

“ESTUDIO DE POLIMORFISMOS DE ADN EN MANCHAS DE SANGRE Y OTRAS MUESTRAS BIOLÓGICAS”

CROMOSOMAS SEXUALES

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Cuerpo Médico Forense
Poder Judicial de Mendoza
Mendoza - Argentina

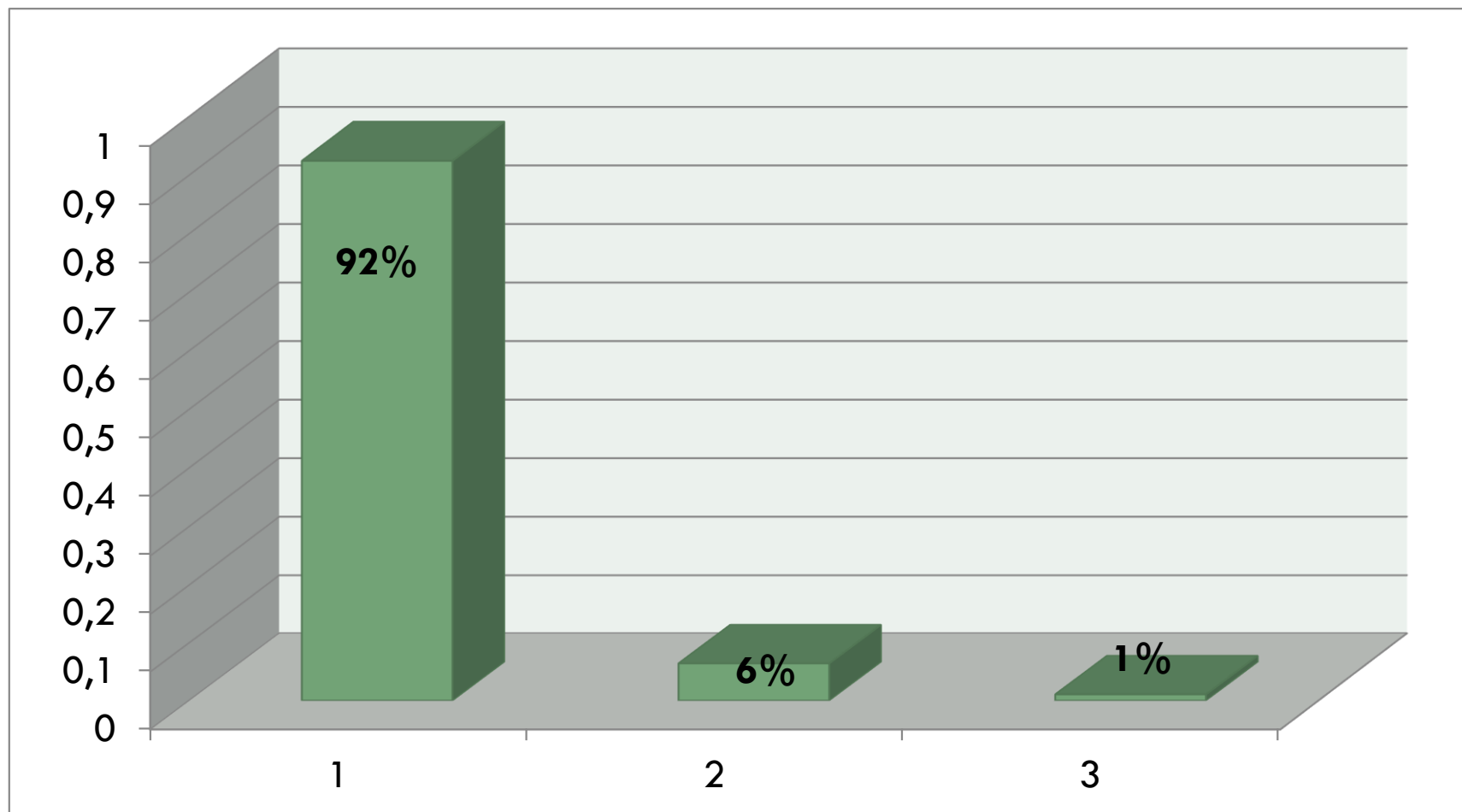
ghep-isfg

XX JORNADAS del GHEP-ISFG

31 de Agosto – 1 de Septiembre de 2015, Cracovia, Polonia

Nro. de kits utilizados

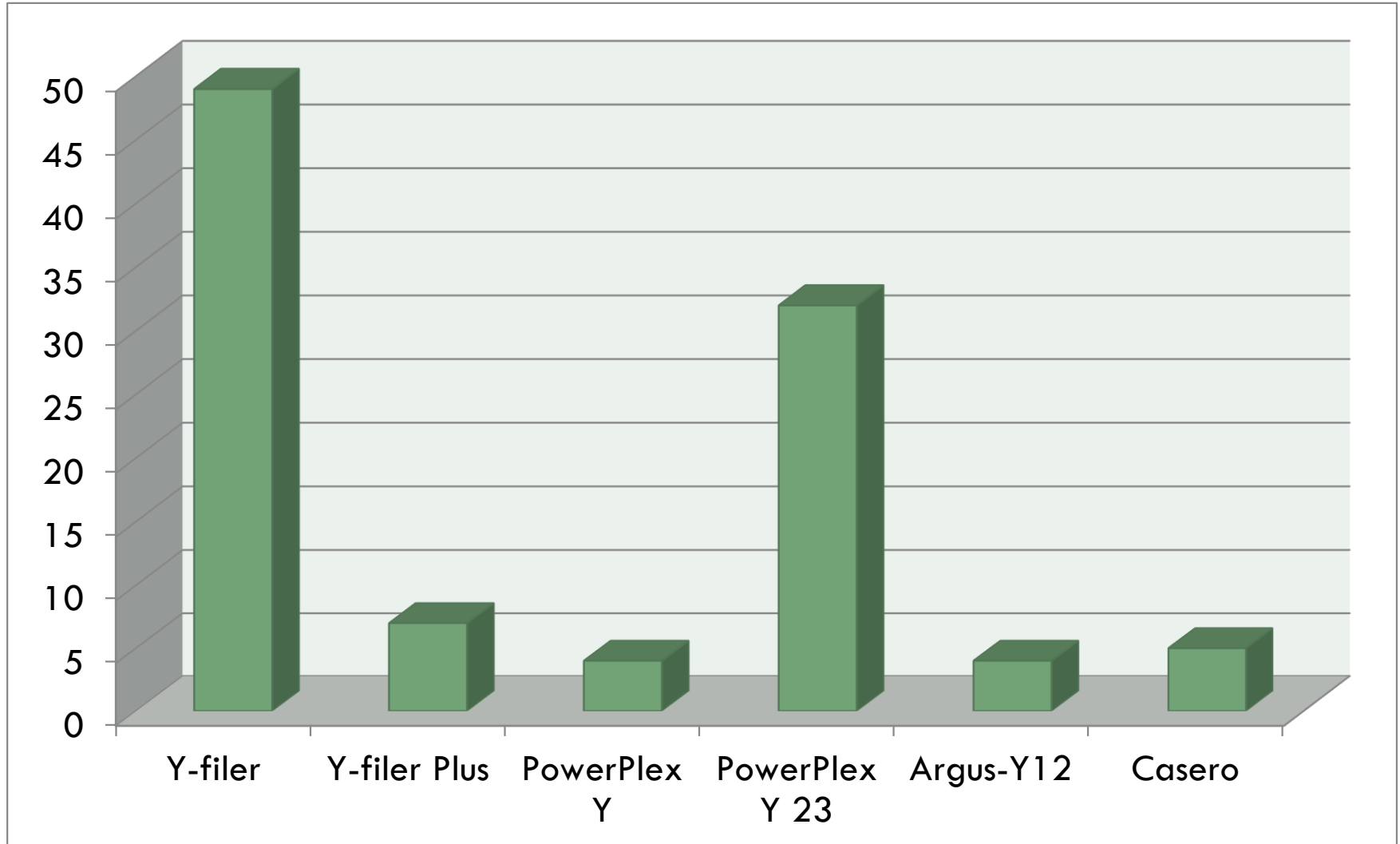
2



Mínimo de marcadores analizados 8; Máximo de marcadores analizados 27

Kits utilizados Y-STRs

3



CROMOSOMA Y MÓDULO BÁSICO

Participación Básico

5

121 Laboratorios
analizan Aut-STRs

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graph TD; A[121 Laboratorios analizan Aut-STRs] --> B[76,86% (93) analizan Y-STRs  
(en 2014 fue un 72,22%)]; A --> C[29,76% (36) analizan X-STRs  
(en 2014 fue un 32,54%)];
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76,86% (93) analizan
Y-STRs
(en 2014 fue un 72,22%)

29,76% (36) analizan
X-STRs
(en 2014 fue un 32,54%)

M2

6

Marcador/Marker	M2	N	n	% Consenso
DYS_456	15	82	80	97,56
DYS_389_I	12	93	93	100
DYS_390	23	92	92	100
DYS_389_II	31	91	91	100
DYS_458	18	82	82	100
DYS_19	13	90	90	100
DYS_385	16-17	93	93	100
DYS_393	13	93	93	100
DYS_391	10	93	91	97,85
DYS_439_GATA_A4	12	91	91	100
DYS_635_GATA_C4	22	85	85	100
DYS_392	11	92	91	98,91
GATA_H4	9	83	82	98,8
DYS_437	14	91	91	100
DYS_438	10	92	92	100
DYS_448	20	82	82	100
DYS_460_GATA_A71	11	11	11	100
DYS_576	19	36	36	100
DYS_481	27	35	35	100
DYS_549	11	31	31	100
DYS_533	10	36	35	97,22
DYS_570	20	36	36	100
DYS_643	12	30	30	100

Total N= 1640
n= 1633 (99,57%)

Errores= 7 (0,43%)

3 errores (43%) concentrados en 1 laboratorio 303299

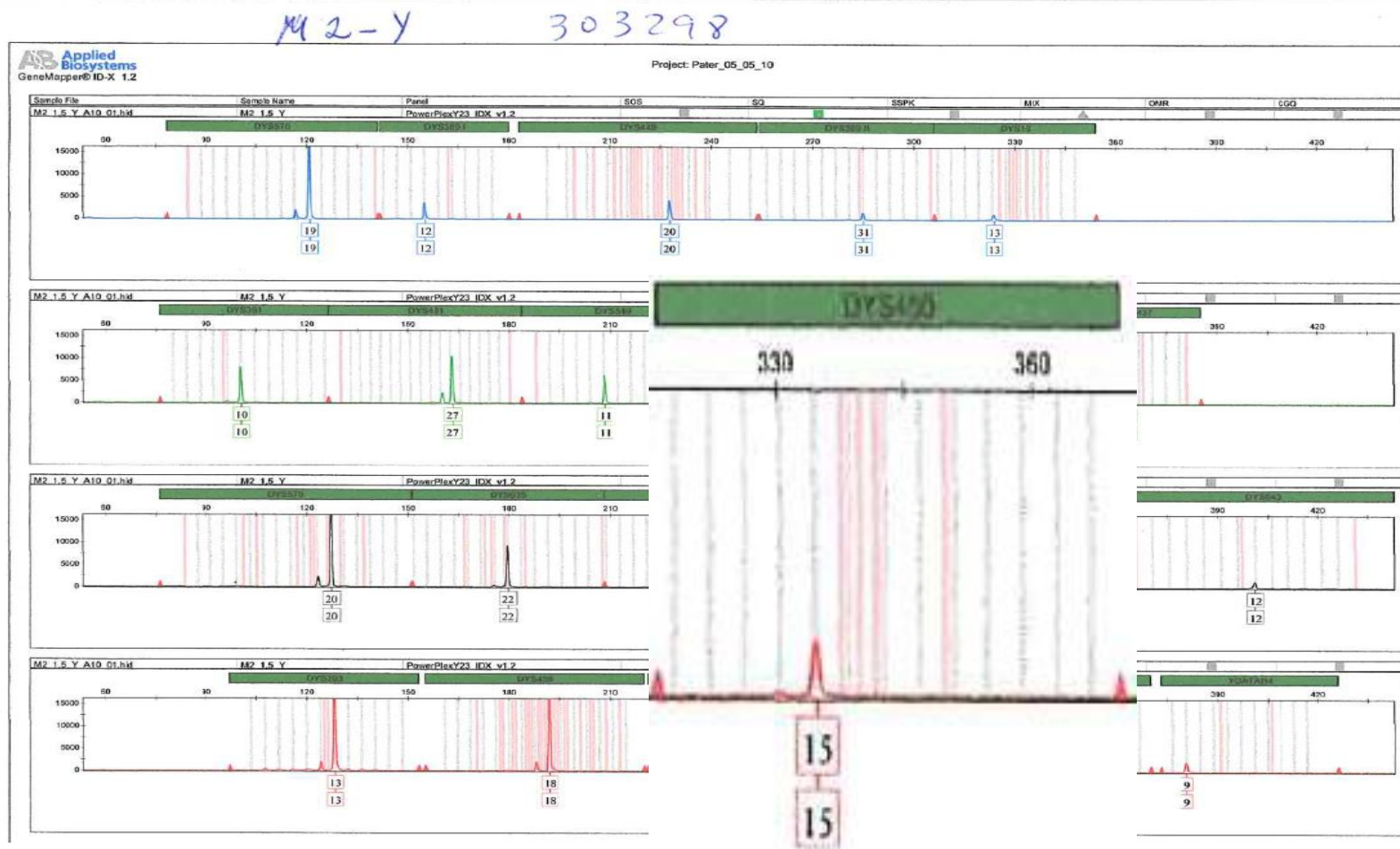
1 error de transcripción 303298

1 error de transcripción 303299 en DYS533

1 error de nomenclatura 303268 en GATA_H4

303298 informa 13 en DYS456

7

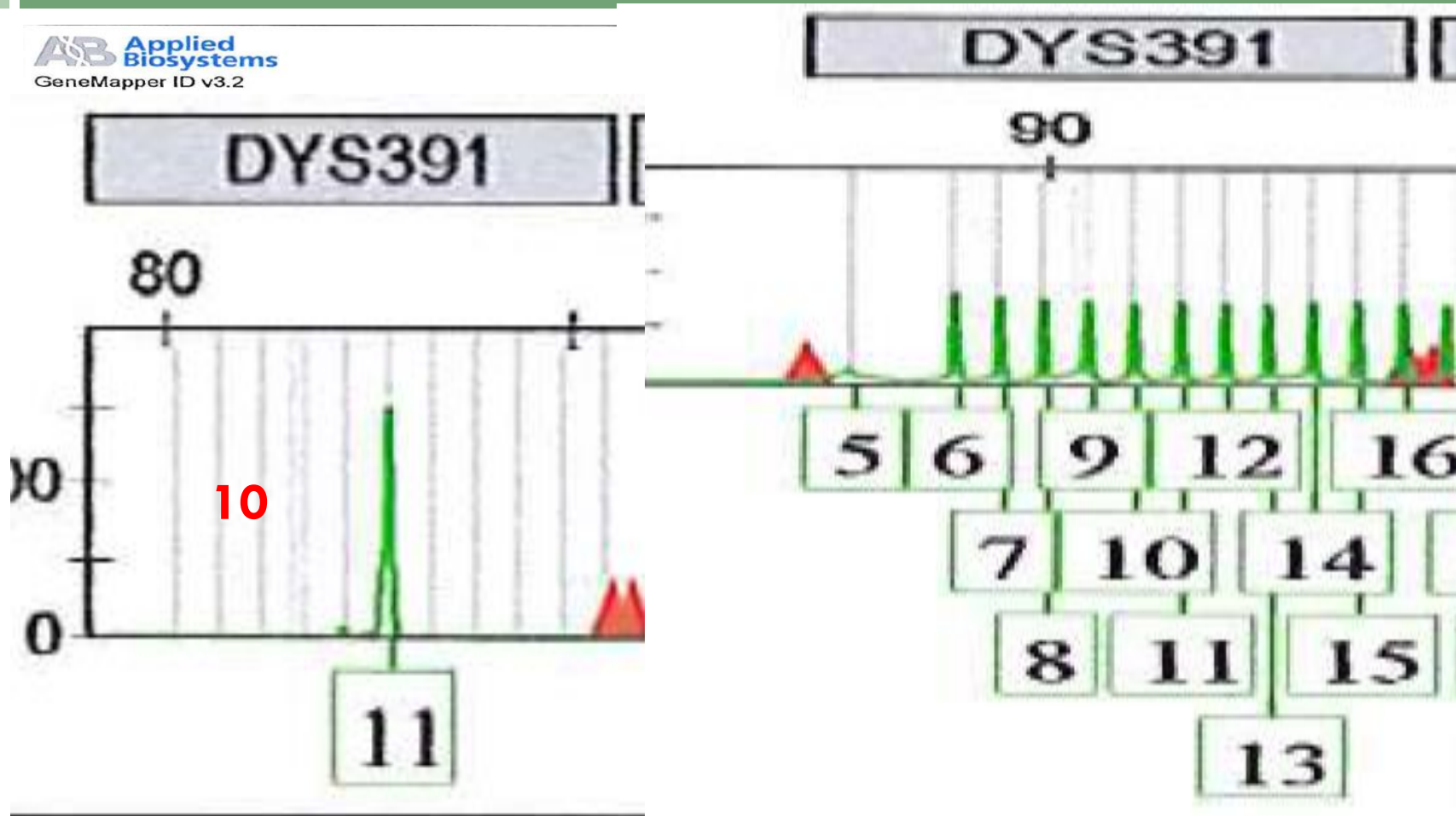


8



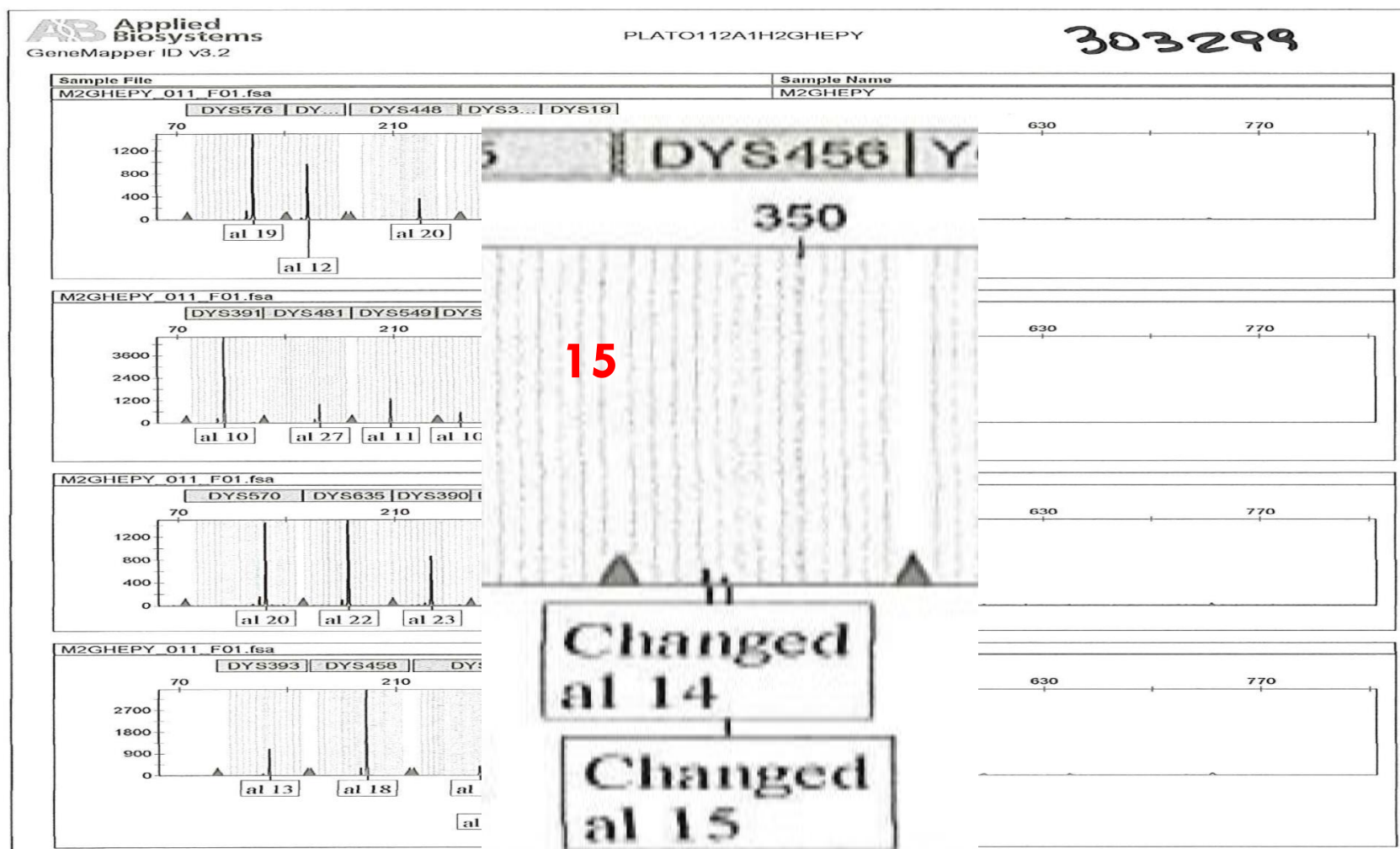
303335 informa 11 en DYS391

9



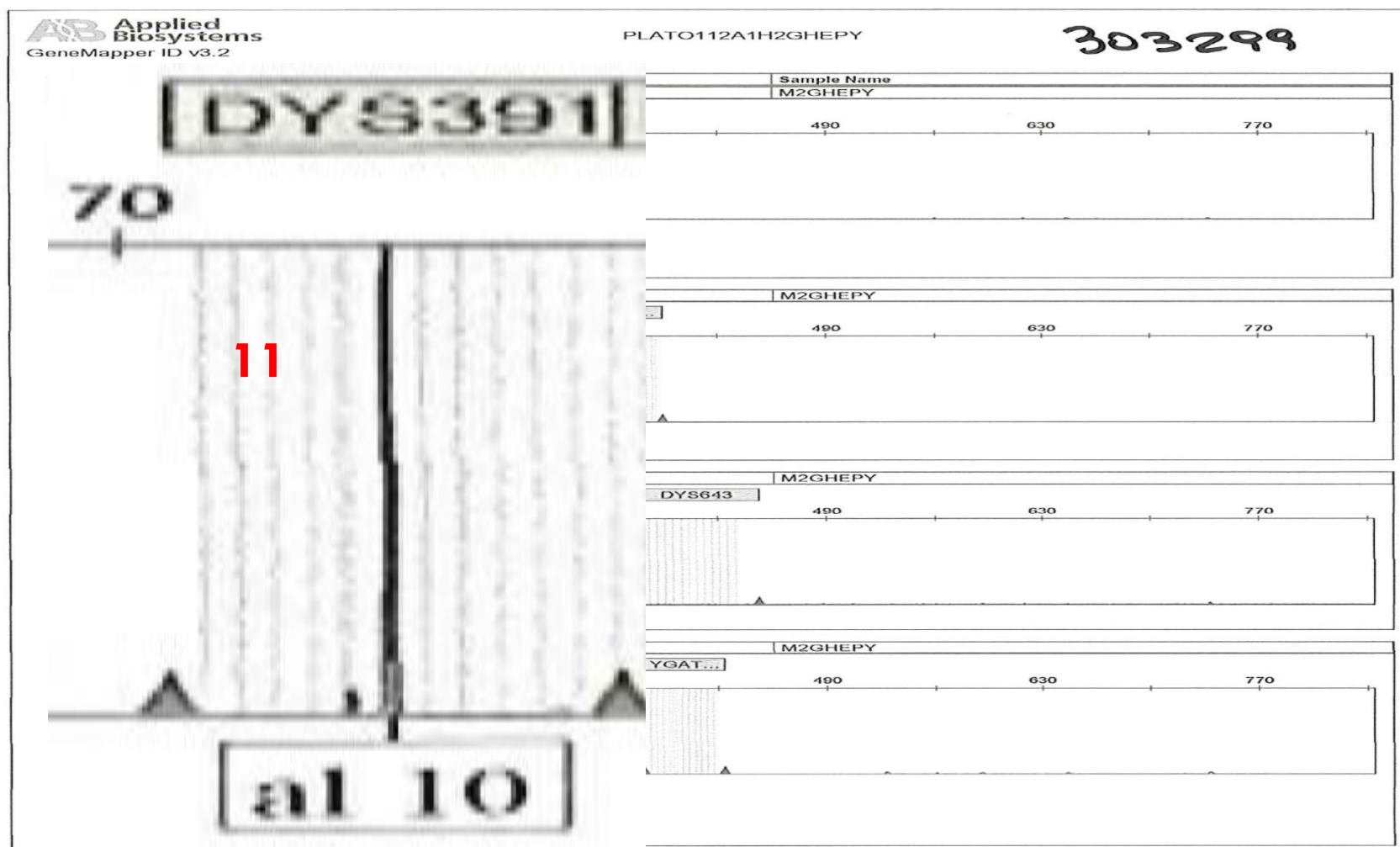
303299 informa 14 en DYS456

10



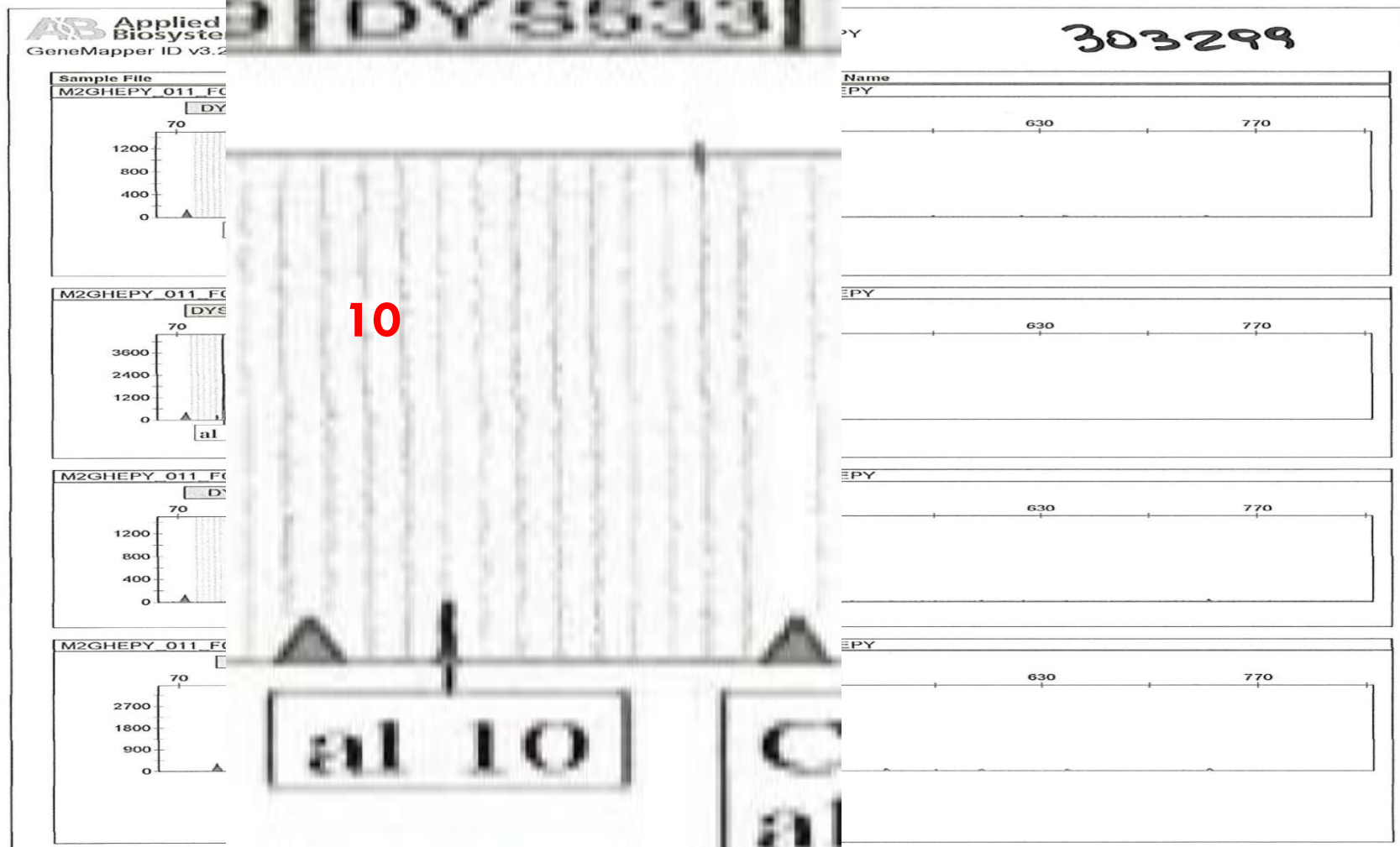
303299 informa 10 en DYS392

11



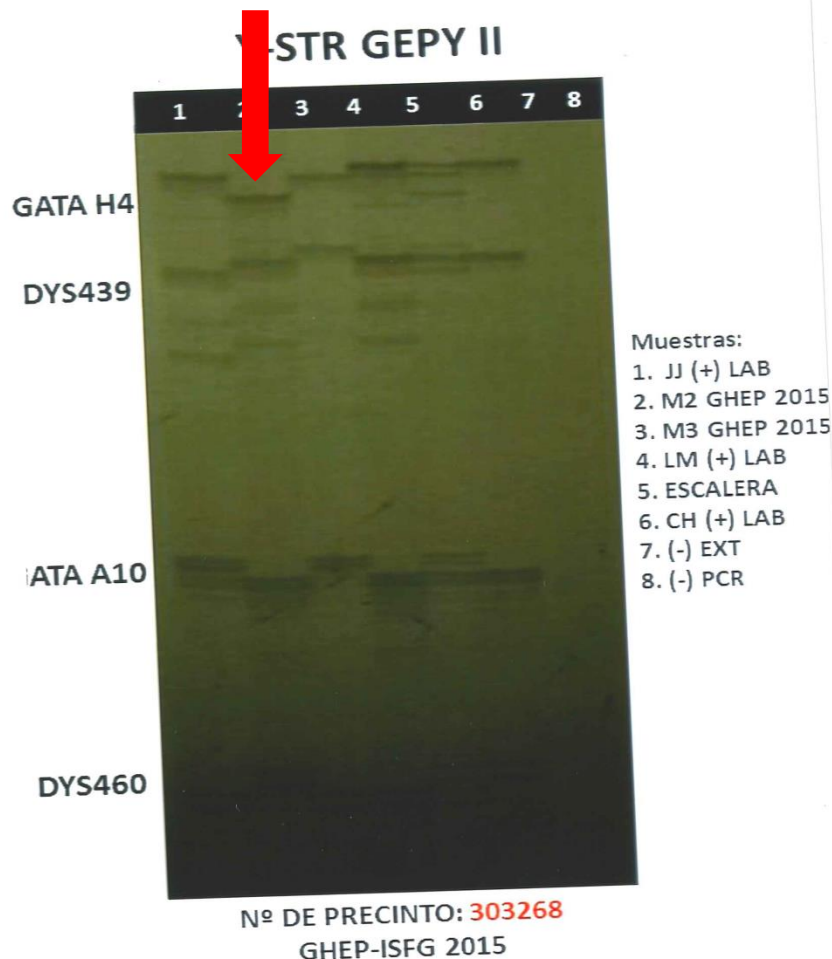
303299 informa 12 en DYS533

12



303268 informa 25 en GATA_H4

13



Utiliza nomenclatura anterior, aplicando la corrección la asignación sería correcta

Letter to the Editor—Nomenclature and Allele Repeat Structure Update for the Y-STR Locus GATA H4

J Forensic Sci, May 2006, Vol. 51, No. 3
doi:10.1111/j.1556-4029.2006.00149.x

Available online at: www.blackwell-synergy.com

mendations of the ISFG Commission should add a correction factor of nine to the Yfiler allele number, and they should refer to this marker as GATA H4.1. Employing the ISFG proposed allele designation for GATA H4.1 changes the Yfiler kit allelic ladder range from 8–13 to 17–22. Alternatively, those who amplify the entire GATA H4 region (GATA H4.1 and GATA H4.2) should add a correction factor of 16 to the Yfiler kit allele number. In this case, the Yfiler kit allelic ladder for GATA H4 ranges from 24 to 29.

M3

14

Marcador/Marker	M3	N	n	% Consenso
DYS_456	14	83	83	100
DYS_389_I	12	94	94	100
DYS_390	22	93	93	100
DYS_389_II	28	93	93	100
DYS_458	15	83	82	98,80
DYS_19	13	91	91	100
DYS_385	13-15	92	92	100
DYS_393	13	94	94	100
DYS_391	10	94	92	97,87
DYS_439_GATA_A4	13	91	91	100
DYS_635_GATA_C4	20	85	85	100
DYS_392	11	91	91	100
GATA_H4	11	86	85	98,84
DYS_437	16	92	92	100
DYS_438	10	91	91	100
DYS_448	20	82	82	100
DYS_460_GATA_A71	10	11	11	100
DYS_576	17	37	37	100
DYS_481	26	36	36	100
DYS_549	12	32	32	100
DYS_533	12	37	36	97,30
DYS_570	18	37	37	100
DYS_643	12	32	32	100

Total N= 1657
n= 1652 (99,70%)

Errores= 5 (0,3%)

1 error de transcripción 303298

1 error de transcripción 303299

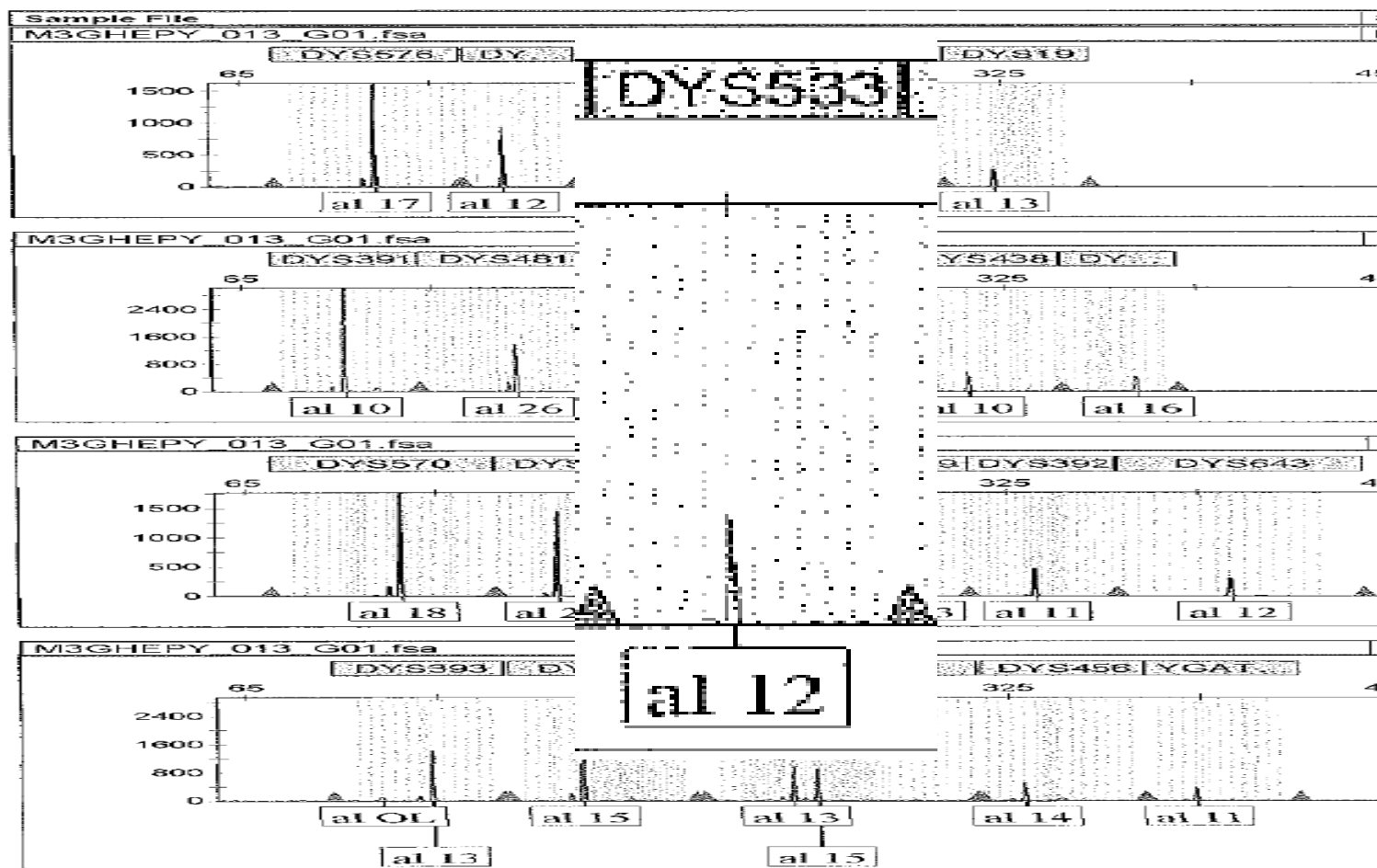
1 error de nomenclatura 303268
en GATA_H4

15



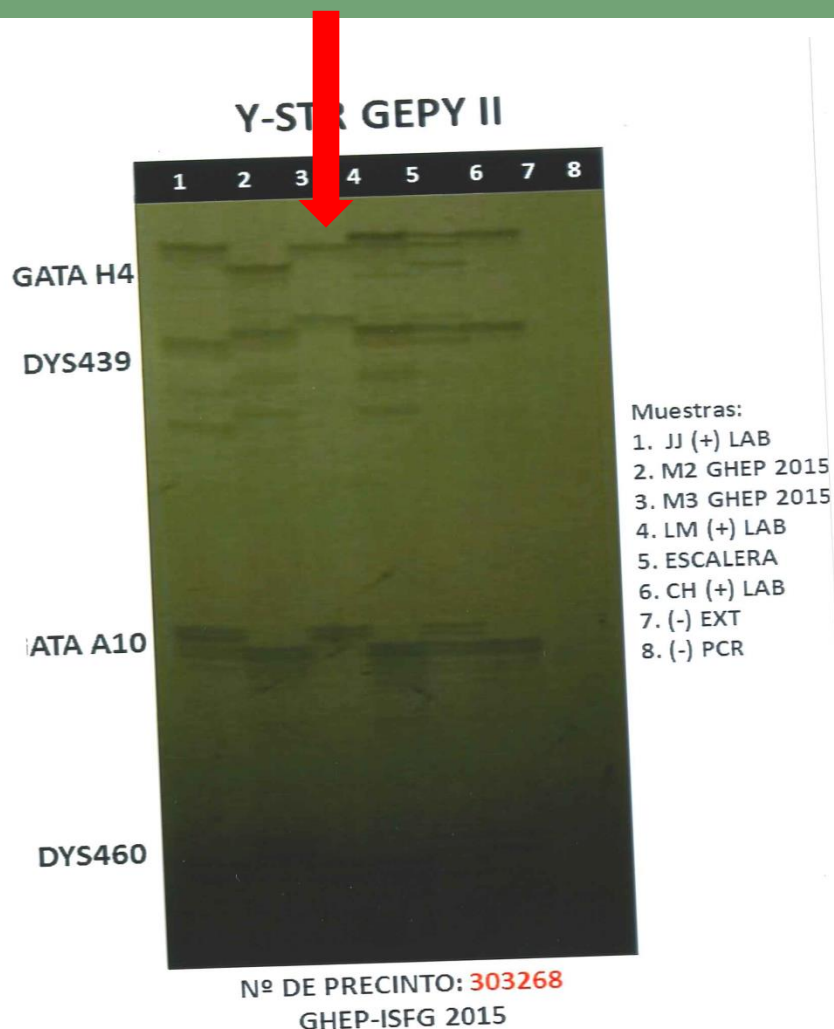
303299 informa 10 en DYS533

16



303268 informa 27 en GATA_H4

17



Utiliza nomenclatura anterior, aplicando la corrección la asignación sería correcta

Letter to the Editor—Nomenclature and Allele Repeat Structure Update for the Y-STR Locus GATA H4

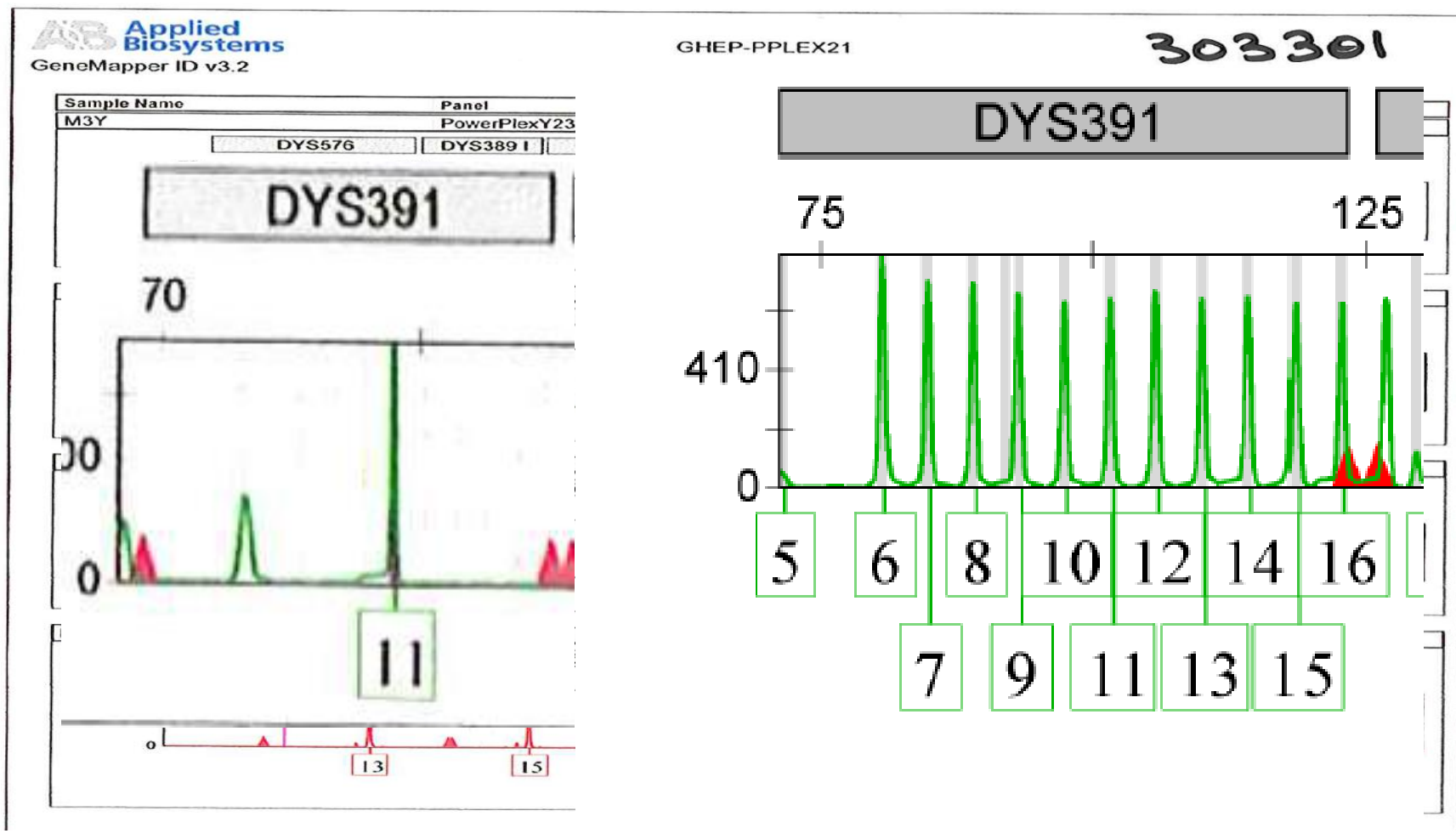
J Forensic Sci, May 2006, Vol. 51, No. 3
doi:10.1111/j.1556-4029.2006.00149.x

Available online at: www.blackwell-synergy.com

mendations of the ISFG Commission should add a correction factor of nine to the Yfiler allele number, and they should refer to this marker as GATA H4.1. Employing the ISFG proposed allele designation for GATA H4.1 changes the Yfiler kit allelic ladder range from 8–13 to 17–22. Alternatively, those who amplify the entire GATA H4 region (GATA H4.1 and GATA H4.2) should add a correction factor of 16 to the Yfiler kit allele number. In this case, the Yfiler kit allelic ladder for GATA H4 ranges from 24 to 29.

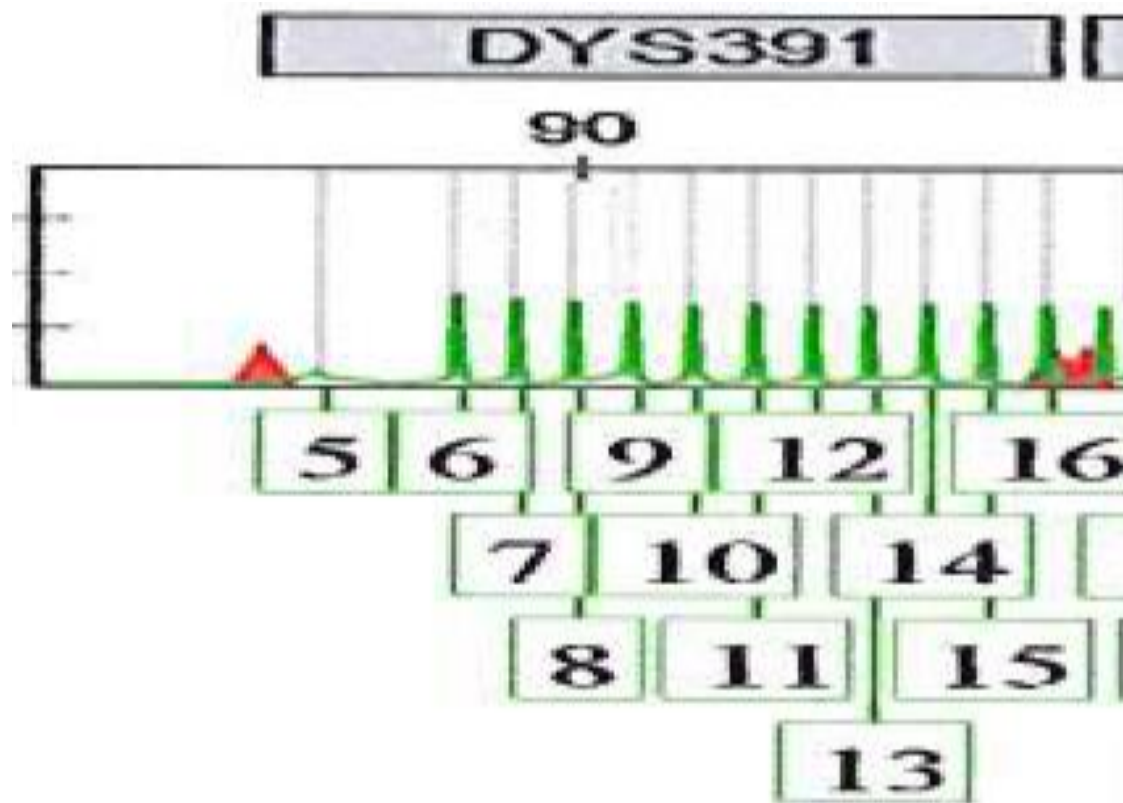
303301 informa 11 en DYS391

18



303335 informa 11 en DYS391

19



M4

20

Marcador/ <i>Marker</i>	M4 Total	Saliva varón	Semen varón M4 2da frac	N	n	% Coincidencia con valor conocido
DYS_456	15-16	15	16	57	53	92,98
DYS_389_I	12-14	12	14	62	58	93,55
DYS_390	23-24	23	24	61	58	95,08
DYS_389_II	31	31	31	59	55	93,22
DYS_458	16-18	18	16	59	55	93,22
DYS_19	13-14	13	14	60	57	95,00
DYS_385	11-14-16-17	16-17	11-14	60	56	93,33
DYS_393	13	13	13	63	59	93,65
DYS_391	10	10	10	63	59	93,65
DYS_439_GATA_A4	12	12	12	61	56	91,80
DYS_635_GATA_C4	22-24	22	24	58	54	93,10
DYS_392	11-13	11	13	59	54	91,53
GATA_H4	9-11	9	11	59	54	91,53
DYS_437	14	14	14	62	58	93,55
DYS_438	9-10	10	9	61	56	91,80
DYS_448	18-20	20	18	57	52	91,23
DYS_576	18-19	19	18	26	25	96,15
DYS_481	22-27	27	22	25	23	92,00
DYS_549	11-13	11	13	21	19	90,48
DYS_533	10-13	10	13	26	24	92,31
DYS_570	17-20	20	17	26	24	92,31
DYS_643	10-12	12	10	19	17	89,47

Errores

21

- Total $N = 1104$
 $n = 1026 (92,93\%)$

- Errores = 78 (7,07%)
 - 42 Discrepancias concentrado en 11 laboratorios
 - 36 Errores de Formato concentrado en 2 laboratorios

Marcador/ <i>Marker</i>	M4 Total	Saliva varón	Semen varón	N	n	% Coincidencia con valor conocido
DYS_456	15-16	15	16	57	55	96,49
DYS_389_I	12-14	12	14	62	60	96,77
DYS_390	23-24	23	24	61	60	98,36
DYS_389_II	31	31	31	59	56	94,92
DYS_458	16-18	18	16	59	57	96,61
DYS_19	13-14	13	14	60	59	98,33
DYS_385	11-14-16-17	16-17	11-14	60	57	95,00
DYS_393	13	13	13	63	61	96,83
DYS_391	10	10	10	63	61	96,83
DYS_439_GATA_A4	12	12	12	61	58	95,08
DYS_635_GATA_C4	22-24	22	24	58	56	96,55
DYS_392	11-13	11	13	59	56	94,92
GATA_H4	9-11	9	11	59	57	96,61
DYS_437	14	14	14	62	60	96,77
DYS_438	9-10	10	9	61	58	95,08
DYS_448	18-20	20	18	57	54	94,74
DYS_576	18-19	19	18	26	26	100,00
DYS_481	22-27	27	22	25	24	96,00
DYS_549	11-13	11	13	21	20	95,24
DYS_533	10-13	10	13	26	25	96,15
DYS_570	17-20	20	17	26	25	96,15
DYS_643	10-12	12	10	19	17	89,47

Errores

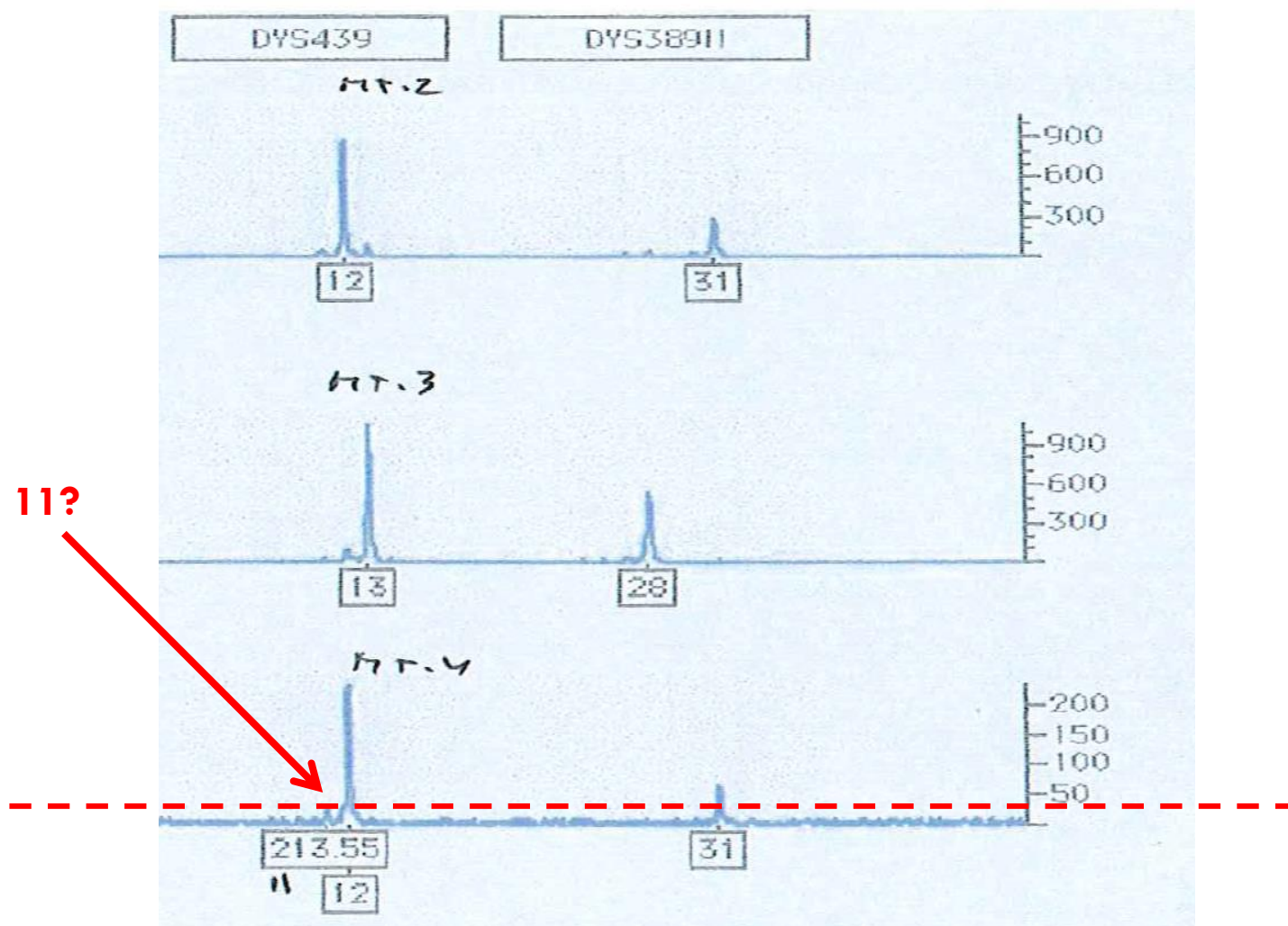
23

- Total N= 1104
 n= 1062 (96,20%)

- Errores= **42 (3,80%)**
 - 42 Discrepancias (63% concentrado en 2 laboratorios)
 - ~~■ 36 Errores de Formato concentrado en 2 laboratorios~~

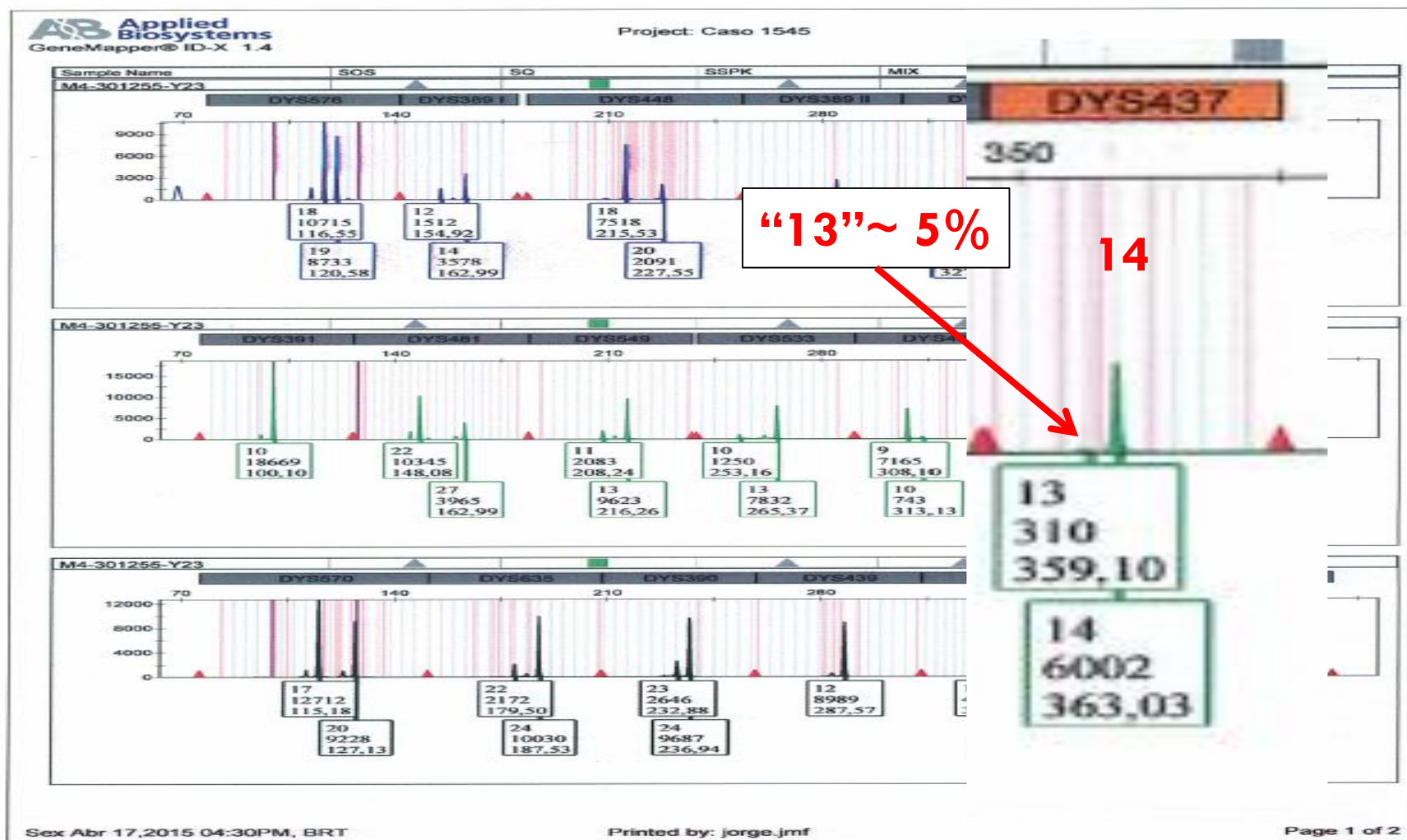
301244 informa 11-12

24



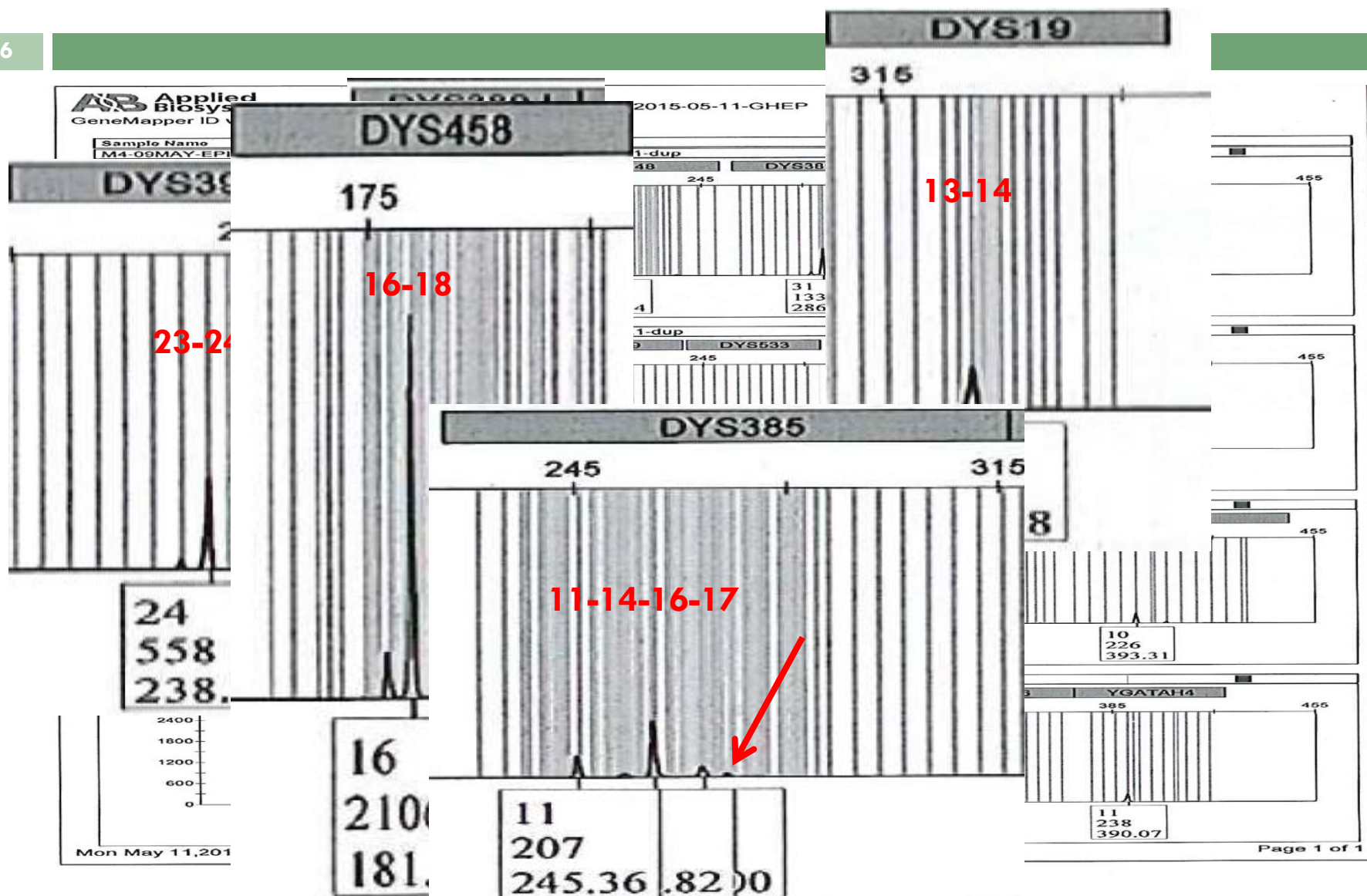
301255

25



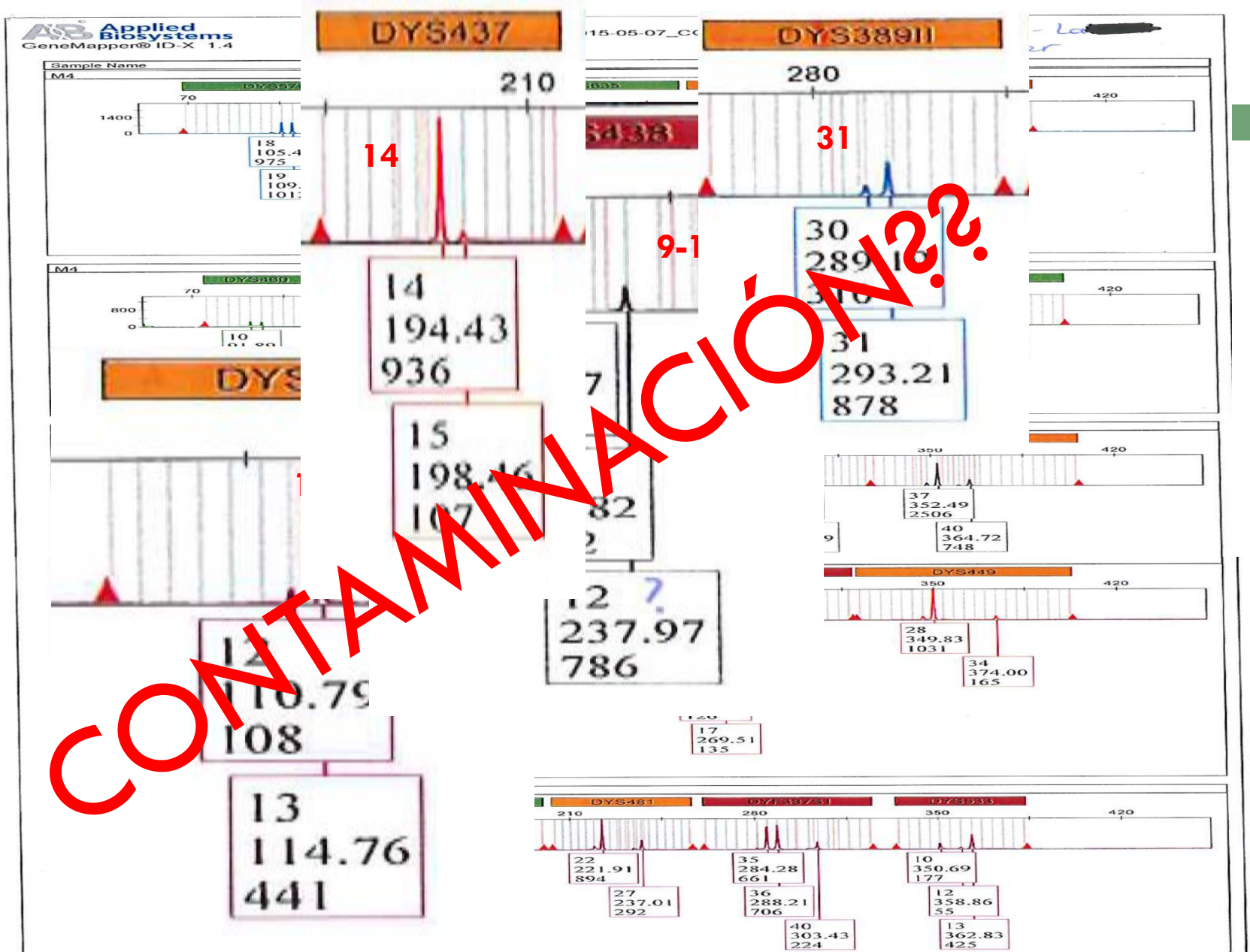
301265

26



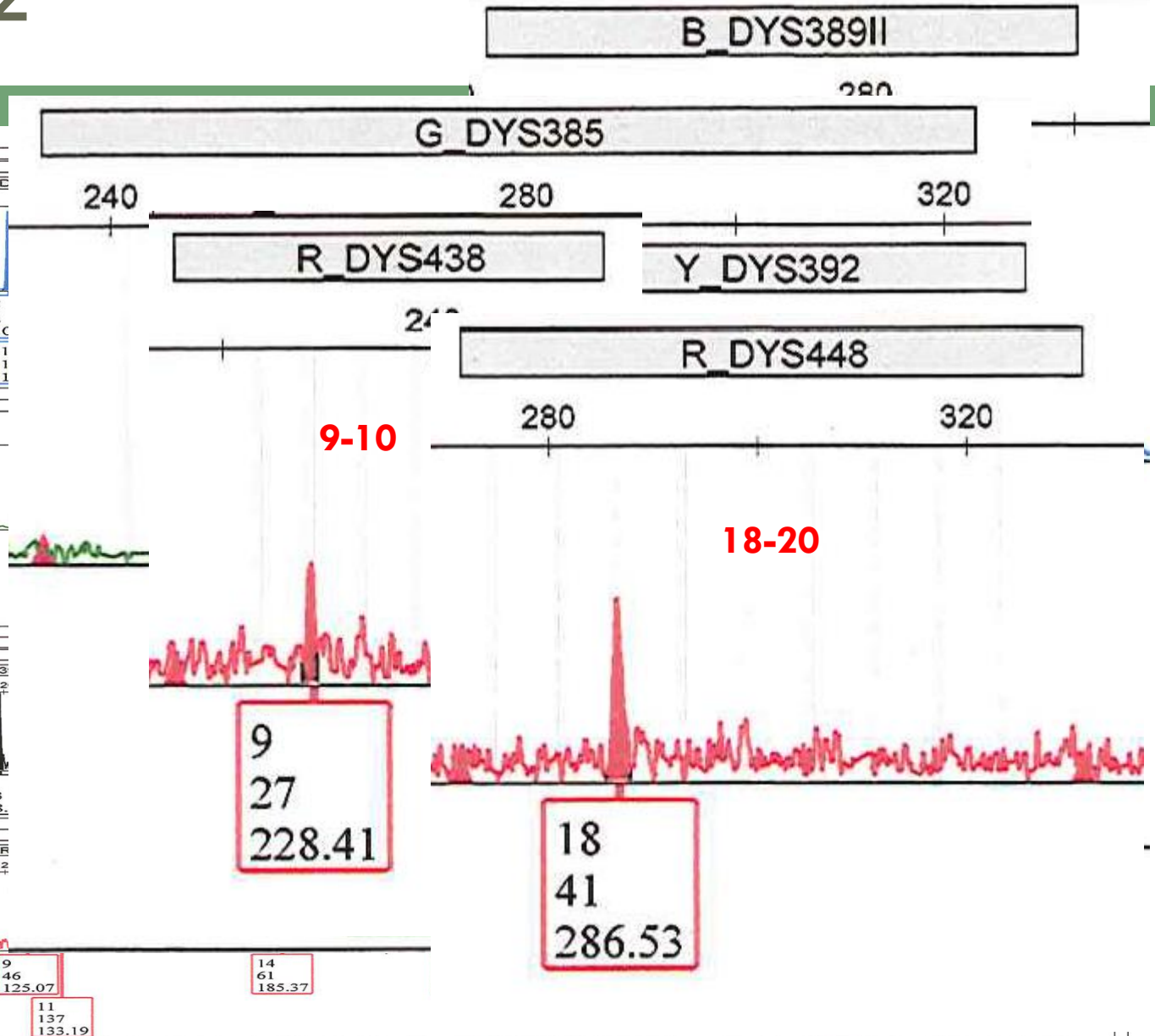
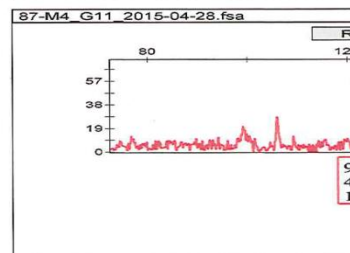
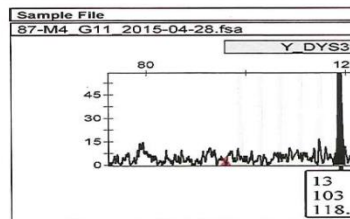
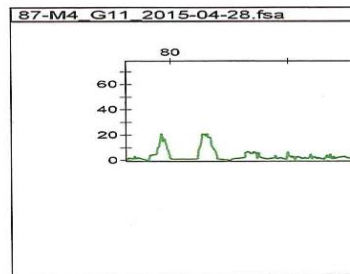
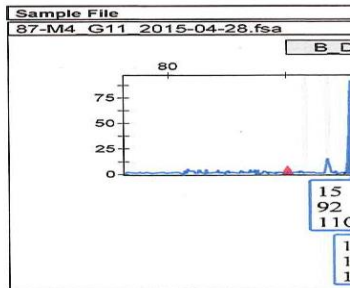
303259

27



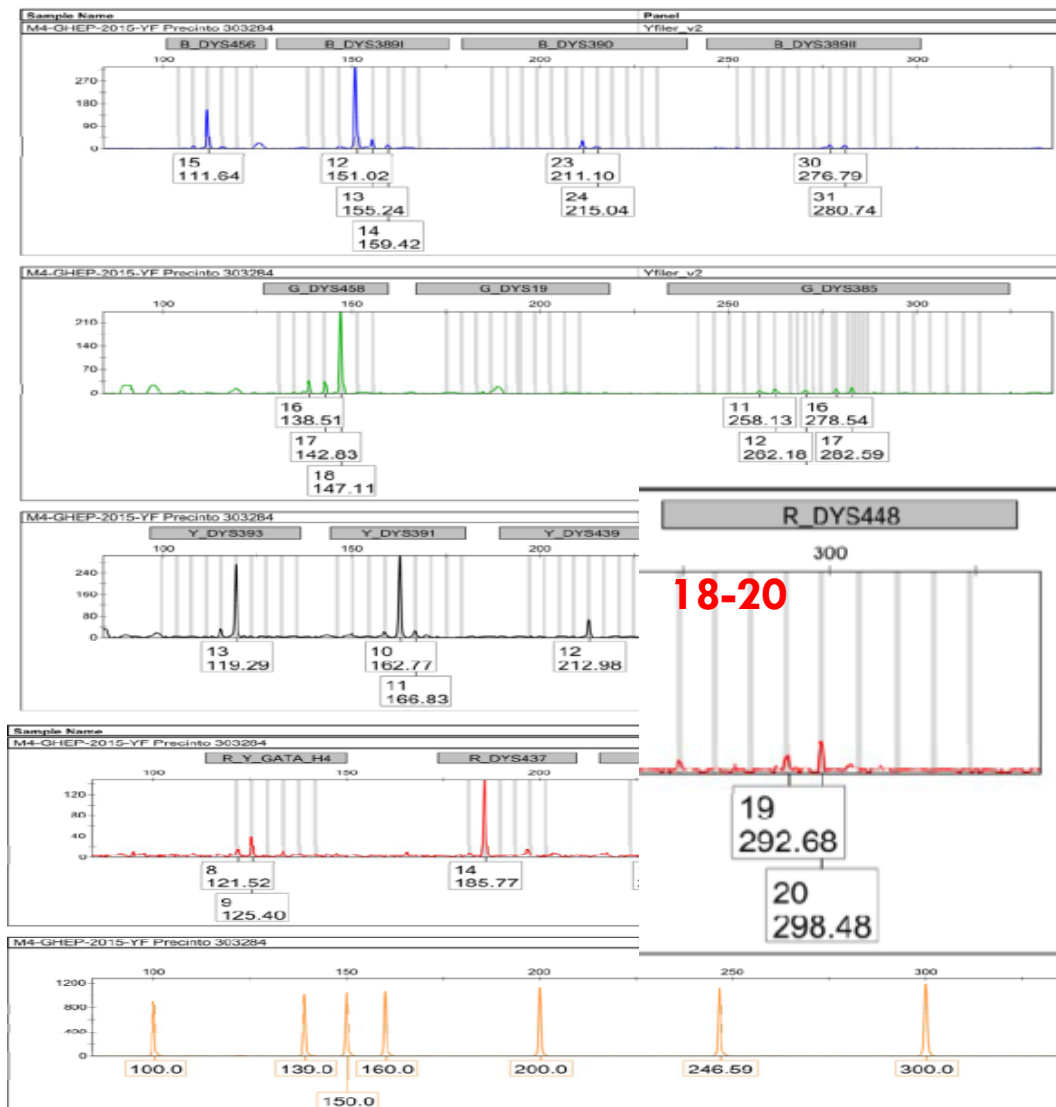
303292

28



303284

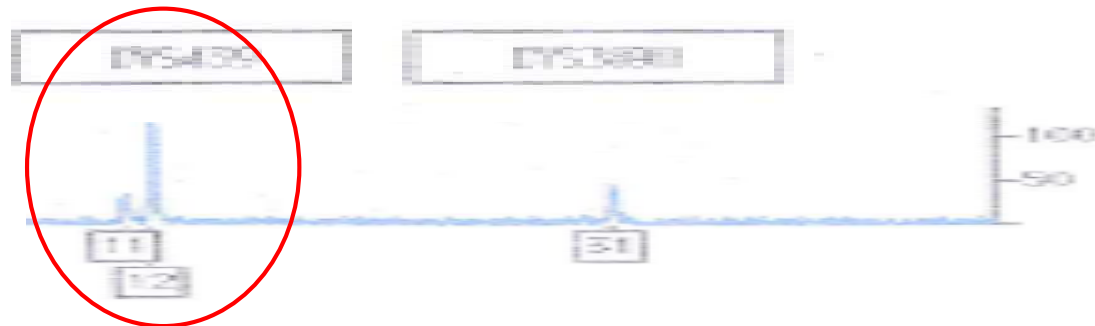
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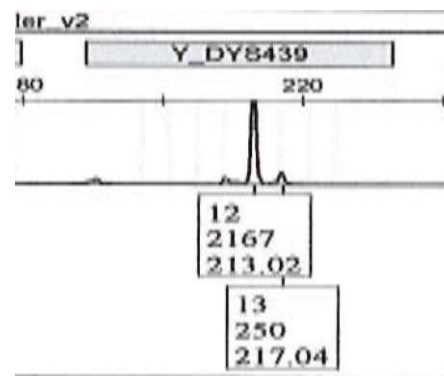
□ 303257 en GATA H4 usa otra nomenclatura

* nomenclatura dos alelos para o locus GATA H4.1 efectuada de acordo com as recomendações da ISFG (J.J. Mulero et al., J. Forensic Sci., 2006, 51: 694). Utilizando o ladder do kit Y Filer, corresponde a menos 9 repetições.

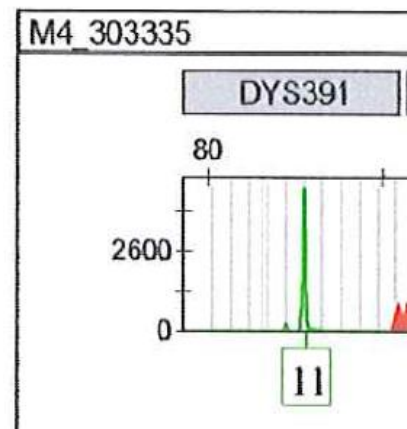
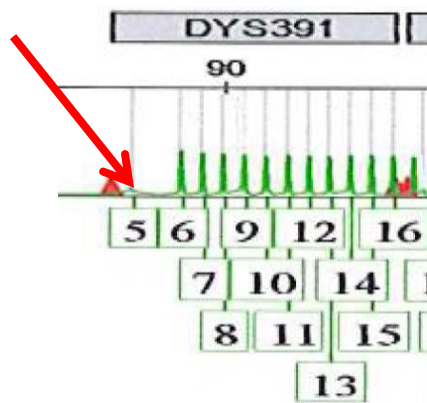
□ 303300 en DYS439 informa 11-12 (12)



- 303311 en DYS439 informa 12-13 (12)



- 303335 en DYS391 informa 11 (10)

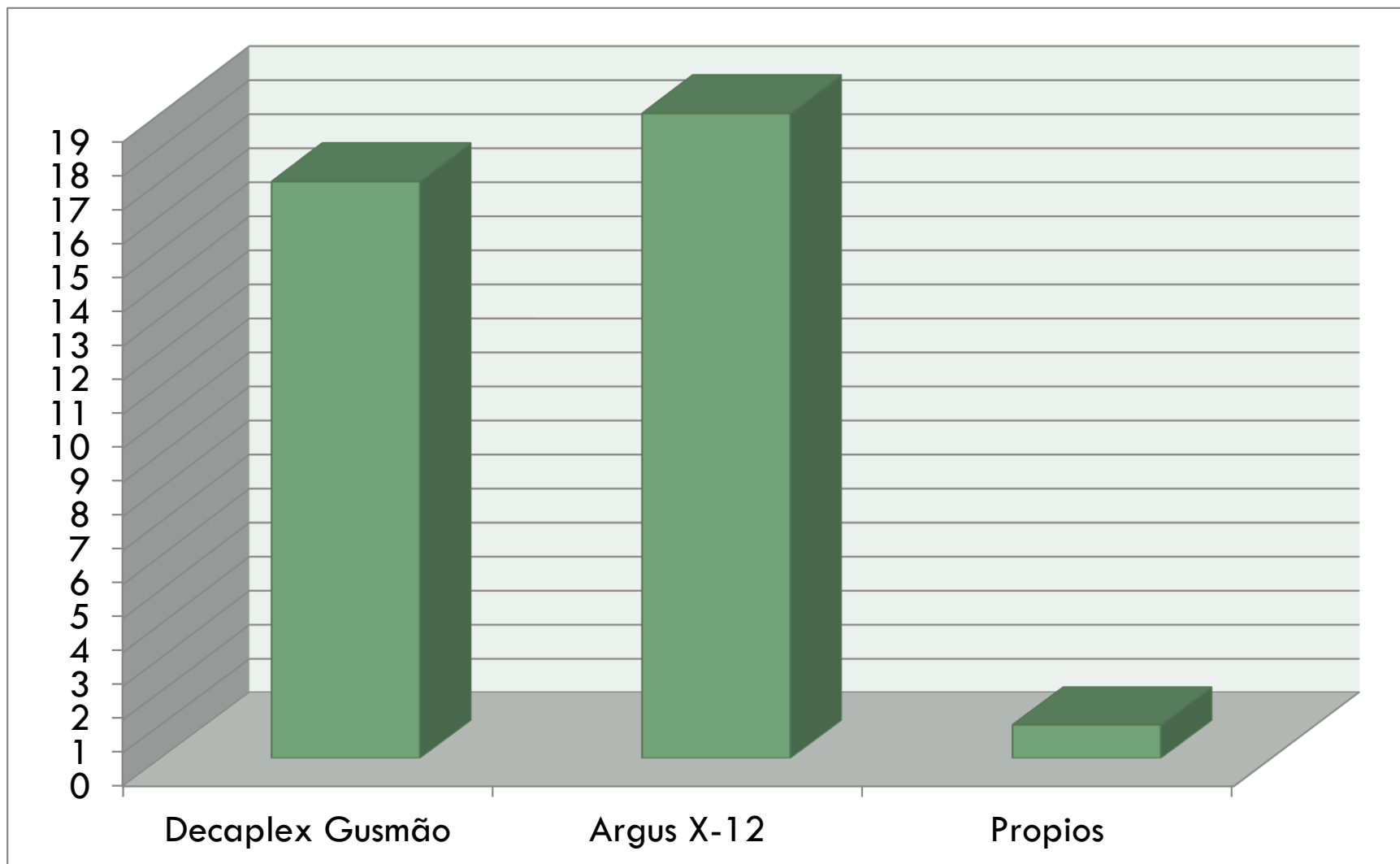


CROMOSOMA X

MÓDULO BÁSICO

Kits utilizados X-STRs

33



M1

34

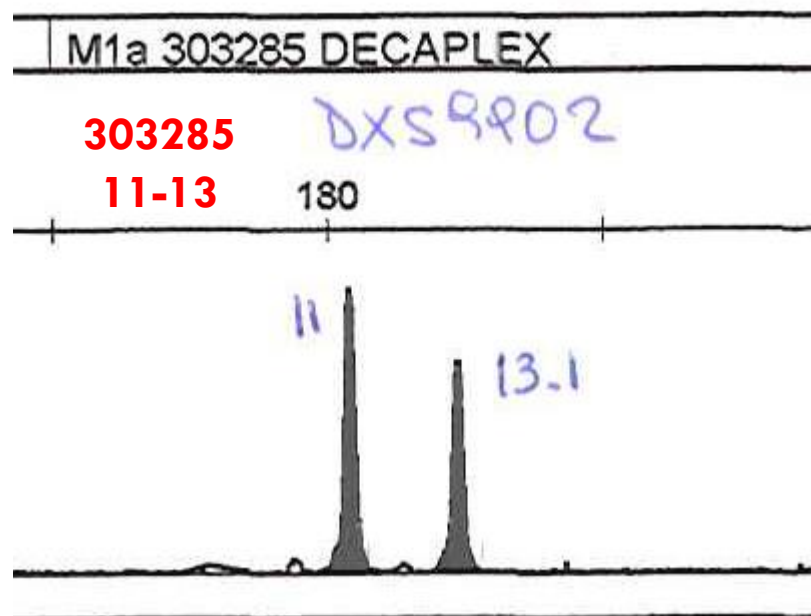
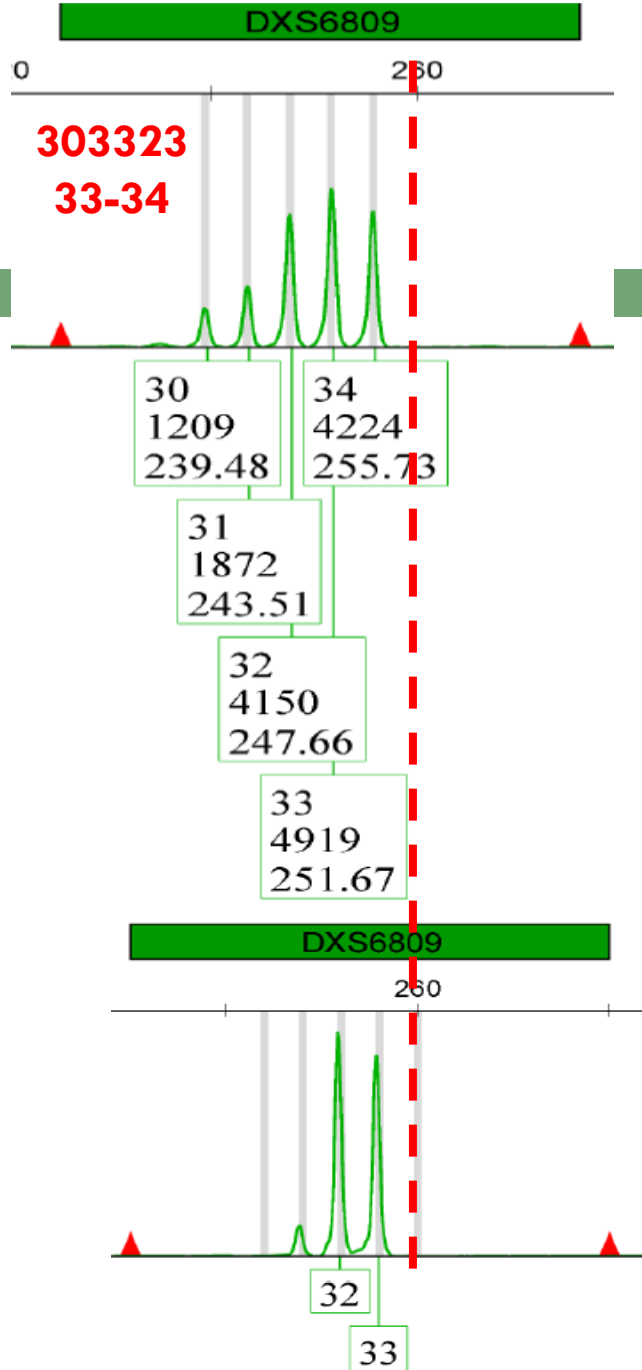
Marcador/Marker	M1	N	n	% Consenso
DXS8378	10-12	34	33	97,06
DXS9898	8.3-11	21	21	100,00
DXS7133	9	21	21	100,00
GATA31E08	13	19	19	100,00
GATA172D05	9-12	21	21	100,00
DXS7423	13-14	36	36	100,00
DXS6809	33-34	21	20	95,24
DXS7132	13-14	34	34	100,00
DXS9902	11-13	19	18	94,74
DXS6789	20-21	20	20	100,00
DXS10103	17-19	19	18	94,74
DXS10134	37-39.3	18	18	100,00
DXS10074	16-18	19	19	100,00
DXS10101	31-34	18	18	100,00
DXS10135	20-26	20	20	100,00
DXS10146	24-26	19	19	100,00
DXS10079	20-21	19	19	100,00
DXS10148	24.1-26.1	18	18	100,00
HPRTB	13-14	20	20	100,00

Total N= 416
n= 412 (99,04%)

Errores= 4 (0,96%)

2 errores de transcripción
303284 y 303285

35



M2

36

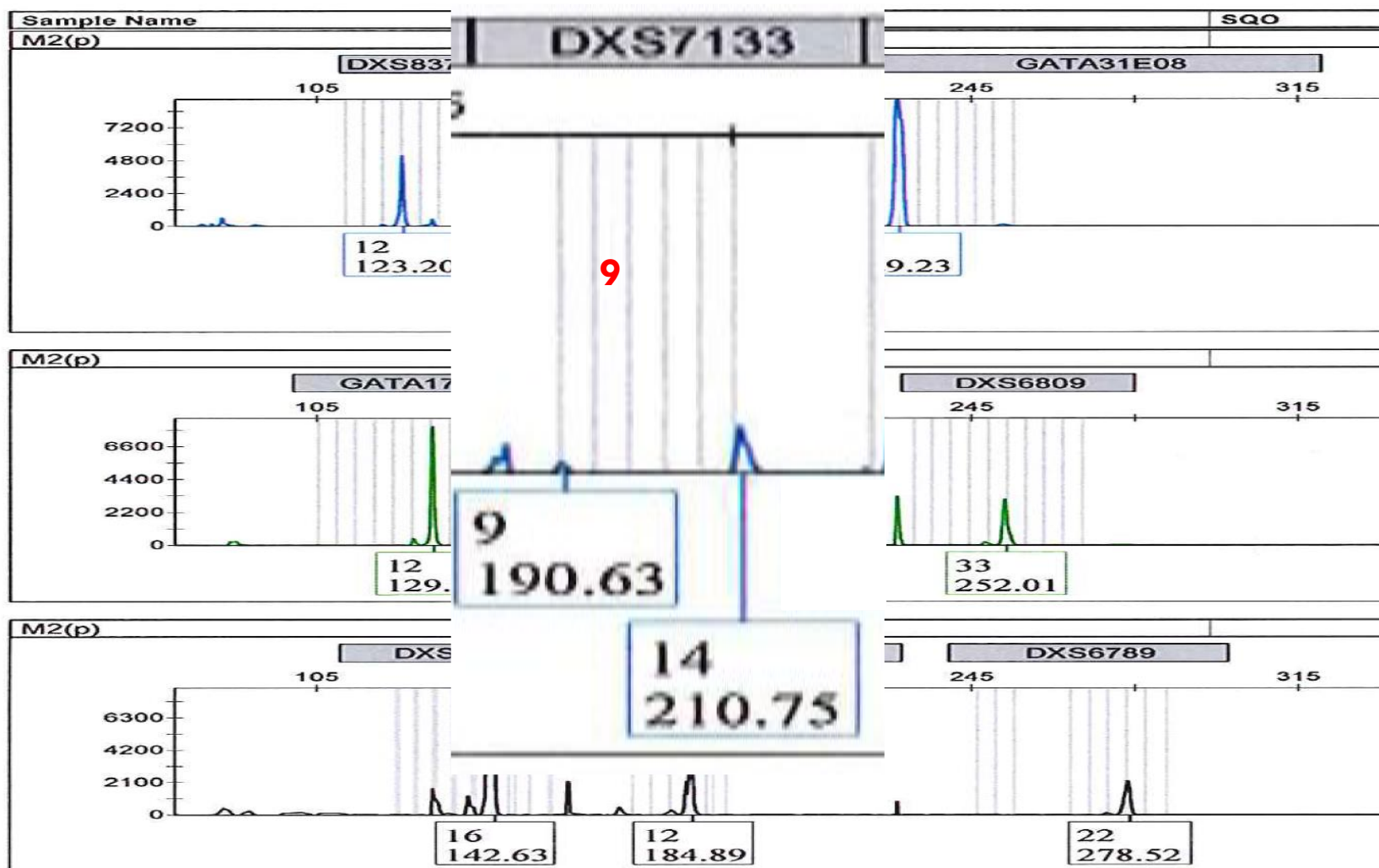
Marcador/Marker	M2	N	n	% Consenso
DXS8378	12	35	35	100,00
DXS9898	11	21	21	100,00
DXS7133	9	20	19	95,00
GATA31E08	9	19	19	100,00
GATA172D05	12	21	21	100,00
DXS7423	15	36	36	100,00
DXS6809	33	21	21	100,00
DXS7132	16	34	32	94,12
DXS9902	12	19	19	100,00
DXS6789	22	20	20	100,00
DXS10103	19	19	19	100,00
DXS10134	35	18	18	100,00
DXS10074	17	19	19	100,00
DXS10101	29.2	18	18	100,00
DXS10135	21.1	20	18	90,00
DXS10146	30	19	19	100,00
DXS10079	17	19	19	100,00
DXS10148	20	18	18	100,00
HPRTB	11	20	20	100,00

Total N= 416
n= 411 (98,80%)

Errores= 5 (1,20%)

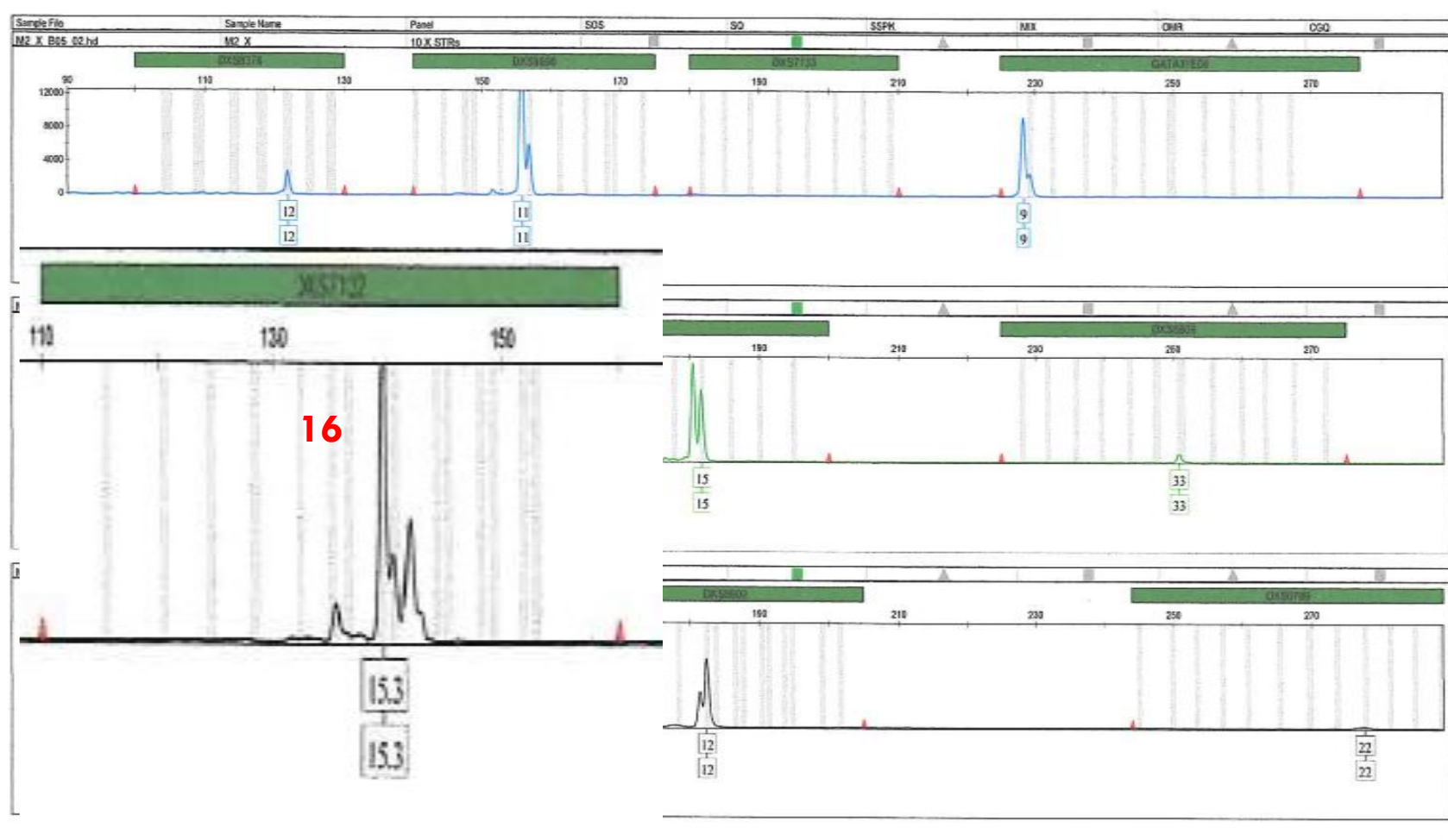
301272

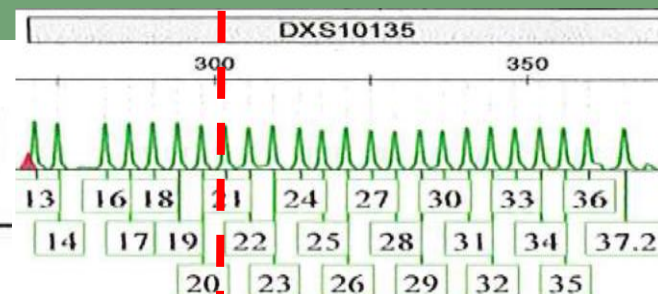
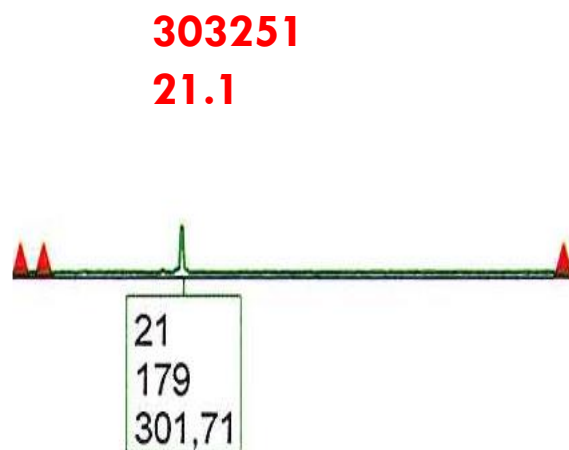
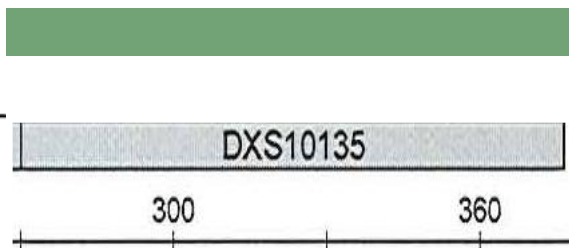
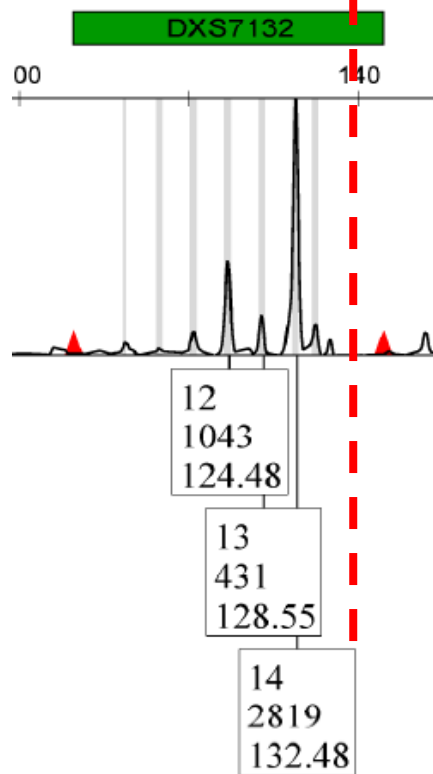
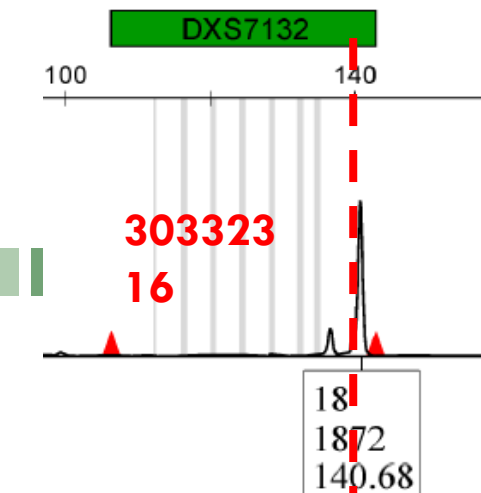
37



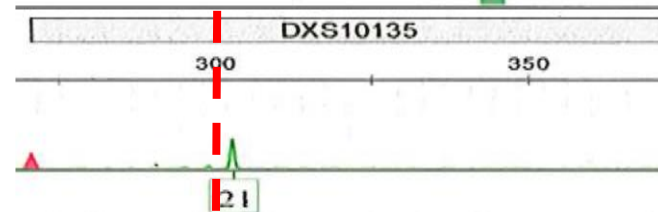
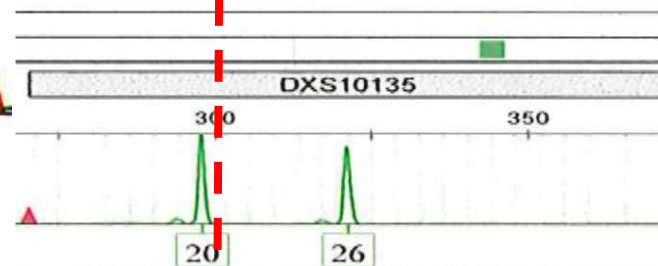
303298

38





303301
21.1



M3

40

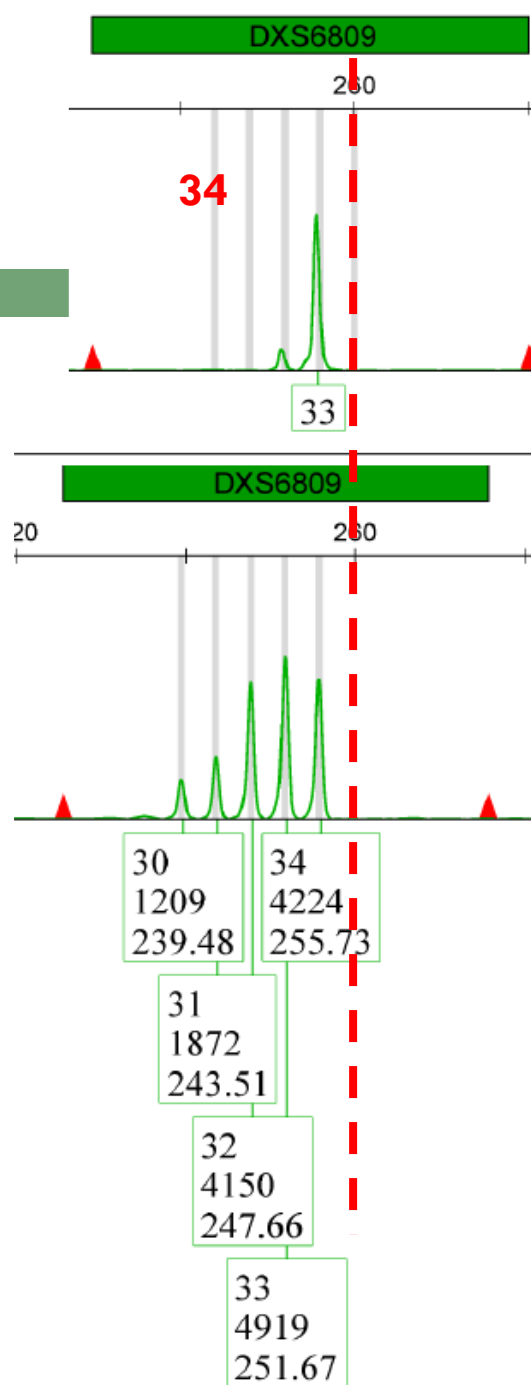
Marcador/ <i>Marker</i>	M3	N	n	% Consenso
DXS8378	12	35	35	100,00
DXS9898	8.3	21	21	100,00
DXS7133	11	20	20	100,00
GATA31E08	12	19	19	100,00
GATA172D05	10	21	21	100,00
DXS7423	14	36	36	100,00
DXS6809	34	21	20	95,24
DXS7132	15	34	34	100,00
DXS9902	11	19	19	100,00
DXS6789	20	20	20	100,00
DXS10103	19	19	19	100,00
DXS10134	34	18	18	100,00
DXS10074	9	19	19	100,00
DXS10101	31.2	18	18	100,00
DXS10135	23	20	20	100,00
DXS10146	28	19	19	100,00
DXS10079	17	19	19	100,00
DXS10148	27.1	18	18	100,00
HPRTB	12	20	20	100,00

Total N= 416
n= 415 (99,76%)

Errores= 1 (0,24%)

303323

41



Marcador/ <i>Marker</i>	M4T	M2		N	n	% Coincidencia con valor conocido
DXS8378	10-12	12	10	16	13	81,25
DXS9898	11-12	11	12	9	8	88,89
DXS7133	9	9	9	8	8	100,00
GATA31E08	9-11	9	11	8	7	87,50
GATA172D05	12	12	12	9	6	66,67
DXS7423	14-15	15	14	17	17	100,00
DXS6809	32-33	33	32	8	6	75,00
DXS7132	13-16	16	13	16	14	87,50
DXS9902	10-12	12	10	8	6	75,00
DXS6789	20-22	22	20	8	8	100,00
DXS10103	19	19	19	8	8	100,00
DXS10134	35-38	35	38	9	9	100,00
DXS10074	15-17	17	15	9	9	100,00
DXS10101	29.2-32.2	29.2	32.2	9	9	100,00
DXS10135	21.1-27	21.1	27	10	9	90,00
DXS10146	30-40.2	30	40.2	9	9	100,00
DXS10079	17	17	17	9	9	100,00
DXS10148	20-24	20	24	9	8	88,89
HPRTB	11-12	11	12	9	9	100,00

CROMOSOMA Y MÓDULO AVANZADO

Participación Avanzado

44

58 Laboratorios
analizan Au-
STRs

```
graph TD; A[58 Laboratorios analizan Au-STRs] --> B[81,03% (47) analizan Y-STRs  
(en 2014 fue un 90,38%)]; A --> C[22,41% (13) analizan X-STRs  
(en 2014 fue un 30,77%)];
```

81,03% (47) analizan
Y-STRs
(en 2014 fue un 90,38%)

22,41% (13) analizan
X-STRs
(en 2014 fue un 30,77%)

Marcador/ <i>Marker</i>	M6	N	n	% Consenso
DYS_456	14	47	47	100,00
DYS_389_I	12	47	47	100,00
DYS_390	22	47	47	100,00
DYS_389_II	28	47	47	100,00
DYS_458	15	47	47	100,00
DYS_19	13	47	46	97,87
DYS_385	13-15	47	47	100,00
DYS_393	13	47	47	100,00
DYS_391	10	47	47	100,00
DYS_439_GATA_A4	13	47	47	100,00
DYS_635_GATA_C4	20	47	47	100,00
DYS_392	11	47	47	100,00
GATA_H4	11	47	47	100,00
DYS_437	16	47	47	100,00
DYS_438	10	47	47	100,00
DYS_448	20	47	47	100,00
DYS_460_GATA_A71	10	8	8	100,00
DYS_576	17	21	21	100,00
DYS_481	26	21	21	100,00
DYS_549	12	16	16	100,00
DYS_533	12	21	21	100,00
DYS_570	18	21	21	100,00
DYS_643	12	16	16	100,00
DYS_449	30	7	7	100,00
DYF_387S1	36-39	7	7	100,00
DYS_627	18	7	7	100,00
DYS_518	35	7	7	100,00

- Total N= 904
 n= 880 (97,35%)

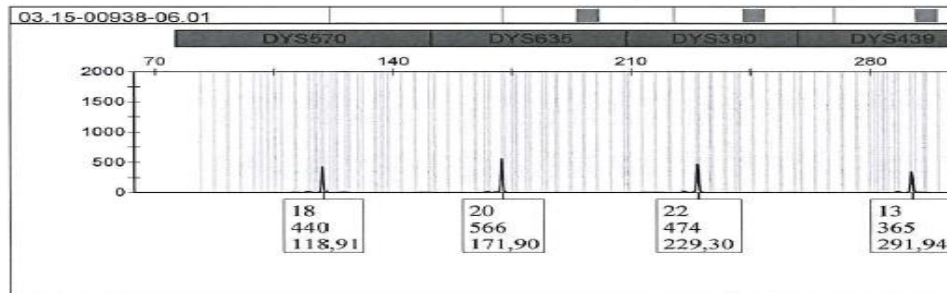
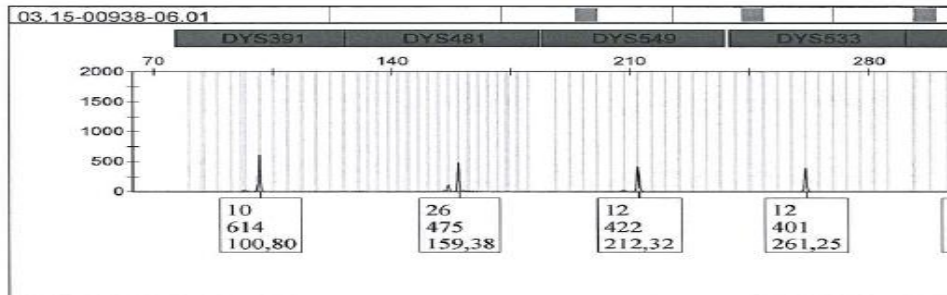
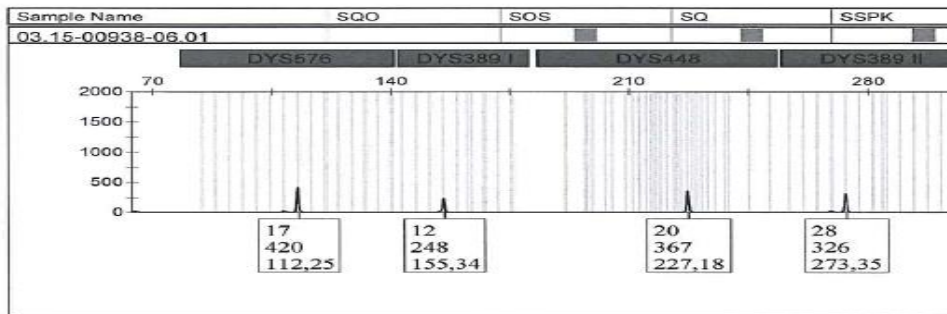
- Errores= 0??? o 24 (2,65%)
 - 22 Errores de Formato de 301250. Coloca en la columna de M6 total el número de alelos hallados y no los alelos

 - 1 Error de nomenclatura de 303257 en GATA H4 usa otra nomenclatura

* nomenclatura dos alelos para o locus GATA H4.1 efectuada de acordo com as recomendações da ISFG (J.J. Mulero et al., J. Forensic Sci., 2006, 51: 694). Utilizando o ladder do kit Y Filer, corresponde a menos 9 repetições.

303244 DYS19

47



DYS19

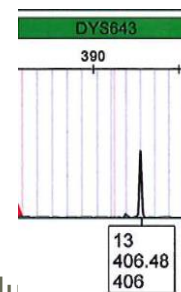
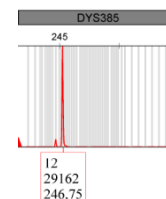
350

Transcribe 10

13
292
323,04

Marcador/Marker	M8	N	n	% Consenso
DYS_456	14	45	45	100,00
DYS_389_I	13	45	45	100,00
DYS_390	23	45	45	100,00
DYS_389_II	28	45	45	100,00
DYS_458	18	45	45	100,00
DYS_19	16	45	45	100,00
DYS_385	12	45	45	100,00
DYS_393	13	45	44	97,78
DYS_391	10	45	45	100,00
DYS_439_GATA_A4	12	44	44	100,00
DYS_635_GATA_C4	22	45	45	100,00
DYS_392	11	45	45	100,00
GATA_H4	12	45	45	100,00
DYS_437	15	45	45	100,00
DYS_438	10	45	45	100,00
DYS_448	21	45	45	100,00
DYS_460_GATA_A71	10	7	7	100,00
DYS_576	18	20	20	100,00
DYS_481	23	20	20	100,00
DYS_549	10	16	16	100,00
DYS_533	12	20	20	100,00
DYS_570	19	20	20	100,00
DYS_643	13	16	16	100,00
DYS_449	29	6	6	100,00
DYF_387S1	35-38	6	6	100,00
DYS_627	20	6	6	100,00
DYS_518	38	6	6	100,00

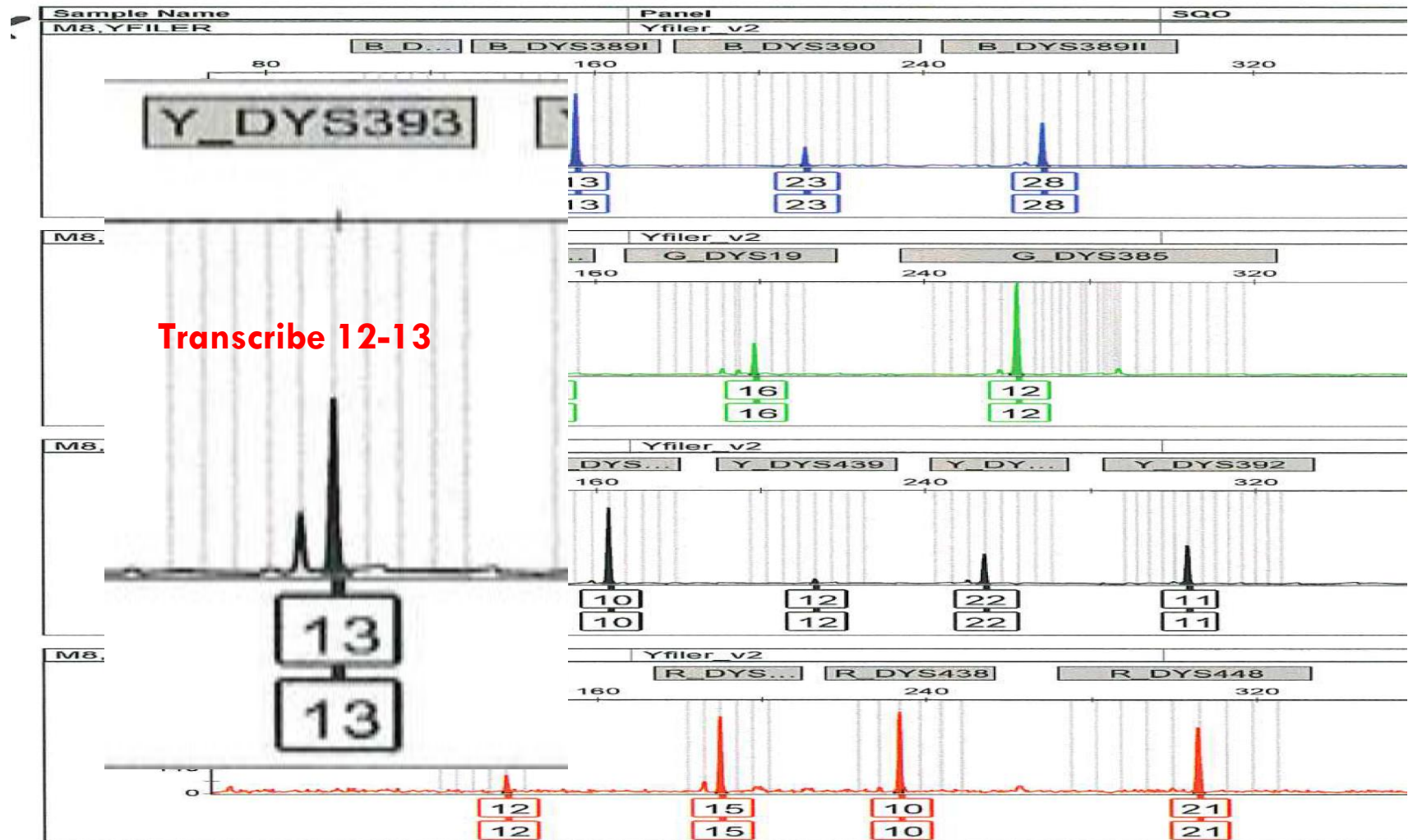
- Total N= 862
n= 836 (96,98%)
- Errores= 1??? (0,12%) o 26 (3,02%)
 - 22 Errores de Formato de 301250. Coloca en la columna de M8 total el número de alelos hallados y no los alelos
 - 1 error de transcripción de 301254 DYS385
 - 1 Error de nomenclatura de 303257 en GATA H4 usa otra nomenclatura
- 1 error de transcripción de 303260 DYS643



* nomenclatura dos alelos para o locus GATA H4.1 efectuada de acordo com as recomendações da ISFG (J.J. Mulero et al., J. Forensic Sci., 2006, 51: 694). Utilizando o ladder do kit Y Filer, corresponde a menos 9 repetições.

303319

50



CROMOSOMA X

MÓDULO AVANZADO

Marcador/ <i>Marker</i>	M6	M3	D06	D10	N	n	% Consenso
DXS8378	10-12	12	12	10	11	8	72,73
DXS9898	8.3-12-14	8.3	12-14	12	5	5	100,00
DXS7133	9-11-13	11	9-13	9	4	3	75,00
GATA31E08	9-12-13	12	9-13	9	5	5	100,00
GATA172D05	6-8-10	10	6-10	8	5	3	60,00
DXS7423	14-15	14	14-15	14	11	10	90,91
DXS6809	32-33-34	34	33	32	5	4	80,00
DXS7132	13-14-15	15	14	13	11	11	100,00
DXS9902	11-12-13	11	12-13	11	5	5	100,00
DXS6789	20-21-22	20	21-22	21	5	5	100,00
DXS10103	19	19	19	19	6	6	100,00
DXS10134	34-35-37-40.3	34	35-40.3	37	6	6	100,00
DXS10074	9-16-18	9	18	16	7	6	85,71
DXS10101	30.2-31.2	31.2	30.2-31.2	30.2	6	6	100,00
DXS10135	21-23-25	23	21-25	21	6	6	100,00
DXS10146	27-28-29-40.2	28	29-40.2	27	7	6	85,71
DXS10079	17-20-21-23	17	20-23	21	7	6	85,71
DXS10148	24.1-26.1-27.1	27.1	24.1	26.1	6	6	100,00
HPRTB	12-14	12	12-14	14	7	7	100,00

Marcador/Marker	M7	N	n	% Consenso
DXS8378	10-11	13	13	100,00
DXS9898	11-12	6	6	100,00
DXS7133	9-11	6	6	100,00
GATA31E08	9-13	6	6	100,00
GATA172D05	6	6	6	100,00
DXS7423	14-15	13	13	100,00
DXS6809	29-34	6	5	83,33
DXS7132	14-15	13	13	100,00
DXS9902	11-12	6	6	100,00
DXS6789	20	6	6	100,00
DXS10103	19	9	9	100,00
DXS10134	35-39	9	9	100,00
DXS10074	16-17	8	8	100,00
DXS10101	28-31	9	9	100,00
DXS10135	18-28	9	8	88,89
DXS10146	28-31	9	9	100,00
DXS10079	19	10	10	100,00
DXS10148	24.1-25.1	9	9	100,00
HPRTB	12-14	9	9	100,00

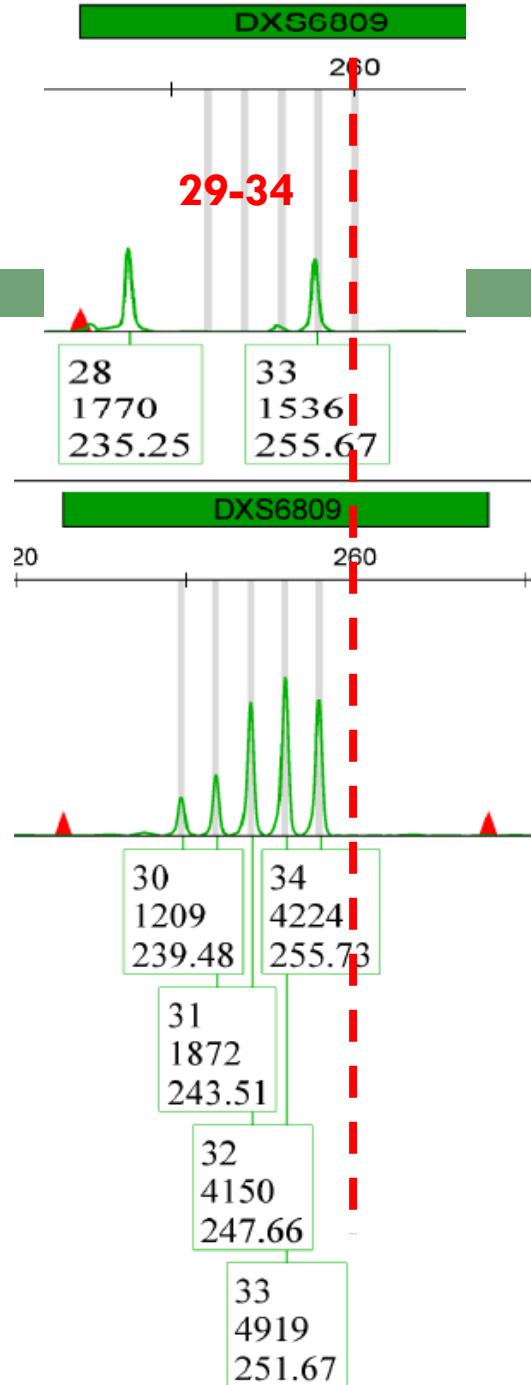
Total N= 162

n= 160 (98,77%)

Errores= 2(1,23%)

303323

54



Marcador/ <i>Marker</i>	M8	N	n	% Consenso
DXS8378	10	12	12	100,00
DXS9898	12	5	5	100,00
DXS7133	9	5	5	100,00
GATA31E08	12	5	5	100,00
GATA172D05	11	5	5	100,00
DXS7423	16	12	11	91,67
DXS6809	33	4	4	100,00
DXS7132	12	12	12	100,00
DXS9902	11	5	5	100,00
DXS6789	22	5	5	100,00
DXS10103	19	9	9	100,00
DXS10134	35	9	9	100,00
DXS10074	16	9	9	100,00
DXS10101	31.2	9	9	100,00
DXS10135	35	9	9	100,00
DXS10146	39.2	9	9	100,00
DXS10079	22	10	10	100,00
DXS10148	22.1	9	9	100,00
HPRTB	12	9	9	100,00

Total N= 152

n= 151 (99,34%)

Errores= 1 (0,66%)

303323

56

