



Cell Line Authentication Service

STR Profile Report

Sample Submitted By: NIH/NCI
Shouhui Yang

Email Address: shouhui.yang@nih.gov

ATCC Sales Order: SO0895664

FTA Barcode: STRB8048

Cell Line Designation: CFPAC-1

Date Sample Received: Monday, October 04, 2021

Report Date: Friday, October 15, 2021

Methodology: Seventeen short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, were amplified using the commercially available PowerPlex® 18D Kit from Promega. The cell line sample was processed using the ABI Prism® 3500xl Genetic Analyzer. Data were analyzed using GeneMapper® ID-X v1.2 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) Authentication of Human Cell Lines: Standardization of STR Profiling 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*. 2012 Nov 8. doi: 10.1002/ijc.27931

ATCC performs STR Profiling following ISO 9001:2008 and ISO/IEC 17025:2005 quality standards.

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Technical questions?

ATCC Technical Support
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tech@atcc.org

Ordering questions?

800-638-6597 or 703-365-2700
Fax 703-365-2750
Email: sales@atcc.org



| Test Results for Submitted Sample | | | | ATCC Reference Database Profile | | | |
|---|------------------------|------|--|---|----|--|-----|
| Locus | Query Profile: CFPAC-1 | | | Database Profile: CFPAC-1; Pancreatic Carcinoma; Human (Homo sapiens) | | | |
| D3S1358 | 16 | | | | | | |
| TH01 | 8 | | | 8 | | | |
| D21S11 | 30 | 31.2 | | | | | |
| D18S51 | 12 | | | | | | |
| Penta_E | 10 | 12 | | | | | |
| D5S818 | 10 | 11 | | 10 | 11 | | |
| D13S317 | 12 | | | 12 | | | |
| D7S820 | 8 | 10 | | 8 | 10 | | |
| D16S539 | 9 | 11 | | 9 | 11 | | |
| CSF1PO | 10 | | | 10 | | | |
| Penta_D | 11 | 13 | | | | | |
| Amelogenin | X | Y | | X | Y | | |
| vWA | 17 | | | 17 | | | |
| D8S1179 | 11 | 15 | | | | | |
| TPOX | 8 | | | 8 | | | |
| FGA | 21 | 22 | | | | | |
| D19S433 | 13 | 15 | | | | | |
| D2S1338 | 18 | 23 | | | | | |
| Number of shared alleles between query sample and database profile: | | | | | | | 13 |
| Total number of alleles in the database profile: | | | | | | | 13 |
| Percent match between the submitted sample and the database profile: | | | | | | | 100 |
| <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> | | | | | | | |
| 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. Electropherograms showing raw data are attached. | | | | | | | |

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 ATCC STR database.
- The submitted profile is an exact match for the following ATCC human cell line(s) in the ATCC STR database (8 core loci plus Amelogenin): CRL-1918
- The submitted profile is similar to the following ATCC human cell line(s):
- An STR profile could not be generated.

Additional Comments:

n/a

| | |
|--------------------------|-------------------|
| e-Signature, Technician: | gsykes 10/15/2021 |
| e-Signature, Reviewer: | Bchase 10/15/2021 |





Addendum: Comparative Output from the ATCC STR Profile Database

| % Match | ATCC® Cat. No. | Designation | D5S818 | D13S317 | D7S820 | D16S539 | vWA | TH01 | AMEL | TPOX | CSF1PO |
|---------|----------------|--|--------|---------|--------|---------|-----|------|------|------|--------|
| 100 | STRB8048 | CFPAC-1 | 10,11 | 12 | 8,10 | 9,11 | 17 | 8 | X,Y | 8 | 10 |
| 100 | CRL-1918 | CFPAC-1; Pancreatic Carcinoma; Human (Homo sapiens) | 10,11 | 12 | 8,10 | 9,11 | 17 | 8 | X,Y | 8 | 10 |

Definitions of terms used in this report:

Peak Area Difference (PAD):

Refers to a heterozygous peak imbalance.

Two alleles at a single locus should amplify in a similar manner; and therefore produce peaks of similar height and area. Peaks which are above threshold (50 rfu) but are not of similar area, within 50% of each other, are referred to as a PAD. Due to their nature cell lines do not amplify in the same manner as a sample taken from a fresh buccal swab. PAD is far more common in cell line samples.

Stutter:

A stutter peak is a small peak which occurs immediately before the true peak. It is defined as being a single repeat unit smaller than the true peak. The stutter peak should be less than 15% of the true peak. The stutter is caused by the polymerase.

+4 Peak:

A +4 is similar to a stutter but occurs immediately after the true peak. A stutter peak should be less than 5% for a homozygous and 10% for a heterozygous.

Below Threshold Peak(s):

Cell lines can produce unusual profiles and occasionally a peak will amplify poorly and be below threshold. Where we find a below threshold peak which we believe is valid we indicate it as a below threshold peak. Our cell line analysis criteria, Homozygous and Heterozygous peaks must be equal to or above the set height threshold for it to be considered a true peak.

Ladder/ Off Ladder Peak(s):

The allelic ladder consists of most or all known alleles in the population and allows for precise assignment of alleles. Those which do not align are termed 'off ladder'.

Artifact:

A non-allelic product of the amplification process, an anomaly of the detection process, or a by-product of primer synthesis

Pull-up:

A term used to describe when signal from one dye color channel produces artificial peaks in another, usually adjacent, color.

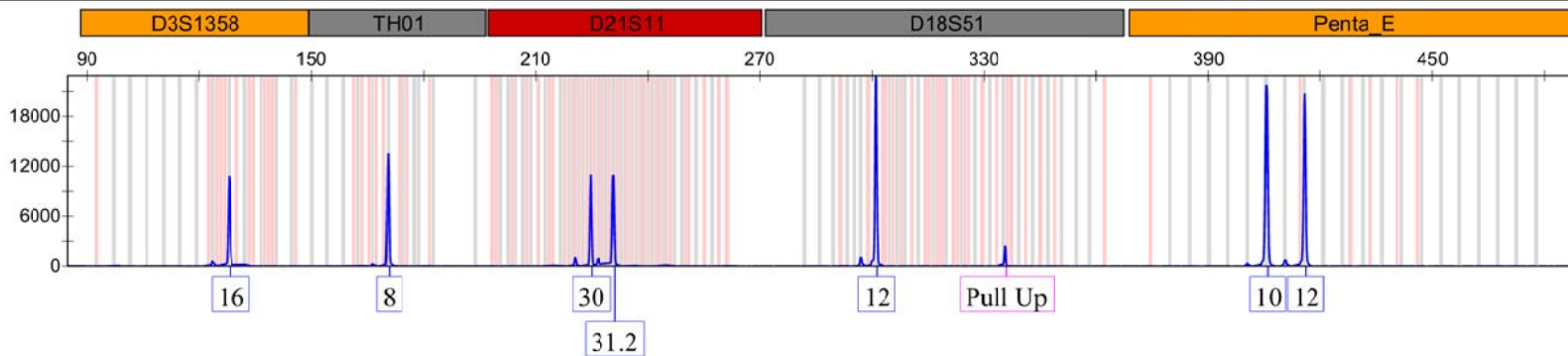
Spike:

An extraneous peak resulting from dust, dried polymer, an air bubble, or an electrical surge.

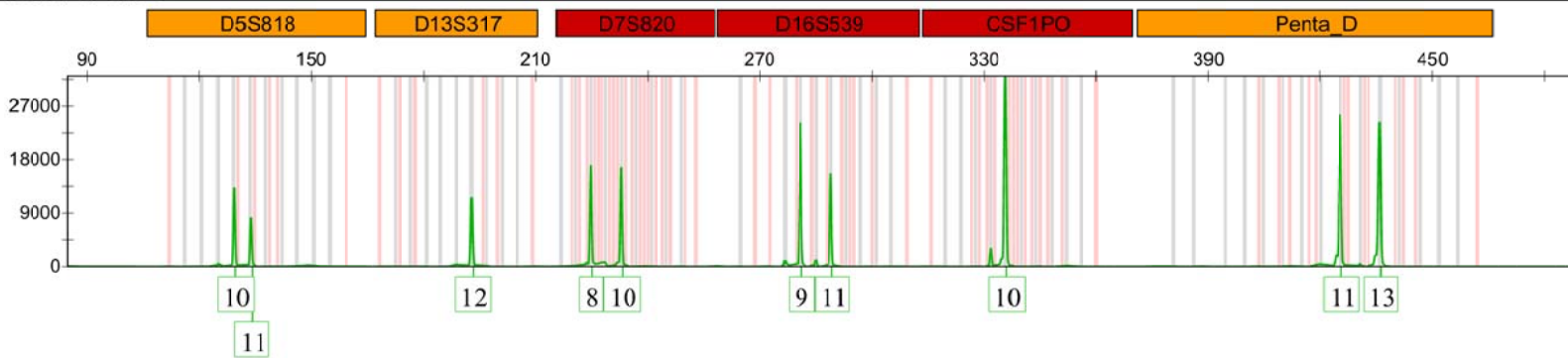
Dye blob:

Free dye not coupled to primer that can be injected into the capillary (A known and documented dye blob is often found at the D3S1358 locus.)

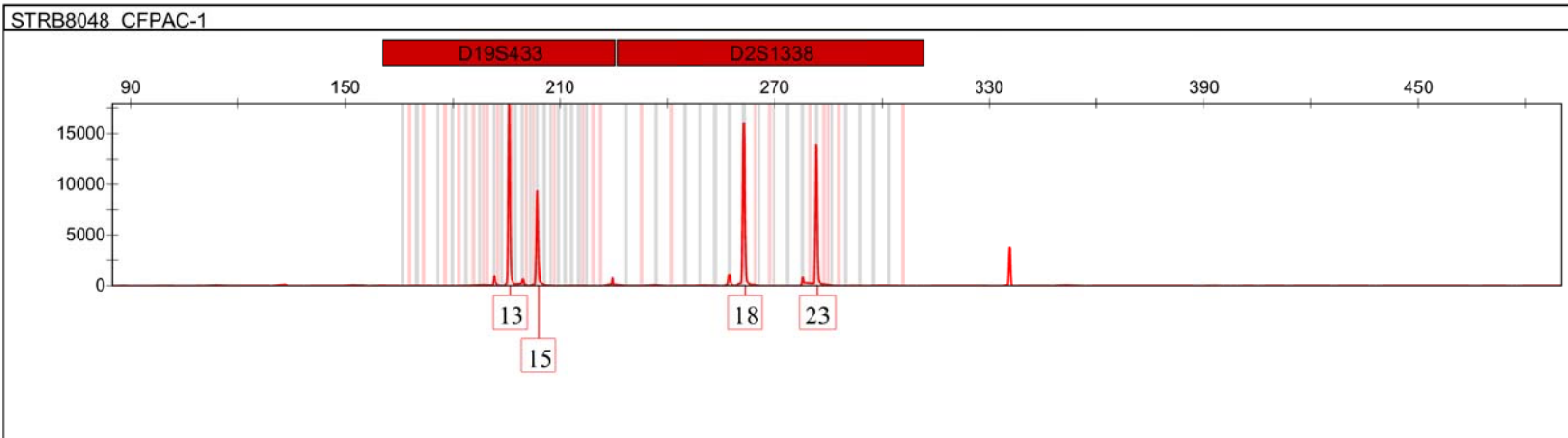
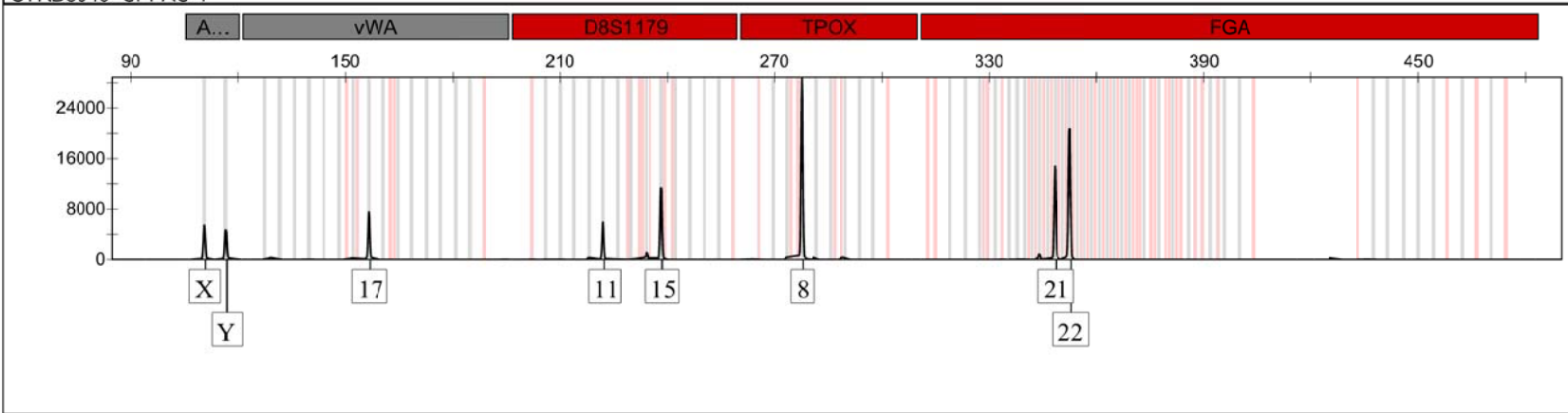
Sample Name
STRB8048_CFPAC-1



STRB8048_CFPAC-1



Sample Name
STRB8048_CFPAC-1





Cell Line Authentication Service

STR Profile Report

Sample Submitted By: National Institutes of Health
Shouhui Yang

Email Address: shouhui.yang@nih.gov

ATCC Sales Order: SO0895664

FTA Barcode: STRB8050

Cell Line Designation: Capan-2 P9

Date Sample Received: Monday, March 28, 2022

Report Date: Wednesday, March 30, 2022

Methodology: Seventeen short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, were amplified using the commercially available PowerPlex® 18D Kit from Promega. The cell line sample was processed using the ABI Prism® 3500xl Genetic Analyzer. Data were analyzed using GeneMapper® ID-X v1.2 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) Authentication of Human Cell Lines: Standardization of STR Profiling 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*. 2012 Nov 8. doi: 10.1002/ijc.27931

ATCC performs STR Profiling following ISO 9001:2008 and ISO/IEC 17025:2005 quality standards.

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tech@atcc.org

Ordering questions?

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Fax 703-365-2750
Email: sales@atcc.org



| Test Results for Submitted Sample | | | | ATCC Reference Database Profile | | | |
|---|---------------------------|----|--|---|----|--|-----|
| Locus | Query Profile: Capan-2 P9 | | | Database Profile: Capan-2; Pancreatic Carcinoma; Human (Homo sapiens) | | | |
| D3S1358 | 17 | 18 | | | | | |
| TH01 | 9.3 | | | 9.3 | | | |
| D21S11 | 31 | | | | | | |
| D18S51 | 13 | | | | | | |
| Penta_E | 11 | | | | | | |
| D5S818 | 11 | 12 | | 11 | 12 | | |
| D13S317 | 11 | 12 | | 11 | 12 | | |
| D7S820 | 9 | 11 | | 9 | 11 | | |
| D16S539 | 9 | 13 | | 9 | 13 | | |
| CSF1PO | 11 | 12 | | 11 | 12 | | |
| Penta_D | 13 | 15 | | | | | |
| Amelogenin | X | | | X | | | |
| vWA | 17 | | | 17 | | | |
| D8S1179 | 12 | 13 | | | | | |
| TPOX | 8 | | | 8 | | | |
| FGA | 21 | 24 | | | | | |
| D19S433 | 13 | 15 | | | | | |
| D2S1338 | 19 | 25 | | | | | |
| Number of shared alleles between query sample and database profile: | | | | | | | 14 |
| Total number of alleles in the database profile: | | | | | | | 14 |
| Percent match between the submitted sample and the database profile: | | | | | | | 100 |
| <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> | | | | | | | |
| 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. Electropherograms showing raw data are attached. | | | | | | | |

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 ATCC STR database.
- The submitted profile is an exact match for the following ATCC human cell line(s) in the ATCC STR database (8 core loci plus Amelogenin): HTB-80
- The submitted profile is similar to the following ATCC human cell line(s):
- An STR profile could not be generated.

Additional Comments:

n/a

| | |
|--------------------------|------------------|
| e-Signature, Technician: | lchamp 3/30/2022 |
| e-Signature, Reviewer: | Bchase 3/30/2022 |





Addendum: Comparative Output from the ATCC STR Profile Database

| % Match | ATCC® Cat. No. | Designation | D5S818 | D13S317 | D7S820 | D16S539 | vWA | TH01 | AMEL | TPOX | CSF1PO |
|---------|----------------|---|--------|---------|--------|---------|-----|------|------|------|--------|
| 100 | STRB8050 | Capan-2 P9 | 11,12 | 11,12 | 9,11 | 9,13 | 17 | 9.3 | X | 8 | 11,12 |
| 100 | HTB-80 | Capan-2; Pancreatic Carcinoma; Human (Homo sapiens) | 11,12 | 11,12 | 9,11 | 9,13 | 17 | 9.3 | X | 8 | 11,12 |

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Artifact:

A non-allelic product of the amplification process, an anomaly of the detection process, or a by-product of primer synthesis

Pull-up:

A term used to describe when signal from one dye color channel produces artificial peaks in another, usually adjacent, color.

Spike:

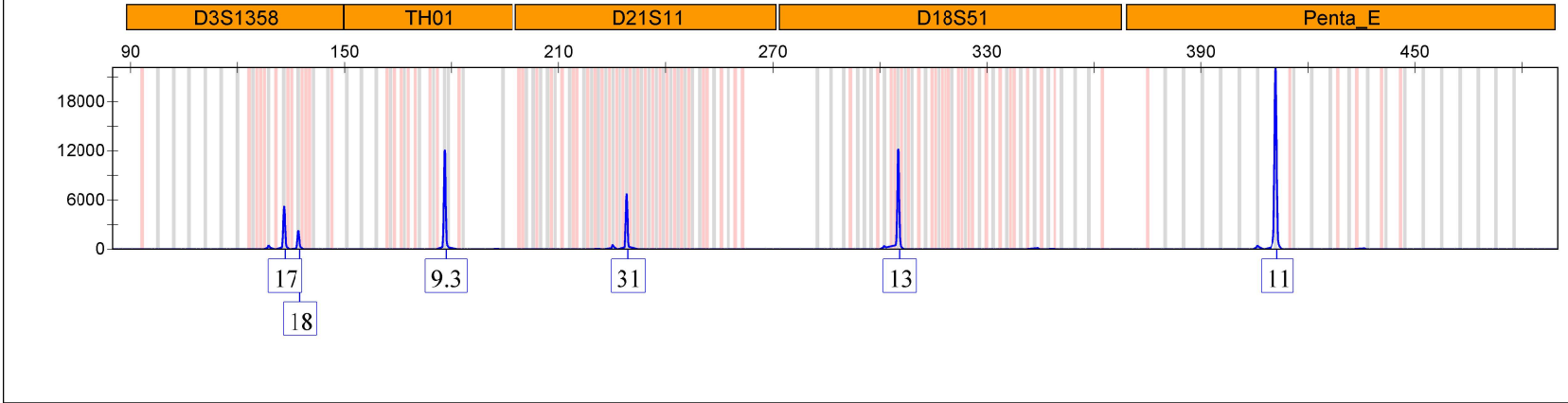
An extraneous peak resulting from dust, dried polymer, an air bubble, or an electrical surge.

Dye blob:

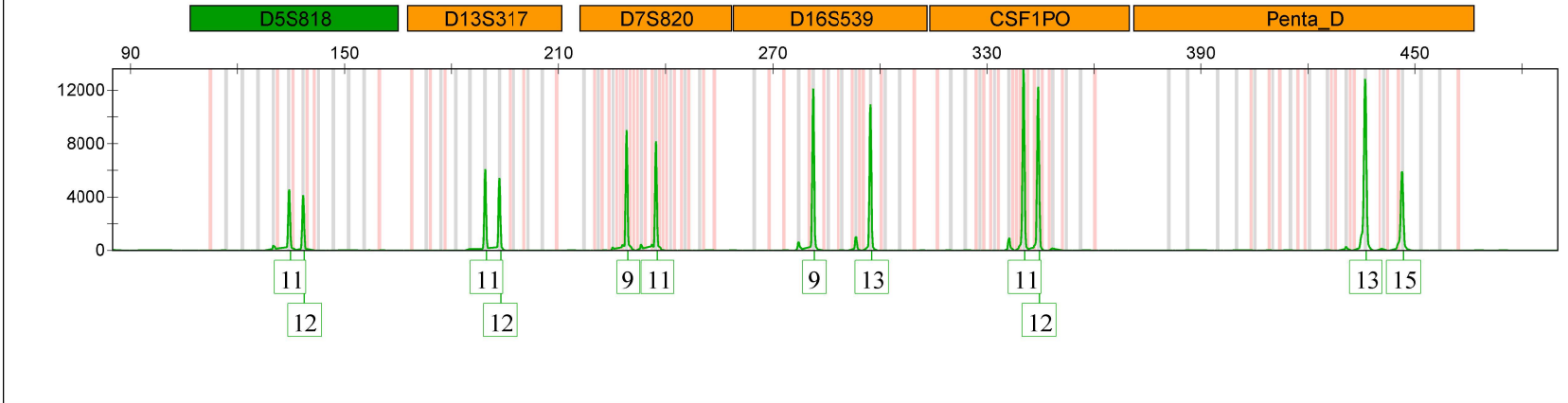
Free dye not coupled to primer that can be injected into the capillary (A known and documented dye blob is often found at the D3S1358 locus.)

Sample Name

STRB8050 Capan-2 P9

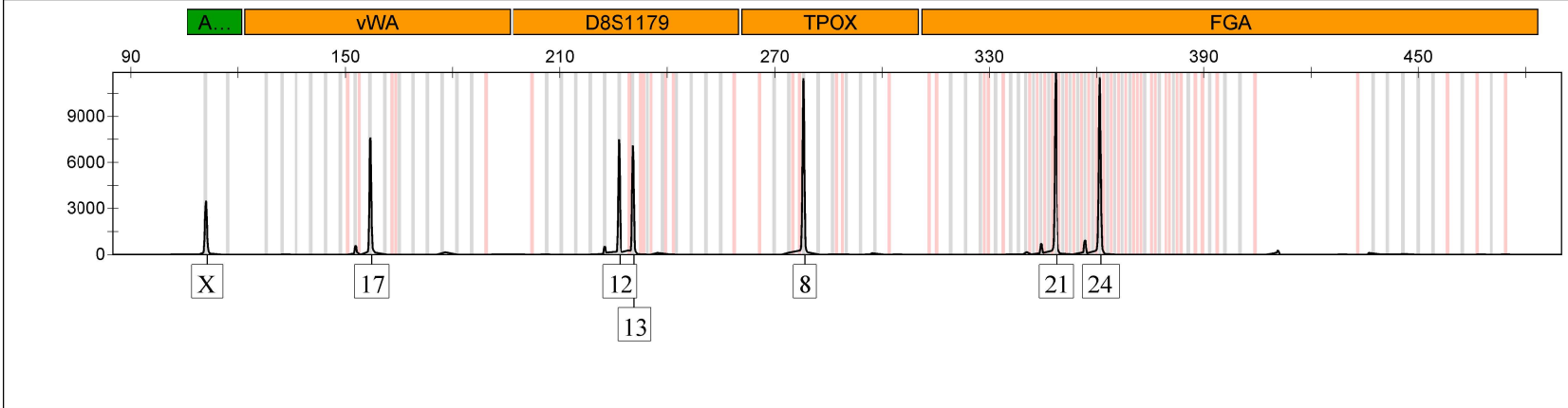


STRB8050 Capan-2 P9

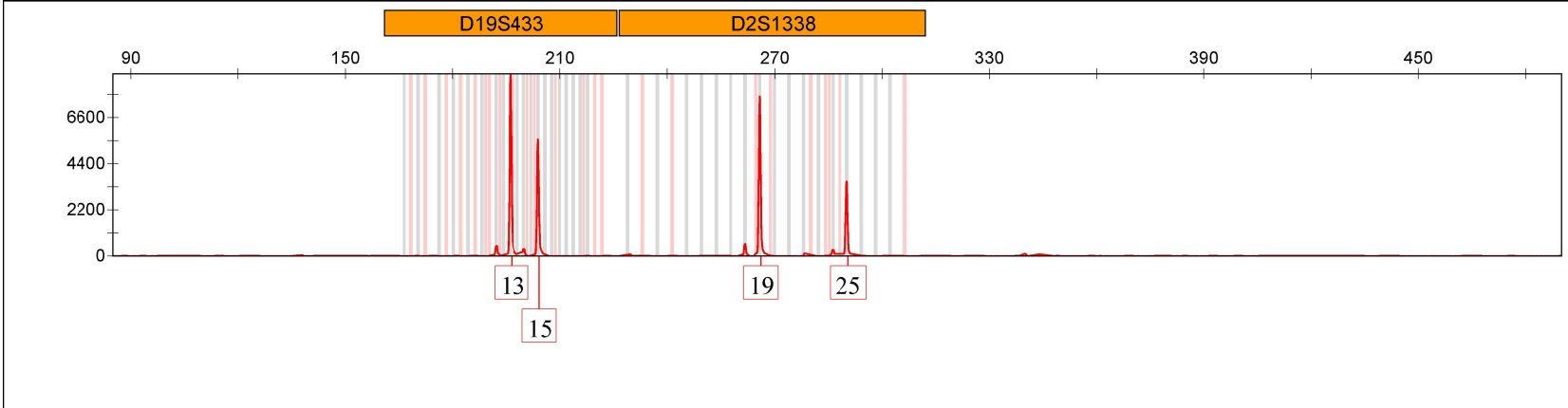


Sample Name

STRB8050 Capan-2 P9



STRB8050 Capan-2 P9





Cell Line Authentication Service

STR Profile Report

Sample Submitted By: National Institutes of Health
Shouhui Yang

Email Address: shouhui.yang@nih.gov

ATCC Sales Order: SO0895664

FTA Barcode: STRB8042

Cell Line Designation: ASPC-1

Date Sample Received: Monday, March 28, 2022

Report Date: Wednesday, March 30, 2022

Methodology: Seventeen short tandem repeat (STR) loci plus the gender determining locus, Amelogenin, were amplified using the commercially available PowerPlex® 18D Kit from Promega. The cell line sample was processed using the ABI Prism® 3500xl Genetic Analyzer. Data were analyzed using GeneMapper® ID-X v1.2 software (Applied Biosystems). Appropriate positive and negative controls were run and confirmed for each sample submitted.

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| Test Results for Submitted Sample | | | | ATCC Reference Database Profile | | | |
|---|-----------------------|-----|--|---|-----|--|-----|
| Locus | Query Profile: ASPC-1 | | | Database Profile: AsPC-1; Pancreatic Cancer; Human (Homo sapiens) | | | |
| D3S1358 | 16 | | | | | | |
| TH01 | 7 | 9.3 | | 7 | 9.3 | | |
| D21S11 | 28 | 30 | | | | | |
| D18S51 | 18 | | | | | | |
| Penta_E | 5 | 12 | | | | | |
| D5S818 | 12 | | | 12 | | | |
| D13S317 | 9 | 12 | | 9 | 12 | | |
| D7S820 | 12 | 13 | | 12 | 13 | | |
| D16S539 | 11 | | | 11 | | | |
| CSF1PO | 10 | 13 | | 10 | 13 | | |
| Penta_D | 9 | 12 | | | | | |
| Amelogenin | X | | | X | | | |
| vWA | 17 | | | 17 | | | |
| D8S1179 | 13 | 15 | | | | | |
| TPOX | 8 | 10 | | 8 | 10 | | |
| FGA | 24 | | | | | | |
| D19S433 | 14 | | | | | | |
| D2S1338 | 22 | 23 | | | | | |
| Number of shared alleles between query sample and database profile: | | | | | | | 14 |
| Total number of alleles in the database profile: | | | | | | | 14 |
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Additional Comments:

n/a

| | |
|--------------------------|------------------|
| e-Signature, Technician: | lchamp 3/30/2022 |
| e-Signature, Reviewer: | Bchase 3/30/2022 |





Addendum: Comparative Output from the ATCC STR Profile Database

| % Match | ATCC® Cat. No. | Designation | D5S818 | D13S317 | D7S820 | D16S539 | vWA | TH01 | AMEL | TPOX | CSF1PO |
|---------|----------------|---|--------|---------|--------|---------|-----|-------|------|------|--------|
| 100 | STRB8042 | ASPC-1 | 12 | 9,12 | 12,13 | 11 | 17 | 7,9,3 | X | 8,10 | 10,13 |
| 100 | CRL-1682 | AsPC-1; Pancreatic Cancer; Human (Homo sapiens) | 12 | 9,12 | 12,13 | 11 | 17 | 7,9,3 | X | 8,10 | 10,13 |

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Spike:

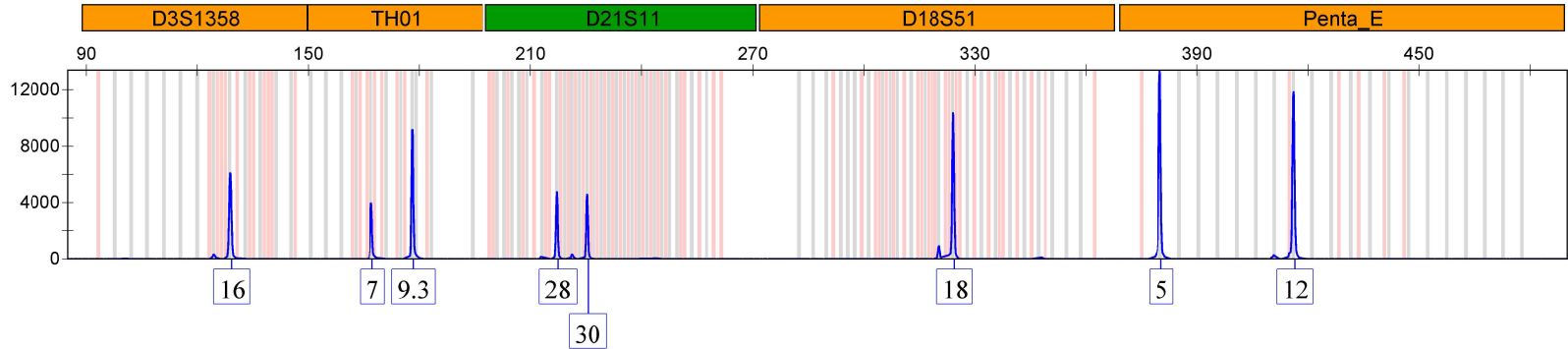
An extraneous peak resulting from dust, dried polymer, an air bubble, or an electrical surge.

Dye blob:

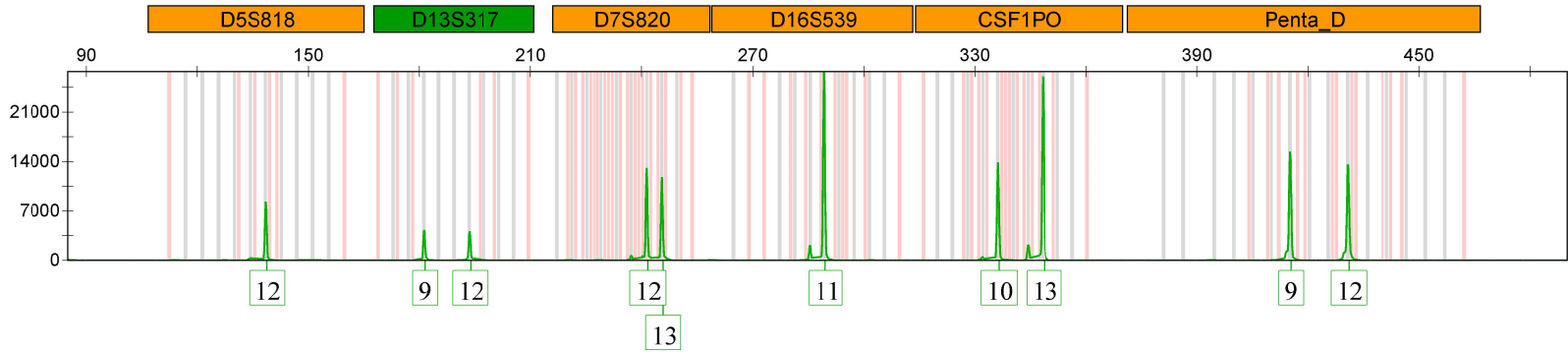
Free dye not coupled to primer that can be injected into the capillary (A known and documented dye blob is often found at the D3S1358 locus.)

Sample Name

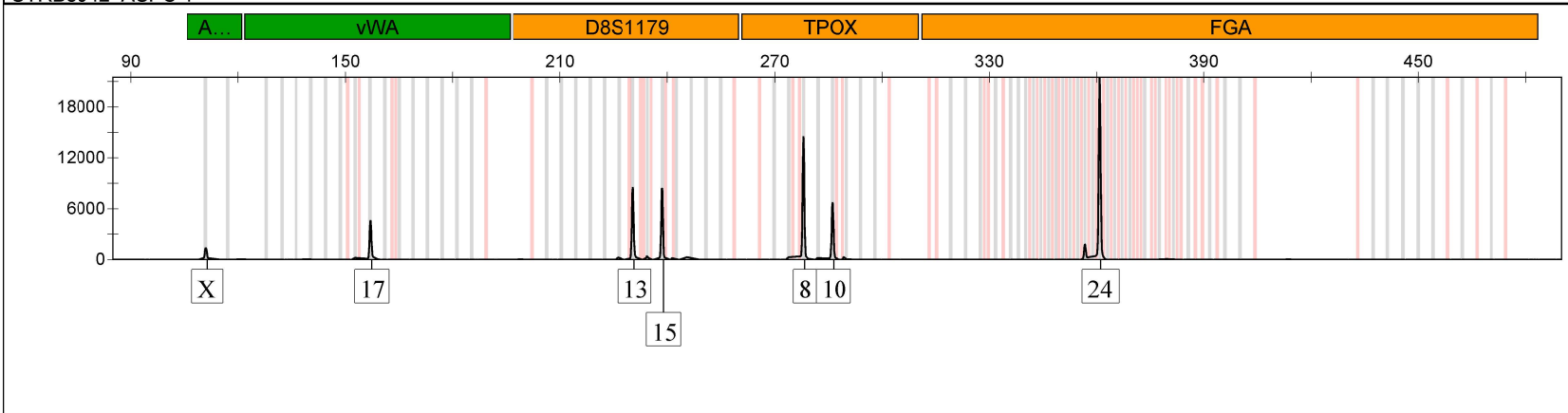
STRB8042 ASPC-1



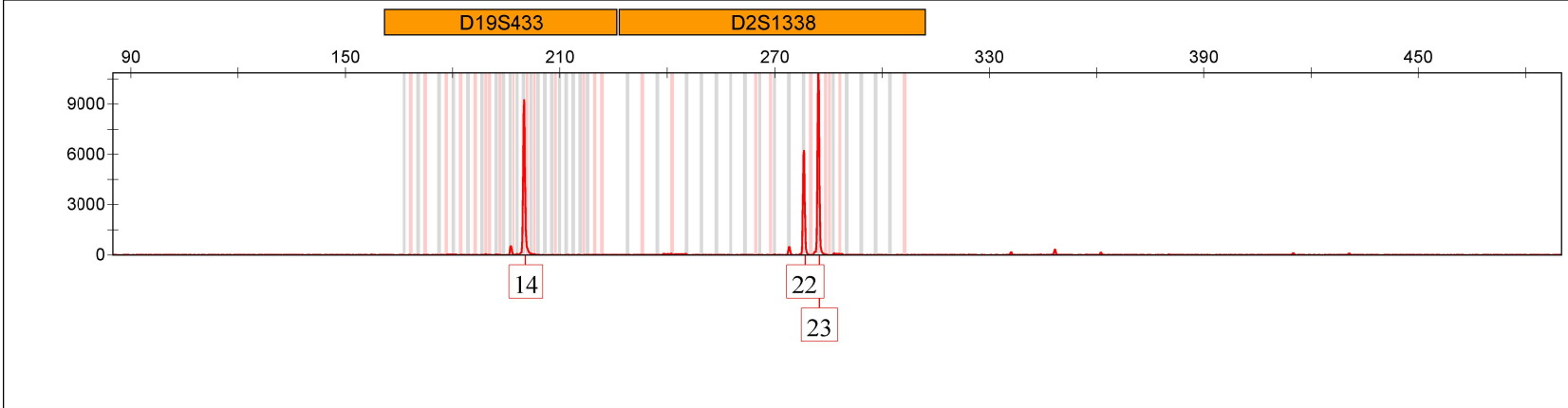
STRB8042 ASPC-1



Sample Name
STRB8042 ASPC-1



STRB8042 ASPC-1





Frederick National Laboratory for Cancer Research

DATE: July 10th, 2015

TO: Perwez Hussain, Ph.D.

THROUGH: Carissa Grose
Group Leader, Cloning and Nucleic Acids
Protein Expression Laboratory

FROM: Allison Meade
Research Associate I
Molecular Detection Group
Protein Expression Laboratory

SUBJECT: Short Tandem Repeat Analysis (STR) CSAS 17674

SAMPLES: 7 cell lines

MDG received the above DNA samples from your laboratory for STR analysis. DNA was extracted from each sample and was amplified by PCR using the AmpF ℓ STR $\text{\textcircled{R}}$ Identifiler PCR amplification kit. This is a STR multiplex assay that amplifies 15 tetranucleotide repeat loci and the Amelogenin gender determination marker in a single PCR amplification. Sample PCR amplicon, as well as positive control amplicon, were then denatured at 95 $^{\circ}$ C and the fragments analyzed on an Applied Biosystems 3130xl genetic analyzer in Hi-Di formamide with a size standard. Fragments were labeled and identified using GeneMapper 4.0.

The resulting allelic distributions of the samples are listed in the attached table. The numerical values represent the number of tetramer repeats for each allele of the 16 target loci. The allelic distribution of the positive control is also provided as a reference.

RESULTS:

| | Panc-1 | MiaPaCa-2 | Capan-1 | Capan-2 | CFPAC-1 | Pancn10.05 | ASPC-1 | Test Positive Control | Expected Positive Control |
|------------|--------|-----------|---------|----------|----------|------------|--------|-----------------------|---------------------------|
| D8S1179 | 14, 15 | 16, 16 | 14,16 | 12, 13 | 11, 15 | 13, 14 | 13, 15 | 13, 13 | 13, 13 |
| D21S11 | 28, 28 | 29, 31.2 | 28, 30 | 31, 31 | 30, 31.2 | 30, 30 | 28, 30 | 30, 30 | 30, 30 |
| D7S820 | 8, 10 | 12, 13 | 10, 11 | 9, 11 | 8, 10 | 8, 9 | 12, 13 | 10, 11 | 10, 11 |
| CSF1P0 | 10, 12 | 10, 10 | 11, 11 | 11, 12 | 10, 10 | 12, 12 | 10, 13 | 10, 12 | 10, 12 |
| D3S1358 | 17, 17 | 16, 16 | 15, 15 | 17, 18 | 16, 16 | 14, 14 | 16, 16 | 14, 15 | 14, 15 |
| TH01 | 7, 8 | 9, 10 | 6, 6 | 9.3, 9.3 | 8, 8 | 6, 9.3 | 7, 9.3 | 8, 9.3 | 8, 9.3 |
| D13S317 | 11, 11 | 12, 13 | 9, 9 | 11, 12 | 12, 12 | 12, 12 | 9, 12 | 11, 11 | 11, 11 |
| D16S539 | 11, 11 | 10, 13 | 13, 14 | 9, 13 | 9, 11 | 9, 12 | 11, 11 | 11, 12 | 11, 12 |
| D2S1338 | 23, 24 | 25, 25 | 20, 24 | 19, 25 | 18, 23 | 17, 18 | 22, 23 | 19, 23 | 19, 23 |
| D19S433 | 11, 16 | 15, 15 | 14, 15 | 13, 15 | 13, 15 | 13, 14 | 14, 14 | 14, 15 | 14, 15 |
| vWA | 15, 15 | 15, 15 | 16, 16 | 17, 17 | 17, 17 | 16, 16 | 17, 17 | 17, 18 | 17, 18 |
| TPOX | 8, 11 | 9, 9 | 8, 11 | 8, 8 | 8, 8 | 11, 11 | 8, 10 | 8, 8 | 8, 8 |
| D18S51 | 12, 12 | 12, 12 | 12, 12 | 13, 13 | 12, 12 | 15, 15 | 18, 18 | 15, 19 | 15, 19 |
| D5S818 | 11, 13 | 12, 13 | 11, 11 | 11, 12 | 10, 11 | 13, 13 | 12, 12 | 11, 11 | 11, 11 |
| FGA | 21, 21 | 22, 22 | 24, 24 | 21, 24 | 21, 22 | 20, 20 | 24, 24 | 23, 24 | 23, 24 |
| Amelogenin | X, X | X, X | X, X | X, X | X, Y | X, X | X, X | X, X | X, X |

If you have any questions, please feel free to contact me.

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DISCLAIMER: Characterization of a cell line by examining differences in the number of short tandem repeats (STR) is a technology originally developed for use as a forensic tool. While this technology has been applied for the identification and characterization of human tumor cell lines, there are some technical issues to be considered in the interpretation of the data obtained. Issues that may be encountered are polyploidy and increased mutation rates (loss/gain of number of STR) due to continuous cell culture¹.

References:

¹ Parson W., Kirchbner R., Mühlmann R., Renner K., Kofler A., Schmidt S., Kofler R. (2005) *FASEB J.* 19, 434-436.