

Supplementary Table 1 data from ENSEMBL homo_sapiens_variation_57_37b database
(ftp://ftp.ensembl.org/pub/current_mysql/homo_sapiens_variation_57_37b/)

#SNPs	category	HGDP		ALFRED	
		3840		671	
		matches	% ^a	matches	% ^a
REGULATORY_REGION	GEN	6	0.1	3	0.3
NON_SYNONYMOUS_CODING	GEN	78	1.4	19	2.2
DOWNSTREAM	GEN	673	12.0	163	18.7
FRAMESHIFT_CODING	GEN	2	0.0	0	0.0
INTRONIC	GEN	1829	32.7	346	39.7
5PRIME_UTR	GEN	45	0.8	6	0.7
UPSTREAM	GEN	595	10.6	158	18.1
WITHIN_NON_CODING_GENE	GEN	1369	24.5	129	14.8
SPLICE_SITE,INTRONIC	GEN	7	0.1	3	0.3
ESSENTIAL_SPLICE_SITE,INTRONIC	GEN	3	0.1	0	0.0
3PRIME_UTR	GEN	112	2.0	27	3.1
SYNONYMOUS_CODING	GEN	58	1.0	15	1.7
SPLICE_SITE,5PRIME_UTR	GEN	1	0.0	1	0.1
STOP_GAINED	GEN	1	0.0	0	0.0
NON_SYNONYMOUS_CODING,SPLICE_SITE	GEN	0	0.0	2	0.2
INTERGENIC	INT	819	14.6	165	18.9
	total matches	5598		872	

^a% is referred to total matches

Supplementary Table 2

Summary statistics for genetic distance distributions. Shapiro test of normality.

			Min.	1st qu	Median	Mean	3rd qu	Max.	Shapiro		
										S	p-value
Reynolds	HGDP	SNP_ALL	0.000	0.011	0.022	0.048	0.034	0.200	0.66	<0.001	
		SNP_GEN	0.000	0.011	0.020	0.047	0.031	0.198	0.66	<0.001	
		SNP_INT	-0.011	0.013	0.022	0.045	0.031	0.185	0.66	<0.001	
		STR	0.005	0.013	0.016	0.022	0.022	0.063	0.74	<0.001	
	ALFRED	ALL	0.258	0.272	0.282	0.288	0.293	0.356	0.84	<0.001	
		GEN	0.262	0.284	0.293	0.298	0.307	0.362	0.91	<0.001	
		INT	0.189	0.243	0.263	0.270	0.285	0.390	0.94	<0.001	
F _{ST}	HGDP	SNP_ALL	-0.009	0.011	0.022	0.044	0.033	0.181	0.68	<0.001	
		SNP_GEN	-0.009	0.011	0.020	0.044	0.030	0.180	0.68	<0.001	
		SNP_INT	-0.011	0.013	0.022	0.045	0.031	0.185	0.69	<0.001	
		STR	0.005	0.012	0.016	0.022	0.021	0.061	0.74	<0.001	
	ALFRED	ALL	0.227	0.238	0.246	0.250	0.254	0.299	0.85	<0.001	
		GEN	0.230	0.247	0.254	0.258	0.264	0.304	0.92	<0.001	
		INT	0.172	0.216	0.231	0.236	0.248	0.323	0.96	0.003	

Supplementary Table3 Mantel correlation and partial correlation coefficients, between genetic (SNP), linguistic (LAN) and geographic (GEODIR, GEOAFR) matrices for populations in the HGDP and ALFRED datasets. ALFRED_10 is a subset of ALFRED database that include only populations present in the HGDP panel. Linguistic distances based on the Parametric Comparison Method. Genetic distances calculated according to Reynolds using all SNPs in the datasets (ALL) or only those in “genic” or “intergenic” regions (GEN and INT, respectively). r = Spearman correlation coefficient. Statistical significance at the $P < 0.05$ level highlighted in boldtype. All correlations are statistically significant after Bonferroni correction

		ALFRED				ALFRED_10				HGDP			
		Reynolds		Weir and Cockerham		Reynolds		Weir and Cockerham		Reynolds		Weir and Cockerham	
		r	P	r	P	r	P	r	P	r	P	r	P
ALL	$r_{\text{SNP,LAN}}$	0.20	0.123	0.20	0.122	0.47	0.017	0.47	0.015	0.56	0.005	0.06	0.006
	$r_{\text{SNP,GEODIR}}$	0.06	0.276	0.06	0.278	0.19	0.155	0.19	0.162	0.40	0.021	0.40	0.020
	$r_{\text{SNP, GEOAFR}}$	0.24	0.099	0.24	0.103	0.48	0.032	0.48	0.030	0.70	0.000	0.70	0.002
	$r_{\text{SNP,LAN,GEODIR}}$	0.19	0.133	0.19	0.128	0.47	0.018	0.47	0.019	0.58	0.004	0.58	0.005
	$r_{\text{SNP,LAN,GEOAFR}}$	0.15	0.179	0.15	0.174	0.39	0.052	0.39	0.049	0.51	0.013	0.51	0.015
GEN	$r_{\text{SNP,LAN}}$	0.24	0.098	0.24	0.097	0.48	0.020	0.48	0.018	0.57	0.005	0.57	0.003
	$r_{\text{SNP,GEODIR}}$	-0.10	0.751	-0.10	0.746	-0.10	0.681	-0.10	0.683	0.41	0.018	0.41	0.019
	$r_{\text{SNP, GEOAFR}}$	0.09	0.241	0.09	0.239	0.23	0.187	0.23	0.176	0.70	0.001	0.70	0.001
	$r_{\text{SNP,LAN,GEODIR}}$	0.26	0.070	0.26	0.073	0.49	0.016	0.49	0.016	0.59	0.004	0.59	0.004
	$r_{\text{SNP,LAN,GEOAFR}}$	0.22	0.096	0.22	0.100	0.44	0.035	0.44	0.351	0.53	0.011	0.53	0.012
INT	$r_{\text{SNP,LAN}}$	0.18	0.141	0.18	0.139	0.36	0.076	0.36	0.071	0.49	0.026	0.49	0.031
	$r_{\text{SNP,GEODIR}}$	0.37	0.011	0.37	0.010	0.51	0.002	0.51	0.003	0.34	0.055	0.34	0.054
	$r_{\text{SNP, GEOAFR}}$	0.51	0.002	0.51	0.001	0.74	0.000	0.74	0.000	0.66	0.002	0.66	0.003
	$r_{\text{SNP,LAN,GEODIR}}$	0.13	0.211	0.13	0.212	0.37	0.074	0.37	0.069	0.49	0.026	0.49	0.030
	$r_{\text{SNP,LAN,GEOAFR}}$	0.06	0.329	0.06	0.336	0.22	0.175	0.22	0.176	0.40	0.061	0.40	0.058