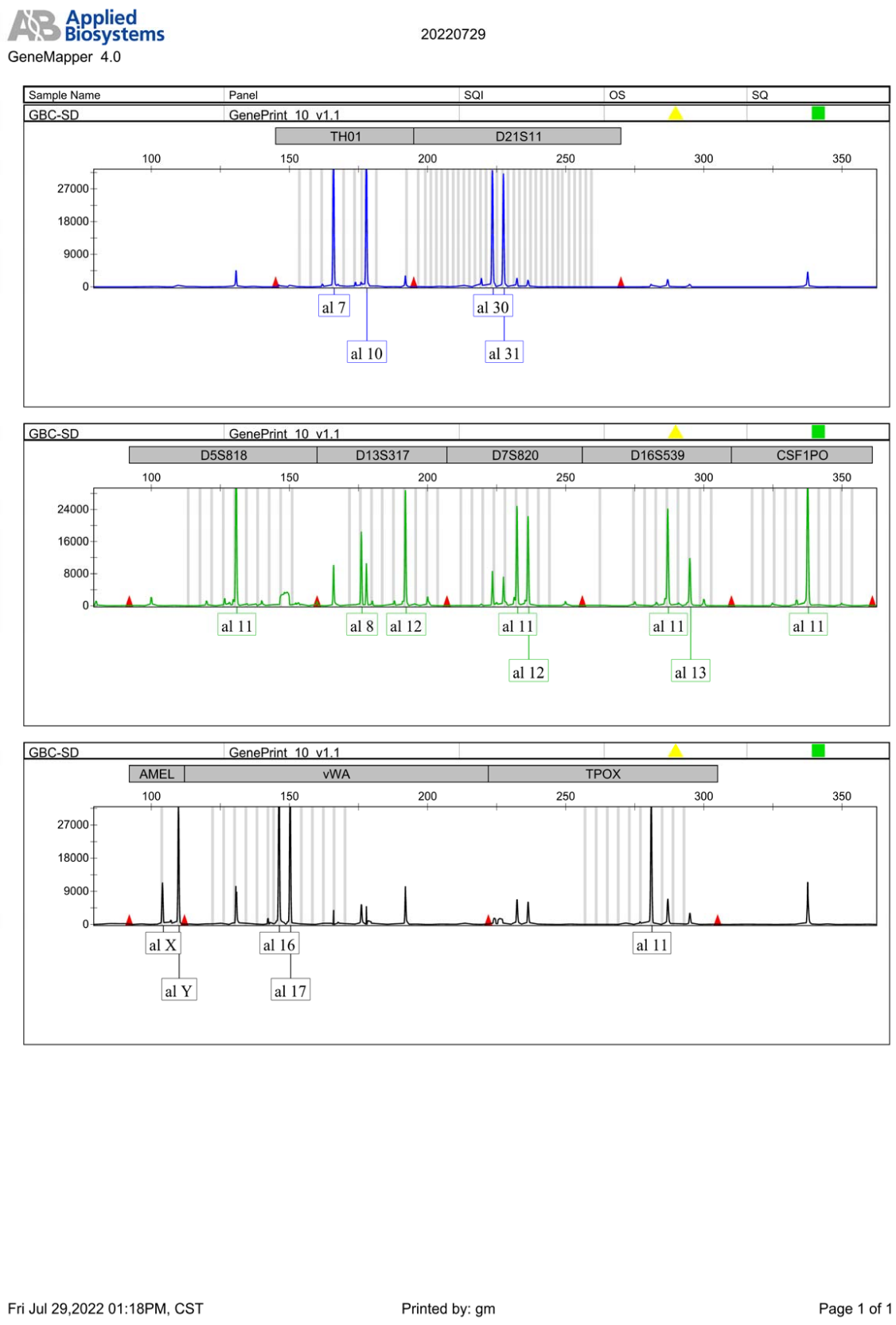
1. P=100% x (2xM)/N; M=16, N=36 P=100% x (2x16)/36=88.89%

M: number of the matching peaks;　　N: number of all peaks

2. Based on the ANSI Standard, cell lines with ≥80% match are considered to be related; i.e., derived from a common ancestry. Cell lines with between a 55% to 80% match require further profiling for authentication of relatedness.

3. The short tandem repeat (STR) profile generated by Azenta is indicative only of the sample sent to Azenta at the time it was sent. This data and analysis are for research use only.

2) Electrophoretogram