Characterization of Additional STR Loci Beyond the 13 CODIS Loci

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National Institute of Standards and Technology

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Outline of Topics to Discuss

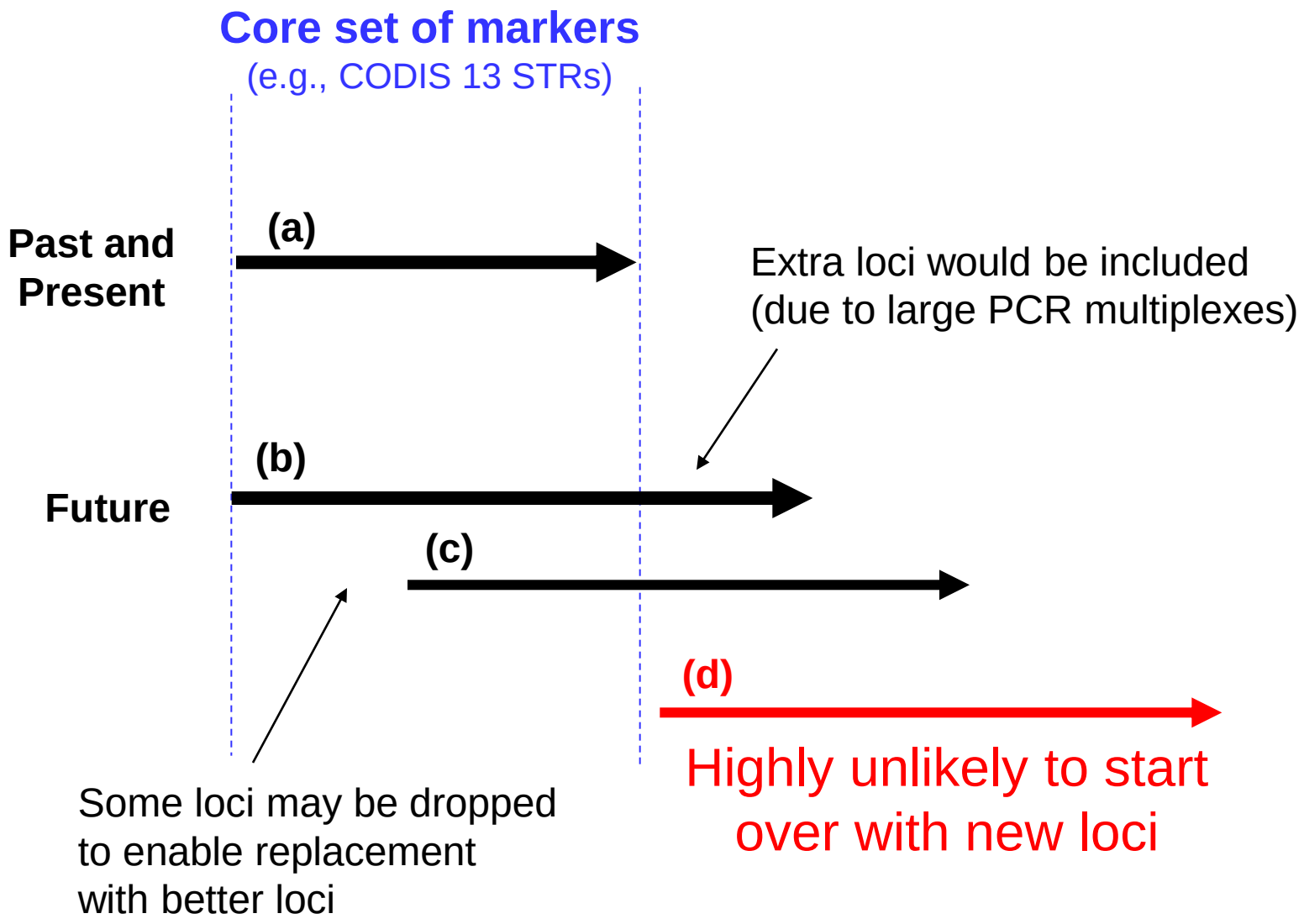
- Need for additional loci
  - Growth in U.S. and other national DNA databases
- Locus characteristics
- Population data and statistical analysis
- New STR kits available with additional loci
  - GlobalFiler (Life Technologies)
  - PowerPlex Fusion (Promega)

Need for Additional Loci

Additional STR Loci in the Future?

- More loci will be needed for more complex kinship analyses and extended applications
  - Example: Y-STRs needed for familial searching
- Immigration testing needs more than 13 STRs
- Larger DNA databases will require more loci
  - CODIS database currently has 11.5 million profiles and it continues to quickly grow

Possible scenarios for extending sets of genetic markers to be used in national DNA databases



Position of Forensic STR Markers on Human Chromosomes

13 Core U.S. STR Loci

1997

TPOX
D3S1358
D5S818
FGA
CSF1PO
D8S1179
D7S820
TH01
VWA

1 2 3 4 5 6 7 8 9 10 11 12

8 STR loci overlap between U.S. and Europe

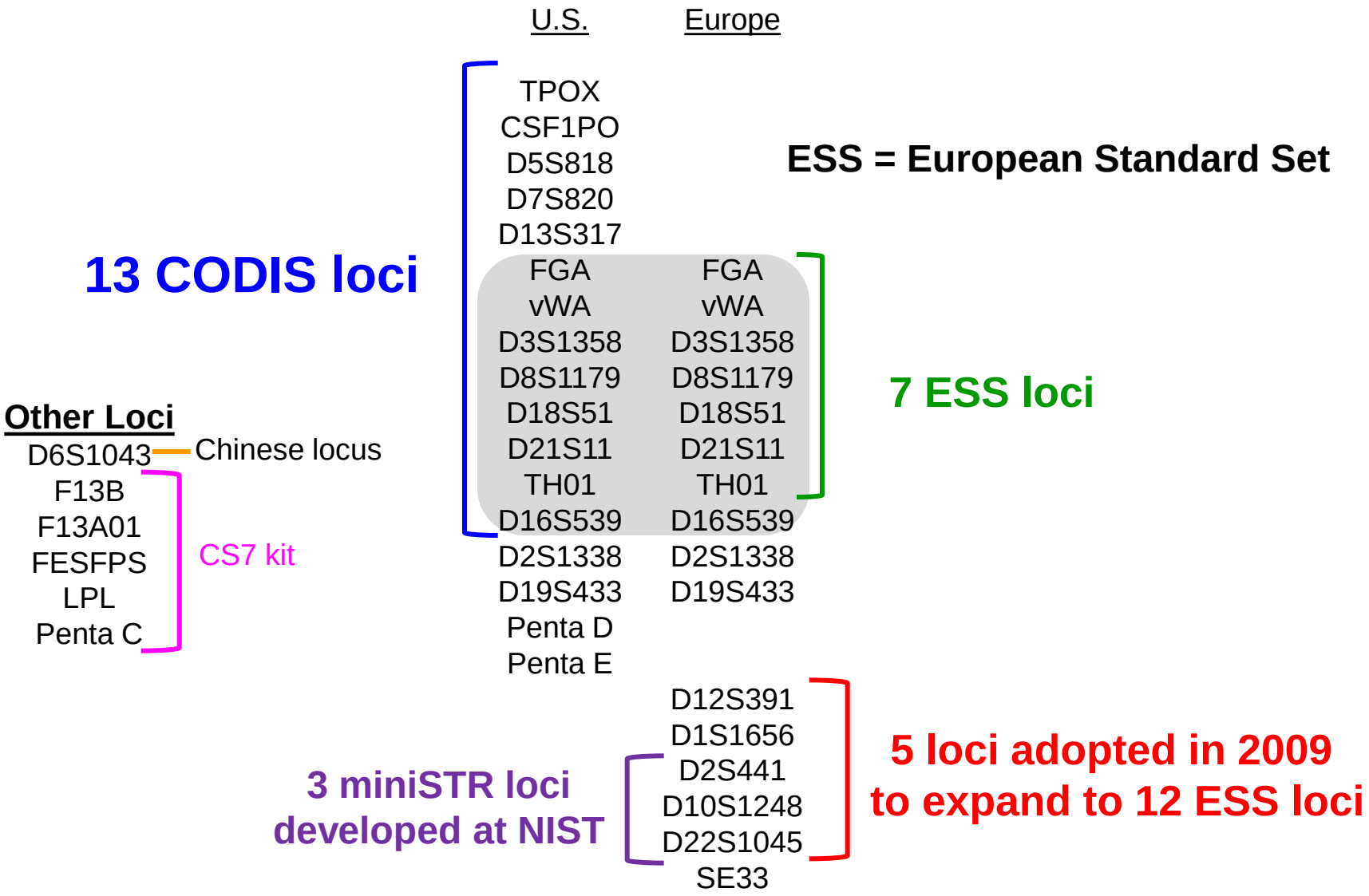
D13S317
D16S539
D18S51
D21S11
AMEL
AMEL

Sex-typing

13 14 15 16 17 18 19 20 21 22 X Y

29 Autosomal STR Markers

Present in Commercial STR Multiplex Kits



Expanded U.S. Core Loci

Forensic Science International: Genetics 6 (2012) e52–e54

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Letter to the Editor

Expanding the CODIS core loci in the United States

Dear Editor:

After over a decade of operation, the National DNA Index System (NDIS) continues to grow in importance and size [1]. While the STR DNA technology has remained relatively consistent, other key aspects of the NDIS program have been reevaluated and revisions implemented. For example, based upon recommendations of the Scientific Working Group on DNA Analysis Methods, the Director of the Federal Bureau of Investigation (FBI) issued revised Quality Assurance Standards (QAS) for Forensic DNA

major reasons for expanding the CODIS core loci in the United States:

(1) To reduce the likelihood of adventitious matches [7] as the number of profiles stored at NDIS continues to increase each year (expected to total over 10 million profiles by the time of this publication). There are no signs that this trend will slow down as States expand the coverage of their DNA database programs and increase laboratory efficiency and capacity.

(2) To increase international compatibility to assist law enforcement data sharing efforts.

(3) To increase discrimination power to aid missing persons cases.

Hares, D.R. (2012a) Expanding the CODIS core loci in the United States. *Forensic Sci. Int. Genet.* 6(1), e52-4.

Forensic Science International: Genetics 6 (2012) e135

Contents lists available at SciVerse ScienceDirect

Forensic Science International: Genetics

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Letter to the Editor

Addendum to expanding the CODIS core loci in the United States

Dear Editor,

An important objective in proposing new CODIS core loci is to ensure that all loci would be available for all potential manufacturers. During the evaluation process, appropriate steps were taken to document access to all proposed core loci. Since

publication of the proposed list of core loci, additional information has come to our attention indicating that there may be outstanding issues with respect to some of the proposed loci. Consequently, to ensure the availability for all interested manufacturers in accordance with our stated objective, we are withdrawing Penta D and Penta E as proposed CODIS core loci and recommending the revised listing of core loci in Table 1. Manufacturers are still encouraged to attempt loci in Section B, in ranked order of preference, for inclusion in potential kits provided the impact on the kit's sensitivity and overall performance is negligible. Please

Hares, D.R. (2012b) Addendum to expanding the CODIS core loci in the United States. *Forensic Sci. Int. Genet.* 6(5), e135.

Required and Recommended CODIS Core Loci

Table 1
Revised ranked list of CODIS core loci.

Locus
Section A (required) **Required Loci**
Amelogenin
D18S51
FGA
D21S11
D8S1179
vWA
D13S317
D16S539
D7S820
TH01
D3S1358
D5S818
CSF1PO
D2S1338
D19S433
D1S1656
D12S391
D2S441
D10S1248
DYS391
Section B (in order of preference) **Recommended Loci**
TPOX
D22S1045
SE33

Penta D and Penta E were removed from this list in the addendum

Y-STR to confirm Amelogenin null alleles

No longer required

Commercially Available STR Kits

Applied Biosystems (18)

- ~~AmpFlSTR Blue (1996)~~
- ~~AmpFlSTR Green I (1997)~~
- Profiler (1997)
- Profiler Plus (1997)
- COfiler (1998)
- SGM Plus (1999)
- **Identifiler** (2001)
- Profiler Plus ID (2001)
- ~~SEfiler (2002)~~
- Yfiler (2004)
- MiniFiler (2007)
- SEfiler Plus (2007)
- Sinofiler (2008) – China only
- **Identifiler Direct** (2009)
- NGM (2009)
- **Identifiler Plus** (2010)
- NGM SElect (2010)
- **GlobalFiler** (2012)

Promega Corporation (17)

- PowerPlex 1.1 (1997)
- PowerPlex 1.2 (1998)
- PowerPlex 2.1 (1999)
- **PowerPlex 16** (2000)
- PowerPlex ES (2002)
- PowerPlex Y (2003)
- PowerPlex S5 (2007)
- **PowerPlex 16 HS** (2009)
- PowerPlex ESX 16 (2009)
- PowerPlex ESX 17 (2009)
- PowerPlex ESI 16 (2009)
- PowerPlex ESI 17 (2009)
- PowerPlex CS7 (2009)
- PowerPlex 18D (2011)
- PowerPlex Y23 (2012)
- PowerPlex 21 (2012)
- **PowerPlex Fusion** (2012)

Qiagen (10) kits in 2010

Primarily selling kits in Europe

Due to patent restrictions cannot sell in U.S.

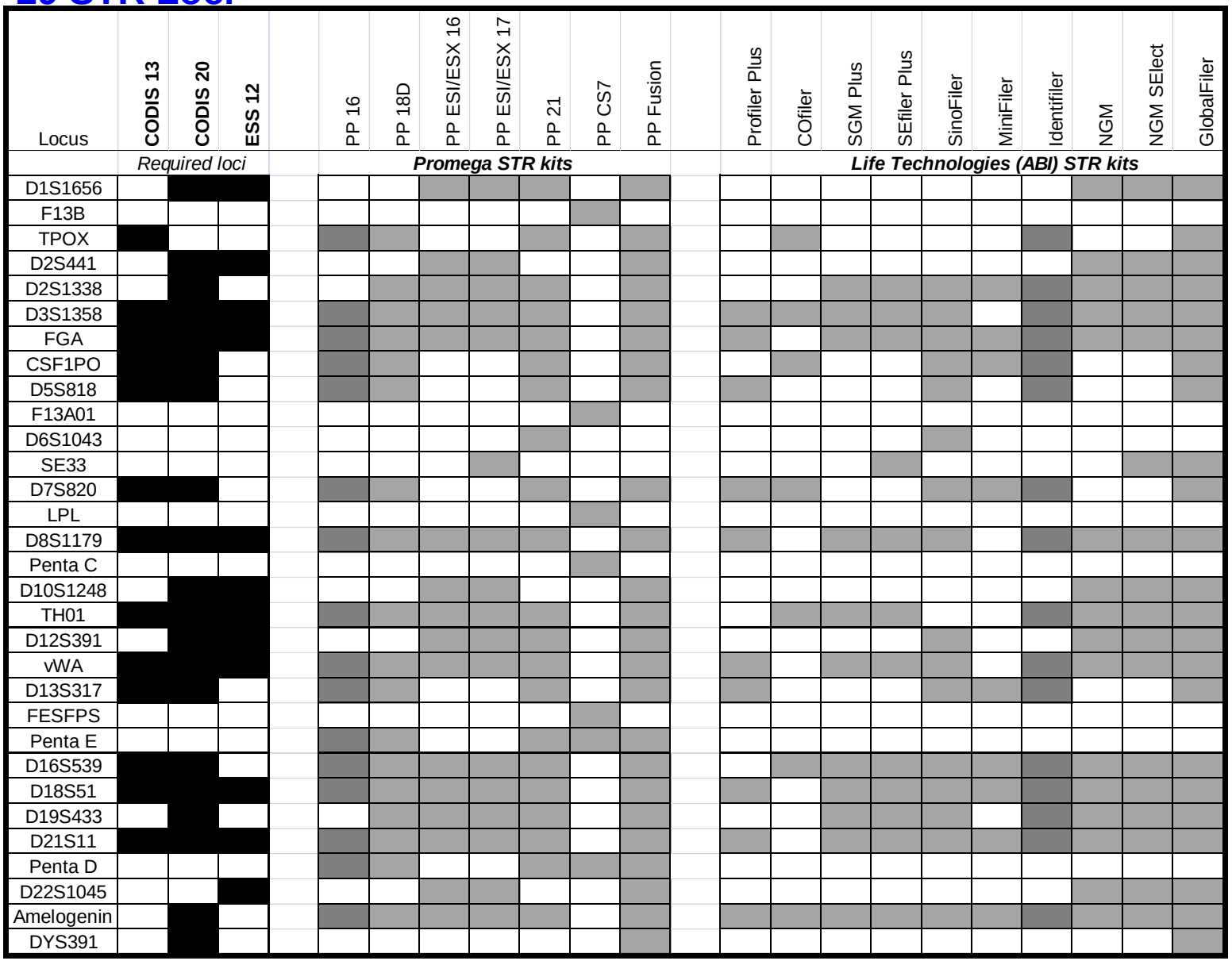
Investigator kits

- ESSplex
- ESSplex SE
- Decaplex SE
- IDplex
- Nonaplex ESS
- Hexaplex ESS
- HDplex
- Triplex AFS QS
- Triplex DSF
- Argus X-12

>1/3 of all STR kits were released in the last four years

Most Commonly Used STR Kits in the U.S.

29 STR Loci



Butler, J.M., Hill, C.R., Coble, M.D. (2012) *Profiles in DNA,* Variability of New STR Loci and Kits in U.S. Population Groups.

NIST U.S. Population Samples

NIST 1036 U.S. Population Samples

- 1032 males + 4 females
  - 361 Caucasians (2 female)
  - 342 African Americans (1 female)
  - 236 Hispanics
  - 97 Asians (1 female)

***Unrelated* samples**
All known or potential related individuals (based on autosomal & lineage marker testing) have been removed from the 1036 data set (e.g., only sons were used from father-son samples)

- Anonymous donors with self-identified ancestry
  - Interstate Blood Bank (Memphis, TN) – obtained in 2002
  - Millennium Biotech, Inc. (Ft. Lauderdale, FL) – obtained in 2001
  - DNA Diagnostics Center (Fairfield, OH) – obtained in 2007

- **Complete profiles with 29 autosomal STRs + PowerPlex Y23**
  - **Examined with multiple kits** and in-house primer sets enabling concordance

- Additional DNA results available on subsets of these samples
  - mtDNA control region/whole genome (AFDIL)
  - >100 SNPs (AIMs), 68 InDel markers, X-STRs (AFDIL)
  - NIST assays: miniSTRs, 26plex, >100 Y-STRs, 50 Y-SNPs

Data available on STRBase: **http://www.cstl.nist.gov/biotech/strbase/NISTpop.htm**

Benefits of NIST 1036 Data Set

- **Elimination of potential null alleles due to primer binding site mutations** through extensive concordance testing performed with different PCR primer sets from all available commercial STR kits

- **Ancestry testing performed** on DNA samples with autosomal SNPs, Y-SNPs, and mtDNA sequencing to verify self-declared ancestry categorization

- **Related individuals removed** based on Y-STR and mtDNA results

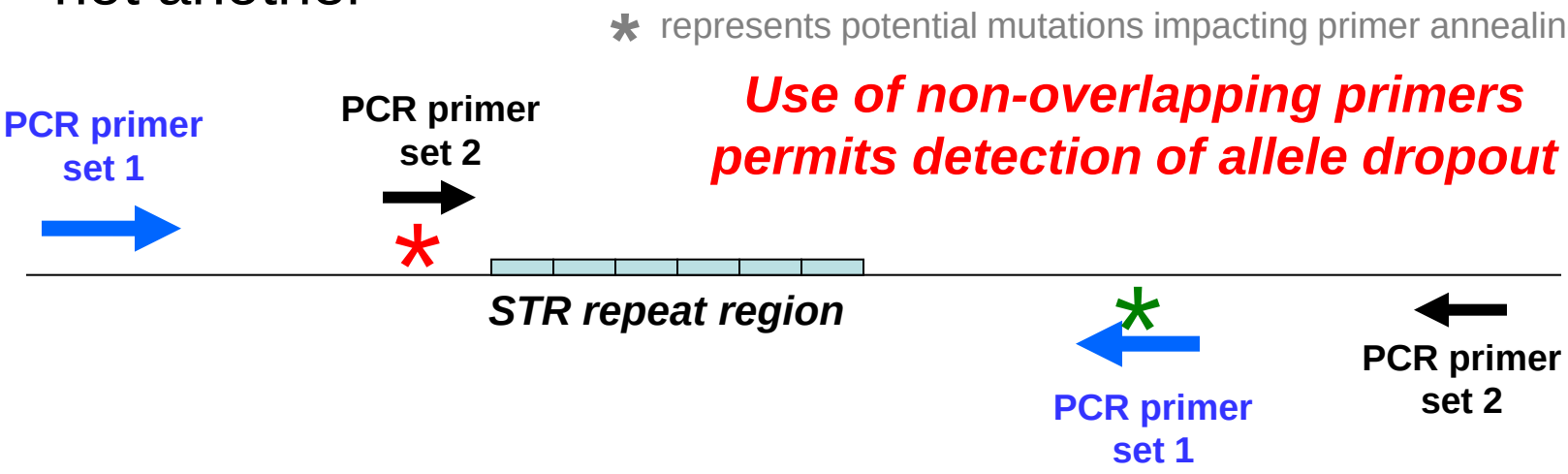
Concordance Testing at NIST

STR Kit Concordance Testing

- Many of these STR kits have different primer sequences for amplifying the same STR locus
- Need to analyze the same DNA samples with different STR typing kits looking for differences
- In some rare cases, allele dropout may occur due to mutations in primer binding regions

Purpose of Concordance Studies

When different primer sets are utilized, there is a concern that allele dropout may occur due to primer binding site mutations that impact one set of primers but not another

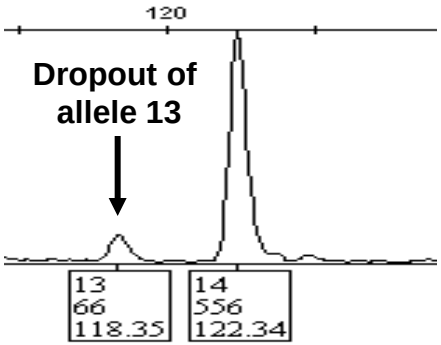


If no primer binding site mutations

If a primer binding site mutation exists

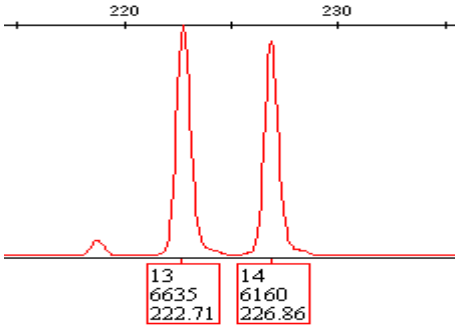
Example Primer Binding Site Mutation that Causes a Null Allele

Identifiler = 14,14



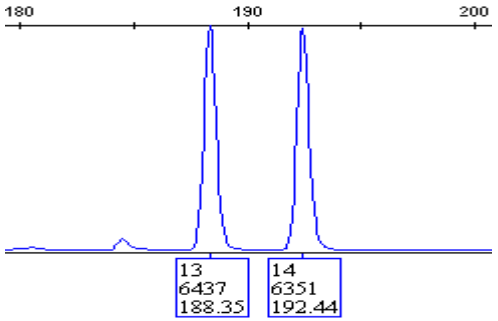
PHR = 11.9%

PP ESX 17 = 13,14



PHR = 92.8%

PP ESI 17 = 13,14



PHR = 98.7%

D19S433 repeat region

G → A SNP

ggaaagaaggtaggaaggaaggaaggaagtaagtaaggaaggaaggaaggaaggaaggaaggagagaggaagaaagagagaagatttttattcgggtaat

X

This region could potentially represent where the reverse primer is located to include the primer binding site mutation

*Applied Biosystems does not publish their primer sequences

Completed Concordance Studies

Kits compared	Samples	Loci Compared	Comparisons	# Differences	Concordance (%)
ID/SGM+	1424	11	15,664	1	99.994
ID/Pro+	1415	10	14,150	1	99.993
ID/IDplex	1426	16	22,816	29	99.873
ID/PP16	662	14	9,268	4	99.957
ID/MiniFiler	1137	9	10,233	26	99.746
ID/NGM	1437	11	15,807	3	99.981
ID/NGMs	663	11	7,293	0	100.000
ID/ESX17	1443	11	15,873	5	99.968
ID/ESI17	1443	11	15,873	4	99.975
ID/ESSplex	1433	11	15,763	28	99.822
ID/ESSplexSE	662	11	7,282	17	99.767
ID/Hexaplex	653	2	1,306	1	99.923
PP16/SGM+	651	9	5,859	1	99.983
PP16/Pro+	647	10	6,470	2	99.969
PP16/IDplex	657	14	9,198	3	99.967
PP16/MiniFiler	656	8	5,248	14	99.733
PP16/NGM	657	9	5,913	3	99.949
PP16/NGMs	662	9	5,958	1	99.983
PP16/ESX17	662	9	5,958	1	99.983
PP16/ESI17	662	9	5,958	0	100.000
PP16/ESSplex	653	9	5,877	16	99.728
PP16/ESSplexSE	662	9	5,958	16	99.731
PP16/Hexaplex	653	2	1,306	1	99.923
SGM+/Pro+	1415	7	9,905	0	100.000
SGM+/IDplex	1424	11	15,664	5	99.968
SGM+/MiniFiler	1137	6	6,822	10	99.853
SGM+/NGM	1424	11	15,664	4	99.974
SGM+/NGMs	651	11	7,161	0	100.000
SGM+/ESX17	1424	11	15,664	6	99.962
SGM+/ESI17	1424	11	15,664	5	99.968
SGM+/ESS	1424	11	15,664	5	99.968
SGM+/ESSplexSE	651	11	7,161	5	99.930
SGM+/Hexaplex	651	2	1,302	1	99.923
Pro+/IDplex	1415	10	14,150	5	99.965
Pro+/MiniFiler	1137	6	6,822	16	99.765
Pro+/NGM	1415	7	9,905	4	99.960
Pro+/NGMs	647	7	4,529	0	100.000
Pro+/ESX17	1415	7	9,905	4	99.960
Pro+/ESI17	1415	7	9,905	3	99.970
Pro+/ESS	1415	7	9,905	4	99.960
Pro+/ESSplexSE	647	7	4,529	4	99.912
Pro+/Hexaplex	647	1	647	1	99.845
IDplex/MiniFiler	1137	9	10,233	48	99.531
IDplex/NGM	1426	11	15,686	30	99.809
IDplex/NGMs	657	11	7,227	17	99.765
IDplex/ESX17	1426	11	15,686	28	99.821
IDplex/ESI17	1426	11	15,686	27	99.828
IDplex/-ESS	1426	11	15,686	1	99.994
IDplex/ESSplexSE	657	11	7,227	1	99.986
IDplex/Hexaplex	653	2	1,306	1	99.923
MiniFiler/NGM	1137	6	6,822	13	99.809
MiniFiler/NGMs	656	6	3,936	10	99.746
MiniFiler/ESX17	1137	6	6,822	10	99.853
MiniFiler/ESI17	1137	6	6,822	9	99.868
MiniFiler/ESS	1137	6	6,822	35	99.487
MiniFiler/ESSplexSE	656	6	3,936	35	99.111
MiniFiler/Hexaplex	653	1	653	1	99.847
NGM/NGMs	657	16	10,512	14	99.867
NGM/ESX17	1437	16	22,992	16	99.930
NGM/ESI17	1437	16	22,992	18	99.922
NGM/ESS	1433	16	22,928	42	99.817
NGM/ESSplexSE	657	16	10,512	22	99.791
NGM/Hexaplex	653	7	4,571	9	99.803
NGMs/ESX17	662	17	11,254	4	99.964
NGMs/ESI17	662	17	11,254	14	99.876
NGMs/ESS	653	16	10,448	17	99.837
NGMs/ESSplexSE	662	17	11,254	34	99.698
NGMs/Hexaplex	653	7	4,571	3	99.934
ESX17/ESI17	1443	17	24,531	19	99.923
ESX17/ESS	653	16	10,448	34	99.675
ESX17/ESSplexSE	662	17	11,254	25	99.778
ESX17/Hexaplex	657	7	4,599	6	99.870
ESI17/ESS	653	16	10,448	28	99.732
ESI17/ESSplexSE	662	17	11,254	30	99.733
ESI17/Hexaplex	657	7	4,599	3	99.935
ESS/ESSplexSE	653	16	10,448	0	100.000
ESS/Hexaplex	653	7	4,571	3	99.934
ESSplexSE/Hexaplex	653	7	4,571	3	99.934
SE33/ESX17	1443	1	1,443	6	99.584
SE33/ESI17	1443	1	1,443	17	98.822
SE33/NGMs	663	1	663	4	99.397
SE33/ESSplexSE	662	1	662	21	96.828
ESI17p/ESX17	477	17	8,109	7	99.914
ESI17p/NGMs	477	17	8,109	2	99.975
ESI17p/ESSplexSE	477	17	8,109	42	99.482
ESI17p/SE33	477	1	477	4	99.161
PP18D/ID	50	16	800	2	99.750
PP18D/PP16	703	16	11,248	1	99.991
ESX17*/ESX17	1443	17	24531	4	99.984
ESX17*/ESI17p	477	17	8109	3	99.963
ESX17*/NGM	1437	16	22992	22	99.904
ESX17*/NGMs	663	17	11271	4	99.965
ESX17*/ESS	1433	16	22928	30	99.869
ESX17*/ESSplexSE	662	17	11254	44	99.609
ESX17*/Hexaplex	653	7	4571	2	99.956
26plex/ESX17	1443	3	4329	4	99.908
26plex/ESI17	1443	3	4329	0	100.000
26plex/NGM	1437	3	4311	11	99.745
26plex/NGMs	663	3	1989	0	100.000
26plex/ESS	1433	3	4299	0	100.000
26plex/ESSplexSE	662	3	1986	0	100.000
26plex/Hexaplex	653	3	1959	2	99.898
26plex/ESX17*	663	3	1989	0	100.000
miniSTRs/ESX17	663	3	1989	3	99.849
miniSTRs/ESI17	663	3	1989	0	100.000
miniSTRs/NGM	657	3	1971	3	99.848
miniSTRs/NGMs	663	3	1989	0	100.000
miniSTRs/ESS	653	3	1959	0	100.000
miniSTRs/ESSplexSE	662	3	1986	0	100.000
miniSTRs/Hexaplex	653	3	1959	2	99.898
miniSTRs/ESX17*	663	3	1989	0	100.000
PP21*/Identifiler	761	16	12176	6	99.951
PP21*/PP16	761	16	12176	3	99.975
PP21/SGM+	761	11	8371	4	99.952
PP21/Pro+	761	10	7610	2	99.974
PP21/IDplex	761	16	12176	20	99.836
PP21/MiniFiler	761	9	6849	14	99.796
PP21/ESX17	761	13	9893	1	99.990
PP21/ESI17	761	13	9893	0	100.000
PP21/NGM	761	13	9893	5	99.949
PP21/NGMs	568	13	7384	1	99.986
PP21/ESS	761	13	9893	18	99.818
PP21/ESSplexSE	568	13	7384	16	99.783
PP21/Hexaplex	568	4	2272	1	99.956
PP21/Sinofiler	568	16	9088	1	99.989
PP21nk/Identifiler	639	16	10224	4	99.961
PP21nk/PP16	639	16	10224	1	99.990
Totals	**114144**	**1245**	**1,104,031**	**1224**	**99.889**

1,104,031 allele comparisons

1,224 total differences

99.89% concordance

*Kits (except Identifiler) were kindly provided by **Promega, Qiagen and Applied Biosystems** for concordance testing performed at NIST*

Final Concordance Results

Marker	Kits with Correct Genotype	# Kits Compared	Correct Type	Kits with Null Allele/Discordant Genotype	Incorrect Type	Total Samples	Sequence Issue
Amel	ID/ESX17/ESI17/PP16/MiniFiler/Pro+/SGM+/ESS/ESSplexSE/IDplex/NGMs/Hexaplex	13	X,Y	NGM*	Y,Y	657	yet to be determined
Amel	ID/ESX17/ESI17/PP16/MiniFiler/Pro+/SGM+/ESS/ESSplexSE/IDplex/NGMs/Hexaplex	13	X,Y	NGM*	Y,Y	657	yet to be determined
Amel	ID/ESX17/ESI17/Pro+/SGM+/ESS/IDplex	8	X,Y	NGM*	Y,Y	780	yet to be determined
Amel	ESS/ESSplexSE/IDplex/Hexaplex call	13	X,Y	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+/PP18D	Y,Y	653	yet to be determined
CSF1PO	PP16/MiniFiler/IDplex/PP18D	5	11,11	ID call	11,11.1	656	1 bp ins in ID amplicon outside of PP16 and MiniFiler primers [2]
CSF1PO	ID/MiniFiler/IDplex/PP18D	5	9,12	PP16 call	12,12	662	C/T SNP 16 bp ds from repeat
D10S1248	ESX17/ESI17/NGM/NGMs/ESS/ESSplexSE	7	14,16	Hexaplex	14,14	653	G/T SNP 24 bp ds from repeat
D10S1248	ESX17/ESI17/NGM/NGMs/ESS/ESSplexSE	7	14,16	Hexaplex	14,14	653	G/T SNP 24 bp ds from repeat
D13S317	Pro+/ID/PP16/IDplex	5	9, 11	MiniFiler	11, 11	656	4 bp del in the rev MiniFiler primer binding site [2]
D13S317	Pro+/ID/PP16/IDplex	5	9, 11	MiniFiler	11, 11	656	4 bp del in the rev MiniFiler primer binding site [2]
D13S317	Pro+/ID/PP16/IDplex	5	9, 13	MiniFiler	13, 13	656	4 bp del in the rev MiniFiler primer binding site [2]
D13S317	Pro+/ID/PP16/IDplex	5	9, 12	MiniFiler	12, 12	656	4 bp del in the rev MiniFiler primer binding site [2]
D13S317	Pro+/ID/PP16/IDplex	5	8, 12	MiniFiler	12, 12	656	4 bp del in the rev MiniFiler primer binding site [2]
D13S317	Pro+/ID/PP16/IDplex	5	8, 11	MiniFiler	11, 11	656	4 bp del in the rev MiniFiler primer binding site [2]
D13S317	Pro+/ID/PP16/IDplex	5	10, 13	MiniFiler	13, 13	656	4 bp del in the rev MiniFiler primer binding site [2]
D13S317	Pro+/ID/PP16/IDplex	5	9, 11	MiniFiler	11, 11	656	4 bp del in the rev MiniFiler primer binding site [2]
D13S317	Pro+/ID/PP16/IDplex	5	9, 12	MiniFiler	12, 12	656	4 bp del in the rev MiniFiler primer binding site [2]
D13S317	Pro+/ID/PP16/IDplex	5	9, 14	MiniFiler	14, 14	656	4 bp del in the rev MiniFiler primer binding site [2]
D13S317	Pro+/ID/IDplex	4	9,10	MiniFiler	10,10	481	4 bp del in the rev MiniFiler primer binding site [2]
D13S317	Pro+/ID/IDplex	4	10,11	MiniFiler	11,11	481	4 bp del in the rev MiniFiler primer binding site [2]
D13S317	Pro+/ID/IDplex	4	8,10	MiniFiler	8,8	481	4 bp del in the rev MiniFiler primer binding site [2]
D13S317	Pro+/ID/IDplex	4	10,12	MiniFiler	12,12	481	4 bp del in the rev MiniFiler primer binding site [2]
D16S539	ID/MiniFiler/ESI17/PP16/NGM/NGMs/SGM+/ESS/ESSplexSE/IDplex	11	12,13	ESX17	12,12	660	yet to be determined
D16S539	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+/IDplex	11	9,11	ESS/ESSplexSE	11,11	653	C/G SNP 10 bp us from repeat
D16S539	ID/ESX17/ESI17/PP16/NGM/NGMs/SGM+/ESS/ESSplexSE/IDplex	11	9,11	MiniFiler	9,9	656	A/G SNP in MiniFiler primer binding site [2]
D16S539	ID/ESX17/ESI17/PP16/NGM/NGMs/SGM+/ESS/ESSplexSE/IDplex	11	11,12	MiniFiler	12,12	656	A/G SNP in MiniFiler primer binding site [2]
D16S539	ID/ESX17/ESI17/PP16/NGM/NGMs/SGM+/ESS/ESSplexSE/IDplex	11	9,11	MiniFiler	9,9	656	A/G SNP in MiniFiler primer binding site [2]
D16S539	ID/ESX17/ESI17/NGM/SGM+/ESS/IDplex	8	11,14	MiniFiler	14,14	481	A/G SNP in MiniFiler primer binding site [2]
D16S539	ID/ESX17/ESI17/NGM/SGM+/ESS/IDplex	8	9,11	MiniFiler	9,9	481	A/G SNP in MiniFiler primer binding site [2]
D16S539	ID/ESX17/ESI17/NGM/SGM+/ESS/IDplex	8	11,13	MiniFiler	13,13	481	A/G SNP in MiniFiler primer binding site [2]
D16S539	ID/ESX17/ESI17/NGM/SGM+/ESS/IDplex	8	11,12	MiniFiler	12,12	481	A/G SNP in MiniFiler primer binding site [2]
D16S539	ID/ESX17/ESI17/NGM/SGM+/ESS/IDplex	8	11,12	MiniFiler	12,12	481	A/G SNP in MiniFiler primer binding site [2]
D16S539	ID/ESX17/ESI17/NGM/SGM+/ESS/IDplex	8	9,12	MiniFiler	9,9	481	A/G SNP in MiniFiler primer binding site [2]
D18S51	ESX17/ESI17/PP16/MiniFiler/ESS/ESSplexSE/IDplex	12	13,15	ID/NGM/NGMs/Pro+/SGM+	15,15	660	G/A SNP 172 bp ds from repeat
D19S433	ESX17/ESI17	7	13,14	ID/NGM/SGM+/ESS/IDplex	14,14	785	G/A SNP 32 bp ds from repeat
D19S433	ESX17/ESI17	7	13,14.2	ID/NGM/SGM+/ESS/IDplex	14.2,14.2	785	G/A SNP 32 bp ds from repeat
D1S1656	ESI17/NGM/ESSplex	4	14,15.3	ESX17	15.3,15.3	786	C/T SNP 30 bp us from repeat
D22S1045	miniSTR/23plex/NGMs/ESI17/ESS/ESSplexSE/Hexaplex	8	15,17	ESX17*/NGM*	17,17	663	G/T SNP 15 bp us from repeat
D22S1045	miniSTR/23plex/NGMs/ESI17/ESS/ESSplexSE/Hexaplex	8	15,17	ESX17*/NGM*	17,17	663	G/T SNP 15 bp us from repeat
D22S1045	miniSTR/23plex/NGMs/ESI17/ESS/ESSplexSE/Hexaplex	8	15,17	ESX17*/NGM*	17,17	663	G/T SNP 15 bp us from repeat
D22S1045	23plex/ESI17/NGMs/ESS	6	15,16	ESX17*/NGM*	16,16	789	G/T SNP 15 bp us from repeat
D2S1338	PP18D	2	17,23	ID	23,23	50	G/A SNP 174 bp ds from repeat
D2S441	ESX17/ESI17/23plex/ESS/NGMs	6	9.1,11	NGM*	11,11	780	A ins adjacent to the 5' end of repeat
D2S441	ESX17/ESI17/23plex/ESS/NGMs	6	9.1,12	NGM*	12,12	780	A ins adjacent to the 5' end of repeat
D2S441	ESX17/ESI17/23plex/ESS/NGMs	6	9.1,10	NGM*	10,10	780	A ins adjacent to the 5' end of repeat
D2S441	ESX17/ESI17/23plex/ESS/NGMs	6	9.1,11	NGM*	11,11	780	A ins adjacent to the 5' end of repeat
D2S441	ESX17/ESI17/23plex/ESS/NGMs	6	9.1,11	NGM*	11,11	780	A ins adjacent to the 5' end of repeat
D2S441	ESX17/ESI17/23plex/ESS/NGMs	6	9.1,10	NGM*	10,10	780	A ins adjacent to the 5' end of repeat
D2S441	ESX17/ESI17/23plex/ESS/NGMs	6	9.1,11	NGM*	11,11	780	A ins adjacent to the 5' end of repeat
D3S1358	ESX17/ESI17/ESS/IDplex	8	14,17	ID/NGM/Pro+/SGM+	14,14	785	G/C SNP 12 bp us from repeat
D7S820	Pro+/ID	5	8, 9.3	PP16/MiniFiler/IDplex	8, 11	656	5 bp del 114 bp ds from repeat
D8S1179	ID/ESX17/ESI17/NGM/ESS/IDplex	8	14,15	Pro+/SGM+	14,14	773	A/G SNP 15 bp us from repeat
SE33	ESX17/ESI17/NGMs/ESSplexSE	5	26.2,27.2	SE33 Monoplex (SE33)	26.2,26.2	663	C/T SNP 110 bp us from repeat
SE33	ESX17/ESI17/NGMs/ESSplexSE	5	24.2,28.2	SE33 Monoplex (SE33)	28.2,28.2	663	C/T SNP 110 bp us from repeat
SE33	ESX17/ESI17/NGMs/ESSplexSE	5	21.2,26.2	SE33 Monoplex (SE33)	21.2,21.2	663	C/T SNP 110 bp us from repeat
SE33	ESX17/ESI17/NGMs/ESSplexSE	5	24.2,25.2	SE33 Monoplex (SE33)	24.2,24.2	663	C/T SNP 110 bp us from repeat
SE33	SE33/NGMs	5	20,29.2	ESX17/ESI17/ESSplexSE	20,28.3	663	TTG del 28 bp ds from repeat
SE33	SE33/NGMs	3	19,25.2	ESX17	19,19	663	C/T SNP 60 bp ds from repeat
SE33	SE33/NGMs	4	19,25.2	ESI17*/ESSplexSE	19,25.3	663	C/T SNP 60 bp ds from repeat
SE33	SE33/ESX17/NGMs	5	13.2,18	ESI17*/ESSplexSE	13.3,18	50	G/A SNP 68 bp ds from the repeat
SE33	SE33/ESX17/NGMs	5	15.2,19	ESI17*/ESSplexSE	15.3,19	50	G/A SNP 68 bp ds from the repeat
SE33	SE33/ESX17/NGMs	5	15.2,28.2	ESI17*/ESSplexSE	15.3,28.2	50	G/A SNP 68 bp ds from the repeat
SE33	SE33/ESX17/NGMs	5	19,23.2	ESI17*/ESSplexSE	19,23.3	663	G/A SNP 68 bp ds from the repeat
SE33	SE33/ESX17/NGMs	5	16.2,18	ESI17*/ESSplexSE	16.3,18	663	G/A SNP 68 bp ds from the repeat
SE33	SE33/ESX17/NGMs	5	12.2,27.2	ESI17*/ESSplexSE	12.3,27.2	663	G/A SNP 68 bp ds from the repeat
SE33	SE33/ESX17/NGMs	5	16.2,21	ESI17*/ESSplexSE	16.3,21	663	G/A SNP 68 bp ds from the repeat
SE33	SE33/ESX17/NGMs	5	16.2,28.2	ESI17*/ESSplexSE	16.3,28.2	663	G/A SNP 68 bp ds from the repeat
SE33	SE33/ESX17/NGMs	5	13.2,19	ESI17*/ESSplexSE	13.3,19	663	G/A SNP 68 bp ds from the repeat
SE33	SE33/ESX17/NGMs	5	13.2,20	ESI17*/ESSplexSE	13.3,20	789	G/A SNP 68 bp ds from the repeat
SE33	SE33/ESX17/NGMs	5	15.2,27.2	ESI17*/ESSplexSE	15.3,27.2	789	G/A SNP 68 bp ds from the repeat
SE33	ESX17/ESI17/SE33/NGMs	5	13,18	ESSplexSE	18,18	662	AAAA del 85 bp us of the repeat
SE33	ESX17/ESI17/SE33/NGMs	5	15,17	ESSplexSE	15,15	662	AAAA del 85 bp us of the repeat
SE33	ESX17/ESI17/SE33/NGMs	5	16,17	ESSplexSE	17,17	662	AAAA del 85 bp us of the repeat
SE33	ESX17/ESI17/SE33/NGMs	5	15,19	ESSplexSE	19,19	662	AAAA del 85 bp us of the repeat
TH01	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+/Hexaplex	12	6,7	ESSplex/ESSplexSE/IDplex	6,6	653	G/A SNP 37 bp ds from the repeat
vWA	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+	11	12,16	ESS/ESSplexSE/IDplex	16,16	653	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+	11	13,18	ESS/ESSplexSE/IDplex	18,18	653	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+	11	14,15	ESS/ESSplexSE/IDplex	15,15	653	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+	11	14,15	ESS/ESSplexSE/IDplex	15,15	653	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+	11	14,16	ESS/ESSplexSE/IDplex	16,16	653	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+	11	14,17	ESS/ESSplexSE/IDplex	17,17	653	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+	11	14,17	ESS/ESSplexSE/IDplex	17,17	653	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+	11	14,17	ESS/ESSplexSE/IDplex	17,17	653	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+	11	14,19	ESS/ESSplexSE/IDplex	19,19	653	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+	11	14,19	ESS/ESSplexSE/IDplex	19,19	653	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+	11	14,19	ESS/ESSplexSE/IDplex	19,19	653	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+	11	15,16	ESS/ESSplexSE/IDplex	16,16	653	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/PP16/NGM/NGMs/SGM+	11	15,17	ESS/ESSplexSE/IDplex	17,17	653	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/NGM/SGM+	8	13,15	ESS/IDplex	15,15	780	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/NGM/SGM+	8	13,15	ESS/IDplex	15,15	780	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/NGM/SGM+	8	13,16	ESS/IDplex	16,16	780	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/NGM/SGM+	8	13,17	ESS/IDplex	17,17	780	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/NGM/SGM+	8	13,19	ESS/IDplex	19,19	780	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/NGM/SGM+	8	14,16	ESS/IDplex	16,16	780	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/NGM/SGM+	8	14,17	ESS/IDplex	17,17	780	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/NGM/SGM+	8	14,17	ESS/IDplex	17,17	780	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/NGM/SGM+	8	14,18	ESS/IDplex	18,18	780	ATCCATCC del 4 bp ds from repeat
vWA	ID/MiniFiler/ESI17/ESX17/NGM/SGM+	8	14,18	ESS/IDplex	18,18	780	ATCCATCC del 4 bp ds from repeat

- All up-to-date results can be found on STRBase:
  - ISFG poster (Vienna, Austria), 8/31-9/2, 2011, "Concordance Testing Comparing STR Multiplex Kits with a Standard Data Set"
  - Promega ISHI (National Harbor, MD), 10/4-10/5, 2011, "Concordance Testing Comparing STR Multiplex Kits with a Standard Data Set"

Characterization of STR Loci

Available in Commercial Kits

The 10 STR Loci Beyond the CODIS 13

STR Locus	Location	Repeat Motif	Allele Range*	# Alleles*
D2S1338	2q35	TGCC/TTCC	10 to 31	40
D19S433	19q12	AAGG/TAGG	5.2 to 20	36
Penta D	21q22.3	AAAGA	1.1 to 19	50
Penta E	15q26.2	AAAGA	5 to 32	53
D1S1656	1q42	TAGA	8 to 20.3	25
D12S391	12p13.2	AGAT/AGAC	13 to 27.2	52
D2S441	2p14	TCTA/TCAA	8 to 17	22
D10S1248	10q26.3	GGAA	7 to 19	13
D22S1045	22q12.3	ATT	7 to 20	14
SE33	6q14	AAAG‡	3 to 49	**178**

5 new European loci

**Allele range and number of observed alleles from Appendix 1, J.M. Butler (2011) Advanced Topics in Forensic DNA Typing: Methodology; ‡SE33 alleles have complex repeat structure*

25 Alleles Reported in the Literature for **D1S1656**

15 NIST observed alleles circled in red

Allele (Repeat #)	Promega ESX 17	Promega ESI 17	ABI NGM	Repeat Structure $[TAGA]_4[TGA]_{0-1}[TAGA]_nTAGG[TG]_5$	Reference
8	133 bp	222 bp	171 bp	$[TAGA]_8[TG]_5$	Phillips *et al.* (2010)
9	137 bp	226 bp	175 bp	$[TAGA]_9[TG]_5$	Phillips *et al.* (2010)
10 (a)	141 bp	230 bp	179 bp	$[TAGA]_{10}[TG]_5$	Lareu *et al.* (1998)
10 (b)	141 bp	230 bp	179 bp	$[TAGA]_{10}TAGG[TG]_5$	Phillips *et al.* (2010)
11	145 bp	234 bp	183 bp	$[TAGA]_{11}[TG]_5$	Lareu *et al.* (1998)
12 (a)	149 bp	238 bp	187 bp	$[TAGA]_{12}[TG]_5$	Lareu *et al.* (1998)
12 (b)	149 bp	238 bp	187 bp	$[TAGA]_{11}TAGG[TG]_5$	Lareu *et al.* (1998)
13 (a)	153 bp	242 bp	191 bp	$[TAGA]_{12}TAGG[TG]_5$	Lareu *et al.* (1998)
13 (b)	153 bp	242 bp	191 bp	$[TAGA]_{13}[TG]_5$	Phillips *et al.* (2010)
13.3	156 bp	245 bp	194 bp	$[TAGA]_1TGA[TAGA]_{11}TAGG[TG]_5$	Phillips *et al.* (2010)
14 (a)	157 bp	246 bp	195 bp	$[TAGA]_{13}TAGG[TG]_5$	Lareu *et al.* (1998)
14 (b)	157 bp	246 bp	195 bp	$[TAGA]_{14}[TG]_5$	Phillips *et al.* (2010)
14.3	160 bp	249 bp	198 bp	$[TAGA]_4TGA[TAGA]_9TAGG[TG]_5$	Phillips *et al.* (2010)
15	161 bp	250 bp	199 bp	$[TAGA]_{14}TAGG[TG]_5$	Lareu *et al.* (1998)
15.3	164 bp	253 bp	202 bp	$[TAGA]_4TGA[TAGA]_{10}TAGG[TG]_5$	Lareu *et al.* (1998)
16	165 bp	254 bp	203 bp	$[TAGA]_{15}TAGG[TG]_5$	Lareu *et al.* (1998)
16.3	168 bp	257 bp	206 bp	$[TAGA]_4TGA[TAGA]_{11}TAGG[TG]_5$	Lareu *et al.* (1998)
17	169 bp	258 bp	207 bp	$[TAGA]_{16}TAGG[TG]_5$	Lareu *et al.* (1998)
17.1	170 bp	259 bp	208 bp	Not published	Schröer *et al.* (2000)
17.3	172 bp	261 bp	210 bp	$[TAGA]_4TGA[TAGA]_{12}TAGG[TG]_5$	Lareu *et al.* (1998)
18	173 bp	262 bp	211 bp	$[TAGA]_{17}TAGG[TG]_5$	Phillips *et al.* (2010)
18.3	176 bp	265 bp	214 bp	$[TAGA]_4TGA[TAGA]_{13}TAGG[TG]_5$	Lareu *et al.* (1998)
19	177 bp	266 bp	215 bp	Not published	Asamura *et al.* (2008)
19.3	180 bp	269 bp	218 bp	$[TAGA]_4TGA[TAGA]_{14}TAGG[TG]_5$	Lareu *et al.* (1998)
20.3	184 bp	273 bp	222 bp	Not published	Gamero *et al.* (2000)

from Appendix 1, J.M. Butler (2011) Advanced Topics in Forensic DNA Typing: Methodology

NIST **U.S. Population Allele Frequencies**

D1S1656 (15 different alleles)

15 different alleles

Allele	African American (n=342)	Asian (n=97)	Caucasian (n=361)	Hispanic (n=236)
10	0.0146	0.0000	0.0028	0.0064
11	0.0453	0.0309	0.0776	0.0275
12	0.0643	0.0464	0.1163	0.0890
13	0.1009	0.1340	0.0665	0.1144
14	**0.2573**	0.0619	0.0789	0.1165
14.3	0.0073	0.0000	0.0028	0.0042
15	0.1579	**0.2784**	**0.1496**	0.1377
15.3	0.0292	0.0000	0.0582	0.0508
16	0.1096	0.2010	0.1357	**0.1758**
16.3	0.1023	0.0155	0.0609	0.0508
17	0.0278	0.0722	0.0471	0.0424
17.3	0.0497	0.0876	0.1330	0.1483
18	0.0029	0.0155	0.0055	0.0064
18.3	0.0234	0.0515	0.0499	0.0254
19.3	0.0073	0.0052	0.0152	0.0042

N=1036

(only unrelated samples used; fathers removed from this sample set)

D1S1656 Characteristics

- **15 alleles** observed
- **93 genotypes** observed
- **>89% heterozygotes** (heterozygosity = 0.8890)
- **0.0224 Probability of Identity** (P_I)

$$P_I = \sum (genotype\ frequencies)^2$$

These values have been calculated for all 29 STR loci across the U.S. population samples examined

Loci sorted on Probability of Identity (P_I) values

Locus	Alleles Observed	Genotypes Observed	Het (obs)	P_I Value n=1036
SE33	52	304	0.9353	0.0066
Penta E	23	138	0.8996	0.0147
D2S1338	13	68	0.8793	0.0220
D1S1656	15	93	0.8890	0.0224
D18S51	22	93	0.8687	0.0258
D12S391	24	113	0.8813	0.0271
FGA	27	96	0.8745	0.0308
D6S1043	27	109	0.8494	0.0321
Penta D	16	74	0.8552	0.0382
D21S11	27	86	0.8330	0.0403
D8S1179	11	46	0.7992	0.0558
D19S433	16	78	0.8118	0.0559
vWA	11	39	0.8060	0.0611
F13A01	16	56	0.7809	0.0678
D7S820	11	32	0.7944	0.0726
D16S539	9	28	0.7761	0.0749
D13S317	8	29	0.7674	0.0765
TH01	8	24	0.7471	0.0766
Penta C	12	49	0.7732	0.0769
D2S441	15	43	0.7828	0.0841
D10S1248	12	39	0.7819	0.0845
D3S1358	11	30	0.7519	0.0915
D22S1045	11	44	0.7606	0.0921
F13B	7	20	0.6911	0.0973
CSF1PO	9	31	0.7558	0.1054
D5S818	9	34	0.7297	0.1104
FESFPS	12	36	0.7230	0.1128
LPL	9	27	0.7027	0.1336
TPOX	9	28	0.6902	0.1358

Better for mixtures (more alleles seen)

29 STR Loci present in STR kits

rank ordered by their variability

N=1036

(only unrelated samples used)

There are several loci more polymorphic than the **current CODIS 13 STRs**

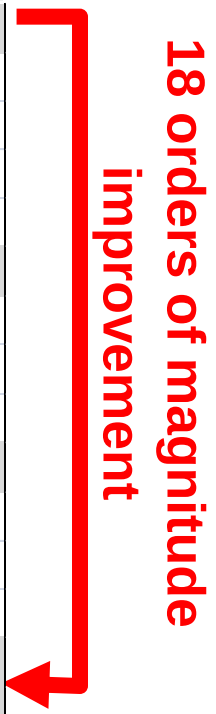
361 Caucasians
342 African Americans
236 Hispanics
97 Asians

Better for kinship (low mutation rate)

Butler, J.M., Hill, C.R., Coble, M.D. (2012) *Profiles in DNA,* Variability of New STR Loci and Kits in U.S. Population Groups.

Probability of Identity Combinations
(assuming unrelated individuals)

STR Kit or Core Set of Loci	Total N=1036	Caucasians (n=361)	African Am. (n=342)	Hispanics (n=236)	Asians (n=97)
CODIS 13	5.02E-16	2.97E-15	1.14E-15	1.36E-15	1.71E-14
Identifiler	6.18E-19	6.87E-18	1.04E-18	2.73E-18	5.31E-17
PowerPlex 16	2.82E-19	4.24E-18	6.09E-19	1.26E-18	2.55E-17
PowerPlex 18D	3.47E-22	9.82E-21	5.60E-22	2.54E-21	7.92E-20
ESS 12	3.04E-16	9.66E-16	9.25E-16	2.60E-15	3.42E-14
ESI 16 / ESX 16 / NGM	2.80E-20	2.20E-19	6.23E-20	4.03E-19	9.83E-18
ESI 17 / ESX 17 / NGM SElect	1.85E-22	1.74E-21	6.71E-22	3.97E-21	1.87E-19
CODIS 20	9.35E-24	7.32E-23	6.12E-23	8.43E-23	4.22E-21
GlobalFiler	7.73E-28	1.30E-26	3.20E-27	2.27E-26	1.81E-24
PowerPlex Fusion	6.58E-29	2.35E-27	1.59E-28	2.12E-27	1.42E-25
All 29 autosomal STRs	2.24E-37	7.36E-35	3.16E-37	2.93E-35	4.02E-32
29 autoSTRs + DYS391	1.07E-37	3.26E-35	1.77E-37	1.29E-35	2.81E-32



Butler, J.M., Hill, C.R., Coble, M.D. (2012) *Profiles in DNA,* Variability of New STR Loci and Kits in U.S. Population Groups.

NIST U.S. Population Data

- We plan on making the data from our 1036 U.S. population samples available on STRBase:

  http://www.cstl.nist.gov/biotech/strbase/NISTpop.htm

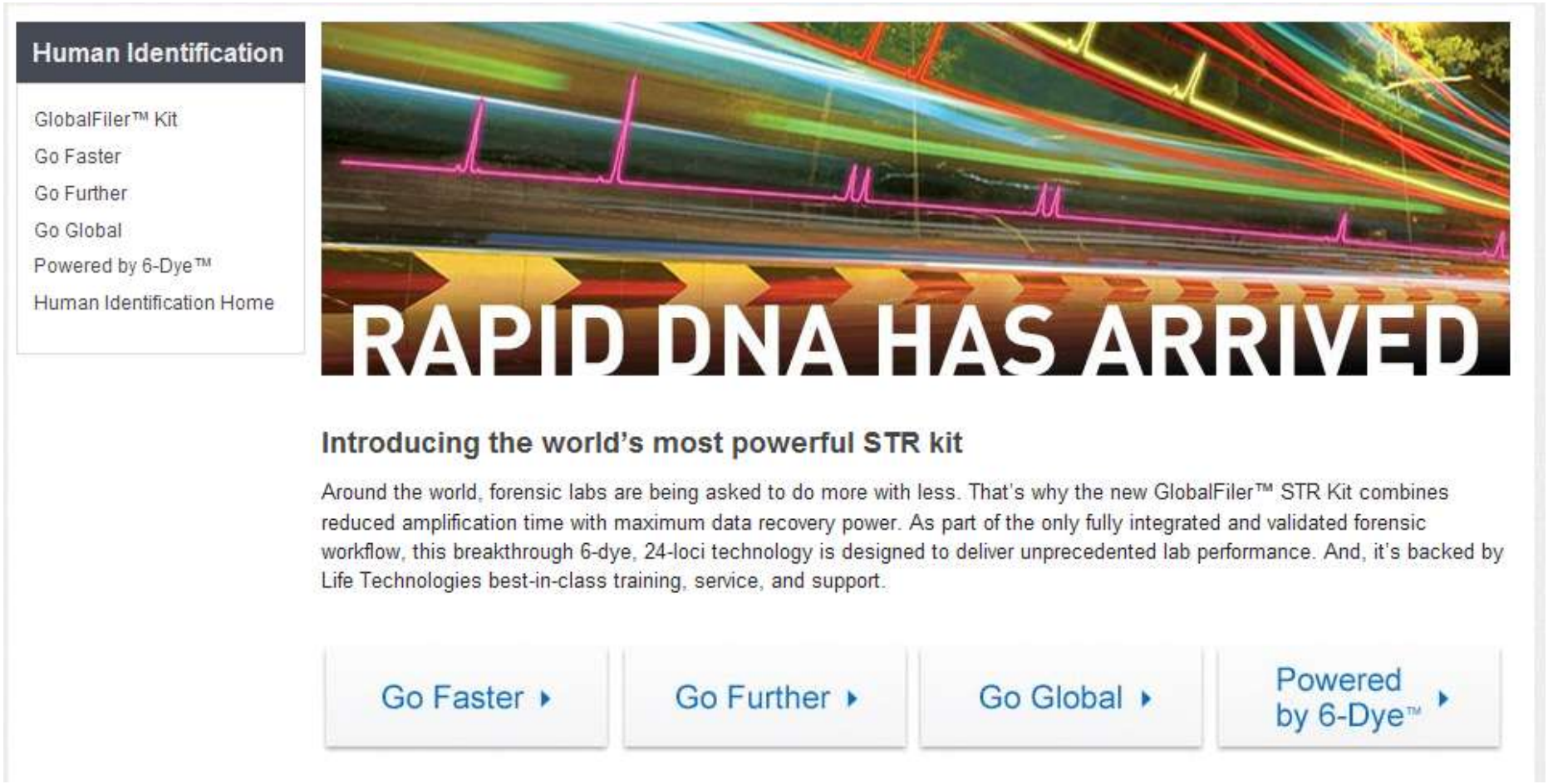
- A summary of the NIST 1036 data set was recently submitted to *Profiles in DNA* for autosomal and YSTR loci
- Population Data announcements will be summited to FSI: Genetics (soon!) for
  - 29 autosomal STR loci (*Hill et al*)
  - 23 Y-STR loci (*Coble et al*)

New STR Multiplex Kits

Recently Launched

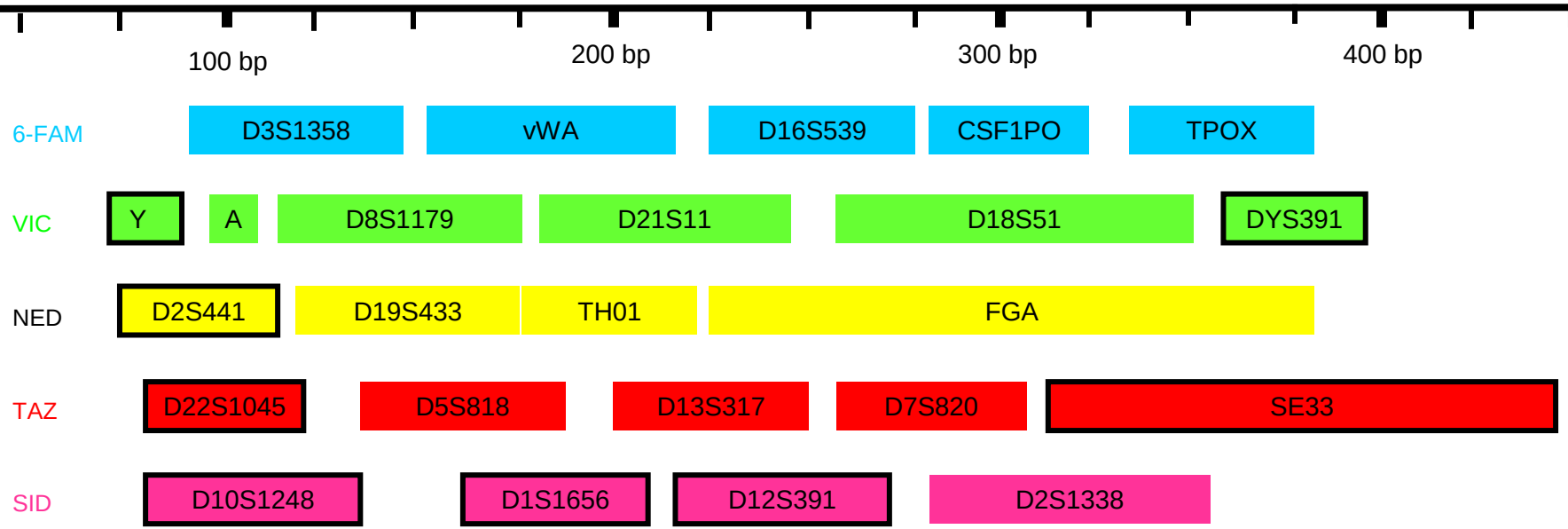
GlobalFiler STR Kit

Launched Friday, September 14, 2012



http://www.invitrogen.com/site/us/en/home/Products-and-Services/Applications/Human-Identification/globalfiler_str_kit.html

Applied Biosystems **GlobalFiler** **24plex**



- 24 STR loci in 6 dyes (3500 instrument use only)
- Direct amplification capabilities
  - Single Source Samples: 40 min amplification
  - Casework Samples: 80 min amplification
- Largest products <460 bp, 10 markers <220 bp (miniSTRs)
- Allelic ladder includes 343 total alleles

PowerPlex Fusion

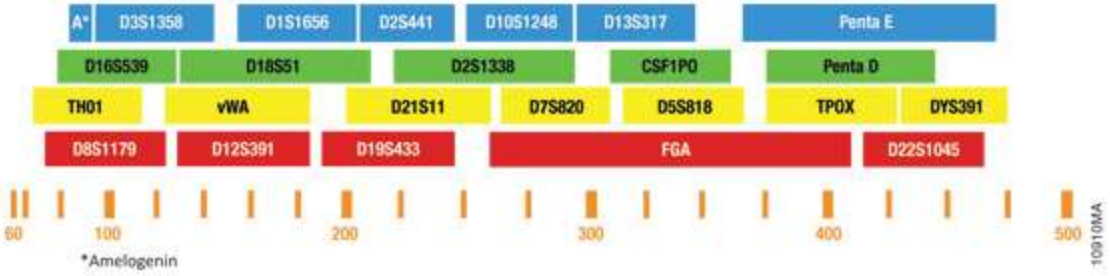
PowerPlex® Fusion System

Launched Friday, September 14, 2012

Designed to meet CODIS and European standards, the PowerPlex® Fusion System enables laboratories to:

- Achieve the most inter database compatibility and highest discrimination of any autosomal STR kit.
- Improve laboratory efficiencies with rapid cycling and direct amplification protocols.
- Obtain a higher success rate with difficult casework samples due to robustness and sensitivity.
- Simplify validation and QC efforts by using one kit for both casework and databasing sections.

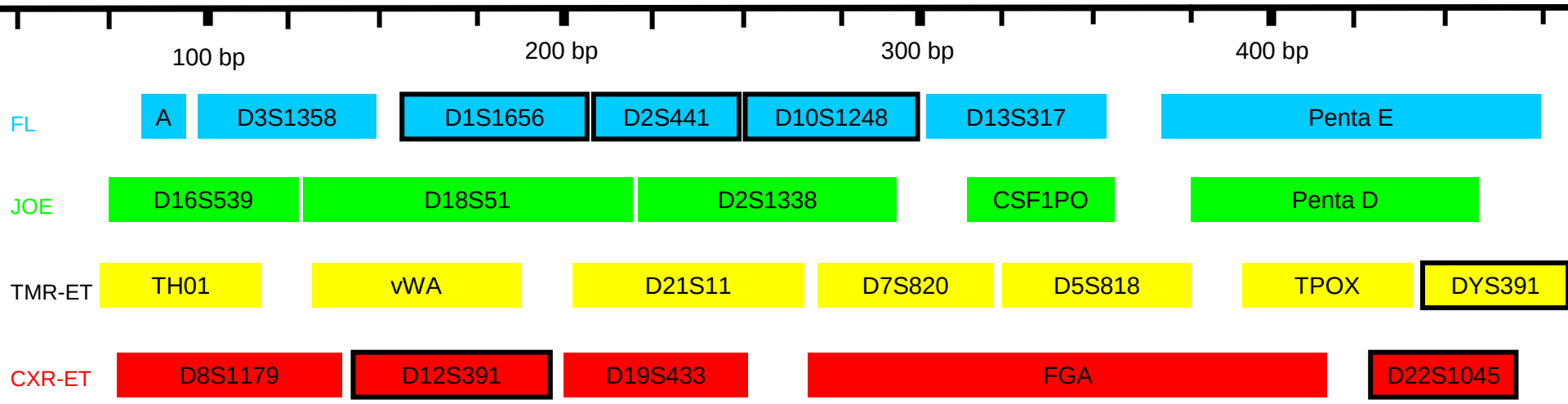
The PowerPlex® Fusion System provides all of the materials needed for co-amplification and five-color fluorescent detection of 24 loci (23 STR loci and Amelogenin), including the CODIS core loci and the European Standard Set (ESS) loci. With 24 loci, the system offers the most STR loci and highest discrimination from a single reaction and delivers more information in demanding forensic, paternity and relationship testing cases. Utilizing proven STR chemistries on existing instrument platforms and software, the PowerPlex® Fusion System requires no software or instrument upgrades.



http://www.promega.com/products/pm/genetic-identity/powerplex-fusion/

Promega PowerPlex **FUSION**

24plex

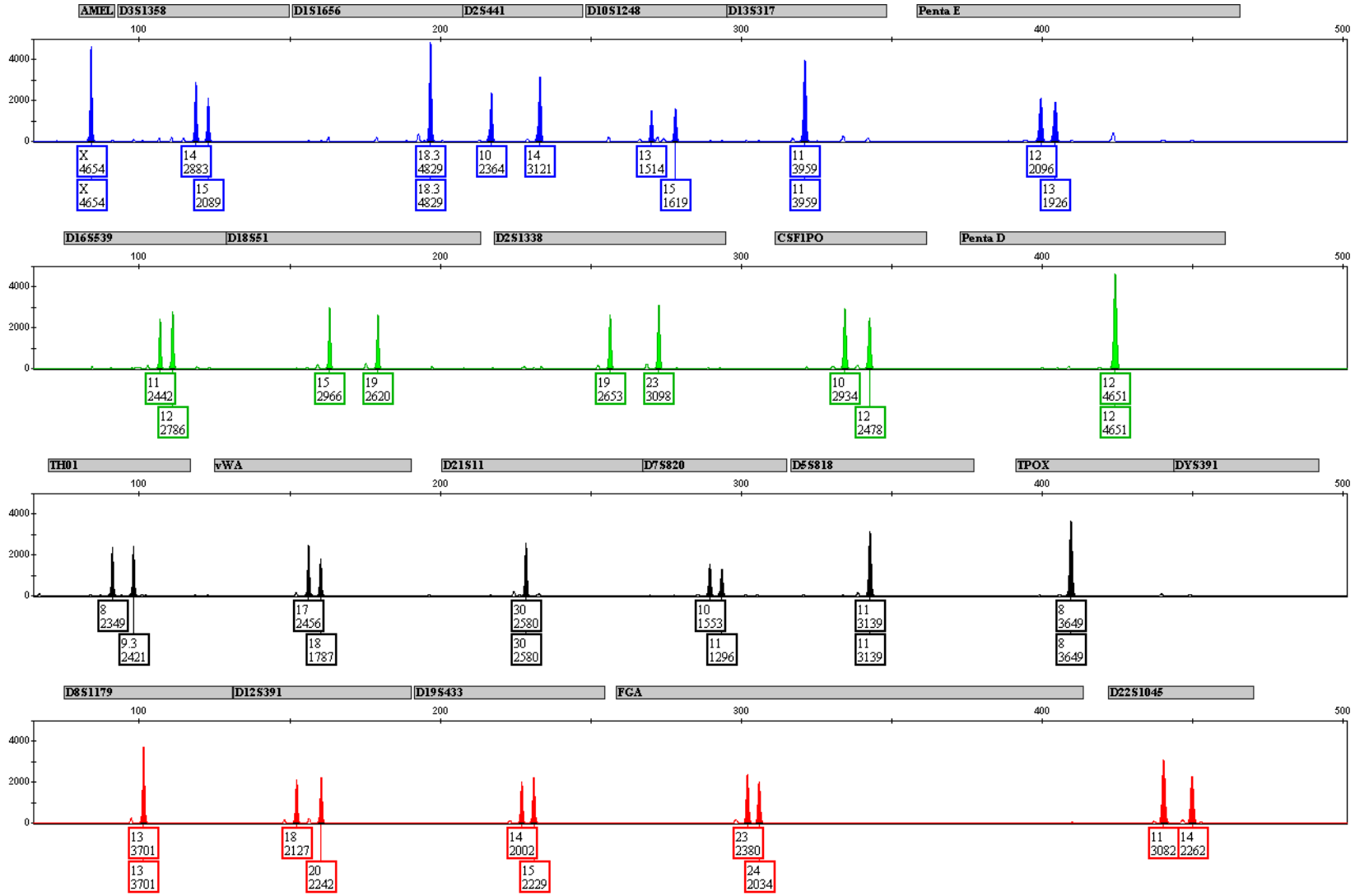


- 24 STR loci in 5 dyes (3130 and 3500 instrument use)
- Direct amplification capabilities: 85 min amp
- Largest products <500 bp
- Full profiles using 100 pg at 30 cycles

NIST Concordance Testing with PowerPlex Fusion

- PP Fusion results compared to all other kits tested including: Sinofiler/NGM/Identifiler/Yfiler/IDplex/ESSplex/PP16/ PP21 kits with **652 unrelated individuals** (NIST U.S. population set)
- PP Fusion is **fully concordant with NIST SRMs 2391b&c** certified values
- No PP Fusion **null alleles**
- No PP Fusion **discordance** with other PowerPlex kits, discordance with ABI or Qiagen kits is on their end and are previously documented

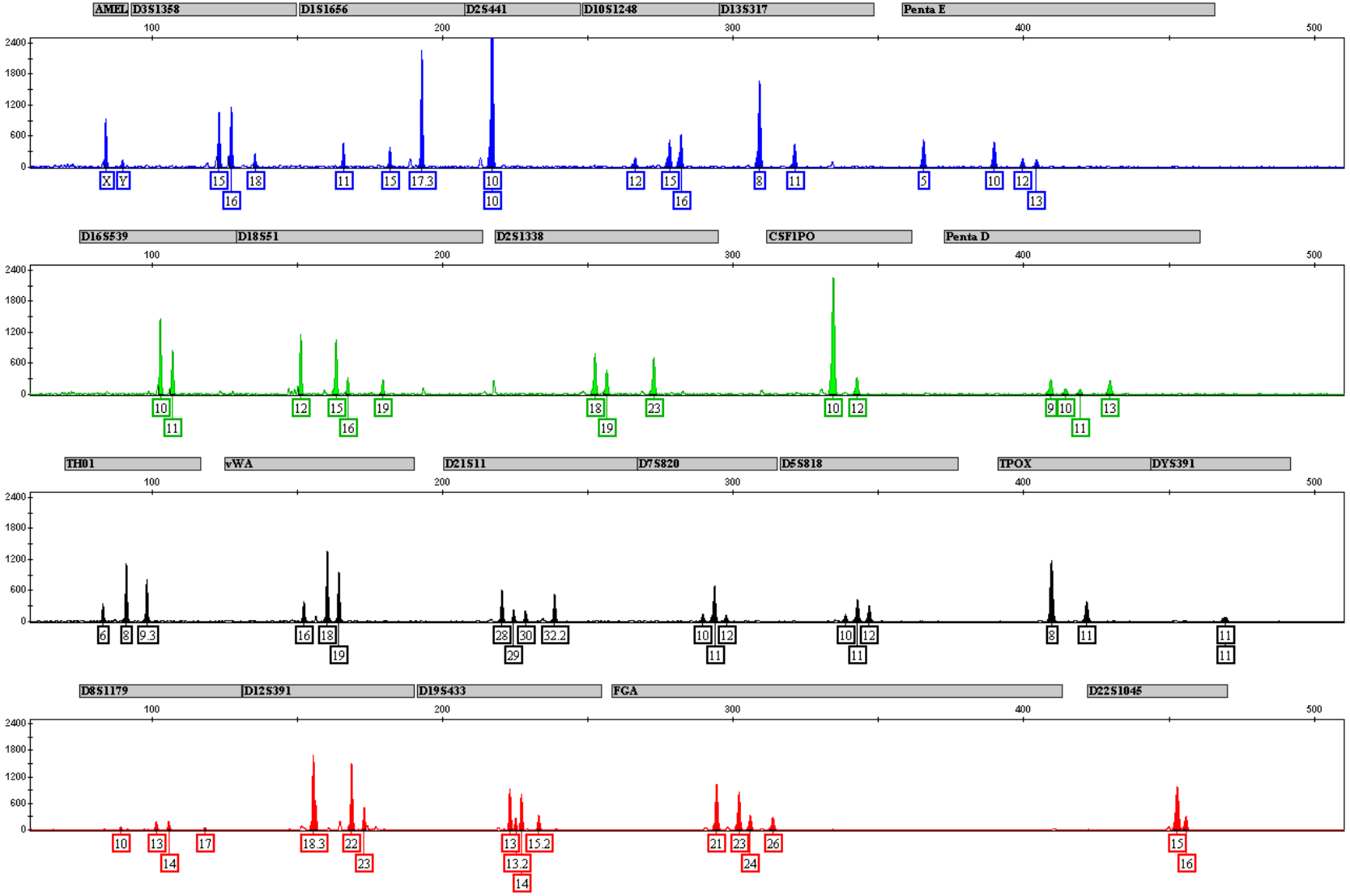
SRM 2391b&c were **fully concordant** at all loci for PP Fusion kit – **9947A Profile**



1 ng DNA, 30 cycles

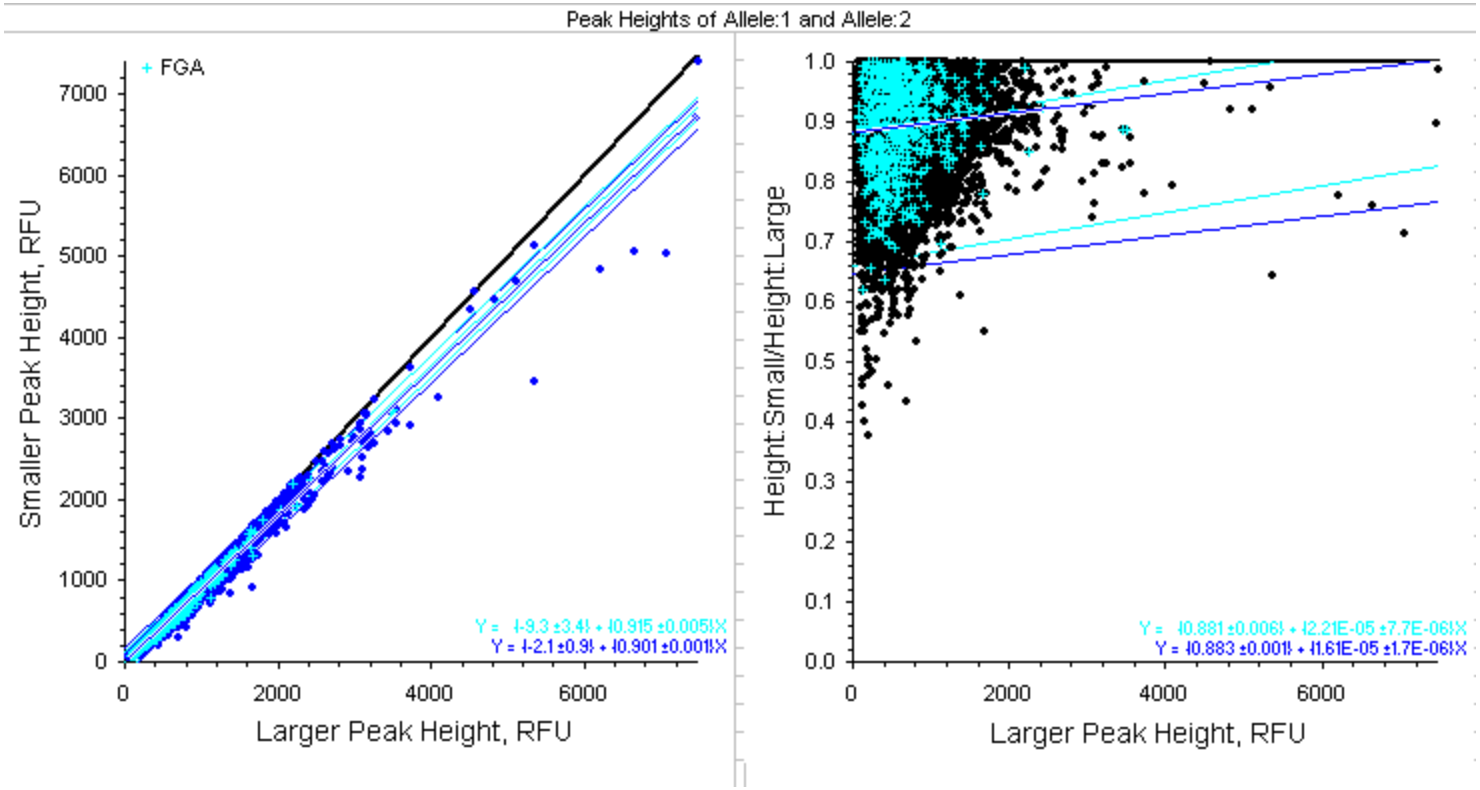
1 ng DNA, 30 cycles

SRM 2391c Mixture Component D

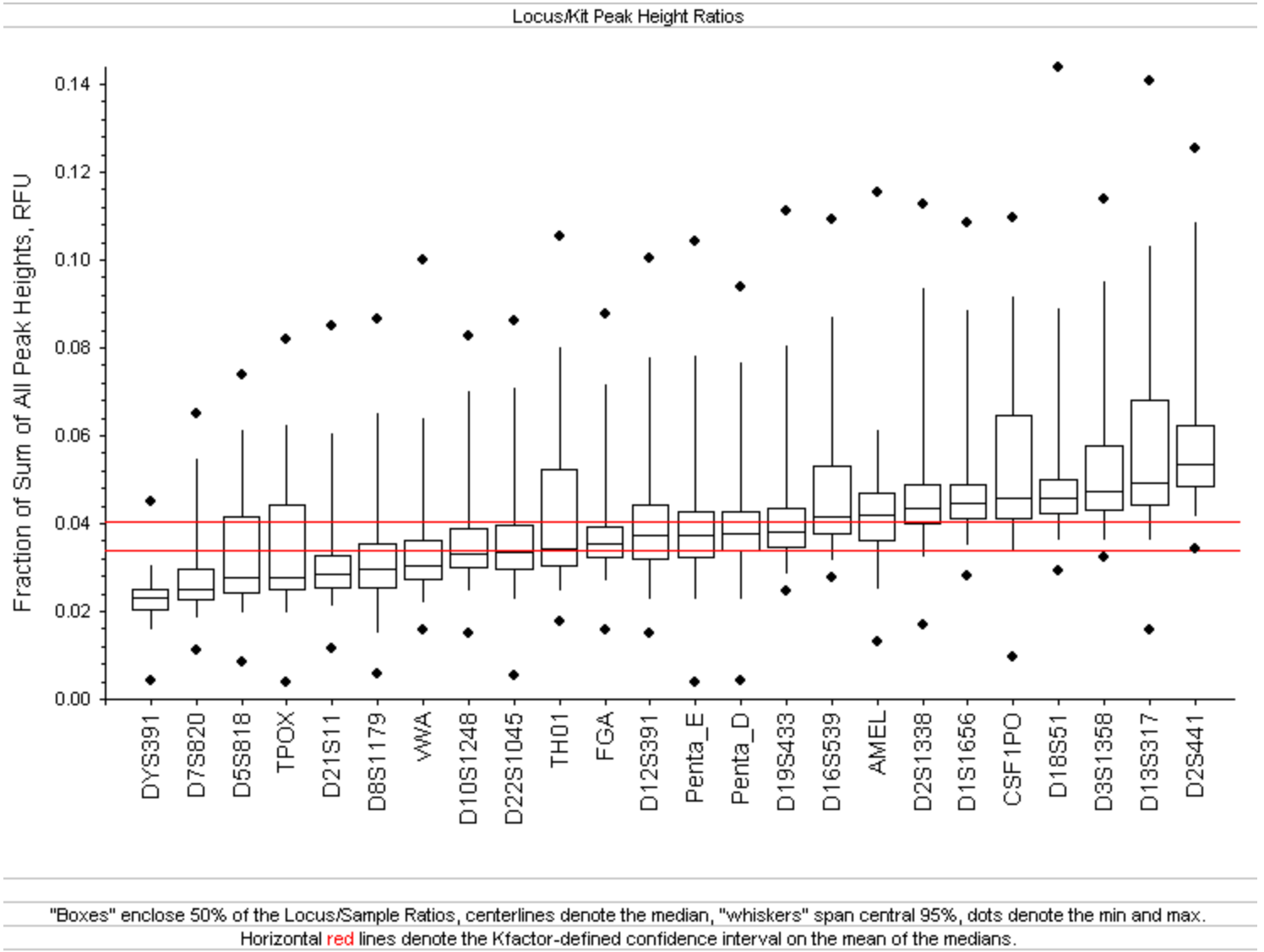


*This sample was low-injected because the default had too much bleed through

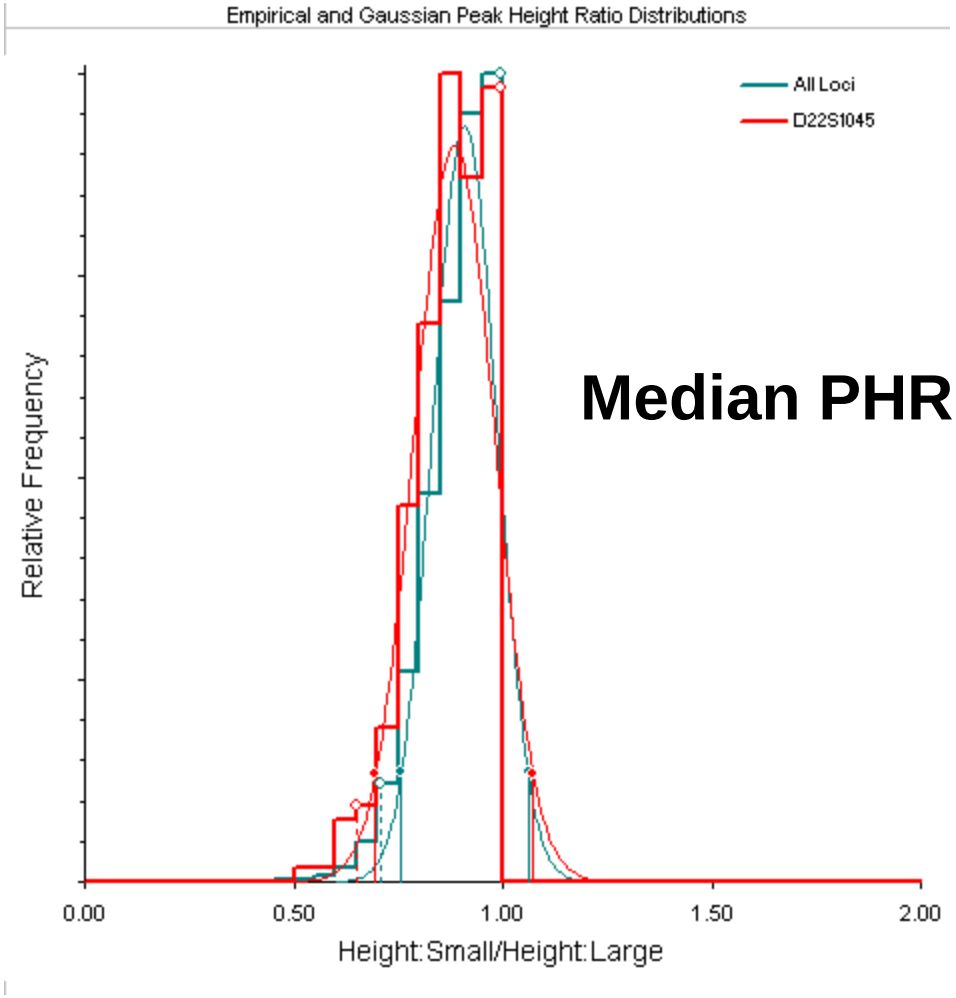
Peak Height Ratios



PHR Balance Across All Loci

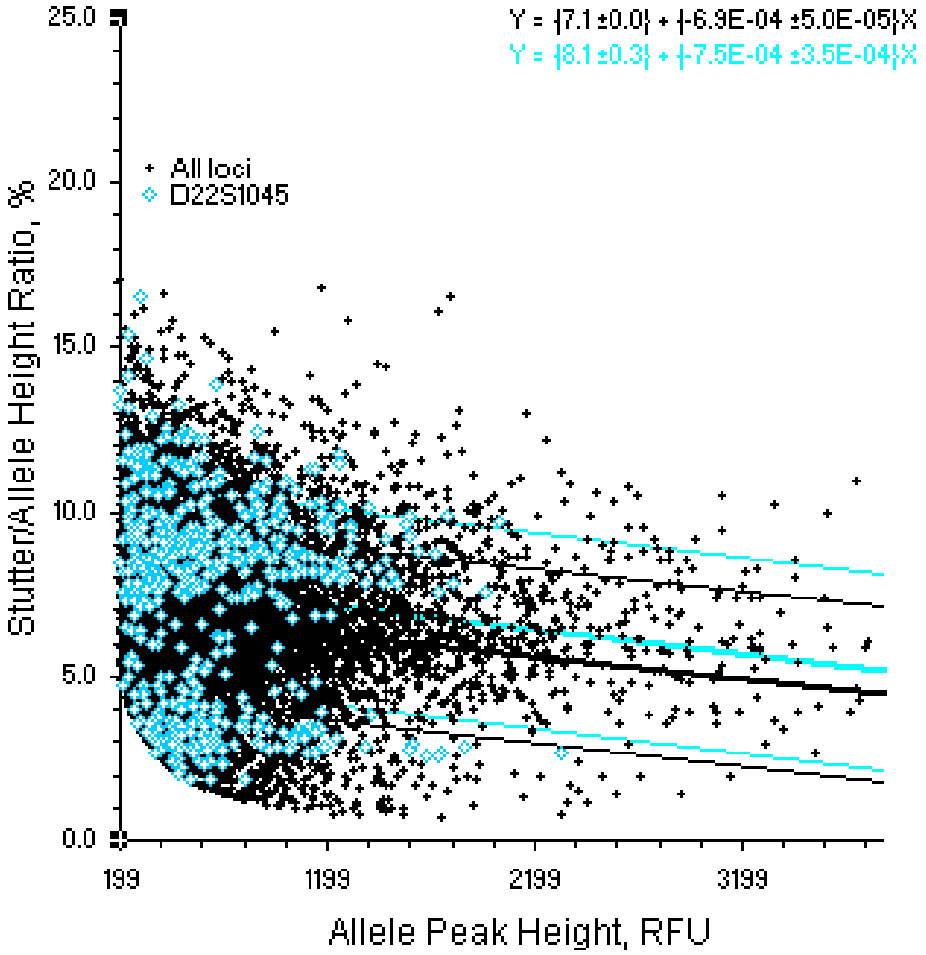


Heterozygote Peak Balance



Median PHR = 90.9%

Minus Stutter Observed
(Big Picture View)



*D22S1045
stutter is in blue
(trinucleotide locus)

Locus-Specific Stutter Values

Created on:	23-May-12 16:37:36
From Version:	29-Feb-12

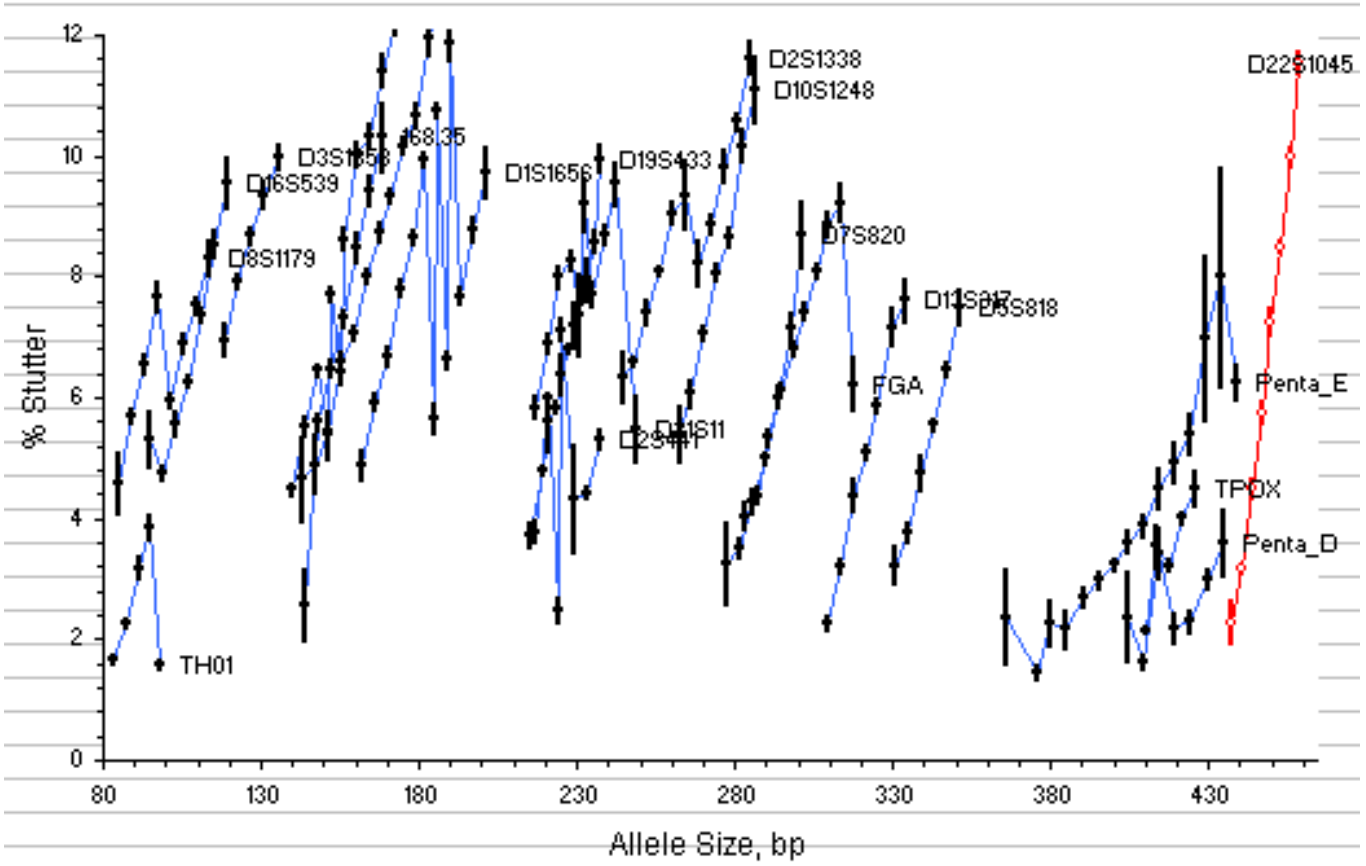
Filter	Setting
Fetch	Stored profiles
Min PkHt	200
Max PkHt	4000
Max %Stutter	30
Allow Forwards	No
Min #Ratio	7
BpWin	0.50

			Percentage Stutter															
Locus	#Ratio	Mean	SD	Median	MADe	Min	1%	2.5%	5%	10%	25%	75%	90%	95%	97.5%	99%	Max
TH01	432	2.5	1.1	2.2	1.0	0.9	1.1	1.2	1.3	1.4	1.7	3.2	4.0	4.5	5.2	5.8	10.0
Penta_D	427	2.9	1.6	2.5	1.2	0.7	0.8	1.0	1.1	1.3	1.8	3.5	4.9	5.9	6.4	7.4	12.7
TPOX	452	3.3	1.3	3.2	1.5	0.9	1.5	1.6	1.7	1.8	2.2	4.1	4.9	5.8	6.3	6.9	9.6
Penta_E	685	4.0	2.4	3.5	1.6	0.7	0.9	1.1	1.3	1.7	2.6	4.7	6.8	8.8	11.3	12.8	15.3
D7S820	428	5.2	1.7	4.9	1.6	1.8	2.5	2.7	2.8	3.1	4.0	6.2	7.5	8.7	9.1	10.3	11.2
D2S441	711	5.1	1.6	5.1	1.5	1.0	1.9	2.3	2.7	3.2	4.0	6.1	6.9	7.7	8.7	9.7	14.7
D13S317	526	5.1	1.9	5.2	1.7	1.2	1.7	1.8	2.0	2.5	4.0	6.2	7.4	8.1	8.8	10.0	17.1
D5S818	388	5.8	1.6	5.9	1.3	1.8	2.6	3.0	3.4	3.8	4.9	6.7	7.6	8.2	9.1	9.8	13.7
CSF1PO	452	6.1	1.6	6.0	1.4	1.6	2.4	2.8	3.4	4.2	5.2	7.0	8.3	9.0	9.8	10.6	12.4
D16S539	496	6.5	1.7	6.3	1.7	2.3	3.6	3.8	4.0	4.4	5.3	7.6	8.9	9.5	10.3	10.8	14.3
D19S433	588	6.6	1.6	6.5	1.4	1.8	3.3	3.6	4.3	4.7	5.6	7.5	8.6	9.4	10.2	10.7	12.9
D8S1179	522	6.8	1.5	6.7	1.4	2.5	3.3	3.8	4.3	5.1	5.8	7.8	8.6	9.4	10.2	10.9	11.8
vWA	461	6.9	2.3	6.8	1.9	0.9	1.2	1.5	2.3	4.3	5.6	8.2	9.6	10.4	11.4	12.3	20.6
FGA	644	6.9	1.7	6.8	1.7	3.4	3.7	3.9	4.2	4.7	5.7	8.1	9.2	9.8	10.3	11.0	12.6
D10S1248	453	8.0	1.8	7.7	1.6	3.7	4.7	5.0	5.5	6.0	6.8	8.9	10.5	11.4	12.0	13.2	15.3
D21S11	633	8.1	1.6	8.0	1.4	4.1	4.9	5.3	5.7	6.1	7.1	9.0	10.2	10.8	12.0	12.9	15.3
D1S1656	813	8.2	2.0	8.1	2.2	2.3	4.2	4.9	5.3	5.8	6.7	9.7	10.9	11.5	12.2	12.8	15.6
D22S1045	552	7.6	3.0	8.3	2.7	1.8	2.2	2.4	2.8	3.0	4.5	9.6	11.2	11.7	12.4	13.5	16.6
D12S391	696	8.6	2.7	8.3	3.0	3.7	4.0	4.3	4.6	5.0	6.5	10.5	12.4	13.2	14.3	15.3	16.8
D18S51	745	8.4	2.2	8.4	2.3	3.6	4.3	4.8	5.1	5.4	6.8	9.8	11.4	12.4	13.1	13.6	16.6
D2S1338	834	8.7	1.9	8.5	2.0	4.0	5.4	5.6	5.9	6.3	7.2	9.9	11.2	11.8	12.7	13.4	14.9
D3S1358	484	8.6	1.6	8.5	1.5	3.1	5.4	5.9	6.2	6.7	7.5	9.5	10.6	11.2	11.8	12.6	16.1

Settings Used for Analysis

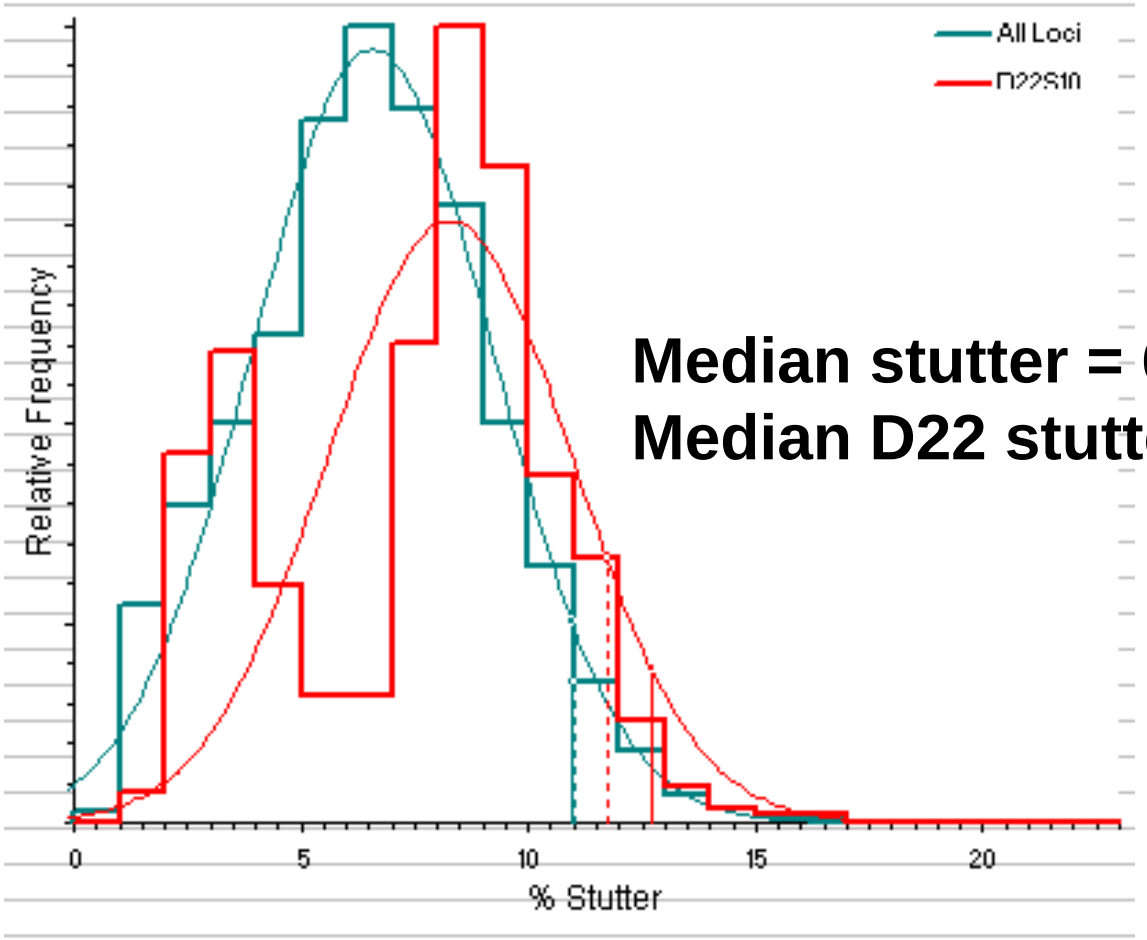
*Verified Max stutter amounts

Stutter Trends (Size Scale)



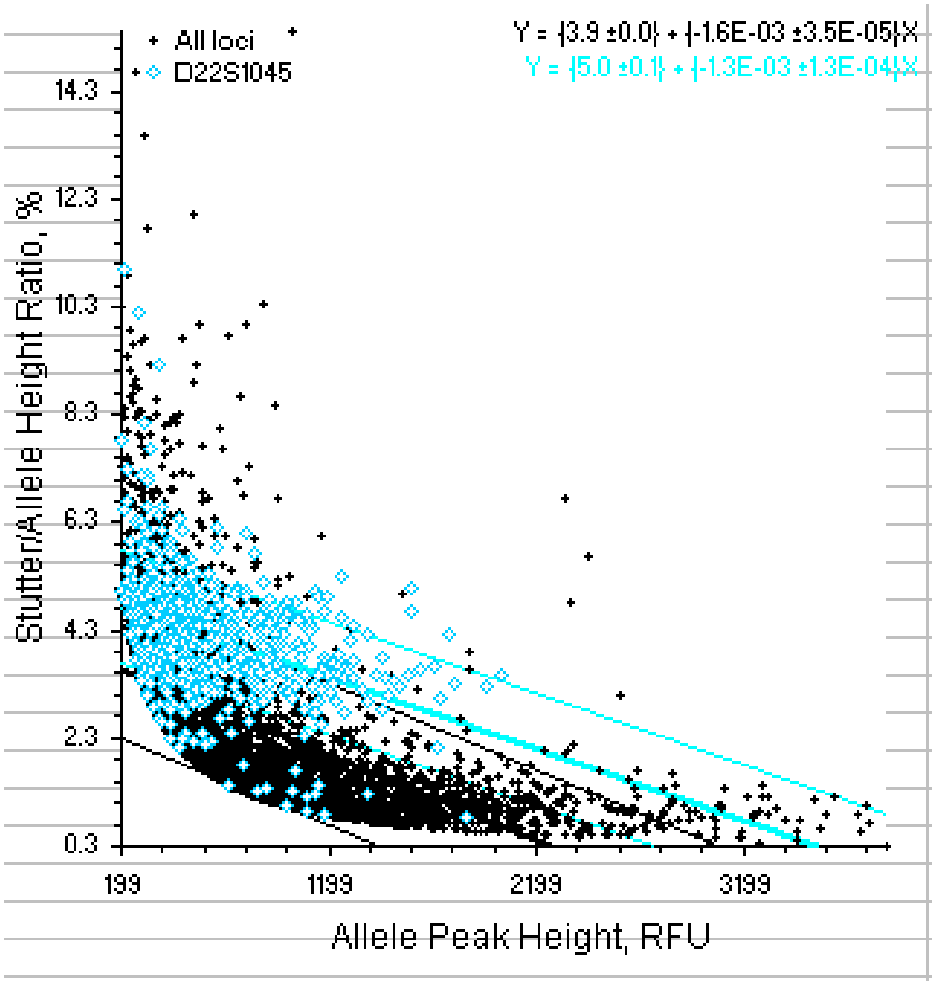
*D22S1045 is in red

Stutter Density Plot



Median stutter = 6.57%
Median D22 stutter (in red) = 8.26%

Forward Stutter Observed
(Big Picture View)



*D22S1045 stutter is in blue (trinucleotide locus)

Locus-Specific Stutter Values

Created on:	23-May-12 17:00:59
From Version:	29-Feb-12

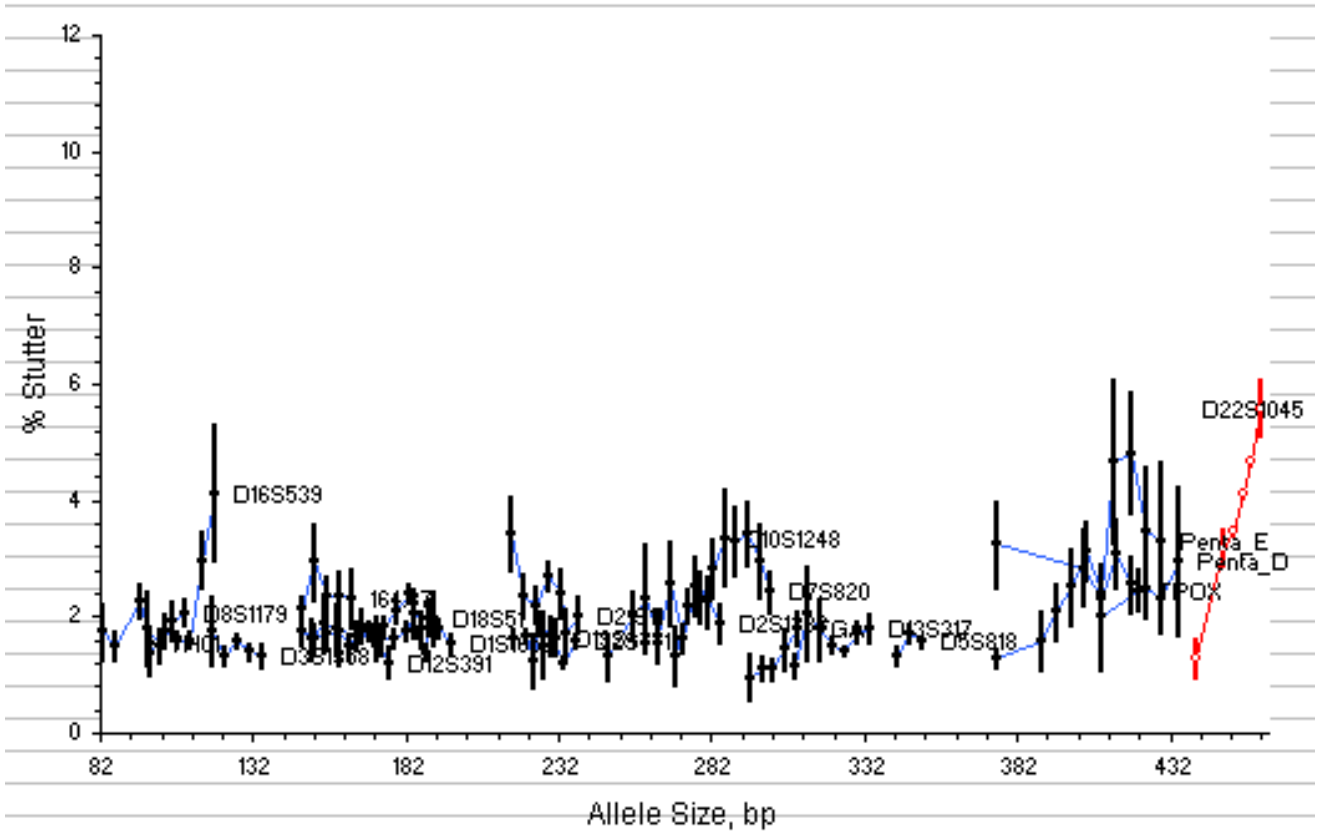
Filter	Setting
Fetch	Stored profiles
Min PkHt	200
Max PkHt	4000
Max %Stutter	30
Allow Forwards	No
Min #Ratio	7
BpWin	0.50

			Percentage Stutter															
Locus	#Ratio	Mean	SD	Median	MADe	Min	1%	2.5%	5%	10%	25%	75%	90%	95%	97.5%	99%	Max
FGA	92	1.7	1.0	1.3	0.8	0.4	0.4	0.5	0.5	0.6	1.0	2.1	3.1	3.5	4.1	5.4	6.0
D3S1358	316	1.9	1.2	1.5	0.7	0.4	0.5	0.6	0.7	0.8	1.1	2.2	3.4	4.5	5.4	6.0	7.0
D19S433	26	1.9	1.5	1.5	0.6	0.3	0.4	0.4	0.6	0.9	1.1	2.0	3.2	3.7	5.5	7.2	8.3
D13S317	348	1.8	1.2	1.5	0.6	0.4	0.6	0.7	0.8	0.9	1.2	2.1	3.0	3.9	4.4	8.4	10.2
D2S441	417	1.9	1.2	1.6	0.8	0.4	0.6	0.6	0.7	0.8	1.1	2.2	3.2	4.0	4.7	5.5	9.9
D5S818	169	1.9	1.1	1.6	0.6	0.6	0.6	0.7	0.8	1.0	1.2	2.1	3.5	4.2	4.8	5.4	6.3
D12S391	133	1.9	1.2	1.6	0.7	0.3	0.5	0.6	0.7	0.8	1.2	2.1	3.2	4.5	4.9	6.2	7.3
D1S1656	514	2.0	1.0	1.7	0.7	0.3	0.7	0.8	0.9	1.1	1.3	2.3	3.3	4.1	4.9	5.5	8.2
TH01	56	2.1	1.2	1.8	0.8	0.3	0.4	0.7	0.9	1.0	1.4	2.5	3.5	4.1	5.2	6.2	6.8
D16S539	329	2.4	1.8	1.8	1.0	0.5	0.7	0.7	0.8	1.0	1.3	3.0	4.5	6.2	8.0	8.3	11.7
D8S1179	67	2.1	1.6	1.8	0.7	0.7	0.9	1.0	1.0	1.0	1.2	2.3	3.1	4.2	4.4	7.5	13.4
D18S51	441	2.2	1.3	1.9	0.9	0.6	0.6	0.8	0.9	1.0	1.3	2.7	3.7	4.7	5.7	6.9	8.8
D2S1338	176	2.4	1.5	2.0	1.1	0.5	0.5	0.7	0.8	1.0	1.3	2.9	4.0	5.6	6.9	7.7	8.5
CSF1PO	422	2.6	1.5	2.3	1.1	0.6	0.7	0.8	1.0	1.2	1.5	3.1	4.5	5.2	7.1	7.9	11.1
D21S11	289	2.6	1.4	2.4	1.2	0.8	0.8	0.9	1.0	1.2	1.6	3.4	4.7	5.2	6.1	6.6	9.8
vWA	113	2.7	1.7	2.4	1.1	0.7	0.8	0.9	0.9	1.2	1.7	3.1	4.0	5.2	6.0	6.5	15.4
D10S1248	159	2.7	1.6	2.4	1.4	0.5	0.5	0.7	0.8	1.0	1.6	3.5	4.9	5.5	6.1	7.8	10.9
TPOX	35	2.8	1.6	2.4	1.3	0.6	0.6	0.6	0.7	1.0	1.7	3.5	5.2	5.6	6.1	6.5	6.8
Penta_D	188	3.0	1.9	2.6	1.5	0.6	0.7	0.8	0.9	1.2	1.7	3.9	5.3	6.4	7.6	9.4	14.6
Penta_E	177	3.6	2.4	2.8	1.8	0.5	0.7	1.0	1.1	1.3	1.9	4.6	7.3	8.4	9.2	10.0	12.0
D7S820	124	3.2	1.6	3.2	1.7	0.6	0.8	0.9	1.0	1.2	1.9	4.2	5.4	5.9	6.5	7.3	7.8
D22S1045	540	4.1	1.1	4.1	0.9	0.6	1.1	1.5	2.4	2.9	3.5	4.7	5.2	5.9	6.4	7.5	11.0

Settings Used for Analysis

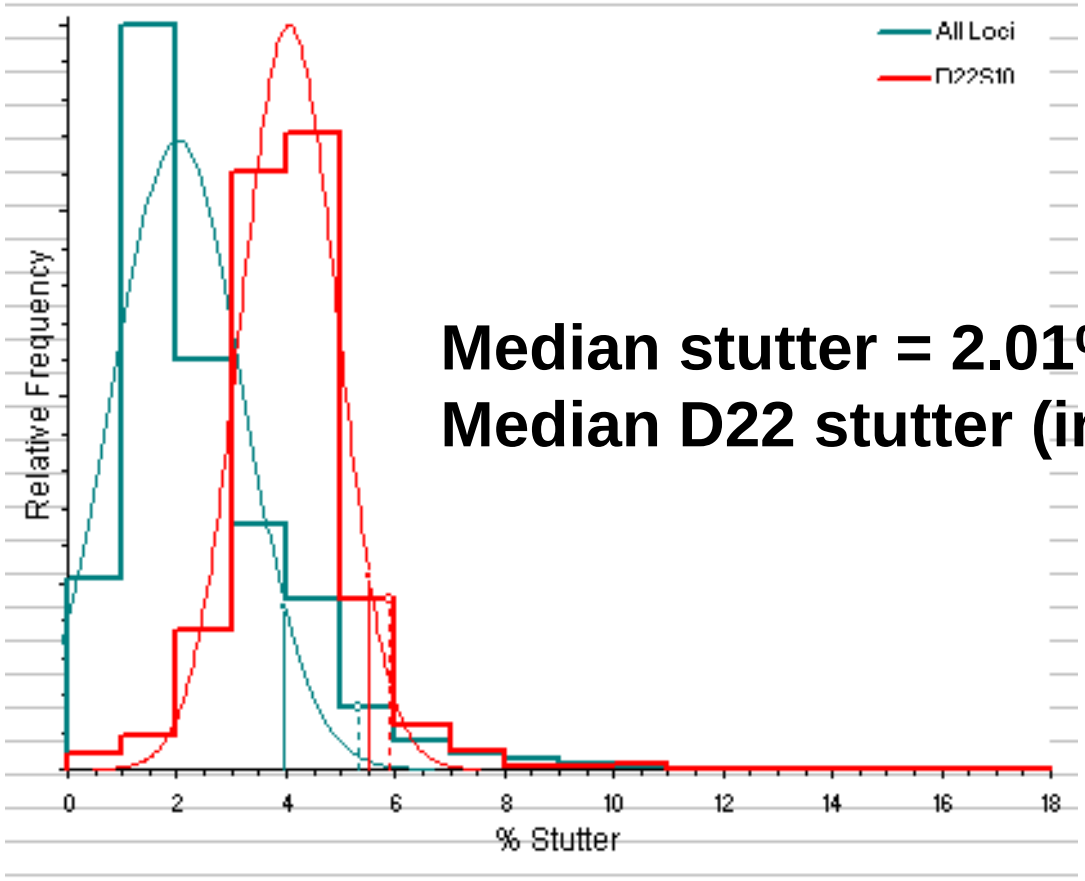
*Verified Max stutter amounts

Stutter Trends (Size Scale)



*D22S1045 is in red

Stutter Density Plot



Median stutter = 2.01%
Median D22 stutter (in red) = 4.05%

Summary

- Additional STR loci are important as DNA databases grow larger each year
- NIST has a set of 1036 U.S. Population Samples that have been used to fully characterize 29 autosomal STR loci
- Commercial companies are continuing to release larger STR multiplexes to meet the needs of the forensic community

SAVE THE DATE

Forensics@NIST 2012

Three day symposium on cutting edge forensic science research at NIST

Date: November 28-30th, 2012
Time: 9:00 am to 5:00 pm
Location: NIST (Gaithersburg, Maryland)

For more information:
www.nist.gov/oles/forensics-2012.cfm
Note: registration is required (free)

FORENSIC SCIENCES

Acknowledgments

NIST Funding: Interagency Agreement 2008-DN-R-121 between the National Institute of Justice and NIST Office of Law Enforcement Standards

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Points of view are mine and do not necessarily represent the official position or policies of the US Department of Justice or the National Institute of Standards and Technology.

NIST Team for This Work


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Dave Duewer


Margaret Kline


Mike Coble

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