

Fig. S1. The heat map of the average peak height about different cycle numbers and annealing temperatures.

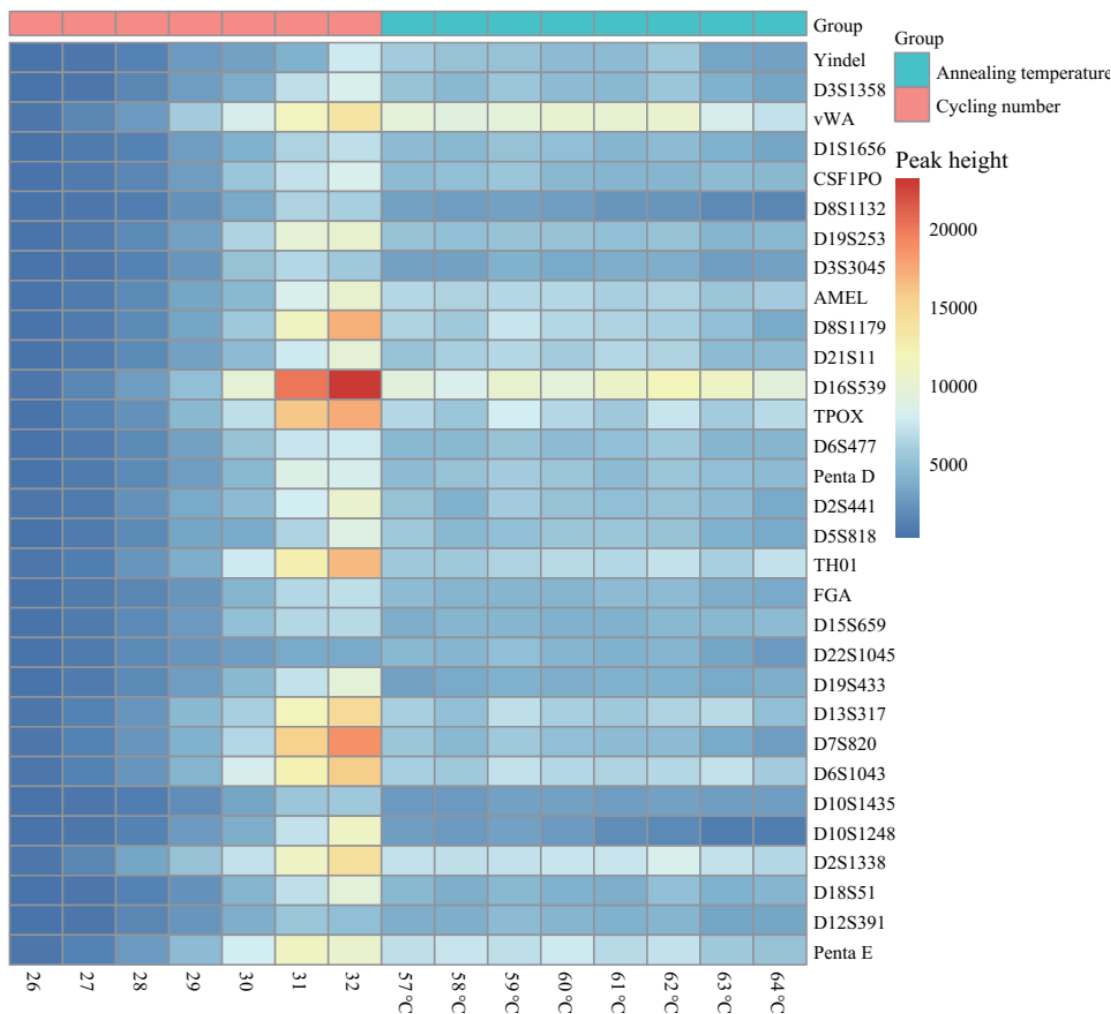


Fig. S2. The electrophoresis results of amplification specificity under different SUPER MIX concentrations.

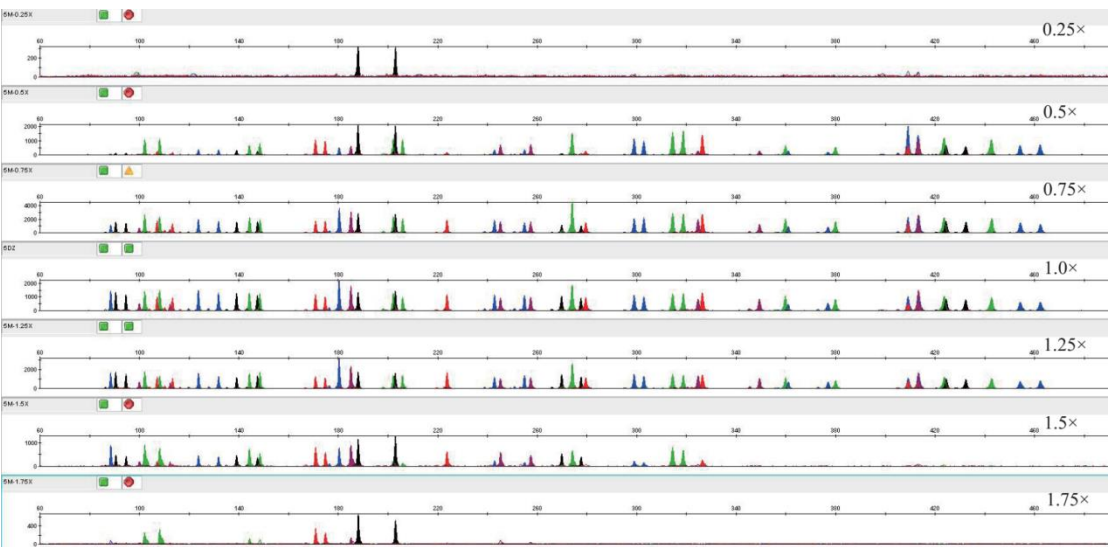


Fig. S3. The electrophoresis results of amplification specificity under different primer concentrations.

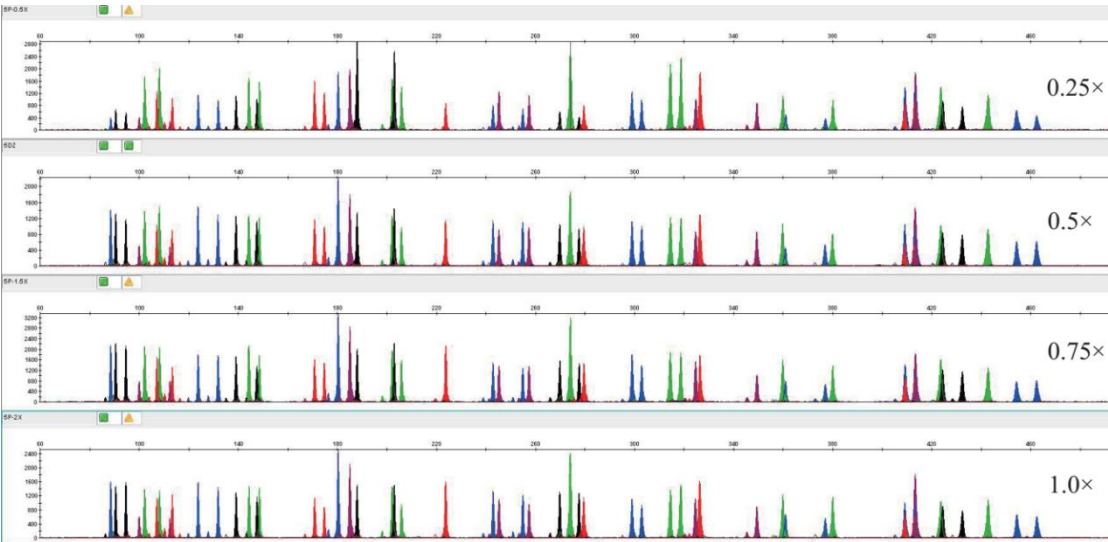
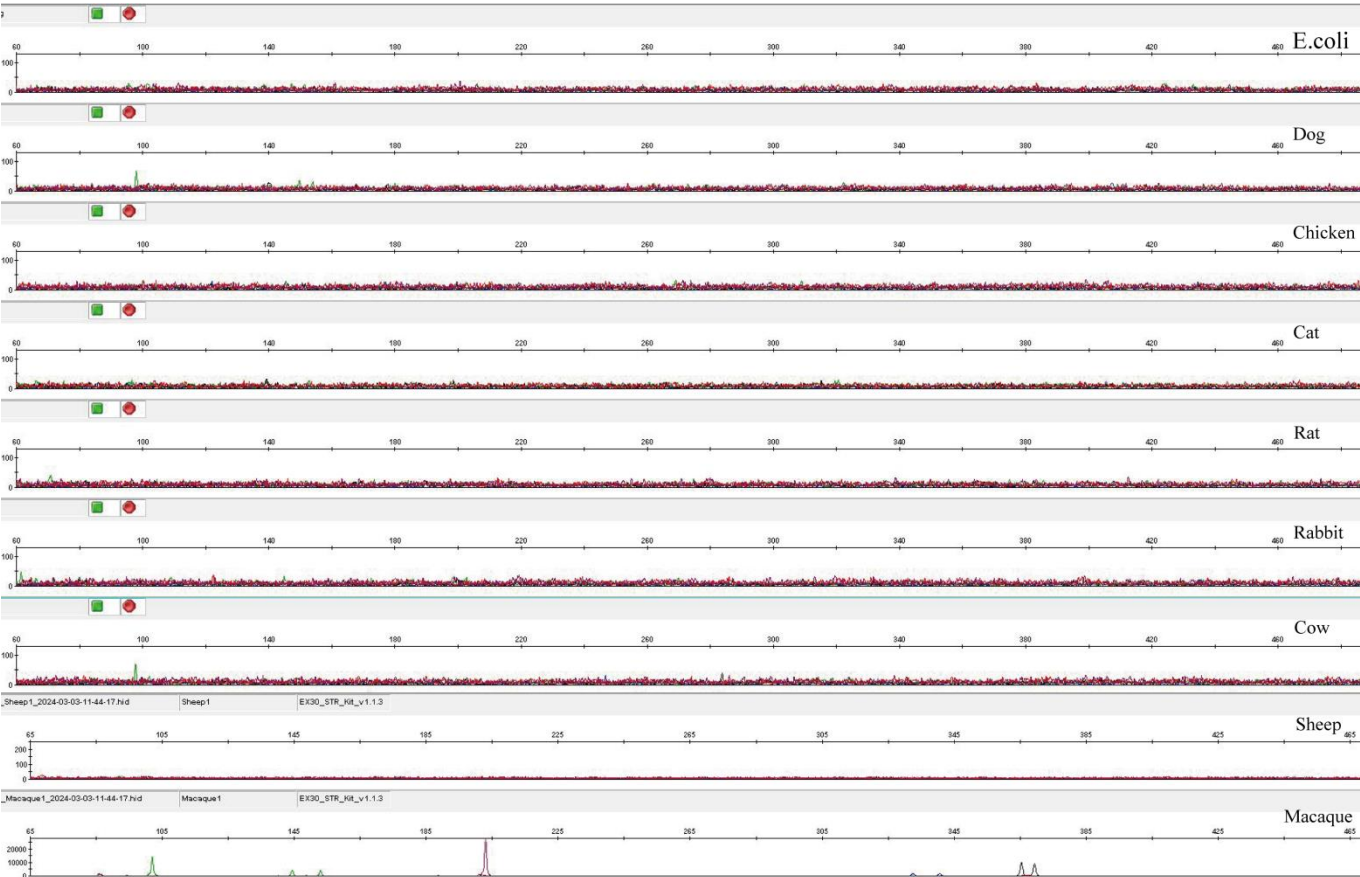


Fig. S4. The electrophoresis results of non-human DNA samples.



Supplementary Table 1 Primer details of for 31 loci.

Fluorescent		
Loci	labels	Primer sequence (5'-3')
Yindel	FAM	GCACATGCCTTCTCACTTCT
		GCGGAATGAAATACTTTTGAGTAAAG

D3S135		GCCTTATACTCATGAAATCAA
8		TTATCAGTCCAATCTGGGTGACAG
vWA		GGGTAAGAATAATCAGTATGTGAC
		AGCTAGAGACAGGATAGATGATAA
D1S165		TCATGTTGAGTAGGCTGAGAAG
6		TCAGGATTCTTCAGAGAAATAG
CSF1P		TGGTGCCAGACTGAGCCTTCT
O		ATTAGATTGTACAGAGGAGGCA
D8S113		ATTCTGTTGGTCATTGAGGGTTATAAC
2		GTCGTAGAATTTCTACTTGCACAA
D19S25		TTCCCCCTGTTCCCTGGGAT
3		GCACCACCAGTGTCCCTGATTCT
D3S304		GAAGATTACCTCCAGTGTTCT
5		GTTGTTTCTCACAATTGGTATCCCT
AMEL		TTTGCGTTAACAATGCCCTG
		GGGAAGCTGGTGGTAGGAACT
D8S117		TTCAGGCCCACTGGGCTCTTT
9		GTTATTTTCACTGTGGGGAATAG
D21S11		GCCTTTTCTCAGTCTCCATAAAT
		GGGTAGATAGACTGGATAGATA
D16S53		TAGTGTACAAGTGCCAGATG
9	HEX	GATACCATTTAGCGTTTGTGTGT
TPOX		ACCCATGTTCCCACTGGCCTGT
		CCCACAGGTTAATTAAGAGATTCA
D6S477		GGTGACTCTGAAACCAGAGTTGTTTC
		GGCTCTAAGAGTTATGATTTAGC
Penta D		TGGTGAGGCTGAAGTAGGATCACT
		GCTCTTTAATCTGGACACAAGTCCT
D2S441	SUM	GGAAGTGTGGCTCATCTATGA

		GGCTGTGGTGTTATGATATAGA
D5S818		GCTTTAATAGCAAGTATGTGACAAG
		GCCGTATCTTTATCTGTATCCTT
TH01		GTCCTGTTCCCTCCCTTATTTCCCT
		TAGGTTCTGAGTGCCCAAGGAGGCA
FGA		GCGTTAGGCATATTTACAAGCTAG
		TGCTTTGCGCTTCAGGACTTCAATTC
D15S65		GTTCAGATTTAGCCCAATTTTTCCCT
9		GGGAGAGGCTTAAACAAGAAGATA
D22S10		ATAGCTGCTATGGGGGCTAGAT
45		GCCGGATTGGCAATATTTTTATAAC
D19S43		GCAGAATAAGATTCTGTTGAAGG
3		GTCGTTCTTTAGCAGTGATTTCTG
D13S31		TCTGGGATGTGGAGGAGAGTT
7	LYN	TGTTGGTCAAATCTCCTCCTTCAA
D7S820		TCCGGACTATGGAGTTATTTTAAGGT
		GCTCTGAGGTATCAAAAACCTCAGAG
D6S104		GGAATGGCACTCTTATTCATCTAGT
3		CATGTTTTGAAGGCTTTGACTTGGAC
D10S14		TTCATAAGTCAGGAGAGAAGAGATG
35		GCAACATGGTGAAATCCCATCTCT
D10S12		GGAACAAATGAGTGAGTGGA
48		CTTGTTATTAAAGGAACAACCTCTGGT
D2S133		TGTGGGAGGGAGCCAGTGGATTTG
8	PUR	GGTGGCCCATAATCATGAGTTAT
D18S51		GTGACAAATTGAGACCTTGTCTCA
		ACAACACAAATAAACAAACCGTCAGC
D12S39		GTAAGGCTTCTCCAGAGAGAAAG
1		ATACCAGGGGCACTCCAGGTTCT

Penta E

GTATTACCTGAGCTCAGGAGAT

ACTCATTACCTTGCATGCATG

Supplementary Table 2 Values of stutter ratio and recommended filter for 31 loci.

Locus	Minim	Maximum	Mean	SD	Recommended
	um				filter(Mean+3*SD)
Yindel	0.0024	0.0100	0.0049	0.0025	0.0124
AMEL	0.0046	0.0500	0.0096	0.0106	0.0415
Penta D	0.0070	0.0456	0.0183	0.0086	0.0441
TH01	0.0113	0.0656	0.0333	0.0102	0.0640
TPOX	0.0176	0.0809	0.0354	0.0134	0.0755
D3S3045	0.0102	0.0905	0.0417	0.0216	0.1064
Penta E	0.0100	0.1224	0.0504	0.0207	0.1126
D13S317	0.0239	0.1292	0.0596	0.0242	0.1321
D7S820	0.0279	0.1172	0.0618	0.0189	0.1184
D2S441	0.0106	0.1066	0.0624	0.0205	0.1238
D1S1656	0.0122	0.1448	0.0748	0.0349	0.1794
D16S539	0.0071	0.1493	0.0757	0.0260	0.1536
CSF1PO	0.0370	0.1319	0.0778	0.0183	0.1327
D19S253	0.0270	0.1523	0.0778	0.0290	0.1649
D5S818	0.0192	0.1476	0.0787	0.0231	0.1480
FGA	0.0405	0.1259	0.0789	0.0190	0.1360
D10S1435	0.0299	0.1318	0.0804	0.0216	0.1452
D19S433	0.0100	0.2200	0.0819	0.0241	0.1541
D6S477	0.0544	0.1370	0.0839	0.0152	0.1296
D18S51	0.0400	0.1621	0.0841	0.0248	0.1584
D15S659	0.0396	0.2194	0.0855	0.0236	0.1562
D8S1179	0.0200	0.2163	0.0892	0.0233	0.1590
D6S1043	0.0531	0.1781	0.0920	0.0194	0.1501
D22S1045	0.0100	0.2348	0.0945	0.0460	0.2326

vWA	0.0200	0.1700	0.1020	0.0265	0.1814
D10S1248	0.0340	0.1834	0.1033	0.0230	0.1722
D2S1338	0.0547	0.1917	0.1049	0.0220	0.1711
D21S11	0.0500	0.1732	0.1059	0.0171	0.1574
D8S1132	0.0447	0.1760	0.1060	0.0232	0.1756
D3S1358	0.0593	0.2480	0.1090	0.0230	0.1780
D12S391	0.0512	0.2006	0.1171	0.0249	0.1919

Supplementary Table 3 Allelic frequencies and relevant forensic parameters for 29 autosomal loci.

Allele	CSF1P	D10S12	D10S14	D12S3	D13S3	D15S6	D16S5	D18S	D19S2	D19S4	D1S16	D21S	D22S10	D2S13	D2S4
	O	48	35	91	17	59	39	51	53	33	56	11	45	38	41
5					0.0024										
6															
7	0.0071								0.1517						
8	0.0047	0.0024	0.0142		0.2725		0.0024		0.0166						
9	0.0308		0.0047		0.1588	0.0024	0.2820		0.0095						
9.1															0.0190
9.3															
10	0.2204		0.0332		0.1706		0.1303		0.0190		0.0024				0.2062
10.1															0.0071
10.3			0.0024												
11	0.2559	0.0071	0.1303		0.2275	0.0142	0.2962	0.0071	0.1706		0.0592		0.1777		0.3104
11.3															0.0972
12	0.3957	0.0592	0.4218		0.1256	0.1540	0.2156	0.0569	0.3057	0.0332	0.0569				0.1967
12.3															0.0047
13	0.0735	0.3365	0.2346		0.0332	0.1991	0.0640	0.1801	0.2322	0.2915	0.0948		0.0024		0.0190
13.2										0.0284					
14	0.0118	0.2488	0.1445		0.0095	0.1161	0.0071	0.2014	0.0687	0.2630	0.1090		0.0403		0.1280
14.2										0.1209					
15		0.2180	0.0142	0.0190		0.0592	0.0024	0.1991	0.0261	0.0711	0.2701		0.3128		0.0118

15.2					0.1303			
15.3						0.0024		
16	0.0972	0.0071	0.1422	0.1422	0.0237	0.2038	0.2109	0.0095
16.2					0.0355			
16.3						0.0071		
17	0.0284	0.0616	0.1919	0.0545		0.0853	0.2109	0.0806
17.2					0.0024			
17.3						0.0735		
18	0.0024	0.2299	0.1019	0.0403		0.0118	0.0450	0.0829
18.3						0.0237		
19		0.1611	0.0166	0.0379				0.2204
20		0.1517	0.0024	0.0213				0.1327
20.3								
21		0.1327		0.0237				0.0332
21.2								
22		0.1137		0.0213				0.0355
22.2								
23		0.0687		0.0095				0.1635
23.2								
24		0.0427		0.0047				0.1588
24.2								
25		0.0095						0.0664
25.2								
26		0.0024						0.0118
27								0.0024
28						0.0379		0.0024
28.2						0.0024		
29						0.2867		
30						0.2725		

30.2												0.0047			
30.3												0.0024			
31												0.0758			
31.2												0.0758			
32												0.0166			
32.2												0.1517			
33												0.0095			
33.2												0.0616			
34.2												0.0024			
GD	0.7245	0.7653	0.7294	0.8588	0.8046	0.8538	0.7669	0.8583	0.7963	0.8074	0.8465	0.8053	0.7798	0.8635	0.7976
PIC	0.6771	0.7266	0.6889	0.8408	0.7737	0.834	0.7264	0.8403	0.7652	0.7802	0.8276	0.7776	0.7432	0.8465	0.7669
PM	0.1309	0.092	0.1104	0.0392	0.0696	0.0416	0.0967	0.0396	0.07	0.0622	0.0437	0.0654	0.0844	0.0384	0.0705
PD	0.8691	0.908	0.8896	0.9608	0.9304	0.9584	0.9033	0.9604	0.93	0.9378	0.9563	0.9346	0.9156	0.9616	0.9295
Hobs	0.7773	0.763	0.6635	0.8104	0.8199	0.8199	0.7773	0.8531	0.7583	0.8057	0.872	0.7678	0.7678	0.891	0.7773
PE	0.5575	0.5323	0.3741	0.6185	0.6365	0.6365	0.5575	0.7009	0.5241	0.6096	0.7387	0.5407	0.5407	0.7771	0.5575
TPI	2.2447	2.11	1.4859	2.6375	2.7763	2.7763	2.2447	3.4032	2.0686	2.5732	3.9074	2.1531	2.1531	4.587	2.2447
P-val															
ue	0.6626	0.9050	0.5157	0.0352	0.9513	0.3170	0.0798	0.6275	0.7651	0.9650	0.5823	0.1185	0.4420	0.6252	0.3998

10.3												
11		0.0308	0.2749	0.1232		0.3720		0.1374		0.1232	0.1825	0.0024 0.2749
11.3												
12		0.1256	0.2607	0.1398	0.0403	0.2275		0.1161		0.1635	0.1019	0.0190
12.3												
13	0.0024	0.2891	0.1256	0.1445	0.2275	0.0379		0.1896	0.0024	0.0948	0.0687	0.0024
13.2												
14	0.0498	0.1351	0.0047	0.1161	0.1754	0.0047		0.1374	0.0024	0.0379	0.0948	0.2346
14.2												
15	0.3104	0.0569		0.0166	0.3389			0.1825		0.0095	0.0900	0.0213
15.2												
15.3												
16	0.3033	0.0047			0.1682		0.0142	0.0711	0.0047		0.0592	0.1564
16.2												
16.3												
17	0.2464			0.0474	0.0308		0.0829	0.0118			0.0664	0.2773
17.2												
17.3												
18	0.0806			0.1659	0.0095		0.2204	0.0071	0.0190		0.0687	0.1967
18.3												
19	0.0047			0.1469	0.0024		0.2133		0.0592		0.0474	0.0877
20	0.0024			0.0474			0.1611		0.0521		0.0379	0.0213
20.3				0.0024								
21				0.0071			0.1256		0.1185		0.0284	0.0024
21.2									0.0071			
22				0.0024			0.0972		0.1825		0.0166	
22.2									0.0024			
23							0.0592		0.2227		0.0237	
23.2									0.0118			

24							0.0213		0.1493		0.0071			
24.2									0.0071					
25							0.0024		0.1043					
25.2									0.0142					
26							0.0024		0.0332					
27									0.0024					
28									0.0047					
28.2														
29														
30														
30.2														
30.3														
31														
31.2														
32														
32.2														
33														
33.2														
34.2														
GD	0.7437	0.7721	0.7896	0.8778	0.7735	0.7628	0.8457	0.8547	0.8637	0.7895	0.9145	0.7028	0.5971	0.7982
PIC	0.6968	0.7366	0.7554	0.8627	0.7371	0.7266	0.8248	0.8348	0.847	0.7638	0.9061	0.6582	0.5375	0.766
PM	0.1106	0.0948	0.0772	0.0326	0.089	0.0901	0.0427	0.0405	0.0364	0.0717	0.0193	0.1412	0.2259	0.0741
PD	0.8894	0.9052	0.9228	0.9674	0.911	0.9099	0.9573	0.9595	0.9636	0.9283	0.9807	0.8588	0.7741	0.9259
Hobs	0.7488	0.8152	0.7962	0.8673	0.7678	0.7156	0.8009	0.8483	0.8626	0.7583	0.9289	0.6445	0.5924	0.8009
PE	0.5077	0.6275	0.592	0.7292	0.5407	0.4529	0.6008	0.6916	0.7198	0.5241	0.8548	0.3478	0.2819	0.6008
TPI	1.9906	2.7051	2.4535	3.7679	2.1531	1.7583	2.5119	3.2969	3.6379	2.0686	7.0333	1.4067	1.2267	2.5119
P-value	0.6393	0.0997	0.9555	0.2929	0.8385	0.1242	0.5239	0.9879	0.9378	0.1426	0.2049	0.0190	0.3846	0.6136

Supplementary Table 4 CPD and CPE of the 29-plex STR multiplex system for 211 Guangdong Han individuals in different commercial kits

Kit	N	CPD	CPE
CODIS core STR loci	13	1-6.12E-15	1-1.74E-05
Promega PowerPlex 16 System	15	1-8.46E-18	1-1.20E-06
Microreader™ 20A ID system	19	1-2.58E-23	1-1.08E-08
GlobalFiler™ PCR Amplification Kit**	20	1-1.37E-23	1-1.43E-08
Promega PowerPlex 21 System	20	1-1.13E-24	1-2.82E-09
Promega PowerPlex Fusion System*	22	1-1.90E-26	1-9.89E-10
VeriFiler™ Plus System	23	1-6.18E-28	1-2.68E-10
29-plex STR multiplex system	29	1-7.16E-35	1-1.98E-12

N, number of STRs; **CPD**, combined power of discrimination; **CPE**, cumulative power of exclusion.

*, except DYS391; **, except SE33 and DYS391.