

SUPPLEMENTARY DATA

	9947A	9948
Amelogenin	X : X	X : Y
D13S317	11 : 11	11 : 11
D16S539	11 : 12	11 : 11
D18S51	15 : 19	15 : 18
D21S11	30 : 30	29 : 30
D3S1358	14 : 15	15 : 17
D5S818	11 : 11	11 : 13
D7S820	10 : 11	11 : 11
D8S1179	13 : 13	12 : 13
FGA	23 : 24	24 : 26
CD4	5 : 5	4 : 4
TH01	8 : 9.3	6 : 9.3
TPOX	8 : 8	8 : 9
vWA	17 : 18	17 : 17
SE33	19 : 29.2	23.2 : 26.2

Supplementary Table 1: True STR-profile of the examined reference samples as confirmed by capillary electrophoresis.

	Forward primer	Concentration (μM)	Reverse Primer	Concentration (μM)
Amelogenin	CCCTGGGCTCTGTAAAGAA	0.5	ATCAGAGCTTAAACTGGGAAGCTG	0.5
D13S317	ATTACAGAAGTCTGGGATGTGGAGGA	0.5	GGCAGCCCCAAAAAGACAGA	0.5
D16S539	GGGGGTCTAAGAGCTTGAAAAAG	0.8	GTTTGTGTGTCATCTGTAAGCATGTATC	0.8
D18S51	TTCTTGAGCCCAGAAGGTTA	0.5	ATTCTACCAGCAACAACAAAATAAAC	0.5
D21S11	ATATGTGAGTCAATCCCCAAG	0.5	TGTATTAGTCAATGTTCTCCAGAGAC	0.5
D3S1358	ACTGCAGTCCAATCTGGGT	0.5	ATGAAATCAACAGAGGCTTGC	0.5
D5S818	GGTGATTTTCCTCTTTGGTATCC	0.5	AGCCACAGTTTACAACATTTGTATCT	0.5
D7S820	ATGTTGGTCAGGCTGACTATG	0.6	GATCCACATTTATCCTCATTGAC	0.6
D8S1179	ATIGCAACTTATATGTATTTTTGTATTTTCATG	1	ACCAAATTGTGTTTCATGAGTATAGTTTC	1
FGA	GGCTGCAGGGCATAACATTA	0.5	ATTCTATGACTTTGCGCTTCAGGA	0.5
CD4	TTACCGGTTTGGAGTCGCAAGCTGAACTAGCG	0.15	CCAGGAAGTTGAGGCTGCAGTGAA	0.6
TH01	GTGATTCCCATGGCCTGTC	0.5	ATTCCTGTGGGCTGAAAAGCTC	0.5
TPOX	GCACAGAACAGGCACTTAGG	0.25	CGCTCAAACGTGAGGTTG	0.25
vWA	GCCCTAGTGGATGATAAGAATAATCAGTATGTG	0.5	GGACAGATGATAAATACATAGGATGGATGG	0.5
SE33	ACATCTCCCCTACCGCTATA	0.5	AATCTGGGCGACAAGAGTGA	1

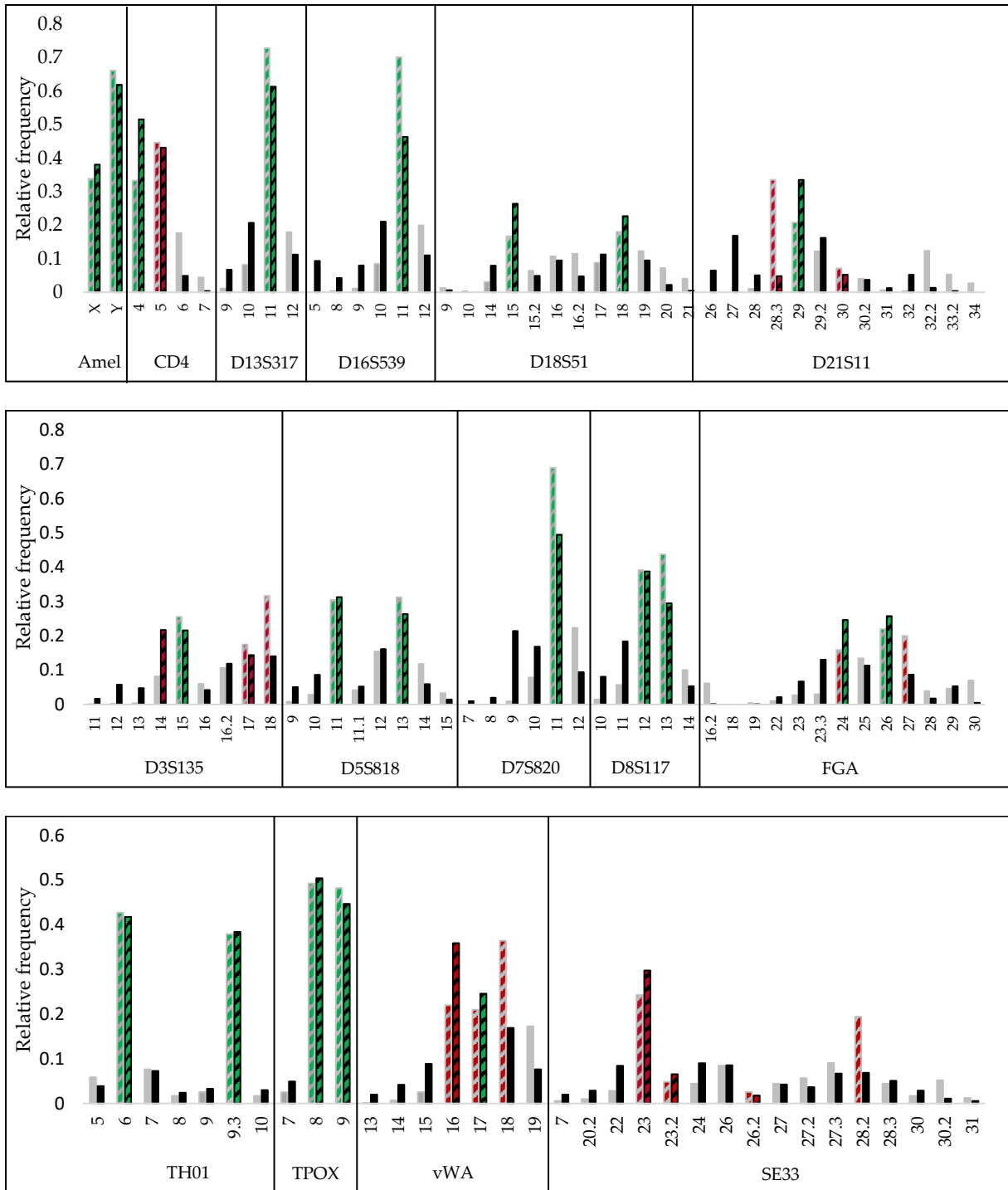
Supplementary Table 2: Forward and reverse primer sequences and concentrations used in the STR multiplex PCR reaction.

Locus	Allele	Locus	Allele	Locus	Allele	Locus	Allele	Locus	Allele	Locus	Allele	Locus	Allele	
Amelogenin	X	D7S820	7	D21S11	26	D16S539	5	D8S1179	10	SE33	7	SE33	26.2	
	Y		8		27		6		11		8		27	
CD4	4		9		28		7		12		9		27.2	
	5		10		29		8		13		10		27.3	
	6		11		29.2		9		14		10.2		28.2	
	7		12		30		10		15		11		28.3	
	8		13		30.2		11		16		12		29.2	
	9		14		30.3		12		17		13		30	
	10		D18S51		9		31		13		18		13.2	30.2
	11				10		31.2		14		FGA		15.2	31
	D16S317		7		11		32		15				19	16
		8	12	32.2	16	20	17	32						
9		13	33	TPOX	6	21	17.2	32.2						
10		13.2	33.1		7	22	17.3	33						
11		14	33.2	8	23	18	34							
12		14.2	34	9	23.3	18.3	34.2							
13		15	35	10	24	19	35							
14		15.2	36	11	25	19.2	36							
15		16	37	vWA	11	26	20							
D5S818		7	16.2		38	12	27	20.2						
	8	17	39	13	D3S1358	11	21							
	9	18	TH01	5		12	21.2							
	10	19		6		13	22							
	11	20		7		14	22.2							
	12	21		8		15	23							
	13	21.2		9		16	23.2							
	14	22		9.3		17	24							
	15	23		10		18	24.2							
	16	24		11		19	25.2							
						20	26							

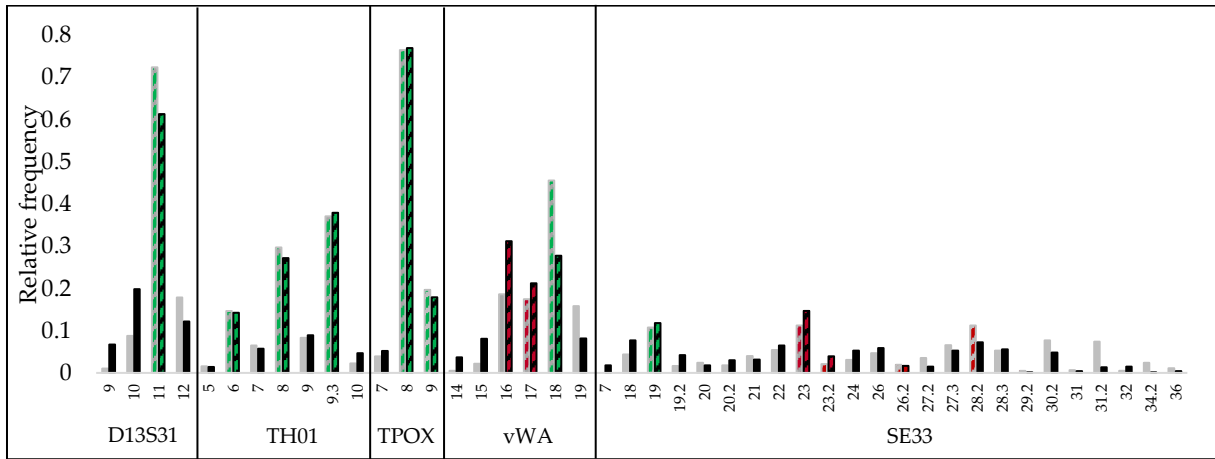
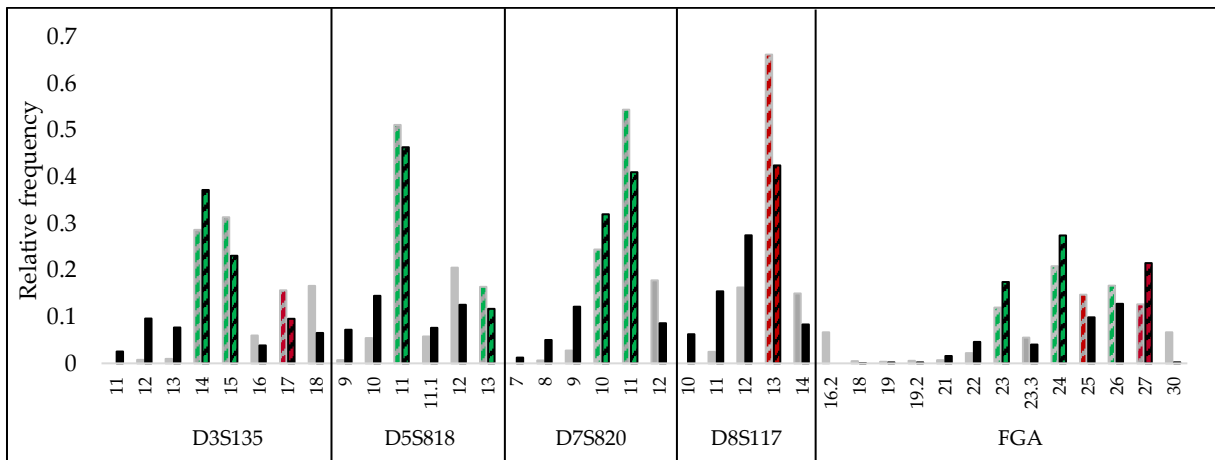
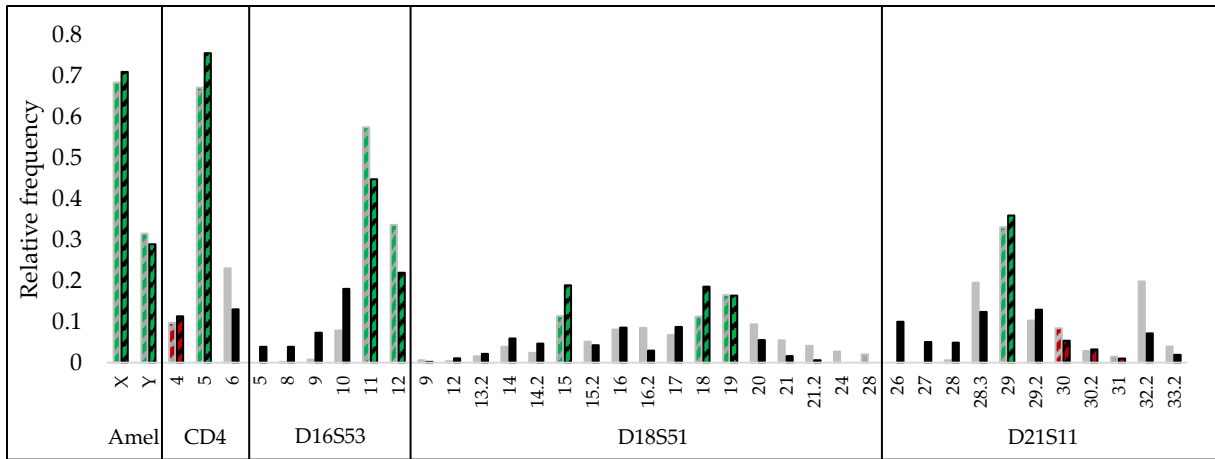
Supplementary Table 3: Alleles encompassed in reference database for alignment.

Locus	Allele	Sample A	Sample B	Sample C	Locus	Allele	Sample A	Sample B	Sample C	
Amel	X	100%	100%	100%	D8S1179	11	1%	6%	4%	
	Y	0%	94%	27%		12	10%	100%	37%	
CD4	4	2%	100%	59%		13	100%	80%	100%	
	5	100%	0%	100%		14	1%	0%	1%	
D13S317	9	1%	1%	1%	FGA	16.2	7%	10%	0%	
	10	9%	10%	9%		22	13%	10%	0%	
	11	100%	100%	100%		23	100%	10%	75%	
	12	1%	1%	1%		24	73%	100%	100%	
D16S539	8	0%	1%	2%		25	0%	0%	0%	
	9	1%	0%	2%		26	7%	30%	25%	
	10	10%	9%	14%		27	0%	0%	25%	
	11	100%	100%	100%		28	0%	10%	0%	
	12	76%	0%	33%		29	7%	0%	0%	
D18S51	13	2%	0%	0%	TH01	5	1%	5%	2%	
	14	14%	11%	13%		6	1%	94%	36%	
	15	100%	100%	100%		7	5%	1%	4%	
	17	0%	11%	8%		8	96%	0%	68%	
	18	5%	53%	29%		9	4%	3%	4%	
	19	34%	0%	54%		9.3	100%	100%	100%	
D21S11	27	0%	2%	1%		10	1%	1%	1%	
	28	2%	11%	5%		TPOX	7	3%	4%	5%
	29	16%	100%	41%			8	100%	100%	100%
	30	100%	77%	100%			9	0%	84%	15%
	31	1%	2%	1%	vWA	15	3%	3%	3%	
D3S1358	12	1%	0%	1%		16	16%	15%	15%	
	13	9%	1%	7%		17	100%	100%	100%	
	14	100%	11%	74%		18	73%	1%	39%	
	15	88%	100%	100%		19	1%	0%	1%	
	16	0%	14%	7%		20	1%	0%	0%	
D5S818	17	0%	81%	37%	SE33	18	18%	0%	18%	
	7	2%	5%	4%		19	100%	1%	100%	
	8	0%	1%	1%		20	5%	1%	7%	
	9	2%	2%	1%		21	1%	1%	1%	
	10	10%	11%	10%		22	2%	0%	4%	
	11	100%	100%	100%		22.2	1%	11%	8%	
	12	1%	14%	4%		23	1%	2%	6%	
	13	0%	96%	26%		23.2	0%	100%	68%	
14	0%	1%	1%	24		1%	0%	0%		
D7S820	8	1%	0%	1%		24.2	1%	4%	4%	
	9	8%	2%	4%		25.2	1%	11%	9%	
	10	100%	9%	54%		26	1%	0%	0%	
	10.3	6%	9%	8%		26.2	0%	57%	48%	
	11	86%	100%	100%		27.2	3%	5%	4%	
	13	0%	0%	0%	28.2	7%	4%	13%		
	14	0%	0%	0%	29.2	55%	1%	29%		

Supplementary Table 4: Allele representation by Illumina reads for all samples. Grey indicates true alleles.



Supplementary Figure 1: Relative frequency of aligned reads per locus, sample B. Grey indicates R9.4 data, black indicates R10 data. Green colored bars indicate true positive alleles, red colored bars indicate drop-ins or drop-outs.



Supplementary Figure 2: Relative frequency of aligned reads per locus, sample C. Grey indicates R9.4 data, black indicates R10 data. Green colored bars indicate true positive alleles, red colored bars indicate drop-ins or drop-outs.