SUPPLEMENTARY INFORMATION

Methods

Bootstrap and Jackknife Sensitivity analyses

We performed resampling tests to evaluate the robustness of our results in both the MANCOVA and linear mixed effects models for associations between phonemes and RU1-1 frequencies among the 43 populations we studied (Table S5). Confidence intervals for parameter estimates in the linear mixed effects model were generated through 10,000 bootstraps with the *bootMer* function in the R package *lme4* (1).

To quantify the sensitivity of the results to individual populations and population grouping by region, we performed leave-one out and leave-n out jackknifing, respectively, under both the MANCOVA and linear mixed effects models. Leave-one out jackknife tests entailed excluding a single population, among the 43 in our sample, and fitting both the MANCOVA and linear mixed effects models over the remaining 42 populations. Similarly, we assessed sensitivity of our results to regional differences through leave-n out jackknife tests, where a jackknife sample was formed by excluding n populations from four regional groupings of the populations in Africa, Europe, Asia, and the Americas, respectively.

Migratory distances

We modeled migratory distances between populations and the putative location of human origin using an undirected acyclic graph with nodes corresponding to the respective 43 populations in our sample (Figure S5). Six hub nodes were also instantiated for five migratory waypoints defined by Ramachandran, et al., (2007) (2), located in Cairo (30N, 31E), Istanbul (41N, 29E), Phnom Penh (12N, 105E), Anadyr (64N, 177E), and Prince Rupert Island (54N, 130W), as well as at one putative location of human origin in South Africa (22S, 20E) proposed by Henn, et al. (2011) (3). Edges were also drawn connecting South Africa to Cairo, Cairo to Istanbul, Cairo to Phnom Penh, Cairo to Anadyr, and Anadyr to Prince Rupert Island. Each of the 43 populations were then connected to the hub node where their migration passed through most recently. Each edge was weighted by the great circle distance between the respective two nodes it connected. The migratory distance from any population center to either South Africa or another population center was computed using the shortest distance on this graph with the *igraph* package in R (4).

Quadratic term for RU1-1 univariate analysis

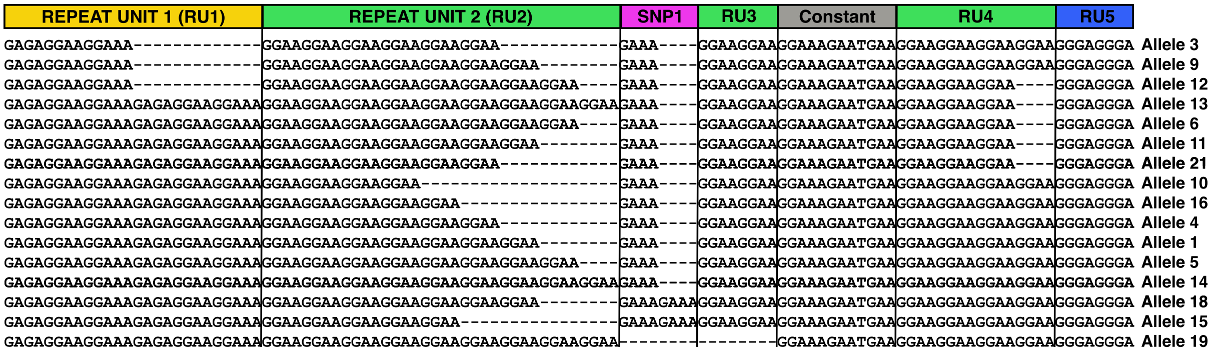
To test whether the fit for the analyses depicted in Figure 2 and Table 2 could be improved, we performed the post hoc univariate analysis of the effect of RU1-1 using a quadratic term for RU1-1 (Table S6). RU1-1 was modeled by an orthogonal polynomial basis of order two for the RU1-1 frequencies (using the poly function in R) to remove collinearity between first-order (linear) and second-order (quadratic) terms. We repeated this analysis over the sample of 43 populations. Although in this sample the quadratic model was a better fit and provided a better explanation for variation in the log-transformed consonant counts than a model with only linear terms, this could change with expanded datasets in the future. We chose to use only the simplest model in our main text as it is the most conservative solution.

References

1. Bates D, Mächler M, Bolker B, & Walker S (2015) Fitting Linear Mixed-Effects Models Using lme4. *2015* 67(1):48.
2. Ramachandran S & Rosenberg NA (2011) A test of the influence of continental axes of orientation on patterns of human gene flow. *American journal of physical anthropology* 146(4):515-529.
3. Henn BM*, et al.* (2011) Hunter-gatherer genomic diversity suggests a southern African origin for modern humans. *Proceedings of the National Academy of Sciences of the United States of America* 108(13):5154-5162.
4. Csardi G & Nepusz T (2006) The igraph software package for complex network research. *InterJournal, Complex Systems* 1695(5):1-9.
5. Rajeevan H*, et al.* (2003) ALFRED: the ALelle FREquency Database. Update. *Nucleic acids research* 31(1):270-271.

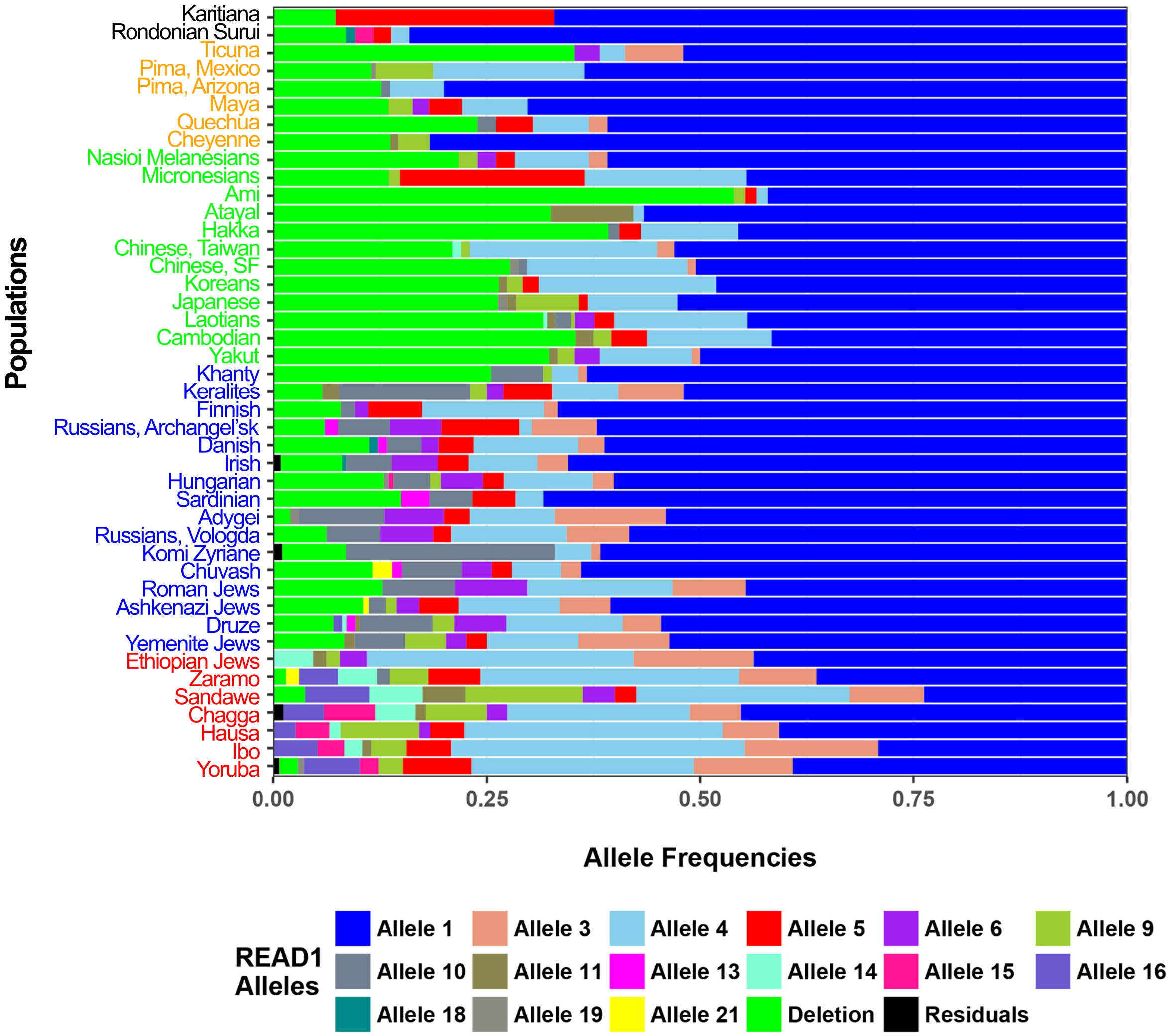
SUPPLEMENTARY FIGURES

Supplementary Figure S1. Alignment of the 16 most common human READ1 sequences. READ1 is composed of seven repeat units: RU1 is GAGAGGAAGGAAA, RU2 is GGAA, SNP1 is GAAA, RU3 is GGAA, Constant Region is GGAAGAATGAA, RU4 is GGAA, RU5 is GGGA.

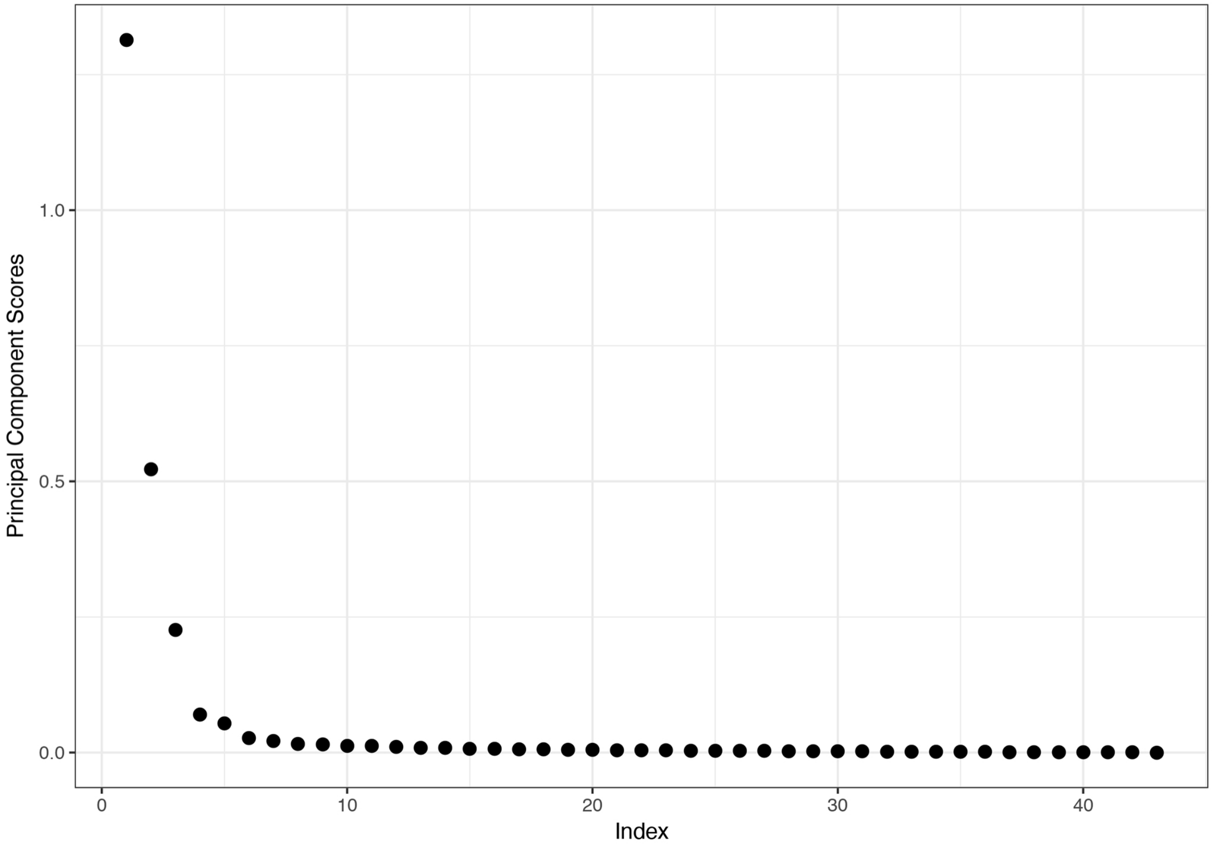


REPEAT UNIT 1 (RU1)	REPEAT UNIT 2 (RU2)	SNP1	RU3	Constant	RU4	RU5	
GAGAGGAAGGAAA-------------	GGAAGGAAGGAAGGAAGGAAGGAA------------	GAAA----	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAAGGAA	GGGAGGGA	**Allele 3**
GAGAGGAAGGAAA-------------	GGAAGGAAGGAAGGAAGGAAGGAAGGAA--------	GAAA----	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAAGGAA	GGGAGGGA	**Allele 9**
GAGAGGAAGGAAA-------------	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA----	GAAA----	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAA----	GGGAGGGA	**Allele 12**
GAGAGGAAGGAAAGAGAGGAAGGAAA	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA	GAAA----	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAA----	GGGAGGGA	**Allele 13**
GAGAGGAAGGAAAGAGAGGAAGGAAA	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA----	GAAA----	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAA----	GGGAGGGA	**Allele 6**
GAGAGGAAGGAAAGAGAGGAAGGAAA	GGAAGGAAGGAAGGAAGGAAGGAAGGAA--------	GAAA----	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAA----	GGGAGGGA	**Allele 11**
GAGAGGAAGGAAAGAGAGGAAGGAAA	GGAAGGAAGGAAGGAAGGAAGGAA------------	GAAA----	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAA----	GGGAGGGA	**Allele 21**
GAGAGGAAGGAAAGAGAGGAAGGAAA	GGAAGGAAGGAAGGAA--------------------	GAAA----	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAAGGAA	GGGAGGGA	**Allele 10**
GAGAGGAAGGAAAGAGAGGAAGGAAA	GGAAGGAAGGAAGGAAGGAA----------------	GAAA----	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAAGGAA	GGGAGGGA	**Allele 16**
GAGAGGAAGGAAAGAGAGGAAGGAAA	GGAAGGAAGGAAGGAAGGAAGGAA------------	GAAA----	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAAGGAA	GGGAGGGA	**Allele 4**
GAGAGGAAGGAAAGAGAGGAAGGAAA	GGAAGGAAGGAAGGAAGGAAGGAAGGAA--------	GAAA----	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAAGGAA	GGGAGGGA	**Allele 1**
GAGAGGAAGGAAAGAGAGGAAGGAAA	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA----	GAAA----	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAAGGAA	GGGAGGGA	**Allele 5**
GAGAGGAAGGAAAGAGAGGAAGGAAA	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA	GAAA----	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAAGGAA	GGGAGGGA	**Allele 14**
GAGAGGAAGGAAAGAGAGGAAGGAAA	GGAAGGAAGGAAGGAAGGAAGGAAGGAA--------	GAAAGAAA	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAAGGAA	GGGAGGGA	**Allele 18**
GAGAGGAAGGAAAGAGAGGAAGGAAA	GGAAGGAAGGAAGGAAGGAA----------------	GAAAGAAA	GGAAGGAA	GGAAAGAATGAA	GGAAGGAAGGAAGGAA	GGGAGGGA	**Allele 15**
GAGAGGAAGGAAAGAGAGGAAGGAAA	GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAA	--------	--------	GGAAAGAATGAA	GGAAGGAAGGAAGGAA	GGGAGGGA	**Allele 19**

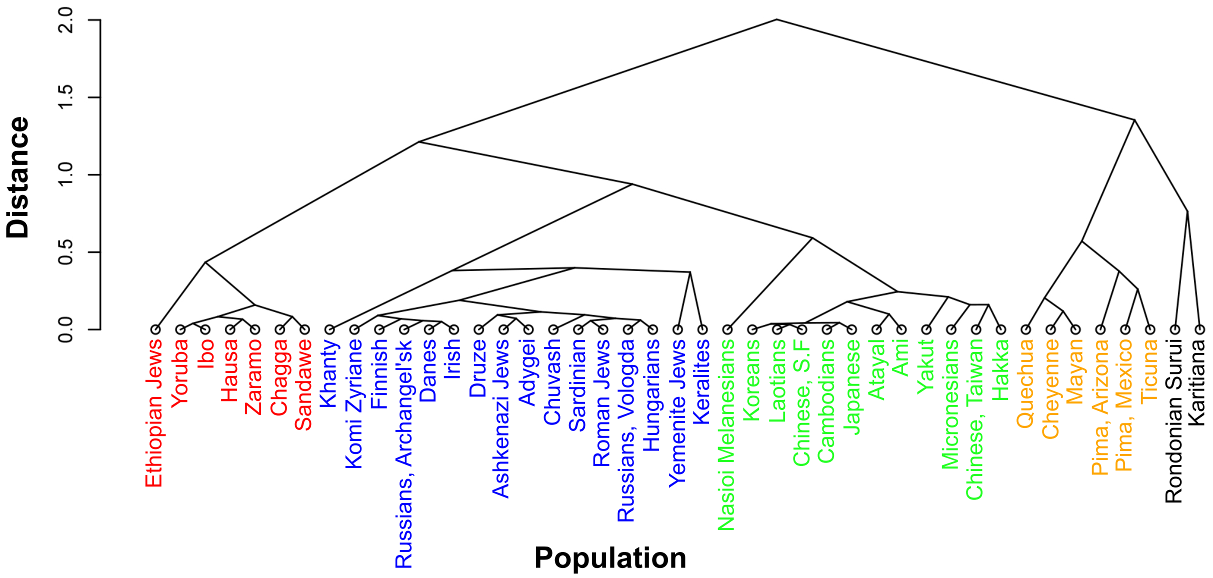
Supplementary Figure S2. READ1 allele distributions among world populations. READ1 was sequenced in samples from 43 populations. The populations are arranged on the y-axis reflecting their migrational history, going from Africa to the southern tip of the Americas. Alleles are represented on the x-axis as percentages of the whole. In green is the frequency of a complete deletion of READ1. Black represents residual alleles (sum of all rare alleles). Alleles that are only seen in one population and at a frequency less than 0.02 are assigned to the residual alleles group.



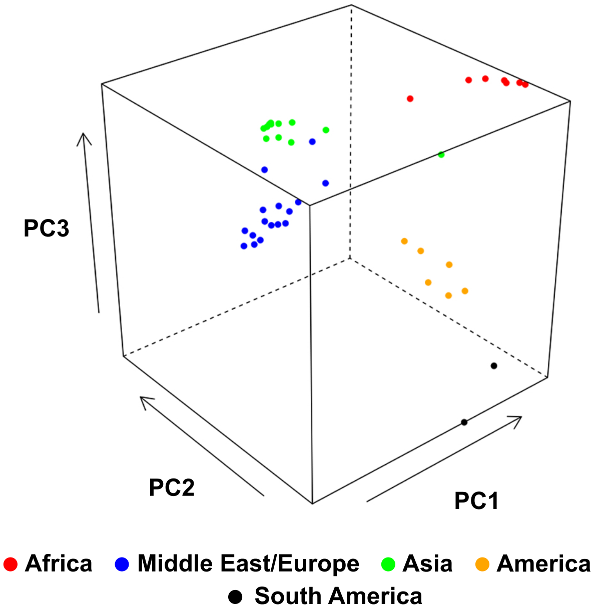
Supplementary Figure S3. Distribution of principal component scores of the tau matrix. Principal component one (PC1) accounts for 82.63% of the variation, PC2 accounts for 14.68%, and PC3 accounts for 2.05%.



Supplementary Figure S4. Continental clustering. Dendrograms generated from centroid clustering of the tau genetic relatedness matrix. Populations are colored by the continental group to which they are assigned: Africa (red), Middle East and Europe (blue), Asia (green), America (orange), South America (black).

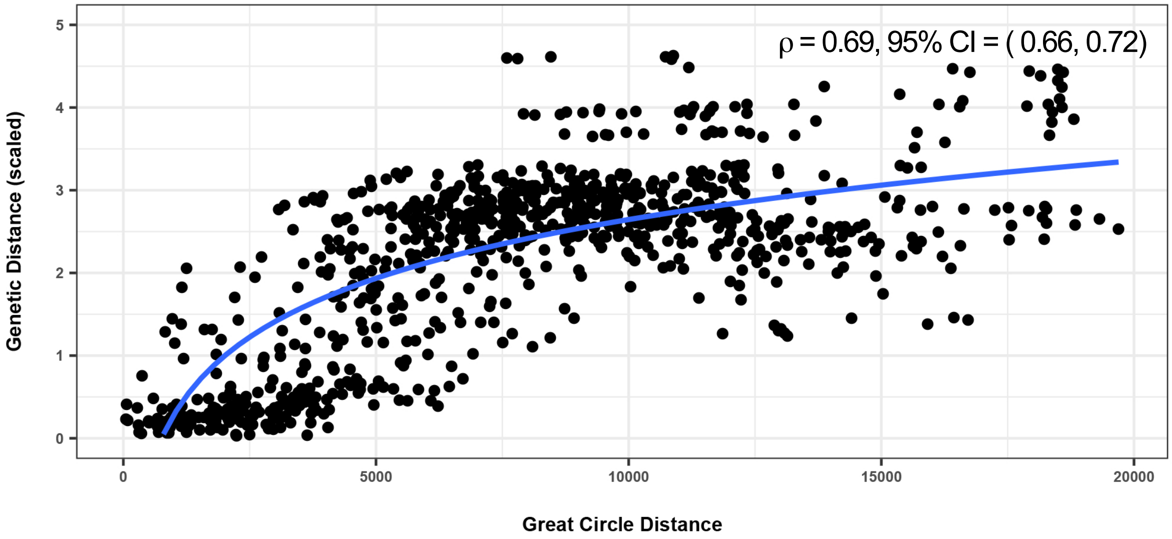


Supplementary Figure S5. 3D representation of the first three principal components of the tau genetic relatedness matrix, colored by continental groups. PCs represent geographical diversity. Populations map to continental groupings using first three PCs of the tau genetic relatedness matrix

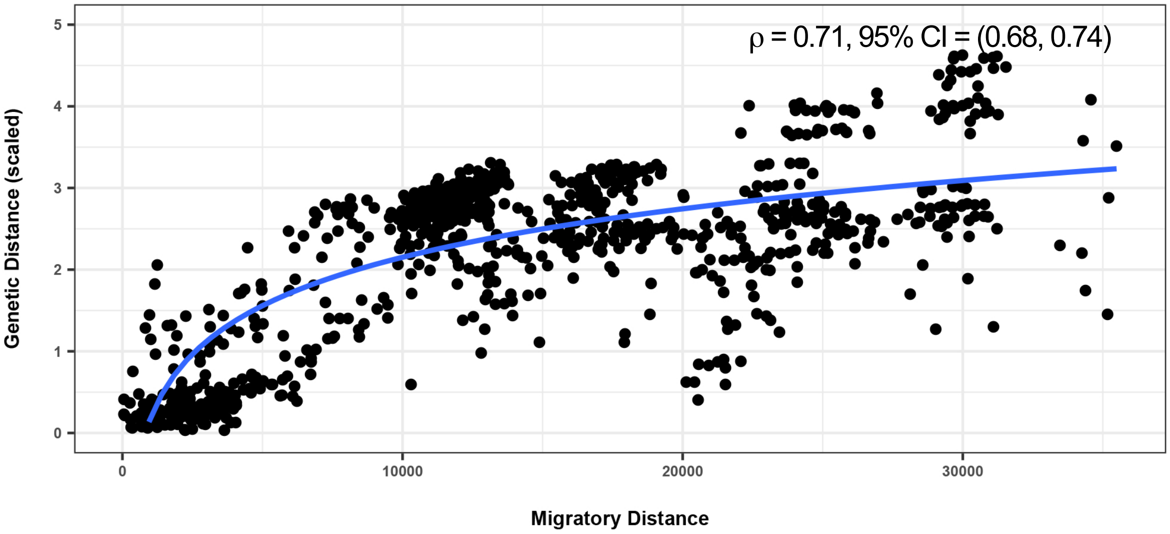


Supplementary Figure S6. Population pairwise comparisons of genetic distance and geographic distance. (a) Logarithms of kilometer geographic distances between pairs of populations are plotted on the x-axis, whereas genetic distances (using the first three PCs of the tau genetic relatedness matrix) are plotted on the y-axis (Pearson's product-moment correlation ρ = 0.69, 95% CI = (0.66, 0.72)). (b) Geographic distances between populations using migratory way points and a proposed origin in South Africa are plotted on the x-axis, genetic distances are plotted on the y-axis (Pearson's product-moment correlation ρ = 0.71, 95% CI = (0.68, 0.74)). (c) Geographic distances from South Africa for each population using migratory way points are plotted on the x-axis, Principal Component 1 scores are plotted on the y-axis. Points are colored by continental group.

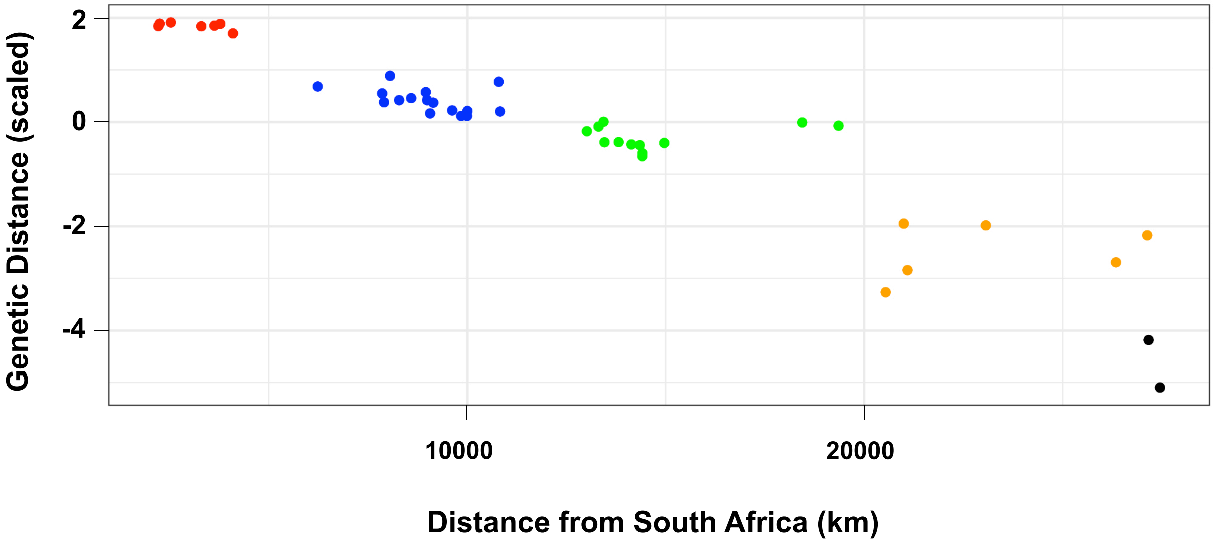
(a)



(b)


ρ = 0.71, 95% CI = (0.68, 0.74)
Genetic Distance (scaled)
Migratory Distance
0
1
2
3
4
5
0
10000
20000
30000

(c)


Genetic Distance (scaled)
Distance from South Africa (km)
2
0
-2
-4
10000
20000

Supplementary Table S1. READ1 alleles observed in previous studies.

Allele	Repeat unit 1	Repeat unit 2	SNP1	Repeat unit 3	Const. Region	Repeat unit 4	Repeat Unit 5	Length
1	(GAGAGGAAGGAAA)2	(GGAA)7	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	102
2	(GAGAGGAAGGAAA)1	(GGAA)9	(GAAA)0	(GGAA)0	GGAAAGAATGAA	(GGAA)4	(GGGA)2	85
3	(GAGAGGAAGGAAA)1	(GGAA)6	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	85
4	(GAGAGGAAGGAAA)2	(GGAA)6	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	98
5	(GAGAGGAAGGAAA)2	(GGAA)8	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	106
6	(GAGAGGAAGGAAA)2	(GGAA)8	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)3	(GGGA)2	102
7	(GAGAGGAAGGAAA)2	(GGAA)8	(GAAA)1	(GGAA)1	GGAAAGAATGAA	(GGAA)4	(GGGA)2	102
8	(GAGAGGAAGGAAA)2	(GGAA)7	(GAAA)0	(GGAA)0	GGAAAGAATGAA	(GGAA)4	(GGGA)2	90
9	(GAGAGGAAGGAAA)1	(GGAA)7	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	89
10	(GAGAGGAAGGAAA)2	(GGAA)4	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	90
11	(GAGAGGAAGGAAA)2	(GGAA)7	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)3	(GGGA)2	98
12	(GAGAGGAAGGAAA)1	(GGAA)8	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)3	(GGGA)2	89
13	(GAGAGGAAGGAAA)2	(GGAA)9	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)3	(GGGA)2	106
14	(GAGAGGAAGGAAA)2	(GGAA)9	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	110
15	(GAGAGGAAGGAAA)2	(GGAA)5	(GAAA)2	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	98
16	(GAGAGGAAGGAAA)2	(GGAA)5	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	94
17	(GAGAGGAAGGAAA)2	(GGAA)4	(GAAA)2	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	94
18	(GAGAGGAAGGAAA)2	(GGAA)7	(GAAA)2	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	106
19	(GAGAGGAAGGAAA)2	(GGAA)9	(GAAA)0	(GGAA)0	GGAAAGAATGAA	(GGAA)4	(GGGA)2	98
20	(GAGAGGAAGGAAA)2	(GGAA)10	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	114
21	(GAGAGGAAGGAAA)2	(GGAA)6	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)3	(GGGA)2	94
22	(GAGAGGAAGGAAA)2	(GGAA)10	(GAAA)0	(GGAA)0	GGAAAGAATGAA	(GGAA)4	(GGGA)2	102
23	(GAGAGGAAGGAAA)2	(GGAA)11	(GAAA)0	(GGAA)0	GGAAAGAATGAA	(GGAA)4	(GGGA)2	106
24	(GAGAGGAAGGAAA)2	(GGAA)6	(GAAA)2	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	102
25	(GAGAGGAAGGAAA)1	(GGAA)8	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	93
26	(GAGAGGAAGGAAA)2	(GGAA)5	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)3	(GGGA)2	90
27	(GAGAGGAAGGAAA)1	(GGAA)5	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	81
28	(GAGAGGAAGGAAA)2	(GGAA)7	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)5	(GGGA)2	106
29	(GAGAGGAAGGAAA)2	(GGAA)5+(GGGA)1+(GGAA)1	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	102
30	(GAGAGGAAGGAAA)2	(GGAA)5	(GAAA)1	(GGAA)4	GGAAAGAATGAA	(GGAA)4	(GGGA)2	102

31	(GAGAGGAAGGAAA)2	(GGAA)7	(GAAA)1	(GGAA)1+(GGGA)1	GGAAAGAATGAA	(GGAA)4	(GGGA)2	102
32	(GAGAGGAAGGAAA)2	(GGAA)8	(GAAA)0	(GGAA)0	GGAAAGAATGAA	(GGAA)4	(GGGA)2	94
33	(GAGAGGAAGGAAA)2	(GGAA)6	(GAAA)0	(GGAA)0	GGAAAGAATGAA	(GGAA)3	(GGGA)2	82
34	(GAGAGGAAGGAAA)2	(GGAA)7	(GAAA)2	(GGAA)2	GGAAAGAATGAA	(GGAA)3	(GGGA)2	102
35	(GAGAGGAAGGAAA)1+(GAGAGGAAGAAAA)1	(GGAA)7	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	102
36	(GAGAGGAAGGAAA)1+(GAGAGGAAGGAA)1	(GGAA)9	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	109
37	(GAGAGGAAGGAAA)2	(GGAA)6	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)1+(GAAA)1+(GGAA)2	(GGGA)2	98
38	(GAGAGGAAGGAAA)1	(GGAA)10	(GAAA)0	(GGAA)0	GGAAAGAATGAA	(GGAA)4	(GGGA)2	89
39	(GAGAGGAAGGAAA)1	(GGAA)5	(GAAA)2	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	85
40	(GAGAGGAAGGAAA)2	(GGAA)2+(GGAAA)1+(GGAA)7	(GAAA)1	(GGAA)2	GGAAAGAATGAA	(GGAA)4	(GGGA)2	115
Del	x	x	x	x	x	x	x	x

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Supplementary Table S2: READ1 allele frequencies in populations studied. Included are all alleles observed in at least one population.

Population	N	Deletion	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 9	Allele 10	Allele 11	Allele 12	Allele 13	Allele 14	Allele 15	Allele 16
Yoruba	69	0.022	0.391	0.000	0.116	0.261	0.080	0.000	0.029	0.000	0.000	0.007	0.000	0.000	0.022	0.065
Ibo	48	0.000	0.292	0.000	0.156	0.344	0.052	0.000	0.042	0.000	0.010	0.000	0.000	0.021	0.031	0.052
Hausa	38	0.000	0.408	0.000	0.066	0.303	0.039	0.013	0.092	0.000	0.000	0.000	0.000	0.013	0.039	0.026
Chagga	42	0.000	0.452	0.000	0.060	0.214	0.000	0.024	0.071	0.000	0.012	0.000	0.000	0.048	0.060	0.048
Sandawe	40	0.038	0.238	0.000	0.088	0.250	0.025	0.038	0.138	0.000	0.050	0.000	0.000	0.063	0.000	0.075
Zaramo	33	0.015	0.364	0.000	0.091	0.303	0.061	0.000	0.045	0.015	0.000	0.000	0.000	0.045	0.000	0.045
Ethiopian Jews	32	0.000	0.438	0.000	0.141	0.313	0.000	0.031	0.016	0.000	0.016	0.000	0.000	0.047	0.000	0.000
Yemenite Jews	42	0.083	0.536	0.000	0.107	0.107	0.024	0.024	0.048	0.060	0.012	0.000	0.000	0.000	0.000	0.000
Druze	99	0.071	0.545	0.000	0.045	0.136	0.000	0.061	0.025	0.086	0.005	0.000	0.010	0.005	0.000	0.010
Ashkenazi Jews	76	0.105	0.605	0.000	0.059	0.118	0.046	0.026	0.013	0.020	0.000	0.000	0.000	0.000	0.000	0.000
Roman Jew	24	0.128	0.447	0.000	0.085	0.170	0.000	0.085	0.000	0.085	0.000	0.000	0.000	0.000	0.000	0.000
Chuvash	43	0.116	0.640	0.000	0.023	0.058	0.023	0.035	0.000	0.070	0.000	0.000	0.012	0.000	0.000	0.000
Komi	47	0.074	0.617	0.011	0.011	0.043	0.000	0.000	0.000	0.245	0.000	0.000	0.000	0.000	0.000	0.000
Russian, Vologda	48	0.063	0.583	0.000	0.073	0.135	0.021	0.063	0.000	0.063	0.000	0.000	0.000	0.000	0.000	0.000
Adygei	50	0.020	0.540	0.000	0.130	0.100	0.030	0.070	0.000	0.100	0.000	0.000	0.000	0.000	0.000	0.000
Sardinian	30	0.150	0.683	0.000	0.000	0.033	0.050	0.000	0.000	0.050	0.000	0.000	0.033	0.000	0.000	0.000
Hungarians	82	0.129	0.601	0.000	0.025	0.104	0.025	0.049	0.012	0.043	0.000	0.000	0.000	0.000	0.006	0.000
Irish	112	0.072	0.655	0.000	0.036	0.081	0.036	0.054	0.000	0.054	0.000	0.000	0.000	0.000	0.000	0.000
Danes	49	0.112	0.612	0.000	0.031	0.122	0.041	0.020	0.000	0.041	0.000	0.000	0.010	0.000	0.000	0.000

Russian, Archangel'sk	33	0.061	0.621	0.000	0.076	0.015	0.091	0.061	0.000	0.061	0.000	0.000	0.015	0.000	0.000	0.000
Finns	32	0.079	0.667	0.000	0.016	0.143	0.063	0.016	0.000	0.016	0.000	0.000	0.000	0.000	0.000	0.000
Keralites	26	0.058	0.519	0.000	0.077	0.077	0.058	0.019	0.019	0.154	0.019	0.000	0.000	0.000	0.000	0.000
Khanty	49	0.255	0.633	0.000	0.010	0.031	0.000	0.000	0.010	0.061	0.000	0.000	0.000	0.000	0.000	0.000
Yakut	51	0.324	0.500	0.000	0.010	0.108	0.000	0.029	0.020	0.000	0.010	0.000	0.000	0.000	0.000	0.000
Cambodians	24	0.354	0.417	0.000	0.000	0.146	0.042	0.000	0.021	0.000	0.021	0.000	0.000	0.000	0.000	0.000
Laotians	109	0.317	0.445	0.000	0.000	0.156	0.023	0.023	0.005	0.018	0.009	0.000	0.000	0.005	0.000	0.000
Japanese	48	0.263	0.526	0.000	0.000	0.105	0.011	0.000	0.074	0.000	0.011	0.000	0.000	0.000	0.000	0.000
Koreans	53	0.264	0.481	0.000	0.000	0.208	0.019	0.000	0.019	0.000	0.009	0.000	0.000	0.000	0.000	0.000
Chinese, S.F.	51	0.277	0.505	0.000	0.010	0.188	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000
Chinese, Taiwan	50	0.210	0.530	0.000	0.020	0.220	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.010	0.000	0.000
Hakka	40	0.392	0.456	0.000	0.000	0.114	0.025	0.000	0.000	0.013	0.000	0.000	0.000	0.000	0.000	0.000
Atayal	42	0.325	0.566	0.000	0.000	0.012	0.000	0.000	0.000	0.000	0.096	0.000	0.000	0.000	0.000	0.000
Ami	38	0.539	0.421	0.000	0.000	0.013	0.013	0.000	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Micronesians	37	0.135	0.446	0.000	0.000	0.189	0.216	0.000	0.014	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Nasioi Melanesians	23	0.217	0.609	0.000	0.022	0.087	0.022	0.022	0.022	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Cheyenne	55	0.138	0.817	0.000	0.000	0.000	0.000	0.000	0.037	0.000	0.009	0.000	0.000	0.000	0.000	0.000
Quechua	23	0.239	0.609	0.000	0.022	0.065	0.043	0.000	0.000	0.022	0.000	0.000	0.000	0.000	0.000	0.000
Maya	52	0.135	0.702	0.000	0.000	0.077	0.038	0.019	0.029	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Pima, Arizona	48	0.126	0.800	0.000	0.000	0.063	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000
Pima, Mexico	96	0.115	0.635	0.000	0.000	0.177	0.000	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Ticuna	51	0.353	0.520	0.000	0.069	0.029	0.000	0.029	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Rondonian Surui	47	0.085	0.840	0.000	0.000	0.021	0.021	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.021	0.000
Karitiana	41	0.073	0.671	0.000	0.000	0.000	0.256	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Population	N	Allele 18	Allele 19	Allele 20	Allele 21	Allele 22
Yoruba	69	0.000	0.007	0.000	0.000	0.000
Ibo	48	0.000	0.000	0.000	0.000	0.000
Hausa	38	0.000	0.000	0.000	0.000	0.000
Chagga	42	0.000	0.000	0.000	0.000	0.000
Sandawe	40	0.000	0.000	0.000	0.000	0.000
Zaramo	33	0.000	0.000	0.000	0.015	0.000
Ethiopian Jews	32	0.000	0.000	0.000	0.000	0.000
Yemenite Jews	42	0.000	0.000	0.000	0.000	0.000
Druze	99	0.000	0.000	0.000	0.000	0.000
Ashkenazi Jews	76	0.000	0.000	0.000	0.007	0.000
Roman Jews	24	0.000	0.000	0.000	0.000	0.000
Chuvash	43	0.000	0.000	0.000	0.023	0.000
Komi	47	0.000	0.000	0.000	0.000	0.000
Russian, Vologda	48	0.000	0.000	0.000	0.000	0.000
Adygei	50	0.000	0.010	0.000	0.000	0.000
Sardinian	30	0.000	0.000	0.000	0.000	0.000
Hungarians	82	0.000	0.006	0.000	0.000	0.000

Irish	112	0.004	0.000	0.000	0.000	0.009
Danes	49	0.010	0.000	0.000	0.000	0.000
Russian, Archangel'sk	33	0.000	0.000	0.000	0.000	0.000
Finns	32	0.000	0.000	0.000	0.000	0.000
Keralites	26	0.000	0.000	0.000	0.000	0.000
Khanty	49	0.000	0.000	0.000	0.000	0.000
Yakut	51	0.000	0.000	0.000	0.000	0.000
Cambodians	24	0.000	0.000	0.000	0.000	0.000
Laotians	109	0.000	0.000	0.000	0.000	0.000
Japanese	48	0.000	0.011	0.000	0.000	0.000
Koreans	53	0.000	0.000	0.000	0.000	0.000
Chinese, S.F.	51	0.000	0.010	0.000	0.000	0.000
Chinese, Taiwan	50	0.000	0.000	0.000	0.000	0.000
Hakka	40	0.000	0.000	0.000	0.000	0.000
Atayal	42	0.000	0.000	0.000	0.000	0.000
Ami	38	0.000	0.000	0.000	0.000	0.000
Micronesians	37	0.000	0.000	0.000	0.000	0.000
Nasioi Melanesians	23	0.000	0.000	0.000	0.000	0.000
Cheyenne	55	0.000	0.000	0.000	0.000	0.000
Quechua	23	0.000	0.000	0.000	0.000	0.000
Maya	52	0.000	0.000	0.000	0.000	0.000

Pima, Arizona	48	0.000	0.000	0.000	0.000	0.000
Pima, Mexico	96	0.000	0.005	0.000	0.000	0.000
Ticuna	51	0.000	0.000	0.000	0.000	0.000
Rondonian Surui	47	0.011	0.000	0.000	0.000	0.000
Karitiana	41	0.000	0.000	0.000	0.000	0.000

Supplementary Table S3: Summary of populations and linguistic data. Included are continental location, population name, abbreviation, language name, language family, top-level language family, ISO code for the language assignment, listing of numbers of phonemes, consonants, vowels, and database sources for phoneme counts. General descriptions of these populations can be found in alfred.med.yale.edu (5).

Continental Group	Population	popcode	Language	Family	Top-level family	ISO	Phonemes	Consonants	Vowels	Source
Africa	Yoruba	YOR	Yoruba	Ede	Atlantic-Congo	yor	30	18.25	10.25	(1-4)
Africa	Ibo	IBO	Igbo	Igboid	Atlantic-Congo	ibo	49.25	36	11.75	(4-7)
Africa	Hausa	HSA	Hausa	Chadic	Afroasiatic	hau	39.4	30.6	7.6	(4, 8-10)
Africa	Chagga	CGA	Moshi	Narrow Bantu	Atlantic-Congo	old	25	20	5	(11)
Africa	Sandawe	SND	Sandawe	Isolate	Isolate	sad	56	44.33	9	(4, 12, 13)
Africa	Zaramo	ZRM	Zaramo	Narrow Bantu	Atlantic-Congo	zaj	24	19	5	(14, 15)
Africa	Ethiopian Jews	ETJ	Qimant	Agaw	Afro-Asiatic	ahg	39	28	7	(16)
Middle East, Europe	Yemenite Jews	YMJ	Ancient Hebrew	Semitic	Afro-Asiatic	hbo	33	27	6	(17)
Middle East, Europe	Druze	DRU	Arabic, North Levantine	Semitic	Afro-Asiatic	apc	27.5	20	7.5	(4, 18)
Middle East, Europe	Ashkenazi Jews	ASH	Ancient Hebrew	Semitic	Afro-Asiatic	hbo	33	27	6	(17)
Middle East, Europe	Roman Jews	RMJ	Ancient Hebrew	Semitic	Afro-Asiatic	hbo	33	27	6	(17)
Middle East, Europe	Chuvash	CHV	Chuvash	Turkic	Turkic	chv	31.33	22.33	9	(4, 19, 20)
Middle East, Europe	Komi-Zyrian	KMZ	Komi-Zyrian	Uralic	Uralic	kpv	33.67	26.67	7	(4, 21, 22)
Middle East, Europe	Russian, Vologda	RUV	Russian	Slavic	Indo-European	rus	37	31.67	5.33	(4, 23, 24)
Middle East, Europe	Adygei	ADY	Adyghe	Circassian	Abkhaz-Adyghe	ady	48.5	44	4.5	(4, 25)
Middle East, Europe	Sardinian	SRD	Sardinian	Romance	Indo-European	srd	33	28	5	(26)

Middle East, Europe	Hungarian	HGR	Hungarian	Uralic	Uralic	hun	45	33	12	(4, 27, 28)
Middle East, Europe	Irish	IRI	Irish	Celtic	Indo-European	gle	54	36	18	(4, 29, 30)
Middle East, Europe	Danish	DAN	Danish	Germanic	Indo-European	dan	32	16	16	(4, 31)
Middle East, Europe	Russian, Archangel'sk	RUA	Russian	Slavic	Indo-European	rus	37	31.67	5.33	(4, 23, 24)
Middle East, Europe	Finnish	FIN	Finnish	Uralic	Uralic	fin	29.33	18.33	11	(4, 32, 33)
Middle East, Europe	Khanty	KTY	Khanty	Uralic	Uralic	kca	31	18	13	(34)
Middle East, Europe	Keralites	KER	Malayalam	Dravidian	Dravidian	mal	39	29.5	9.5	(4, 35)
Asia	Yakut	YAK	Yakut	Turkic	Turkic	sah	36.33	24.33	12	(4, 36, 37)
Asia	Cambodian	CBD	Khmer	Austronesian	Austronesian	khm	38	21	17	(4, 38, 39)
Asia	Laotian	LAO	Lao	Tai-Kadai	Tai-Kadai	lao	40	28	12	(4, 40)
Asia	Japanese	JPN	Japanese	Japonic	Japonic	jpn	27.67	19.33	7	(4, 41, 42)
Asia	Korean	KOR	Korean	Koreanic	Koreanic	kor	34.67	21.33	12.67	(4, 43)
Asia	Chinese, S.F.	CHS	Cantonese	Sinitic	Sino-Tibetan	yue	30	20.33	6	(4, 44, 45)
Asia	Chinese, Taiwan	CHT	Taiwanese	Sinitic	Sino-Tibetan	nan	25	19	6	(46)
Asia	Hakka	HKA	Hakka	Sinitic	Sino-Tibetan	hak	27	18	5.67	(4, 47, 48)
Asia	Atayal	ATL	Atayal	Austronesian	Austronesian	tay	25.67	19	6.67	(4, 49)
Asia	Ami	AMI	Amis	Austronesian	Austronesian	ami	21	17.5	3.5	(4, 50)
Asia	Micronesian	MCR	Nauruan	Malayo-Polynesian	Austronesian	nau	27.5	18.5	9	(4, 51)
Asia	Nasioi Melanesian	NAS	Nasioi	South Bougainville	South Bougainville	nas	15.33	8	6.67	(4, 52, 53)
North America	Cheyenne	CHY	Cheyenne	Algonquian	Algic	chy	15	10	3	(4, 54)
North America	Pima, Arizona	PMA	O'odham	Uto-Aztecan	Uto-Aztecan	ood	26.33	19.33	7	(4, 55, 56)

North America	Pima, Mexico	PMM	Pima Bajo	Uto-Aztecan	Uto-Aztecan	pia	21.5	15.5	6	(4, 57)
North America	Mayan	MAY	Yucatec	Mayan	Mayan	yua	28.5	20	7.5	(4, 58)
South America	Quechua	QUE	Quechua	Quechuan	Quechuan	quz	29.5	25.5	4	(4, 59)
South America	Ticuna	TIC	Ticuna	Ticuna-Yuri	Ticuna-Yuri	tca	32.75	17	11.5	(4, 60-62)
South America	Rondonian Surui	SUR	Surui	Tupian	Tupian	sru	25.5	18	7.5	(4, 63)
South America	Karitiana	KAR	Karitiâna	Tupian	Tupian	ktn	25	11	14	(64)

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Supplementary Table S4. SNPs used for calculating tau scores. Listed are the 165 SNPs genotyped on the 43 populations studied.

SNP	Alleles
rs10007810	AG
rs10108270	AC
rs10236187	AC
rs1040045	AG
rs1040404	AG
rs10496971	GT
rs10497191	CT
rs10510228	AG
rs10511828	CT
rs10512572	AG
rs10513300	CT
rs10839880	CT
rs10954737	CT
rs11227699	AG
rs11652805	CT
rs12130799	AG
rs12439433	AG
rs12498138	AG
rs12544346	AG
rs12629908	AG
rs12657828	AG
rs12913832	AG
rs1296819	AC
rs1325502	AG
rs13400937	GT
rs1800414	TC
rs1834619	AG
rs1837606	CT
rs1871428	AG
rs1871534	CG
rs1876482	AG
rs1879488	AC
rs192655	AG
rs1950993	GT
rs2001907	CT
rs200354	GT
rs2024566	AG
rs2030763	AG
rs2033111	AG
rs2042762	CT
rs2070586	AG
rs2073821	CT
rs2125345	CT
rs214678	CT
rs2166624	AG
rs2196051	AG
rs2238151	AG
rs2269793	GT
rs2306040	CT
rs2330442	AG
rs2986742	CT
rs310644	CT
rs3118378	AG
rs316598	CT
rs316873	CT
rs32314	CT
rs37369	TC
rs3737576	CT
rs3745099	AG
rs3784230	AG
rs3793451	CT
rs3793791	CT
rs3811801	AG
rs3814134	AG
rs3823159	AG
rs3827760	AG
rs385194	AG
rs3907047	CT
rs3916235	CT
rs3943253	AG
rs4411548	CT
rs4458655	CT
rs4463276	AG
rs4471745	AG
rs459920	CT
rs4951629	CT
rs4955316	GT
rs4984913	AG
rs5768007	CT
rs6104567	GT
rs6422347	CT
rs6451722	AG
rs6464211	CT
rs647325	AG
rs6541030	AG
rs6548616	CT
rs6556352	CT
rs671	AG
rs6754311	CT
rs6990312	GT
rs705308	AC
rs7226659	GT
rs7238445	AG
rs7251928	AC
rs731257	AG
rs7326934	CG
rs734873	AG
rs735480	CT
rs7421394	AG
rs7554936	CT
rs917115	CT
rs9291090	AC
rs9319336	CT
rs946918	GT
rs948028	AC
rs9522149	CT
rs9530435	CT
rs9809104	CT
rs9845457	AG

rs1407434	AG
rs1426654	AG
rs1462906	CT
rs1471939	CT
rs1500127	CT
rs1513056	AG
rs1513181	AG
rs1569175	CT
rs1572018	CT
rs16891982	CG
rs1693425	TC
rs174570	CT
rs1760921	CT
rs17642714	AT
rs2357442	AC
rs2397060	CT
rs2416791	AG
rs2504853	CT
rs2532060	CT
rs2593595	AG
rs260690	AC
rs2627037	AG
rs2702414	AG
rs2814778	CT
rs2835370	CT
rs2899826	AG
rs2946788	GT
rs2966849	AG
rs4666200	AG
rs4670767	GT
rs4717865	AG
rs4746136	AG
rs4781011	GT
rs4798812	AG
rs4800105	CT
rs4821004	CT
rs4833103	CA
rs4880436	TC
rs4891825	AG
rs4908343	AG
rs4918664	AG
rs4918842	CT
rs7657799	GT
rs7722456	CT
rs772262	AG
rs7745461	AG
rs7803075	AG
rs7844723	CT
rs798443	AG
rs7997709	CT
rs8021730	GT
rs8035124	AC
rs8113143	AC
rs818386	CT
rs874299	CT
rs881728	AC

Supplementary Table S5. Jackknife sensitivity analyses. Leave-one out and leave-n out jackknifing, respectively, under both the MANCOVA and linear mixed effects models. Jackknife samples ordered by Incremental R2 in association between RU1-1 and consonants. Incremental R2 (Inc R2) is the change in adjusted R2 from the model fits over the full model and the null model where RU1-1 has no effect.

	MANCOVA model						Linear mixed effects model		
	Consonants			Vowels			Slopes		Log-likelihood ratio
Sample	Beta	Inc R2	P	Beta	Inc R2	P	Consonants	Vowels	Jackknife/Full
Full sample (n=43)	1.75	0.14	0.003	-0.61	-0.01	0.471	0.0020	-0.0023	-
Removed population									
Nasioi Melanesians	1.35	0.09	0.013	-0.71	-0.01	0.424	0.0019	-0.0023	0.97
Sandawe	1.50	0.09	0.015	-0.87	0.00	0.340	0.0016	-0.0023	0.98
Adygei	1.58	0.10	0.011	-0.25	-0.03	0.774	0.0017	-0.0019	0.97
Finns	1.67	0.12	0.005	-0.54	-0.02	0.531	0.0020	-0.0023	0.96
Danes	1.67	0.13	0.004	-0.49	-0.02	0.554	0.0022	-0.0027	0.97
Zaramo	1.71	0.13	0.004	-0.75	-0.01	0.380	0.0019	-0.0024	0.97
Ibo	1.67	0.13	0.004	-0.75	-0.01	0.374	0.0019	-0.0024	0.96
Chagga	1.72	0.13	0.004	-0.75	-0.01	0.381	0.0019	-0.0024	0.97
Yoruba	1.70	0.13	0.004	-0.53	-0.02	0.530	0.0020	-0.0023	0.96
Rondonian Surui	1.70	0.13	0.004	-0.62	-0.01	0.472	0.0020	-0.0023	0.96
Khanty	1.71	0.13	0.004	-0.52	-0.02	0.541	0.0020	-0.0023	0.96
Chuvash	1.74	0.13	0.004	-0.59	-0.01	0.493	0.0019	-0.0023	0.96
Keralites	1.73	0.13	0.004	-0.66	-0.01	0.441	0.0020	-0.0023	0.97
Russian, Archangel'sk	1.74	0.14	0.004	-0.50	-0.02	0.560	0.0020	-0.0022	0.96
Micronesians	1.77	0.14	0.003	-0.57	-0.02	0.511	0.0020	-0.0023	0.97
Koreans	1.75	0.14	0.003	-0.65	-0.01	0.440	0.0020	-0.0024	0.96
Russian, Vologda	1.74	0.14	0.004	-0.53	-0.02	0.527	0.0020	-0.0023	0.96
Druze	1.75	0.14	0.003	-0.61	-0.01	0.475	0.0021	-0.0022	0.96
Yakut	1.75	0.14	0.003	-0.62	-0.01	0.460	0.0020	-0.0023	0.96
Hakka	1.75	0.14	0.003	-0.66	-0.01	0.438	0.0020	-0.0024	0.96
Ethiopian Jews	1.76	0.14	0.003	-0.60	-0.01	0.489	0.0020	-0.0023	0.97

Chinese, S.F.	1.76	0.14	0.003	-0.62	-0.01	0.467	0.0020	-0.0023	0.96
Ashkenazi Jews	1.76	0.14	0.003	-0.59	-0.01	0.483	0.0020	-0.0023	0.96
Cambodians	1.77	0.14	0.003	-0.49	-0.02	0.549	0.0020	-0.0023	0.97
Atayal	1.77	0.14	0.003	-0.64	-0.01	0.453	0.0020	-0.0024	0.97
Ami	1.76	0.14	0.003	-0.59	-0.01	0.469	0.0020	-0.0023	0.96
Chinese, Taiwan	1.77	0.14	0.003	-0.56	-0.02	0.509	0.0020	-0.0022	0.96
Komi	1.78	0.14	0.003	-0.65	-0.01	0.450	0.0020	-0.0024	0.97
Roman Jew	1.78	0.14	0.003	-0.54	-0.02	0.526	0.0020	-0.0022	0.97
Maya	1.78	0.14	0.003	-0.61	-0.01	0.477	0.0020	-0.0023	0.96
Karitiana	1.72	0.14	0.004	-0.49	-0.02	0.549	0.0020	-0.0023	0.96
Ticuna	1.83	0.14	0.003	-0.85	0.00	0.325	0.0020	-0.0026	0.99
Hausa	1.78	0.15	0.002	-0.60	-0.01	0.480	0.0020	-0.0023	0.97
Pima, Mexico	1.82	0.15	0.003	-0.56	-0.02	0.519	0.0020	-0.0021	0.97
Pima, Arizona	1.82	0.15	0.002	-0.62	-0.01	0.469	0.0021	-0.0024	0.97
Hungarians	1.82	0.15	0.002	-0.53	-0.02	0.532	0.0021	-0.0022	0.97
Laotians	1.85	0.15	0.002	-0.52	-0.02	0.537	0.0022	-0.0019	0.98
Japanese	1.95	0.15	0.002	-0.60	-0.02	0.506	0.0020	-0.0021	1.00
Irish	1.81	0.15	0.002	-0.49	-0.02	0.550	0.0021	-0.0018	0.96
Yemenite Jews	1.99	0.16	0.002	-0.47	-0.02	0.601	0.0020	-0.0020	1.00
Cheyenne	1.77	0.16	0.002	-0.59	-0.01	0.469	0.0020	-0.0023	0.96
Quechua	1.89	0.16	0.001	-0.77	0.00	0.359	0.0021	-0.0025	0.98
Sardinian	2.00	0.16	0.001	-1.03	0.01	0.244	0.0020	-0.0027	1.00
Removed region									
Africa (n=7)	1.22	0.05	0.056	-1.31	0.03	0.182	0.0014	-0.0024	0.78
Americas (n=8)	1.47	0.10	0.012	-1.22	0.02	0.203	0.0020	-0.0025	0.80
EastAsia (n=16)	1.66	0.12	0.015	-0.51	-0.03	0.599	0.0021	-0.0021	0.63
Europe (n=12)	1.90	0.13	0.030	0.47	-0.04	0.694	0.0021	-0.0013	0.52

Supplementary Table S6. RU1-1 Univariate regression using a quadratic term.

Model	**R2**	**p-value**	**AIC**	**Significance (p-value) in ANOVA vs 3 PCs Model**
3 PCs	0.3	0.001207	-51.61	N/A
Linear RU1-1	0.4	$5.275e^{-05}$	-55.19	0.0028
Quadratic RU1-1	0.5	8.015e-^{06}	-60.67	0.0005