Analysis of 21 autosomal STRs in Saudi Arabia reveals population structure and the influence of consanguinity

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Running head: Diversity of 21 autosomal STRs in Saudi Arabia

Abstract

Variation in the 21 autosomal STRs detected by the GlobalFiler multiplex was investigated in a sample of 523 indigenous male Arabs from five geographic regions of Saudi Arabia. Although allele frequencies for the entire dataset were found to be broadly similar to those determined in previous studies of Saudi citizens, significant differences were found among regions. Heterozygote deficiency was observed at nearly all loci in all regions, probably as a consequence of high levels of consanguineous marriage; in the case of D2S1338, which showed the largest deviation from Hardy-Weinberg equilibrium, the presence of a null allele also played a part. Genetic distances were greatest between the Northern and Southern regions, whilst the West, Central and East appeared most similar to each other, and to previously published surveys. This contrasts with previously described variation among paternal lineages in the same sample-set: Y-chromosome variation was limited within the North/Central/South core compared with the more diverse East and West. Differences between autosomal and Y-chromosomal patterns probably reflect genetic drift on the Y chromosome, exacerbated by prevalent patrilineal descent groups in different regions.

Keywords:

Saudi Arabia, autosomal STRs, population structure, heterozygosity, consanguinity, GlobalFiler

Highlights

- GlobalFiler (21-STR) genotypes reported for 523 Saudi Arabian males
- Significant differences in allele frequencies among five geographical sub-regions
- Heterozygote deficiency observed at nearly all loci in all regions, likely reflecting history of consanguineous marriage
- Genetic distances greatest between Northern and Southern regions, with West, Central and East most similar to each other
- Autosomal pattern of sub-regional differentiation contrasts with previously described pattern of Y-STR variation in the same sample-set
- Population structure and heterozygote deficiency should be accounted for in forensic interpretation of STR profiles in Saudi Arabia

Introduction

The Kingdom of Saudi Arabia (KSA) is located in the southwest corner of Asia at the junction between the three old-world continents of Asia, Africa and Europe. It constitutes the majority of the Arabian Peninsula along with Kuwait, Qatar and the United Arab Emirates to the east, Yemen and Oman to the south, and both Jordan and Iraq to the north. It also faces Egypt, Sudan and Eritrea over the Red Sea to the west, and Iran over the Arabian Gulf to the east. The country is populated by approximately 32.5 million people of whom 20.4 million are Saudi nationals according to Saudi Arabian General Authority for Statistics (last accessed 01/10/2018). Administratively, the country is divided into 13 regions across five geographical areas namely: Central (Riyadh, Al-Qassim), Northern (Northern borders region, Tabuk, Al-Jawf and Hail), Southern (Asir, Jazan, Al-Bahah and Najran), Eastern (Eastern province) and Western (Makkah and Al-Madinah) (Figure 1a).

Several previous studies have investigated autosomal allele frequencies in Saudi Arabia, initially covering just eight STRs among 207 individuals [1], then 190 individuals from the Riyadh region analysed with the 15-STR Identifiler multiplex [2], and 500 individuals from six cities spread across the five regions with the 21 STRs of the GlobalFiler system [3]. Further studies examined variation at 13 (Profiler Plus) and 15 STRs (Identifiler) in Saudis resident in the bordering countries of Dubai [4] and Kuwait [5] respectively. Whilst these studies determined autosomal STR allele frequencies in Saudi nationals, they did not explore population structure within KSA. Analysis of the sample-set described here, which includes approximately equal representation of the five regions of the Kingdom, has previously revealed striking population structure in Y-chromosome variation, with greater diversity in the East and West and relative homogeneity within the North to South central axis of the country [6]. Here we ask whether population structure can also be detected with autosomal markers, and if so whether it presents a similar geographical pattern to that of the patrilineal variation.

Materials and Methods

DNA sampling

Samples were collected from indigenous Saudi Arabian males [6] with continuous paternal ancestry back to their great-grandfather within each of the five geographical subdivisions of the country (Figure 1a; Central N =115, Northern N =104, Southern N =103, Eastern N =88, and Western N =113) ensuring that all donors were separated by at least three generations. Ethical review for recruitment and analysis was provided by the Saudi General Administration for Forensic Evidence and the University of Leicester Research Ethics Committee. Informed consent was provided by all participants.

DNA Extraction and Quantification

DNA from FTA blood-spot samples (Whatman, UK) was extracted, purified and quantified as previously described [6].

DNA amplification and fragment detection

The GlobalFiler® PCR amplification kit was used to generate profiles based on 21 autosomal STRs: D3S1358, vWA, D16S539, CSF1PO, TPOX, D8S1179, D21S11, D18S51, D2S441, D19S433, TH01, FGA, D22S1045, D5S818, D13S317, D7S820, SE33, D10S1248, D1S1656, D12S391 and D2S1338, along with three additional markers used in sex determination (DYS391, Y indel and Amelogenin).

Amplification was performed on a Veriti PCR machine (Thermo Fisher Scientific) and fragment detection on an ABI3500 Genetic Analyzer (Thermo Fisher Scientific) in accordance with the manufacturer's recommended protocols. GeneMapper IDX software V1.4 was used for allele calling and interpretation.

This work followed the guidelines of *FSI:Genetics* for publication of population genetic data [7-9] and for allele nomenclature [10]. The dataset has been QC checked via STRidER [11], with the dataset reference STR000119.

Forensic and statistical analysis

PowerStats v1.2 software (Promega Corporation, Madison, WI, USA) [12] was used to calculate allele frequencies, Random Match Probability (PM), Power of Discrimination (PD), Power of Exclusion (PE), Typical Paternity Index (TPI), observed homozygosity and observed heterozygosity. Arlequin v 3.5 [13] was used to test Hardy-Weinberg equilibrium, calculate expected heterozygosity, perform AMOVA to investigate genetic diversity within and between the five geographical regions, and undertake population differentiation tests for KSA and neighbouring countries. F_{IS} was calculated using FSTAT [14]. Average pairwise F_{ST} values for 13 loci (CSF1PO, D13S317, D16S539, D18S51, D21S11, D3S1358, D5S818, D7S820, D8S1179, FGA, TH01, TPOX, vWA) shared with other studies of Saudi Arabians and neighbouring populations were used to generate multidimensional scaling (MDS) plots using the (MASS) package [15] in the R library.

Results

1- Data descriptions and forensic statistics

The 21 autosomal STRs targeted by the GlobalFiler kit were amplified from 523 Saudi Arabian males. Table 1 presents allele frequency data and forensic statistics for the whole KSA dataset; these measures are also provided for each of the five geographical subdivisions (Figure 1a) in Table S1.

The least variable loci are TPOX and D22S1045, each with seven allelic variants in the KSA dataset, and the most variable locus was SE33 with 42 alleles. These respective loci had the lowest and highest Probabilities of Discrimination (0.820, 0.837 and 0.993 respectively), and conversely the highest and lowest major allele frequencies: TPOX allele 8 had a frequency of 0.552 in the total KSA dataset, being most frequent in the North (0.596) and rarest in the Central region (0.517), whilst SE33 allele 18, the most common variant at that locus, was detected at a frequency of just 0.107 in the KSA dataset overall. The combined

origin showed that the North and South sub-regions were also the most differentiated from most other nearby populations (Figure 1d). The results of per-locus population differentiation tests between the KSA and regional datasets, previously published Saudi datasets and neighbouring countries are presented in Table S3.

Discussion

In our analysis of diversity at the 21 autosomal STR loci of the GlobalFiler multiplex we found no previously unreported alleles among 523 indigenous Saudi Arabian individuals and no evidence of genetic differentiation between the combined KSA dataset and previously published Saudi autosomal datasets, through exact tests of allele frequency. In common with previous studies [1-3, 5], a tendency towards heterozygote deficiency was observed affecting almost all loci, although only two retained significance following Bonferroni correction. This observation, and the elevated F_{IS} values, are likely to reflect historical marriage practices in KSA in which partners are usually from within the same tribal group, and rates of first-cousin marriages are high, at around 30% [17]. One of the two loci that showed significant deviation from Hardy-Weinberg equilibrium due to heterozygote deficiency (D2S1338) also showed evidence of the presence of a null allele, identified through a null homozygote. We assume that the combined effect of consanguinity [17] and presence of null alleles in the heterozygous state produced the apparent excess of CE length “homozygotes” ($P = 0.00001$). It is unclear whether both factors, or only inbreeding, contributed to the significant but slightly weaker distortion observed at vWA ($P = 0.00006$).

Interestingly, a null has previously been reported at D2S1338 with the Identifiler multiplex, which could be weakly detected as a visible allele with the NGM kit [18]. Identifiler, NGM and GlobalFiler are all Thermo Fisher multiplexes and share exactly the same primers at this locus (Matt Phipps, ThermoFisher personal communication). The same SNP (rs567937457) which lies 174bp downstream of the repeat array was also identified by NIST as causing discordance between Identifiler and Promega PP18 kits (http://strbase.nist.gov/pub_pres/NIST-Update-EDNAP-Apr2011.pdf). It has been suggested that the discrepancy between Identifiler and NGM is related to the longer annealing/extension time (3 min vs. 1 min) in the latter, which may permit amplification from the poorly matched primer [18]; however, in our homozygous null individual, extending the annealing/extension time to 3 minutes did not yield a detectable peak. Subsequent amplification with the

MiniFiler kit which has a 183bp shorter amplicon also yielded no result. The positions of the MiniFiler primers are proprietary information but can encompass at most 60bp of flanking region which must exclude the aforementioned SNP as the cause, and would imply either a substantial deletion affecting both downstream primers or a polymorphism upstream of the repeat, where the primer is already close to the repeat array. Unfortunately we are unable to explore the nature of this polymorphism any further due to the limitations of the DNA donor consent.

This study is the first to specifically address the question of sub-structure within the indigenous Saudi Arabian population using autosomal STR markers. Our population sample, which has approximately equal representation of the five geographic regions of the Kingdom, has previously been shown to display striking differentiation in Y-chromosomal haplogroup (Y-SNP) and haplotype (Y-STR, Yfiler Plus) distributions [6], suggesting that the country is genetically substructured at least with respect to male-specific markers.

A different picture emerged when we explored the genetic diversity of the geographic sub-regions with GlobalFiler. Significantly different pairwise F_{ST} values were noted between the South, North and Central/West regions, with the East appearing intermediate, and not significantly differentiated from any other region (Figure 1b). The combined KSA dataset is virtually indistinguishable from sets of Saudi donors sampled in Dubai and Kuwait [4, 5] and the previous multi-city GlobalFiler survey within Saudi Arabia [3], but somewhat different from the Identifiler dataset derived from bone marrow donors at a Riyadh hospital [2], which is an outlier (Figure 1c). However, after division of our dataset into the five regions (Figure 1d) we see that sample-sets from the previously published population surveys now cluster most closely with the Eastern region. Also, the North and South are the most differentiated from each other and from the other regions, with the exception of the bone marrow donor set [2], which shows similarity with the South.

Autosomal differentiation between North and South may be a

consequence of historically limited migration between these regions. Migrants are now primarily attracted by the oil industry in the East, the holy cities of the West and the capital in the Central region [19]. Prior to the establishment of the Kingdom of Saudi Arabia the interior was sparsely populated by sedentary farmers or nomads who moved within their tribal areas, reflected by some of the current administrative boundaries. The rapid growth of the Saudi population, stimulated by the discovery of oil, has involved movement into the cities from the surrounding areas, but the rural populations have not generally moved between regions. Our regional patrilineal criterion for inclusion in the dataset [6] meant that the results of Y-chromosome tests reflect the historic boundaries of tribal groups, and these are strongest and most stable in the North and Central regions. By contrast, the East and West received the greatest inward migration in recent centuries, as they were outward facing and the destinations of traders and pilgrims. The autosomal results also reflect the movement of women, who are likely to move to their husband's home. We applied no restriction on the origin of the maternal line, and as a consequence a different pattern reflecting more recent migration patterns is unsurprising.

Conclusion

This study is in concordance with the high discrimination power of GlobalFiler in the Saudi population, which makes it suitable for the purposes of forensic DNA identification and paternity testing; the allele frequencies derived in this study can be utilised by Saudi forensic providers for DNA interpretation purposes. Whilst the observed allele frequency variation between regions will have limited influence on interpretation issues, the high level of consanguinity and presence of null alleles should be taken into account.

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Conflicts of interest

None

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Figure legends

Figure 1: Map of sample locations, and multidimensional scaling (MDS) plots based on pairwise F_{ST} values derived from autosomal STR data.

a) Map of Saudi Arabia, showing location of the five geographical sub-regions; b) MDS plot comparing the five KSA sub-regions; c) MDS comparison of combined KSA dataset (encircled K) compared to previously published Saudi Arabian datasets and neighbouring countries; d) Five KSA sub-regions (encircled N - northern; S - southern; E - eastern; W - western; C- central) compared to previously published Saudi Arabian datasets and neighbouring countries.

Comparative data sources and population abbreviations are as follows: BAH - Bahrain [20], EGY1, EGY2 - Egypt, respectively [5, 21]; IRN1, IRN2 - Iran, respectively [5, 22]; IRQ1, IRQ2 - Iraq, respectively [5, 23]; JOR - Jordan [24]; KUW - Kuwait [5]; OMN - Oman [4]; QAT - Qatar [25]; SA1, SA2, SA3, SA4 - Saudi Arabia, respectively [2-5]; UAE1, UAE2 - United Arab Emirates, respectively [26, 27]; YEM - Yemen [4].

Tables

Main text tables:

Table 1: KSA allele frequencies and forensic statistics.

MP: Random Match Probability, PE: Power of Exclusion, O-Het: observed heterozygosity, E-Het: expected heterozygosity, HWE p-value: probability of deviation from Hardy Weinberg equilibrium, F_{IS} p-value: significance of F_{IS} .

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Allele	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
4											0.001										
6					0.002						0.339										
6.3																	0.005				
7				0.001	0.001						0.162				0.001	0.012					
7.3																	0.005				
8			0.031	0.005	0.552	0.002					0.110			0.011	0.105	0.165			0.001		
9			0.113	0.011	0.163	0.007			0.011		0.282			0.076	0.033	0.111	0.004	0.018			
9.3											0.096										
10			0.128	0.304	0.113	0.038		0.001	0.124	0.001	0.010		0.003	0.123	0.062	0.361	0.001		0.002		
11			0.359	0.294	0.157	0.137		0.021	0.358	0.011	0.001		0.107	0.262	0.255	0.183	0.001	0.009	0.042		
11.2																	0.002				
11.3									0.077												
12			0.212	0.345	0.012	0.188		0.144	0.080	0.095			0.011	0.346	0.341	0.146	0.006	0.037	0.131		
12.2										0.009											
13	0.007	0.002	0.137	0.033		0.185		0.210	0.010	0.168				0.171	0.147	0.020	0.015	0.167	0.099		
13.2										0.046							0.001				
13.3			0.001						0.001								0.001				
14	0.060	0.029	0.017	0.006		0.192		0.122	0.300	0.209			0.058	0.011	0.054	0.001	0.052	0.362	0.125	0.002	0.004
14.2										0.048											
15	0.239	0.157	0.002			0.201		0.119	0.033	0.141			0.508	0.001	0.001		0.030	0.257	0.136	0.025	
15.2	0.001							0.003		0.126											
15.3																			0.033		
16	0.314	0.282				0.043		0.118	0.006	0.074			0.258				0.058	0.105	0.251	0.011	0.077
16.2	0.001							0.006		0.053											
16.3																			0.054		
17	0.267	0.272				0.008		0.094		0.007			0.054				0.075	0.043	0.074	0.110	0.225
17.2								0.002		0.012											
17.3																			0.022		
18	0.105	0.179						0.073				0.007					0.107	0.001	0.003	0.149	0.098
18.3																			0.020	0.004	
19	0.007	0.066						0.041				0.064					0.064		0.001	0.133	0.127
19.3																			0.006	0.005	
20		0.012						0.026				0.070					0.044			0.100	0.239
20.2																	0.007				
21		0.001						0.008				0.139					0.018			0.089	0.047
21.2												0.001					0.076				
22								0.009				0.122					0.002			0.123	0.014
22.2												0.002					0.018				
22.3												0.002									
23								0.004				0.185								0.140	0.068
23.2												0.002					0.020				
24								0.001				0.226					0.001			0.057	0.064

24.2																		0.028			
25											0.112									0.041	0.030
25.2																		0.027			
26											0.052									0.007	0.006
26.2																		0.050			
27							0.011				0.008									0.004	0.001
27.2																		0.050			
28							0.131				0.006										
28.2																		0.042			
29							0.270				0.003										
29.2																		0.036			
30							0.256				0.001										
30.2							0.011											0.043			
31							0.046											0.001			
31.2							0.103				0.001							0.049			
32							0.007														
32.2							0.112											0.038			
33																		0.005			
33.2							0.039											0.007			
34																		0.005			
34.2							0.007											0.005			
35							0.005											0.002			
35.2							0.001											0.001			
36							0.001														
36.2																		0.001			
37							0.001											0.001			

	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
MP	0.097	0.078	0.081	0.147	0.180	0.052	0.056	0.029	0.100	0.030	0.097	0.038	0.163	0.092	0.081	0.081	0.007	0.096	0.032	0.024	0.040
PE	0.474	0.471	0.490	0.385	0.287	0.644	0.556	0.685	0.443	0.656	0.486	0.659	0.291	0.461	0.452	0.490	0.832	0.566	0.634	0.659	0.570
O-Het	0.729	0.727	0.738	0.671	0.597	0.824	0.778	0.845	0.709	0.830	0.736	0.832	0.600	0.721	0.715	0.738	0.918	0.782	0.818	0.832	0.784
E-Het	0.759	0.785	0.777	0.701	0.632	0.832	0.818	0.876	0.754	0.871	0.759	0.857	0.658	0.762	0.779	0.775	0.948	0.761	0.864	0.890	0.850
P-value	0.264	<0.0001	0.019	0.141	0.444	0.944	0.637	0.226	0.004	0.874	0.092	0.130	0.029	0.158	0.020	0.374	0.053	0.364	0.559	0.068	<0.0001
Alleles	9	9	9	8	7	10	15	18	10	14	8	18	7	8	9	8	42	9	16	16	14

F _{IS}	0.037	0.072	0.050	0.043	0.058	0.010	0.047	0.032	0.064	0.045	0.027	0.027	0.086	0.049	0.078	0.049	0.032	-0.036	0.055	0.065	0.076
P-value	0.072	0.001	0.014	0.070	0.020	0.321	0.011	0.029	0.005	0.005	0.135	0.067	0.001	0.022	0.001	0.020	0.002	0.952	0.001	<0.0001	<0.0001

Table 2: Pairwise F_{ST} between regional sub-populations.

Region	C	E	N	S	W
C	*	0.0322	0.0020	<0.0001	0.5664
E	0.0017	*	0.1006	0.1084	0.8291
N	0.0028	0.0013	*	<0.0001	0.0010
S	0.0041	0.0012	0.0053	*	0.0166
W	0.0001	0	0.0040	0.0021	*

Figures upper-right are p-values, with significant values in bold.

Figure 1.

Supplementary material, Table S1a. Allele frequencies and forensic statistics (Central region)

Allele	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
4																					
6											0.404										
6.3																	0.004				
7											0.135				0.004	0.004					
7.3																	0.004				
8			0.035		0.517						0.096			0.009	0.087	0.196			0.004		
9			0.100	0.013	0.152	0.013			0.009		0.287			0.065	0.026	0.096		0.017			
9.3											0.074										
10			0.078	0.317	0.135	0.022			0.157	0.004	0.004		0.004	0.100	0.061	0.374					
11			0.391	0.261	0.174	0.157		0.022	0.365	0.004			0.078	0.235	0.278	0.157			0.043		
11.2																					
11.3									0.074												
12			0.257	0.374	0.022	0.196		0.174	0.057	0.100			0.004	0.404	0.343	0.148	0.004	0.030	0.130		
12.2											0.009										
13	0.004		0.117	0.022		0.157		0.217	0.013	0.130				0.178	0.157	0.026	0.013	0.126	0.130		
13.2										0.030											
13.3			0.004														0.004				
14	0.070	0.026	0.013	0.013		0.183		0.117	0.287	0.204			0.083	0.009	0.043		0.052	0.357	0.122		0.004
14.2										0.087											
15	0.261	0.130	0.004			0.226		0.100	0.039	0.143			0.517				0.035	0.309	0.126	0.035	
15.2								0.004		0.104											
15.3																			0.043		
16	0.313	0.235				0.043		0.130		0.104			0.248				0.039	0.113	0.226	0.004	0.113
16.2								0.013		0.061											
16.3																			0.026		
17	0.213	0.317				0.004		0.087		0.009			0.065				0.083	0.048	0.100	0.083	0.217
17.2										0.009											
17.3																			0.017		
18	0.130	0.200						0.070				0.004					0.117		0.009	0.100	0.091
18.3																			0.004	0.009	
19	0.009	0.078						0.030				0.043					0.057			0.143	0.126
19.3																			0.017	0.004	
20		0.013						0.013				0.065					0.065			0.113	0.283
20.2																	0.009				
21								0.009				0.126					0.017			0.083	0.022

21.2			0.070		
22	0.004	0.083		0.148	0.013
22.2			0.026		
22.3		0.004			
23	0.009	0.261		0.170	0.052
23.2		0.004	0.022		
24		0.226	0.004	0.057	0.061
24.2			0.022		
25		0.122		0.039	0.013
25.2			0.026		
26		0.043		0.004	
26.2			0.043		
27	0.013	0.009		0.009	0.004
27.2			0.043		
28	0.096	0.004			
28.2			0.043		
29	0.257	0.004			
29.2			0.013		
30	0.270				
30.2	0.004		0.052		
31	0.043				
31.2	0.152		0.052		
32					
32.2	0.100		0.030		
33			0.009		
33.2	0.048		0.013		
34					
34.2	0.009		0.013		
35	0.009		0.009		
35.2					
36					
36.2			0.004		
37					

	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
MP	0.107	0.084	0.105	0.169	0.165	0.060	0.058	0.039	0.115	0.033	0.118	0.051	0.172	0.112	0.092	0.092	0.014	0.101	0.035	0.026	0.053
PD	0.893	0.916	0.895	0.831	0.835	0.940	0.942	0.961	0.885	0.967	0.882	0.949	0.828	0.888	0.908	0.908	0.986	0.899	0.965	0.974	0.947

PIC	0.729	0.747	0.715	0.629	0.618	0.802	0.791	0.854	0.712	0.864	0.678	0.815	0.609	0.696	0.732	0.733	0.943	0.706	0.856	0.875	0.811
PE	0.552	0.477	0.449	0.449	0.395	0.648	0.583	0.682	0.536	0.615	0.358	0.632	0.323	0.358	0.370	0.435	0.876	0.422	0.716	0.615	0.567
TPI	2.212	1.855	1.742	1.742	1.554	2.875	2.396	3.194	2.130	2.614	1.438	2.738	1.337	1.438	1.474	1.691	8.214	1.643	3.594	2.614	2.300
Ho	0.226	0.270	0.287	0.287	0.322	0.174	0.209	0.157	0.235	0.191	0.348	0.183	0.374	0.348	0.339	0.296	0.061	0.304	0.139	0.191	0.217
Ht	0.774	0.730	0.713	0.713	0.678	0.826	0.791	0.843	0.765	0.809	0.652	0.817	0.626	0.652	0.661	0.704	0.939	0.696	0.861	0.809	0.783
Alleles	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230

MP: Random Match Probability, PD: Power of Discrimination, PIC: Polymorphism information content, PE: Power of Exclusion, TPI: Typical Paternity Index, Ho: Homozygosity, Ht: Heterozygosity

Supplementary material, Table S1b. Allele frequencies and forensic statistics (Eastern region)

Allele	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
4																					
6					0.011						0.335										
6.3																	0.011				
7											0.153					0.011					
7.3																					
8			0.034	0.023	0.585	0.006					0.102			0.017	0.119	0.153					
9			0.148	0.011	0.114	0.006			0.011		0.295			0.068	0.028	0.114	0.006				
9.3											0.080										
10			0.148	0.324	0.091	0.034		0.006	0.085		0.034			0.085	0.068	0.381					
11			0.341	0.261	0.193	0.102		0.028	0.381	0.017			0.142	0.335	0.273	0.170			0.063		
11.2																					
11.3									0.080												
12			0.222	0.330	0.006	0.182		0.119	0.080	0.091			0.011	0.330	0.301	0.148		0.063	0.136		
12.2																					
13		0.011	0.108	0.045		0.205		0.176	0.006	0.182				0.153	0.159	0.023	0.017	0.210	0.085		
13.2										0.028											
13.3																					
14	0.057	0.023		0.006		0.205		0.074	0.313	0.216			0.063	0.006	0.051		0.045	0.369	0.131	0.006	
14.2										0.017											
15	0.239	0.193				0.210		0.153	0.045	0.142			0.517	0.006			0.057	0.216	0.153	0.011	
15.2										0.131											
15.3																			0.028		
16	0.267	0.324				0.045		0.131		0.063			0.199				0.063	0.102	0.210	0.023	0.034
16.2								0.006		0.085											
16.3																			0.051		
17	0.295	0.188				0.006		0.108		0.017			0.068				0.080	0.034	0.080	0.119	0.222
17.2								0.006		0.011											
17.3																			0.040		
18	0.136	0.165						0.074				0.006					0.068	0.006		0.159	0.119
18.3																			0.023		
19	0.006	0.080						0.034				0.057					0.057			0.125	0.108
19.3																			0.006		
20		0.017						0.057				0.080					0.034		0.080	0.233	
20.2																	0.006				
21								0.006				0.153					0.023			0.091	0.057
21.2																	0.028				
22								0.017				0.125					0.006			0.125	

22.2		0.006		0.023	
22.3		0.006			
23		0.148			0.108 0.068
23.2				0.023	
24	0.006	0.244			0.091 0.097
24.2				0.028	
25		0.131			0.051 0.045
25.2				0.051	
26		0.034			0.006 0.017
26.2				0.063	
27	0.011	0.006			
27.2				0.057	
28	0.142	0.006			
28.2				0.034	
29	0.318				
29.2				0.080	
30	0.182				
30.2	0.011			0.045	
31	0.045				
31.2	0.119			0.051	
32	0.011				
32.2	0.114			0.040	
33					
33.2	0.034				
34					
34.2	0.011				
35					
35.2					
36					
36.2					
37				0.006	

	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
MP	0.099	0.084	0.081	0.132	0.209	0.057	0.061	0.033	0.126	0.042	0.107	0.044	0.157	0.109	0.079	0.095	0.015	0.115	0.038	0.028	0.046
PD	0.901	0.916	0.919	0.868	0.791	0.943	0.939	0.967	0.874	0.958	0.893	0.956	0.843	0.891	0.921	0.905	0.985	0.885	0.962	0.972	0.954
PIC	0.723	0.758	0.746	0.662	0.557	0.801	0.792	0.875	0.696	0.847	0.722	0.834	0.625	0.702	0.757	0.736	0.946	0.721	0.861	0.881	0.833
PE	0.549	0.472	0.491	0.401	0.198	0.591	0.510	0.768	0.435	0.677	0.529	0.570	0.308	0.401	0.570	0.591	0.791	0.791	0.549	0.699	0.591
TPI	2.200	1.833	1.913	1.571	1.023	2.444	2.000	4.400	1.692	3.143	2.095	2.316	1.294	1.571	2.316	2.444	4.889	4.889	2.200	3.385	2.444
Ho	0.227	0.273	0.261	0.318	0.489	0.205	0.250	0.114	0.295	0.159	0.239	0.216	0.386	0.318	0.216	0.205	0.102	0.102	0.227	0.148	0.205

Ht	0.773	0.727	0.739	0.682	0.511	0.795	0.750	0.886	0.705	0.841	0.761	0.784	0.614	0.682	0.784	0.795	0.898	0.898	0.773	0.852	0.795
Alleles	176	176	176	176	176	176	176	176	176	176	176	176	176	176	176	176	176	176	176	176	176

MP: Random Match Probability, PD: Power of Discrimination, PIC: Polymorphism information content, PE: Power of Exclusion, TPI: Typical Paternity Index, Ho: Homozygosity, Ht: Heterozygosity

Supplementary material, Table S1c. Allele frequencies and forensic statistics (Northern region)

Allele	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
4																					
6											0.313										
6.3																	0.005				
7				0.005							0.173					0.010					
7.3																					
8			0.024		0.596						0.135			0.005	0.072	0.149					
9			0.091	0.005	0.154	0.005			0.005		0.250			0.130	0.063	0.173	0.010	0.019			
9.3											0.120										
10			0.149	0.279	0.087	0.043			0.139		0.005			0.154	0.077	0.337			0.010		
11			0.361	0.298	0.149	0.154		0.014	0.351	0.005	0.005		0.115	0.303	0.274	0.236		0.014	0.053		
11.2																	0.005				
11.3									0.096												
12			0.212	0.380	0.014	0.183		0.091	0.067	0.101			0.014	0.240	0.269	0.087	0.010	0.014	0.111		
12.2										0.005											
13			0.149	0.029		0.173		0.250	0.010	0.183				0.144	0.159	0.010	0.010	0.101	0.043		
13.2										0.038							0.005				
13.3									0.005												
14	0.053	0.034	0.010	0.005		0.149		0.178	0.288	0.245			0.053	0.024	0.082		0.058	0.365	0.149	0.005	
14.2										0.038											
15	0.240	0.163	0.005			0.221		0.144	0.029	0.168			0.563		0.005		0.024	0.313	0.154	0.005	
15.2	0.005									0.111											
15.3																			0.019		
16	0.404	0.250				0.058		0.115	0.010	0.048			0.221				0.067	0.139	0.293		0.087
16.2								0.005		0.058											
16.3																			0.038		
17	0.212	0.317				0.014		0.082					0.034				0.072	0.034	0.082	0.082	0.216
17.2																					
17.3																			0.010		
18	0.082	0.159						0.067				0.005					0.111		0.005	0.207	0.091
18.3																			0.024		
19	0.005	0.072						0.010				0.077					0.077		0.005	0.163	0.101
19.3																			0.005	0.005	
20		0.005						0.024				0.043					0.029			0.120	0.245
20.2																					
21								0.010				0.125					0.010			0.096	0.038
21.2																	0.058				
22								0.005				0.159					0.005			0.091	

22.2													0.019							
22.3																				
23	0.005								0.154								0.111		0.091	
23.2																	0.019			
24									0.212								0.058		0.091	
24.2																	0.019			
25									0.135								0.043		0.029	
25.2																	0.005			
26									0.067								0.005		0.010	
26.2																	0.063			
27	0.005								0.010								0.010			
27.2																	0.043			
28	0.111								0.010											
28.2																	0.038			
29	0.284								0.005											
29.2																	0.058			
30	0.322																			
30.2	0.014																0.043			
31	0.043																			
31.2	0.048																0.048			
32	0.014																			
32.2	0.111																0.072			
33																	0.005			
33.2	0.038																0.010			
34																				
34.2	0.005																0.005			
35	0.005																			
35.2																				
36																				
36.2																				
37																				

	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
MP	0.123	0.086	0.093	0.164	0.211	0.055	0.082	0.042	0.096	0.048	0.087	0.040	0.193	0.077	0.073	0.092	0.015	0.121	0.048	0.035	0.047
PD	0.877	0.914	0.907	0.836	0.789	0.945	0.918	0.958	0.904	0.952	0.913	0.960	0.807	0.923	0.927	0.908	0.985	0.879	0.952	0.965	0.953
PIC	0.681	0.745	0.740	0.626	0.551	0.815	0.757	0.835	0.724	0.830	0.743	0.844	0.573	0.757	0.779	0.737	0.939	0.696	0.826	0.862	0.831
PE	0.347	0.416	0.402	0.416	0.275	0.650	0.493	0.613	0.446	0.706	0.510	0.687	0.253	0.578	0.526	0.416	0.823	0.578	0.687	0.632	0.493
TPI	1.405	1.625	1.576	1.625	1.209	2.889	1.926	2.600	1.733	3.467	2.000	3.250	1.156	2.364	2.080	1.625	5.778	2.364	3.250	2.737	1.926
Ho	0.356	0.308	0.317	0.308	0.413	0.173	0.260	0.192	0.288	0.144	0.250	0.154	0.433	0.212	0.240	0.308	0.087	0.212	0.154	0.183	0.260

Ht	0.644	0.692	0.683	0.692	0.587	0.827	0.740	0.808	0.712	0.856	0.750	0.846	0.567	0.788	0.760	0.692	0.913	0.788	0.846	0.817	0.740
Alleles	208	208	208	208	208	208	208	208	208	208	208	208	208	208	208	208	208	208	208	208	208

MP: Random Match Probability, PD: Power of Discrimination, PIC: Polymorphism information content, PE: Power of Exclusion, TPI: Typical Paternity Index, Ho: Homozygosity, Ht: Heterozygosity

Supplementary material, Table S1d. Allele frequencies and forensic statistics (Southern region)

Allele	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
4											0.005										
6											0.262										
6.3																	0.005				
7					0.005						0.189					0.034					
7.3																	0.015				
8			0.044		0.534	0.005					0.097			0.015	0.155	0.121					
9			0.146	0.015	0.194	0.005			0.019		0.296			0.058	0.024	0.058		0.019			
9.3											0.141										
10			0.141	0.320	0.126	0.073			0.107		0.010			0.160	0.049	0.383	0.005				
11			0.320	0.359	0.136	0.146		0.024	0.335	0.010			0.083	0.194	0.199	0.199	0.005	0.015	0.029		
11.2																					
11.3									0.078												
12			0.136	0.267	0.005	0.155		0.126	0.112	0.083			0.005	0.393	0.364	0.184	0.005	0.024	0.121		
12.2										0.010											
13	0.024		0.170	0.039		0.180		0.209	0.005	0.194				0.170	0.146	0.015	0.015	0.262	0.146		
13.2										0.078											
13.3																					
14	0.053	0.034	0.044			0.204		0.146	0.301	0.204			0.053	0.010	0.063	0.005	0.044	0.335	0.131		0.010
14.2										0.053											
15	0.204	0.117				0.189		0.068	0.034	0.121			0.505				0.015	0.218	0.146	0.039	
15.2										0.126											
15.3																			0.024		
16	0.262	0.320				0.039		0.097	0.010	0.068			0.316				0.063	0.092	0.262	0.015	0.063
16.2								0.005		0.039											
16.3																			0.068		
17	0.350	0.296				0.005		0.107		0.005			0.039				0.087	0.034	0.049	0.131	0.248
17.2										0.010											
17.3																			0.010		
18	0.097	0.165						0.102				0.010					0.126			0.165	0.092
18.3																			0.015	0.010	
19	0.010	0.058						0.073				0.073					0.068			0.136	0.150

22.2					0.010							
22.3												
23					0.160					0.117	0.053	
23.2					0.005					0.024		
24					0.214					0.029	0.029	
24.2									0.034			
25					0.073					0.019	0.039	
25.2									0.019			
26					0.063					0.010		
26.2									0.015			
27	0.010				0.005							
27.2									0.049			
28	0.155				0.005							
28.2									0.034			
29	0.296											
29.2									0.029			
30	0.257											
30.2	0.015								0.024			
31	0.039											
31.2	0.078								0.034			
32												
32.2	0.126								0.019			
33									0.010			
33.2	0.019								0.010			
34									0.024			
34.2												
35												
35.2									0.005			
36												
36.2												
37	0.005											

	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
MP	0.102	0.099	0.072	0.149	0.177	0.054	0.069	0.032	0.088	0.037	0.094	0.046	0.181	0.108	0.079	0.095	0.015	0.106	0.043	0.030	0.049
PD	0.898	0.901	0.928	0.851	0.823	0.946	0.931	0.968	0.912	0.963	0.906	0.954	0.819	0.892	0.921	0.905	0.985	0.894	0.957	0.970	0.951
PLC	0.716	0.728	0.780	0.635	0.598	0.817	0.770	0.864	0.732	0.854	0.743	0.847	0.576	0.714	0.745	0.727	0.932	0.723	0.831	0.873	0.832
PE	0.457	0.539	0.628	0.330	0.305	0.684	0.592	0.665	0.356	0.703	0.628	0.742	0.293	0.506	0.442	0.489	0.861	0.592	0.665	0.665	0.557
TPI	1.776	2.146	2.711	1.355	1.288	3.219	2.452	3.029	1.431	3.433	2.711	3.962	1.256	1.981	1.717	1.907	7.357	2.452	3.029	3.029	2.239
Ho	0.282	0.233	0.184	0.369	0.388	0.155	0.204	0.165	0.350	0.146	0.184	0.126	0.398	0.252	0.291	0.262	0.068	0.204	0.165	0.165	0.223

Ht	0.718	0.767	0.816	0.631	0.612	0.845	0.796	0.835	0.650	0.854	0.816	0.874	0.602	0.748	0.709	0.738	0.932	0.796	0.835	0.835	0.777
Alleles	206	206	206	206	206	206	206	206	206	206	206	206	206	206	206	206	206	206	206	206	206

MP: Random Match Probability, PD: Power of Discrimination, PIC: Polymorphism information content, PE: Power of Exclusion, TPI: Typical Paternity Index, Ho: Homozygosity, Ht: Heterozygosity

Allele	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
4																					
6										0.372											
6.3																					
7										0.159						0.004					
7.3																	0.004				
8			0.018	0.004	0.535					0.119		0.009	0.097	0.199							
9			0.088	0.013	0.195	0.004			0.009	0.283		0.058	0.022	0.115	0.004	0.031					
9.3										0.066											
10			0.133	0.283	0.119	0.022			0.124			0.009	0.115	0.058	0.336						
11			0.376	0.292	0.137	0.119		0.018	0.358	0.022		0.124	0.257	0.252	0.155			0.013	0.027		
11.2																	0.004				
11.3									0.062												
12			0.230	0.367	0.013	0.221		0.199	0.088	0.097		0.022	0.354	0.416	0.164	0.009	0.058	0.155			
12.2										0.018											
13	0.004		0.137	0.035		0.212		0.195	0.013	0.159			0.204	0.119	0.027	0.022	0.150	0.088			
13.2										0.053											
13.3																					
14	0.066	0.027	0.018	0.004		0.221		0.093	0.314	0.181		0.040	0.004	0.035		0.058	0.385	0.097		0.004	
14.2										0.035											
15	0.248	0.186				0.159		0.133	0.022	0.133		0.442				0.022	0.221	0.106	0.031		
15.2								0.009		0.159											
15.3																			0.049		
16	0.314	0.292				0.031		0.115	0.009	0.080		0.296				0.062	0.080	0.261	0.018	0.080	
16.2	0.004									0.027											
16.3																			0.084		
17	0.274	0.230				0.009		0.088		0.004		0.066				0.053	0.062	0.058	0.137	0.221	
17.2								0.004		0.031											
17.3																			0.035		
18	0.084	0.199						0.053				0.009				0.106				0.124	0.102
18.3																			0.035		
19	0.004	0.044						0.058				0.071				0.062			0.097	0.146	
19.																					

22.2		0.004		0.013	
22.3					
23	0.004	0.186		0.181	0.075
23.2				0.013	
24		0.235		0.058	0.049
24.2				0.035	
25		0.102		0.053	0.027
25.2				0.035	
26		0.049		0.009	0.004
26.2				0.066	
27	0.013	0.009			
27.2				0.058	
28	0.155	0.004			
28.2				0.058	
29	0.208	0.004			
29.2				0.013	
30	0.239	0.004			
30.2	0.013			0.049	
31	0.058			0.004	
31.2	0.115	0.004		0.058	
32	0.009				
32.2	0.111			0.031	
33					
33.2	0.053				
34					
34.2	0.009			0.004	
35	0.009				
35.2	0.004				
36	0.004				
36.2					
37					

	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338
MP	0.104	0.079	0.092	0.144	0.171	0.066	0.043	0.039	0.107	0.032	0.109	0.046	0.143	0.102	0.118	0.084	0.014	0.093	0.037	0.033	0.041
PD	0.896	0.921	0.908	0.856	0.829	0.934	0.957	0.961	0.893	0.968	0.891	0.954	0.857	0.898	0.882	0.916	0.986	0.907	0.963	0.967	0.959
PIC	0.711	0.751	0.727	0.639	0.598	0.790	0.825	0.854	0.707	0.864	0.695	0.839	0.647	0.711	0.698	0.751	0.941	0.736	0.850	0.875	0.836
PE	0.484	0.455	0.498	0.338	0.262	0.642	0.592	0.712	0.441	0.592	0.455	0.642	0.282	0.484	0.400	0.544	0.801	0.529	0.544	0.694	0.642
TPI	1.883	1.766	1.948	1.378	1.177	2.825	2.457	3.531	1.712	2.457	1.766	2.825	1.228	1.883	1.569	2.173	5.136	2.093	2.173	3.324	2.825
Ho	0.265	0.283	0.257	0.363	0.425	0.177	0.204	0.142	0.292	0.204	0.283	0.177	0.407	0.265	0.319	0.230	0.097	0.239	0.230	0.150	0.177

Ht	0.735	0.717	0.743	0.637	0.575	0.823	0.796	0.858	0.708	0.796	0.717	0.823	0.593	0.735	0.681	0.770	0.903	0.761	0.770	0.850	0.823
Alleles	226	226	226	226	226	226	226	226	226	226	226	226	226	226	226	226	226	226	226	226	226

MP: Random Match Probability, PD: Power of Discrimination, PIC: Polymorphism information content, PE: Power of Exclusion, TPI: Typical Paternity Index, Ho: Homozygosity, Ht: Heterozygosity

Table S2: Per-locus observed and expected heterozygosity values.

Central SA

Locus	Genotype	alleles	O-Het	E-Het	P-value
D3S1358	230	7	0.774	0.770	0.051
vWA	230	7	0.730	0.784	0.119
D16S539	230	9	0.713	0.753	0.079
CSF1PO	230	6	0.713	0.694	0.313
TPOX	230	5	0.678	0.663	0.074
D8S1179	230	9	0.826	0.829	0.609
D21S11	230	11	0.800	0.820	0.832
D18S51	230	15	0.843	0.871	0.093
D2S441	230	8	0.765	0.753	0.012
D19S433	230	14	0.809	0.880	0.492
TH01	230	6	0.652	0.725	0.239
FGA	230	14	0.826	0.839	0.694
D22S1045	230	7	0.626	0.657	0.039
D5S818	230	7	0.652	0.738	0.152
D13S317	230	8	0.661	0.770	0.031
D7S820	230	7	0.704	0.769	0.099
SE33	230	32	0.939	0.950	0.338
D10S1248	230	7	0.696	0.749	0.703
D1S1656	230	14	0.861	0.873	0.759
D12S391	230	15	0.809	0.890	0.720
D2S1338	230	13	0.783	0.834	0.108

Northern SA

Genotype	alleles	O-Het	E-Het	P-value
208	7	0.644	0.728	0.077
208	7	0.692	0.782	0.049
208	8	0.683	0.776	0.021
208	7	0.692	0.692	0.873
208	5	0.587	0.594	0.757
208	9	0.827	0.840	0.217
208	12	0.740	0.789	0.163
208	14	0.808	0.855	0.663
208	10	0.712	0.763	0.556
208	11	0.856	0.851	0.577
208	7	0.750	0.781	0.553
208	12	0.846	0.864	0.927
208	6	0.567	0.620	0.627
208	7	0.788	0.792	0.947
208	8	0.760	0.809	0.250
208	7	0.692	0.775	0.028
208	30	0.913	0.947	0.312
208	8	0.788	0.741	0.556
208	15	0.846	0.846	0.506
208	14	0.817	0.878	0.124
208	10	0.740	0.852	0.007

Eastern SA

Locus	Genotype	alleles	O-Het	E-Het	P-value
D3S1358	176	6	0.773	0.767	0.997
vWA	176	8	0.727	0.793	0.053
D16S539	176	6	0.739	0.783	0.873
CSF1PO	176	7	0.682	0.720	0.733
TPOX	176	6	0.511	0.602	0.365
D8S1179	176	10	0.795	0.830	0.811
D21S11	176	11	0.750	0.819	0.473
D18S51	176	16	0.886	0.891	0.823
D2S441	176	8	0.705	0.739	0.029
D19S433	176	12	0.841	0.867	0.645
TH01	176	6	0.761	0.763	0.464
FGA	176	13	0.784	0.856	0.269
D22S1045	176	6	0.614	0.668	0.412
D5S818	176	8	0.682	0.747	0.240
D13S317	176	7	0.784	0.792	0.875
D7S820	176	7	0.795	0.771	0.313
SE33	176	26	0.898	0.954	0.099
D10S1248	176	7	0.898	0.762	0.335
D1S1656	176	11	0.773	0.879	0.022
D12S391	176	14	0.852	0.896	0.723
D2S1338	176	10	0.795	0.855	0.081

Southern SA

Genotype	alleles	O-Het	E-Het	P-value
206	7	0.718	0.758	0.410
206	8	0.767	0.768	0.195
206	7	0.816	0.809	0.199
206	5	0.631	0.699	0.192
206	6	0.612	0.646	0.380
206	10	0.845	0.842	0.433
206	10	0.796	0.802	0.925
206	12	0.835	0.880	0.733
206	9	0.650	0.769	0.033
206	13	0.854	0.872	0.528
206	7	0.816	0.782	0.882
206	13	0.874	0.866	0.072
206	6	0.602	0.637	0.729
206	7	0.748	0.753	0.089
206	7	0.709	0.779	0.614
206	8	0.738	0.763	0.700
206	31	0.932	0.940	0.763
206	8	0.796	0.764	0.390
206	11	0.835	0.852	0.955
206	14	0.835	0.889	0.719
206	11	0.777	0.852	0.031

Western SA

Locus	Genotype	alleles	O-Het	E-Het	P-value
D3S1358	226	8	0.735	0.756	0.153
vWA	226	7	0.717	0.788	0.511
D16S539	226	7	0.743	0.764	0.816
CSF1PO	226	7	0.637	0.701	0.385
TPOX	226	5	0.575	0.645	0.210
D8S1179	226	9	0.823	0.819	0.684
D21S11	226	14	0.796	0.847	0.784
D18S51	226	15	0.858	0.872	0.152
D2S441	226	9	0.708	0.748	0.490
D19S433	226	13	0.796	0.880	0.161
TH01	226	5	0.717	0.741	0.968
FGA	226	15	0.823	0.858	0.079
D22S1045	226	7	0.593	0.698	0.022
D5S818	226	7	0.735	0.754	0.805
D13S317	226	7	0.681	0.738	0.010
D7S820	226	7	0.770	0.786	0.293
SE33	226	28	0.903	0.948	0.182
D10S1248	226	8	0.761	0.769	0.117
D1S1656	226	12	0.770	0.867	0.088
D12S391	226	13	0.850	0.890	0.120
D2S1338	226	12	0.823	0.856	0.377

O-het: observed heterozygosity; E-het: expected heterozygosity; P-values in bold are significant at <0.05.

Table S3a. Population differentiation exact tests, overall KSA sample.

locus	C	E	N	S	W	SA3	SA1	SA2	SA4	BAH	QAT	UAE1	UAE2	KUW	OMN	YEM	JOR	IRQ2	EGY2	IRN2	IRQ1	IRN1	EGY1	locus
CSF1PO	0.68675	0.3375	0.78628	0.32963	0.9927	0.00136	0.18811	0.61228	<0.0001	0.00198	0.08727	0.0259	0.00023	0.57535	0.05938	0.5571	0.01212	0.02161	0.00591	0.18279	0.15909	0.06856	0.01695	CSF1PO
D10S1248	0.61773	0.1364	0.08436	0.13509	0.36028	0.26353	N/A	N/A	N/A	N/A	N/A	0.2874	0.43145	N/A	N/A	N/A	<0.0001	N/A	N/A	N/A	N/A	N/A	N/A	D10S1248
D12S391	0.63325	0.80068	0.21843	0.60036	0.69018	0.27407	N/A	N/A	N/A	N/A	N/A	<0.0001	<0.0001	N/A	N/A	N/A	<0.0001	N/A	N/A	N/A	N/A	N/A	N/A	D12S391
D13S317	0.86089	0.98558	0.08216	0.45329	0.59847	0.02519	0.00994	0.27857	0.00117	0.19317	0.22372	0.02837	0.02601	0.15936	0.27437	0.40151	<0.0001	0.00968	<0.0001	0.00003	<0.0001	<0.0001	<0.0001	D13S317
D16S539	0.25951	0.55678	0.88908	0.02908	0.94227	0.00938	0.00031	0.02254	0.02364	0.00018	0.00085	0.03079	0.0016	0.10634	0.68846	0.16411	0.00004	0.6094	0.00872	0.08969	<0.0001	0.3097	0.00575	D16S539
D18S51	0.24444	0.02997	0.09447	0.14698	0.04673	0.56262	<0.0001	0.03719	0.05323	<0.0001	0.68918	0.09519	0.01505	0.11118	0.01929	0.74604	<0.0001	0.01063	<0.0001	<0.0001	0.00013	<0.0001	<0.0001	D18S51
D19S433	0.4009	0.52539	0.79493	0.93757	0.3869	0.77219	0.03507	N/A	0.48908	<0.0001	<0.0001	0.00301	<0.0001	0.59908	N/A	N/A	<0.0001	<0.0001	<0.0001	0.00009	<0.0001	0.01949	<0.0001	D19S433
D1S1656	0.21824	0.94538	0.14234	0.81615	0.49421	0.43964	N/A	N/A	N/A	N/A	N/A	<0.0001	<0.0001	N/A	N/A	N/A	<0.0001	N/A	N/A	N/A	N/A	N/A	N/A	D1S1656
D21S11	0.67154	0.76454	0.46433	0.75716	0.53915	0.4978	0.00097	0.7527	0.01945	<0.0001	0.21814	0.03651	0.00186	0.89496	0.01452	0.33799	<0.0001	0.12099	0.03702	0.04149	0.00848	0.40104	0.0292	D21S11
D22S1045	0.50099	0.54197	0.66981	0.62462	0.18886	0.27287	N/A	N/A	N/A	<0.0001	<0.0001	N/A	<0.0001	N/A	N/A	N/A	<0.0001	N/A	N/A	N/A	N/A	N/A	N/A	D22S1045
D2S1338	0.36883	0.18771	0.65221	0.18698	0.99408	0.15699	0.11169	N/A	0.24582	<0.0001	0.00146	<0.0001	<0.0001	0.00832	N/A	N/A	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	D2S1338
D2S441	0.84498	0.93551	0.84909	0.78023	0.97228	0.65053	N/A	N/A	N/A	N/A	N/A	0.00004	<0.0001	N/A	N/A	N/A	0.01983	N/A	N/A	N/A	N/A	N/A	N/A	D2S441
D3S1358	0.73349	0.78443	0.18899	0.09561	0.90737	0.29665	0.00008	0.81527	0.84694	0.00222	0.00903	0.25465	0.18757	0.05296	0.04812	0.6403	<0.0001	0.05185	0.05133	0.00449	0.03438	<0.0001	0.04521	D3S1358
D5S818	0.84216	0.27247	0.0048	0.34179	0.90275	0.13995	0.03743	0.27293	0.27452	0.52234	<0.0001	0.04764	0.10723	0.49105	0.71019	0.46638	<0.0001	0.76229	0.01478	0.07939	0.16541	0.00516	<0.0001	D5S818
D7S820	0.815	0.99587	0.04306	0.01585	0.71499	0.31666	0.66937	0.47717	0.00545	<0.0001	0.77043	<0.0001	<0.0001	0.74671	0.10513	0.57131	<0.0001	0.07453	<0.0001	<0.0001	0.00831	<0.0001	0.12457	D7S820
D8S1179	0.83906	0.95789	0.81535	0.64644	0.60746	0.07812	0.00184	0.88743	0.69144	<0.0001	0.11152	<0.0001	<0.0001	0.01206	0.57333	0.00546	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	D8S1179
FGA	0.5029	0.96811	0.86825	0.77806	0.95124	0.47695	0.00081	0.34892	0.23857	<0.0001	0.02468	0.02868	0.0024	0.41467	0.02672	0.08161	<0.0001	0.00395	0.00133	<0.0001	<0.0001	<0.0001	<0.0001	FGA
SE33	0.96352	0.70959	0.93042	0.31427	0.98446	<0.0001	N/A	N/A	N/A	N/A	N/A	<0.0001	<0.0001	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	SE33
TH01	0.59308	0.39875	0.52141	0.15708	0.64356	0.32657	<0.0001	0.00012	0.01531	<0.0001	0.62753	0.00308	0.00334	<0.0001	0.00006	0.68552	<0.0001	0.00159	<0.0001	0.00171	0.01391	0.00479	<0.0001	TH01
TPOX	0.71056	0.13962	0.84245	0.55218	0.84701	0.39203	0.48248	0.83267	0.32614	<0.0001	0.00118	<0.0001	<0.0001	0.0362	<0.0001	0.67754	<0.0001	0.00188	0.00009	<0.0001	<0.0001	0.00028	0.00002	TPOX
vWA	0.68854	0.10522	0.86834	0.56565	0.62025	0.27522	0.00026	0.3068	0.21439	<0.0001	0.00356	0.00024	0.00068	0.51918	0.05505	<0.0001	<0.0001	0.00007	0.00001	<0.0001	<0.0001	<0.0001	<0.0001	vWA

Table S3b. Population differentiation exact test, Central subregion.

locus	K	E	N	S	W	SA3	SA1	SA2	SA4	BAH	QAT	UAE1	UAE2	KUW	OMN	YEM	JOR	IRQ2	EGY2	IRN2	IRQ1	IRN1	EGY1	locus
CSF1PO	0.68675	0.22582	0.7338	0.05758	0.77089	0.02711	0.90817	0.28113	0.00867	0.03938	0.04075	0.19776	0.09154	0.74681	0.14187	0.58021	0.20936	0.02359	0.04761	0.10111	0.48408	0.03193	0.08605	CSF1PO
D10S1248	0.61773	0.02465	0.56914	0.00717	0.10645	0.66965	N/A	N/A	N/A	N/A	N/A	0.33886	0.29529	N/A	N/A	N/A	<0.0001	N/A	N/A	N/A	N/A	N/A	N/A	D10S1248
D12S391	0.63325	0.17138	0.04995	0.20202	0.49286	0.02082	N/A	N/A	N/A	N/A	N/A	<0.0001	<0.0001	N/A	N/A	N/A	0.03837	N/A	N/A	N/A	N/A	N/A	N/A	D12S391
D13S317	0.86089	0.96799	0.21159	0.23649	0.75656	0.13833	0.01544	0.23255	0.00722	0.33341	0.55543	0.17471	0.20106	0.21857	0.84442	0.22352	0.01139	0.07464	0.00286	0.02386	0.00787	0.00007	0.00871	D13S317
D16S539	0.25951	0.18926	0.34155	0.00194	0.4507	0.20751	0.0602	0.72212	0.3667	0.236	0.53841	0.15436	0.0926	0.36536	0.32535	0.81856	0.1207	0.12206	0.08022	0.08752	0.06512	0.72629	0.0087	D16S539
D18S51	0.24444	0.14791	0.23866	0.20062	0.68977	0.7586	0.18555	0.28872	0.84735	0.0035	0.22812	0.08265	0.01452	0.8033	0.02481	0.9623	0.01947	0.19534	0.00887	0.00127	0.02464	0.00306	0.00263	D18S51
D19S433	0.4009	0.11121	0.21224	0.29356	0.05319	0.2044	0.00523	N/A	0.08009	<0.0001	0.00199	0.02313	<0.0001	0.07374	N/A	N/A	0.01969	<0.0001	0.00321	0.00118	0.00035	0.0246	0.00248	D19S433
D1S1656	0.21824	0.27076	0.03437	0.11371	0.00997	0.13543	N/A	N/A	N/A	N/A	N/A	0.03078	0.00751	N/A	N/A	N/A	0.00349	N/A	N/A	N/A	N/A	N/A	N/A	D1S1656
D21S11	0.67154	0.26485	0.03423	0.05876	0.56249	0.24954	0.03923	0.73156	0.04018	0.00844	0.13281	0.06133	0.06667	0.44091	0.04505	0.1093	0.13382	0.07262	0.05614	0.50653	0.08385	0.08957	0.62774	D21S11
D22S1045	0.50099	0.26651	0.21881	0.48074	0.07257	0.38474	N/A	N/A	N/A	N/A	N/A	0.02321	0.0078	N/A	N/A	N/A	0.24947	N/A	N/A	N/A	N/A	N/A	N/A	D22S1045
D2S1338	0.36883	0.00355	0.24266	0.01738	0.53283	0.03135	0.06776	N/A	0.00301	<0.0001	0.00008	<0.0001	<0.0001	0.00356	N/A	N/A	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	D2S1338
D2S441	0.84498	0.62035	0.89521	0.26473	0.68695	0.67568	N/A	N/A	N/A	N/A	N/A	0.25682	0.05401	N/A	N/A	N/A	0.59515	N/A	N/A	N/A	N/A	N/A	N/A	D2S441
D3S1358	0.73349	0.60291	0.31077	0.01995	0.57316	0.57403	0.03141	0.44837	0.49343	0.51192	0.34065	0.91087	0.99565	0.50984	0.39859	0.57955	0.56716	0.35265	0.58358	0.60289	0.74382	<0.0001	0.7834	D3S1358
D5S818	0.84216	0.38549	0.00131	0.60971	0.91681	0.53032	0.82545	0.49991	0.62102	0.95168	0.00926	0.67315	0.60958	0.93265	0.93386	0.84217	<0.0001	0.7019	0.39877	0.49172	0.74684	0.37947	0.05802	D5S818
D7S820	0.815	0.88101	0.00967	0.03275	0.979	0.71805	0.25347	0.68972	0.0236	0.00109	0.63627	0.03136	0.00655	0.88374	0.14031	0.60149	0.04522	0.02606	0.00801	0.00025	0.03939	<0.0001	0.23033	D7S820
D8S1179	0.83906	0.70463	0.786	0.24122	0.35672	0.03077	0.00407	0.61627	0.2646	<0.0001	0.03404	0.00067	0.00011	0.0409	0.15112	0.0319	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.00258	D8S1179	
FGA	0.5029	0.58971	0.07848	0.05252	0.79619	0.03182	0.00301	0.32887	0.57764	0.00247	0.00494	0.09369	0.00753	0.18317	0.02546	0.01308	0.00012	0.00066	0.03351	<0.0001	0.0093	<0.0001	0.00046	FGA
SE33	0.96352	0.19348	0.42646	0.39905	0.87716	0.00134	N/A	N/A	N/A	N/A	N/A	0.06633	0.00145	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	SE33
TH01	0.59308	0.22986	0.14765	0.0113	0.8231	0.05924	0.00043	0.00602	0.00295	<0.0001	0.21265	0.02249	0.00435	<0.0001	<0.0001	0.51311	0.00001	<0.0001	<0.0001	0.00083	0.01667	0.00176	0.00006	TH01
TPOX	0.71056	0.14632	0.36765	0.34748	0.57179	0.75408	0.06171	0.6114	0.67958	0.06615	0.16393	0.51411	0.60807	0.21758	0.01001	0.78935	0.09548	0.10405	0.0822	0.02037	0.06006	0.21005	0.00273	TPOX
vWA	0.68854	0.02532	0.81971	0.45718	0.13949	0.51254	0.00273	0.39756	0.59695	0.00276	0.08762	0.45245	0.36965	0.60716	0.3199	0.00146	0.04274	0.02303	0.39773	0.10779	0.36052	<0.0001	0.01838	vWA

Table S3c. Population differentiation exact tests, Eastern subregion.

locus	K	C	N	S	W	SA3	SA1	SA2	SA4	BAH	QAT	UAE1	UAE2	KUW	OMN	YEM	JOR	IRQ2	EGY2	IRN2	IRQ1	IRN1	EGY1	locus
CSF1PO	0.68675	0.22582	0.25975	0.12998	0.6679	0.68821	0.09569	0.88949	0.76175	0.58601	0.90592	0.474	0.07181	0.71545	0.69215	0.61136	0.81835	0.68551	0.44157	0.03858	0.48567	0.09057	0.82176	CSF1PO
D10S1248	0.61773	0.02465	0.00039	0.12498	0.08318	0.1823	N/A	N/A	N/A	N/A	N/A	0.16433	0.08238	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	D10S1248
D12S391	0.63325	0.17138	0.38173	0.30876	0.57428	0.72899	N/A	N/A	N/A	N/A	N/A	0.07643	0.10129	N/A	N/A	N/A	0.2007	N/A	N/A	N/A	N/A	N/A	N/A	D12S391
D13S317	0.86089	0.96799	0.40396	0.54869	0.4441	0.23627	0.03176	0.57906	0.17885	0.72209	0.44871	0.68403	0.73427	0.74513	0.47063	0.48422	0.11708	0.12484	0.0825	0.15818	0.16226	0.00267	0.05365	D13S317
D16S539	0.25951	0.18926	0.49648	0.01845	0.25785	0.20392	0.00601	0.01382	0.17943	0.7897	0.05484	0.66012	0.60778	0.7031	0.5824	0.3423	0.2554	0.61664	0.08388	0.42769	0.18544	0.2257	0.03009	D16S539
D18S51	0.24444	0.14791	0.04378	0.04884	0.07847	0.14402	0.00112	0.04425	0.10799	0.00122	0.12234	0.08752	0.00404	0.01177	0.01032	0.39957	0.03891	0.05271	0.00172	0.00064	0.00031	0.00021	0.02801	D18S51
D19S433	0.4009	0.11121	0.4422	0.25372	0.13165	0.09851	0.01838	N/A	0.49724	0.00016	0.00754	0.13411	<0.0001	0.66602	N/A	N/A	0.01555	0.00055	0.00791	0.05856	0.0293	0.11025	0.00187	D19S433
D1S1656	0.21824	0.27076	0.4267	0.24141	0.4379	0.98921	N/A	N/A	N/A	N/A	N/A	0.89884	0.79519	N/A	N/A	N/A	0.89937	N/A	N/A	N/A	N/A	N/A	N/A	D1S1656
D21S11	0.67154	0.26485	0.07001	0.44501	0.64966	0.3474	0.43253	0.76319	0.08815	0.46566	0.0792	0.60486	0.4311	0.90229	0.86926	0.61697	0.30908	0.37546	0.24625	0.58205	0.71015	0.95889	0.72665	D21S11
D22S1045	0.50099	0.26651	0.58464	0.05732	0.25269	0.65424	N/A	N/A	N/A	N/A	N/A	0.67281	0.35516	N/A	N/A	N/A	0.05868	N/A	N/A	N/A	N/A	N/A	N/A	D22S1045
D2S1338	0.36883	0.00355	0.56459	0.01153	0.16096	0.04476	0.07176	N/A	0.23641	<0.0001	0.07646	0.03199	0.0139	0.03253	N/A	N/A	<0.0001	0.01547	0.00206	0.00299	0.0009	0.00301	0.00582	D2S1338
D2S441	0.84498	0.62035	0.70201	0.88224	0.78122	0.7408	N/A	N/A	N/A	N/A	N/A	0.13084	0.07564	N/A	N/A	N/A	0.52633	N/A	N/A	N/A	N/A	N/A	N/A	D2S441
D3S1358	0.73349	0.60291	0.04741	0.28143	0.61724	0.91168	0.32829	0.98173	0.58689	0.88846	0.4626	0.86345	0.83095	0.84192	0.22365	0.81549	0.68559	0.44114	0.96511	0.5039	0.95763	0.00081	0.38002	D3S1358
D5S818	0.84216	0.38549	0.0158	0.03802	0.47808	0.95776	0.14377	0.78977	0.92869	0.20164	0.02105	0.4655	0.13322	0.53098	0.34089	0.19088	<0.0001	0.61634	0.1	0.35519	0.4786	0.17191	0.03177	D5S818
D7S820	0.815	0.88101	0.17329	0.24812	0.82466	0.88702	0.9831	0.4479	0.39484	0.00886	0.89624	0.12496	0.09348	0.97506	0.37963	0.58186	0.36457	0.23174	0.06184	0.00853	0.54205	0.00162	0.57207	D7S820
D8S1179	0.95789	0.70463	0.76052	0.90617	0.79854	0.65903	0.62179	0.98802	0.99911	0.19681	0.83705	0.68184	0.51838	0.98716	0.98353	0.2753	0.03258	0.06783	0.10005	0.00036	0.13087	0.00448	0.63245	D8S1179
FGA	0.5029	0.58971	0.70135	0.71947	0.99191	0.89072	0.16764	0.89908	0.48699	0.35871	0.14939	0.98106	0.86842	0.86816	0.57149	0.79902	0.2008	0.28718	0.24256	0.4856	0.65079	0.05065	0.40343	FGA
SE33	0.96352	0.19348	0.48951	0.00177	0.21521	0.00468	N/A	N/A	N/A	N/A	N/A	0.98895	0.95817	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	SE33
TH01	0.59308	0.22986	0.17408	0.16339	0.12411	0.31649	0.0041	0.01554	0.05024	0.00017	0.08151	0.39534	0.12104	<0.0001	0.00092	0.78821	0.48487	0.05674	0.11424	0.08337	0.22232	0.00597	0.02229	TH01
TPOX	0.71056	0.14632	0.34267	0.04107	0.04271	0.27242	0.06144	0.53195	0.35419	0.51912	0.52698	0.16799	0.34393	0.08944	0.00675	0.23278	0.42215	0.34282	0.16811	0.20697	0.09956	0.07656	0.03732	TPOX
vWA	0.68854	0.02532	0.06767	0.05344	0.49898	0.01593	0.00391	0.37689	0.09417	0.00001	0.01029	0.00031	0.00236	0.04388	0.05682	0.00004	0.02966	0.02371	0.00049	<0.0001	0.00124	<0.0001	0.00001	vWA

Table S3d. Population differentiation exact test, Northern subregion.

locus	K	C	E	S	W	SA3	SA1	SA2	SA4	BAH	QAT	UAE1	UAE2	KUW	OMN	YEM	JOR	IRQ2	EGY2	IRN2	IRQ1	IRN1	EGY1	locus
CSF1PO	0.68675	0.22582	0.25975	0.13782	0.96677	0.04099	0.81335	0.54205	0.01729	0.07878	0.08996	0.29083	0.13506	0.80722	0.07494	0.59895	0.18337	0.04431	0.26281	0.45666	0.29287	0.11901	0.43915	CSF1PO
D10S1248	0.61773	0.02465	0.00039	0.00098	0.01671	0.03538	N/A	N/A	N/A	N/A	N/A	0.07382	0.07936	N/A	N/A	N/A	<0.0001	N/A	N/A	N/A	N/A	N/A	N/A	D10S1248
D12S391	0.63325	0.17138	0.38173	0.04721	0.00379	0.30177	N/A	N/A	N/A	N/A	N/A	0.00573	0.00833	N/A	N/A	N/A	0.00308	N/A	N/A	N/A	N/A	N/A	N/A	D12S391
D13S317	0.86089	0.96799	0.40396	0.00832	0.00971	0.00137	0.0002	0.27553	0.00057	0.01705	0.35944	0.00201	0.00074	0.00947	0.03976	0.01315	0.00142	0.0109	0.00152	0.00167	0.00031	0.00039	0.01245	D13S317
D16S539	0.25951	0.18926	0.49648	0.04736	0.9707	0.10775	0.00341	0.0141	0.01782	0.20111	0.01915	0.06082	0.02047	0.19161	0.48892	0.20659	0.03092	0.36479	0.03012	0.04428	0.0112	0.3	0.01717	D16S539
D18S51	0.24444	0.14791	0.04378	0.01304	0.00319	0.43625	0.018	0.0121	0.44025	0.03503	0.13026	0.16037	0.12082	0.16419	0.0237	0.41536	0.02326	0.01261	<0.0001	0.00142	0.03651	0.00327	0.00026	D18S51
D19S433	0.4009	0.11121	0.4422	0.53025	0.03343	0.24134	0.15387	N/A	0.79787	0.01078	0.00087	0.9351	<0.0001	0.92544	N/A	N/A	0.68151	0.04773	0.24022	0.28758	0.27279	0.27104	0.47736	D19S433
D1S1656	0.21824	0.27076	0.4267	0.0453	0.00966	0.01755	N/A	N/A	N/A	N/A	N/A	0.00942	0.00056	N/A	N/A	N/A	0.00007	N/A	N/A	N/A	N/A	N/A	N/A	D1S1656
D21S11	0.67154	0.26485	0.07001	0.43857	0.14017	0.6988	0.14416	0.33876	0.35765	0.00119	0.65986	0.09767	0.0344	0.37117	0.00349	0.3996	0.02088	0.0435	0.0254	0.00752	0.09219	0.05396	0.36815	D21S11
D22S1045	0.50099	0.26651	0.58464	0.28721	0.08976	0.37997	N/A	N/A	N/A	N/A	N/A	0.01979	0.00194	N/A	N/A	N/A	0.00352	N/A	N/A	N/A	N/A	N/A	N/A	D22S1045
D2S1338	0.36883	0.00355	0.56459	0.00469	0.39171	0.04522	0.04409	N/A	0.13022	<0.0001	0.01102	0.00068	0.00014	0.06722	N/A	N/A	<0.0001	0.00006	<0.0001	<0.0001	0.00003	<0.0001	0.00032	D2S1338
D2S441	0.84498	0.62035	0.70201	0.6539	0.91598	0.53709	N/A	N/A	N/A	N/A	N/A	0.13458	0.02836	N/A	N/A	N/A	0.85372	N/A	N/A	N/A	N/A	N/A	N/A	D2S441
D3S1358	0.73349	0.60291	0.04741	0.00051	0.48441	0.02086	0.00581	0.02124	0.44837	0.00928	0.0193	0.06702	0.04889	0.00319	0.00922	0.22025	0.00028	0.00161	0.0039	0.0029	0.01134	<0.0001	0.00863	D3S1358
D5S818	0.84216	0.38549	0.0158	0.00121	0.0023	0.00165	0.00088	0.00208	0.00245	<0.0001	0.00495	<0.0001	0.00008	<0.0001	0.00537	0.01829	0.00001	0.00247	0.00007	0.00001	0.00037	0.00086	0.00006	D5S818
D7S820	0.815	0.88101	0.17329	0.00086	0.01202	0.28636	0.40385	0.01343	0.11184	0.00004	0.19176	0.00516	0.0283	0.03666	0.07061	0.55569	0.14127	0.06722	0.01092	0.00054	0.16662	<0.0001	0.1659	D7S820
D8S1179	0.81535	0.70463	0.76052	0.61248	0.14688	0.51703	0.02211	0.76665	0.57781	0.002	0.3703	0.12559	0.07882	0.16049	0.25266	0.31924	<0.0001	0.00004	0.00313	<0.0001	<0.0001	<0.0001	0.01564	D8S1179
FGA	0.5029	0.58971	0.70135	0.50257	0.68497	0.51074	0.0559	0.12989	0.20581	0.13065	0.00146	0.85953	0.54504	0.51537	0.82005	0.14548	0.19688	0.24222	0.34429	0.08061	0.26124	0.01045	0.67245	FGA
SE33	0.96352	0.19348	0.48951	0.02639	0.35793	<0.0001	N/A	N/A	N/A	N/A	N/A	0.22205	0.03041	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	SE33
TH01	0.59308	0.22986	0.17408	0.57206	0.22687	0.31767	0.14685	0.00719	0.26056	0.01123	0.61278	0.92854	0.79799	<0.0001	0.03915	0.2066	0.27187	0.17111	0.00204	0.55887	0.52467	0.55614	0.00088	TH01
TPOX	0.71056	0.14632	0.34267	0.3771	0.54906	0.58243	0.39836	0.53651	0.50135	0.02906	0.01239	0.02344	0.1202	0.58751	0.00111	0.36807	0.15584	0.06598	0.12403	0.00559	0.02607	0.00879	0.02513	TPOX
vWA	0.68854	0.02532	0.06767	0.6751	0.17784	0.35446	0.10481	0.26752	0.80603	0.01214	0.10503	0.37534	0.34307	0.92811	0.18352	<0.0001	0.25116	0.00995	0.30516	0.16733	0.23645	<0.0001	0.04407	vWA

K – KSA overall sample, C – Central SA, E – Eastern SA, N – Northern SA, S – Southern SA, W – Western SA (all our data), BAH – Bahrain [1], EGY1, EGY2 – Egypt, respectively [2, 3]; IRN1, IRN2 – Iran, respectively [3, 4]; IRQ1, IRQ2 – Iraq, respectively [3, 5]; JOR – Jordan [6];

KUW – Kuwait [3]; OMN – Oman [7]; QAT –

Table S3e. Population differentiation exact tests, Southern subregion.

locus	K	C	E	N	W	SA3	SA1	SA2	SA4	BAH	QAT	UAE1	UAE2	KUW	OMN	YEM	JOR	IRQ2	EGY2	IRN2	IRQ1	IRN1	EGY1	locus
CSFIPO	0.68675	0.22582	0.25975	0.13782	0.24895	0.34843	0.01021	0.07463	0.00304	0.26844	0.14945	0.52304	0.22219	0.09879	0.02784	0.4157	0.60664	0.43605	0.19156	0.60559	0.28355	0.26545	0.09494	CSFIPO
D10S1248	0.61773	0.02465	0.00039	0.00098	0.06929	0.00274	N/A	N/A	N/A	N/A	N/A	0.25364	0.23021	N/A	N/A	N/A	<0.0001	N/A	N/A	N/A	N/A	N/A	N/A	D10S1248
D12S391	0.63325	0.17138	0.38173	0.04721	0.17609	0.33686	N/A	N/A	N/A	N/A	N/A	0.74451	0.71026	N/A	N/A	N/A	0.82237	N/A	N/A	N/A	N/A	N/A	N/A	D12S391
D13S317	0.86089	0.96799	0.40396	0.00832	0.28614	0.32652	0.32207	0.08266	0.38902	0.05615	0.02141	0.14359	0.27724	0.32294	0.05489	0.83369	0.00276	0.00777	0.03203	0.00636	0.00395	<0.0001	0.02855	D13S317
D16S539	0.25951	0.18926	0.49648	0.04736	0.02392	0.0024	0.00012	0.00317	0.00056	0.00246	0.0004	0.00002	<0.0001	0.00005	0.15126	0.00033	0.00027	0.069	0.0021	0.01372	0.00184	0.0702	0.01053	D16S539
D18S51	0.24444	0.14791	0.04378	0.01304	0.00232	0.3098	<0.0001	0.00649	0.23242	0.00028	0.89713	0.37104	0.06443	0.01824	0.15182	0.24518	0.184	0.24598	0.07701	0.02145	0.0924	0.00037	0.01126	D18S51
D19S433	0.4009	0.11121	0.4422	0.53025	0.73612	0.92482	0.49716	N/A	0.96632	0.12431	0.00179	0.36547	<0.0001	0.70408	N/A	N/A	0.05012	0.01481	0.04505	0.23265	0.03522	0.10127	0.0181	D19S433
D1S1656	0.21824	0.27076	0.4267	0.0453	0.21826	0.45407	N/A	N/A	N/A	N/A	N/A	0.06756	0.01782	N/A	N/A	N/A	0.0103	N/A	N/A	N/A	N/A	N/A	N/A	D1S1656
D21S11	0.67154	0.26485	0.07001	0.43857	0.22524	0.88613	0.04392	0.4274	0.16967	0.0311	0.32994	0.57611	0.20823	0.71905	0.04769	0.74561	0.01775	0.23011	0.07005	0.08368	0.6585	0.64421	0.81566	D21S11
D22S1045	0.50099	0.26651	0.58464	0.28721	0.20284	0.38819	N/A	N/A	N/A	N/A	N/A	0.00379	0.00186	N/A	N/A	N/A	0.08014	N/A	N/A	N/A	N/A	N/A	N/A	D22S1045
D2S1338	0.36883	0.00355	0.56459	0.00469	0.88676	0.89921	0.43281	N/A	0.23048	<0.0001	0.04721	0.02236	0.00965	0.09697	N/A	N/A	<0.0001	0.01529	0.00181	<0.0001	<0.0001	<0.0001	0.02609	D2S1338
D2S441	0.84498	0.62035	0.70201	0.6539	0.8891	0.45772	N/A	N/A	N/A	N/A	N/A	0.00566	0.00692	N/A	N/A	N/A	0.0423	N/A	N/A	N/A	N/A	N/A	N/A	D2S441
D3S1358	0.73349	0.60291	0.04741	0.00051	0.24714	0.01382	0.02298	0.38784	0.03022	0.16654	0.05778	0.01167	0.00422	0.01051	0.01353	0.139	0.01032	0.00913	0.04321	<0.0001	0.00151	<0.0001	0.00249	D3S1358
D5S818	0.84216	0.38549	0.0158	0.00121	0.50895	0.0142	0.1696	0.05942	0.05923	0.41131	0.06144	0.17181	0.29423	0.23433	0.9758	0.92176	<0.0001	0.0718	0.13151	0.01403	0.02177	0.02522	0.13816	D5S818
D7S820	0.815	0.88101	0.17329	0.00086	0.00971	0.0073	0.0373	0.11754	0.00058	0.02937	0.02049	0.0192	0.00774	0.00646	0.56223	0.00816	0.00501	0.10405	0.0157	0.00092	0.00438	0.01236	0.0359	D7S820
D8S1179	0.64644	0.70463	0.76052	0.61248	0.18112	0.48078	0.25593	0.81266	0.88514	0.25249	0.87154	0.3998	0.31568	0.58628	0.56782	0.63579	0.00864	0.08712	0.06289	0.00142	0.04104	0.00526	0.57634	D8S1179
FGA	0.5029	0.58971	0.70135	0.50257	0.72867	0.95824	0.11057	0.4612	0.06571	0.77532	0.44317	0.976	0.74401	0.25584	0.32681	0.17228	0.47935	0.79016	0.29382	0.39735	0.82924	0.09441	0.66482	FGA
SE33	0.96352	0.19348	0.48951	0.02639	0.14881	<0.0001	N/A	N/A	N/A	N/A	N/A	0.00039	<0.0001	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	SE33
TH01	0.59308	0.22986	0.17408	0.57206	0.01203	0.36805	0.00733	0.00017	0.31227	0.05653	0.1092	0.78628	0.42087	<0.0001	0.01096	0.39218	0.34276	0.7518	0.09073	0.20991	0.27839	0.16788	0.04238	TH01
TPOX	0.71056	0.14632	0.34267	0.3771	0.94066	0.50331	0.48816	0.50193	0.12158	0.00409	0.01113	0.01335	0.01626	0.01593	0.00141	0.7826	0.00442	0.00051	0.00377	<0.0001	0.00001	0.0009	0.01258	TPOX
vWA	0.68854	0.02532	0.06767	0.6751	0.18432	0.86104	0.00879	0.36288	0.61975	0.02889	0.03277	0.23519	0.25382	0.30711	0.33496	0.00039	0.1016	0.00472	0.0313	0.04107	0.15314	<0.0001	0.02703	vWA

Table S3f. Population differentiation exact tests, Western subregion.

locus	K	C	E	N	S	SA3	SA1	SA2	SA4	BAH	QAT	UAE1	UAE2	KUW	OMN	YEM	JOR	IRQ2	EGY2	IRN2	IRQ1	IRN1	EGY1	locus
CSFIPO	0.68675	0.22582	0.25975	0.13782	0.24895	0.34481	0.74705	0.90899	0.16405	0.34197	0.50523	0.80024	0.41604	0.994	0.21913	0.82896	0.65674	0.32221	0.64539	0.70225	0.93252	0.26277	0.71777	CSFIPO
D10S1248	0.61773	0.02465	0.00039	0.00098	0.06929	0.12027	N/A	N/A	N/A	N/A	N/A	0.01471	0.00776	N/A	N/A	N/A	<0.0001	N/A	N/A	N/A	N/A	N/A	N/A	D10S1248
D12S391	0.63325	0.17138	0.38173	0.04721	0.17609	0.2134	N/A	N/A	N/A	N/A	N/A	<0.0001	0.00001	N/A	N/A	N/A	0.01788	N/A	N/A	N/A	N/A	N/A	N/A	D12S391
D13S317	0.86089	0.96799	0.40396	0.00832	0.28614	0.73315	0.06095	0.11088	0.00742	0.14809	0.04741	0.33185	0.24481	0.2388	0.74767	0.46024	0.00746	0.10092	0.0041	0.10649	0.02515	<0.0001	0.00469	D13S317
D16S539	0.25951	0.18926	0.49648	0.04736	0.02392	0.09887	0.05935	0.03913	0.04686	0.11691	0.00678	0.15582	0.06301	0.20553	0.45786	0.1907	0.0588	0.36189	0.12652	0.1068	0.03997	0.27889	0.01723	D16S539
D18S51	0.24444	0.14791	0.04378	0.01304	0.00232	0.34796	0.0447	0.34362	0.15895	0.00044	0.00553	0.02304	0.00054	0.34893	0.00416	0.44326	<0.0001	0.04178	0.0042	0.00014	0.00022	0.00018	0.04472	D18S51
D19S433	0.4009	0.11121	0.4422	0.53025	0.73612	0.23119	0.04744	N/A	0.54678	0.00006	<0.0001	0.00179	<0.0001	0.16381	N/A	N/A	0.00007	<0.0001	0.00014	0.00102	0.00082	0.00049	<0.0001	D19S433
D1S1656	0.21824	0.27076	0.4267	0.0453	0.21826	0.37711	N/A	N/A	N/A	N/A	N/A	0.00108	0.00102	N/A	N/A	N/A	0.00842	N/A	N/A	N/A	N/A	N/A	N/A	D1S1656
D21S11	0.67154	0.26485	0.07001	0.43857	0.22524	0.57706	0.15076	0.56388	0.18083	0.37482	0.4607	0.86289	0.72299	0.8924	0.79367	0.79844	0.60383	0.8383	0.05572	0.83943	0.366	0.85853	0.64738	D21S11
D22S1045	0.50099	0.26651	0.58464	0.28721	0.20284	0.82428	N/A	N/A	N/A	N/A	N/A	0.42422	0.23785	N/A	N/A	N/A	0.0375	N/A	N/A	N/A	N/A	N/A	N/A	D22S1045
D2S1338	0.36883	0.00355	0.56459	0.00469	0.88676	0.98975	0.78943	N/A	0.76145	0.0001	0.23525	0.14231	0.03209	0.78568	N/A	N/A	<0.0001	0.05518	0.00317	<0.0001	0.00127	<0.0001	0.01826	D2S1338
D2S441	0.84498	0.62035	0.70201	0.6539	0.8891	0.88912	N/A	N/A	N/A	N/A	N/A	0.11455	0.06394	N/A	N/A	N/A	0.42606	N/A	N/A	N/A	N/A	N/A	N/A	D2S441
D3S1358	0.73349	0.60291	0.04741	0.00051	0.24714	0.37149	0.02144	0.78518	0.92286	0.23471	0.12645	0.30433	0.31904	0.46656	0.08555	0.36738	0.02699	0.08538	0.35761	0.02363	0.14397	<0.0001	0.21611	D3S1358
D5S818	0.84216	0.38549	0.0158	0.00121	0.50895	0.75378	0.42378	0.81083	0.86264	0.98772	0.06969	0.868	0.95141	0.96357	0.75901	0.7016	<0.0001	0.97862	0.42281	0.79932	0.85415	0.06651	0.03669	D5S818
D7S820	0.815	0.88101	0.17329	0.00086	0.00971	0.8213	0.2819	0.40826	0.1866	0.00353	0.80386	0.02501	0.01082	0.64179	0.08431	0.52396	0.12494	0.04121	0.00638	0.00094	0.11869	0.00028	0.11987	D7S820
D8S1179	0.60746	0.70463	0.76052	0.61248	0.18112	0.11011	0.01193	0.43662	0.47862	0.00003	0.45589	0.00285	0.00567	0.02531	0.43615	0.00056	<0.0001	0.00021	<0.0001	<0.0001	0.00022	0.006	0.00022	D8S1179
FGA	0.5029	0.58971	0.70135	0.50257	0.72867	0.83884	0.1794	0.64702	0.57517	0.12597	0.15975	0.82335	0.24886	0.54165	0.37676	0.09996	0.03559	0.07346	0.13056	0.02332	0.16597	0.00018	0.09824	FGA
SE33	0.96352	0.19348	0.48951	0.02639	0.14881	0.00236	N/A	N/A	N/A	N/A	N/A	0.01958	0.00365	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	SE33
TH01	0.59308	0.22986	0.17408	0.57206	0.01203	0.05845	0.00832	0.00046	0.01292	<0.0001	0.75602	0.12555	0.02421	<0.0001	0.00141	0.32629	0.00035	0.001	<0.0001	0.00207	0.02761	0.00132	0.00008	TH01
TPOX	0.71056	0.14632	0.34267	0.3771	0.94066	0.75835	0.40615	0.44431	0.34701	0.0031	0.01263	0.01837	0.03283	0.08441	0.00109	0.83569	0.0093	0.00626	0.0171	0.00001	0.00007	0.00353	0.01066	TPOX
vWA	0.68854	0.02532	0.06767	0.6751	0.18432	0.18594	0.00506	0.52491	0.08461	0.00004	0.00944	0.04211	0.06971	0.59219	0.18152	<0.0001	0.02772	0.04915	0.00996	0.00011	0.00593	<0.0001	0.00317	vWA

K – KSA overall sample, C – Central SA, E – Eastern SA, N – Northern SA, S – Southern SA, W – Western SA (all our data), BAH – Bahrain [1], EGY1, EGY2 – Egypt, respectively [2, 3]; IRN1, IRN2 – Iran, respectively [3, 4]; IRQ1, IRQ2 – Iraq, respectively [3, 5]; JOR – Jordan [6]; KUW – Kuwait [3