GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Genetic analysis of 30 InDel markers for forensic use in five different Chinese populations

C.T. Li, S.H. Zhang and S.M. Zhao

Shanghai Key Laboratory of Forensic Medicine,
Institute of Forensic Sciences, Ministry of Justice, Shanghai, P.R. China

Corresponding author: S.M. Zhao
E-mail: zhaoshuminxl@hotmail.com

Genet. Mol. Res. 10 (2): 964-979 (2011)
Received October 1, 2010
Accepted November 30, 2010
Published May 24, 2011
DOI 10.4238/vol10-2gmr1082

ABSTRACT. Allele frequencies of 30 insertion/deletion polymorphism (InDel) markers previously selected and validated for forensic purposes were assessed in 419 unrelated individuals originating from five different populations of P.R. China, including Chinese Han, Chinese Hui, Uighur, Mongolians, and Tibetans. Hardy-Weinberg equilibrium tests and linkage disequilibrium analysis were performed; the allele frequency distributions of the 30 InDel markers met the conditions for genetic equilibrium in all five populations and the InDel markers on the same chromosome did not generate any linkage blocking. Analysis of molecular variance indicated that genetic variation among the five populations represents only 4% of the total genetic diversity. We determined the cumulative power of discrimination for each population: 0.99999999999841 in Chinese Han, 0.99999999999690 in Chinese Hui, 0.99999999999709 in Uighur, 0.99999999999772 in Mongolians, and 0.99999999999854 in Tibetans.

Key words: Insertion/deletion polymorphism (InDel); China; Forensic genetics; Allele frequency; Population genetics

METHODOLOGY

A total of 419 unrelated individuals were randomly selected from the five main populations in P.R. China, including Chinese Han (N = 108), Chinese Hui (N = 71), Uighur (N = 96), Mongolian (N = 58), and Tibetan (N = 86). All persons gave their informed consent prior to inclusion in the study.

DNA extraction

Genomic DNA was extracted from blood samples using a QIAamp DNA mini kit according to manufacturer instructions (Qiagen, Hilden, Germany). The quantity of recovered DNA was determined spectrophotometrically.

Selection of highly informative InDel markers

All highly informative InDel markers with average heterozygosity ≥0.400 in the 22 human autosomes were screened with the Human Genome Browser in Galaxy system (http://main.g2.bx.psu.edu/) and with similar tools in dbSNP (http://www.ncbi.nlm.nih.gov/SNP/) in the present study, and 837 InDel markers were selected and imported into a sub-database. Next, 30 candidate InDel markers were picked out according to the following criteria: i) the minor allele frequency in East Asia was ≥0.200; ii) allele length variation was 3-30 bp; iii) the InDel marker was located in an intron; iv) all selected InDel markers in the same chromosome were unlinked, and v) all selected InDel markers could be amplified with a multiplex reaction in a single tube.

Typing

All 30 InDel markers were determined in a single multiplex polymerase chain reaction (PCR) by multicolor fluorescence and capillary electrophoresis using the Qiagen Multiplex PCR kit (Qiagen) at 1X concentration, 0.1 µM of all primers and 0.5 ng genomic DNA in a 25-µL final reaction volume. Thermocycling conditions were as follows: 30 cycles of 95°C for 11 min, 94°C for 30 s, 57°C for 90 s; 72°C for 90 s, and 60°C for 60 min.

The amplified products were separated by capillary electrophoresis on ABI PRISM 3130 Genetic Analyzers (Applied Biosystems, Foster City, CA, USA) according to manufacturer protocols using the filter set G5 and the POP4 polymer (Applied Biosystems). The sample run data were analyzed using the GeneMapper v4.0 software (Applied Biosystems) with the analysis method developed by the authors.

Quality control

The 9947A DNA (0.1 ng/µL; Promega) was routinely used as amplification positive controls and to test the overall performance of the multiplex genotyping protocol.

Analysis of data

Basic statistical computations including allele frequency, observed heterozygosity, expected

heterozygosity, power of discrimination, power of exclusion, probability of matching, polymorphism information content, and typical paternity index were performed with PowerStats V12.xls (http://www.promega.com/geneticidtools/powerstats/). The χ^2 test for RXC tables was employed to test the deviation of allele frequencies among different populations, and pairwise population comparisons were made with the Fisher exact test. Test size α was equal to 0.05, P value was corrected by Bonferroni's adjustment and $P < 0.0125$ (0.05/4, 4 = number of comparisons performed) was considered to be statistically significant with the Fisher exact test. Hardy-Weinberg equilibrium tests for the 30 InDel markers in the 5 populations studied and linkage disequilibrium (LD) analysis among the InDel markers distributed on the same chromosome were performed with SNPAnalyzer 2.0 (http://snp.istech21.com/snpanalyzer/2.0/).

Analysis of molecular variance (AMOVA) of the 30 InDel markers in the 5 populations was done with the GenAlEx v6.3 software (http://www.anu.edu.au/BoZo/GenAlEx/) (Peakall and Smouse, 2006).

RESULTS

Hardy-Weinberg equilibrium tests demonstrated no significant deviation from expected values ($P > 0.0017$, after Bonferroni's correction for multiple testing) for all 30 InDel markers in the 5 populations studied: Chinese Han, Chinese Hui, Uighur, Mongolian, and Tibetan (see Supplementary Tables 1-5). Detailed information of the 30 InDel markers is shown in Table 1.

Table 1. Details of the selected 30 InDel markers.

InDel	rs#	Allele 1/Allele 2	Chr	SNP to Chr	Chr Pos (Genome build 37.1)	Group label
1	rs2307963	-/TTAGCCCTTTCCCCCTTAAGGT	1	-	245551961:245551982	GRCh37
2	rs2308276	-/TTTAA	2	+	172915805:172915806	GRCh37
3	rs2307975	-/CTT	3	-	16427710:16427712	GRCh37
4	rs1611088	-/TAC	5	+	102432775:102432777	GRCh37
5	rs2307661	-/TTCT	5	-	34893909:34893910	GRCh37
6	rs1610949	-/ATA	5	-	96329011	GRCh37
7	rs1160953	-/TCTA	5	-	115626076:115626077	GRCh37
8	rs1610903	-/GGTGAGGGTGAGGGTATATGGGGAGT	5	-	11312823:11312824	GRCh37
9	rs2308116	-/GGA	6	-	11715435:11715437	GRCh37
10	rs2308139	-/TAA	6	-	152778334	GRCh37
11	rs16458	-/TTCC	7	+	122151327:122151328	GRCh37
12	rs2307783	-/CCCA	7	-	23307635:23307638	GRCh37
13	rs10666410	-/AGTG	8	+	61190688:61190689	GRCh37
14	rs34535242	-/GTAG	8	+	18429416	GRCh37
15	rs2307850	-/GGTG	9	-	135380186:135380189	GRCh37
16	rs16721	-/TTGC	11	+	32121863	GRCh37
17	rs35248926	-/TCTCT	11	+	117052070:117052074	GRCh37
18	rs35833136	-/AAATA	11	+	77997682:77997683	GRCh37
19	rs16660	-/TGG	12	+	120900933:120900934	GRCh37
20	rs2308232	-/AGTTTA	12	-	96991884:96991885	GRCh37
21	rs2307805	-/CCATAAACC	12	-	67705010:67705011	GRCh37
22	rs3049448	-/TCTGATCC	13	-	96127408:96127415	GRCh37
23	rs3032356	-/TTCCATC	14	+	32943593:32943594	GRCh37
24	rs2307537	-/AAG	14	+	77762948:77762949	GRCh37
25	rs1610878	-/ACAG	16	-	58763163:58763166	GRCh37
26	rs34999022	-/TAAAA	18	+	33050322:33050323	GRCh37
27	rs2307561	-/AGTGTT	18	+	24503507	GRCh37
28	rs2308278	-/TAAG	20	-	35315632	GRCh37
29	rs3034941	-/ATT	21	+	43182953:43182954	GRCh37
30	rs34543832	-/TCA	21	+	19706182:19706183	GRCh37

rs# = reference clustered SNPID; Chr = chromosome; Chr Pos = chromosome position. The chromosome position of the selected 30 InDel markers was obtained from a provisional release of dbSNP build 132.

Genotyping data of the 5 populations were imported into SNPAnalyzer2.0, a web-based integrated workbench for LD analysis in order to construct the LD map of the InDels on the same chromosome in each population. The results showed that there was no significant LD among the InDels on the same chromosome in all 5 populations, and consequently, the assumption of independence among all selected markers was reasonable.

Allele frequencies of the 30 InDel markers and the results of pairwise comparisons between Chinese Han and the other four populations are listed in Table 2. The power of discrimination values of the 30 InDel markers in the 5 populations studied are listed in Table 3. Cumulative power of discrimination for each population was 0.99999999999841 in Chinese Han, 0.99999999999690 in Chinese Hui, 0.99999999999709 in Uighur, 0.99999999999772 in Mongolian, and 0.99999999999854 in Tibetan.

AMOVA of the 30 InDel markers indicates that genetic variation among the populations studied represents only 4.0% of the total genetic diversity, meaning that individual components of genetic variation account for most of the human genetic diversity for these markers.

Access to the data

Available upon request: zhaoshuminxl@hotmail.com.

DISCUSSION

Chinese Han is the largest population in P.R China, accounting for approximately 91% of the country's total population. The Chinese Hui, Uighur, Mongolian, and Tibetan populations are minority ethnic groups in P.R. China, and the total population of each is more than 5 million. Genetic data resulting from the typing of 419 unrelated individuals originating from the 5 populations confirmed the high information content of the selected InDel markers (see Supplementary Tables 6-10). The average observed heterozygosity value calculated for the panel of 30 InDel markers in the populations studied is 0.476 for Chinese Han, 0.476 for Chinese Hui, 0.461 for Uighur, 0.469 for Mongolian, and 0.463 for Tibetan.

Allele frequencies of the 30 InDel markers in the 4 minority ethnic groups including Chinese Hui, Uighur, Mongolian, and Tibetan were compared to those in the Chinese Han population at the same markers (Table 2). P values were corrected by Bonferroni's adjustment and $P < 0.0125$ (0.05/4, 4 = number of comparisons performed) was considered to be significant. The Fisher exact test showed that there were statistically significant differences in some InDel markers between the Chinese Han and Uighur (7), Mongolian (3) and Tibetan (7) populations. There were no statistically significant differences between Chinese Han and Chinese Hui in allele distribution of the 30 InDel markers, in line with the results of AMOVA between the 2 populations, which indicated that genetic variation within the two populations represents 0.0% of the total genetic diversity.

Several different InDel marker panels have been published in the last two years (Edelmann et al., 2009; Pereira et al., 2009; Li et al., 2010; Pimenta and Pena, 2010), including the 29plex panel with the SNPlex genotyping system in our previous study (Li et al., 2010). This report of allele frequencies of 30 new InDel markers would serve as a valuable reference database for individual identification in the 5 Chinese populations studied in the future. This database may also be useful for other population genetics and diversity studies. There was no conflict of interest.

Table 2. Allele frequencies of the 30 InDel markers and population comparisons between Chinese Han and the other four populations.

Locus	Allele	Han	Hui	Uigur	Mongolian	Tibetan	χ^2_{CMH}	P (α = 0.05)	P' of the Fisher exact test (α' = 0.0125)			
		(2N = 216)	(2N = 142)	(2N = 192)	(2N = 116)	(2N = 172)			Han *vs* Hui	Han *vs* Ui	Han *vs* Mon	Han *vs* Tib
1	0/1	0.347/0.653	0.246/0.754	0.219/0.781	0.560/0.440	0.390/0.610	45.155	<0.0001	0.047	**0.0044**	**2.84E-04**	0.3982
2	0/1	0.352/0.648	0.380/0.620	0.302/0.698	0.353/0.647	0.448/0.552	8.710	0.0688	/	/	/	/
3	0/1	0.324/0.676	0.394/0.606	0.313/0.688	0.353/0.647	0.297/0.703	4.095	0.3934	/	/	/	/
4	0/1	0.370/0.630	0.296/0.704	0.271/0.729	0.362/0.638	0.302/0.698	6.219	0.1834				
5	0/1	0.458/0.542	0.387/0.613	0.380/0.620	0.422/0.578	0.459/0.541	4.207	0.3788	/	/	/	/
6	0/1	0.625/0.375	0.514/0.486	0.542/0.458	0.543/0.457	0.372/0.628	25.182	<0.0001	0.0486	0.1071	0.1601	**8.47E-07**
7	0/1	0.403/0.597	0.415/0.585	0.505/0.495	0.440/0.560	0.453/0.547	4.934	0.2941	/	/	/	/
8	0/1	0.426/0.574	0.380/0.620	0.260/0.740	0.595/0.405	0.488/0.512	38.881	<0.0001	0.4418	**5.71E-04**	**0.004**	0.2589
9	0/1	0.718/0.282	0.627/0.373	0.354/0.646	0.603/0.397	0.616/0.384	59.453	<0.0001	0.0821	**1.90E-13**	0.0369	0.0388
10	0/1	0.356/0.644	0.345/0.655	0.318/0.682	0.310/0.690	0.442/0.558	7.868	0.0965	/	/	/	/
11	0/1	0.588/0.412	0.535/0.465	0.563/0.438	0.612/0.388	0.581/0.419	1.870	0.7596	/	/	/	/
12	0/1	0.287/0.713	0.246/0.754	0.286/0.714	0.716/0.284	0.558/0.442	102.009	<0.0001	0.4660	1.0000	**8.04E-14**	**9.29E-08**
13	0/1	0.477/0.523	0.528/0.472	0.474/0.526	0.543/0.457	0.552/0.448	3.872	0.4237	/	/	/	/
14	0/1	0.472/0.528	0.437/0.563	0.594/0.406	0.534/0.466	0.436/0.564	12.973	0.0114	0.5175	0.0170	0.3013	0.5383
15	0/1	0.384/0.616	0.366/0.634	0.438/0.563	0.345/0.655	0.471/0.529	6.946	0.1388	/	/	/	/
16	0/1	0.273/0.727	0.260/0.739	0.203/0.797	0.233/0.767	0.407/0.593	21.064	0.0003	0.8086	0.1052	0.5114	0.0066
17	0/1	0.454/0.546	0.472/0.528	0.630/0.370	0.474/0.526	0.651/0.349	25.977	<0.0001	0.7463	**4.85E-04**	0.7305	**1.42E-04**
18	0/1	0.616/0.384	0.549/0.451	0.677/0.323	0.664/0.336	0.802/0.198	25.477	<0.0001	0.2280	0.2144	0.4056	**8.89E-05**
19	0/1	0.310/0.690	0.330/0.669	0.292/0.708	0.319/0.681	0.320/0.680	0.683	0.9534	/	/	/	/
20	0/1	0.310/0.690	0.310/0.690	0.328/0.672	0.302/0.698	0.291/0.709	0.629	0.9598	/	/	/	/
21	0/1	0.676/0.324	0.613/0.387	0.448/0.552	0.586/0.414	0.628/0.372	23.929	<0.0001	0.2571	**3.91E-06**	0.1183	0.3352
22	0/1	0.389/0.611	0.408/0.592	0.417/0.583	0.371/0.629	0.360/0.640	1.588	0.8109	/	/	/	/
23	0/1	0.343/0.657	0.275/0.725	0.375/0.625	0.422/0.578	0.395/0.605	7.842	0.0975				
24	0/1	0.509/0.491	0.514/0.486	0.474/0.526	0.543/0.457	0.517/0.483	1.544	0.8189	/	/	/	/
25	0/1	0.384/0.616	0.310/0.690	0.583/0.417	0.448/0.552	0.401/0.599	29.337	<0.0001	0.1755	**6.95E-05**	0.2919	0.7543
26	0/1	0.426/0.574	0.500/0.500	0.547/0.453	0.362/0.638	0.576/0.424	18.697	0.0009	0.1932	0.0172	0.2916	**0.0042**
27	0/1	0.426/0.574	0.401/0.599	0.333/0.667	0.466/0.534	0.564/0.436	20.857	0.0003	0.6625	0.0661	0.4896	**0.0079**
28	0/1	0.667/0.333	0.690/0.310	0.698/0.302	0.655/0.345	0.610/0.390	3.679	0.4511	/	/	/	/
29	0/1	0.634/0.366	0.640/0.359	0.411/0.589	0.664/0.336	0.640/0.360	32.872	<0.0001	0.9111	**7.55E-06**	0.6316	1.0000
30	0/1	0.333/0.667	0.268/0.732	0.365/0.635	0.241/0.759	0.273/0.727	8.002	0.0915	/	/	/	/

Allele 0 = allele deletion of the InDel marker; Allele 1 = allele insertion of the InDel marker; Han = Chinese Hans; Hui = Chinese Hui; Ui = Uigur; Mon = Mongolian; Tib = Tibetan. The statistically significant P values ($P' < 0.0125$) of the Fisher exact tests are indicated in bold. "/" Indicates that the pairwise comparison would not be necessary because of the $P > 0.05$ in the χ^2_{CMH} test.

Table 3. PD and CPD values of the 30 InDel markers in the 5 populations studied.

Locus	rs#	PD values				
		Han	Hui	Uighur	Mongolia	Tibetan
1	rs2307963	0.574	0.530	0.508	0.576	0.541
2	rs2308276	0.604	0.606	0.572	0.609	0.630
3	rs2307975	0.586	0.565	0.590	0.621	0.583
4	rs1611088	0.559	0.538	0.556	0.609	0.583
5	rs2307661	0.595	0.588	0.630	0.628	0.609
6	rs1610949	0.606	0.666	0.647	0.662	0.616
7	rs1160953	0.601	0.599	0.595	0.599	0.570
8	rs1610903	0.643	0.538	0.546	0.649	0.630
9	rs2308116	0.535	0.609	0.601	0.549	0.592
10	rs2308139	0.588	0.610	0.573	0.592	0.624
11	rs16458	0.636	0.632	0.580	0.532	0.606
12	rs2307783	0.568	0.538	0.556	0.490	0.530
13	rs10666410	0.650	0.627	0.646	0.602	0.647
14	rs34535242	0.640	0.598	0.555	0.644	0.655
15	rs2307850	0.624	0.586	0.617	0.615	0.665
16	rs16721	0.553	0.551	0.490	0.523	0.623
17	rs35248926	0.575	0.595	0.605	0.582	0.621
18	rs35833136	0.603	0.630	0.581	0.607	0.469
19	rs16660	0.579	0.594	0.577	0.600	0.598
20	rs2308232	0.584	0.582	0.607	0.562	0.575
21	rs2307805	0.597	0.615	0.609	0.601	0.586
22	rs3049448	0.600	0.605	0.559	0.550	0.567
23	rs3032356	0.584	0.557	0.604	0.594	0.569
24	rs2307537	0.641	0.596	0.638	0.602	0.624
25	rs1610878	0.583	0.549	0.600	0.537	0.546
26	rs34999022	0.555	0.577	0.561	0.595	0.614
27	rs2307561	0.604	0.558	0.579	0.661	0.604
28	rs2308278	0.560	0.593	0.556	0.568	0.628
29	rs3034941	0.615	0.574	0.631	0.571	0.592
30	rs34543832	0.598	0.553	0.607	0.533	0.550
CDP		0.99999999999841	0.99999999999690	0.99999999999709	0.99999999999772	0.99999999999854

PD = power of discrimination; CPD = cumulative power of discrimination.

ACKNOWLEDGMENTS

Research supported by the Ministry of Finance, P.R. China (#GY0902). We also thank Dr. Shilin Li of the National Ministry of Education Key Laboratory of Contemporary Anthropology at Fudan University for generously providing unrelated individual DNA samples of Mongolian and Tibetan populations.

REFERENCES

Edelmann J, Hering S, Augustin C and Szibor R (2009). Indel polymorphisms - An additional set of markers on the X-chromosome. *Forensic Sci. Int. Genet. Suppl.* 2: 510-512.

Li C, Zhao S, Zhang S, Li L, et al. (2010). Genetic polymorphism of 29 highly informative InDel markers for forensic use in the Chinese Han population. *Forensic Sci. Int. Genet*. 5: 27-30.

Peakall R and Smouse PE (2006). GENALEX 6: genetic analysis in Excel. Population genetic software for teaching and research. *Mol. Ecol. Notes* 6: 288-295.

Pereira R, Phillips C, Alves C, Amorim A, et al. (2009). A new multiplex for human identification using insertion/deletion polymorphisms. *Electrophoresis* 30: 3682-3690.

Pimenta JR and Pena SD (2010). Efficient human paternity testing with a panel of 40 short insertion-deletion polymorphisms. *Genet. Mol. Res.* 9: 601-607.

Supplementary Tables

Supplementary Table 1. Allele frequency and HW test by SNPAnalyzer for Chinese Han.

Marker ID	Allele	Total genotype Cnt	Valid genotype Cnt	Call rate	Allele freq	Chi-square	P value
40_01_rs2307963	0/1	108	108	1	0.347/0.653	1.645	0.1997
35_02_rs2308276	0/1	108	108	1	0.352/0.648	0.071	0.7905
23_03_rs2307975	0/1	108	108	1	0.324/0.676	0.023	0.8804
09_05_rs1611088	0/1	108	108	1	0.370/0.630	3.947	0.0469
28_05_rs2307661	0/1	108	108	1	0.458/0.542	1.085	0.2976
33_05_rs1610949	0/1	108	108	1	0.625/0.375	0.006	0.9386
45_05_rs1160953	0/1	108	108	1	0.403/0.597	0.370	0.5429
48_05_rs1610903	0/1	108	108	1	0.426/0.574	1.798	0.1799
03_06_rs2308116	0/1	108	108	1	0.718/0.282	4.799	0.0285
29_06_rs2308139	0/1	108	108	1	0.356/0.644	0.523	0.4695
07_07_rs16458	0/1	108	108	1	0.588/0.412	1.120	0.2899
53_07_rs2307783	0/1	108	108	1	0.287/0.713	0.002	0.9618
20_08_rs10666410	0/1	108	108	1	0.477/0.523	1.763	0.1843
38_08_rs34535242	0/1	108	108	1	0.472/0.528	0.548	0.4593
05_09_rs2307850	0/1	108	108	1	0.384/0.616	0.697	0.4037
26_11_rs16721	0/1	108	108	1	0.273/0.727	0.263	0.6082
27_11_rs35248926	0/1	108	108	1	0.454/0.546	2.699	0.1004
44_11_rs35833136	0/1	108	108	1	0.616/0.384	0.148	0.7002
10_12_rs16660	0/1	108	108	1	0.310/0.690	0.031	0.8604
18_12_rs2308232	0/1	108	108	1	0.310/0.690	0.075	0.7843
36_12_rs2307805	0/1	108	108	1	0.676/0.324	0.530	0.4666
21_13_rs3049448	0/1	108	108	1	0.389/0.611	0.291	0.5893
12_14_rs3032356	0/1	108	108	1	0.343/0.657	0.513	0.4740
15_14_rs2307537	0/1	108	108	1	0.509/0.491	0.588	0.4434
22_16_rs1610878	0/1	108	108	1	0.384/0.616	1.436	0.2308
08_18_rs34999022	0/1	108	108	1	0.426/0.574	4.844	0.0277
49_18_rs2307561	0/1	108	108	1	0.426/0.574	0.393	0.5308
43_20_rs2308278	0/1	108	108	1	0.667/0.333	3.000	0.0833
02_21_rs3034941	0/1	108	108	1	0.634/0.366	0.415	0.5194
47_21_rs34543832	0/1	108	108	1	0.333/0.667	0.188	0.6650

Data format of the SNPAnalyzer; Marker ID was named by the author with the rules listed below: 40_01_rs2307963: 40 = serial number of the InDel marker used in our study; 01 = chromosome number of the InDel marker; rs2307963 = reference of the InDel marker in dbSNP. Alleles of InDel marker was named as 0 = deletion; 1 = insertion.

Supplementary Table 2. Allele frequency and HW test by SNPAnalyzer for Chinese Hui.

Marker ID	Allele	Total genotype Cnt	Valid genotype Cnt	Call rate	Allele freq	Chi-square	P value
40_01_rs2307963	0/1	71	71	1	0.246/0.754	0.341	0.5591
35_02_rs2308276	0/1	71	71	1	0.380/0.620	0.018	0.8928
23_03_rs2307975	0/1	71	71	1	0.394/0.606	2.285	0.1306
09_05_rs1611088	0/1	71	71	1	0.296/0.704	3.348	0.0673
28_05_rs2307661	0/1	71	71	1	0.387/0.613	0.682	0.4089
33_05_rs1610949	0/1	71	71	1	0.514/0.486	6.188	0.0129
45_05_rs1160953	0/1	71	71	1	0.415/0.585	0.377	0.5390
48_05_rs1610903	0/1	71	71	1	0.380/0.620	4.619	0.0316
03_06_rs2308116	0/1	71	71	1	0.627/0.373	0.003	0.9558
29_06_rs2308139	0/1	71	71	1	0.345/0.655	0.659	0.4169
07_07_rs16458	0/1	71	71	1	0.535/0.465	0.100	0.7521
53_07_rs2307783	0/1	71	71	1	0.246/0.754	0.038	0.8457
20_08_rs10666410	0/1	71	71	1	0.528/0.472	0.009	0.9265
38_08_rs34535242	0/1	71	71	1	0.437/0.563	0.549	0.4589
05_09_rs2307850	0/1	71	71	1	0.366/0.634	0.605	0.4367
26_11_rs16721	0/1	71	71	1	0.260/0.739	0.234	0.6285
27_11_rs35248926	0/1	71	71	1	0.472/0.528	0.740	0.3897
44_11_rs35833136	0/1	71	71	1	0.549/0.451	0.077	0.7819
10_12_rs16660	0/1	71	71	1	0.330/0.669	0.014	0.9054
18_12_rs2308232	0/1	71	71	1	0.310/0.690	0.010	0.9191
36_12_rs2307805	0/1	71	71	1	0.613/0.387	0.030	0.8616
21_13_rs3049448	0/1	71	71	1	0.408/0.592	0.172	0.6781
12_14_rs3032356	0/1	71	71	1	0.275/0.725	0.045	0.8322
15_14_rs2307537	0/1	71	71	1	0.514/0.486	0.702	0.4020
22_16_rs1610878	0/1	71	71	1	0.310/0.690	2.444	0.1180
08_18_rs34999022	0/1	71	71	1	0.500/0.500	1.704	0.1917
49_18_rs2307561	0/1	71	71	1	0.401/0.599	2.887	0.0893
43_20_rs2308278	0/1	71	71	1	0.690/0.310	1.468	0.2257
02_21_rs3034941	0/1	71	71	1	0.640/0.359	1.239	0.2657
47_21_rs34543832	0/1	71	71	1	0.268/0.732	0.003	0.9592

Data format of the SNPAnalyzer; Marker ID was named by the author with the rules listed below: 40_01_rs2307963: 40 = serial number of the InDel marker used in our study; 01 = chromosome number of the InDel marker; rs2307963 = reference of the InDel marker in dbSNP. Alleles of InDel marker was named as 0 = deletion; 1 = insertion.

Supplementary Table 3. Allele frequency and HW test by SNPAnalyzer for Uighur.

Marker ID	Allele	Total genotype Cnt	Valid genotype Cnt	Call rate	Allele freq	Chi-square	P value
40_01_rs2307963	0/1	96	96	1	0.219/0.781	0.016	0.8979
35_02_rs2308276	0/1	96	96	1	0.302/0.698	0.136	0.7128
23_03_rs2307975	0/1	96	96	1	0.313/0.688	0.596	0.4401
09_05_rs1611088	0/1	96	96	1	0.271/0.729	0.000	0.9828
28_05_rs2307661	0/1	96	96	1	0.380/0.620	1.829	0.1763
33_05_rs1610949	0/1	96	96	1	0.542/0.458	1.357	0.2441
45_05_rs1160953	0/1	96	96	1	0.505/0.495	1.044	0.3069
48_05_rs1610903	0/1	96	96	1	0.260/0.740	0.073	0.7868
03_06_rs2308116	0/1	96	96	1	0.354/0.646	0.000	0.9852
29_06_rs2308139	0/1	96	96	1	0.318/0.682	0.633	0.4262
07_07_rs16458	0/1	96	96	1	0.563/0.438	1.959	0.1616
53_07_rs2307783	0/1	96	96	1	0.286/0.714	0.879	0.3485
20_08_rs10666410	0/1	96	96	1	0.474/0.526	0.994	0.3189
38_08_rs34535242	0/1	96	96	1	0.594/0.406	4.200	0.0404
05_09_rs2307850	0/1	96	96	1	0.438/0.563	0.024	0.8764
26_11_rs16721	0/1	96	96	1	0.203/0.797	0.063	0.8020
27_11_rs35248926	0/1	96	96	1	0.630/0.370	0.003	0.9554
44_11_rs35833136	0/1	96	96	1	0.677/0.323	0.222	0.6372
10_12_rs16660	0/1	96	96	1	0.292/0.708	0.820	0.3651
18_12_rs2308232	0/1	96	96	1	0.328/0.672	6.876	0.0087
36_12_rs2307805	0/1	96	96	1	0.448/0.552	0.271	0.6029
21_13_rs3049448	0/1	96	96	1	0.417/0.583	3.840	0.0500
12_14_rs3032356	0/1	96	96	1	0.375/0.625	0.047	0.8276
15_14_rs2307537	0/1	96	96	1	0.474/0.526	0.345	0.5569
22_16_rs1610878	0/1	96	96	1	0.583/0.417	0.490	0.4840
08_18_rs34999022	0/1	96	96	1	0.547/0.453	3.765	0.0523
49_18_rs2307561	0/1	96	96	1	0.333/0.667	0.586	0.4440
43_20_rs2308278	0/1	96	96	1	0.698/0.302	1.786	0.1814
02_21_rs3034941	0/1	96	96	1	0.411/0.589	0.542	0.4614
47_21_rs34543832	0/1	96	96	1	0.365/0.635	0.011	0.9159

Data format of the SNPAnalyzer; Marker ID was named by the author with the rules listed below: 40_01_rs2307963: 40 = serial number of the InDel marker used in our study; 01 = chromosome number of the InDel marker; rs2307963 = reference of the InDel marker in dbSNP. Alleles of InDel marker was named as 0 = deletion; 1 = insertion.

Supplementary Table 4. Allele frequency and HW test by SNPAnalyzer for Mongolian.

Marker ID	Allele	Total genotype Cnt	Valid genotype Cnt	Call rate	Allele freq	Chi-square	P value
40_01_rs2307963	0/1	58	58	1	0.560/0.440	1.389	0.2386
35_02_rs2308276	0/1	58	58	1	0.353/0.647	0.188	0.6647
23_03_rs2307975	0/1	58	58	1	0.353/0.647	7.463	0.0063
09_05_rs1611088	0/1	58	58	1	0.362/0.638	0.051	0.8216
28_05_rs2307661	0/1	58	58	1	0.422/0.578	0.123	0.7261
33_05_rs1610949	0/1	58	58	1	0.543/0.457	4.242	0.0394
45_05_rs1160953	0/1	58	58	1	0.440/0.560	0.417	0.5186
48_05_rs1610903	0/1	58	58	1	0.595/0.405	5.953	0.0147
03_06_rs2308116	0/1	58	58	1	0.603/0.397	2.932	0.0868
29_06_rs2308139	0/1	58	58	1	0.310/0.690	0.752	0.3857
07_07_rs16458	0/1	58	58	1	0.612/0.388	4.251	0.0392
53_07_rs2307783	0/1	58	58	1	0.716/0.284	7.685	0.0056
20_08_rs10666410	0/1	58	58	1	0.543/0.457	0.344	0.5578
38_08_rs34535242	0/1	58	58	1	0.534/0.466	0.570	0.4501
05_09_rs2307850	0/1	58	58	1	0.345/0.655	1.495	0.2215
26_11_rs16721	0/1	58	58	1	0.233/0.767	0.047	0.8289
27_11_rs35248926	0/1	58	58	1	0.474/0.526	1.153	0.2830
44_11_rs35833136	0/1	58	58	1	0.664/0.336	0.722	0.3956
10_12_rs16660	0/1	58	58	1	0.319/0.681	1.610	0.2045
18_12_rs2308232	0/1	58	58	1	0.302/0.698	0.637	0.4250
36_12_rs2307805	0/1	58	58	1	0.586/0.414	0.254	0.6143
21_13_rs3049448	0/1	58	58	1	0.371/0.629	2.794	0.0946
12_14_rs3032356	0/1	58	58	1	0.422/0.578	0.527	0.4678
15_14_rs2307537	0/1	58	58	1	0.543/0.457	0.344	0.5578
22_16_rs1610878	0/1	58	58	1	0.448/0.552	3.766	0.0523
08_18_rs34999022	0/1	58	58	1	0.362/0.638	0.118	0.7316
49_18_rs2307561	0/1	58	58	1	0.466/0.534	3.279	0.0702
43_20_rs2308278	0/1	58	58	1	0.655/0.345	1.215	0.2703
02_21_rs3034941	0/1	58	58	1	0.664/0.336	0.838	0.3599
47_21_rs34543832	0/1	58	58	1	0.241/0.759	0.031	0.8611

Data format of the SNPAnalyzer; Marker ID was named by the author with the rules listed below: 40_01_rs2307963: 40 = serial number of the InDel marker used in our study; 01 = chromosome number of the InDel marker; rs2307963 = reference of the InDel marker in dbSNP. Alleles of InDel marker was named as 0 = deletion; 1 = insertion.

Supplementary Table 5. Allele frequency and HW test by SNPAnalyzer for Tibetan.

Marker ID	Allele	Total genotype Cnt	Valid genotype Cnt	Call rate	Allele freq	Chi-square	P value
40_01_rs2307963	0/1	86	86	1	0.390/0.610	5.243	0.0220
35_02_rs2308276	0/1	86	86	1	0.448/0.552	0.111	0.7388
23_03_rs2307975	0/1	86	86	1	0.297/0.703	5.266	0.0217
09_05_rs1611088	0/1	86	86	1	0.302/0.698	0.339	0.5602
28_05_rs2307661	0/1	86	86	1	0.459/0.541	0.246	0.6199
33_05_rs1610949	0/1	86	86	1	0.372/0.628	0.254	0.6139
45_05_rs1160953	0/1	86	86	1	0.453/0.547	2.572	0.1088
48_05_rs1610903	0/1	86	86	1	0.488/0.512	0.044	0.8331
03_06_rs2308116	0/1	86	86	1	0.616/0.384	0.575	0.4483
29_06_rs2308139	0/1	86	86	1	0.442/0.558	0.008	0.9271
07_07_rs16458	0/1	86	86	1	0.581/0.419	0.225	0.6355
53_07_rs2307783	0/1	86	86	1	0.558/0.442	6.411	0.0113
20_08_rs10666410	0/1	86	86	1	0.552/0.448	1.454	0.2280
38_08_rs34535242	0/1	86	86	1	0.436/0.564	4.155	0.0415
05_09_rs2307850	0/1	86	86	1	0.471/0.529	8.989	0.0027
26_11_rs16721	0/1	86	86	1	0.407/0.593	0.114	0.7356
27_11_rs35248926	0/1	86	86	1	0.651/0.349	4.635	0.0313
44_11_rs35833136	0/1	86	86	1	0.802/0.198	4.796	0.0285
10_12_rs16660	0/1	86	86	1	0.320/0.680	1.196	0.2740
18_12_rs2308232	0/1	86	86	1	0.291/0.709	8.988	0.0027
36_12_rs2307805	0/1	86	86	1	0.628/0.372	0.775	0.3788
21_13_rs3049448	0/1	86	86	1	0.360/0.640	2.205	0.1376
12_14_rs3032356	0/1	86	86	1	0.395/0.605	2.411	0.1205
15_14_rs2307537	0/1	86	86	1	0.517/0.483	0.000	0.9910
22_16_rs1610878	0/1	86	86	1	0.401/0.599	4.720	0.0298
08_18_rs34999022	0/1	86	86	1	0.576/0.424	0.047	0.8283
49_18_rs2307561	0/1	86	86	1	0.564/0.436	0.351	0.5534
43_20_rs2308278	0/1	86	86	1	0.610/0.390	0.782	0.3764
02_21_rs3034941	0/1	86	86	1	0.640/0.360	0.302	0.5828
47_21_rs34543832	0/1	86	86	1	0.273/0.727	0.596	0.4402

Data format of the SNPAnalyzer; Marker ID was named by the author with the rules listed below: 40_01_rs2307963: 40 = serial number of the InDel marker used in our study; 01 = chromosome number of the InDel marker; rs2307963 = reference of the InDel marker in dbSNP. Alleles of InDel marker was named as 0 = deletion; 1 = insertion.

Supplementary Table 6. Forensic parameters of the 30 InDel markers in the Chinese Han populations.

Locus	rs#	Ho	Pm	PD	PIC	PE	$PI_{typical}$
1	rs2307963	0.509	0.426	0.574	0.350	0.196	1.020
2	rs2308276	0.444	0.396	0.604	0.350	0.143	0.900
3	rs2307975	0.444	0.414	0.586	0.340	0.143	0.900
4	rs1611088	0.556	0.441	0.559	0.360	0.241	1.130
5	rs2307661	0.546	0.405	0.595	0.370	0.231	1.100
6	rs1610949	0.472	0.394	0.606	0.360	0.164	0.950
7	rs1160953	0.509	0.399	0.601	0.370	0.196	1.020
8	rs1610903	0.426	0.357	0.643	0.370	0.130	0.870
9	rs2308116	0.491	0.465	0.535	0.320	0.180	0.980
10	rs2308139	0.491	0.412	0.588	0.350	0.180	0.980
11	rs16458	0.435	0.364	0.636	0.370	0.137	0.890
12	rs2307783	0.407	0.432	0.568	0.330	0.118	0.840
13	rs10666410	0.435	0.350	0.650	0.370	0.137	0.890
14	rs34535242	0.463	0.360	0.640	0.370	0.157	0.930
15	rs2307850	0.435	0.376	0.624	0.360	0.137	0.890
16	rs16721	0.417	0.447	0.553	0.320	0.124	0.860
17	rs35248926	0.574	0.425	0.575	0.370	0.261	1.170
18	rs35833136	0.491	0.397	0.603	0.360	0.180	0.980
19	rs16660	0.435	0.421	0.579	0.340	0.137	0.890
20	rs2308232	0.417	0.416	0.584	0.340	0.124	0.860
21	rs2307805	0.407	0.403	0.597	0.340	0.118	0.840
22	rs3049448	0.500	0.400	0.600	0.360	0.188	1.000
23	rs3032356	0.481	0.416	0.584	0.350	0.172	0.960
24	rs2307537	0.463	0.359	0.641	0.370	0.157	0.930
25	rs1610878	0.528	0.417	0.583	0.360	0.213	1.060
26	rs34999022	0.593	0.445	0.555	0.370	0.283	1.230
27	rs2307561	0.519	0.396	0.604	0.370	0.204	1.040
28	rs2308278	0.519	0.440	0.560	0.350	0.204	1.040
29	rs3034941	0.435	0.385	0.615	0.360	0.137	0.890
30	rs34543832	0.426	0.402	0.598	0.350	0.130	0.870

Forensic parameters: Ho = observed heterozygosity; Pm = probability of matching; PD = power of discrimination; PIC = polymorphism information content; PE = power of exclusion; $PI_{typical}$ = typical paternity index.

Supplementary Table 7. Forensic parameters of the 30 InDel markers in the Chinese Hui populations.

Locus	rs#	Ho	Pm	PD	PIC	PE	$PI_{typical}$
1	rs2307963	0.408	0.470	0.530	0.300	0.119	0.850
2	rs2308276	0.479	0.394	0.606	0.360	0.170	0.960
3	rs2307975	0.563	0.435	0.565	0.360	0.249	1.150
4	rs1611088	0.507	0.462	0.538	0.330	0.194	1.010
5	rs2307661	0.521	0.412	0.588	0.360	0.207	1.040
6	rs1610949	0.352	0.334	0.666	0.370	0.087	0.770
7	rs1160953	0.521	0.401	0.599	0.370	0.207	1.040
8	rs1610903	0.592	0.462	0.538	0.360	0.281	1.220
9	rs2308116	0.465	0.391	0.609	0.360	0.159	0.930
10	rs2308139	0.408	0.390	0.610	0.350	0.119	0.850
11	rs16458	0.479	0.368	0.632	0.370	0.170	0.960
12	rs2307783	0.352	0.462	0.538	0.300	0.087	0.770
13	rs10666410	0.493	0.373	0.627	0.370	0.181	0.990
14	rs34535242	0.535	0.402	0.598	0.370	0.220	1.080
15	rs2307850	0.507	0.414	0.586	0.360	0.194	1.010
16	rs16721	0.352	0.449	0.551	0.310	0.087	0.770
17	rs35248926	0.549	0.405	0.595	0.370	0.234	1.110
18	rs35833136	0.479	0.370	0.630	0.370	0.170	0.960
19	rs16660	0.437	0.406	0.594	0.340	0.138	0.890
20	rs2308232	0.423	0.418	0.582	0.340	0.128	0.870
21	rs2307805	0.465	0.385	0.615	0.360	0.159	0.930
22	rs3049448	0.507	0.395	0.605	0.370	0.194	1.010
23	rs3032356	0.408	0.443	0.557	0.320	0.119	0.850
24	rs2307537	0.549	0.404	0.596	0.370	0.234	1.110
25	rs1610878	0.507	0.451	0.549	0.340	0.194	1.010
26	rs34999022	0.577	0.423	0.577	0.380	0.265	1.180
27	rs2307561	0.577	0.442	0.558	0.370	0.265	1.180
28	rs2308278	0.366	0.407	0.593	0.340	0.095	0.790
29	rs3034941	0.521	0.426	0.574	0.350	0.207	1.040
30	rs34543832	0.394	0.447	0.553	0.320	0.111	0.830

Forensic parameters: Ho = observed heterozygosity; Pm = probability of matching; PD = power of discrimination; PIC = polymorphism information content; PE = power of exclusion; $PI_{typical}$ = typical paternity index.

Supplementary Table 8. Forensic parameters of the 30 InDel markers in the Uighur populations.

Locus	rs#	Ho	Pm	PD	PIC	PE	$PI_{typical}$
1	rs2307963	0.354	0.492	0.508	0.280	0.088	0.770
2	rs2308276	0.438	0.428	0.572	0.330	0.138	0.890
3	rs2307975	0.396	0.410	0.590	0.340	0.111	0.830
4	rs1611088	0.396	0.444	0.556	0.320	0.111	0.830
5	rs2307661	0.406	0.370	0.630	0.360	0.118	0.840
6	rs1610949	0.438	0.353	0.647	0.370	0.138	0.890
7	rs1160953	0.552	0.405	0.595	0.370	0.237	1.120
8	rs1610903	0.396	0.454	0.546	0.310	0.111	0.830
9	rs2308116	0.458	0.399	0.601	0.350	0.154	0.920
10	rs2308139	0.469	0.427	0.573	0.340	0.162	0.940
11	rs16458	0.563	0.420	0.580	0.370	0.248	1.140
12	rs2307783	0.448	0.444	0.556	0.330	0.146	0.910
13	rs10666410	0.448	0.354	0.646	0.370	0.146	0.910
14	rs34535242	0.583	0.445	0.555	0.370	0.271	1.200
15	rs2307850	0.500	0.383	0.617	0.370	0.188	1.000
16	rs16721	0.323	0.510	0.490	0.270	0.073	0.740
17	rs35248926	0.469	0.395	0.605	0.360	0.162	0.940
18	rs35833136	0.458	0.419	0.581	0.340	0.154	0.920
19	rs16660	0.375	0.423	0.577	0.330	0.099	0.800
20	rs2308232	0.323	0.393	0.607	0.340	0.073	0.740
21	rs2307805	0.521	0.391	0.609	0.370	0.206	1.040
22	rs3049448	0.583	0.441	0.559	0.370	0.271	1.200
23	rs3032356	0.479	0.396	0.604	0.360	0.170	0.960
24	rs2307537	0.469	0.362	0.638	0.370	0.162	0.940
25	rs1610878	0.521	0.400	0.600	0.370	0.206	1.040
26	rs34999022	0.594	0.439	0.561	0.370	0.283	1.230
27	rs2307561	0.479	0.421	0.579	0.350	0.170	0.960
28	rs2308278	0.479	0.444	0.556	0.330	0.170	0.960
29	rs3034941	0.448	0.369	0.631	0.370	0.146	0.910
30	rs34543832	0.458	0.393	0.607	0.360	0.154	0.920

Forensic parameters: Ho = observed heterozygosity; Pm = probability of matching; PD = power of discrimination; PIC = polymorphism information content; PE = power of exclusion; $PI_{typical}$ = typical paternity index.

Supplementary Table 9. Forensic parameters of the 30 InDel markers in the Mongolian populations.

Locus	rs#	Ho	Pm	PD	PIC	PE	$PI_{typical}$
1	rs2307963	0.569	0.424	0.576	0.370	0.255	1.160
2	rs2308276	0.431	0.391	0.609	0.350	0.134	0.880
3	rs2307975	0.293	0.379	0.621	0.350	0.061	0.710
4	rs1611088	0.448	0.391	0.609	0.360	0.146	0.910
5	rs2307661	0.466	0.372	0.628	0.370	0.159	0.940
6	rs1610949	0.362	0.338	0.662	0.370	0.092	0.780
7	rs1160953	0.534	0.401	0.599	0.370	0.219	1.070
8	rs1610903	0.328	0.351	0.649	0.370	0.076	0.740
9	rs2308116	0.586	0.451	0.549	0.360	0.275	1.210
10	rs2308139	0.379	0.408	0.592	0.340	0.102	0.810
11	rs16458	0.603	0.468	0.532	0.360	0.295	1.260
12	rs2307783	0.569	0.510	0.490	0.320	0.255	1.160
13	rs10666410	0.534	0.398	0.602	0.370	0.219	1.070
14	rs34535242	0.448	0.356	0.644	0.370	0.146	0.910
15	rs2307850	0.379	0.385	0.615	0.350	0.102	0.810
16	rs16721	0.362	0.477	0.523	0.290	0.092	0.780
17	rs35248926	0.569	0.418	0.582	0.370	0.255	1.160
18	rs35833136	0.397	0.393	0.607	0.350	0.112	0.830
19	rs16660	0.362	0.400	0.600	0.340	0.092	0.780
20	rs2308232	0.466	0.438	0.562	0.330	0.159	0.940
21	rs2307805	0.517	0.399	0.601	0.370	0.203	1.040
22	rs3049448	0.569	0.450	0.550	0.360	0.255	1.160
23	rs3032356	0.534	0.406	0.594	0.370	0.219	1.070
24	rs2307537	0.534	0.398	0.602	0.370	0.219	1.070
25	rs1610878	0.621	0.463	0.537	0.370	0.316	1.320
26	rs34999022	0.483	0.405	0.595	0.360	0.173	0.970
27	rs2307561	0.379	0.339	0.661	0.370	0.102	0.810
28	rs2308278	0.517	0.432	0.568	0.350	0.203	1.040
29	rs3034941	0.500	0.429	0.571	0.350	0.188	1.000
30	rs34543832	0.345	0.467	0.533	0.300	0.084	0.760

Forensic parameters: Ho = observed heterozygosity; Pm = probability of matching; PD = power of discrimination; PIC = polymorphism information content; PE = power of exclusion; $PI_{typical}$ = typical paternity index.

Supplementary Table 10. Forensic parameters of the 30 InDel markers in the Tibetan populations.

Locus	rs#	Ho	Pm	PD	PIC	PE	$PI_{typical}$
1	rs2307963	0.593	0.459	0.541	0.360	0.283	1.230
2	rs2308276	0.477	0.370	0.630	0.370	0.168	0.960
3	rs2307975	0.314	0.417	0.583	0.330	0.069	0.730
4	rs1611088	0.395	0.417	0.583	0.330	0.111	0.830
5	rs2307661	0.523	0.391	0.609	0.370	0.209	1.050
6	rs1610949	0.442	0.384	0.616	0.360	0.141	0.900
7	rs1160953	0.581	0.430	0.570	0.370	0.269	1.190
8	rs1610903	0.488	0.370	0.630	0.370	0.178	0.980
9	rs2308116	0.512	0.408	0.592	0.360	0.198	1.020
10	rs2308139	0.488	0.376	0.624	0.370	0.178	0.980
11	rs16458	0.512	0.394	0.606	0.370	0.198	1.020
12	rs2307783	0.628	0.470	0.530	0.370	0.326	1.340
13	rs10666410	0.430	0.353	0.647	0.370	0.133	0.880
14	rs34535242	0.384	0.345	0.655	0.370	0.104	0.810
15	rs2307850	0.337	0.335	0.665	0.370	0.080	0.750
16	rs16721	0.465	0.377	0.623	0.370	0.159	0.930
17	rs35248926	0.349	0.379	0.621	0.350	0.086	0.770
18	rs35833136	0.233	0.531	0.469	0.270	0.039	0.650
19	rs16660	0.384	0.402	0.598	0.340	0.104	0.810
20	rs2308232	0.279	0.425	0.575	0.330	0.055	0.690
21	rs2307805	0.512	0.414	0.586	0.360	0.198	1.020
22	rs3049448	0.535	0.433	0.567	0.350	0.220	1.080
23	rs3032356	0.558	0.431	0.569	0.360	0.244	1.130
24	rs2307537	0.500	0.376	0.624	0.370	0.188	1.000
25	rs1610878	0.593	0.454	0.546	0.370	0.283	1.230
26	rs34999022	0.500	0.386	0.614	0.370	0.188	1.000
27	rs2307561	0.523	0.396	0.604	0.370	0.209	1.050
28	rs2308278	0.430	0.372	0.628	0.360	0.133	0.880
29	rs3034941	0.488	0.408	0.592	0.350	0.178	0.980
30	rs34543832	0.430	0.450	0.550	0.320	0.133	0.880

Forensic parameters: Ho = observed heterozygosity; Pm = probability of matching; PD = power of discrimination; PIC = polymorphism information content; PE = power of exclusion; $PI_{typical}$ = typical paternity index.