SE33 Variant Alleles: Sequences and Implications

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Among the 23 short tandem repeat (STR) loci commonly used in commercial STR kits, SE33 is by far the most polymorphic locus possessing 53 detectable alleles and 292 observed genotypes in 938 unrelated U.S. population samples (a subset of data from Hill et al. 2011). A review of the SE33 literature has found more than 170 alleles when internal sequence rearrangements are included (Butler 2011). The high degree of variation with SE33 can potentially impact PCR primers and amplicon mobility. U.S. population sample sets have been tested with PowerPlex ESX 17 and ESI 17 as well as NGM SElect and the widely used primers (Polymeropoulos et al. 1992) to explore any concordance issues between kits possessing primers in different positions. A G→A mutation 68 bp downstream of the repeat region has been detected in several samples that can cause a mobility shift in PowerPlex ESI 17 and ESSplex SE relative to PowerPlex ESX 17 and NGM SElect SE33 alleles. The observed frequencies and potential implications of flanking region differences are presented here.

23 STR loci present in STR kits rank ordered by their variability across 938 unrelated U.S. population samples

STR Locus	Alleles Observed	Genotypes Observed	Het. (obs)	P_I value N = 938
SE33	53	292	0.9360	0.0069
Penta E*	20	114	0.8799	0.0177
D2S1338	13	68	0.8785	0.0219
D1S1656	15	92	0.8934	0.0220
D18S51	21	91	0.8689	0.0256
D12S391	23	110	0.8795	0.0257
FGA	26	93	0.8742	0.0299
Penta D*	16	71	0.8754	0.0356
D21S11	25	81	0.8358	0.0410
D19S433	16	76	0.8124	0.0561
D8S1179	11	45	0.7878	0.0582
vWA	11	38	0.8060	0.0622
D7S820	11	32	0.8070	0.0734
TH01	8	24	0.7580	0.0784
D16S539	9	28	0.7825	0.0784
D13S317	8	29	0.7655	0.0812
D10S1248	12	39	0.7825	0.0837
D2S441	14	41	0.7772	0.0855
D3S1358	11	30	0.7569	0.0873
D22S1045	11	42	0.7697	0.0933
CSF1PO	9	30	0.7537	0.1071
D5S818	9	34	0.7164	0.1192
TPOX	9	28	0.6983	0.1283

*Penta D and Penta E were only examined at 656 samples in this data set; 10 additional loci beyond the current CODIS 13 core loci shown in blue font; data are a subset of Hill et al. (2011)

Summary of Observations

A total of 22 discordant results have been observed with SE33 testing involving five different kits examined at NIST (ESX 17, ESI 17, NGM SElect, ESSplex SE, and the SE33 monoplex which contains the same primers as SEfiler and PowerPlex ES). In some cases, more than 1500 U.S. population samples have been examined although most of the focus to-date has been on a subset of 663 U.S. Caucasian, African American, and U.S. Hispanic samples.

Four samples (involving alleles 24.2, 25.2, 26.2, and 27.2) possess a C→T SNP 110 bp upstream of the repeat region that results in allele dropout when using the SE33 monoplex (SEfiler and PowerPlex ES) forward primer but correct genotypes with all other kits.

In a single sample, a 3 bp deletion of TTG that is 28-30 bp downstream of the repeat region creates a "28.3" allele with ESX 17, ESI 17, and ESSplex SE kits or a "29.2" allele with the NGM SElect and SE33 monoplex (and thus SEfiler and PowerPlex ES kits).

A 4 bp deletion of AAAA that is 85-88 bp upstream of the repeat region (also reported by Rolf et al. 2011) impacts ESSplex SE forward primer annealing. Four occurrences of this flanking region mutation have been observed with alleles 13, 15, and 17 (twice).

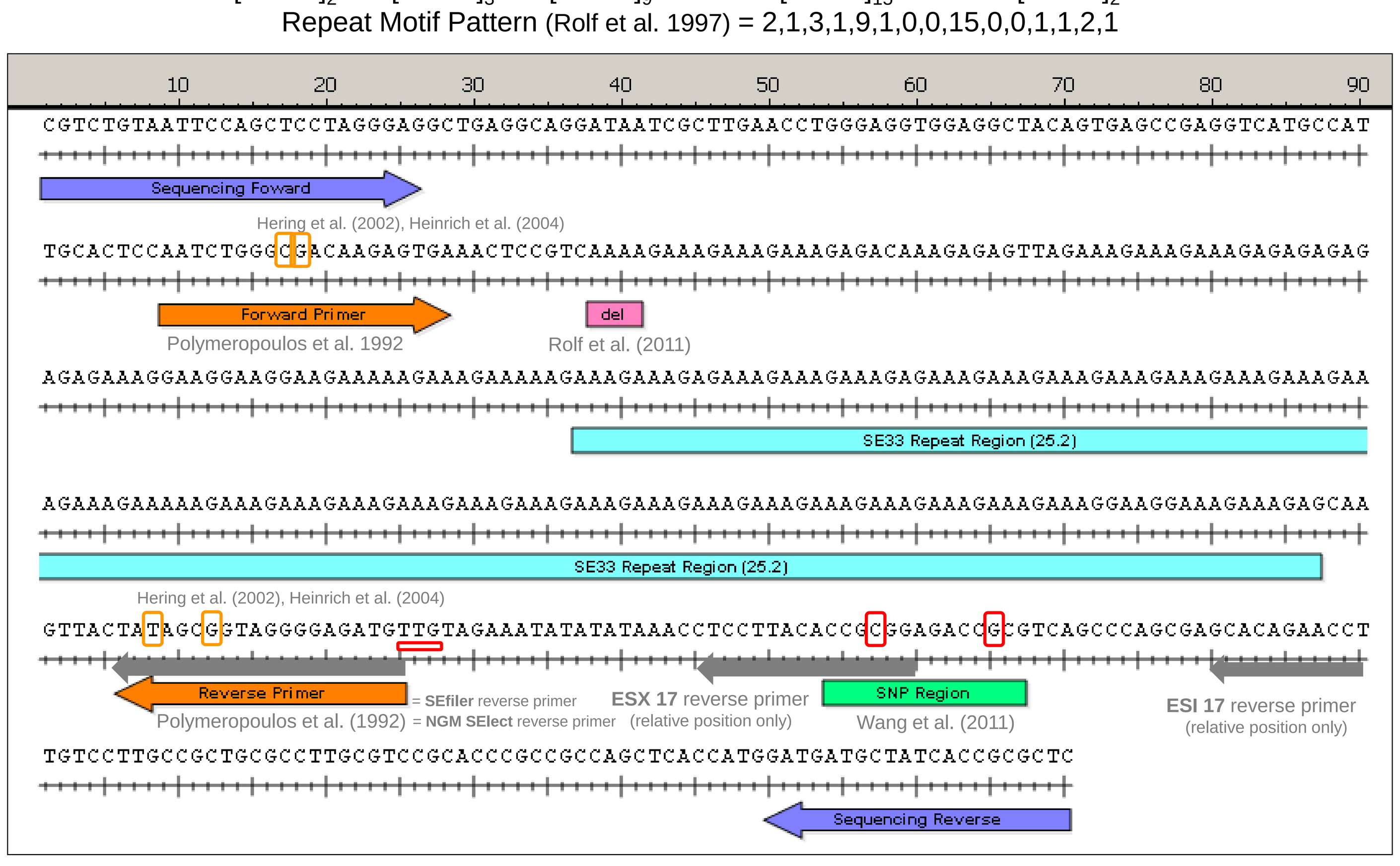
A C→T SNP 60 bp downstream of the repeat region was observed once in an allele 25.2. This flanking mutation resulted in allele dropout with ESX 17 and a +1 base size migration shift in ESI 17 and ESSplex SE ***(see below)***.

A G→A SNP 68 bp downstream of the repeat region was observed in 11 samples [containing alleles 12.2, 13.2 (3x), 15.2 (3x), 16.2 (3x), and 23.2] from the NIST data set, 4 samples [containing alleles 14.2 (2x), 16.2, and 19.2] supplied by two German labs, and 5 samples (containing alleles 13.2, 21.2, 22.2, 23.2, and 24.2) supplied by Applied Biosystems. This mutation led to a migration shift of approximately +1 base for ESI 17 and ESSplex SE amplicons relative to NGM SElect and ESX 17 amplicons ***(see below)***. The newly developed ESI 17 Pro primers corrected this migration shift and re-established full concordance with ESX 17 and NGM SElect on these samples.

No primer pair is immune to potential problems with the highly polymorphic SE33 locus.

Annotated SE33 Allele 25.2 with Known Primer Positions

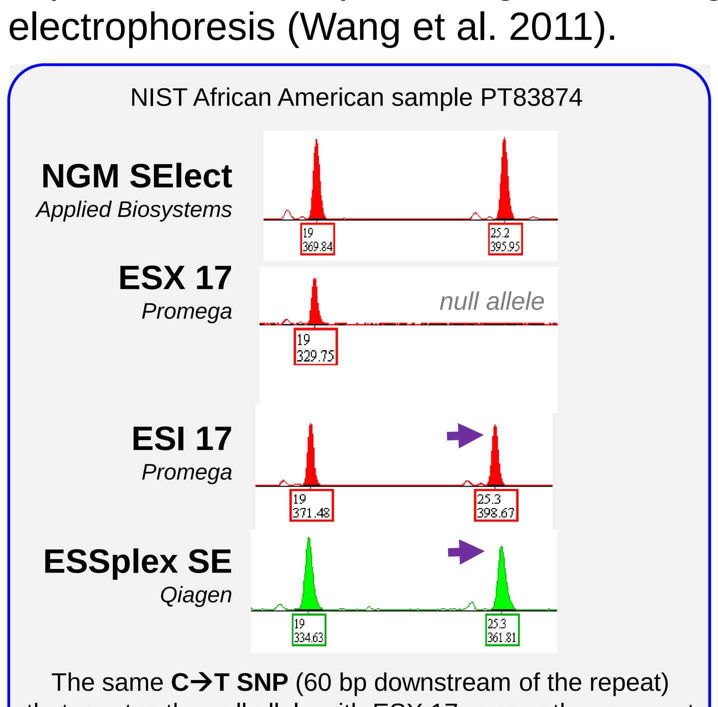
$[AAAG]_2$ AG $[AAAG]_3$ AG $[AAAG]_9$ AAAAAG $[AAAG]_{15}$ G AAGG $[AAAG]_2$ AG
Repeat Motif Pattern (Rolf et al. 1997) = 2,1,3,1,9,1,0,0,15,0,0,1,1,2,1



Hering et al. (2002) and Heinrich et al. (2004) reported primer binding site mutations (boxed in orange) for the widely used Polymeropoulos et al. (1992) primers (orange arrows), which are used in the AmpFlSTR SEfiler and PowerPlex ES kits. NGM SElect uses the Polymeropoulos reverse primer with a new forward primer and creates a 396 bp amplicon with SE33 allele 25.2. We have observed two flanking region mutations (boxed in red) in the Wang et al. (2011) "SNP Region" that impact migration of amplicons created with primers such as ESI 17 that include this SNP region. A 4 bp deletion has been reported by Rolf et al. (2011) and also observed during NIST allele sequencing that will cause STR typing results to differ from the repeat sequence by 4 bp or a single repeat unit. A TTG deletion just downstream of the Polymeropoulos reverse primer was also observed. The sequencing primers used in this study are indicated by the purple arrows and generate a 520 bp product with allele 25.2.

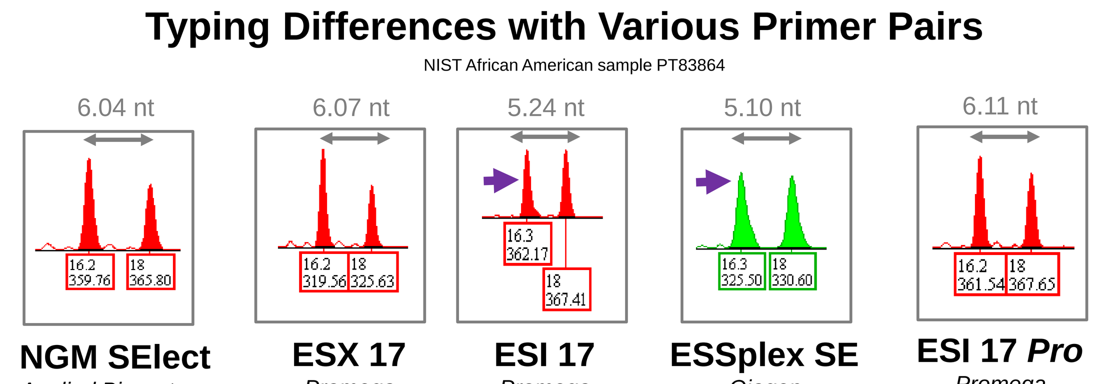
SE33 Flanking Region Mutations that Impact Migration and/or Primer Annealing

Mutations in primer binding regions can create allele dropout. Flanking region variation may also impact local secondary structure in a PCR product and impact how the amplicon migrates during capillary electrophoresis (Wang et al. 2011).

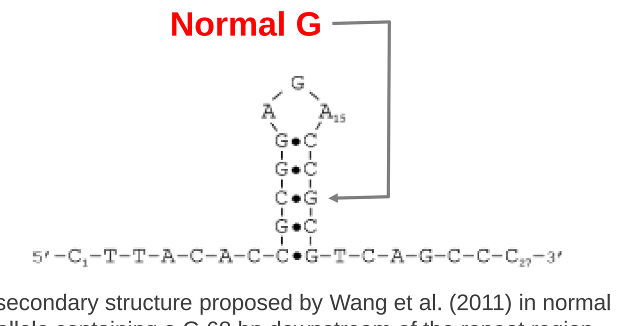


The same **C→T SNP** (60 bp downstream of the repeat) that creates the null allele with ESX 17 causes the apparent +1 nt migration shift with ESI 17 and ESSplex SE.

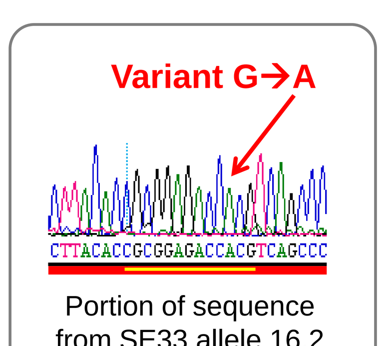
Typing Differences with Various Primer Pairs



The **G → A SNP** disrupts the hairpin structure formed in the 3' flanking region and causes the variant SE33 allele to migrate more slowly in the capillary (36 cm, POP4) – resulting in an "off-ladder" allele exhibiting approximately a +1 nucleotide (nt) shift.

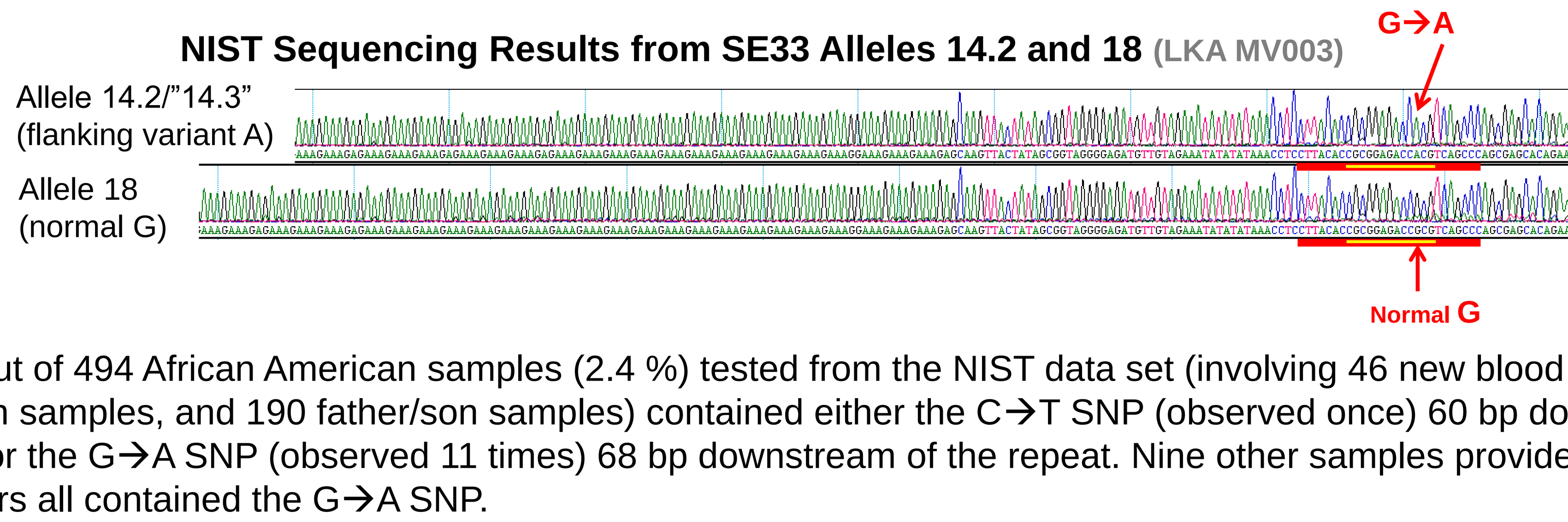


Hairpin secondary structure proposed by Wang et al. (2011) in normal SE33 allele containing a G 68 bp downstream of the repeat region



Portion of sequence from SE33 allele 16.2 (*runs as 16.3 with ESI 17*); PCR product provided by BKA

NIST Sequencing Results from SE33 Alleles 14.2 and 18 (LKA MV003)



A total of 12 out of 494 African American samples (2.4 %) tested from the NIST data set (involving 46 new blood samples, 258 population samples, and 190 father/son samples) contained either the C→T SNP (observed once) 60 bp downstream of the repeat or the G→A SNP (observed 11 times) 68 bp downstream of the repeat. Nine other samples provided to NIST by collaborators all contained the G→A SNP.

The +1 base migration differences between ESX 17 and ESI 17 amplicons were missed in our initial study (Hill et al. 2011) because of poor resolution at the time these samples were run on the NIST ABI 3130xl Genetic Analyzer. Hence, it is important to have good resolution and precise sizing in order to detect potential SE33 variant alleles. However, allele sequencing is still the best way to observe the full extent of variation at the highly polymorphic SE33 locus due to many alleles having internal sequence variation ***(see listing to the right)***.

References

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Reported SE33 Alleles in the Literature or Identified through NIST Allele Sequencing

Shaded alleles have the same size but different internal sequence structures

Repeat Motif Patterns — Motif patterns based on Rolf et al. (1997)

Allele (Repeat #)	ABI SEfiler	Promega ESX 17	Promega ESI 17	AAAG	AG	AAAG	AG	AAAG	AAAAG	AG	AGAAAG	AAAG	AAAAAG	AAAG	G	AAGG	AAAG/ANAG	AG	Reference
				5' flanking				central repeat							3' flanking				
3	197 bp	258 bp	300 bp																STRBase
4.2	203 bp	264 bp	306 bp																PP-ESI ladder
6.3	212 bp	273 bp	315 bp	2	1	3	1	7	0	0	0	0	0	0	0	0	3	1	Rolf *et al.* (1997)
7	213 bp	274 bp	316 bp																Lászik *et al.* (2001)
7.3	216 bp	277 bp	319 bp	2	1	3	1	8	0	0	0	0	0	0	0	0	3	1	Dauber *et al.* (2004)
8	217 bp	278 bp	320 bp																PP-ESI ladder
8.1	218 bp	279 bp	321 bp																Lászik *et al.* (2001)
9 (a)	221 bp	282 bp	324 bp	2	1	3	1	9	0	0	0	0	0	0	1	0	3	1	Dauber *et al.* (2009)
9 (b)	221 bp	282 bp	324 bp	2	1	3	1	9	0	0	0	0	0	0	1	1	2	1	Kline *et al.* (2010)
9.2	223 bp	284 bp	326 bp																Lászik *et al.* (2001)
10	225 bp	286 bp	328 bp																PP-ESI ladder
10.2	227 bp	288 bp	330 bp	2	1	0	0	18	0	0	0	0	0	0	1	0	3	1	Dauber *et al.* (2009)
10.3	228 bp	289 bp	331 bp																Urquhart *et al.* (1993)
11	229 bp	290 bp	332 bp																PP-ESI ladder
11.2	231 bp	292 bp	334 bp	2	1	0	0	15	0	0	0	0	0	0	1	0	3	1	Dauber *et al.* (2004)
12	233 bp	294 bp	336 bp	2	1	3	1	12	0	0	0	0	0	0	1	0	3	1	Rolf *et al.* (1997)
12.2	235 bp	296 bp	338 bp	2	1	3	0	13	0	0	0	0	0	0	1	0	3	1	Rolf *et al.* (1997)
13	237 bp	298 bp	340 bp																PP-ESI ladder
13.2	239 bp	300 bp	342 bp	2	1	3	0	14	0	0	0	0	0	0	1	0	3	1	Rolf *et al.* (1997), Kline *et al.* (2010)
13.3	240 bp	301 bp	343 bp																Poetsch *et al.* (2010)
14 (a)	241 bp	302 bp	344 bp	2	1	3	1	14	0	0	0	0	0	0	1	0	3	1	Rolf *et al.* (1997)
14 (b)	241 bp	302 bp	344 bp	2	1	3	1	14	0	0	0	0	0	0	1	1	2	1	Kline et al. (2010)
14.1	242 bp	303 bp	345 bp																Poetsch *et al.* (2010)
14.2	243 bp	304 bp	346 bp	2	1	3	0	15	0	0	0	0	0	0	1	0	3	1	Kline *et al.* (2010)
14.3	244 bp	305 bp	347 bp																
15	245 bp	306 bp	348 bp	2	1	3	1	15	0	0	0	0	0	0	1	0	3	1	Rolf *et al.* (1997)
15.2	247 bp	308 bp	350 bp																Lászik *et al.* (2001)
16 (a)	249 bp	310 bp	352 bp	2	1	3	1	16	0	0	0	0	0	0	1	0	3	1	Rolf *et al.* (1997)
16 (b)	249 bp	310 bp	352 bp	2	1	3	1	16	0	0	0	0	0	0	1	1	2	1	Kline *et al.* (2010)
16.1	250 bp	311 bp	353 bp																Berti *et al.* (2010)
16.2	251 bp	312 bp	354 bp																Lászik *et al.* (2001)
16.3	252 bp	313 bp	355 bp																Egyed *et al.* (2005)
17	253 bp	314 bp	356 bp	2	1	3	1	17	0	0	0	0	0	0	1	0	3	1	Rolf *et al.* (1997)
17.2	255 bp	316 bp	358 bp																Lászik *et al.* (2001)
17.3	256 bp	317 bp	359 bp																Lászik *et al.* (2001)
18	257 bp	318 bp	360 bp	2	1	3	1	18	0	0	0	0	0	0	1	0	3	1	Rolf *et al.* (1997)
18.2	259 bp	320 bp	362 bp	2	1	3	1	9	1			8	0	0	1	1	2	1	Dauber *et al.* (2009)
18.3	260 bp	321 bp	363 bp																Egyed *et al.* (2005)
19 (a)	261 bp	322 bp	364 bp	2	1	3	1	19	0	0	0	0	0	0	1	0	3	1	Rolf *et al.* (1997)
19 (b)	261 bp	322 bp	364 bp	2	1	3	1	19	0	0	0	0	0	0	1	1	2	1	Kline *et al.* (2010)
19.2	263 bp	324 bp	366 bp	2	1	3	1	10	1	0	0	8	0	0	1	1	2	1	Rolf *et al.* (1997)
19.3	264 bp	325 bp	367 bp																Berti *et al.* (2010)
20 (a)	265 bp	326 bp	368 bp	2	1	3	1	20	0	0	0	0	0	0	1	0	3	1	Rolf *et al.* (1997)
20 (b)	265 bp	326 bp	368 bp	2	1	3	1	20	0	0	0	0	0	0	1	1	2	1	Kline *et al.* (2010)
20.2	267 bp	328 bp	370 bp	2	1	3	1	11	1	0	0	8	0	0	1	1	2	1	Rolf *et al.* (1997)
20.3	268 bp	329 bp	371 bp																
21	269 bp	330 bp	372 bp	2	1	3	1	21	0	0	0	0	0	0	1	0	3	1	Rolf *et al.* (1997)
21.1	270 bp	331 bp	373 bp																
21.2 (a)	271 bp	332 bp	374 bp	2	1	3	1	9	1	0	0	11	0	0	1	1	2	1	Rolf *et al.* (1997)
21.2 (b)	271 bp	332 bp	374 bp	2	1	3	1	11	1	0	0	9	0	0	1	1	2	1	Rolf *et al.* (1997)
21.2 (c)	271 bp	332 bp	374 bp	2	1	3	1	7	0	7	0	11	0	0	1	1	2	1	Kline *et al.* (2010)
22 (a)	273 bp	334 bp	376 bp	2	1	3	1	22	0	0	0	0	0	0	1	0	3	1	Rolf *et al.* (1997)
22 (b)	273 bp	334 bp	376 bp	2	1	3	1	21	0	0	0	0	0	0	1	1	3	1	Kline *et al.* (2010)
22.2 (a)	275 bp	336 bp	378 bp	2	1	3	1	7	1	0	0	14	0	0	1	1	2	1	Rolf *et al.* (1997)
22.2 (b)	275 bp	336 bp	378 bp	2	1	3	1	8	0	5	0	12	0	0	1	1	2	1	Rolf *et al.* (1997)
22.2 (c)	275 bp	336 bp	378 bp	2	1	3	1	9	1	0	0	12	0	0	1	1	2	1	Rolf *et al.* (1997)
22.2 (d)	275 bp	336 bp	378 bp	2	1	3	1	10	1	0	0	11	0	0	1	1	2	1	Rolf *et al.* (1997)
22.2 (e)	275 bp	336 bp	378 bp	2	1	3	1	11	1	0	0	10	0	0	1	1	2	1	Rolf *et al.* (1997)
22.2 (f)	275 bp	336 bp	378 bp	2	1	3	1	12	1	0	0	9	0	0	1	1	2	1	Rolf *et al.* (1997)
22.3	276 bp	337 bp	379 bp																Poetsch *et al.* (2010)
23	277 bp	338 bp	380 bp																Lászik *et al.* (2001)
23.2 (a)	279 bp	340 bp	382 bp	2	1	3	1	7	1	0	0	15	0	0	1	1	2	1	Rolf *et al.* (1997)
23.2 (b)	279 bp	340 bp	382 bp	2	1	3	1	8	1	0	0	14	0	0	1	1	2	1	Rolf *et al.* (1997)
23.2 (c)	279 bp	340 bp	382 bp	2	1	3	1	9	1	0	0	13	0	0	1	1	2	1	Rolf *et al.* (1997)
23.2 (d)	279 bp	340 bp	382 bp	2	1	3	1	10	0	3	0	12	0	0	1	1	2	1	Rolf *et al.* (1997)
23.2 (e)	279 bp	340 bp	382 bp	2	1	3	1	10	1	0	0	12	0	0	1	1	2	1	Rolf *et al.* (1997)
23.2 (f)	279 bp	340 bp	382 bp	2	1	3	1	11	1	0	0	11	0	0	1	1	2	1	Rolf *et al.* (1997)
23.2 (g)	279 bp	340 bp	382 bp	2	1	3	1	12	1	0	0	10	0	0	1	1	2	1	Rolf *et al.* (1997)
24	281 bp	342 bp	384 bp																Lászik *et al.* (2001)
24.2 (a)	283 bp	344 bp	386 bp	2	1	3	1	5	1	0	0	18	0	0	1	1	2	1	Rolf *et al.* (1997)
24.2 (b)	283 bp	344 bp	386 bp	2	1	3	1	7	1	0	0	16	0	0	1	1	2	1	Rolf *et al.* (1997)
24.2 (c)	283 bp	344 bp	386 bp	2	1	3	1	8	1	0	0	15	0	0	1	1	2	1	Rolf *et al.* (1997)
24.2 (d)	283 bp	344 bp	386 bp	2	1	3	1	10	1	0	0	13	0	0	1	1	2	1	Rolf *et al.* (1997)
24.2 (e)	283 bp	344 bp	386 bp	2	1	3	1	11	1	0	0	12	0	0	1	1	2	1	Rolf *et al.* (1997)
24.2 (f)	283 bp	344 bp	386 bp	2	1	3	1	12	1	0	0	11	0	0	1	1	2	1	Rolf *et al.* (1997)
24.2 (g)	283 bp	344 bp	386 bp	2	1	3	1	6	1	0	0	16	0	0	1	1	3	1	U134C-->T -- Kline *et al.* (2010)
25	285 bp	346 bp	388 bp																Lászik *et al.* (2001)
25.2 (a)	287 bp	348 bp	390 bp	2	1	3	1	9	1	0	0	15	0	0	1	1	2	1	Rolf *et al.* (1997)
25.2 (b)	287 bp	348 bp	390 bp	2	1	3	1	10	0	0	1	14	0	0	1	1	2	1	Rolf *et al.* (1997)
25.2 (c)	287 bp	348 bp	390 bp	2	1	3	1	10	1	0	0	14	0	0	1	1	2	1	Rolf *et al.* (1997)
25.2 (d)	287 bp	348 bp	390 bp	2	1	3	1	11	1	0	0	13	0	0	1	1	2	1	Rolf *et al.* (1997)
25.2 (e)	287 bp	348 bp	390 bp	2	1	3	1	12	1	0	0	12	0	0	1	1	2	1	Rolf *et al.* (1997)
25.2 (f)	287 bp	348 bp	390 bp	2	1	3	1	14	1	0	0	10	0	0	1	1	2	1	Rolf *et al.* (1997)
25.2 (g)	287 bp	348 bp	390 bp	2	1	3	1	9	1	0	0	15	0	0	1	1	2	1	D75C-->T -- Kline *et al.* (2010)
25.2 (h)	287 bp	348 bp	390 bp	2	1	3	1	6	1	0	0	17	0	0	1	2	2	1	U134C-->T -- Kline *et al.* (2010)
25.3	288 bp	349 bp	391 bp																Berti *et al.* (2010)
26	289 bp	350 bp	392 bp																Lászik *et al.* (2001)
26.2 (a)	291 bp	352 bp	394 bp	2	1	3	1	8	1	0	0	17	0	0	1	1	2	1	Rolf *et al.* (1997)
26.2 (b)	291 bp	352 bp	394 bp	2	1	3	1	9	1	0	0	16	0	0	1	1	2	1	Rolf *et al.* (1997)
26.2 (c)	291 bp	352 bp	394 bp	2	1	3	1	10	1	0	0	15	0	0	1	1	2	1	Rolf *et al.* (1997)
26.2 (d)	291 bp	352 bp	394 bp	2	1	3	1	11	0	0	1	14	0	0	1	1	2	1	Rolf *et al.* (1997)
26.2 (e)	291 bp	352 bp	394 bp	2	1	3	1	11	1	0	0	14	0	0	1	1	2	1	Rolf *et al.* (1997)
26.2 (f)	291 bp	352 bp	394 bp	2	1	3	1	14	1	0	0	11	0	0	1	1	2	1	Rolf *et al.* (1997)
26.2 (g)	291 bp	352 bp	394 bp	2	1	3	1	6	1	0	0	18	0	0	1	1	3	1	U134C-->T -- Kline *et al.* (2010)
27	293 bp	354 bp	396 bp																Lászik *et al.* (2001)
27.2 (a)	295 bp	356 bp	398 bp	2	1	3	1	8	0	0	1	18	0	0	1	1	2	1	Rolf *et al.* (1997)
27.2 (b)	295 bp	356 bp	398 bp	2	1	3	1	8	1	0	0	18	0	0	1	1	2	1	Rolf *et al.* (1997)
27.2 (c)	295 bp	356 bp	398 bp	2	1	3	1	9	0	0	1	17	0	0	1	3	0	1	Rolf *et al.* (1997)
27.2 (d)	295 bp	356 bp	398 bp	2	1	3	1	10	1	0	0	16	0	0	1	1	2	1	Rolf *et al.* (1997)
27.2 (e)	295 bp	356 bp	398 bp	2	1	3	1	11	1	0	0	15	0	0	1	1	2	1	Rolf *et al.* (1997)
27.2 (f)	295 bp	356 bp	398 bp	2	1	3	1	12	1	0	0	14	0	0	1	1	2	1	Rolf *et al.* (1997)
27.2 (g)	295 bp	356 bp	398 bp	2	1	3	1	12	1	0	0	15	0	0	1	1	2	1	Rolf *et al.* (1997)
27.2 (h)	295 bp	356 bp	398 bp	2	1	3	1	13	0	0	1	13	0	0	1	3	0	1	Rolf *et al.* (1997)
27.2 (i)	295 bp	356 bp	398 bp	2	1	3	1	13	1	0	0	13	0	0	1	1	2	1	Rolf *et al.* (1997)
27.2 (j)	295 bp	356 bp	398 bp	2	1	3	1	15	1	0	0	11	0	0	1	1	2	1	Rolf *et al.* (1997)
27.2 (h)	295 bp	356 bp	398 bp	2	1	3	1	7	0	9	0	15	0	0	1	1	3	1	U134C-->T -- Kline *et al.* (2010)
27.3	296 bp	357 bp	399 bp																Hill *et al.* (2010)
28	297 bp	358 bp	400 bp	2	1	0	0	14	1	0	0	16	0	0	1	1	2	1	Dauber *et al.* (2009)
28.2 (a)	299 bp	360 bp	402 bp	2	1	3	1	8	1	0	0	19	0	0	1	1	2	1	Rolf *et al.* (1997)
28.2 (b)	299 bp	360 bp	402 bp	2	1	3	1	9	0	0	0	18	0	0	1	1	2	1	Rolf *et al.* (1997)
28.2 (c)	299 bp	360 bp	402 bp	2	1	3	1	9	0	0	0	15	0	0	1	1	2	1	Rolf *et al.* (1997)
28.2 (d)	299 bp	360 bp	402 bp	2	1	3	1	9	1	0	0	18	0	0	1	1	2	1	Rolf *et al.* (1997)
28.2 (e)	299 bp	360 bp	402 bp	2	1	3	1	10	1	0	0	17	0	0	1	1	2	1	Rolf *et al.* (1997)
28.2 (f)	299 bp	360 bp	402 bp	2	1	3	1	11	1	0	0	16	0	0	1	1	2	1	Rolf *et al.* (1997)
28.2 (g)	299 bp	360 bp	402 bp	2	1	3	1	12	1	0	0	15	0	0	1	1	2	1	Rolf *et al.* (1997)
28.2 (h)	299 bp	360 bp	402 bp	2	1	3	1	13	1	0	0	14	0	0	1	1	2	1	Rolf *et al.* (1997)
28.2 (i)	299 bp	360 bp	402 bp	2	1	3	1	14	1	0	0	13	0	0	1	1	2	1	Rolf *et al.* (1997)
28.2 (j)	299 bp	360 bp	402 bp	2	1	3	1	14	1	0	0	13	0	0	1	3	0	1	Rolf *et al.* (1997)
28.2 (k)	299 bp	360 bp	402 bp	2	1	3	1	16	1	0	0	11	0	0	1	1	2	1	Rolf *et al.* (1997)
28.3	300 bp	361 bp	403 bp	2	1	3	1	10	1	0	0	12	+A	4	1	1	2	1	Dauber *et al.* (2009)
29	301 bp	362 bp	404 bp	2	1	0	0	15	1	0	0	16	0	0	1	1	2	1	Dauber *et al.* (2009)
29.2 (a)	303 bp	364 bp	406 bp	2	1	3	1	8	1	0	0	20	0	0	1	1	2	1	Rolf *et al.* (1997)
29.2 (b)	303 bp	364 bp	406 bp	2	1	3	1	9	0	0	1	19	0	0	1	1	2	1	Rolf *et al.* (1997)
29.2 (c)	303 bp	364 bp	406 bp	2	1	3	1	9	1	0	0	19	0	0	1	1	2	1	Rolf *et al.* (1997)
29.2 (d)	303 bp	364 bp	406 bp	1	1	3	1	10	1	0	0	19	0	0	1	1	2	1	Rolf *et al.* (1997)
29.2 (e)	303 bp	364 bp	406 bp	2	1	3	1	11	0	5	0	16	0	0	1	1	2	1	Rolf *et al.* (1997)
29.2 (f)	303 bp	364 bp	406 bp	1	1	3	1	11	1	0	0	18	0	0	1	1	2	1	Rolf *et al.* (1997)
29.2 (g)	303 bp	364 bp	406 bp	2	1	3	1	11	1	0	0	17	0	0	1	1	2	1	Rolf *et al.* (1997)
29.2 (h)	303 bp	364 bp	406 bp	2	1	3	1	12	1	0	0	16	0	0	1	1	2	1	Rolf *et al.* (1997)
29.2 (i)	303 bp	364 bp	406 bp	2	1	3	1	13	0	0	1	15	0	0	1	3	0	1	Rolf *et al.* (1997)
29.2 (j)	303 bp	364 bp	406 bp	2	1	3	1	13	1	0	0	15	0	0	1	1	2	1	Rolf *et al.* (1997)
29.2 (k)	303 bp	364 bp	406 bp	2	1	3	1	14	1	0	0	14	0	0	1	1	2	1	Rolf *et al.* (1997)
29.2 (l)	303 bp	364 bp	406 bp	2	1	3	1	16	1	0	0	12	0	0	1	1	2	1	Rolf *et al.* (1997)
29.2 (m)	303 bp	364 bp	406 bp	2	1	3	1	11	1	0	0	17	0	0	1	1	2	1	D41-TTG-deletion -- Kline *et al.* (2010)
29.3	304 bp	365 bp	407 bp																Hill *et al.* (2010)
30	305 bp	366 bp	408 bp																Lászik *et al.* (2001)
30.2 (a)	307 bp	368 bp	410 bp	2	1	3	1	11	1	0	0	18	0	0	1	1	2	1	Rolf *et al.* (1997)
30.2 (b)	307 bp	368 bp	410 bp	2	1	3	1	12	1	0	0	17	0	0	1	1	2	1	Rolf *et al.* (1997)
30.2 (c)	307 bp	368 bp	410 bp	1	1	3	1	12	1	0	0	18	0	0	1	1	2	1	Rolf *et al.* (1997)
30.2 (d)	307 bp	368 bp	410 bp	2	1	3	1	13	1	0	0	16	0	0	1	1	2	1	Rolf *et al.* (1997)
30.2 (e)	307 bp	368 bp	410 bp	2	1	3	1	14	1	0	0	15	0	0	1	1	2	1	Rolf *et al.* (1997)
30.2 (f)	307 bp	368 bp	410 bp	2	1	3	1	15	1	0	0	14	0	0	1	1	2	1	Rolf *et al.* (1997)
31	309 bp	370 bp	412 bp																Lászik *et al.* (2001)
31.2 (a)	311 bp	372 bp	414 bp	1	1	3	1	9	1	0	0	22	0	0	1	1	2	1	Rolf *et al.* (1997)
31.2 (b)	311 bp	372 bp	414 bp	1	1	3	1	10	1	0	0	21	0	0	1	1	2	1	Rolf *et al.* (1997)
31.2 (c)	311 bp	372 bp	414 bp	2	1	3	1	12	1	0	0	18	0	0	1	1	2	1	Rolf *et al.* (1997)
31.2 (d)	311 bp	372 bp	414 bp	2	1	3	1	13	1	0	0	17	0	0	1	1	2	1	Rolf *et al.* (1997)
31.2 (e)	311 bp	372 bp	414 bp	2	1	3	1	14	1	0	0	16	0	0	1	1	2	1	Rolf *et al.* (1997)
32	313 bp	374 bp	416 bp																Lászik *et al.* (2001)
32.1	314 bp	375 bp	417 bp																
32.2 (a)	315 bp	376 bp	418 bp	2	1	3	1	13	1	0	0	18	0	0	1	1	2	1	Rolf *et al.* (1997)
32.2 (b)	315 bp	376 bp	418 bp	2	1	3	1	14	1	0	0	17	0	0	1	1	2	1	Rolf *et al.* (1997)
33 (a)	317 bp	378 bp	420 bp	2	1	2	1	10	1	0	0	12	1	9	1	1	2	1	Rolf *et al.* (1997)
33 (b)	317 bp	378 bp	420 bp	2	1	3	1	10	1	0	0	11	1	9	1	1	2	1	Rolf *et al.* (1997)
33.2 (a)	319 bp	380 bp	422 bp	1	1	3	1	10	1	0	0	23	0	0	1	1	2	1	Rolf *et al.* (1997)
33.2 (b)	319 bp	380 bp	422 bp	2	1	3	1	12	1	0	0	20	0	0	1	1	2	1	Dauber *et al.* (2004)
34	321 bp	382 bp	424 bp	2	1	3	1	9	1	0	0	13	1	9	1	1	2	1	Rolf *et al.* (1997)
34.2	323 bp	384 bp	426 bp	2	1	3	1	13	1	0	0	20	0	0	1	1	2	1	Dauber *et al.* (2004)
35	325 bp	386 bp	428 bp																PP-ESI ladder
35.2	327 bp	388 bp	430 bp	1	1	3	1	13	1	0	0	22	0	0	1	1	2	1	Rolf *et al.* (1997)
36 (a)	329 bp	390 bp	432 bp	2	1	3	1	10	1	0	0	14	1	9	1	1	2	1	Rolf *et al.* (1997)
36 (b)	329 bp	390 bp	432 bp	2	1	3	1	12	1	0	0	10	1	11	1	1	2	1	Dauber *et al.* (2009)
36.2	331 bp	392 bp	434 bp																Lászik *et al.* (2001)
37	333 bp	394 bp	436 bp	2	1	3	1	9	1	0	0	16	1	9	1	1	2	1	Rolf *et al.* (1997)
38	337 bp	398 bp	440 bp																
39	341 bp	402 bp	444 bp																PP-ESI ladder
39.2	343 bp	404 bp	446 bp																Lászik *et al.* (2001)
41	349 bp	410 bp	452 bp																
42	353 bp	414 bp	456 bp																PP-ESI ladder
44	361 bp	422 bp	464 bp																Delghandi *et al.* (2001)
49	381 bp	442 bp	484 bp	2	1	3	1	14	1	0	0	16	1	16	1	1	2	1	Klein *et al.* (2003)

More than 170 alleles are listed here and others continue to be identified…
(we plan to add further information to STRBase to reflect these new alleles as they are discovered)

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