ISHI Workshop on New Loci and Kits
October 2, 2014 (Phoenix, AZ)
New Autosomal and Y-STR Loci and Kits: Making Data Driven Decisions

NIST Studies:

New Y-STR Loci & Kits

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NIST Applied Genetics Group

NIST Applied Genetics

NIST

Product Disclaimer

- **I will mention commercial STR kit names and information, but I am in no way attempting to endorse any specific products.**

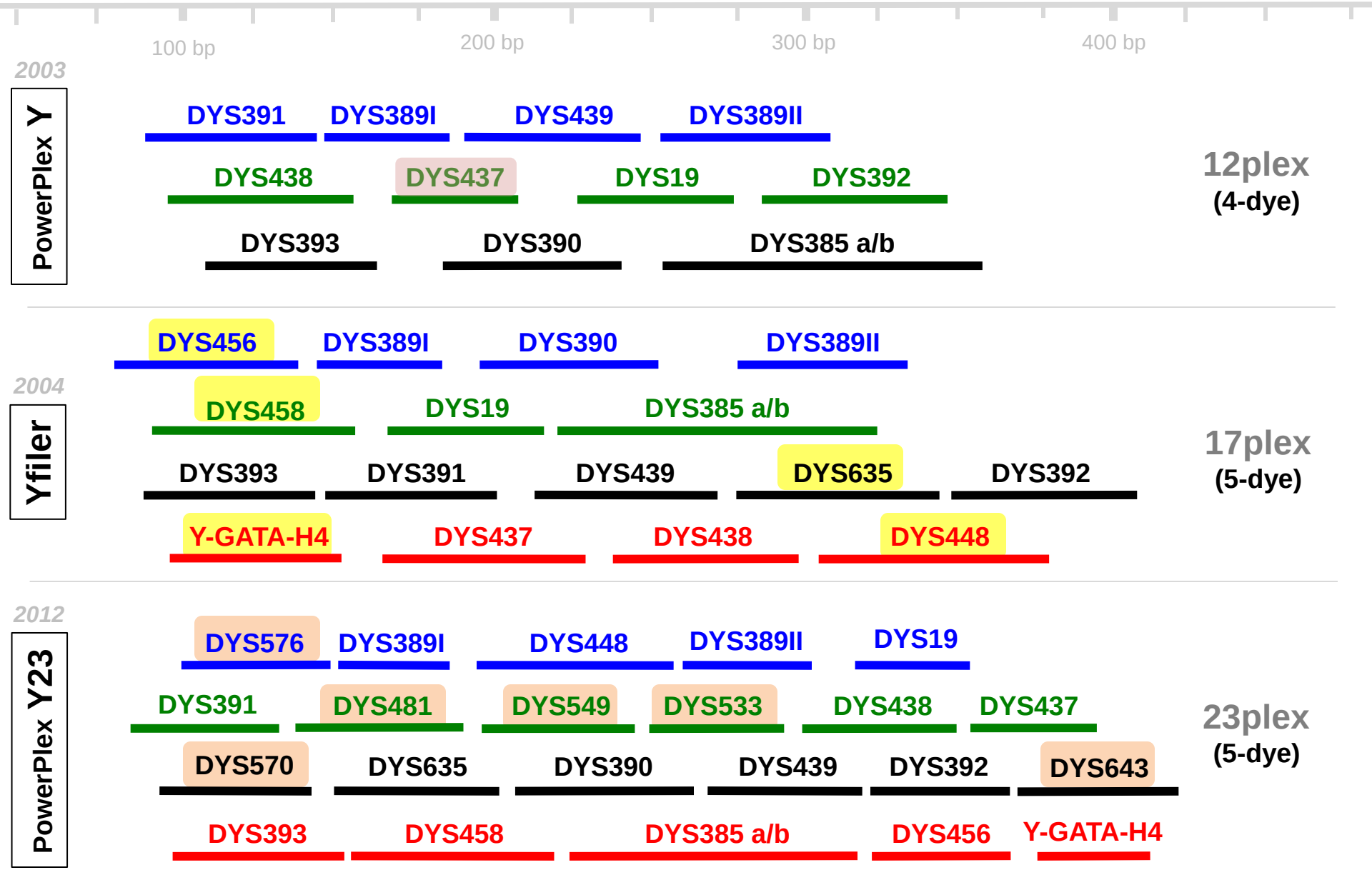
- **NIST Disclaimer**: Certain commercial equipment, instruments and materials are identified in order to specify experimental procedures as completely as possible. In no case does such identification imply a recommendation or it imply that any of the materials, instruments or equipment identified are necessarily the best available for the purpose.

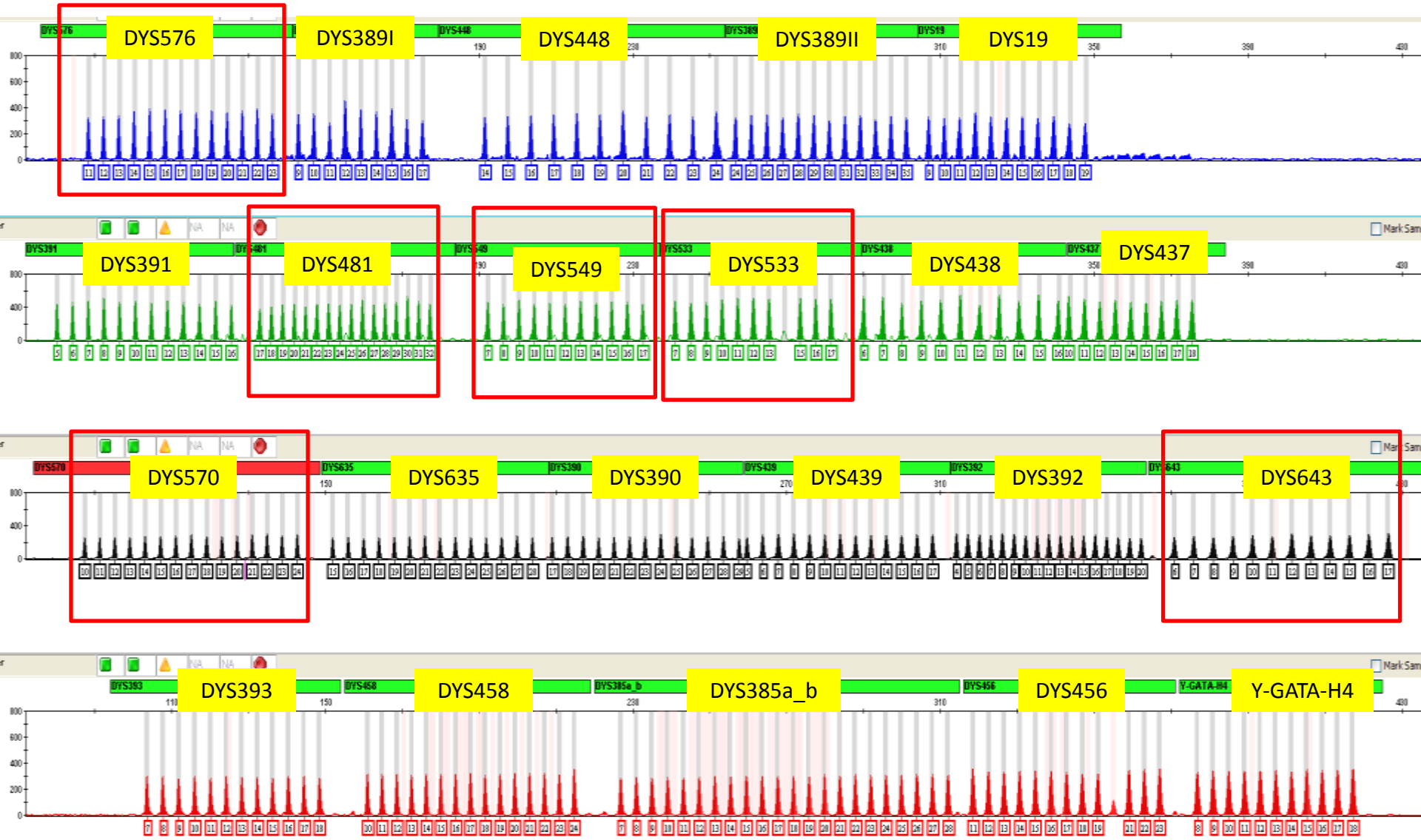
- **Points of view are mine** and do not necessarily represent the official position of the National Institute of Standards and Technology or the U.S. Department of Justice. **Our group receives or has received funding from the FBI Laboratory and the National Institute of Justice.**

What has happened in the past decade…

- **Selection of core Y-STR loci** (SWGDAM Jan 2003)
- "Full" Y-chromosome sequence became available in June 2003; over 700 Y-STR loci identified (only ~20 in 2000)
- **Commercial Y-STR kits released**
  - ~~Y-PLEX 6,5,12 (2001-03)~~, **PowerPlex Y** (9/03), **Yfiler** (12/04), **PPY23** (6/12)
    Yfiler Plus (coming soon)
- Many population studies performed and online databases generated with thousands of Y-STR haplotypes
- Forensic casework demonstrations showing value of Y-STR testing along with court acceptance
- Renewed interest in Y-STRs to aid familial searching

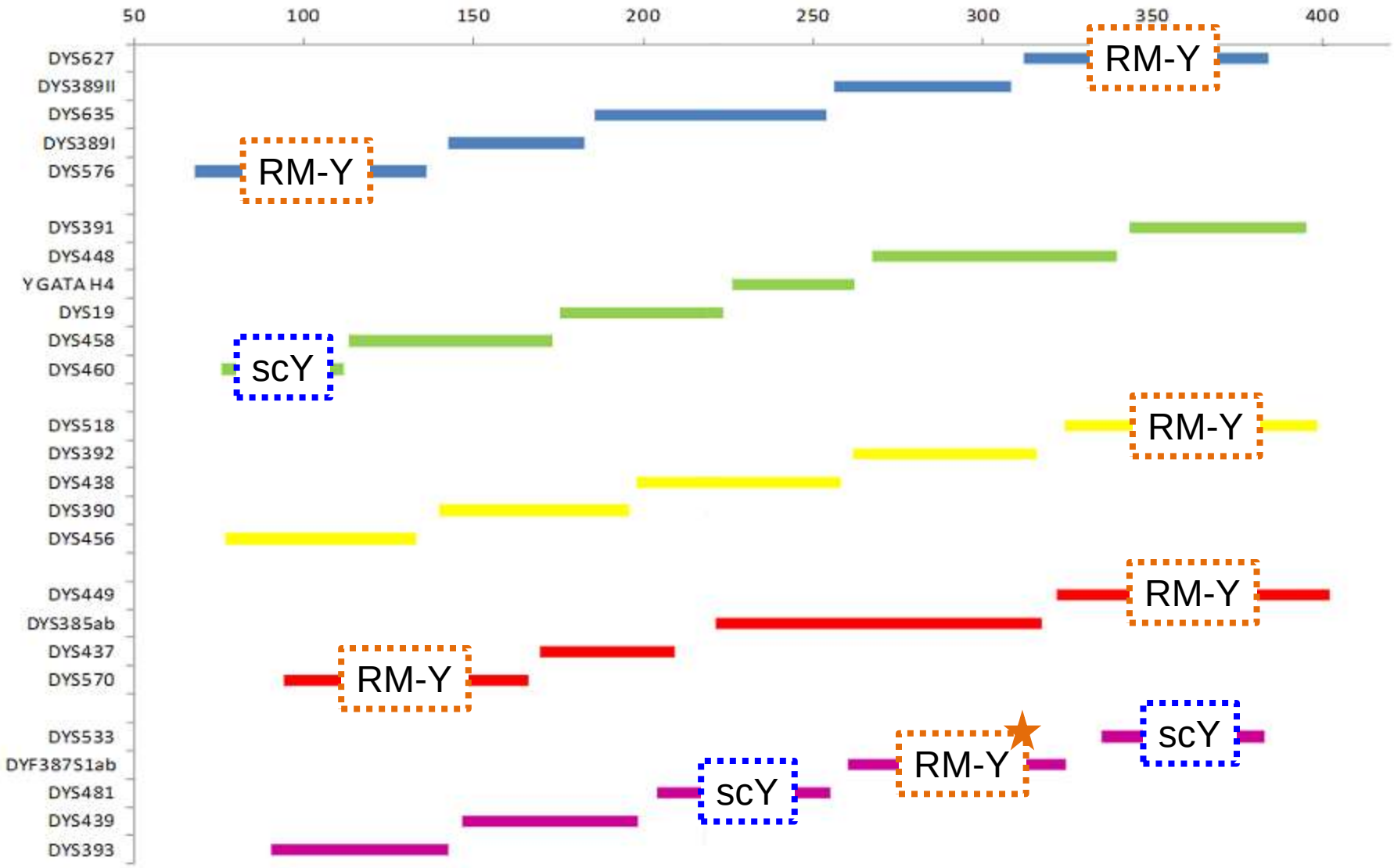
STR Marker Layouts for Y-STR Kits



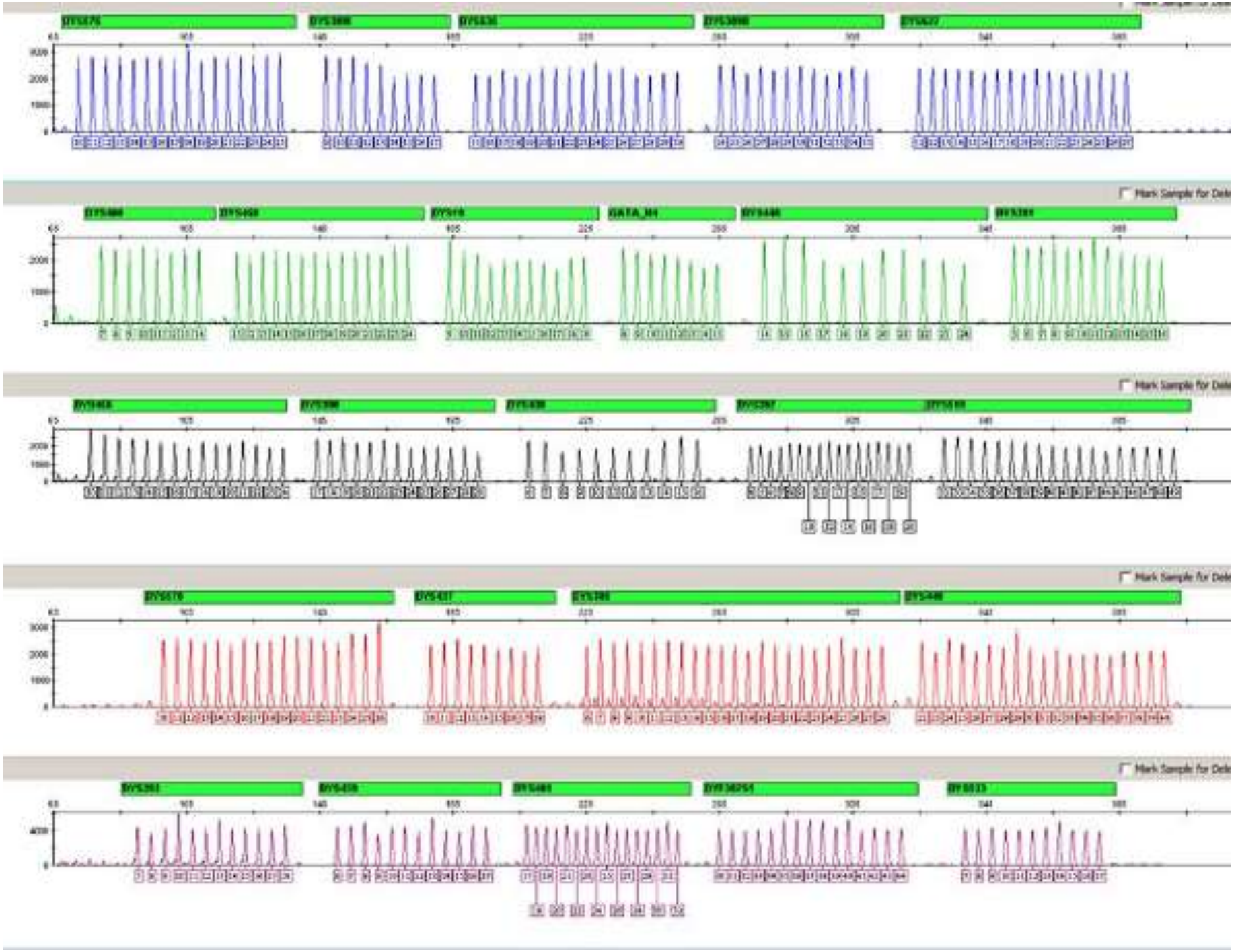


17 Y-Filer + 6 additional loci

Yfiler Plus Kit

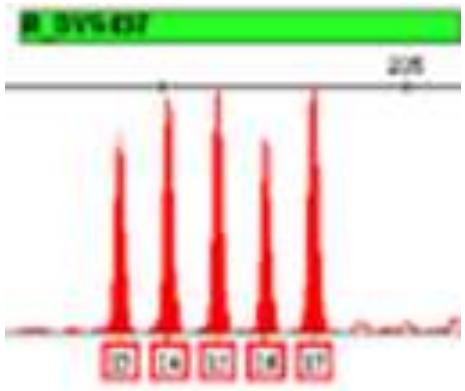


Slide courtesy of Dr. Julio Mulero (Life Technologies)



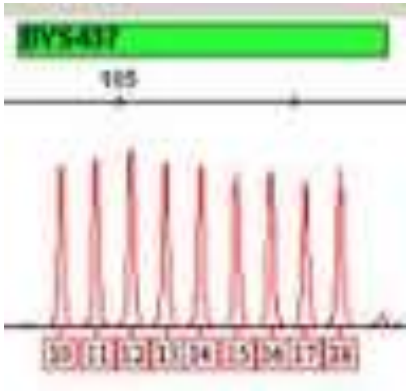
Improved Allelic Ladder (DYS437)

Yfiler



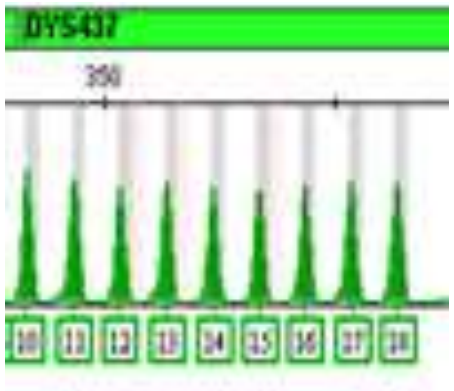
5 Alleles

Yfiler-Plus



9 Alleles

PPY-23



9 Alleles

PowerPlex Y-23

Promega New PowerPlex® Y23 STR System Reveals More Y-STR Loci in Half the Time

MADISON, WISCONSIN (July 12, 2012)

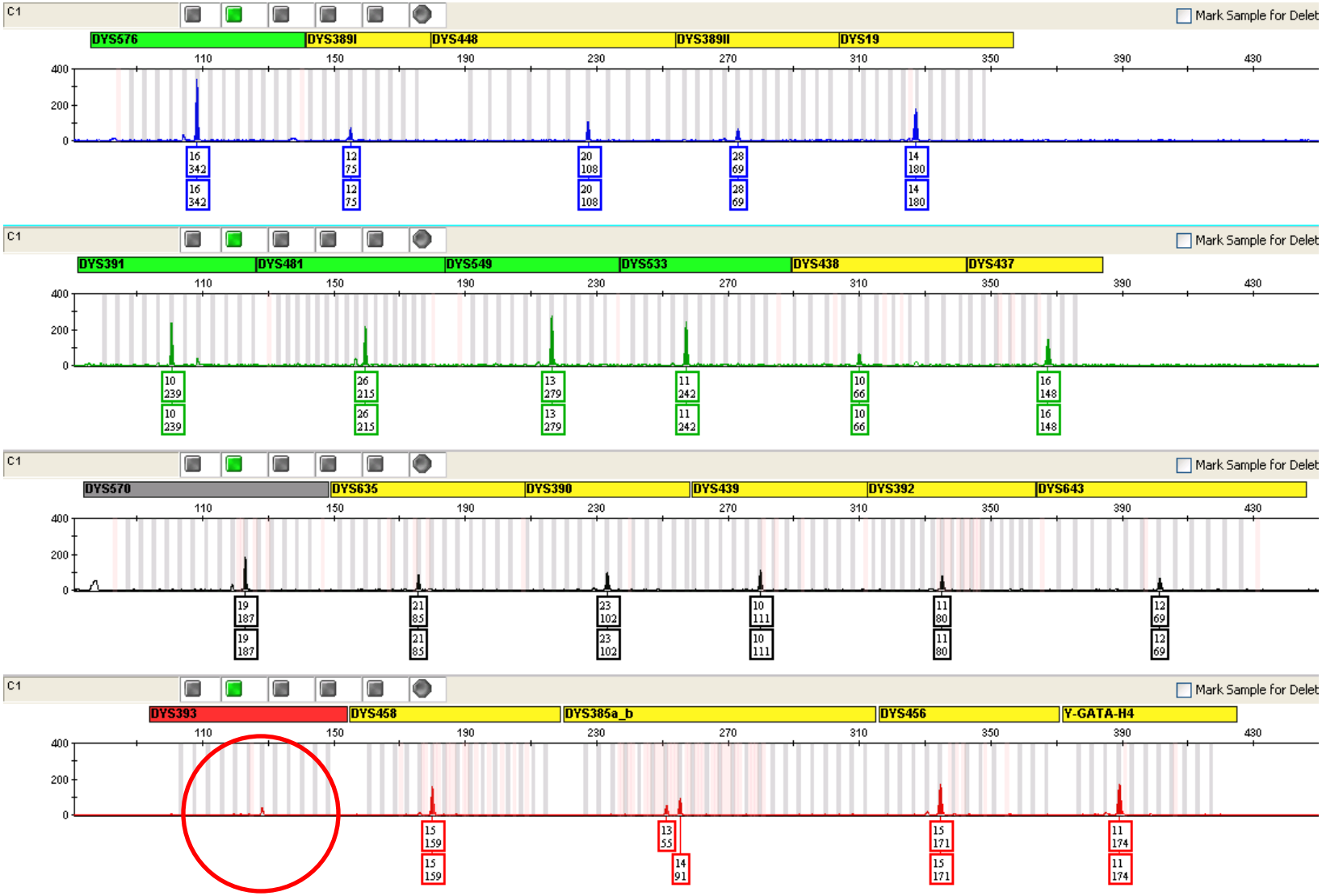
Promega Corporation announces the newest addition to the PowerPlex® STR Systems family, the PowerPlex® Y23 System—a rapid human identification Y-Short Tandem Repeat (Y-STR) assay for forensic casework, offender databasing and relationship testing. Thermal cycling time is cut roughly in half, and the system detects substantially more Y-STR loci than current systems. The multiplex system uses rapid cycling to co-amplify 23 Y-STR loci, which provides maximum discrimination. In addition, these 23 loci include many of the Y-STR loci found in key STR databases in the US and Europe.

The system works with extracted DNA, including difficult samples with lower amounts of template and male:female mixtures. Streamlined protocols also are provided for reference, database and paternity testing. The combination of reduced sample preparation time and shorter cycling times results in a significant reduction in total time to process samples. For many laboratories, this will save more than a half day per plate.

PPY-23 Kit Performance

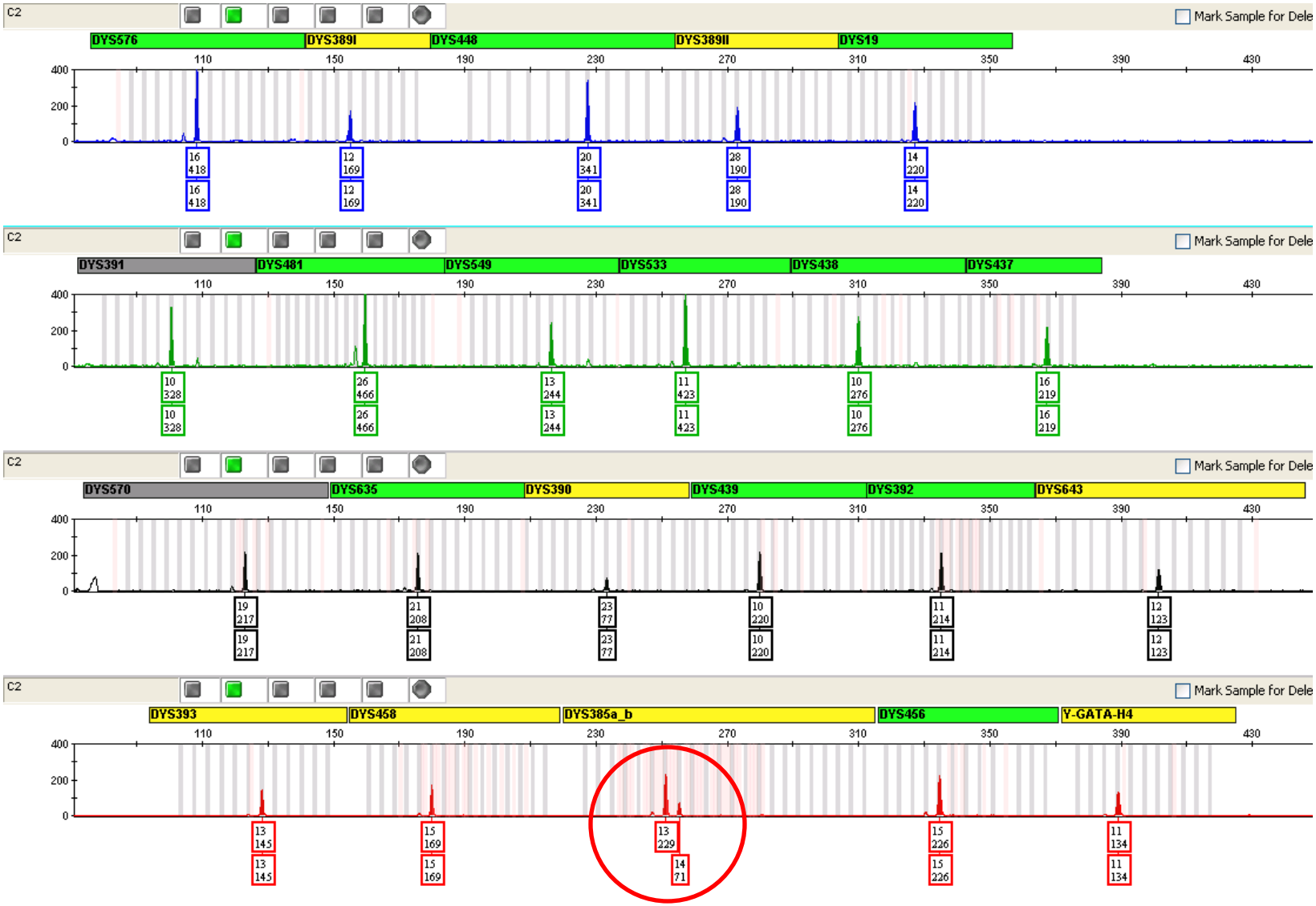
Sensitivity

Sensitivity Study – Sample C (rep 1)



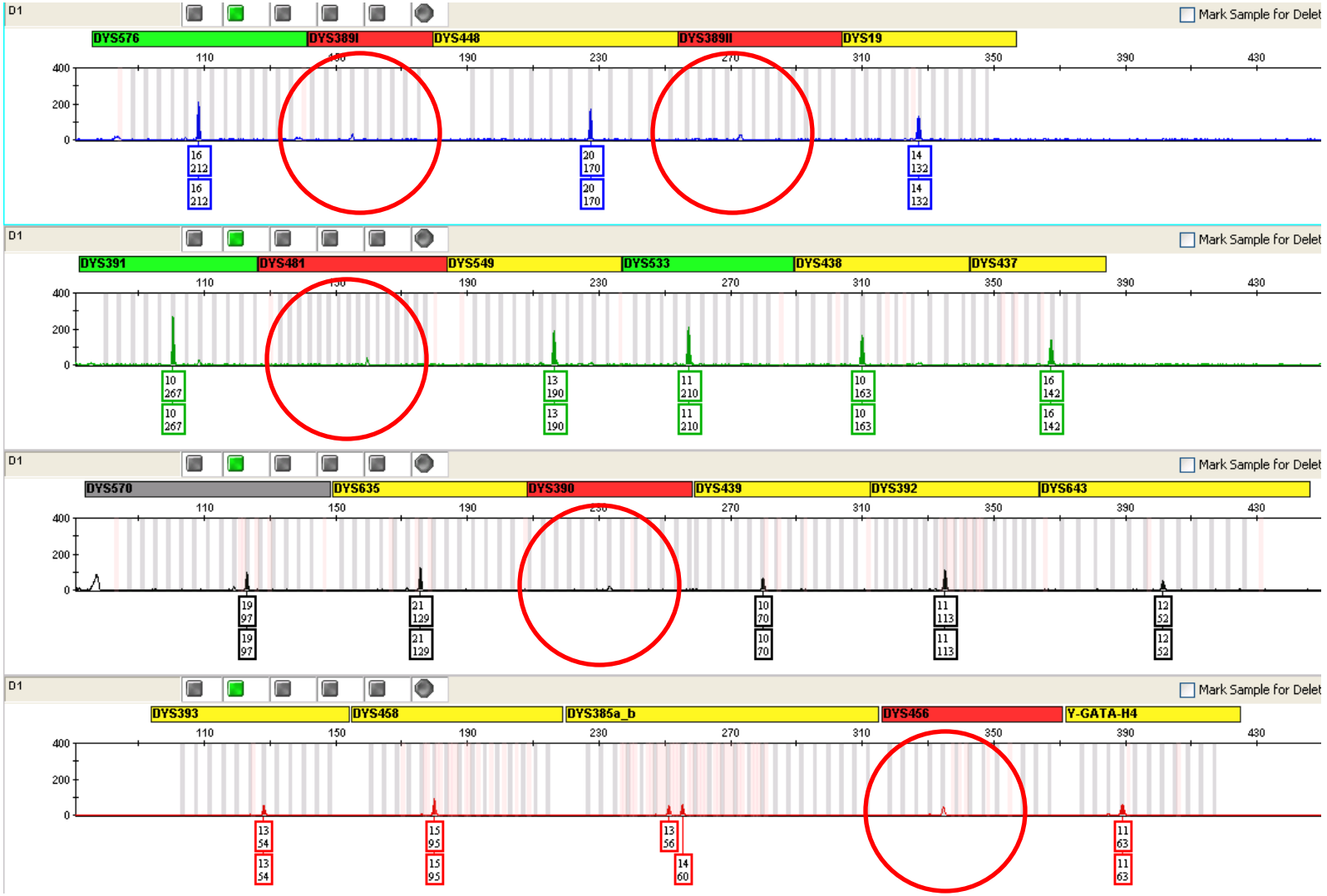
0.125ngQC2 (Tube C)

Sensitivity Study – Sample C (rep 2)



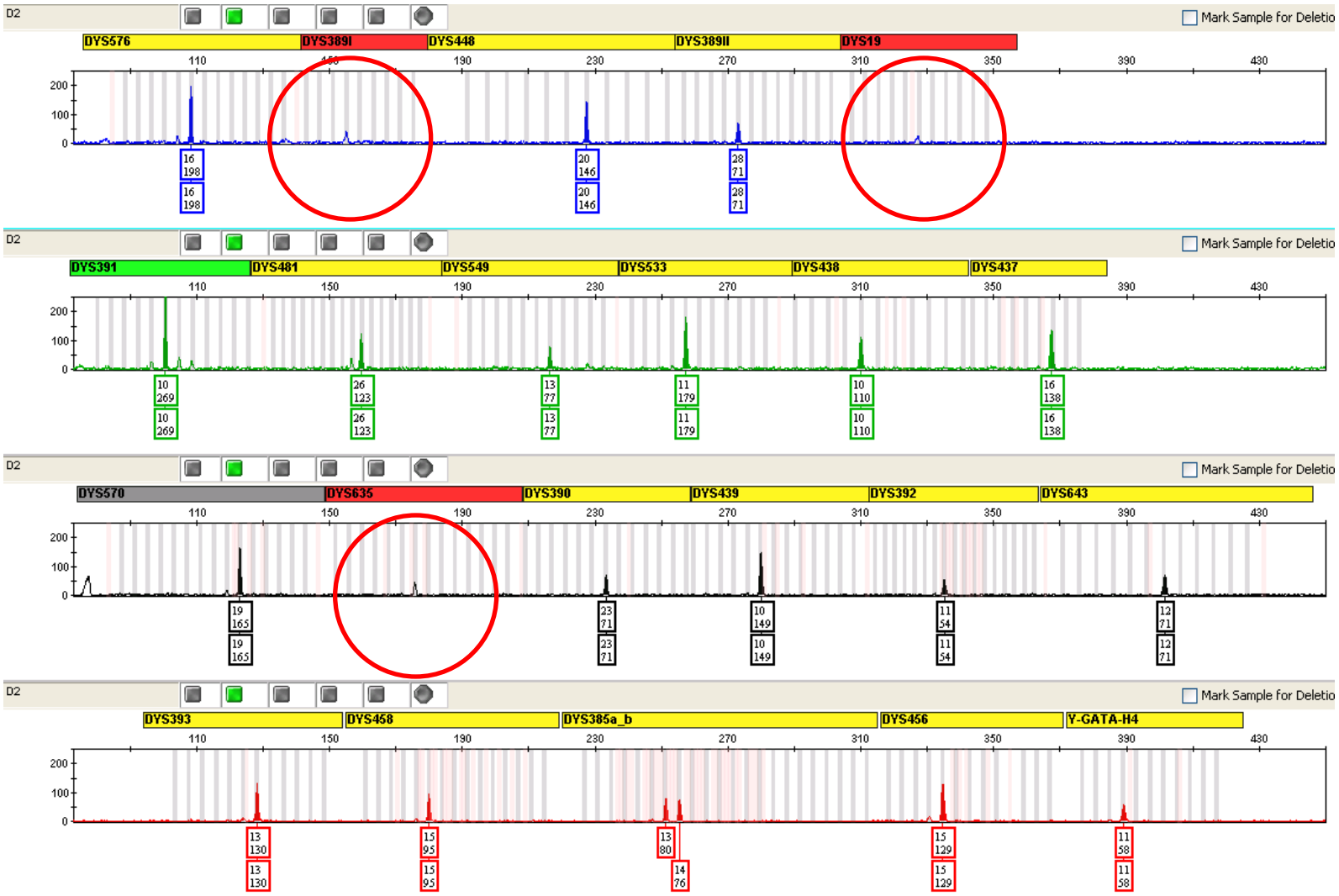
0.125ngQC2 (Tube C)

Sensitivity Study – Sample D (rep 1)



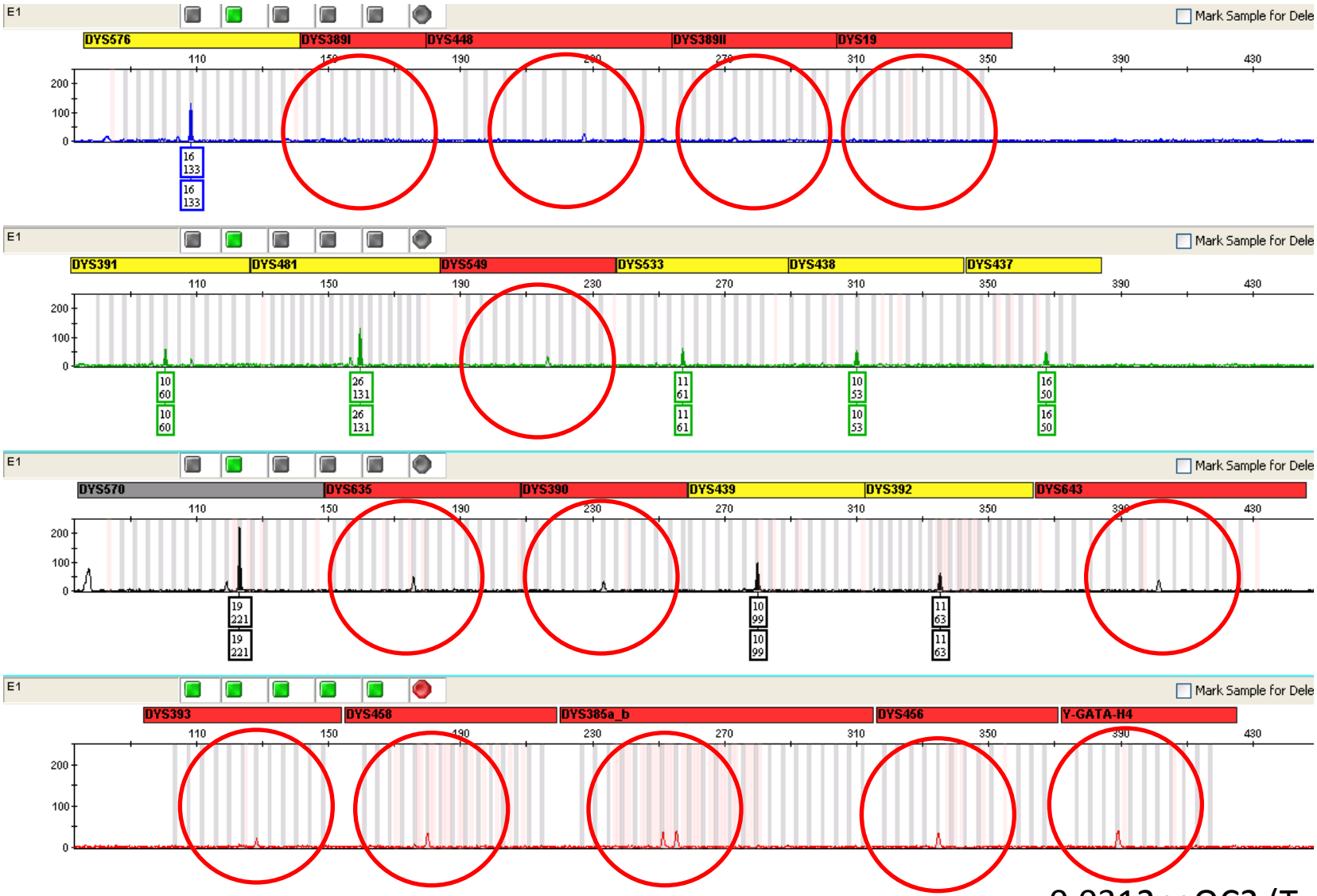
0.0625ngQC2 (Tube D)

Sensitivity Study – Sample D (rep 2)



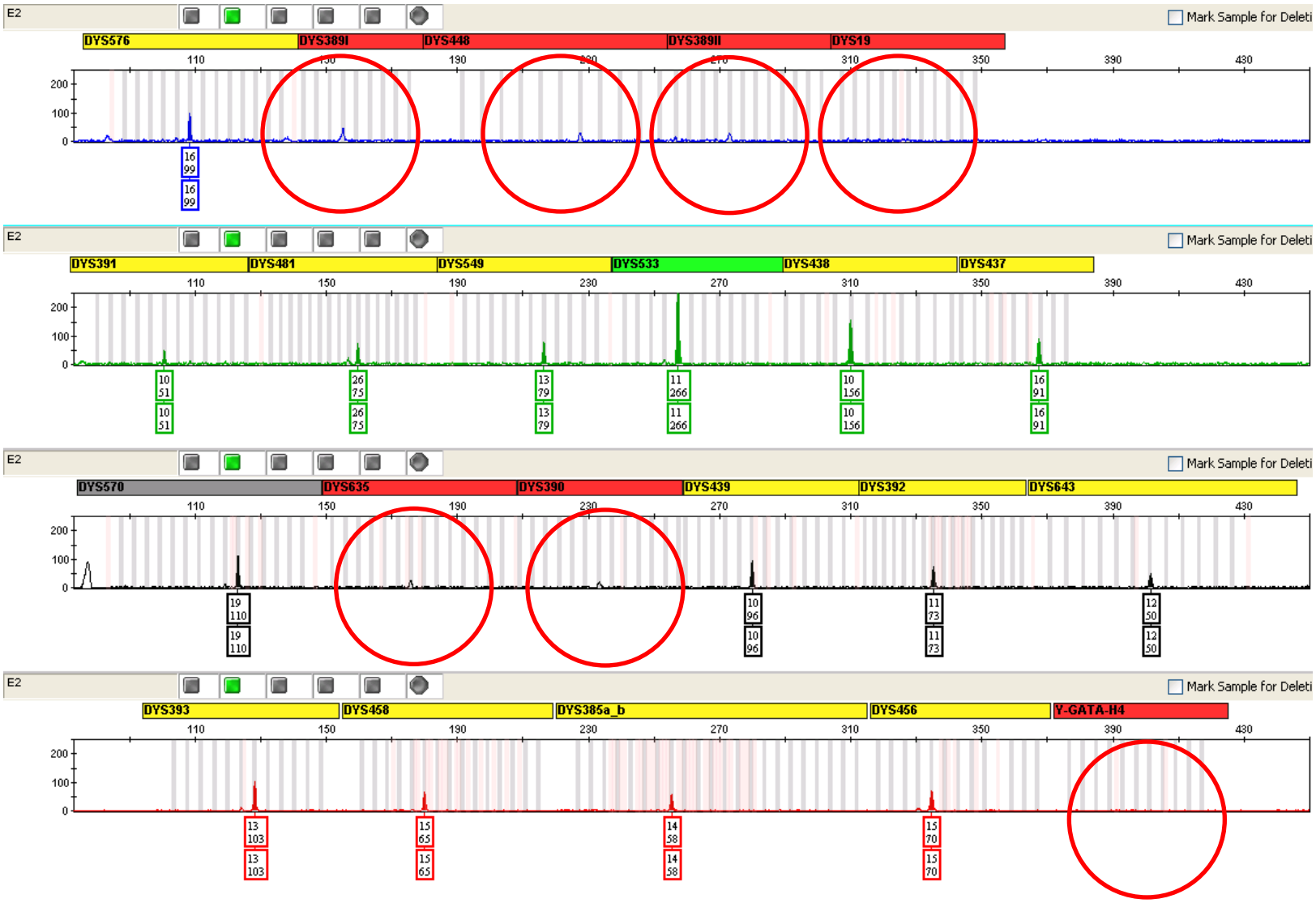
0.0625ngQC2 (Tube D)

Sensitivity Study – Sample E (rep 1)



0.0312ngQC2 (Tube E)

Sensitivity Study – Sample E (rep 2)



0.0312ngQC2 (Tube E)

Performance with related males

Relatives in the NIST Population Samples

Exact matches among the NIST population plates (Y-Filer)

Sample Name	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS385a/b	DYS438	DYS439	DYS437	DYS456	DYS458	DYS635	DYS448	Y-GATA-H4
OT07753	14	13	29	24	11	13	13	11,14	12	12	15	15	17	23	19	12
UC10177	14	13	29	24	11	13	13	11,14	12	12	15	15	17	23	19	12
Y16	17	13	30	21	10	11	14	15,20	11	12	14	15	16	22	21	12
Y17	17	13	30	21	10	11	14	15,20	11	12	14	15	16	22	21	12
ZT79304	16	13	30	21	10	11	13	16,17	11	11	14	15	18	21	22	12
PT84253	16	13	30	21	10	11	13	16,17	11	11	14	15	18	21	22	12
WA29612	14	13	29	23	11	13	12	12,14	12	12	15	15	17	23	19	12
WT52482	14	13	29	23	11	13	12	12,14	12	12	15	15	17	23	19	12
WT52470	14	12	28	23	10	11	13	14,15	10	11	16	14	15	21	20	11
MT94827	14	12												21	20	11
Y27	14	13												23	19	13
Y28	14	13												23	19	13
ZT79994	14	13												23	19	12
ZT79995	14	13												23	19	12
PT84213	14	14												22	20	11
TT51696	14	14												22	20	11
MT94839	15	14	31	25	11	11	13	11,14	11	10	14	15	15	23	20	13
MT97158	15	14	31	25	11	11	13	11,14	11	10	14	15	15	23	20	13
JT51484	17	13	30	21	10	11	14	17,19	11	13	14	16	16	21	21	11
ZT79620	17	13	30	21	10	11	14	17,19	11	13	14	16	16	21	21	11
MT97176	14	13	30	24	11	13	13	11,14	12	12	15	17	16	23	19	12
Y4	14	13	30	24	11	13	13	11,14	12	12	15	17	16	23	19	12
JT51476	14	13	29	25	11	14	13	11,13	12	12	15	17	17	23	18	12
UT58337	14	13	29	25	11	14	13	11,13	12	12	15	17	17	23	18	12
TT51702	14	13	29	24	11	13	13	11,14	12	12	15	16	17	23	19	12
MT97185	14	13	29	24	11	13	13	11,14	12	12	15	16	17	23	19	12
ZT79333	14	13	29	24	11	13	13	11,14	12	12	15	16	17	23	19	12
PT83904	13	15	31	24	9	11	13	13,14	10	10	14	16	18	21	20	12
PT84348	13	15	31	24	9	11	13	13,14	10	10	14	16	18	21	20	12
ZT80369	13	15	31	24	9	11	13	13,14	10	10	14	16	18	21	20	12

12 sets of 2 individuals

2 sets of 3 individuals

Adding 6 markers from PP-Y23

Sample Name	DYS576	DYS570	DYS643	DYS533	DYS481	DYS549
OT07753	18	**17**	10	**12**	**23**	13
UC10177	18	**18**	10	**13**	**22**	13
Y16	14	19	14	11	29	11
Y17	14	19	14	11	29	11
ZT79304	15	19	14	11	28	11
PT84253	15	19	14	11	28	11
WA29612	16	17	10	12	22	**14**
WT52482	16	17	10	12	22	**13**
WT52470	**16**	**23**	12	11	**26**	12
MT94827	**17**	**22**	12	11	**25**	12
Y27	19	17	10	12	22	13
Y28	19	17	10	12	22	13
ZT79994	20	16	10	12	23	12
ZT79995	20	16	10	12	23	12

6 pairs still unresolved

Two Samples from the Population Plates ZT79994 and ZT79995

Match exactly over 23 Y-STRs

ZT79994	Pos	Seq	ZT79995	Pos	Seq
	16172	T - C		16172	T - C
	16219	A - G		16219	A - G
	16311	T - C		16311	T - C
	16344	C -T		16344	C -T
	73	A -G		73	A -G
	263	A- G		263	A- G
	315.1	C		315.1	C
	469	C - T		469	C - T
	523	A-del		523	A-del
	524	C-del		524	C-del

Same mtDNA haplotype (U6a)

Autosomal STR Analysis

Sample Info	CSF1PO 1	CSF1PO 2	D13S317 1	D13S317 2	D16S539 1	D16S539 2	D18S51 1	D18S51 2
ZT79994	9	11	12	14	13	13	13	14
ZT79995	11	12	11	14	11	13	13	14
	D19S433 1	D19S433 2	D21S11 1	D21S11 2	D2S1338 1	D2S1338 2	D3S1358 1	D3S1358 2
ZT79994	13	14	29	30	17	25	16	17
ZT79995	14	16	30	30	17	25	17	18
	D5S818 1	D5S818 2	D7S820 1	D7S820 2	D8S1179 1	D8S1179 2	FGA 1	FGA 2
ZT79994	12	12	7	12	13	13	20	21
ZT79995	13	13	8	12	13	13	20	23
	TH01 1	TH01 2	TPOX 1	TPOX 2	vWA 1	vWA 2	D10S1248	D10S1248
ZT79994	7	9.3	8	8	15	18	14	14
ZT79995	7	9.3	8	11	15	17	14	14
	D12S391	D12S391	D1S1656	D1S1656	D22S1045	D22S1045	D2S441	D2S441
ZT79994	21	21	13	13	15	16	10	11
ZT79995	18.3	20	13	16.3	16	17	10	11
	SE33	SE33	Penta_D	Penta_D	Penta_E	Penta_E	D6S1043	D6S1043
ZT79994	16	17	9	12	13	14	12	18
ZT79995	17	23	11	14	13	14	12	12

24 STR Markers

Kinship Analysis

	Combined
Parent-Child	0
Full Sib	**56327**
Half-Sib*	5692
1st Cousin	264

*Is also the same stat for Aunt/Uncle/Niece/Nephew and Grandparent/Grandchild relationships

Performance with related males

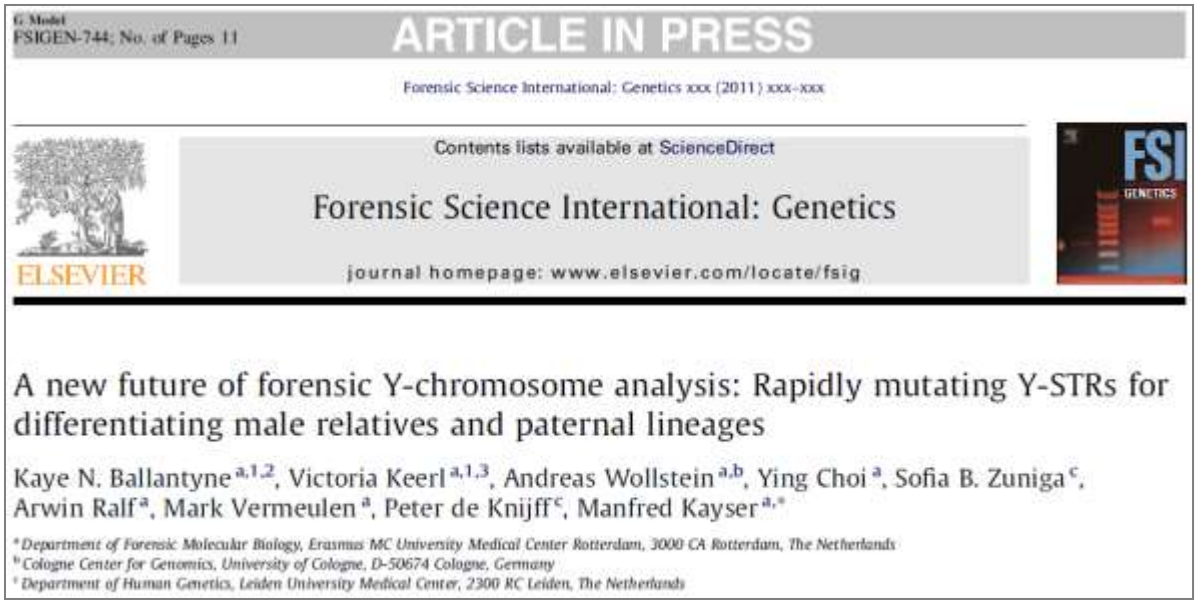
Father-Son Mutation Rates

Father-Son Mutations - Summary

	Meioses	Mutations	
AfAm	85	10	
Asian	101	16	
Caucasian	100	6	
Hispanic	100	12	
Sum	386	44	11.40%

	Father to Son		Father to Son	
	+1 repeat	-1 repeat	+2 repeat	-2 repeat
DYS439	2	4		
DYS389II	3	2		
DYS481	3	2		
DYS570	3	2		
DYS576	2	2		
DYS389I	2	2		
Y-GATA-H4	1	1	1	1
DYS458	2	1		
DYS549	1	1		
DYS635	1	1		
DYS19	1	0		
DYS390	0	1		
DYS643	1	0		
DYS385a	1	0		
DYS448	0	0		
DYS391	0	0		
DYS533	0	0		
DYS438	0	0		
DYS437	0	0		
DYS392	0	0		
DYS393	0	0		
DYS385b	0	0		
DYS456	0	0		
(sum)	23	23	1	1

	Mutations
DYS439	6
DYS389II	5
DYS481	5
→ **DYS570**	5
→ **DYS576**	4
DYS389I	4
Y-GATA-H4	4
DYS458	3
DYS549	2
DYS635	2
DYS19	1
DYS390	1
DYS643	1
DYS385a	1
DYS448	0
DYS391	0
DYS533	0
DYS438	0
DYS437	0
DYS392	0
DYS393	0
DYS385b	0
DYS456	0



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FSIGEN-744; No. of Pages 11

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Forensic Science International: Genetics xxx (2011) xxx–xxx

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Forensic Science International: Genetics

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

A new future of forensic Y-chromosome analysis: Rapidly mutating Y-STRs for differentiating male relatives and paternal lineages

Kaye N. Ballantyne[a,1,2], Victoria Keerl[a,1,3], Andreas Wollstein[a,b], Ying Choi[a], Sofia B. Zuniga[c], Arwin Ralf[a], Mark Vermeulen[a], Peter de Knijff[c], Manfred Kayser[a,*]

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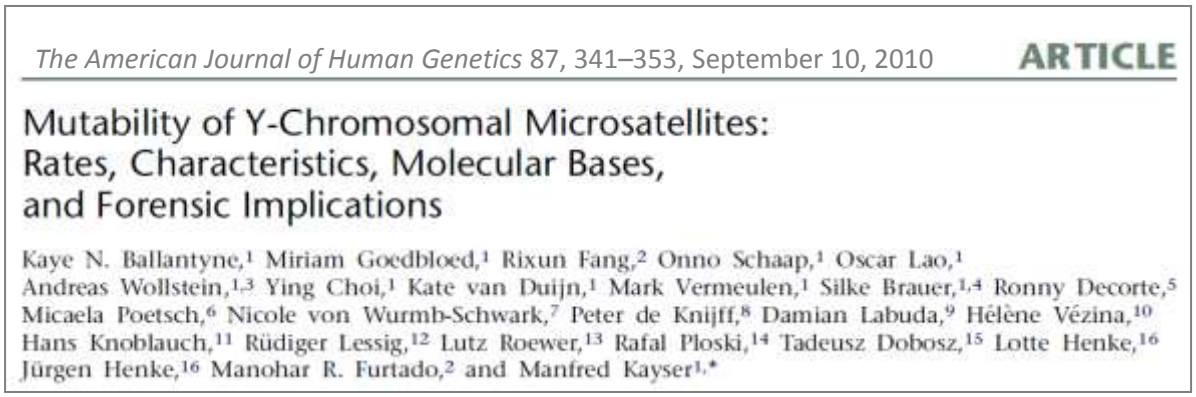


The American Journal of Human Genetics 87, 341–353, September 10, 2010 **ARTICLE**

Mutability of Y-Chromosomal Microsatellites: Rates, Characteristics, Molecular Bases, and Forensic Implications

Kaye N. Ballantyne,[1] Miriam Goedbloed,[1] Rixun Fang,[2] Onno Schaap,[1] Oscar Lao,[1] Andreas Wollstein,[1,3] Ying Choi,[1] Kate van Duijn,[1] Mark Vermeulen,[1] Silke Brauer,[1,4] Ronny Decorte,[5] Micaela Poetsch,[6] Nicole von Wurmb-Schwark,[7] Peter de Knijff,[8] Damian Labuda,[9] Hélène Vézina,[10] Hans Knoblauch,[11] Rüdiger Lessig,[12] Lutz Roewer,[13] Rafal Ploski,[14] Tadeusz Dobosz,[15] Lotte Henke,[16] Jürgen Henke,[16] Manohar R. Furtado,[2] and Manfred Kayser[1,*]

Yfiler Plus Kit

Released August 2014

Yfiler-Plus Kit Performance

Sensitivity

Sensitivity Experiment

Full reaction volumes (25 ul):

- 0.5 ng single amp
- 0.25 ng single amp
- 0.125 ng duplicate amp
- 0.0625 ng duplication amp
- 0.03125 ng duplicate amp

Half reaction volumes (12.5 ul):

- 0.5 ng duplicate amp
- 0.25 ng duplicate amp
- 0.125 ng duplicate amp
- 0.0625 ng duplication amp
- 0.03125 ng duplicate amp

Sensitivity Experiment

FULL REACTION VOLUME (25 ul)								
Marker	0.03125 ng		0.0625 ng		0.125 ng		0.25 ng	0.5 ng
DYS576		184	222	259	491	574	491	2308
DYS389I	96	151	344	318	1083	895	1603	2581
DYS635	195	153	198	152	379	473	1341	2481
DYS389II		115	279	176	725	648	1036	1847
DYS627	142	373	165	140	1257	591	1122	3639
DYS460		463	304	129	263	328	827	2786
DYS458		404	51	261	466	581	1091	3107
DYS19		173	220	143	335	525	1250	2697
GATA_H4	97		159	226	482	153	1896	3212
DYS448	91		154	204	500	196	2255	2489
DYS391	342		231	51	1169	721	2470	3789
DYS456	330	186	269	115	732	241	1524	2143
DYS390		232	123	87	225	331	478	1664
DYS438	144	166	207	205	557	622	999	3563
DYS392		209	53	129	700	156	840	2293
DYS518	232	118	145	185	638	411	619	2322
DYS570		92	163	300	987	327	1673	3398
DYS437	83	248	364	152	749	485	1429	2494
DYS385	109	364	303	135	525	545	1261	2608
DYS385			130		383		1539	1912
DYS449	57	91	321	218	713	482	846	3598
DYS393			485	126	172	389	2184	2353
DYS439		278	130	108	916	313	668	3488
DYS481	254		375	218	1022	588	1707	3605
DYF387S1		203	208	169	413	487	1530	2173
DYF387S1			197	192	696	428	1050	2846
DYS533	209		280	93	942	456	1987	2772

≥ 175 RFU
< 175 RFU

Sensitivity Experiment

HALF REACTION VOLUME (12.5 ul)										
Marker	0.03125 ng		0.0625 ng		0.125 ng		0.25 ng		0.5 ng	
DYS576	84	404	740	484	2271	551	3580	1773	4986	8103
DYS389I		1080	1285	2442	1064	2389	3992	2964	8646	12160
DYS635			331	911	1540	1950	3991	965	7439	5402
DYS389II		1055	717	2561	1026	1985	3080	2211	4781	8069
DYS627			1175	876	1340	2054	2944	2168	12000	4860
DYS460		785	605	1469	2961	2146	4028	2445	3443	5921
DYS458		394	262	2099	2616	1013	4972	2265	5029	6217
DYS19		835	351	1283	1886	1464	2492	2473	4532	4871
GATA_H4		245	475	1690	1766	1274	3980	1493	2813	5701
DYS448			594	1842	1131	1611	4011	2042	3175	5857
DYS391	199	398	1140	398	2861	1632	3359	3067	6691	10923
DYS456	122		121	920	1280	1391	2803	851	3190	6202
DYS390			214	673	771	1428	2059	1212	3429	4472
DYS438	321	155	656	717	2163	1269	2201	1646	5038	6472
DYS392	153		1306	446	1853	858	2242	1960	5151	5722
DYS518	367	262	844	280	771	1661	1657	997	3357	4083
DYS570	196	592	376	1165	1754	1551	3068	2200	4346	7802
DYS437	145	1152	404	325	1424	1582	6373	1199	6266	7528
DYS385	93	613	630	1672	2218	1764	3592	1671	3160	5944
DYS385		197	726	585	1434	894	3548	2302	3706	5323
DYS449	79	112	420	1727	2309	2752	4809	2858	5308	5506
DYS393	77	824	719	621	2240	1716	3786	2111	4809	6484
DYS439		286	841	1266	1449	2781	2165	2468	4563	5620
DYS481	83	618	689	1368	3258	1737	3684	3348	7554	7676
DYF387S1	51	296	842	999	2175	1016	3089	1306	3782	8096
DYF387S1		448	499	1447	1655	2940	2757	2400	4758	4924
DYS533		527	494	4033	2288	952	2599	1869	5163	6919

≥ 175 RFU
< 175 RFU

Yfiler-Plus Kit Performance

F:M Mixtures

High Female [DNA] Experiment

Looking for:

- Artifacts
- Inhibition

Three male samples (B, C, F) were each combined with same female

Input female DNA was constant at approximately 200 ng

Input male DNA at four levels in the range of approx. 1 ng – 0.05 ng

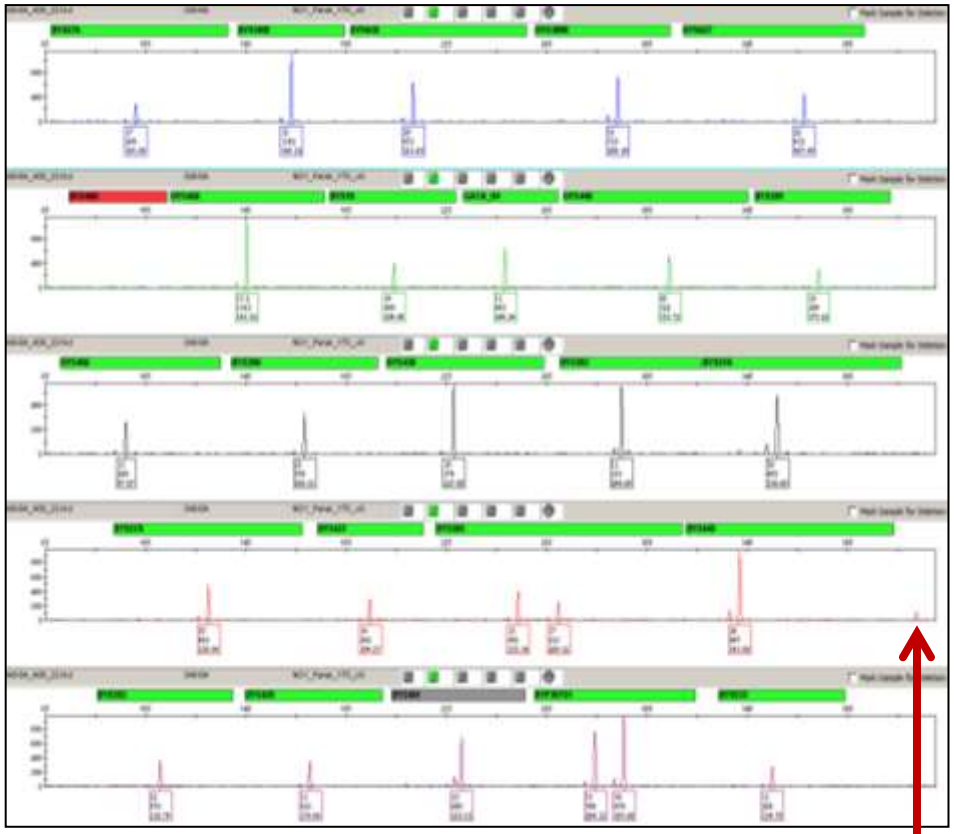
Male only samples for comparison

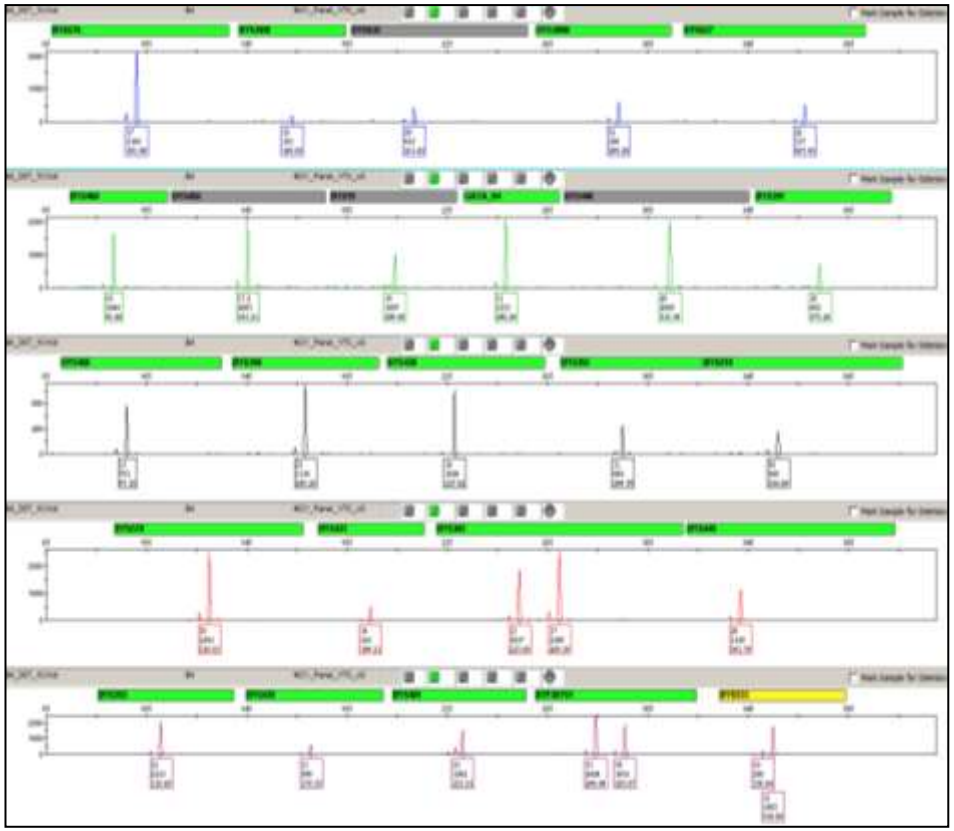
24 samples total

200 : 1  200 ng + 1 ng	 1 ng
700 : 1  200 ng + 0.3 ng	 0.3 ng
2000 : 1  200 ng + 0.1 ng	 0.1 ng
4000 : 1  200 ng + 0.05 ng	 0.05 ng

High Level Female Experiment

Male Sample B





Artifact?

4000 : 1

(approx. 200 ng female + 0.05 ng male)

(approx. 0.05 ng)


349-B1_E08_14.hid
349-B1
NGY_Panel_VTS_v6
Mark Sample for Deletion
330
350
370
390
410
430
450
240
200
160
120
80
40
0
DYS449
200 : 1
26
4291
341.81
349-B2_F08_17.hid
349-B2
NGY_Panel_VTS_v6
Mark Sample for Deletion
700 : 1
26
5173
341.80
349-B3_G08_20.hid
349-B3
NGY_Panel_VTS_v6
Mark Sample for Deletion
2000 : 1
26
763
341.80
349-B4_H08_23.hid
349-B4
NGY_Panel_VTS_v6
Mark Sample for Deletion
4000 : 1
26
967
341.80


B1_A07_01.hid
B1
NGY_Panel_VTS_v6
Mark Sample for Deletion
DYS449
330
350
370
390
410
430
450
240
200
160
120
80
40
0
26
12420
341.79
B2_B07_04.hid
B2
NGY_Panel_VTS_v6
Mark Sample for Deletion
26
8951
341.80
B3_C07_07.hid
B3
NGY_Panel_VTS_v6
Mark Sample for Deletion
26
2009
341.80
B4_D07_10.hid
B4
NGY_Panel_VTS_v6
Mark Sample for Deletion
26
1159
341.79


349-B1_E08_14.hid
349-B1
NGY_Panel_VTS_v6
Mark Sample for Deletion
DYS449
200 : 1
26
4291
341.81
349-B2_F08_17.hid
349-B2
NGY_Panel_VTS_v6
Mark Sample for Deletion
700 : 1
26
5173
341.80
349-B3_G08_20.hid
349-B3
NGY_Panel_VTS_v6
Mark Sample for Deletion
2000 : 1
26
763
341.80
349-B4_H08_23.hid
349-B4
NGY_Panel_VTS_v6
Mark Sample for Deletion
4000 : 1
“TAZ 413” artifact
26
967
341.80

Performance with unrelated males

NIST U.S. Population Samples

Discrimination Capacity

- is a measure of the number of unique haplotypes in a given population

$$DC = \frac{\#H}{N}$$

# of Haplotypes

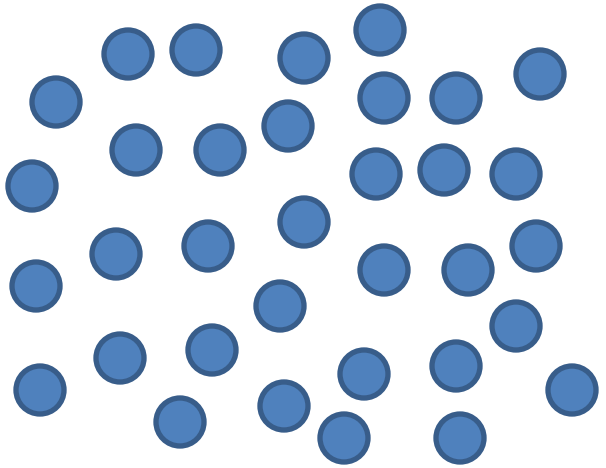
Population size

Results so far (582 individuals)

582 Males

Yfiler Plus

27 Y-STRs

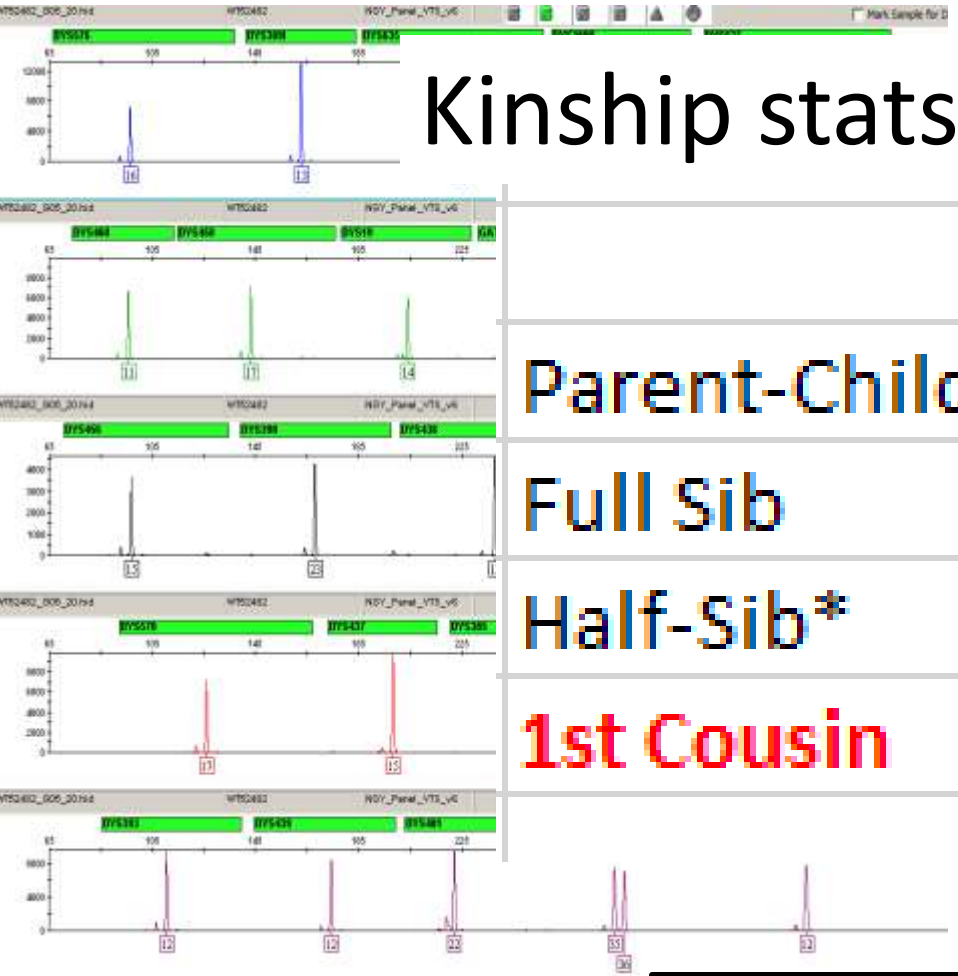


580 Unique Haplotypes

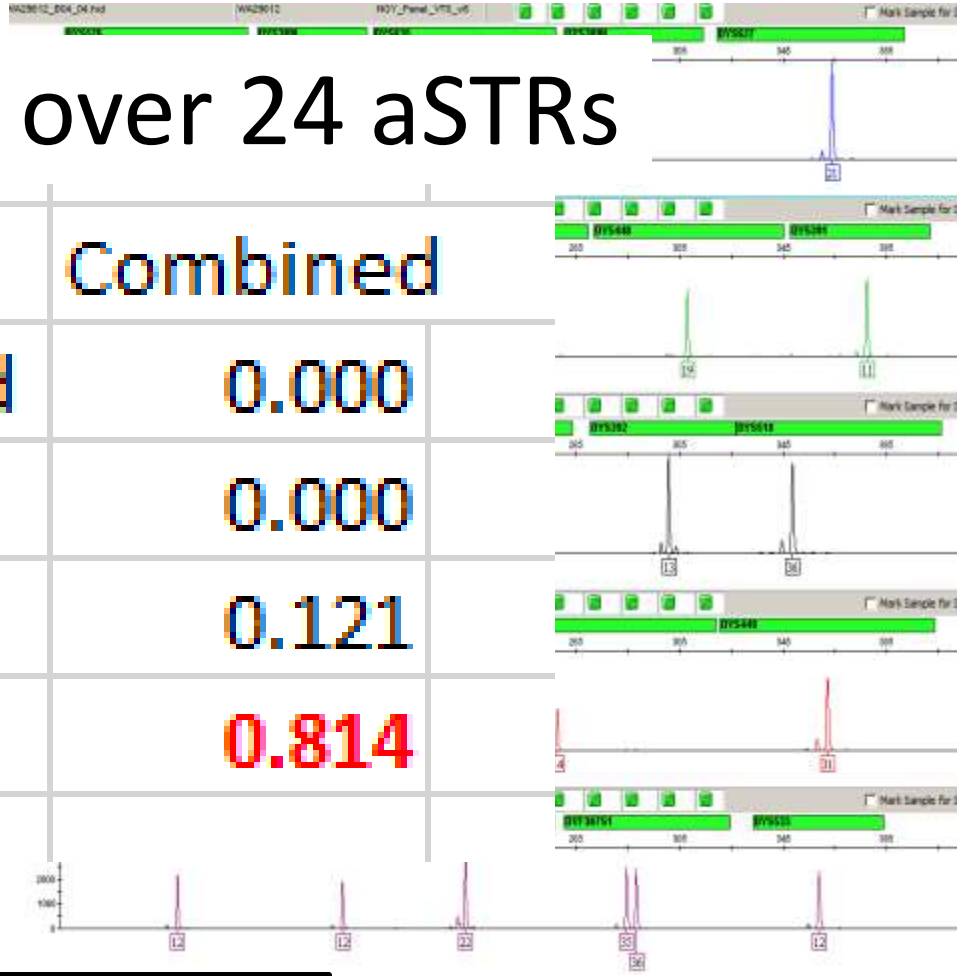
1 Shared Haplotype

DC = 0.998

Kinship stats over 24 aSTRs



	Combined
Parent-Child	0.000
Full Sib	0.000
Half-Sib*	0.121
1st Cousin	0.814



Two Caucasians

Same Haplotype at

Yfiler Plus Loci

N = 948 males	PowerPlex Y
# haplotypes	**816**
discrimination capacity	0.8608

# times haplotype observed	PPY (12 loci)
1	751
2	42
3	12
4	4
5	2
6	2
7	.
8	1
9	.
10	.
11	1
12	.
13	.
14	.
15	.
16	.
17	.
18	.
19	.
20	1

Number of unique and shared haplotypes observed with various combinations of Y-STR loci across 948 U.S. population samples

N = 948 males	Yfiler	New Loci*	Yfiler Plus*
# haplotypes	**930**	**945**	**946**
discrimination capacity	0.9810	0.9842	0.9979
# times haplotype observed	Yfiler (17 loci)	New Loci* (10 loci)	Yfiler Plus (27 loci)
1	916	918	944
2	11	15	2
3	2	.	.
4	1	.	.
5	.	.	.
6	.	.	.
7	.	.	.
8	.	.	.
9	.	.	.
10	.	.	.
11	.	.	.
12	.	.	.
13	.	.	.
14	.	.	.
15	.	.	.
16	.	.	.
17	.	.	.
18	.	.	.
19	.	.	.
20	.	.	.

The new loci alone perform slightly better than Yfiler

Disadvantages of the Y-Chromosome

- Loci are not independent of one another and therefore rare random match probabilities cannot be generated with the product rule; must use haplotypes (combination of alleles observed at all tested loci)

- Not as informative as autosomal STR results
  - **More like addition (10 + 10 + 10 = 30) than multiplication (10 x 10 x 10 = 1,000)**

- **Paternal lineages possess the same Y-STR haplotype** (barring mutation) and thus fathers, sons, brothers, uncles, and paternal cousins cannot be distinguished from one another

Rapidly Mutating (RM) Y-STRs

Trying to separate

close male relatives

Rapidly Mutating Y-STRs

The American Journal of Human Genetics 87, 341–353, September 10, 2010

ARTICLE

Mutability of Y-Chromosomal Microsatellites: Rates, Characteristics, Molecular Bases, and Forensic Implications

Kaye N. Ballantyne,[1] Miriam Goedbloed,[1] Rixun Fang,[2] Onno Schaap,[1] Oscar Lao,[1] Andreas Wollstein,[1,3] Ying Choi,[1] Kate van Duijn,[1] Mark Vermeulen,[1] Silke Brauer,[1,4] Ronny Decorte,[5] Micaela Poetsch,[6] Nicole von Wurmb-Schwark,[7] Peter de Knijff,[8] Damian Labuda,[9] Hélène Vézina,[10] Hans Knoblauch,[11] Rüdiger Lessig,[12] Lutz Roewer,[13] Rafal Ploski,[14] Tadeusz Dobosz,[15] Lotte Henke,[16] Jürgen Henke,[16] Manohar R. Furtado,[2] and Manfred Kayser[1,*]

Manfred Kayser

13 markers evaluated

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A new future of forensic Y-chromosome analysis: Rapidly mutating Y-STRs for differentiating male relatives and paternal lineages

Kaye N. Ballantyne [a,1,2], Victoria Keerl [a,1,3], Andreas Wollstein [a,b], Ying Choi [a], Sofia B. Zuniga [c], Arwin Ralf [a], Mark Vermeulen [a], Peter de Knijff [c], Manfred Kayser [a,*]

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[b] Cologne Center for Genomics, University of Cologne, D-50674 Cologne, Germany
[c] Department of Human Genetics, Leiden University Medical Center, 2300 RC Leiden, The Netherlands

Using Y-STRs with a higher mutation rate, father-son and brother pairs can sometimes be distinguished

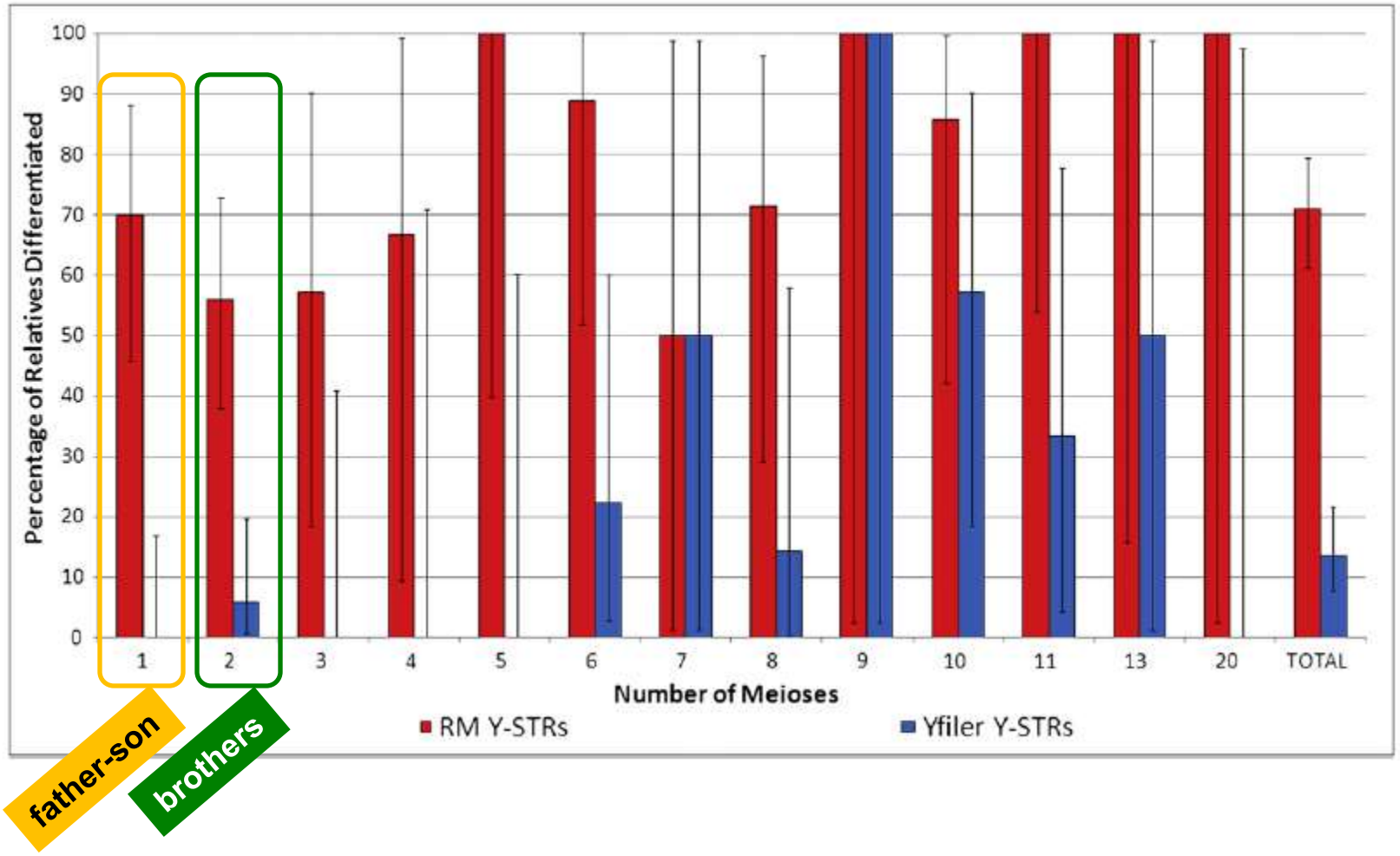


Figure 4. Male Relative Differentiation with Newly Identified 13 RM Y-STRs and Commonly Used 17 Yfiler Y-STRs

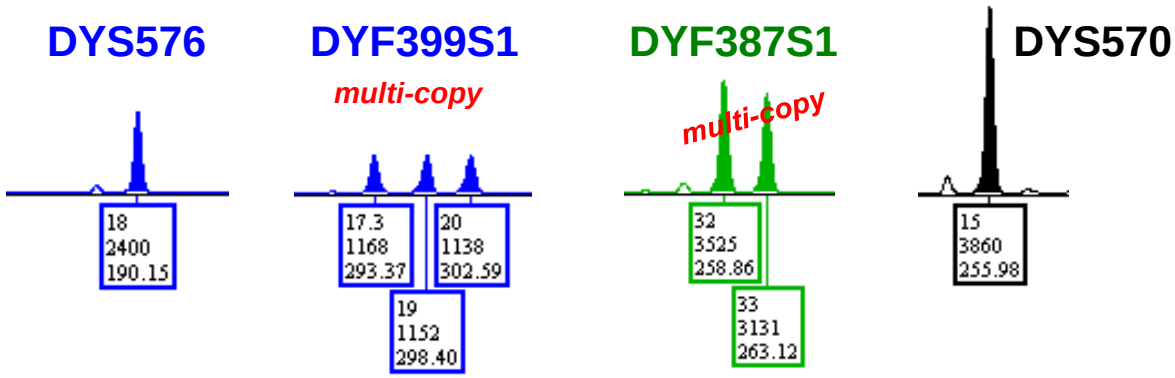
Results from differentiating between male relatives from analyzing 103 pairs from 80 male pedigrees, sorted according to the number of generations separating pedigree members, based on 13 RM Y-STRs (in red) and 17 Yfiler Y-STRs (in blue). Error bars represent 95% binomial confidence intervals. Note that these samples are independent from the father-son pairs initially used to establish the Y-STR mutation rates.

The American Journal of Human Genetics 87, 341–353, September 10, 2010

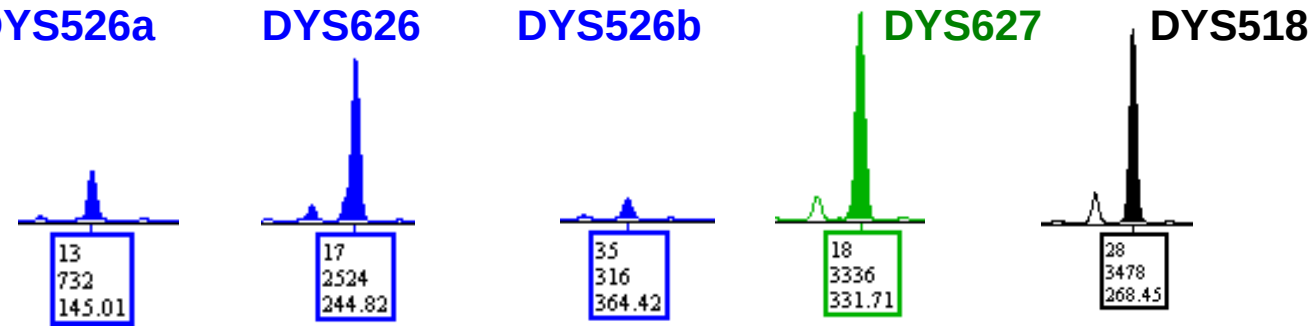
Rapidly Mutating (RM) Y-STRs

NIST supplied data from 1,296 U.S. samples (634 population + 331 father/son pairs)
to RM Y-STR Study Group led by Manfred Kayser

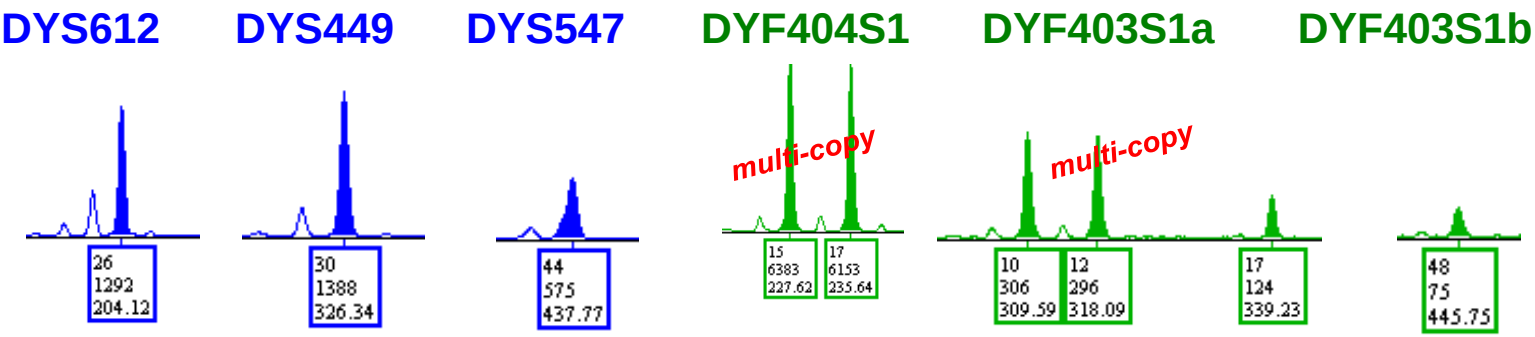
RM Y-STR
Multiplex 1



RM Y-STR
Multiplex 2



RM Y-STR
Multiplex 3

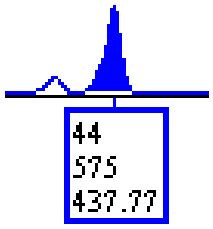


Why do these markers mutate “rapidly”?

Markers in Yfiler Plus

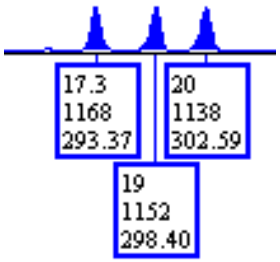
Locus	(average mutation rate)
DYS449	(1.2%)
DYS518	(1.8%)
DYS547	(2.4%)
DYS570	(1.2%)
DYS576	(1.4%)
DYS612	(1.4%)
DYS626	(1.2%)
DYS627	(1.2%)
DYF387S1	(1.6%)
DYF399S1	(7.7%)
DYF403S1 a/b	(3.1/1.2%)
DYF404S1	(1.3%)
DYS526 a/b	(1.3%)

“Large” number of repeats



DYS547

Multi-copy Markers



DYF399S1

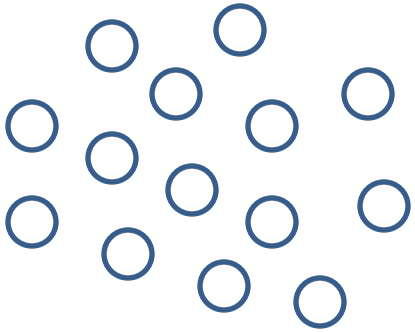
DYS458 (0.64%) is highest in Yfiler loci where average is ~0.2%

Gene Diversity

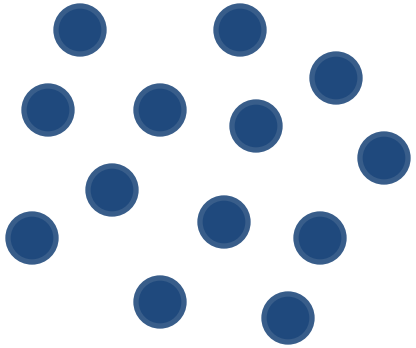
- is a measure of the uniqueness of a particular marker in a given population

$$GD = (1 - \sum_i x_i^2)$$

Relative frequency of each allele



Marker Y



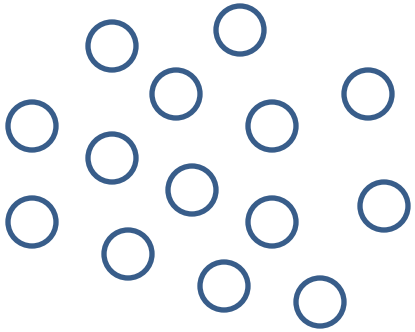
1 type = 100%

N = 100

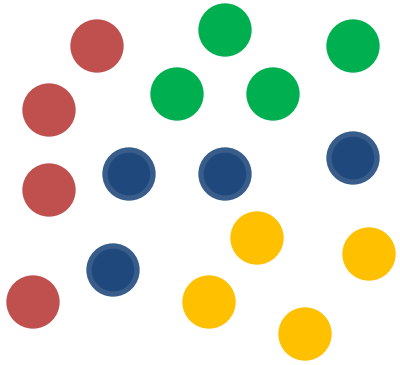
$$GD = (1 - \underbrace{\sum_i x_i^2}_{})$$

0

DC = 1/100 = 0.01



Marker Y



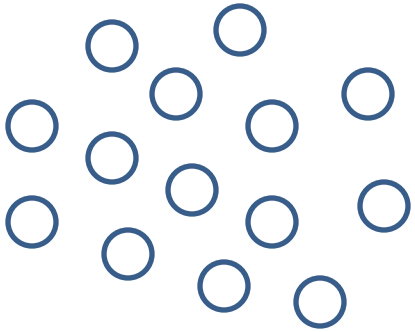
4 types = 25%

N = 100

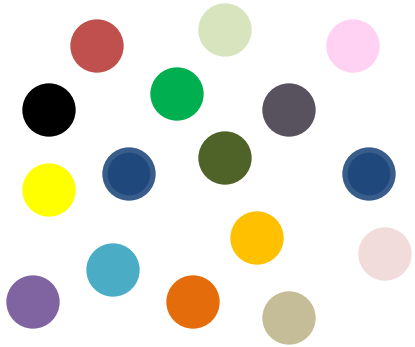
$$GD = (1 - \sum_i x_i^2)$$

0.75

DC = 4/100 = 0.04



Marker Y



100 types = 0%

N = 100

$$GD = (1 - \sum_i x_i^2)$$

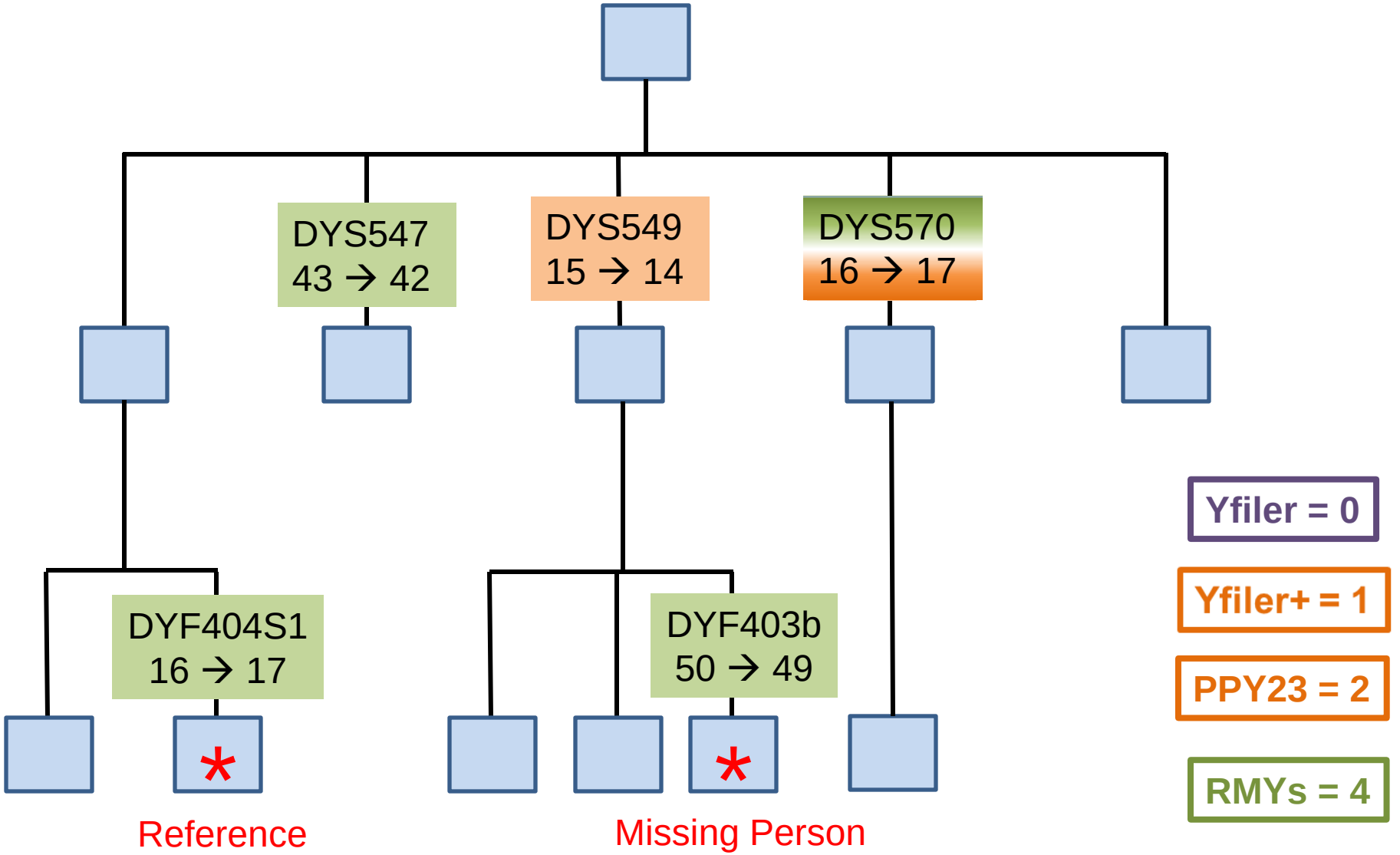
0.99

DC = 100/100 = 1.0

Gene Diversity of the YFP Markers

Locus	Gene Diversity
DYF387S1a/b	0.919
DYS385a/b	0.919
DYS627	0.8584
DYS449	0.8315
DYS481	0.82
DYS518	0.8196
DYS576	0.7954
DYS570	0.7852
DYS458	0.7671
DYS390	0.7645
DYS635	0.7457
DYS389II	0.7375
DYS448	0.7202
DYS456	0.7015
DYS438	0.693
DYS19	0.6681
DYS439	0.6533
DYS533	0.6372
DYS437	0.6305
GATA_H4	0.6026
DYS392	0.6001
DYS460	0.5736
DYS389I	0.548
DYS391	0.5352
DYS393	0.4749

Y-STR mutations in a Paternal Lineage



Mutation Rate Information

Meioses	Mutations	Group
63	15	AfAm
89	25	Asian
91	11	Caucasian
88	20	Hispanic
331	71	total
		(21.4%)

+1 Repeat (Son)	-1 Repeat (Son)	
8	6	AfAm
11	13	Asian
5	6	Caucasian
8	12	Hispanic
+2 Repeat (Son)	-2 Repeat (Son)	
0	1	AfAm
1	0	Asian
0	0	Caucasian
0	0	Hispanic

Marker	# of Mutations
DYF399S1	**15**
DYF403S1a/b	**11**
DYS627	**7**
DYS612	**7**
DYS518	**6**
DYS570	**5**
DYS626	**5**
DYS547	**4**
DYS526a/b	**3**
DYS576	**3**
DYS449	**3**
DYF404S1	**1**
DYF387S1	**1**

Interpretational Issues

- We will need to move away from simply “excluding” based upon a number of discordant markers.
- A Likelihood Ratio can provide weight to the evidence based upon competing propositions.
- This will require information on the haplotype frequency and mutation rate data.

Relating two deep-rooted pedigrees from Central Germany by high-resolution Y-STR haplotyping

Manfred Kayser [a,*], Mark Vermeulen [a,b], Hans Knoblauch [c], Herbert Schuster [d], Michael Krawczak [e], Lutz Roewer [f]

Forensic Science International: Genetics 1 (2007) 125–128.

Summary

- Rapidly Mutating Y-STRs are highly diverse markers that can discriminate common haplotypes and close relatives.

- These markers may create interpretational issues for paternity/missing persons cases, but LRs can be useful for evaluating these situations .

- The Yfiler Plus kit is sensitive and provides improved haplotype discrimination.

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