

Molecular dissection of a crime scene: introducing STR sequencing in routine investigation

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Ludwig Maximilian University of Munich

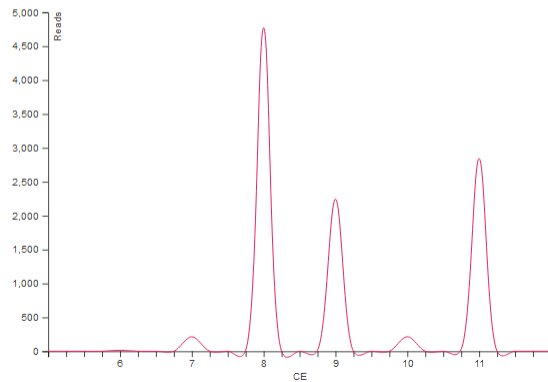


57-Spur3 ▾ / TPOX

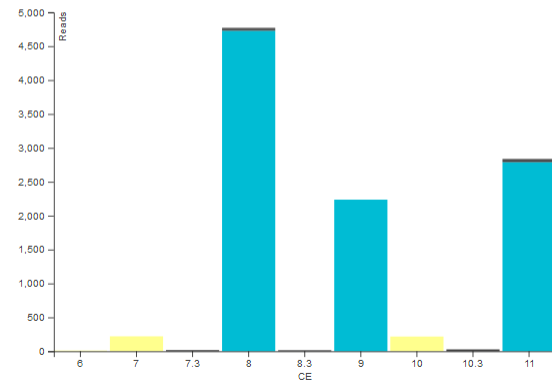
ANALYTICAL THRESHOLD 10 reads

CALLING THRESHOLD 5 % (517 reads)

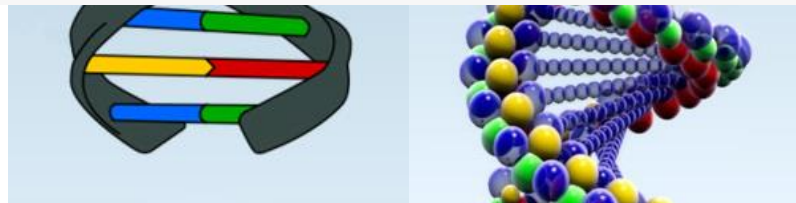
Electropherogram ⓘ



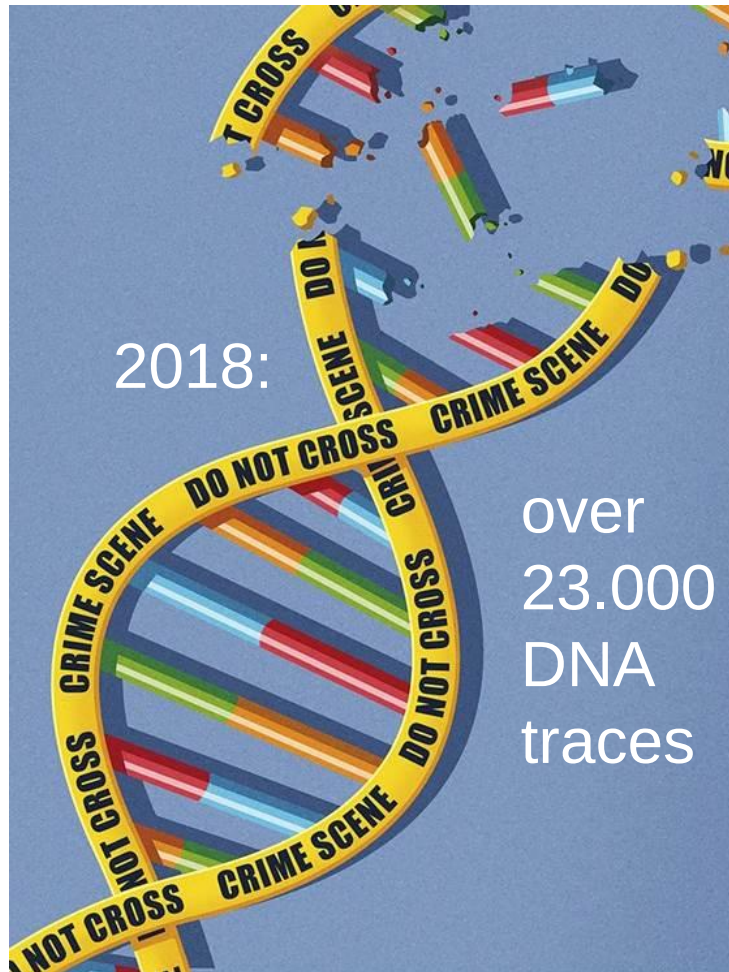
Histogram ⓘ



source: toaSTR



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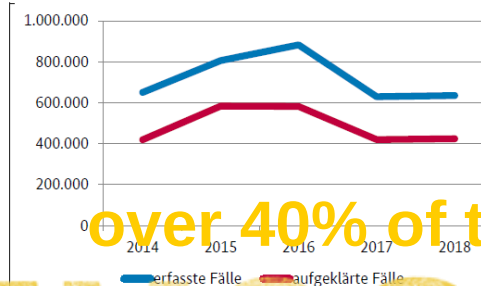
Bayern

Bevölkerungszahlen 2018

insgesamt: 12.997.204
männlich: 6.438.503
weiblich: 6.558.701



Straftaten insgesamt in Bayern



Jahr	Anzahl Fälle		AQ
	erfasst	aufgeklärt	
2014	650.868	419.482	64,4
2015	805.915	584.128	72,5
2016	882.473	581.860	65,9
2017	625.512	420.440	66,8
2018	605.421	401.004	66,2

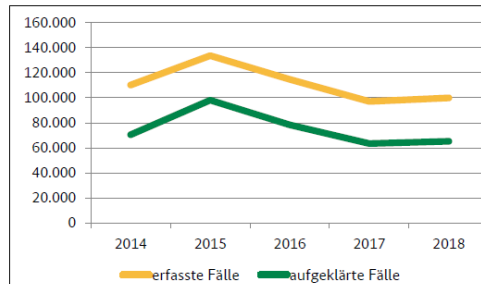
Landeshauptstadt: München

Bevölkerungszahlen 2018

insgesamt: 1.456.039
männlich: 708.422
weiblich: 747.617



Straftaten insgesamt in München



Jahr	Anzahl Fälle		AQ
	erfasst	aufgeklärt	
2014	110.208	70.448	63,9
2015	133.672	97.997	73,3
2016	114.710	78.302	68,3
2017	97.035	63.380	65,3
2018	99.802	65.191	65,3

over 40% of the crimes
UNSOLVED

Tools



Converge

GlobalFiler™ NGS STR Panel v2

Locus	Category
TPOX	CODIS
D3S1358	
FGA	
D5S818	
CSF1PO	
D7S820	
D8S1179	
TH01	
vWA	
D13S317	
D16S539	
D18S51	
D21S11	
D1S1656	
D2S1338	
D2S441	
D10S1248	
D12S391	
D19S433	
D22S1045	

Locus	Category
D1S1677	non-CODIS/other
D2S1776	
D3S4529	
D4S2408	
D5S2800	
D6S1043	
D6S474	
D12ATA63	
D14S1434	
PENTA D	
PENTA E	

Locus	Category
AMEL-X	sex determination
AMEL-Y	
rs2032678	
DYS391	
SRY	

Converge™ Software v2.1



Batch-1037 

Batch Title: R_2019_01_31_09_52_29_user_IRES5D6X-10-Casework

Batch External ID: 92

Status: Processed

Priority:  Normal

Batch Type: NGS Genotype analysis

Materials & Method: NGS Genotype Analysis 5.10.1 - 2.1

Modified By: superUser

Owner: superUser

Creation Date: Jan-31-2019 6:27:53 PM

Last Modified Date: Feb-6-2019 3:22:42 PM

Created By: superUser

Analysis Name: [Auto_user_IRES5D6X-10-Casework_208](#)

Batch Start Date: Jan-31-2019 4:59:27 PM

Batch End Date: Jan-31-2019 8:23:34 PM

Total Samples: 10

Ready Samples: 0

Completed Samples: 10

Incomplete Samples: 0

Batch Description:

Batch Comments :

[Edit](#)

+ Sample 

- Result Card 

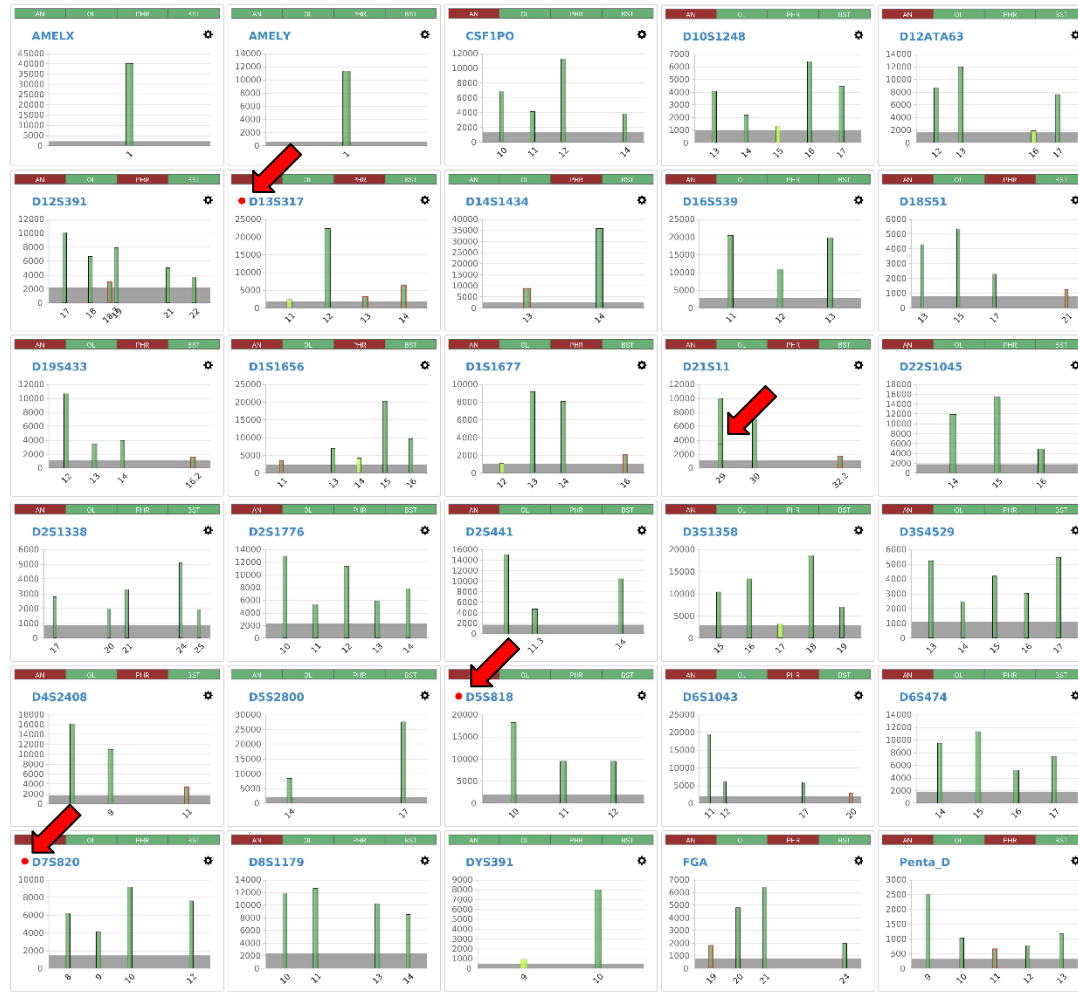
[Export Results](#) [More](#)

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☐	Result ID	Sample Name	Barcode	Sample Type	Batch Processing Status	CGQ at Sample Level	CGQ at Profile Level STR MH	Secondary Analysis Review STR MH	Sample Gender	Profile Gender STR	Action
☐	Result-S-1452.1	C1	IonCode_0138	Unknown	Complete		 N/A		Male Presence	M+	
☐	Result-S-1451.1	C2	IonCode_0139	Unknown	Complete		 N/A		Male Presence	M+	
☐	Result-S-1450.1	C3	IonCode_0140	Unknown	Complete		 N/A		Male Presence	M+	
☐	Result-S-1456.1	C4	IonCode_0141	Unknown	Complete		 N/A		Male Presence	M+	
☐	Result-S-1455.1	C5	IonCode_0142	Unknown	Complete		 N/A		Male Presence	M+	
☐	Result-S-1459.1	C6	IonCode_0143	Unknown	Complete		 N/A		Male Presence	M+	
☐	Result-S-1457.1	C7	IonCode_0144	Unknown	Complete		 N/A		Male Presence	M+	
☐	Result-S-1454.1	C8	IonCode_0145	Unknown	Complete		 N/A		Male Presence	M+	
☐	Result-S-1453.1	C9	IonCode_0146	Unknown	Complete		 N/A		No Male Presence	M-	
☐	Result-S-1458.1	G56_S4	IonCode_0133	Unknown	Complete		 N/A		Male Presence	M+	

Converge™ Software v2.1



Converge™ Software v2.1

appliedbiosystems
by Thermo Fisher Scientific

converge



Case-1047

Case Title: Case1

Creation Date: Feb-5-2019 1:45:18 PM

Owner: superUser

Case Description:

Case Comments :

Case External ID:

Last Modified Date: Feb-6-2019 1:53:19 PM

Requesting Organization:

Status: Open

Created By: superUser

Priority: Normal

Modified By: superUser

Edit

Collapse All

+ Subject

- Profile(s)

+ New Profile

More



Page 1 of 1

20

☐	Profile ID	Subject Name	Profile Category	Kit Name	Locus Type	Sample ID	Sample Name	Action
☐	Profile-1167		Forensic Mixture	PowerPlex_ESX_17	STR			...
☐	Profile-1168		Forensic Mixture	PowerPlex_ESX_17	STR			...
☐	Profile-1169		Forensic Mixture	PowerPlex_ESX_17	STR			...
☐	Profile-1170		Forensic Mixture	PowerPlex_ESX_17	STR			...
☐	Profile-1186		Forensic Mixture	PowerPlex_ESX_17	STR			...
☐	Profile-1171		Forensic Mixture	PowerPlex_ESX_17	STR			...
☐	Profile-1187		Forensic Mixture	PowerPlex_ESX_17	STR			...
☐	Profile-1188		Suspect	PowerPlex_ESX_17	STR			...
☐	Profile-1189		Suspect	PowerPlex_ESX_17	STR			...
☐	Profile-1100			Precision_ID_GlobalFiler_NGS_ST...	STR	S-1452.1	C1	...
☐	Profile-1112			Precision_ID_GlobalFiler_NGS_ST...	STR	S-1455.1	C5	...
☐	Profile-1107			Precision_ID_GlobalFiler_NGS_ST...	STR	S-1456.1	C4	...

+ Sample

+ Kinship

+ Attachment

Sensitivity and mixtures

DNA input	PCR cycles
1ng	23
500pg	23
250pg	25
125pg	26
62pg	28
31pg	

Control DNA 2800M

Mixture	DNA input (1ng final)
M control	1ng male
F control	1ng female
1:1	0.5ng female + 0.5ng male
1:4F	0.8ng female + 0.2ng male
1:9F	0.9ng female + 0.1ng male
1:29F	0.95ng female + 0.05ng male
1:4M	0.8ng male + 0.2ng female
1:9M	0.9ng male + 0.1ng female
1:29M	0.95ng male + 0.05ng female

all amplified in duplicate

Caseworks

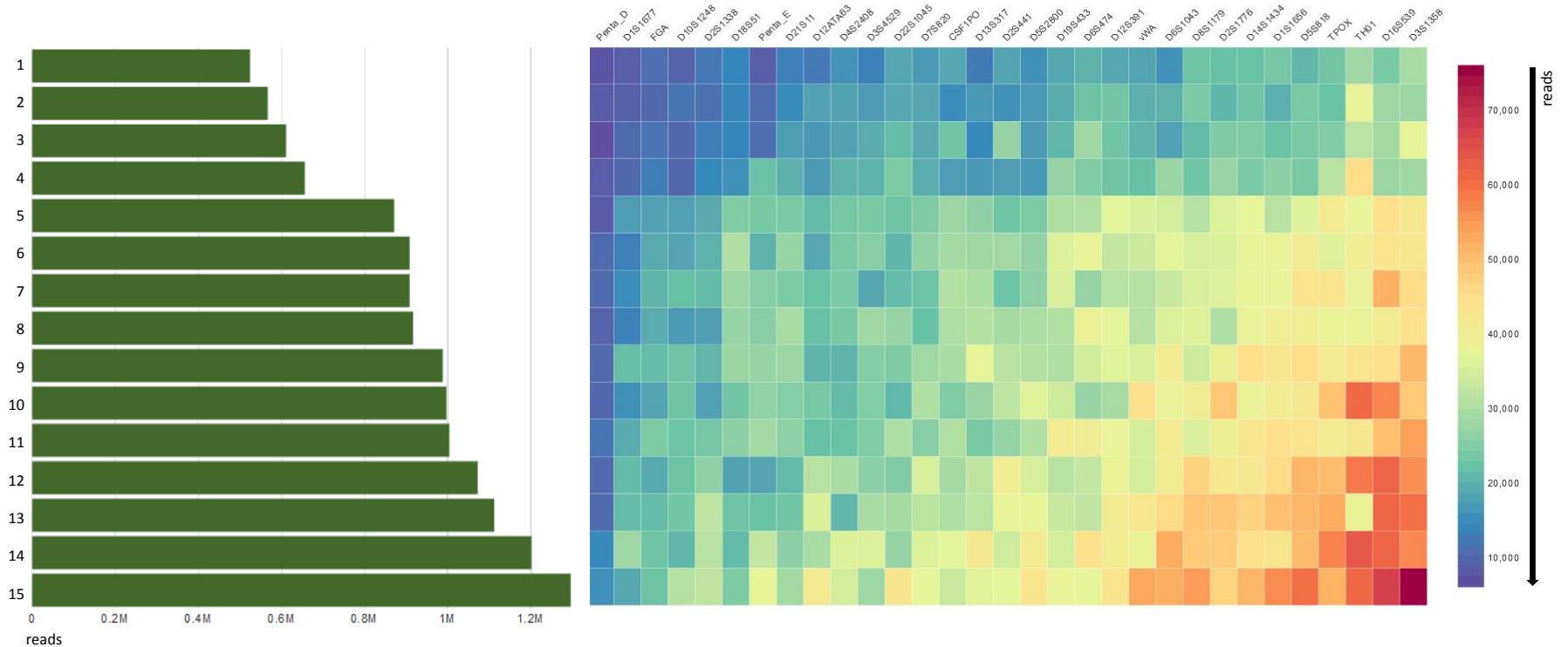


GEDNAP 56 and GEDNAP 57

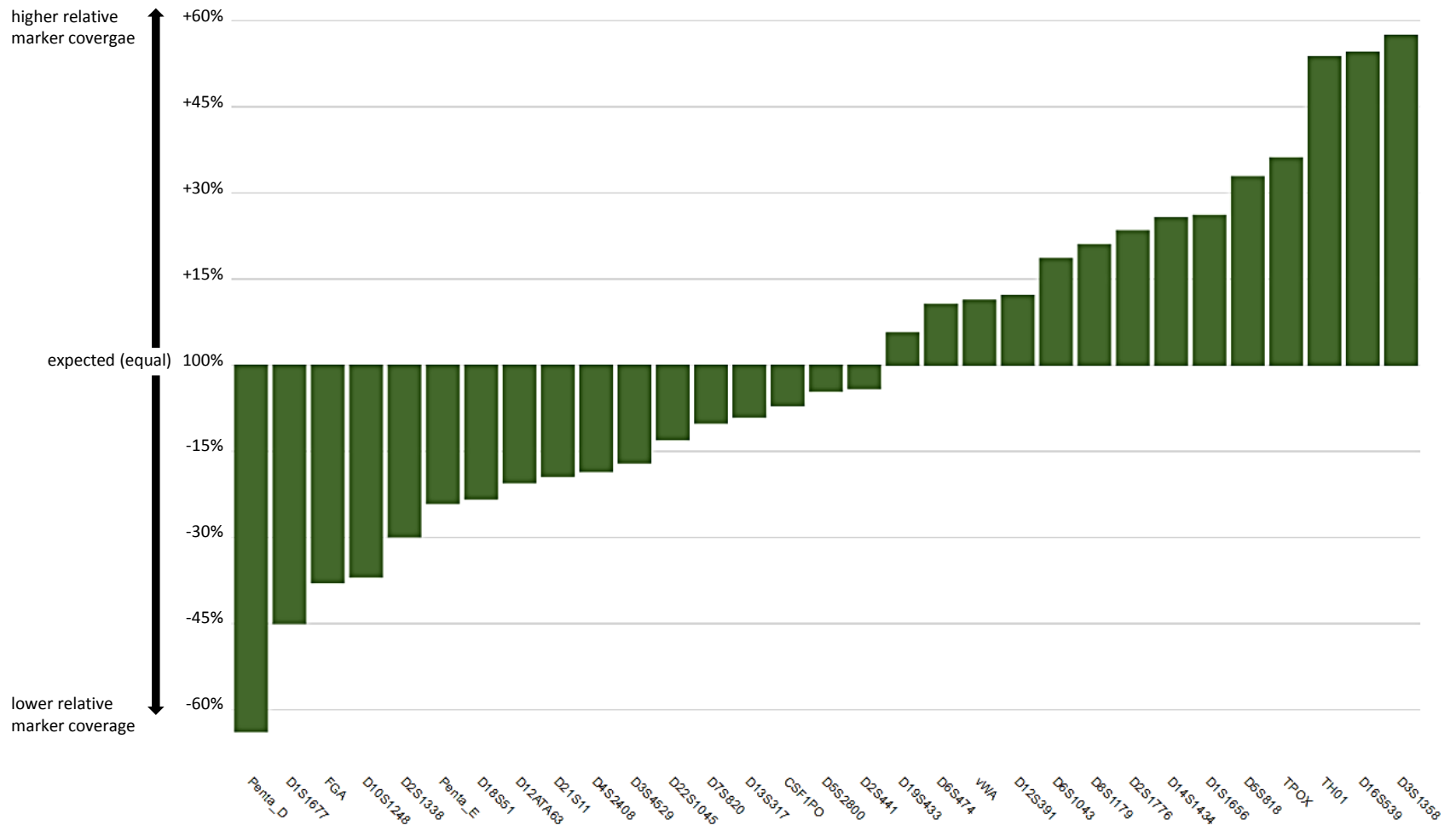


13 samples from 5 crime scenes, amplified in duplicate

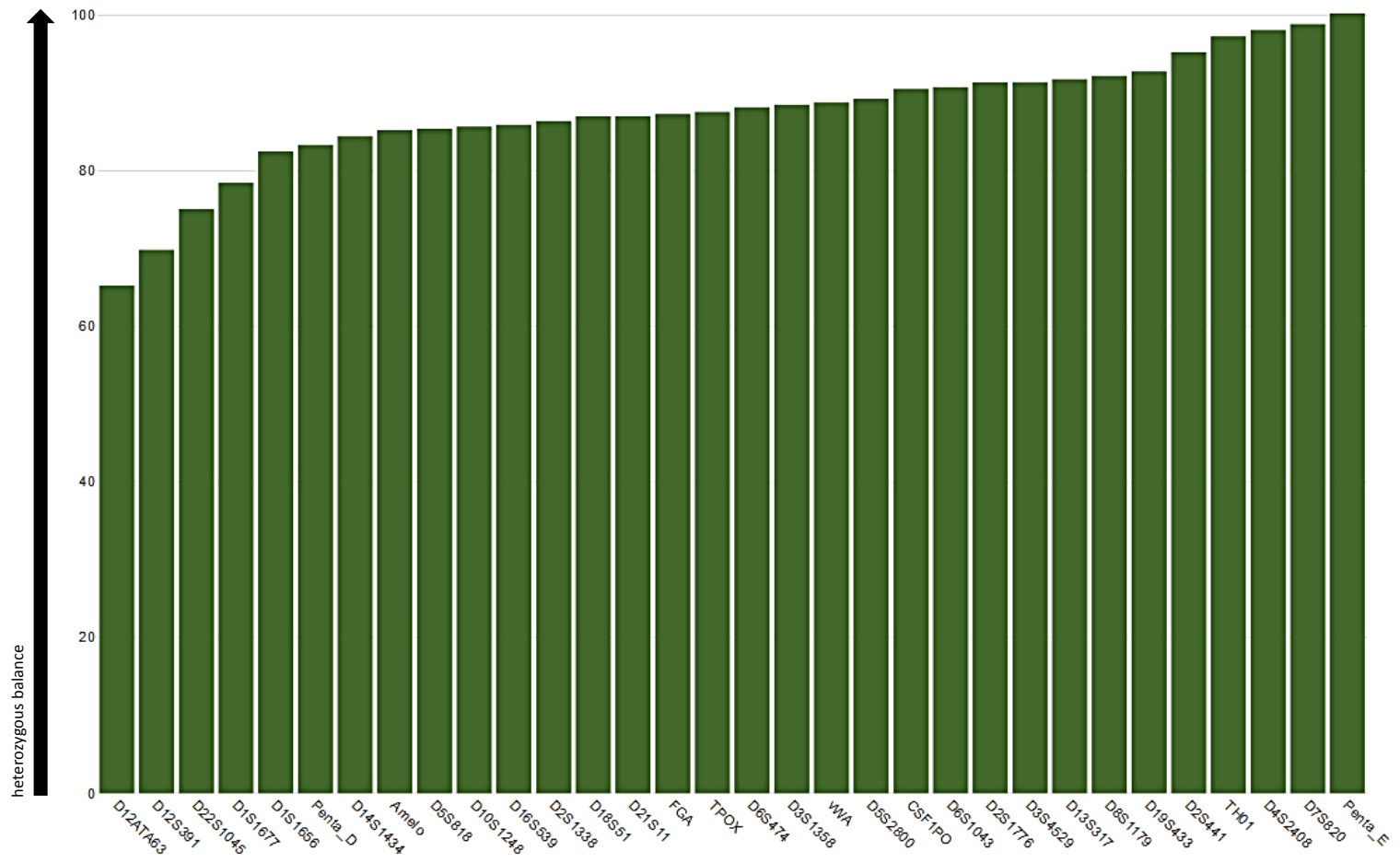
General performance – depth of coverage



General performance – interlocus balance

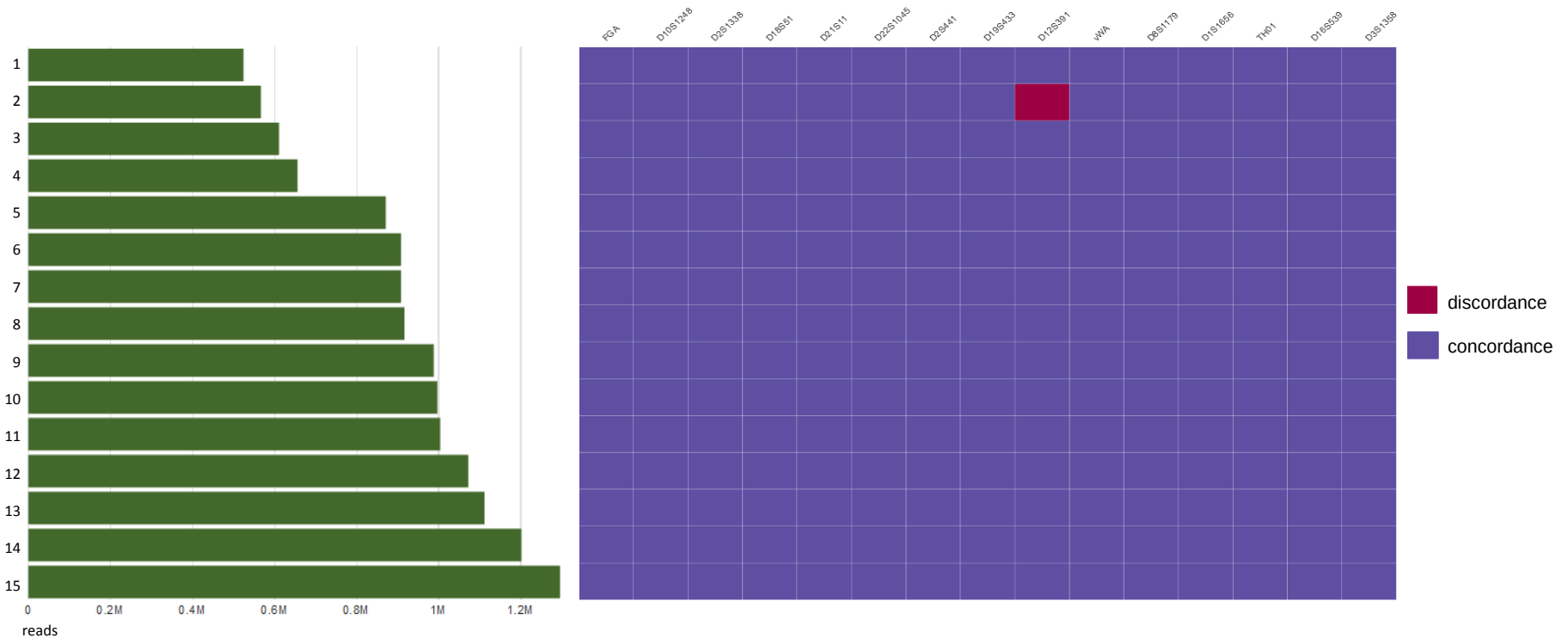


General performance - intralocus balance



General performance – concordance

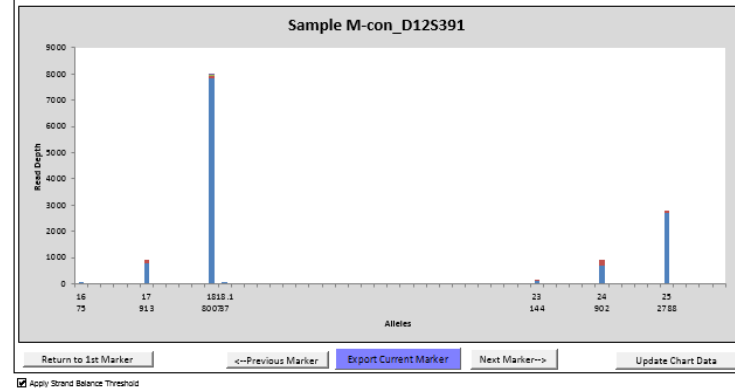
CE: PowerPlex® ESX 17 System



D12S391 - discordance

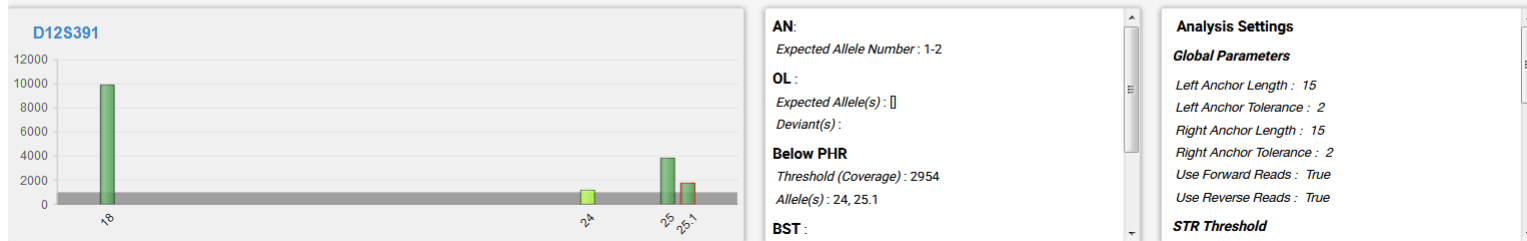
Sample ID	Locus	DoC	String Sequence Data	Length-based		Nomenclature
				Data		
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M-con	D125391	2716	GGATGTCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	25	NovelSeq	
M-con	D125391	756	GGATGTCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACA	17	D125391 [CE 17]-GRCh38-Chr12:12297008-12	
M-con	D125391	687	GGATGTCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	24	D125391 [CE 24]-GRCh38-Chr12:12297008-12	
M-con	D125391	216	GGATGTCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	24	NovelSeq	
M-con	D125391	157	GGATGTCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACA	17	D125391 [CE 17]-GRCh38-Chr12:12297008-12	
M-con	D125391	97	GGATGTCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACA	18	D125391 [CE 18]-GRCh38-Chr12:12297008-12	
M-con	D125391	91	GGATGTCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	23	D125391 [CE 23]-GRCh38-Chr12:12297008-12	
M-con	D125391	75	GGATGTCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACAGACAGACA	16	D125391 [CE 16]-GRCh38-Chr12:12297008-12	
M-con	D125391	72	GGATGTCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	25	NovelSeq	
M-con	D125391	53	GGATGTCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	23	NovelSeq	
M-con	D125391	45	GGATGTCATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACACA	18	NovelSeq	
M-con	D125391	37	GGATGTCATAGGTAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACACA	18	NovelSeq	
M-con	D125391	37	GGATGTCATAGGTAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGACAGACACA	18.1	NovelSeq	
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Determine Nomenclature of Novel Sequence

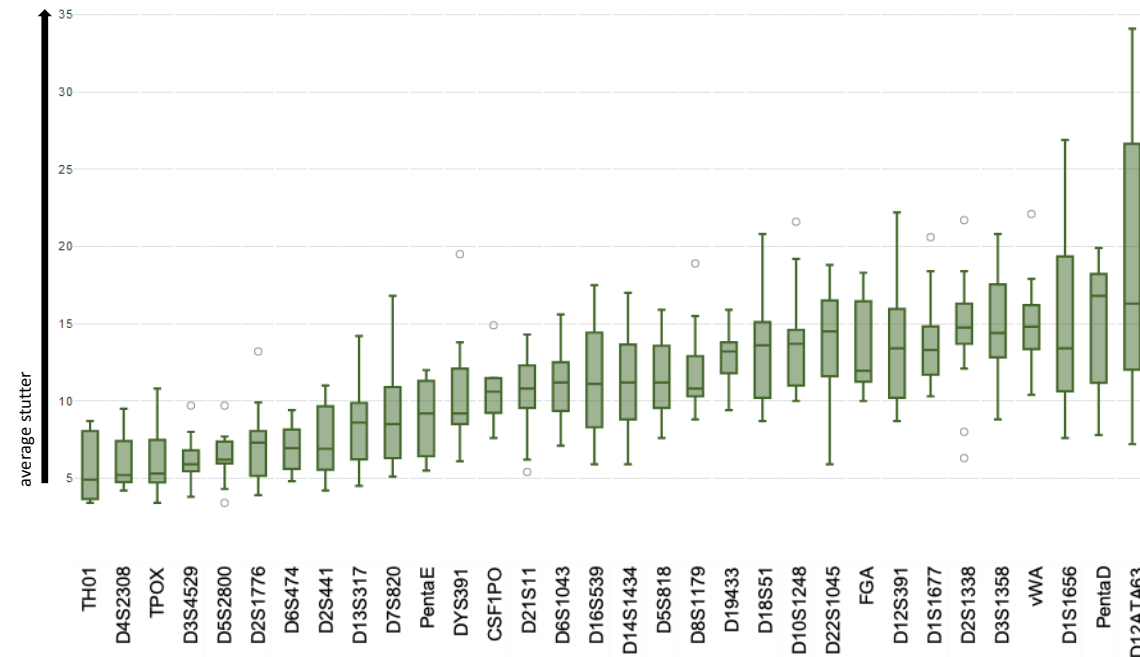


Source: STRait Razor v3

Alle...	Status	Coverage	Sequence	Long Sequence	Ref/A	RS Id's	SNP/Indel Location	Coverage%
18	ABOVE ST	9849	[AGAT]11 [AGAC]6 [AGAT]1	D12S391[CE18]-chr12-hg19 12449954-12450029 [AGAT]11 [AGAC]6 [AGAT]1				
24	STUTTER	1220	[AGAT]15 [AGAC]8 [AGAT]1	D12S391[CE24]-chr12-hg19 12449954-12450029 [AGAT]15 [AGAC]8 [AGAT]1				
25	ABOVE ST	3880	[AGAT]16 [AGAC]8 [AGAT]1	D12S391[CE25]-chr12-hg19 12449954-12450029 [AGAT]16 [AGAC]8 [AGAT]1				
25.1	ABOVE ST	1773	[AGAT]16 [AGAC]8 AGAGT	D12S391[CE25.1]-chr12-hg19 12449954-12450029 [AGAT]16 [AGAC]8 AGAGT				



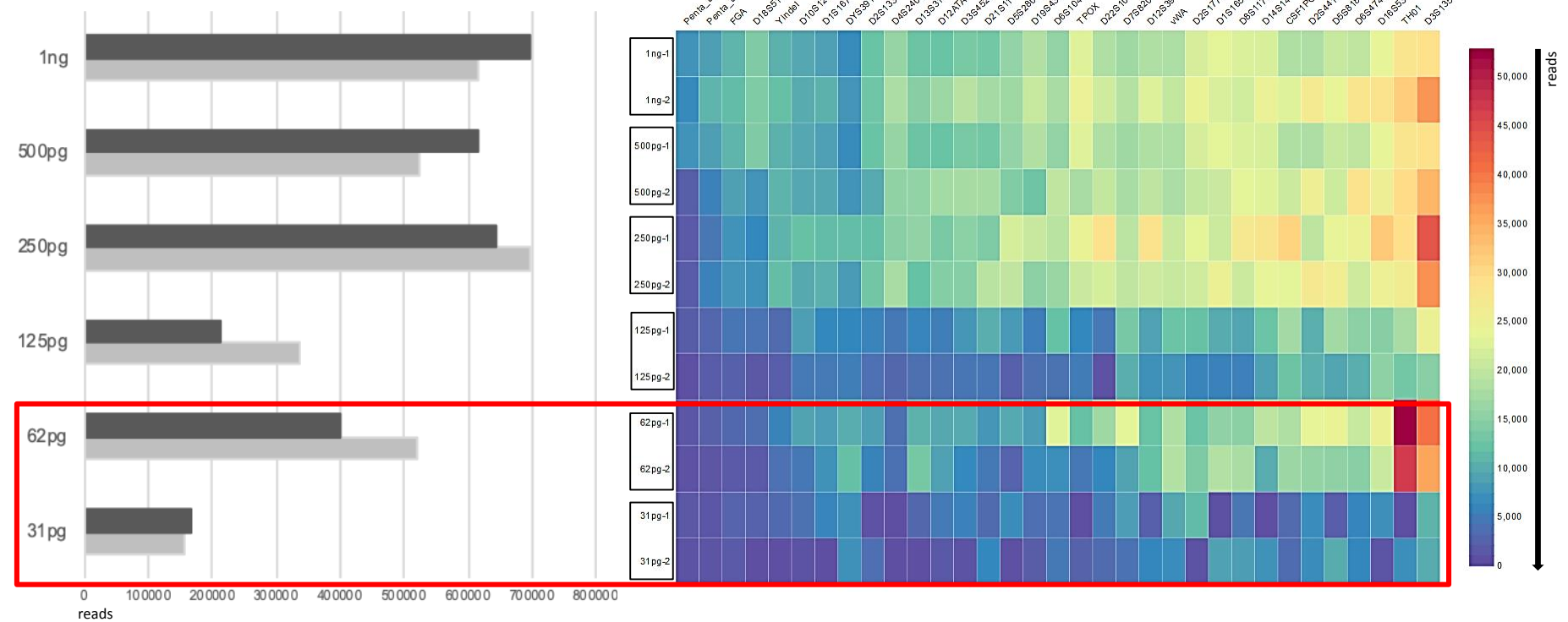
General performance – stutter



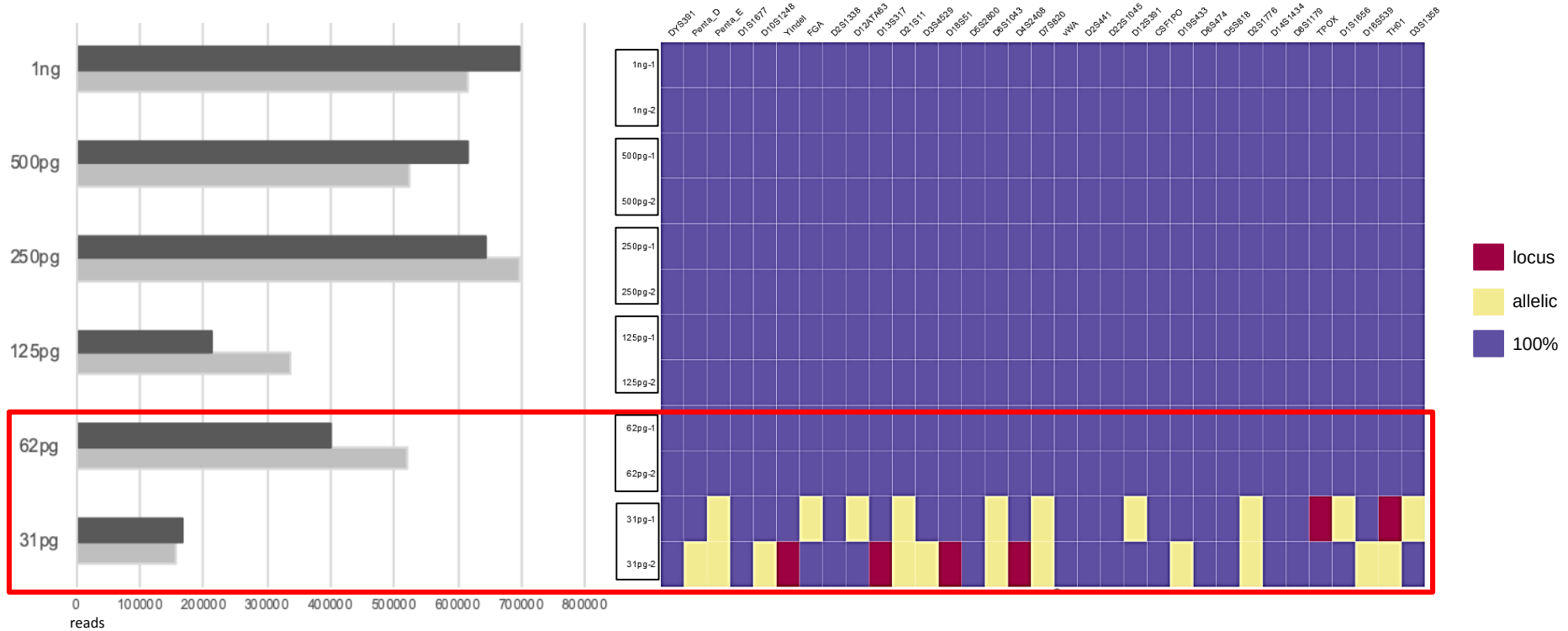
lowest stutter: TH01 (5,5%)

highest stutter: D12ATA63 (18,9%)

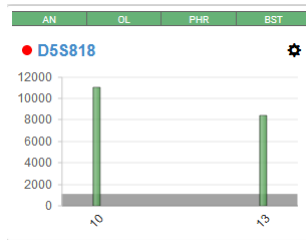
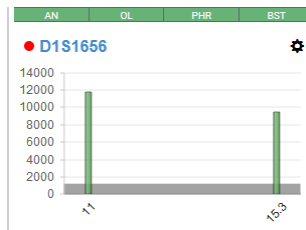
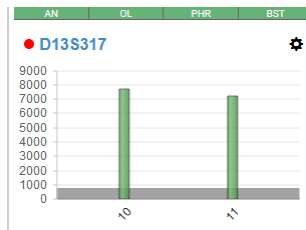
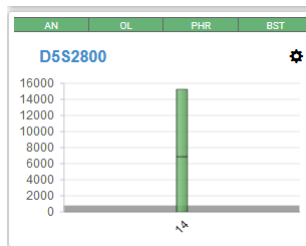
Sensitivity - coverage



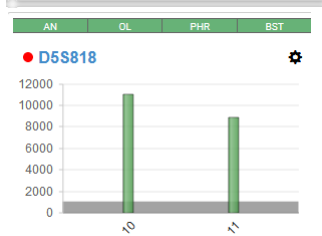
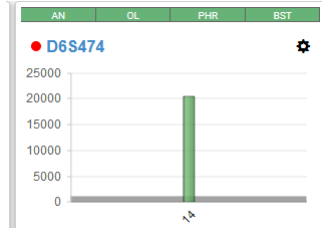
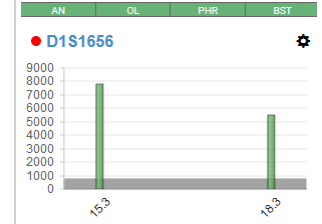
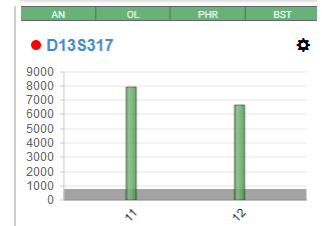
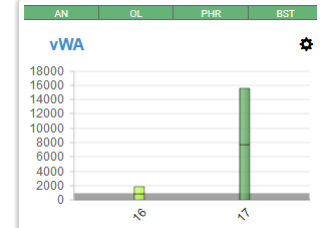
Sensitivity – drop outs



Mixtures

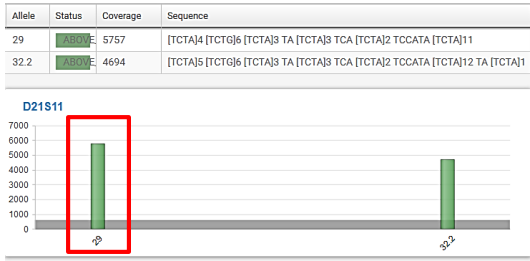


Locus	Female contributor		Male contributor	
	sequence-based	long sequence-based	sequence-based	long-sequence based
Penta_D	13	13	9	9
Penta_E	13,14	13,14	7,17	7,17
D2S1338	19,25	19,25	17,21	17,21
D22S1045	11,16	11,16	11,15	11,15
TPOX	8	8	8	8
D2S1776	9,12	9,12	11	11
D13S317	10,11	10,11	11,12	11,12
D21S11	29,31	29,31	29,32.2	29,32.2
D3S4529	13,15	13,15	13,17	13,17
D18S51	16,17	16,17	15,18	15,18
FGA	23,25	23,25	22,23	22,23
D10S1248	15	15	13	13
D4S2408	9	9	8,9	8,9
D1S1677	15,16	15,16	14	14
D12ATA63	12,19	12,19	12,13	12,13
DYS391	-	-	10	10
D19S433	14,15.2	14,15.2	13	13
D2S441	11,11.3	11,11.3	10,12	10,12
D14S1434	13	13	10,13	10,13
D5S2800	14	14	14,18	14,18
D7S820	10,12	10,12	8,10	8,10
D8S1179	12,13	12,13	12,14	12,14
CSF1PO	10	10	10	10
D1S1656	11,15.3	11,15.3	15.3,18.3	15.3,18.3
vWA	14,16	14,16	17	17
D6S474	14,17	14,17	14	14
D12S391	19,22	19,22	18,25	18,25
D16S539	11,12	11,12	11,13	11,13
D6S1043	11,12	11,12	11,12	11,12
D5S818	10,13	10,13	10,11	10,11
TH01	7,9.3	7,9.3	8,9.3	8,9.3
D3S1358	14	14	13,17	13,17

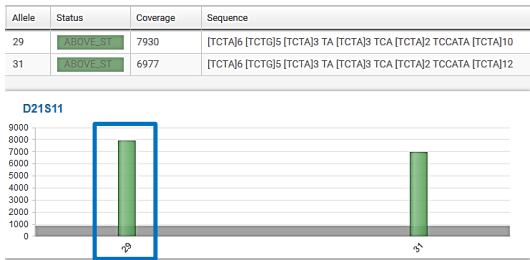


Mixtures – sequence-based alleles

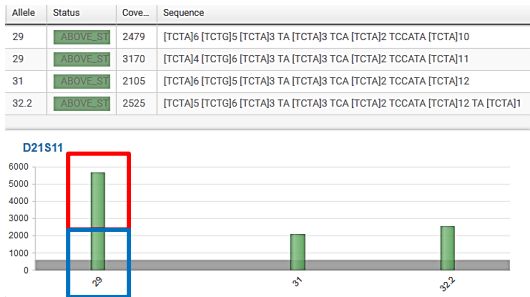
contributor 1



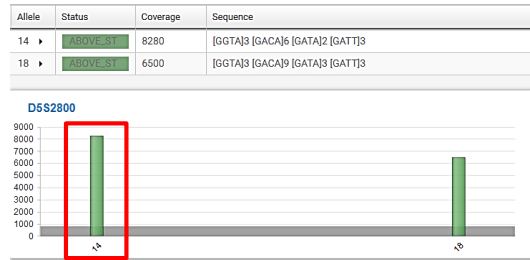
contributor 2



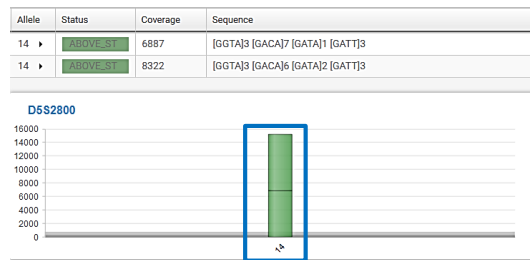
mix 1:1



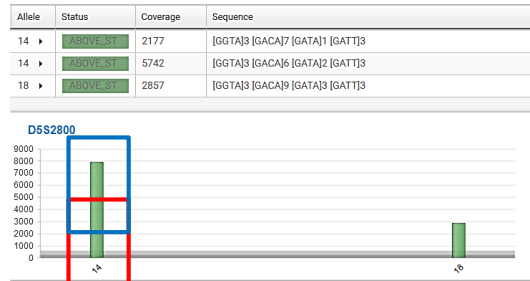
contributor 1



contributor 2

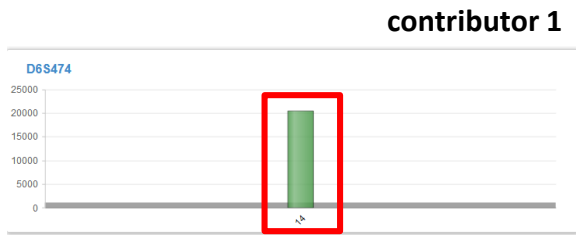


mix 1:1

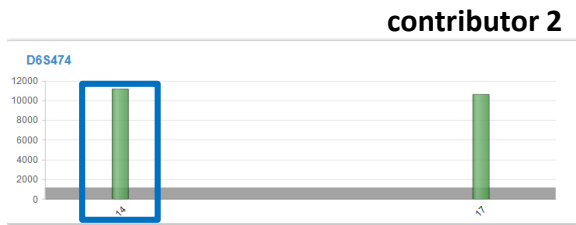


Mixtures – long sequence-based alleles

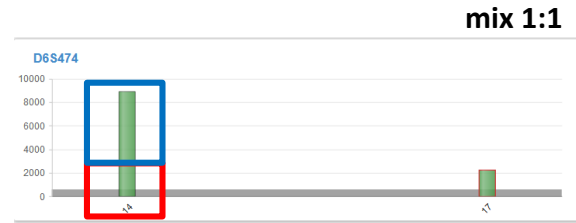
Allele	Status	Coverage	Sequence	Long Sequence	Ref/Alt	RS Id's	SNP/indel Location	Coverage%	Quality
14	ABOVE ST	20428	[AGAT]5 [GATA]	D6S474[CE14]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]9	-	-			
14		9257	[AGAT]5 [GATA]9	D6S474[CE14]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]9	-	-			
14		10988	[AGAT]5 [GATA]9	D6S474[CE14]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]9 112879241-G	A/G	rs62414880			16.96



Allele	Status	Coverage	Sequence	Long Sequence	Ref/Alt	RS Id's	SNP/indel Location	Coverage%	Quality
14	ABOVE ST	11136	[AGAT]5 [GATA]9	D6S474[CE14]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]9	-	-			
14		11116	[AGAT]5 [GATA]9	D6S474[CE14]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]9	-	-			
17	ABOVE ST	10630	[AGAT]5 [GATA]12	D6S474[CE17]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]12					



Allele	Status	Coverage	Sequence	Long Sequence	Ref/Alt	RS Id's	SNP/indel Location	Coverage%	Quality
14	ABOVE ST	8919	[AGAT]5 [GATA]	D6S474[CE14]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]9	-	-			
14		5676	[AGAT]5 [GATA]9	D6S474[CE14]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]9	-	-			
14		3189	[AGAT]5 [GATA]9	D6S474[CE14]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]9 112879241-G	A/G	rs62414880			14.45
17	ABOVE ST	2248	[AGAT]5 [GATA]	D6S474[CE17]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]12					



Casework: GEDNAP

56			57		
	source	contributor		source	contributor
PersonA	blood	male	PersonA	blood	female
PersonB	blood	male	PersonB	blood	male
PersonC	blood	female	PersonC	blood	male
Stain1	blood	male	Stain1	blood	male
Stain2	blood	male	Stain2	sperm	male
Stain3	sperm	male	Stain3	blood	2x female; male
Stain4	blood	2x male	Stain4	blood	female; male

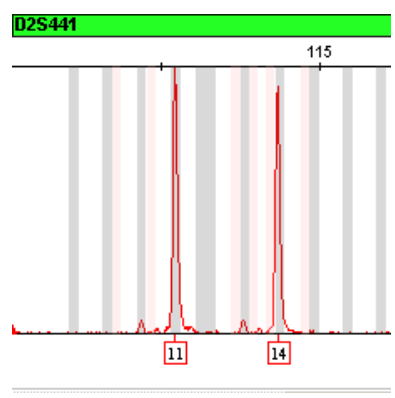
Casework: GEDNAP

56		57	
concordance CE: PowerPlex® ESX 17 System			
PersonA	100%	PersonA	100%
PersonB	100%	PersonB	100%
PersonC	100%	PersonC	100%
Stain1	100%	Stain1	100%
Stain2	100%	Stain2	100%
Stain3	100%	Stain3	100%
Stain4	100%	Stain4	100%

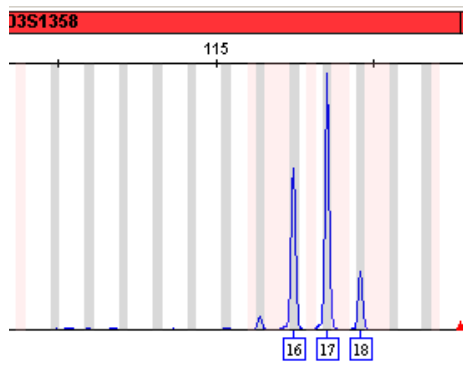
Casework: GEDNAP

56			57		
	sequence-based	long sequence-based		sequence-based	long sequence-based
PersonA		+4	PersonA	+2	+6
PersonB		+5	PersonB		+4
PersonC	+1	+5	PersonC		+3
Stain1		+2	Stain1	+1	+2
Stain2	+1	+5	Stain2	+1	+3
Stain3	+1	+2			

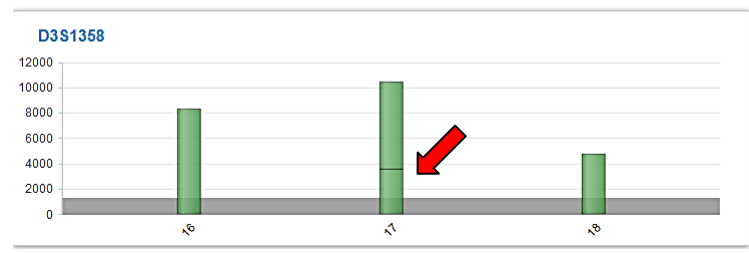
GEDNAP 56 - Stain 4 - 2x male



Allele	Status	Coverage	Sequence
11	ABOVE_ST	4203	[TCTA]11
11 ▶	ABOVE_ST	5385	[TCTA]9 TCTG[TCTA]1
14 ▶	ABOVE_ST	5651	[TCTA]11 TTTA[TCTA]2

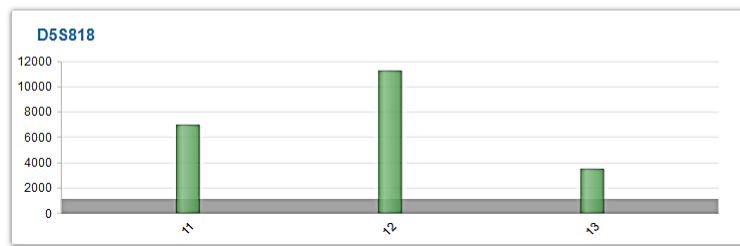


Allele	Status	Coverage	Sequence
16	ABOVE_ST	8353	[TCTA]1 [TCTG]2 [TCTA]13
17 ▶	ABOVE_ST	3585	[TCTA]1 [TCTG]2 [TCTA]14
17 ▶	ABOVE_ST	6858	[TCTA]1 [TCTG]3 [TCTA]13
18	ABOVE_ST	4792	[TCTA]1 [TCTG]3 [TCTA]14



GEDNAP 56 - Stain 4 - 2x male

Allele	Status	Cove...	Sequence	Long Sequence	Ref/Alt	RS Id's	SNP/Indel Location	Coverage%	Quality
11	ABOVE	6975	[AGAT]11	D5S818[CE11]-chr5-hg19 123111250-123111293 [AGAT]11					
12	ABOVE	11257	[AGAT]12	D5S818[CE12]-chr5-hg19 123111250-123111293 [AGAT]12					
12		6482	[AGAT]12	D5S818[CE12]-chr5-hg19 123111250-123111293 [AGAT]12		-			-
12		4742	[AGAT]12	D5S818[CE12]-chr5-hg19 123111250-123111293 [AGAT]12 123111306-G	A/G	rs25768			18.32
13	ABOVE	3483	[AGAT]13	D5S818[CE13]-chr5-hg19 123111250-123111293 [AGAT]13					



AN:
Expected Allele Number : 1-2

OL :
Expected Allele(s) : [6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 10.1, 11.1, 12.1, 12.3]
Deviant(s) :

Below PHR
Threshold (Coverage) : 3377
Allele(s) :

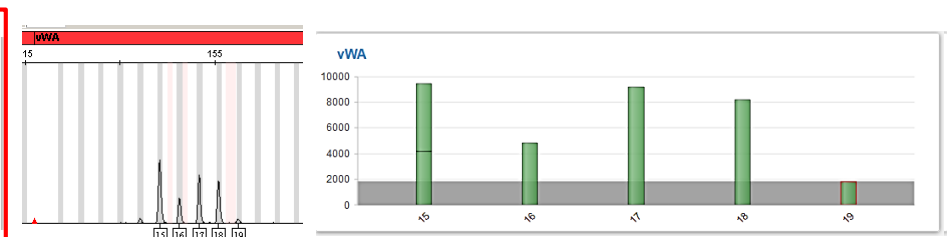
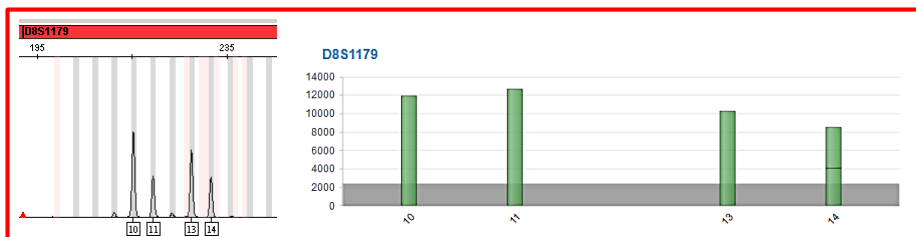
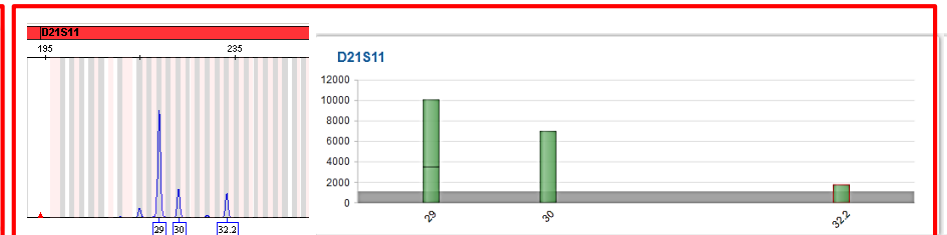
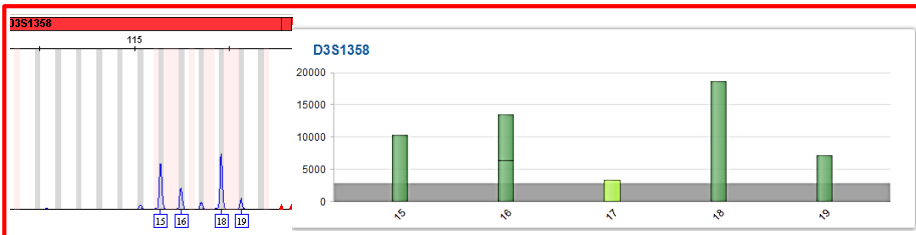
Analysis Settings

Global Parameters

Left Anchor Length : 15
Left Anchor Tolerance : 2
Right Anchor Length : 15
Right Anchor Tolerance : 2
Use Forward Reads : True
Use Reverse Reads : True

STR Threshold

GEDNAP 57 - Stain 3 - 2x female; male



Casework: mixtures

Case	Traces	Source	Contributor	DNA input
1 burglary	M9	swab (bottle)	suspect1	62pg
	M10	cigarette butt	suspect2	1ng
	M11	cigarette butt	mixture	1ng
2 homicide	M6	swab (blood on thumb)	suspect	250pg
	M7	blood (floor at crime scene)	victim	1ng
	M8	blood (knife's blade)	mixture	62pg
3 robbery	M17	swab (handbag at crime scene)	complex mix	250pg
	M18	swab (body)	suspect	1ng

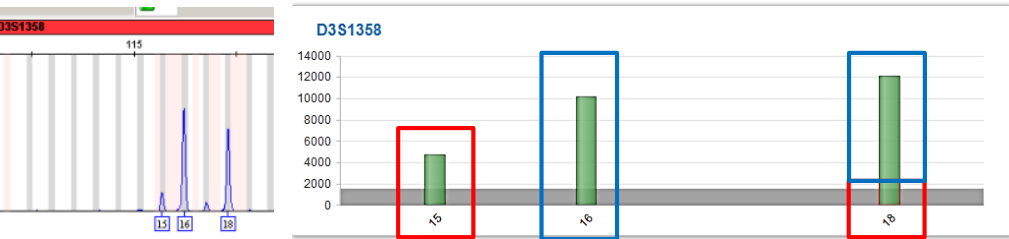
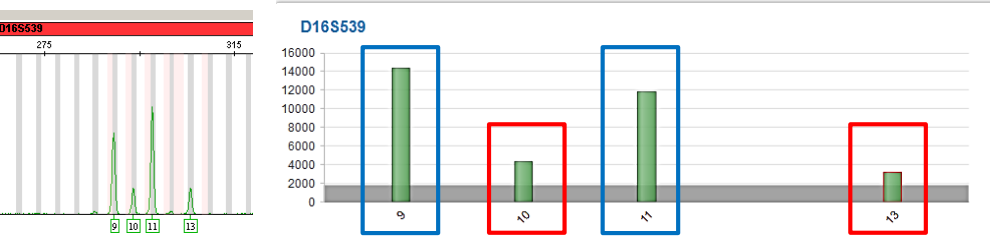
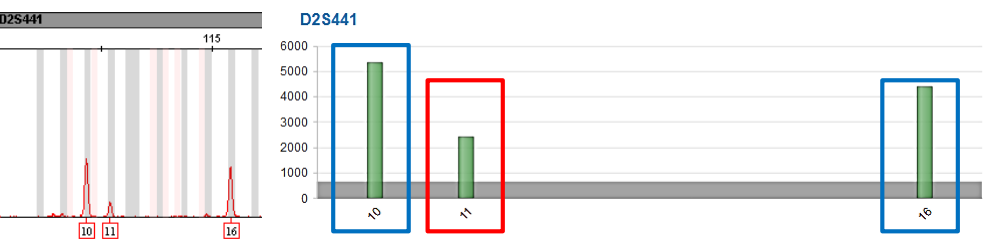
Case 1

Locus	suspect1 CE	suspect1 NGS	suspect2 CE	suspect2 NGS
Amel	XY	XY	XY	XY
D2S1338	17,20	17,20	20,23	20,23
D22S1045	11,15	11,15	11,15	11,15
D21S11	28,30	28,30	28,32.2	28,32.2
D18S51	12,16	12,16	16,17	16,17
FGA	22,23.2	22,23.2	19,23	19,23
D10S1248	15,17	15,17	16,17	16,17
D19S433	13,13	13,13	14,15	14,15
D2S441	11,11	11,11 SNP	10,16	10,16
D8S1179	15,16	15,16	13,14	13,14
D1S1656	13,14	13,14	11,12	11,12
vWA	16,17	16,17	16,17	16,17
D12S391	15,21	15,21	22,25	22,25
D16S539	10,13	10,13 SNP	9,11	9,11 SNP
TH01	7,7	7,7	7,9	7,9
D3S1358	15,18	15,18	16,18	16,18

Case 1

Locus	suspect1 CE	suspect1 NGS	suspect2 CE	suspect2 NGS	mixture CE	mixture NGS
Amel	XY	XY	XY	XY	XY	XY
D2S1338	17,20	17,20	20,23	20,23	17,20,23	17,20,23
D22S1045	11,15	11,15	11,15	11,15	11,15	11,15
D21S11	28,30	28,30	28,32.2	28,32.2	28,30,32.2	28,30,32.2
D18S51	12,16	12,16	16,17	16,17	12,16,17	12,16,17
FGA	22,23.2	22,23.2	19,23	19,23	19,23	19,23
D10S1248	15,17	15,17	16,17	16,17	15,16,17	15,16,17
D19S433	13,13	13,13	14,15	14,15	13,14,15	13,14,15
D2S441	11,11	11,11 SNP	10,16	10,16	10,11,16	10,11,16
D8S1179	15,16	15,16	13,14	13,14	13,14,15,16	13,14,15,16
D1S1656	13,14	13,14	11,12	11,12	11,12,13,14	11,12,13,14
vWA	16,17	16,17	16,17	16,17	16,17	16,17
D12S391	15,21	15,21	22,25	22,25	15,21,22,25	15,21,22,25
D16S539	10,13	10,13 SNP	9,11	9,11 SNP	9,10,11,13	9,10,11,13
TH01	7,7	7,7	7,9	7,9	7,9	7,9
D3S1358	15,18	15,18	16,18	16,18	15,16,18	15,16,18

Case 1 - cigarette butt from the scene



Allele	Stat...	Covera...	Sequence	Long Sequence
10	ABOV	5333	[TCTA]10	D2S441[CE10]-chr2-hg19 68239079-68239126 [TCTA]10
11	ABOV	2419	[TCTA]11	D2S441[CE11]-chr2-hg19 68239079-68239126 [TCTA]11
11	suspect1	1232	[TCTA]11	D2S441[CE11]-chr2-hg19 68239079-68239126 [TCTA]11
11		1180	[TCTA]11	D2S441[CE11]-chr2-hg19 68239079-68239126 [TCTA]11 68239054-A
16	ABOV	4417	[TCTA]13 TTTA[TCTA]2	D2S441[CE16]-chr2-hg19 68239079-68239126 [TCTA]13 TTTA[TCTA]2

Allele	Status	Coverage	Sequence	Long Sequence
9	ABOVE_ST	14380	[GATA]9	D16S539[CE9]-chr16-hg19 86386308-86386351 [GATA]9
9		292	[GATA]9	D16S539[CE9]-chr16-hg19 86386308-86386351 [GATA]9 86386367
9	suspect2	13867	[GATA]9	D16S539[CE9]-chr16-hg19 86386308-86386351 [GATA]9 86386298-G
10	ABOVE_ST	4410	[GATA]10	D16S539[CE10]-chr16-hg19 86386308-86386351 [GATA]10
10		1126	[GATA]10	D16S539[CE10]-chr16-hg19 86386308-86386351 [GATA]10
10	suspect1	3157	[GATA]10	D16S539[CE10]-chr16-hg19 86386308-86386351 [GATA]10 86386367-C
11	ABOVE_ST	11801	[GATA]11	D16S539[CE11]-chr16-hg19 86386308-86386351 [GATA]11
13	ABOVE_ST	3159	[GATA]13	D16S539[CE13]-chr16-hg19 86386308-86386351 [GATA]13

Allele	Status	Coverage	Sequence
15	ABOVE_ST	4772	[TCTA]1 [TCTG]2 [TCTA]12
16	ABOVE_ST	10185	[TCTA]1 [TCTG]2 [TCTA]13
18	ABOVE_ST	2247	[TCTA]1 [TCTG]3 [TCTA]14 suspect1
18	ABOVE_ST	9878	[TCTA]1 [TCTG]4 [TCTA]13 suspect2

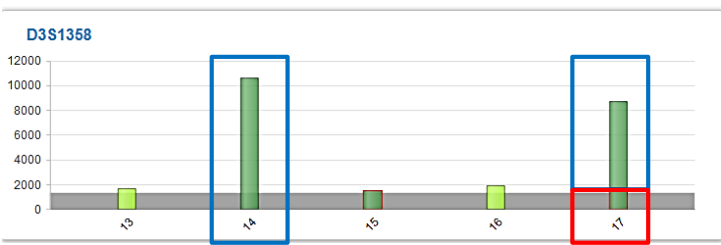
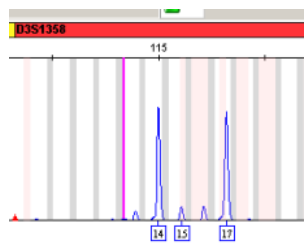
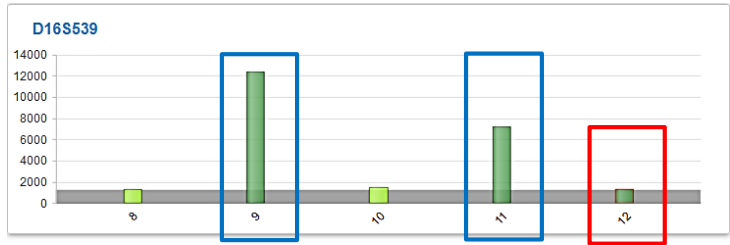
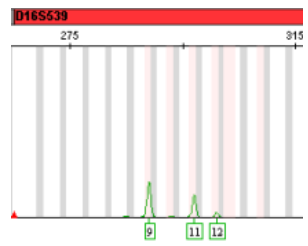
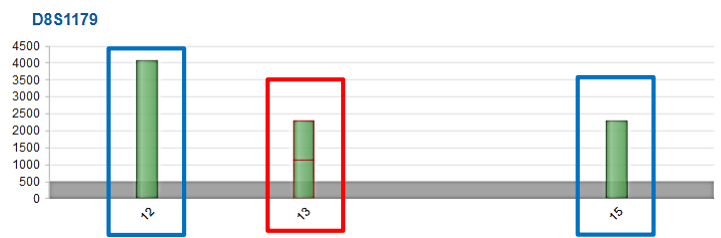
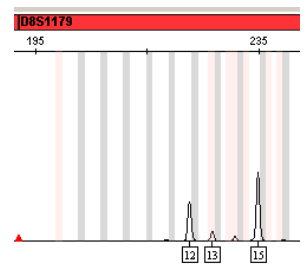
Case 2

Locus	suspect CE	suspect NGS	victim CE	suspect NGS
Amel	XX	XX	XX	XX
D2S1338	22,25	22,25	22,22	22,22
D22S1045	11,14	11,14	11,16	11,16
D21S11	29,31	29,31	30,31	30,31
D18S51	12,16	12,16	15,16	15,16
FGA	26,28	26,28	21,22	21,22
D10S1248	14,14	14,14	13,13	13,13
D19S433	13,13	13,13	13,13	13,13
D2S441	10,14	10,14	14,14	14,14
D8S1179	13,13	13,13 iso	12,15	12,15
D1S1656	17.3,17.3	17.3, 17.3 SNP	14,16.3	14,16.3 SNP
vWA	15,17	15,17	17,18	17,18
D12S391	17,19	17,19	18,18	18,18 iso
D16S539	12,12	12,12	9,11	9,11 SNP
TH01	7,8	7,8	7,9	7,9
D3S1358	17,17	17,17	14,17	14,17

Case 2

Locus	suspect CE	suspect NGS	victim CE	victim NGS	mixture CE	mixture NGS
Amel	XX	XX	XX	XX	XX	XX
D2S1338	22,25	22,25	22,22	22,22	22,25	22
D22S1045	11,14	11,14	11,16	11,16	11,14,16	11,14,16
D21S11	29,31	29,31	30,31	30,31	29,30,31	29,30,31
D18S51	12,16	12,16	15,16	15,16	12,15,16	15,16,17
FGA	26,28	26,28	21,22	21,22	21,22,26,28	21,22
D10S1248	14,14	14,14	13,13	13,13	13,14	13,14
D19S433	13,13	13,13	13,13	13,13	13	13
D2S441	10,14	10,14	14,14	14,14	10,14	10,14
D8S1179	13,13	13,13 iso	12,15	12,15	12,13,15	12,13,15
D1S1656	17.3,17.3	17.3, 17.3 SNP	14,16.3	14,16.3 SNP	14,16.3,17.3	14,16.3,17.3
vWA	15,17	15,17	17,18	17,18	15,17,18	15,17,18
D12S391	17,19	17,19	18,18	18,18 iso	17,18,19	18,18
D16S539	12,12	12,12	9,11	9,11 SNP	9,11,12	9,11,12
TH01	7,8	7,8	7,9	7,9	7,8,9	7,8,9
D3S1358	17,17	17,17	14,17	14,17	14,15,17	14,15,17,17

Case 2 - bloody knife from the scene



Allele	Status	Coverage	Sequence
12	ABOVE_ST	4064	[TCTA]2 TCTG[TCTA]9
13	ABOVE_ST	1134	[TCTA]1 TCTG[TCTA]11
13	ABOVE_ST	1159	[TCTA]2 TCTG[TCTA]10
15	ABOVE_ST	2296	[TCTA]2 TCTG[TCTA]12

suspect

Allele	Status	Coverage	Sequence	Long Sequence	Ref/Alt	RS Id's
8	STUTTER	1378	[GATA]8	D16S539[CE8]-chr16-hg19 86386308-86386351 [GATA]8		
9	ABOVE	12376	[GATA]9	D16S539[CE9]-chr16-hg19 86386308-86386351 [GATA]9		
9		318	[GATA]9	D16S539[CE9]-chr16-hg19 86386308-86386351 [GATA]9	-	
9	victim	11849	[GATA]9	D16S539[CE9]-chr16-hg19 86386308-86386351 [GATA]9 86386367-C	A/C	
10	STUTTER	1478	[GATA]10	D16S539[CE10]-chr16-hg19 86386308-86386351 [GATA]10		
11	ABOVE	7218	[GATA]11	D16S539[CE11]-chr16-hg19 86386308-86386351 [GATA]11		
12	ABOVE	1370	[GATA]12	D16S539[CE12]-chr16-hg19 86386308-86386351 [GATA]12		



Allele	Status	Coverage	Sequence
13	STUTTER	1724	[TCTA]1 [TCTG]2 [TCTA]10
14	ABOVE_ST	10633	[TCTA]1 [TCTG]2 [TCTA]11
15	ABOVE_ST	1537	[TCTA]1 [TCTG]1 [TCTA]13
16	STUTTER	1907	[TCTA]1 [TCTG]1 [TCTA]14
17	ABOVE_ST	1741	[TCTA]1 [TCTG]2 [TCTA]14
17	ABOVE_ST	7004	[TCTA]1 [TCTG]1 [TCTA]15

suspect

victim

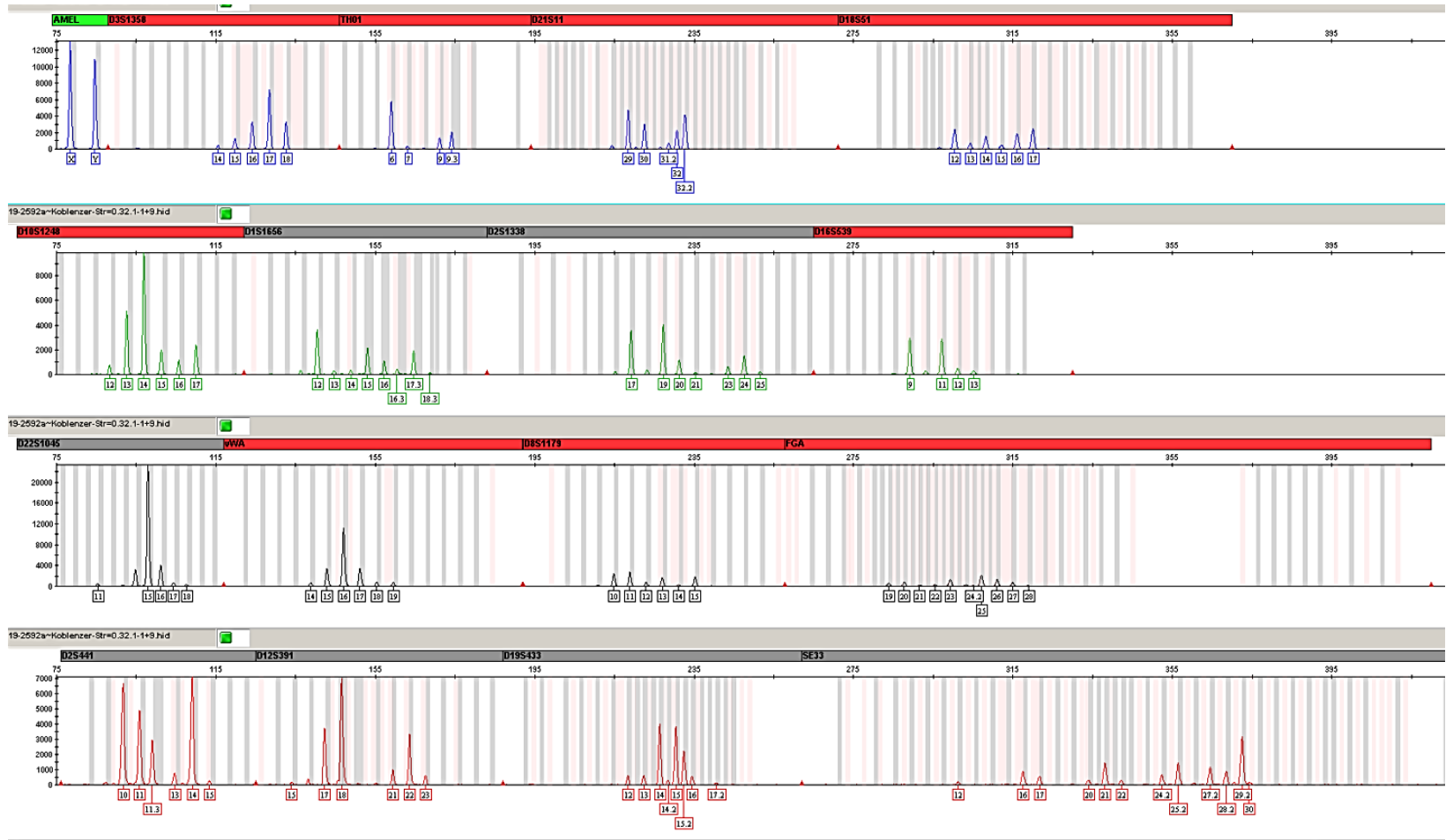
Case 3

Locus	suspect CE	suspect NGS
Amel	XY	XY
D2S1338	19,24	19,24
D22S1045	15,15	15,15
D21S11	32,32.2	32,32.2
D18S51	14,17	14,17
FGA	25,26	25,26
D10S1248	13,14	13,14
D19S433	15,15.2	15,15.2
D2S441	10,11.3	10,11.3
D8S1179	10,15	10,15
D1S1656	12,17.3	12,17.3 SNP
vWA	16,16	16,16
D12S391	18,22	18,22
D16S539	9,11	9,11
TH01	6,6	6,6
D3S1358	17,17	17,17

Case 3

Locus	suspect CE	suspect NGS	mixture CE
Amel	XY	XY	XY
D2S1338	19,24	19,24	17,19,20,23,24,25
D22S1045	15,15	15,15	11,15,16
D21S11	32,32.2	32,32.2	29,30,31.2,32,32.2
D18S51	14,17	14,17	12,13,14,15,16,17
FGA	25,26	25,26	19,20,22,23,25,26,27,28
D10S1248	13,14	13,14	12,13,14,15,16,17
D19S433	15,15.2	15,15.2	13,14,14.2,15,15.2,16
D2S441	10,11.3	10,11.3	10,11,11.3,14,15
D8S1179	10,15	10,15	10,11,12,13,14,15
D1S1656	12,17.3	12,17.3 SNP	12,15,16,16.3,17.3,18.3
vWA	16,16	16,16	15,16,17,18,19
D12S391	18,22	18,22	17,18,21,22,23
D16S539	9,11	9,11	9,11,12,13
TH01	6,6	6,6	6,7,9,9.3
D3S1358	17,17	17,17	14,15,16,17

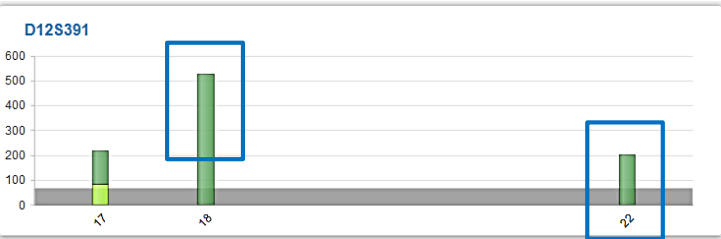
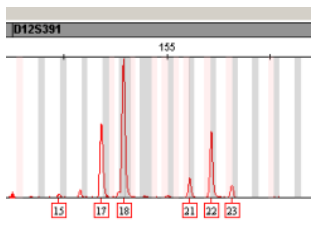
Case 3



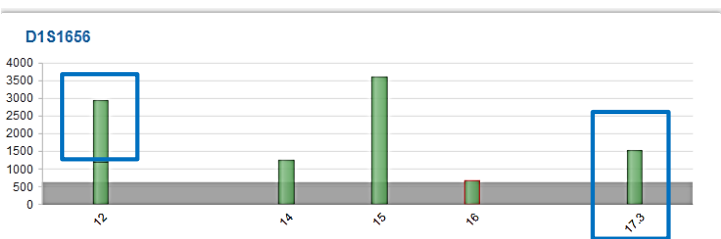
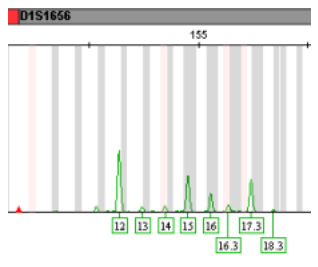
Case 3

Locus	suspect CE	suspect NGS	mixture CE	mixture NGS
Amel	XY	XY	XY	XY
D2S1338	19,24	19,24	17,19,20,23,24,25	17,19,24
D22S1045	15,15	15,15	11,15,16	11,15,16
D21S11	32,32.2	32,32.2	29,30,31.2,32,32.2	29,29,30,31.2,32,32.2
D18S51	14,17	14,17	12,13,14,15,16,17	12,13,14,15,16,17
FGA	25,26	25,26	19,20,22,23,25,26,27,28	19,20,21,22,23,24,25,26
D10S1248	13,14	13,14	12,13,14,15,16,17	12,13,14,15,16,17
D19S433	15,15.2	15,15.2	13,14,14.2,15,15.2,16	13,14,14.2,15,15.2,16
D2S441	10,11.3	10,11.3	10,11,11.3,14,15	10,11,11.3,14
D8S1179	10,15	10,15	10,11,12,13,14,15	10,11,12,13,14,15
D1S1656	12,17.3	12,17.3 SNP	12,15,16,16.3,17.3,18.3	12,12,14,15,16,17.3
vWA	16,16	16,16	15,16,17,18,19	15,16,17,18
D12S391	18,22	18,22	17,18,21,22,23	17,18,18,22
D16S539	9,11	9,11	9,11,12,13	9,11,12
TH01	6,6	6,6	6,7,9,9.3	6,9,9.3
D3S1358	17,17	17,17	14,15,16,17	15,16,17,17,18

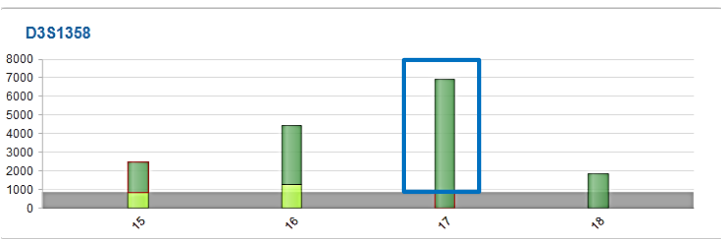
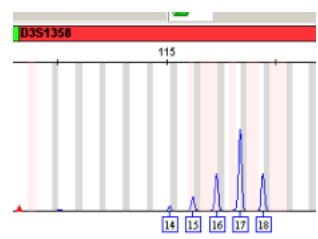
Case 3 - swab from a handbag



Allele	Status	Coverage	Sequence
17	STUTTER	86	[AGAT]10 [AGAC]6 [AGAT]1
17	ABOVE_ST	135	[AGAT]11 [AGAC]5 [AGAT]1
18	ABOVE_ST	187	[AGAT]10 [AGAC]7 [AGAT]1
18	ABOVE_ST	339	[AGAT]11 [AGAC]6 [AGAT]1 suspect
22	ABOVE_ST	204	[AGAT]12 [AGAC]10



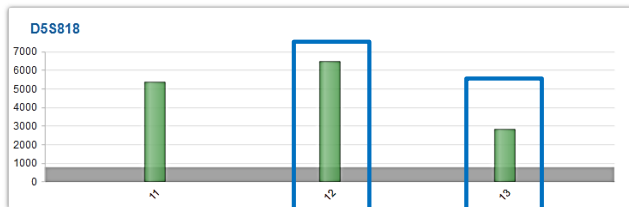
Allele	Status	Coverage	Sequence
12 ▶	ABOVE_ST	1202	[TAGA]11 [TAGG]1
12 ▶	ABOVE_ST	1730	[TAGA]12 suspect
14 ▶	ABOVE_ST	1260	[TAGA]13 [TAGG]1
15 ▶	ABOVE_ST	3599	[TAGA]14 [TAGG]1
16 ▶	ABOVE_ST	681	[TAGA]15 [TAGG]1
17.3 ▶	ABOVE_ST	1524	[TAGA]4 [TGA]1 [TAGA]12 [TAGG]1



Allele	Status	Coverage	Sequence
15	STUTTER	858	[TCTA]1 [TCTG]2 [TCTA]12
15	ABOVE_ST	1618	[TCTA]1 [TCTG]1 [TCTA]13
16	STUTTER	1307	[TCTA]1 [TCTG]3 [TCTA]12
16 ▶	ABOVE_ST	3151	[TCTA]1 [TCTG]2 [TCTA]13
17	ABOVE_ST	932	[TCTA]1 [TCTG]2 [TCTA]14
17	ABOVE_ST	5969	[TCTA]1 [TCTG]3 [TCTA]13 suspect
18	ABOVE_ST	1875	[TCTA]1 [TCTG]3 [TCTA]14

Case 3 - swab from a handbag

Allele	Status	Coverage	Sequence	Long Sequence	Ref/Alt	RS Id's	SNP/Indel Location	Coverage%	Quality
11	ABOVE-ST	5375	[AGAT]11	D5S818[CE11]-chr5-hg19 123111250-123111293 [AGAT]11					
12	ABOVE-ST	6458	[AGAT]12	D5S818[CE12]-chr5-hg19 123111250-123111293 [AGAT]12					
12		349	[AGAT]12	D5S818[CE12]-chr5-hg19 123111250-123111293 [AGAT]12	-	-			-
12	suspect	6098	[AGAT]12	D5S818[CE12]-chr5-hg19 123111250-123111293 [AGAT]12 123111306-G	A/G	rs25768			19.90
13	ABOVE-ST	2851	[AGAT]13	D5S818[CE13]-chr5-hg19 123111250-123111293 [AGAT]13					
13		2840	[AGAT]13	D5S818[CE13]-chr5-hg19 123111250-123111293 [AGAT]13 123111306-G	A/G	rs25768			19.92



AN:
Expected Allele Number : 1-2

OL :
Expected Allele(s) : [6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 10.1, 11.1, 12.1, 12.3]

Deviant(s) :

Below PHR
Threshold (Coverage) : 1937
Allele(s) :

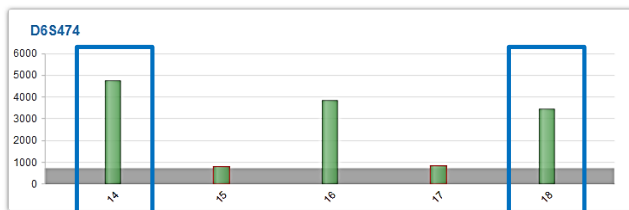
Analysis Settings

Global Parameters

Left Anchor Length : 15
Left Anchor Tolerance : 2
Right Anchor Length : 15
Right Anchor Tolerance : 2
Use Forward Reads : True
Use Reverse Reads : True

STR Threshold

Allele	Status	Coverage	Sequence	Long Sequence	Ref/Alt	RS Id's	SNP/Indel Location	Coverage%	Quality
14	ABOVE-ST	4771	[AGAT]5 [GATA]	D6S474[CE14]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]9					
14		1045	[AGAT]5 [GATA]9	D6S474[CE14]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]9	-	-			-
14	suspect	3659	[AGAT]5 [GATA]9	D6S474[CE14]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]9 112879241-G	A/G	rs62414880			14.22
15	ABOVE-ST	821	[AGAT]5 [GATA]	D6S474[CE15]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]10					
16	ABOVE-ST	3836	[AGAT]5 [GATA]	D6S474[CE16]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]11					
17	ABOVE-ST	854	[AGAT]5 [GATA]	D6S474[CE17]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]12					
18	ABOVE-ST	3468	[AGAT]5 [GATA]	D6S474[CE18]-chr6-hg19 112879153-112879220 [AGAT]5 [GATA]13					



Deviant(s) :

Below PHR
Threshold (Coverage) : 1431
Allele(s) : 15, 17

BST :
Threshold (Coverage) : 719
Allele(s) :

CC :
Expected Value :

Analysis Settings

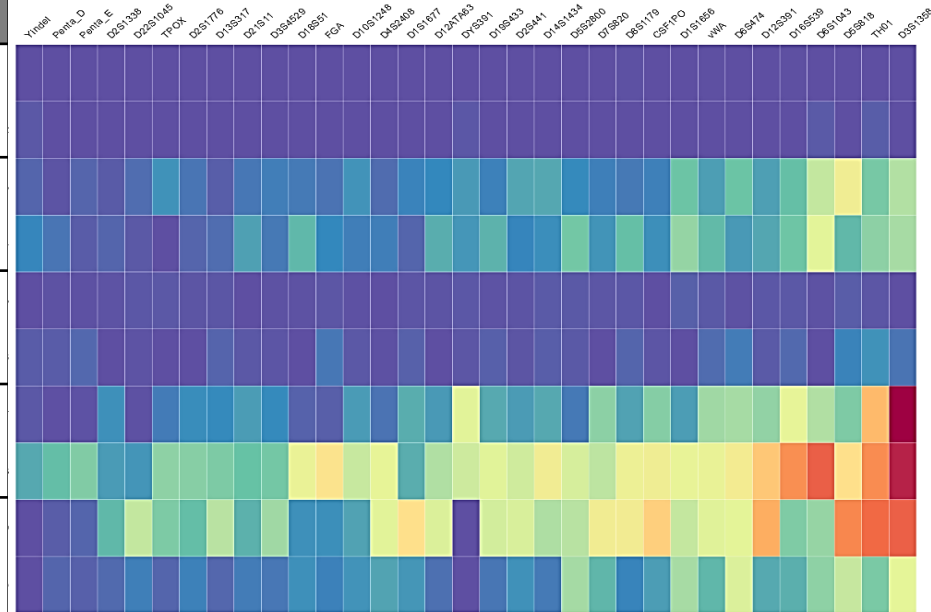
Global Parameters

Left Anchor Length : 15
Left Anchor Tolerance : 2
Right Anchor Length : 15
Right Anchor Tolerance : 2
Use Forward Reads : True
Use Reverse Reads : True

STR Threshold

Casework: cold cases

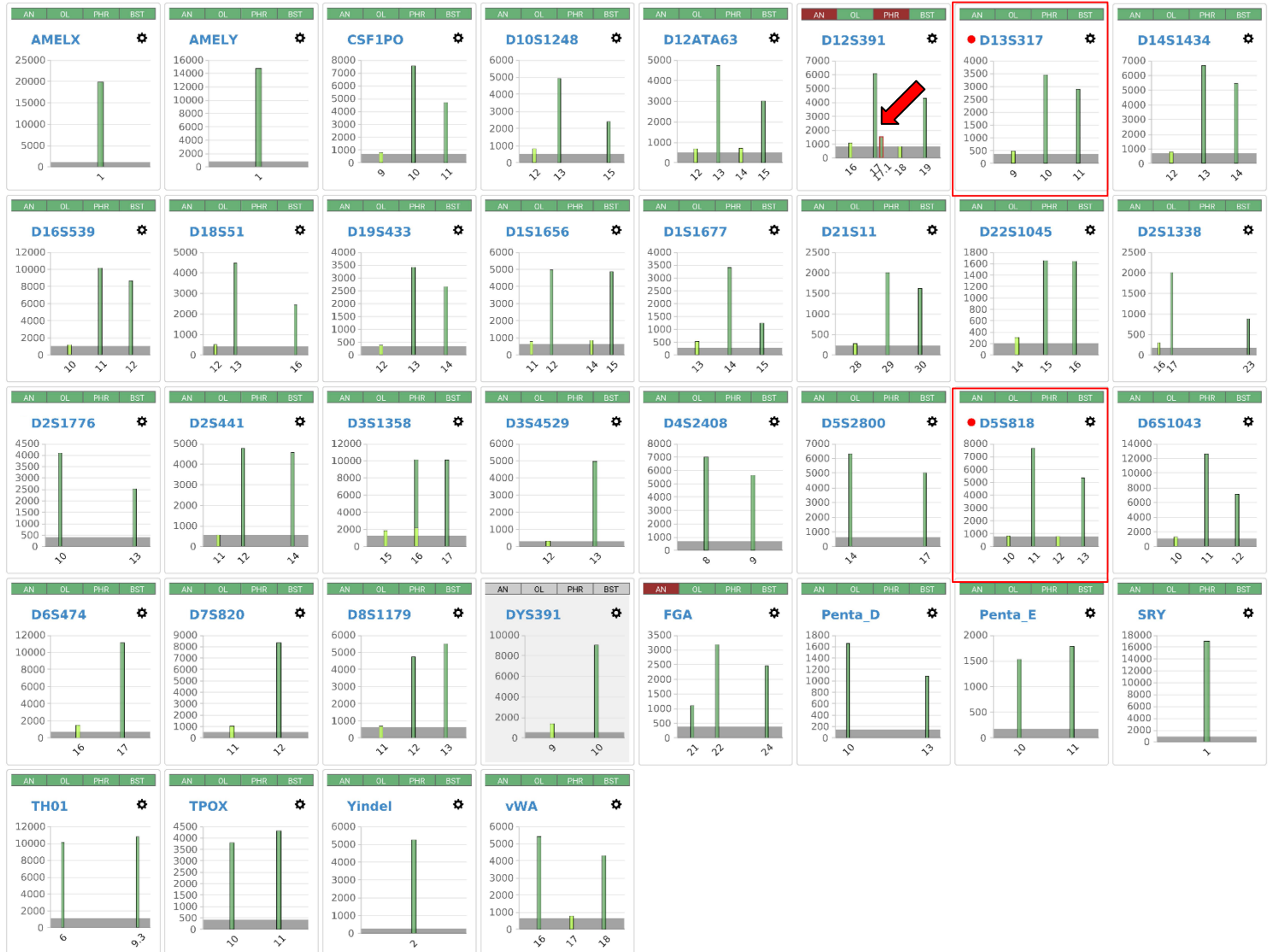
Case	Traces	Source	DNA input (large)	DNA input (small)
1 burglary/ homicide (90s)	CC1	stamp (V)	not determined	7pg
	CC2	stamp (V)	7pg	62pg
	CC3	stamp (V)	7pg	15pg
	CC4	stamp (V)	31pg	250pg
2 homicide (80s)	C9	piece of evidence (C)	15pg	31pg



Locus	C1 CE	C1 NGS	C2 CE	C2 NGS	C3 CE	C3 NGS	C4 CE	C4 NGS	C9 CE	C9 NGS
Amel	(X),Y	XY	XY	XY	XY	XY	XY	XY	XX	XX
D2S1338	-	-	(17)	17,23	(17)	(23)	17,23	17,23	20,25	20,25
D22S1045	(15)	-	(14,15,16)	15,(16)	(15,16)	15,(16)	15,(16)	15,16	15,17	15,17
D21S11	(30)	-	29,30	29,30,(31.2)	(29)	(30)	29,30	29,30	28,33.2	(28),33.2
D18S51	-	-	(13,16)	13,16	(13,15,16)	(16)	13,16	13,16	14,18	14,18
FGA	-	-	(22),24	22,24	(24)	22,(24)	22,24	22,24	20,21	20,21
D10S1248	(15)	-	(13,15)	13,15	(13,15)	(13,15)	13,15	13,15	13,14	13,14,(16)
D19S433	-	-	13,14	13,14	-	13	13,14	13,14	12,14	12,14
D2S441	(12,14)	-	(12,14)	12,14	(12,14)	12	12,14	12,14	10,11.3	10,11.3
D8S1179	-	(13)	12,(13)	12,13	(12,13)	12	12,13	12,13	12,12	12,12
D1S1656	(12)	-	(12),15	12,15	(12,15)	(11,12,15)	12,15	12,15	11,16	11,(16)
vWA	(18)	(16,18)	16,18	16,(18)	16,18	16,18	16,18	16,18	15,20	15,20
D12S391	(17,19)	-	(17,19,20)	17,19	(17,19)	(17,19)	17,19	17,19	20,24	20,24
D16S539	-	(12)	(11,12)	11,12	(11,12)	11,12	11,12	11,12	(12),13	12,13
TH01	(9.3)	-	6,9.3	6,9.3	6,9.3	(6,9.3)	6,9.3	6,9.3	7,9.3	7,9.3
D3S1358	-	-	16,17	16,17	16,17	(16,17)	16,17	16,17	14,14	14,14

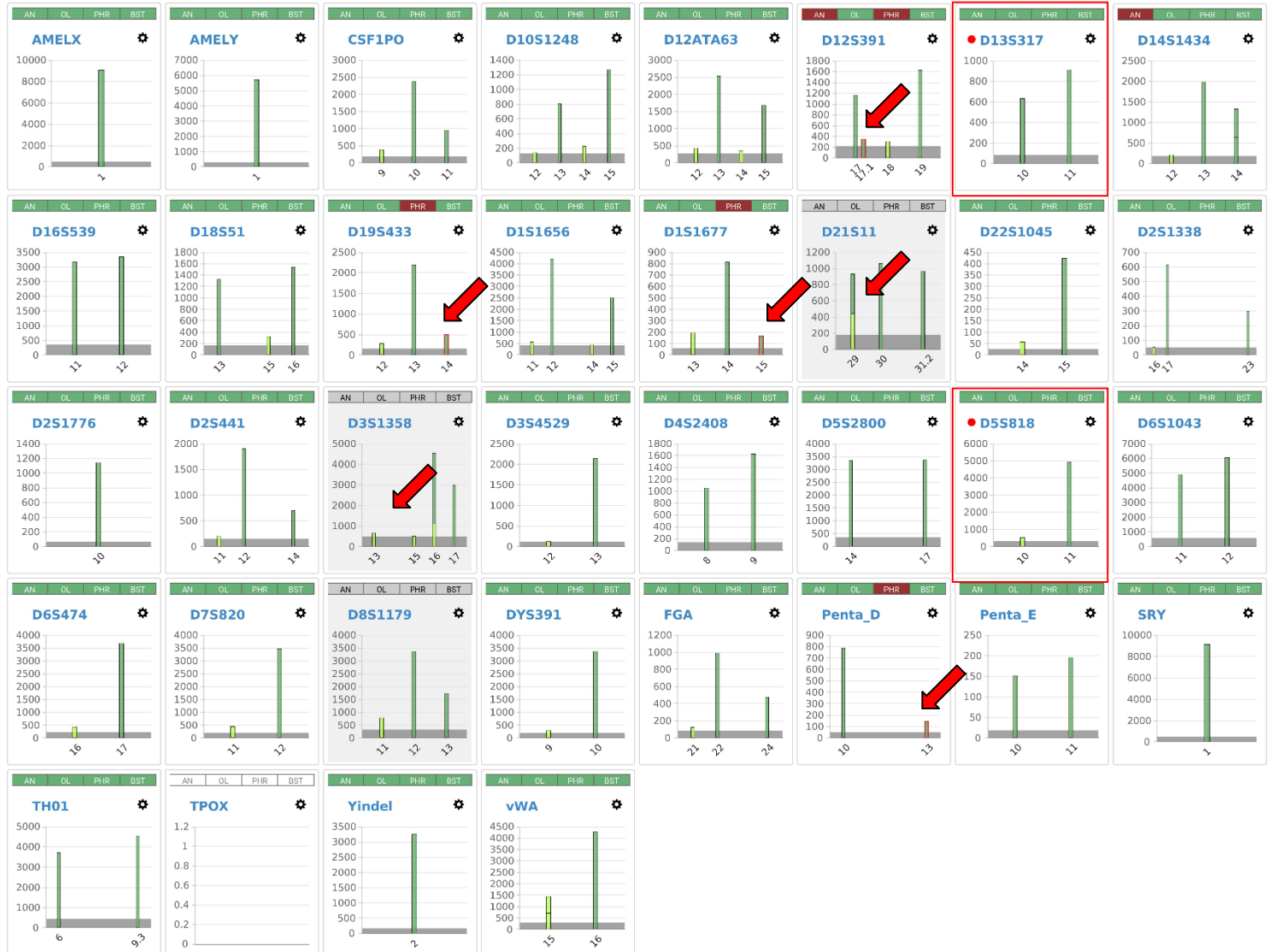
Case 1

31pg



Case 1

7pg



Conclusions and plans:



easy workflow



reliable results



more casework



Acknowledgments:



ThermoFisher
S C I E N T I F I C

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