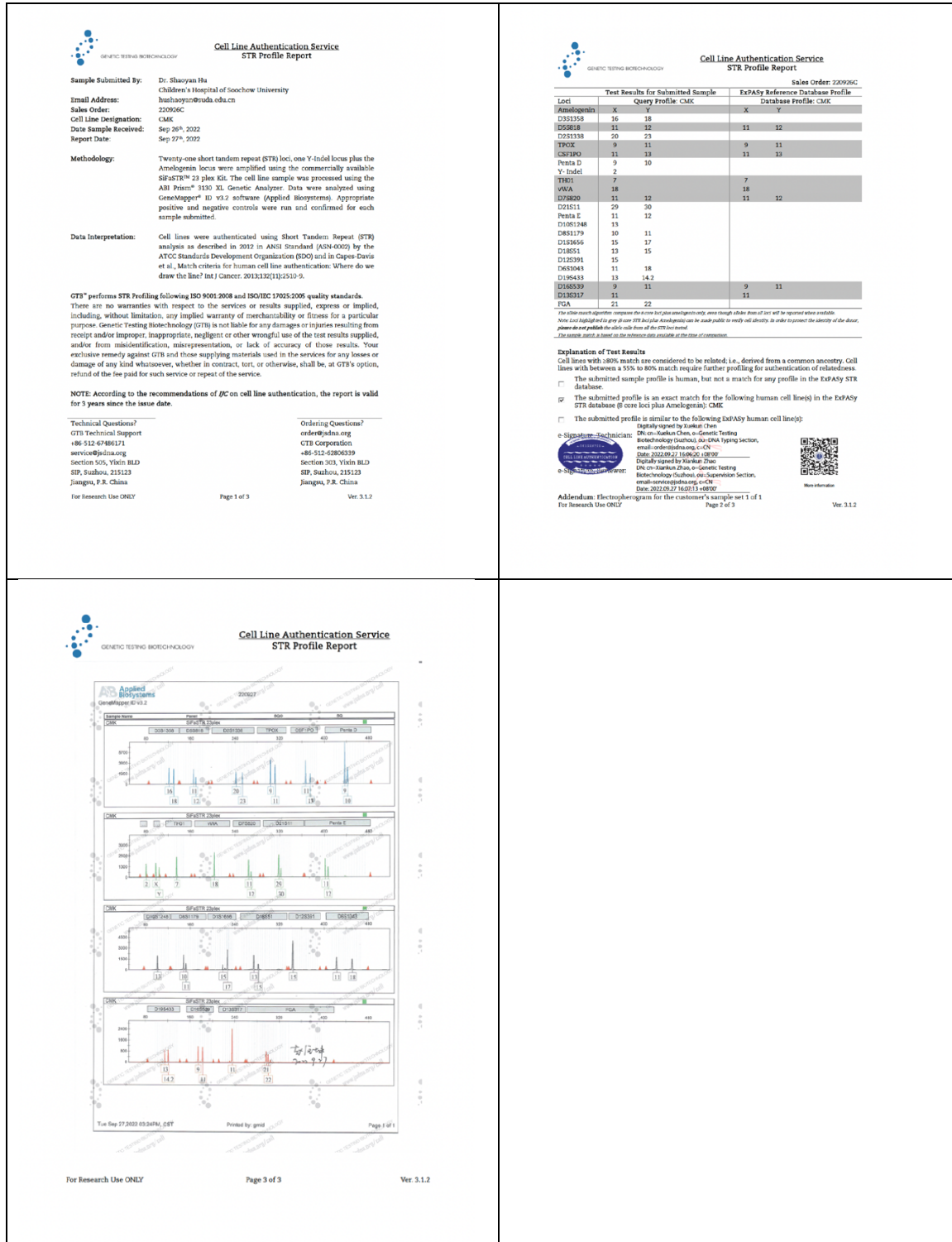


1. STR identification of MEG01 cell lines.

Cell Line Authentication Service STR Profile Report		Cell Line Authentication Service STR Profile Report																																																																																													
Sample Submitted By: Dr. Sudan He Suzhou Institute of Systems Medicine Email Address: hesudan2018@163.com Sales Order: Z20622C Cell Line Designation: MEG-01 Date Sample Received: Jun 22nd, 2022 Report Date: Jun 23rd, 2022 Methodology: Nineteen short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, were amplified using the commercially available Exio kit from AGCU. The cell line sample was processed using the ABI Prism® 3130 XL Genetic Analyzer. Data were analyzed using GeneMapper® ID v3.2 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted. 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. 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GTB Technical Support +86-512-67486171 service@jcdna.org Section 505, Yixin BLD SIP, Suzhou, 215123 Jiangsu, P.R. China Ordering Questions? order@jcdna.org GTB Corporation +86-512-62806339 Section 303, Yixin BLD SIP, Suzhou, 215123 Jiangsu, P.R. China For Research Use ONLY Page 1 of 3 Ver. 3.1.2		Sales Order: Z20622C <table border="1"><thead><tr><th colspan="2">Test Results for Submitted Sample</th><th colspan="2">DSMZ Reference Database Profile</th></tr><tr><th>Loci</th><th>Query Profile: MEG-01</th><th colspan="2">Database Profile: MEG-01</th></tr><tr><th></th><th>X Y</th><th>X</th><th>Y</th></tr></thead><tbody><tr><td>Amelogenin</td><td></td><td></td><td></td></tr><tr><td>D3S1358</td><td>15</td><td></td><td></td></tr><tr><td>D1S1611</td><td>8</td><td>8</td><td></td></tr><tr><td>D7S820</td><td>11</td><td>11</td><td></td></tr><tr><td>D16S0539</td><td>9</td><td>9</td><td></td></tr><tr><td>Penta E</td><td>15</td><td></td><td></td></tr><tr><td>TPOX</td><td>8 11</td><td>8 11</td><td></td></tr><tr><td>TH01</td><td>7</td><td>7</td><td></td></tr><tr><td>D2S1338</td><td>19</td><td></td><td></td></tr><tr><td>CSF1PO</td><td>10</td><td>10</td><td></td></tr><tr><td>Penta D</td><td>11 13</td><td></td><td></td></tr><tr><td>D15S443</td><td>14 15.2</td><td></td><td></td></tr><tr><td>YWA</td><td>16</td><td>16</td><td></td></tr><tr><td>D21S11</td><td>29</td><td></td><td></td></tr><tr><td>D18S51</td><td>18 22</td><td></td><td></td></tr><tr><td>D6S1043</td><td>14 15 18</td><td></td><td></td></tr><tr><td>D8S1179</td><td>14 15</td><td></td><td></td></tr><tr><td>ESX818</td><td>13</td><td>13</td><td></td></tr><tr><td>D12S991</td><td>19</td><td></td><td></td></tr><tr><td>FGA</td><td>26</td><td></td><td></td></tr></tbody></table> <i>The allele match algorithm compares the 8 core loci plus amelogenin only, even though alleles from all loci will be reported when available.</i> <i>Note: Loci highlighted in grey (8 core STR loci plus Amelogenin) can be made public to verify cell identity. In order to protect the identity of the donor, please do not publish the allele calls from all the STR loci tested. The sample match is based on the reference data available at the time of comparison.</i> Explanation of Test Results 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. ☐ 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 DSMZ STR database (8 core loci plus Amelogenin): MEG-01 ☐ The submitted profile is similar to the following DSMZ human cell line(s): e-Signature Technician: Digitally signed by Xiaokun Chen DN: cn=Xiaokun Chen, o=Genetic Testing Biotechnology (GutHub), ou=DNA Typing Section, email=order@jcdna.org, c=CN Date: 2022.06.23 16:23:55 +0800 e-Signature Reviewer: Digitally signed by Xiaokun Zhuo DN: cn=Xiaokun Zhuo, o=Genetic Testing Biotechnology (GutHub), ou=Supervision Section, email=service@jcdna.org, c=CN Date: 2022.06.23 16:36:06 +0800 Addendum: Electropherogram for the customer's sample set 1 of 1 For Research Use ONLY Page 2 of 3 Ver. 3.1.2		Test Results for Submitted Sample		DSMZ Reference Database Profile		Loci	Query Profile: MEG-01	Database Profile: MEG-01			X Y	X	Y	Amelogenin				D3S1358	15			D1S1611	8	8		D7S820	11	11		D16S0539	9	9		Penta E	15			TPOX	8 11	8 11		TH01	7	7		D2S1338	19			CSF1PO	10	10		Penta D	11 13			D15S443	14 15.2			YWA	16	16		D21S11	29			D18S51	18 22			D6S1043	14 15 18			D8S1179	14 15			ESX818	13	13		D12S991	19			FGA	26		
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Cell Line Authentication Service STR Profile Report Genetic Testing Biotechnology Applied Biosystems GeneMapper ID v3.2 STR Profile: MEG-01 Sample: MEG-01 Run: 20220623_1630 File: 20220623_1630 Printed by: gmt The Jan 23, 2022 04:18 PM, GMT For Research Use ONLY Page 3 of 3 Ver. 3.1.2																																																																																															

2. STR identification of CMK cell lines.



3. STR identification of UT-7 cell lines.



**Cell Line Authentication Service
STR Profile Report**

Sample Submitted by: Dr. Jian Pan
Children's Hospital of Soochow University
panjian2008@163.com

Email Address: panjian2008@163.com

Sales Order: 231127D

Cell Line Designation: UT-7

Date Sample Received: Nov 27th, 2023

Report Date: Nov 28th, 2023

Methodology: Twenty-one short tandem repeat (STR) loci plus the Amelogenin locus were amplified using the commercially available Sifast™ Z1 plex Kit. The cell line sample was processed using the ABI Prism® 3130 XL Genetic Analyzer. Data were analyzed using GeneMapper® ID v3.2 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

Data Interpretation: Cell lines were authenticated using Short Tandem Repeat (STR) analysis as described in 2021 in ANSI Standard (ASN-0007) by the ATCC Standards Development Organization (SDO) and in Jamie L. Almeida et al., Authentication of Human and Mouse Cell Lines by Short Tandem Repeat (STR) DNA Genotype Analysis. Assay Guidance Manual. PMID: 23895434. Bookshelf ID: NBK144066.

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NOTE: According to the recommendations of IC® on cell line authentication, the report is valid for 3 years since the issue date.

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**Cell Line Authentication Service
STR Profile Report**

Sales Order: 231127D

Loci	Test Results for Submitted Sample		ExPASy Reference Database Profile	
	Query Profile: UT-7		Database Profile: UT-7	
Amelogenin	X	Y		
D3S1358	16		16	
D5S498	12		12	
D2S1338	18	23		
TPCX	10		10	
CSF1PO	12		12	
Penis D	9	11		
TH01	6	9	6	9
VWA	14	18 19	14	18 19
D7S820	8		8	
D21S11	31.2		31.2	
Penis E	16	17		
D10S1248	14	16		
D8S1179	11	15	11	15
D13S856	15			
D18S51	14	17	14	17
D12S91	18	19		
D6S1043	10	19		
D19S433	14	14.2		
D16S539	10	12	10	12
D13S317	8		8	
FGA	23		23	

The allele match algorithm compares the 13 core STR loci only, even though alleles from all loci will be reported when available.
Note: Loci highlighted in grey (i.e. core STR loci) can be made public to verify cell identity. In order to protect the identity of the donor, please do not publish the allele values from all the STR loci tested.
The sample results are based on the reference data available at the time of comparison.

Explanation of Test Results
Cell lines with >90% match were derived from the same donor. Cell lines with between >70% to 79% match require further profiling for authentication of relatedness. Cell lines with <70% match are very unlikely to be from the same donor.

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

☒ The submitted profile is an exact match for the following human cell line(s) in the ExPASy STR database (13 core STR loci): UT-7

☐ The submitted profile is similar to the following ExPASy human cell line(s):

e-Signature Technician:
DK cn-Xuekun Chen, o-Genetic Testing
Biotechnology (Shanghai), ou-DNA Typing Section,
email=order@gtbna.org c=CN
Date=2023.11.28 17:52:09 +0800

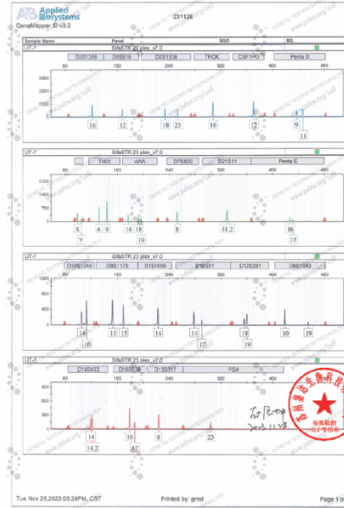
e-Signature Supervisor:
DK cn-Xuekun Zhao, o-Genetic Testing
Biotechnology (Shanghai), ou-Supervision Section,
email=service@gtbna.org c=CN
Date=2023.11.28 17:52:05 +0800

Addendum: Electropherogram for the customer's sample set 1 of 1

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**Cell Line Authentication Service
STR Profile Report**



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**Cell Line Authentication Service
STR Profile Report**

Sales Order: 231127D

Sample Submitted by: Dr. Jian Pan
Children's Hospital of Soochow University
panjian2008@163.com

Email Address: panjian2008@163.com

Sales Order: 231127D

Cell Line Designation: UT-7

Date Sample Received: Nov 27th, 2023

Report Date: Nov 28th, 2023

Methodology: Twenty-one short tandem repeat (STR) loci plus the Amelogenin locus were amplified using the commercially available Sifast™ Z1 plex Kit. The cell line sample was processed using the ABI Prism® 3130 XL Genetic Analyzer. Data were analyzed using GeneMapper® ID v3.2 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

Data Interpretation: Cell lines were authenticated using Short Tandem Repeat (STR) analysis as described in 2021 in ANSI Standard (ASN-0007) by the ATCC Standards Development Organization (SDO) and in Jamie L. Almeida et al., Authentication of Human and Mouse Cell Lines by Short Tandem Repeat (STR) DNA Genotype Analysis. Assay Guidance Manual. PMID: 23895434. Bookshelf ID: NBK144066.

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NOTE: According to the recommendations of IC® on cell line authentication, the report is valid for 3 years since the issue date.

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4. STR identification of M07e cell lines.

**Cell Line Authentication Service
STR Profile Report**

Sample Submitted By: Dr. Jian Pan
Children's Hospital of Soochow University
Email Address: panjian2008@163.com
Sales Order: Z312358
Cell Line Designation: M-07e-New
Date Sample Received: Dec 19th, 2023
Report Date: Dec 19th, 2023

Methodology: Twenty-one short tandem repeat (STR) loci plus the Amelogenin locus were amplified using the commercially available SifastR™ 23 plex Kit. The cell line sample was processed using the ABI Prism® 3130 XL Genetic Analyzer. Data were analyzed using GeneMapper® ID v3.2 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

Data Interpretation: Cell lines were authenticated using Short Tandem Repeat (STR) analysis as described in 2021 in ANSI Standard (ASN-0002) by the ATCC Standards Development Organization (SDO) and in Jamie L. Almeida et al., Authentication of Human and Mouse Cell Lines by Short Tandem Repeat (STR) DNA Genotype Analysis, Assay Guidance Manual. PMID: 23905434. Biocheck ID: N8K140466.

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NOTE: According to the recommendations of $\geq 95\%$ on cell line authentication, the report is valid for 3 years since the issue date.

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**Cell Line Authentication Service
STR Profile Report**

Sales Order: Z312198

Test Results for Submitted Sample		Expasy Reference Database Profile	
Loci	Query Profile: M-07e-New	Database Profile: M-07e	
Amelogenin	X		
DYS19	16 19	16 19	
D5S818	11 11	11	
D2S1338	19 25		
TP2X	8	8	
CSF1PO	9 10	9 10	
Penta D	9		
TH01	6 8	6 8	
vWA	16 18	16 18	
D7S820	11 11	11	
D21S11	30 32.2	30 32.2	
Penta E	12 14		
D10S1248	14 15		
D8S1179	13 16	13 16	
D1S1656	13 16		
D18S51	15 20	15 20	
D12S391	23 24		
D6S1043	13 19		
D19S443	14 15		
D16S539	11	11	
D13S317	10 11	10 11	
FGA	18 22	18 22	

The above match algorithm compares the 15 core STR loci only, even though additional loci will be reported when available.
Note: Loci highlighted in grey (13 core STR loci) can be made public to verify cell identity. In order to protect the identity of the donor, please do not publish the above values of the STR loci tested.
The match results are based on the reference data available at the time of comparison.

Explanation of Test Results
Cell lines with 95% match are derived from the same donor. Cell lines with between a 70% to 79% match require further profiling for authentication of relatedness. Cell lines with <70% match are very unlikely to be from the same donor.

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

☒ The submitted profile is an exact match for the following human cell line(s) in the Expasy STR database (13 core STR loci): M-07e

☐ The submitted profile is similar to the following Expasy human cell line(s):

e-Signature-Technician: Digitally signed by Xiankun Chen, DN: cn=Xiankun Chen, o=Genetic Testing Biotechnology (Suzhou), ou=DNA Typing Section, email=xiaokun@gtbna.org, c=CN, Date: 2023.12.19 15:45:27 +0800

e-Signature-Scientist: Digitally signed by Xiankun Chen, DN: cn=Xiankun Chen, o=Genetic Testing Biotechnology (Suzhou), ou=Supervision Section, email=xiaokun@gtbna.org, c=CN, Date: 2023.12.19 15:17:19 +0800

Addendum: Electropherogram for the customer's sample set 1 of 1

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**Cell Line Authentication Service
STR Profile Report**

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**Cell Line Authentication Service
STR Profile Report**

Addendum: Electropherogram for the customer's sample set 1 of 1

For Research Use ONLY Page 2 of 3 Ver. 3.1.2

Certificate of STR Analysis 细胞遗传学鉴定实验报告 样品名称: 细胞系 样品类型: STR 基因型分析 样品编号: 客户样编号 230 <table border="1"> <tr> <th>客户样编号</th> <th>公司编号</th> </tr> <tr> <td>230</td> <td>20170331-03</td> </tr> </table> 样品数量: 1 样品状态: 细胞系 检测项目: STR 送检单位: 上海中乔新乔生物技术有限公司 检测方法: 用 <i>Ampligen</i> 的基因组抽提试剂盒提取 DNA, 采用 20-STR 扩增方案扩增, 在 ABI 3730 遗传分析仪上对 STR 位点和性别基因 <i>Amelogenin</i> 进行检测。 检测结果: (一) 细胞遗传学结果 <table border="1"> <thead> <tr> <th></th> <th>多态性基因</th> <th>检测加照</th> <th>加照</th> <th>EV 值</th> <th>结果</th> </tr> </thead> <tbody> <tr> <td>20170331-03</td> <td>有</td> <td>K-562</td> <td>DSM2</td> <td>1</td> <td>完全匹配</td> </tr> </tbody> </table> - 多态性基因位于第三及以后位置。 - 本次检测各细胞分型结果良好。	客户样编号	公司编号	230	20170331-03		多态性基因	检测加照	加照	EV 值	结果	20170331-03	有	K-562	DSM2	1	完全匹配	Certificate of STR Analysis (一) 细胞遗传学结果 20170331-03: 该细胞 DNA 分型在细胞系库中匹配到完全匹配的细胞系, DSM2 数据库名为 K-562, 细胞号对应 GCL-263, 本次检测在该细胞系中发展多等位基因。 (二) 细胞分型结果 表 3: 细胞 20170331-03 的 STR 位点和 <i>Amelogenin</i> 位点的基因分型结果 <table border="1"> <thead> <tr> <th rowspan="2">Marker</th> <th colspan="6">样本</th> </tr> <tr> <th>Allele1</th> <th>Allele2</th> <th>Allele3</th> <th>Allele4</th> <th>Allele5</th> <th>Allele6</th> </tr> </thead> <tbody> <tr> <td>D15S818</td> <td>11</td> <td>12</td> <td></td> <td></td> <td>11</td> <td>12</td> </tr> <tr> <td>D15S17</td> <td>8</td> <td>9</td> <td></td> <td></td> <td>8</td> <td>9</td> </tr> <tr> <td>D7S820</td> <td>9</td> <td>11</td> <td></td> <td></td> <td>9</td> <td>11</td> </tr> <tr> <td>D16S539</td> <td>11</td> <td>12</td> <td></td> <td></td> <td>11</td> <td>12</td> </tr> <tr> <td>VWA</td> <td>16</td> <td>16</td> <td></td> <td></td> <td>16</td> <td>16</td> </tr> <tr> <td>TH01</td> <td>9.3</td> <td>9.3</td> <td></td> <td></td> <td>9.3</td> <td>9.3</td> </tr> <tr> <td>AMEL</td> <td>X</td> <td>X</td> <td></td> <td></td> <td>X</td> <td>X</td> </tr> <tr> <td>TPOX</td> <td>8</td> <td>9</td> <td></td> <td></td> <td>8</td> <td>9</td> </tr> <tr> <td>CSF1PO</td> <td>9</td> <td>10</td> <td></td> <td></td> <td>9</td> <td>10</td> </tr> <tr> <td>D12S911</td> <td>23</td> <td>23</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>FGA</td> <td>23</td> <td>24</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>D2S1338</td> <td>17</td> <td>17</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>D21S11</td> <td>29</td> <td>30</td> <td>31</td> <td></td> <td></td> <td></td> </tr> <tr> <td>D18S51</td> <td>15</td> <td>16</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>D16S179</td> <td>12</td> <td>12</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>D15S158</td> <td>16</td> <td>16</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>D16S1043</td> <td>11</td> <td>15</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>PENTAC</td> <td>5</td> <td>14</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>D15S413</td> <td>14</td> <td>14.2</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>PENTAD</td> <td>9</td> <td>13</td> <td></td> <td></td> <td></td> <td></td> </tr> </tbody> </table>	Marker	样本						Allele1	Allele2	Allele3	Allele4	Allele5	Allele6	D15S818	11	12			11	12	D15S17	8	9			8	9	D7S820	9	11			9	11	D16S539	11	12			11	12	VWA	16	16			16	16	TH01	9.3	9.3			9.3	9.3	AMEL	X	X			X	X	TPOX	8	9			8	9	CSF1PO	9	10			9	10	D12S911	23	23					FGA	23	24					D2S1338	17	17					D21S11	29	30	31				D18S51	15	16					D16S179	12	12					D15S158	16	16					D16S1043	11	15					PENTAC	5	14					D15S413	14	14.2					PENTAD	9	13					Certificate of STR Analysis 其他说明: (一) 分型与库中匹配: 列表: 实验与库中匹配 <table border="1"> <thead> <tr> <th></th> <th>方案 1</th> <th>方案 2</th> <th>方案 3</th> <th>方案 4</th> </tr> </thead> <tbody> <tr> <td>1</td> <td>TH01</td> <td>TPOX</td> <td>D15S158</td> <td>AMEL</td> </tr> <tr> <td>2</td> <td>D12S911</td> <td>VWA</td> <td>D15S17</td> <td>D15S18</td> </tr> <tr> <td>3</td> <td>D7S820</td> <td>D15S179</td> <td>D15S1043</td> <td>D15S138</td> </tr> <tr> <td>4</td> <td>CSF1PO</td> <td>PENTAD</td> <td>D16S539</td> <td>D15S11</td> </tr> <tr> <td>5</td> <td>FGA</td> <td></td> <td>D15S413</td> <td>D15S51</td> </tr> <tr> <td>6</td> <td>PENTAC</td> <td></td> <td></td> <td></td> </tr> </tbody> </table>		方案 1	方案 2	方案 3	方案 4	1	TH01	TPOX	D15S158	AMEL	2	D12S911	VWA	D15S17	D15S18	3	D7S820	D15S179	D15S1043	D15S138	4	CSF1PO	PENTAD	D16S539	D15S11	5	FGA		D15S413	D15S51	6	PENTAC			
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6. STR identification of U937 cell lines.


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Cell Line Authentication Report


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Cell Line Authentication Report

Customer: Zhiheng Li

Quotation Number: 80-1139924657_R2

Completion Date: 03/06/2023

1. Sample ID: U937

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 (Locus)	Cell Bank information		Customer sample	
	U-937		U937	
Amelegemin	X	X	X	X
CSF1PO	12	12	12	12
D13S317	10	12	10	12
D16S539	12	12	12	12
D5S818	12	12	12	12
D7S820	9	11	9	11
TH01	6	9,3	6	9,3
TPOX	8	11	8	11
VWA	14	15	14	15
D21S11		27	27	29
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:


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1. $P=100\% \times (2sM)/N$; $M=18$, $N=36$ $P=100\% \times (2s18)/36=100\%$

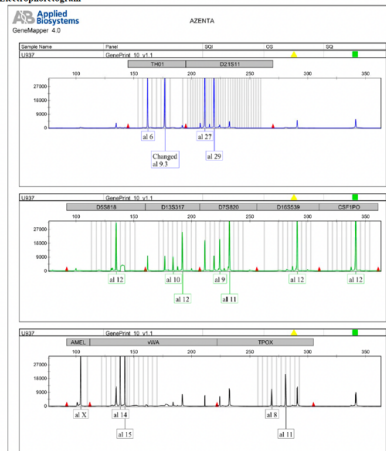
M: number of the matching peaks; N: number of all peaks

2. Based on the ANSI Standard, cell lines with $\geq 80\%$ 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.


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2) Electropherogram



Mon Mar 06 2023 10:09AM CST

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Note: Raw data in appendix