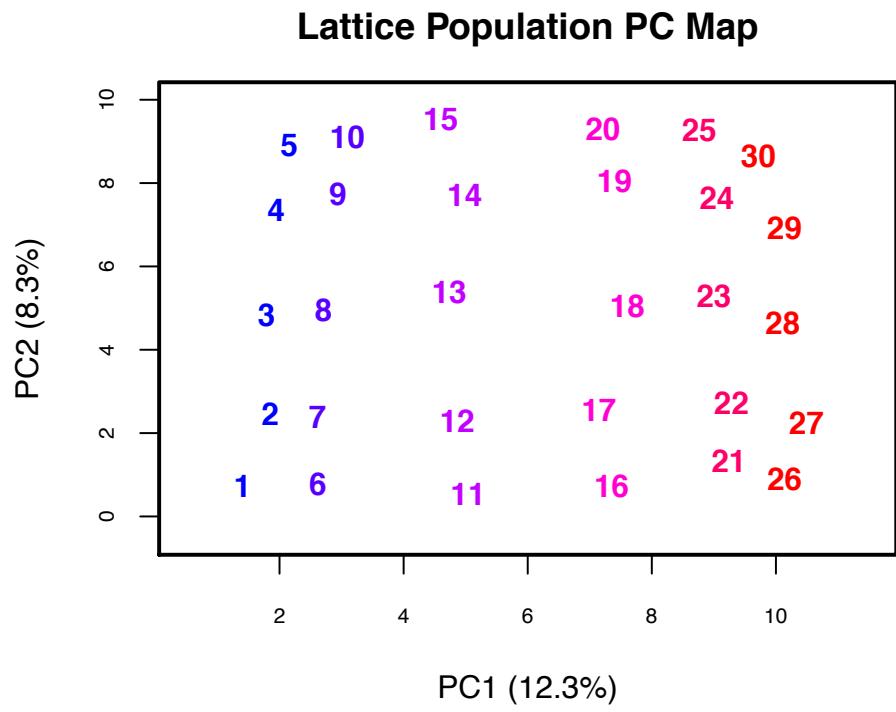
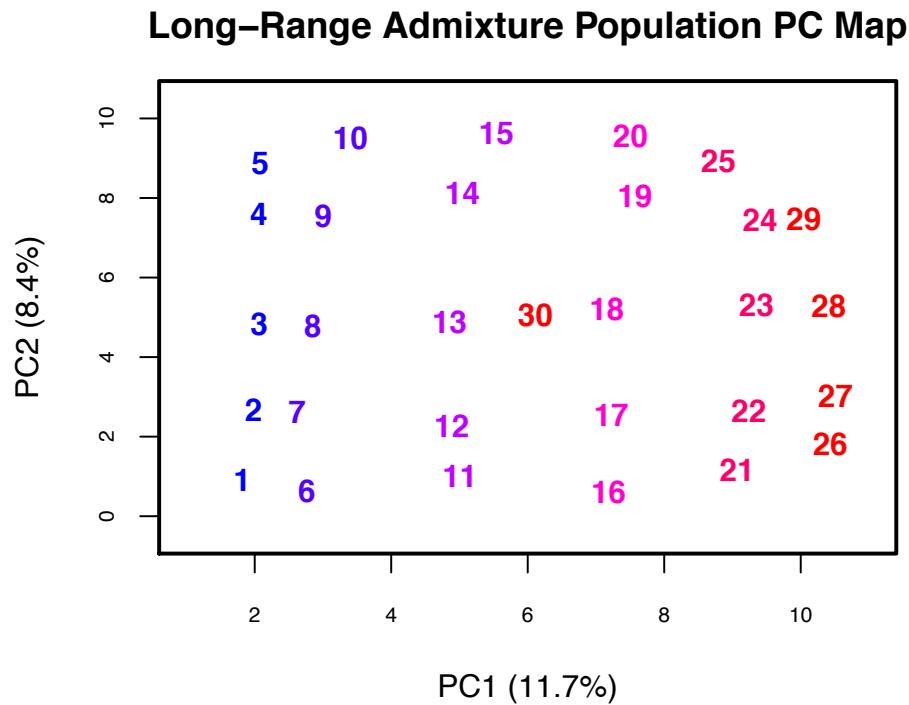


Figure S1. Decays in covariance for four different simulation scenarios (from top to bottom: simple lattice; lattice with barrier; lattice with expansion; lattice with admixture). Left column: sample covariance plotted against observed pairwise distance. Right column: sample covariance plotted against inferred geogenetic distance.



(a)



(b)

Figure S2. Plots of the first two Principal Component axes (with variance explained labeled on the relevant axes) of the mean-centered covariance matrix from simulated spatial scenarios. a) the basic lattice scenario shown in 1a. b) the lattice scenario with admixture from Population 1 into Population 30, shown in 2a

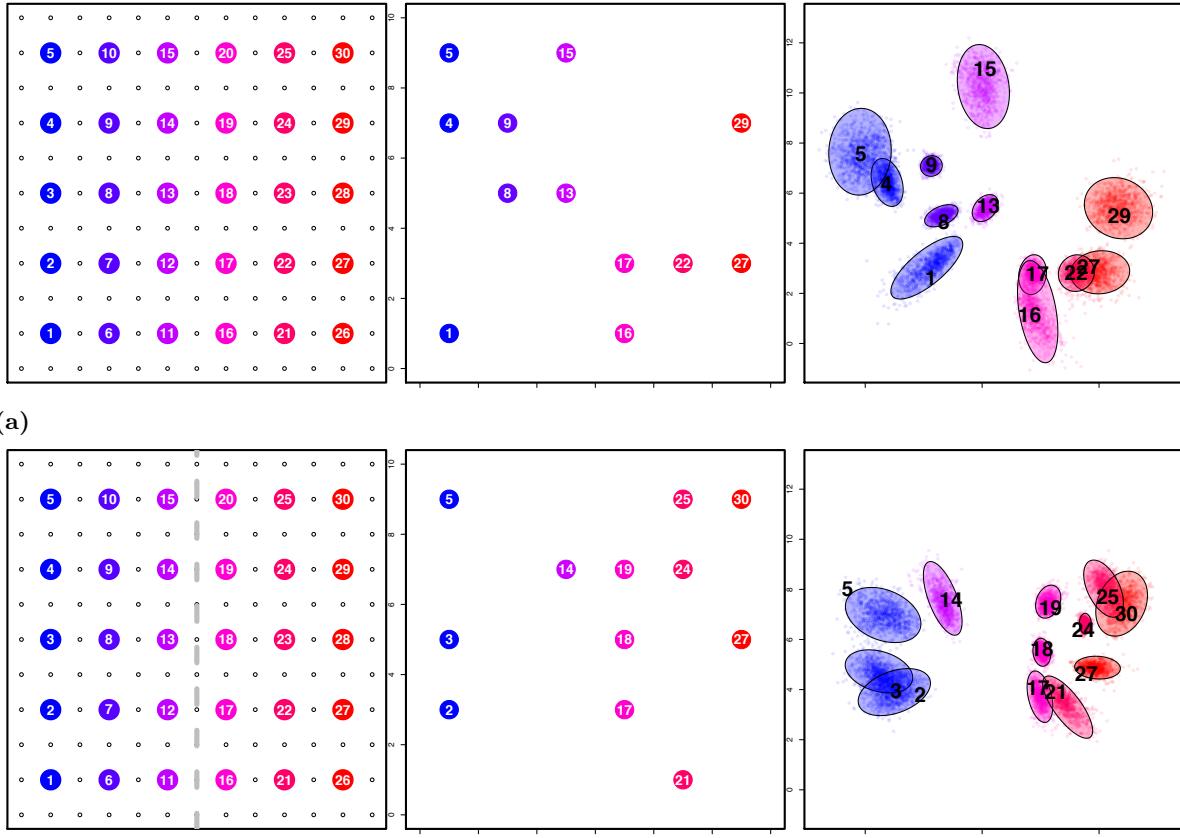
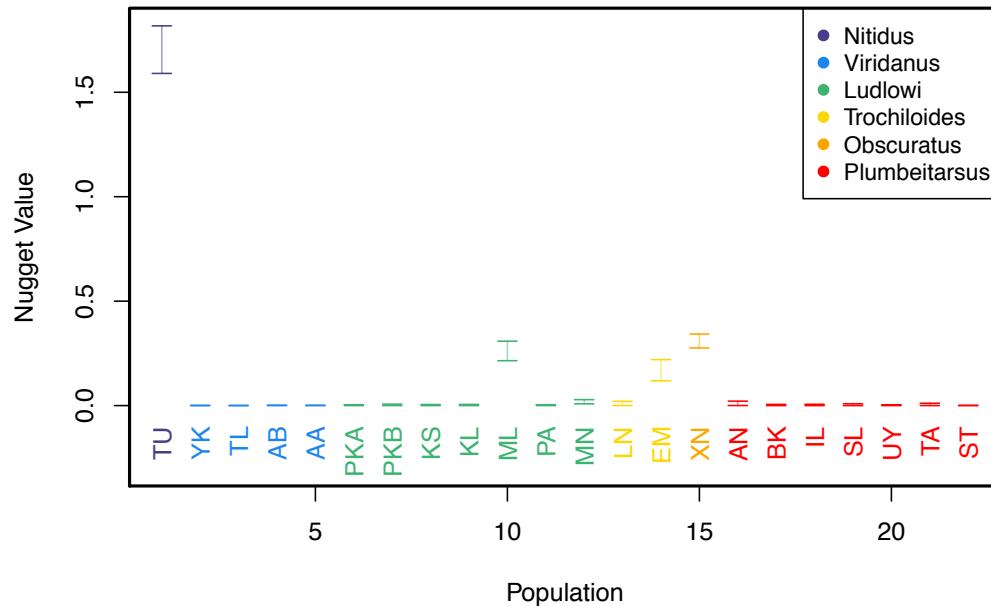


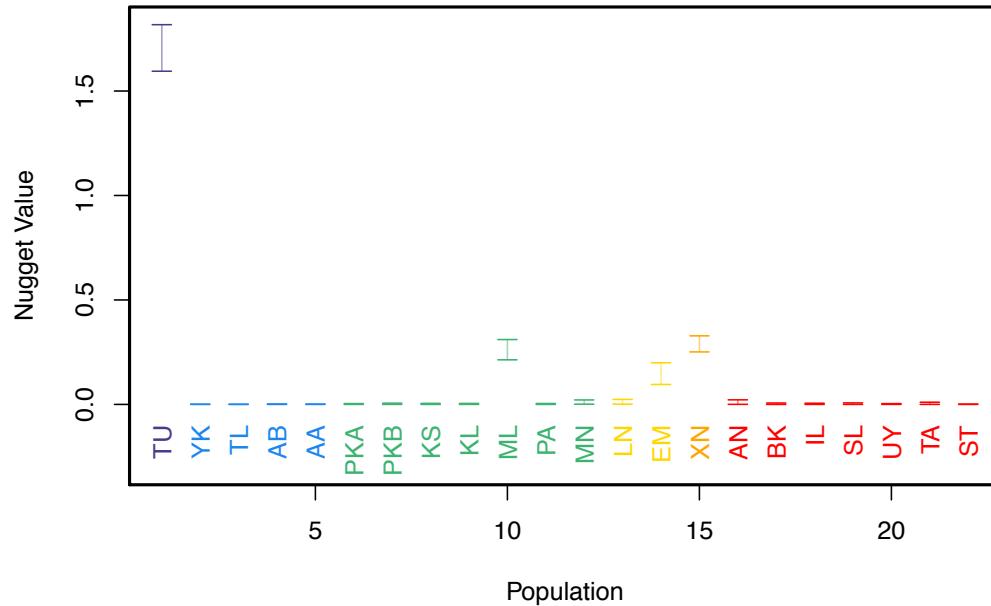
Figure S3. The effect of uneven sampling on inference of geogenetic maps. a) inference using a dataset with a random subsample of 12 populations from the simple lattice scenario with nearest neighbor migration; b) inference using a dataset with a random subsample of 12 populations from the barrier scenario with nearest neighbor migration and a barrier down the center line of longitude. Ellipses denote the 95% credible interval on estimated geogenetic locations.

Warbler Population Nuggets: No Admixture



(a)

Warbler Population Nuggets: Admixture



(b)

Figure S4. Credible intervals on estimated warbler population nugget parameters. a) analysis without admixture; b) analysis with admixture.

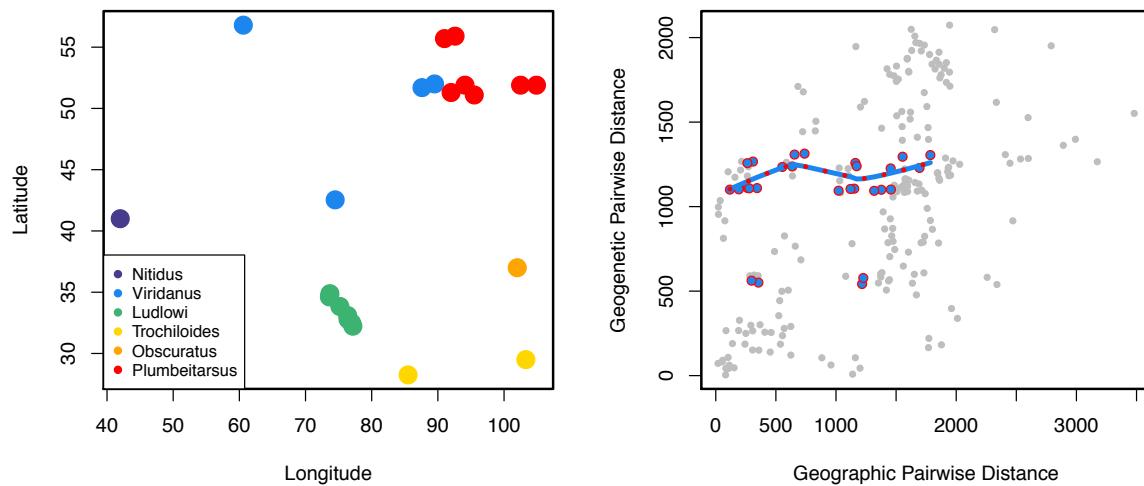


Figure S5. Comparing geographic to geogenetic pairwise distance between warbler populations: a) observed population coordinates; b) pairwise geographic (great-circle) distance between populations compared to that between their geogenetic locations. The highlighted points show distances between populations from the *plumbeitarsus* and *viridanus* subspecies. Notice that, regardless of their observed distance, their geogenetic separations are roughly constant, and much larger than the geographic distance between them.

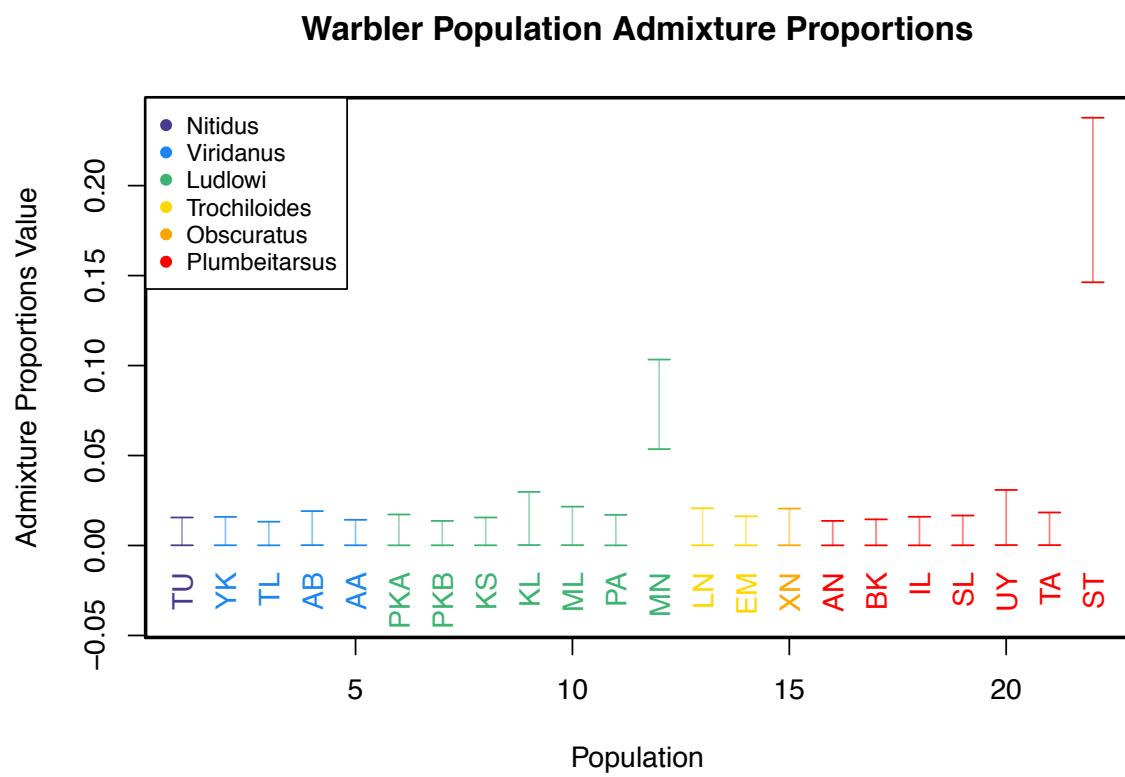
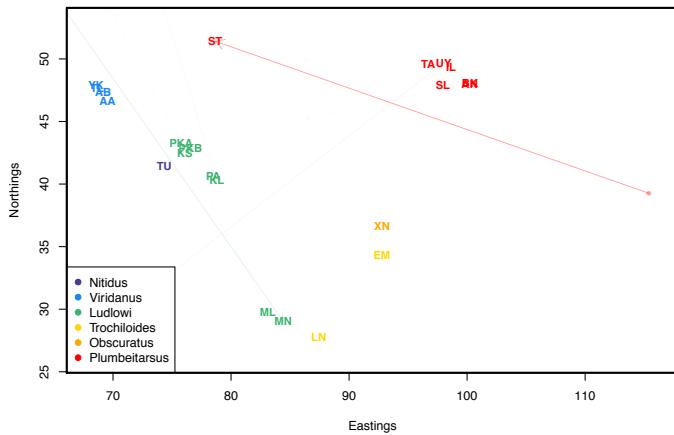
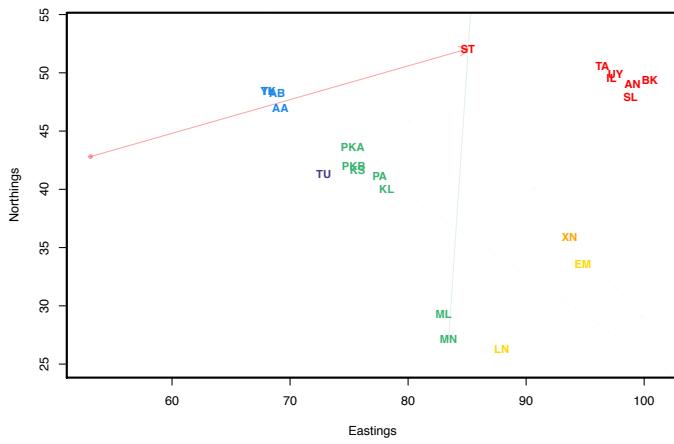


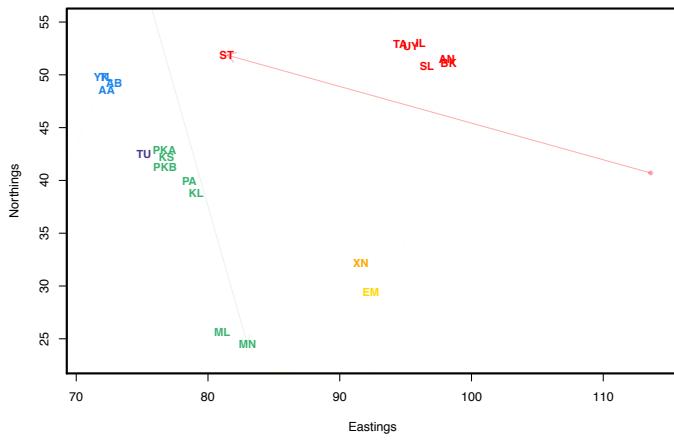
Figure S6. Credible intervals on estimated warbler population admixture proportion parameters.



(a)

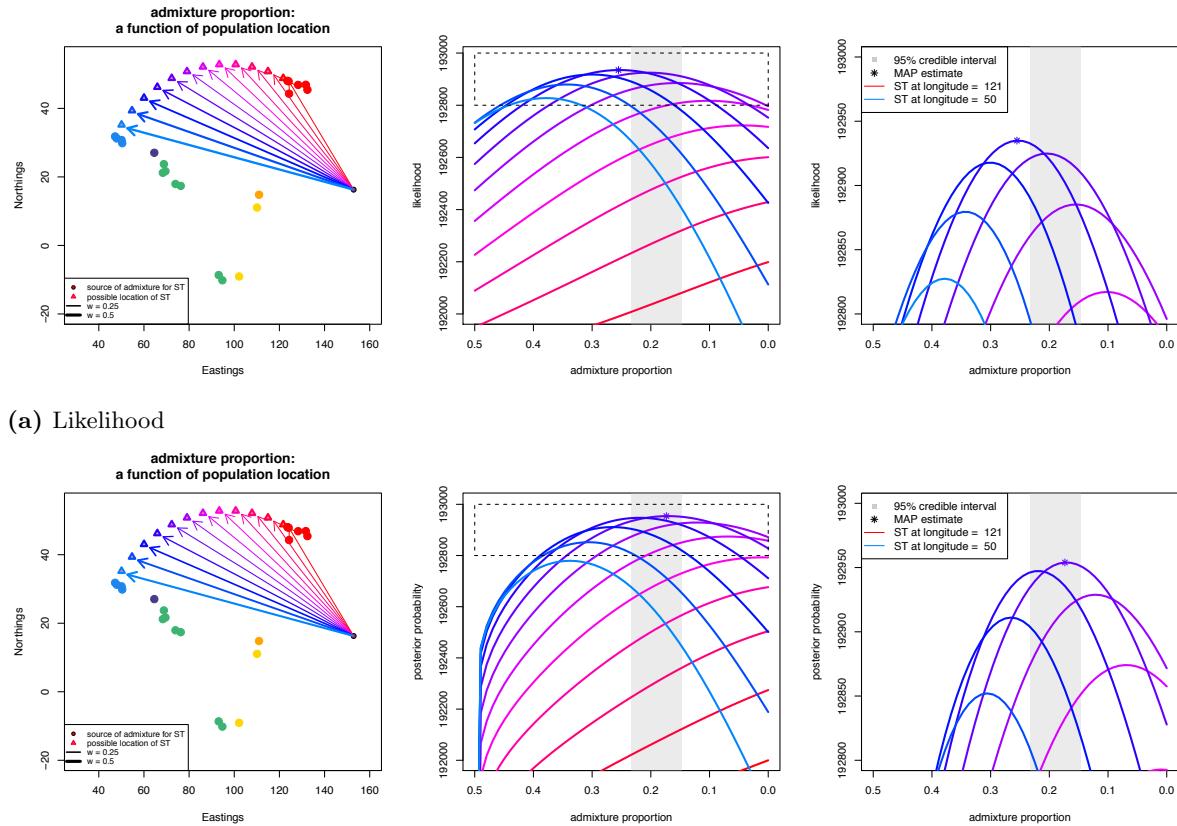


(b)



(c)

Figure S7. Comparison of inferred maps from three independent analyses. (a,b) Results from analysis using observed locations as priors on population locations. (c) Results from analysis using random, uniformly distributed locations within the observed range of latitude and longitude as priors on population locations.



(b) Posterior probability

Figure S8. Likelihood surfaces for different placements of population ST between *plumbeitarsus* and *viridanus* clusters: (a) log likelihood surface; (b) posterior probability surface, incorporating the priors. The maximum a posteriori estimate (MAP) is shown as a star.

Warbler Individual Admixture Proportions

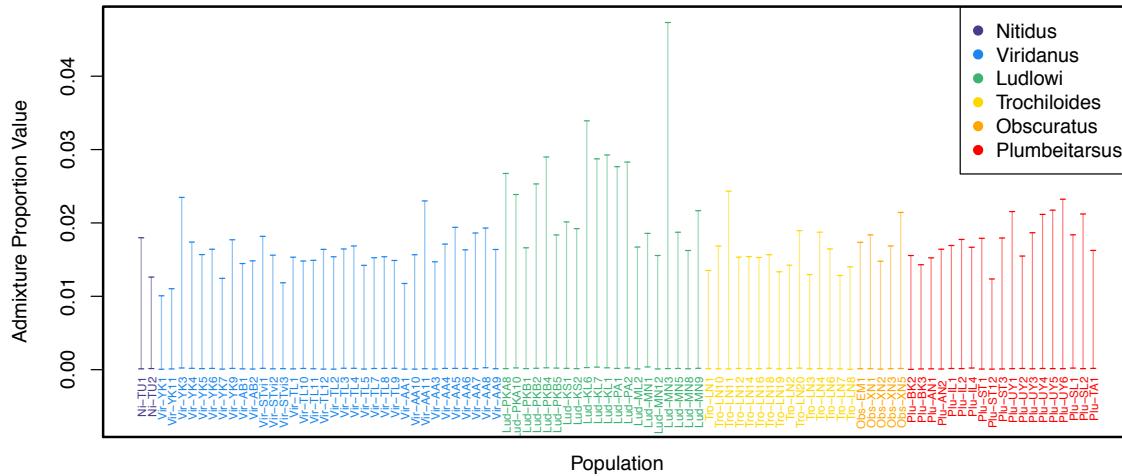
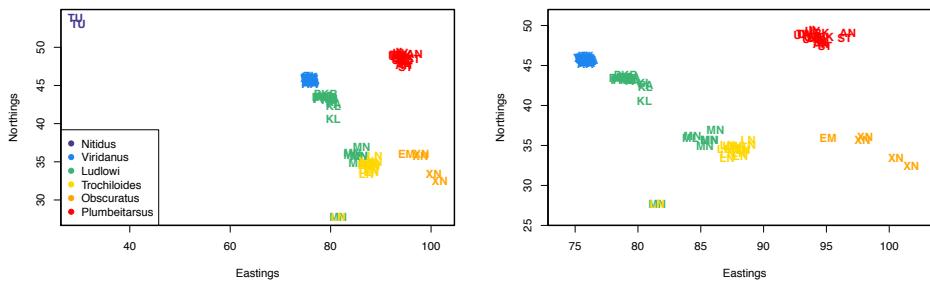


Figure S9. Credible intervals on estimated warbler individual admixture proportion parameters.



(a) Warbler individuals map, no admixture **(b)** Close-up of non-*nitidus* samples

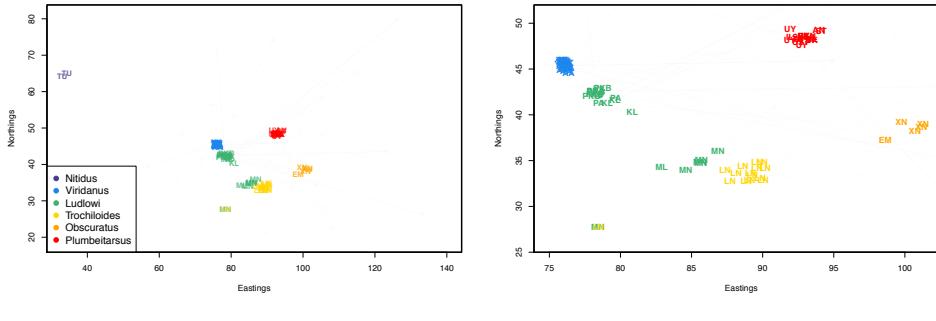
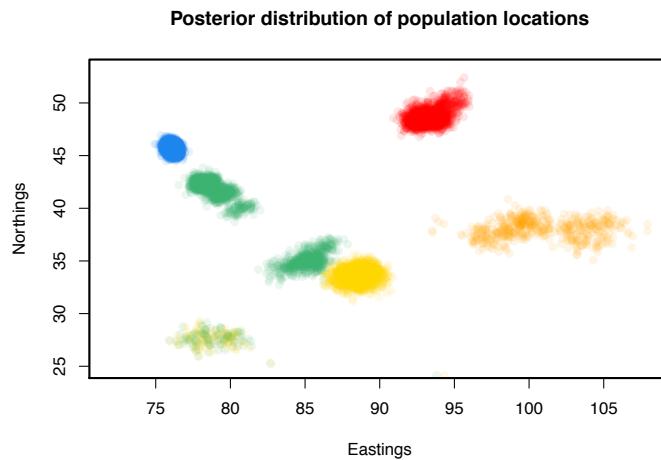
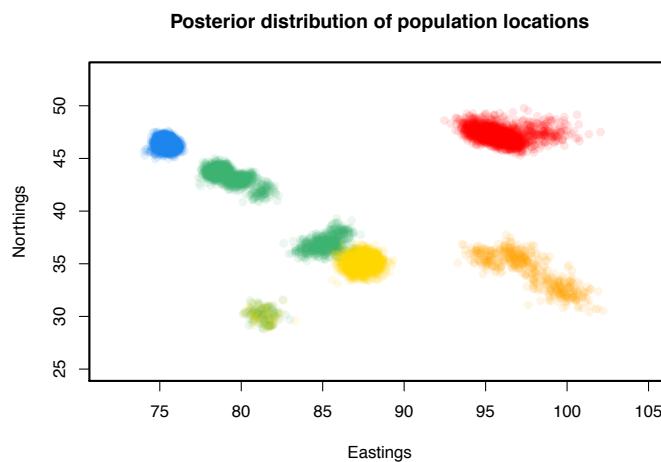


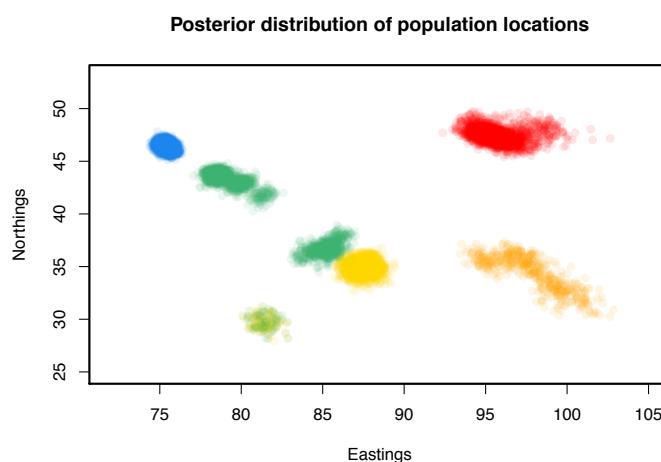
Figure S10. Inferred maps for warbler individuals, colored by subspecies under analyses with and without admixture inference. a) map inferred without admixture; (b) close-up of all non-*nitidus* samples in non-admixture map; c) map inferred with admixture; d) close-up of all non-*nitidus* samples in the admixture map.



(a) random location prior



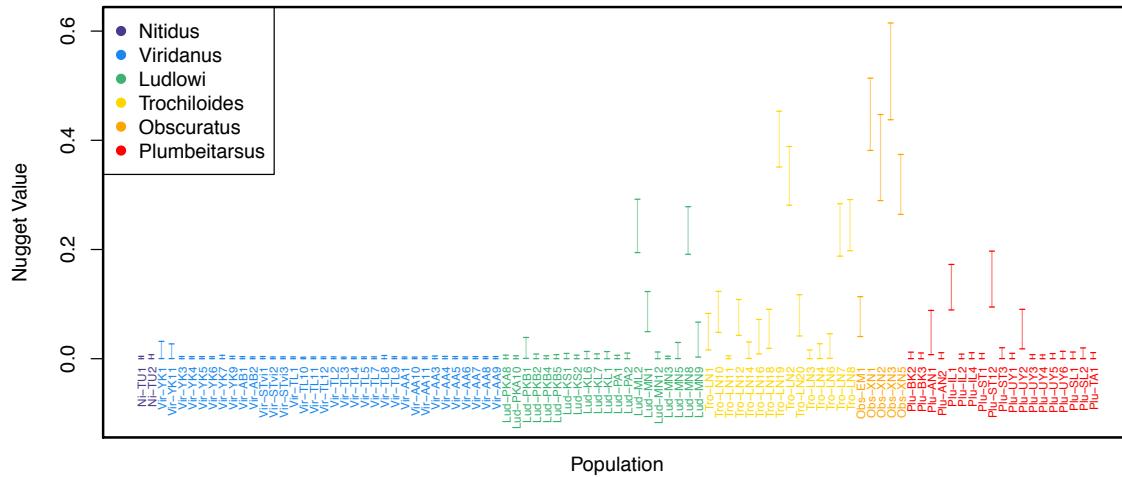
(b) geographic location prior



(c) geographic location prior

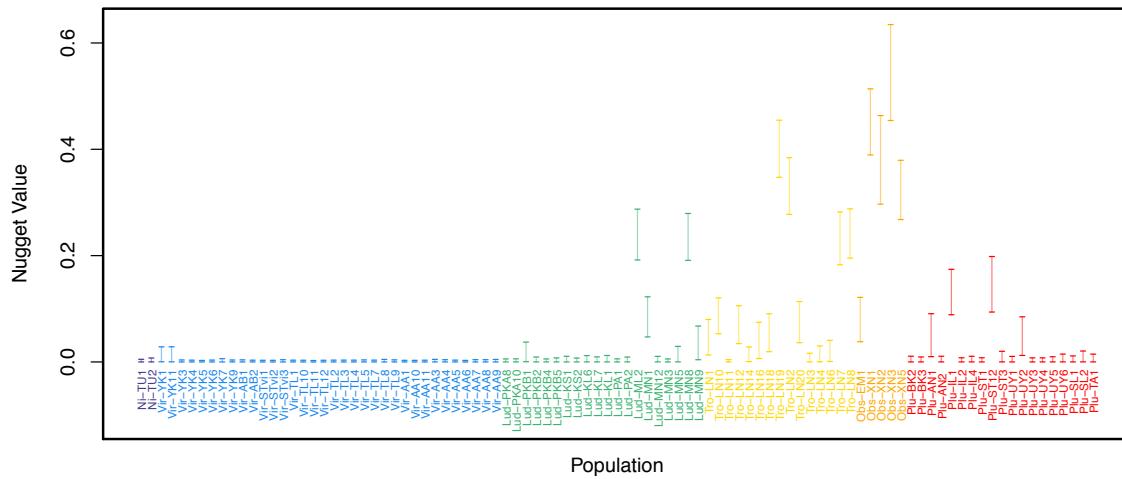
Figure S11. Maps of the posterior distributions on population locations in three separate SpaceMix analyses on the warbler individual dataset.

**Warbler Individual Nuggets:
No Admixture**



(a)

Warbler Individual Nuggets: Admixture



(b)

Figure S12. Credible intervals on estimated warbler individual nugget parameters. a) analysis without admixture; b) analysis with admixture.

Warbler Individuals: Isolation by Distance

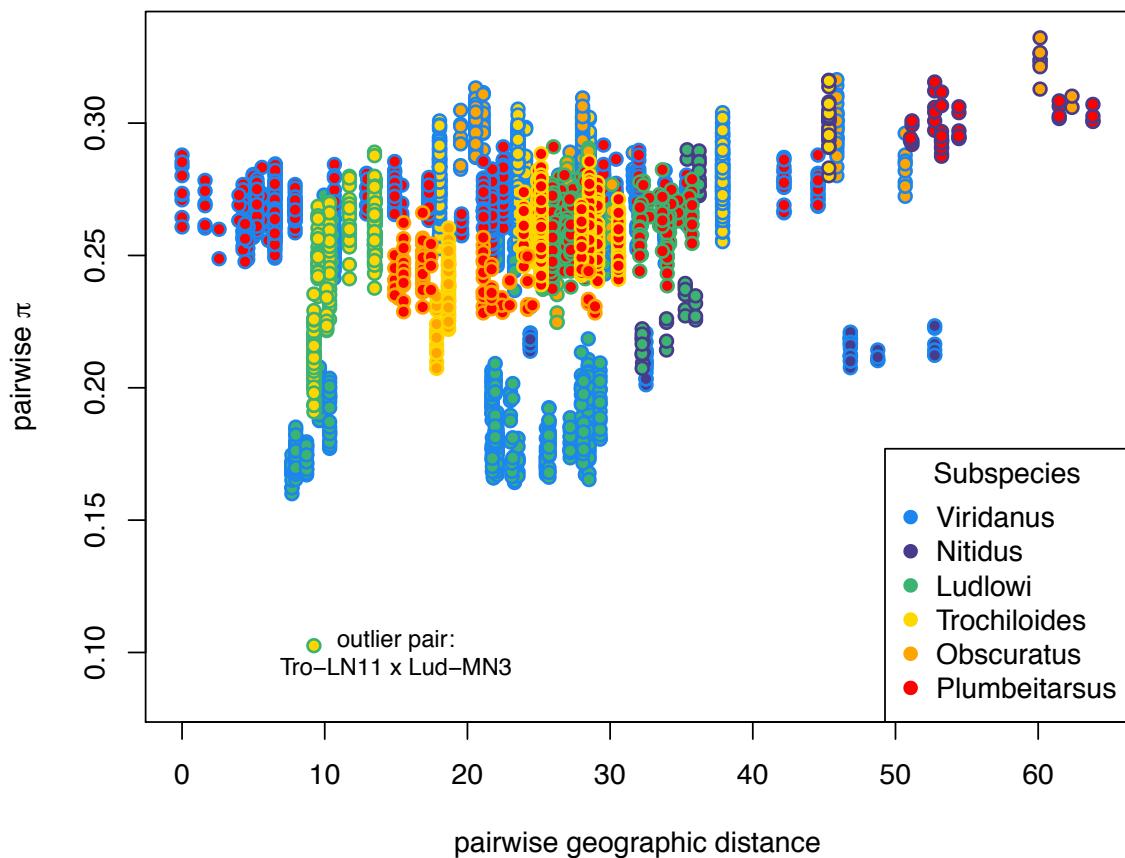


Figure S13. Mean pairwise sequence divergence at polymorphic sites calculated between all pairs of individuals from different subspecies, and colored by the subspecies to which each individual in the comparison is drawn. Note that individuals Tro-LN11 and Lud-MN3 have sequence divergence that is unusually low relative to that of other comparisons between individuals from the same two subspecies.

Warbler Individual PC Map

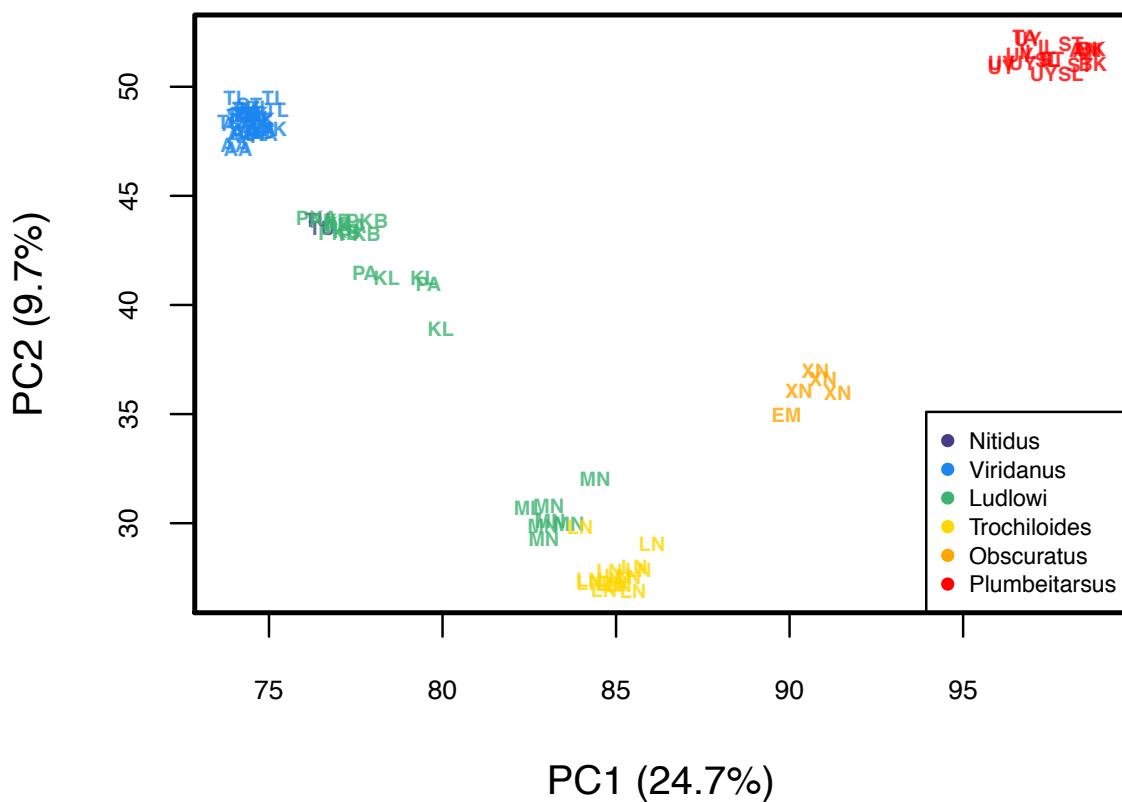
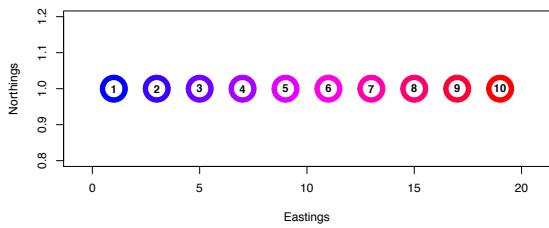
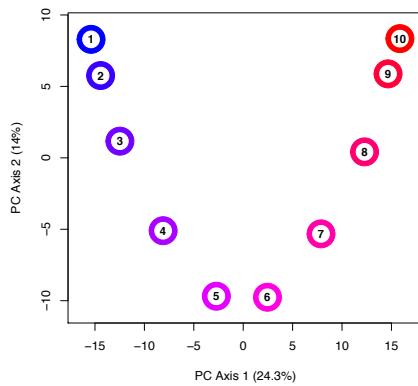


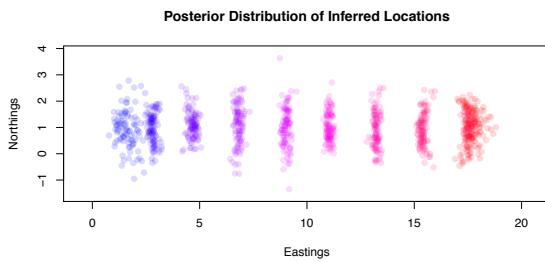
Figure S14. The map of warbler individuals derived from a Principal Components analysis. The PC coordinates have undergone a full Procrustes transformation around the actual sampling coordinates.



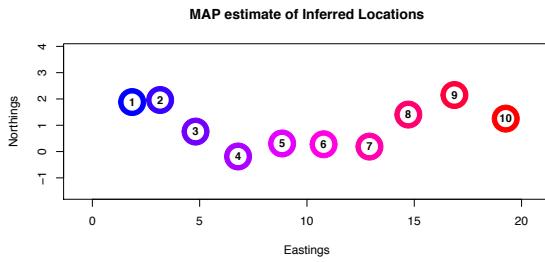
(a) populations on a line



(b) PCA map of line scenario

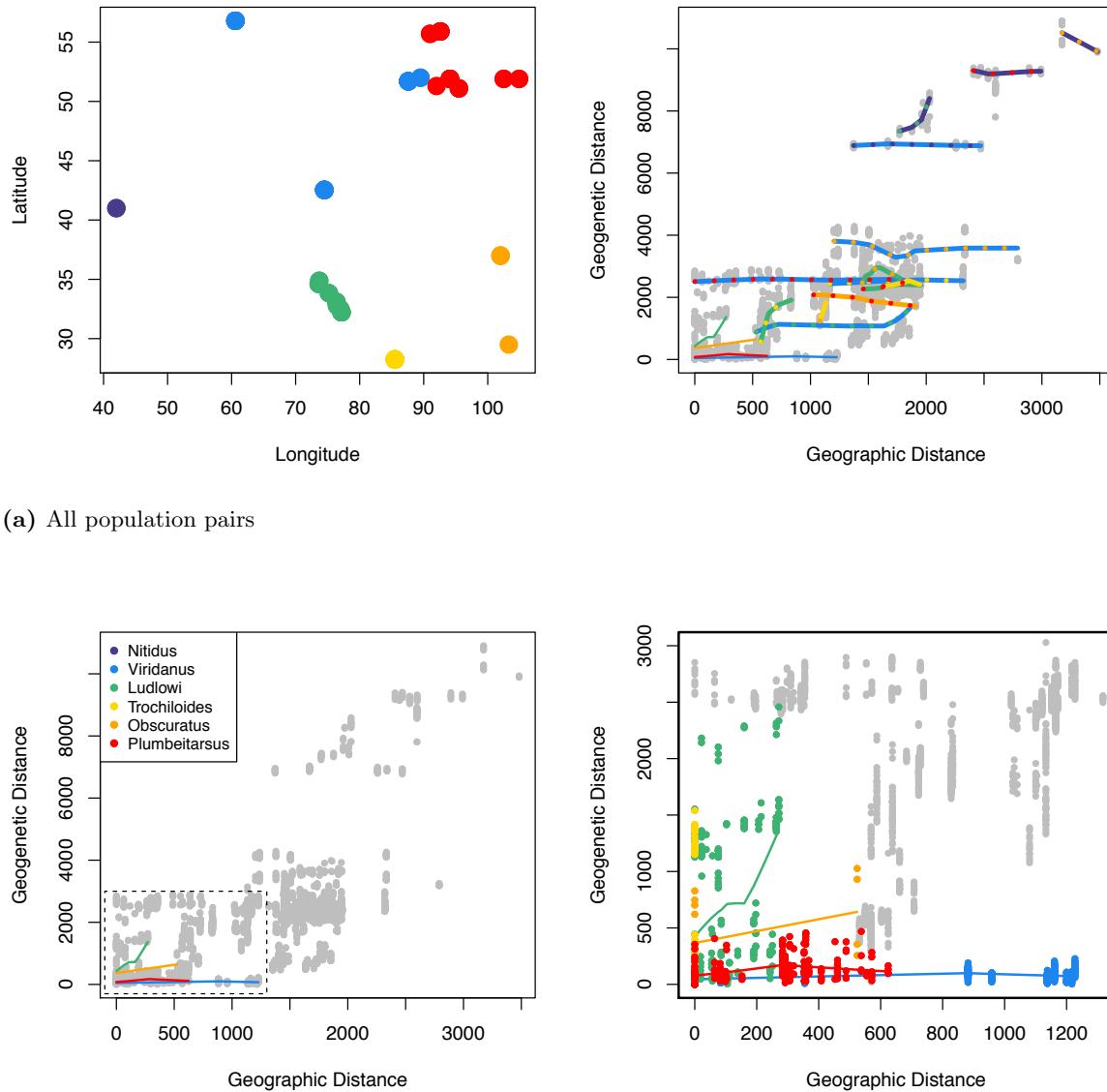


(c) posterior from SpaceMix map of line scenario



(d) MAP estimate from SpaceMix map of line scenario

Figure S15. Simulation scenario of populations on a line, contrasting PCA-based inference and SpaceMix inference. a) Scenario used to simulate data in a spatial coalescent framework with nearest-neighbor migration; b) PCA map of allele frequencies, plotting PC axis 1 against PC axis 2, forming a ‘U’ shape; c) Posterior distribution of SpaceMix location inference, forming a rough line; d) snapshot of the MAP draw from the posterior, again showing a rough line.



(b) Just within population comparisons

Figure S16. Comparing geographic pairwise distance to geogenetic pairwise distance between warbler individuals, (a) between and (b) within subspecies populations.

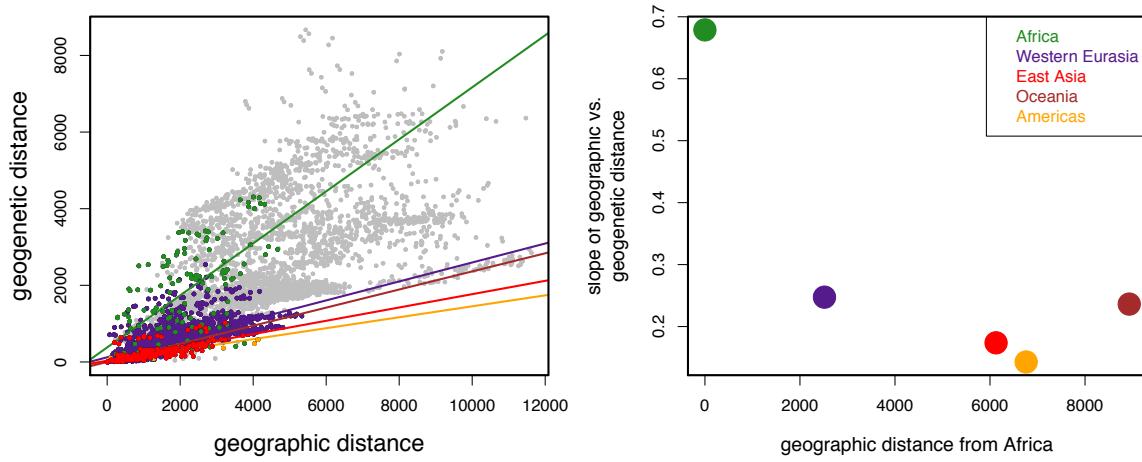
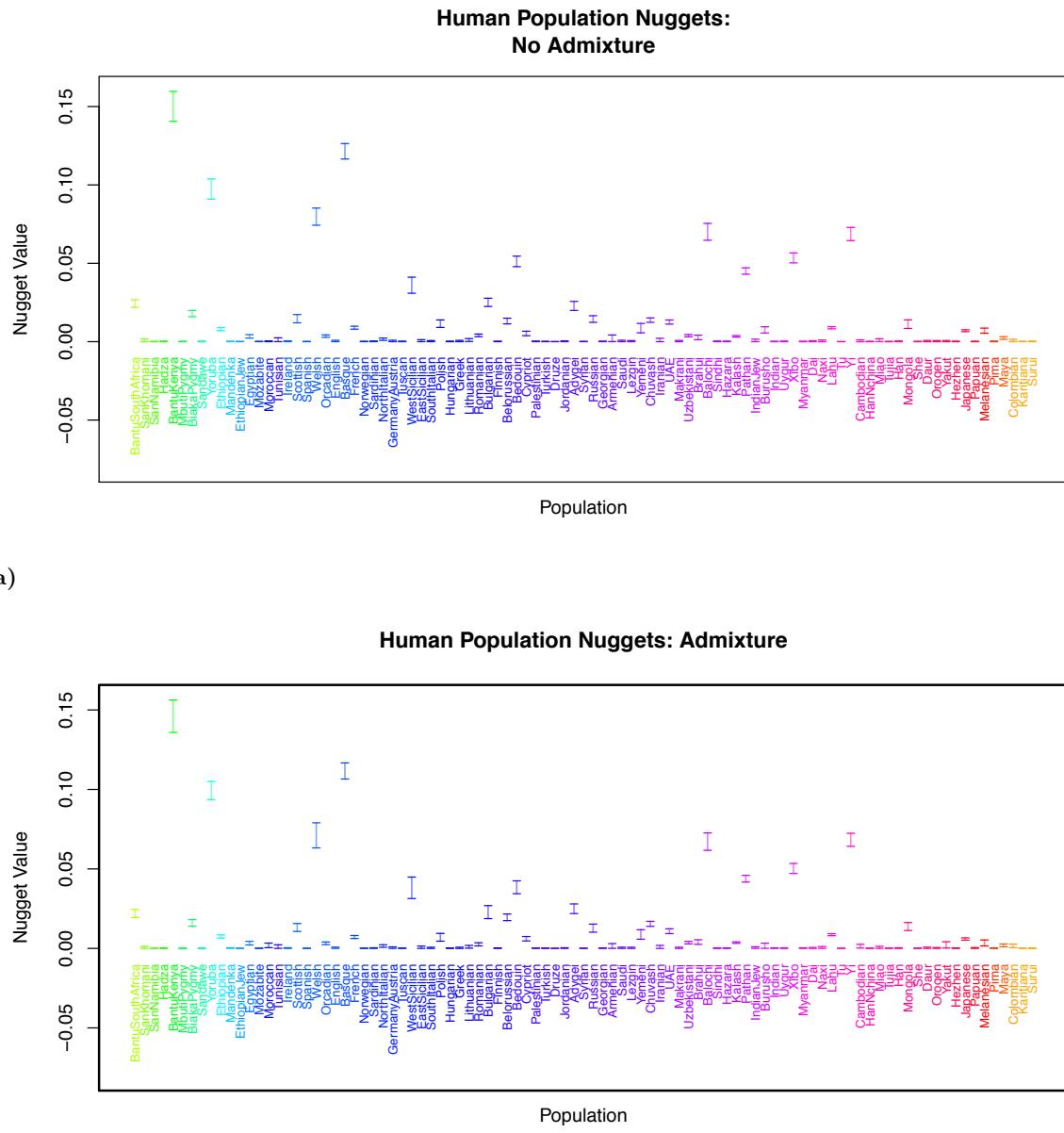
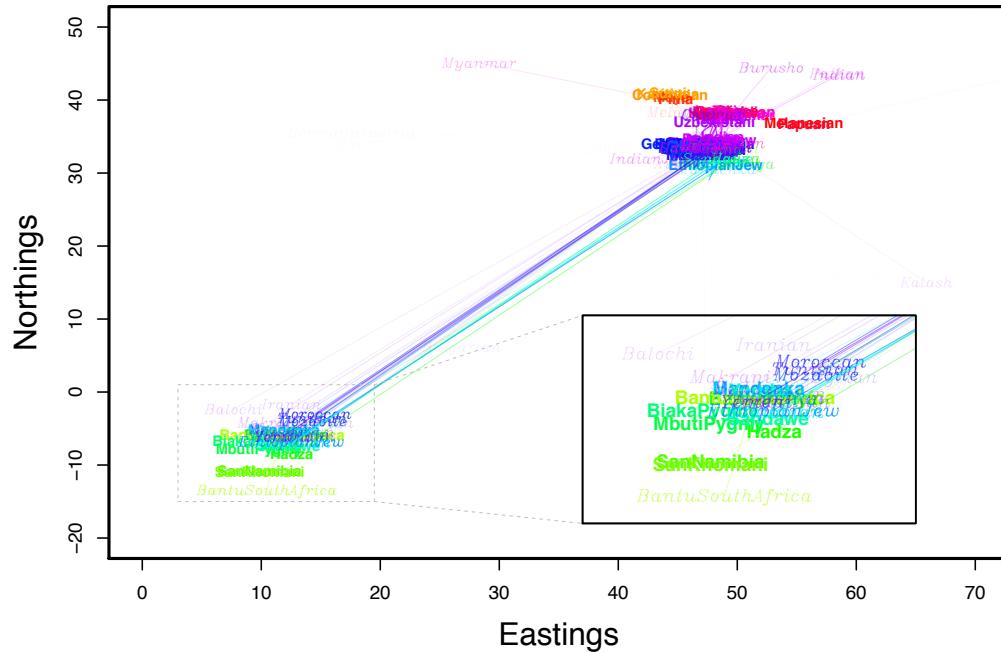


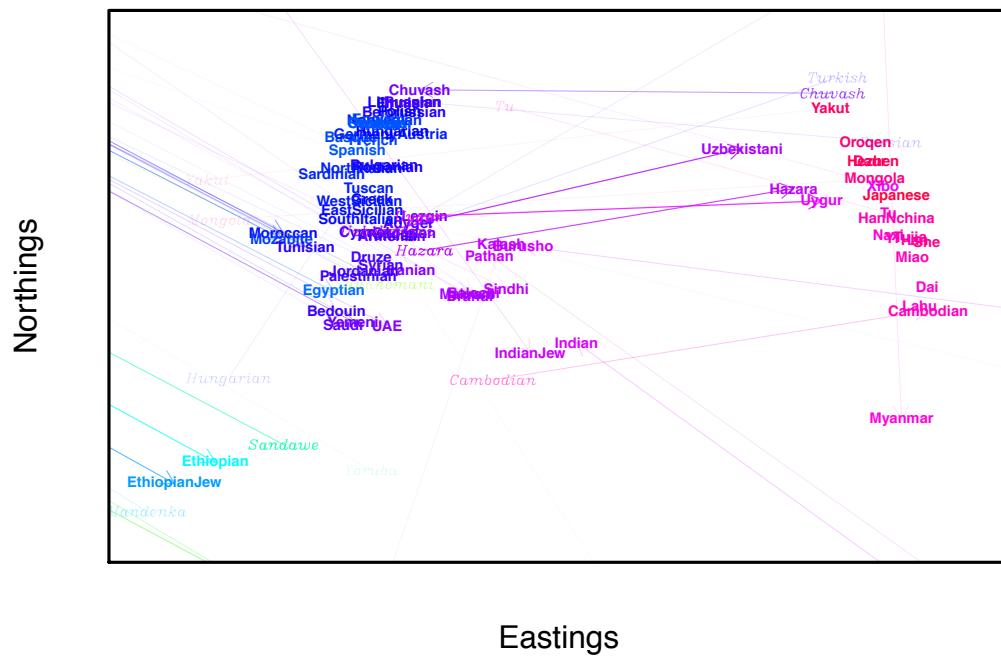
Figure S17. Comparison of geographic pairwise distance to geogenetic pairwise distance between human populations, colored by continent from which populations were sampled (i.e., two populations sampled from Africa are green). Eurasia is divided into Western Eurasia and East Asia.



(b)
Figure S18. Credible intervals on estimated human sample nugget parameters. a) analysis without admixture; a) analysis with admixture.

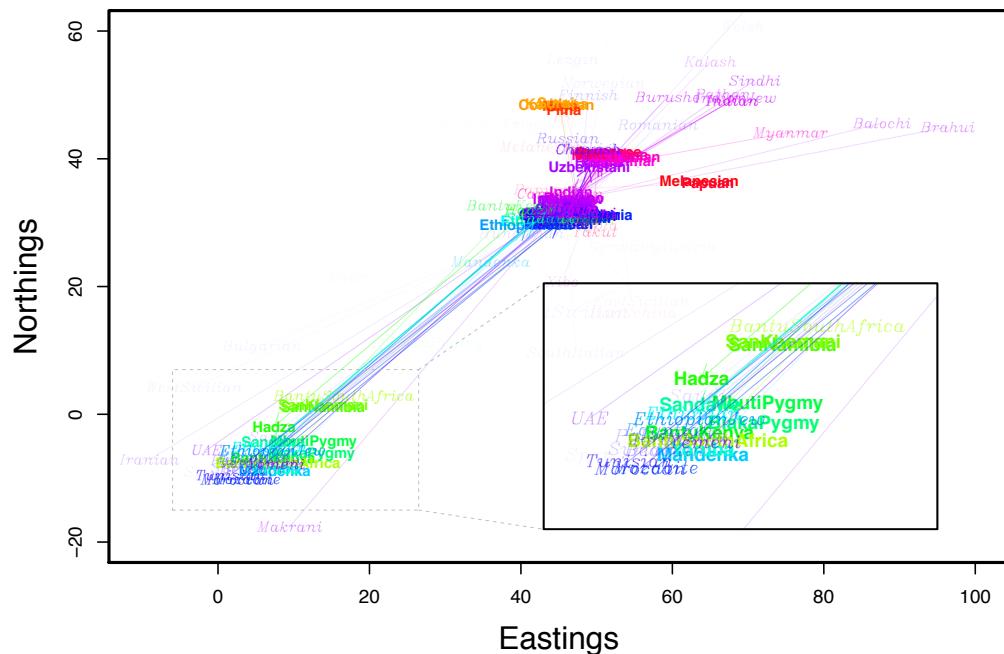


(a) Inferred map of human populations

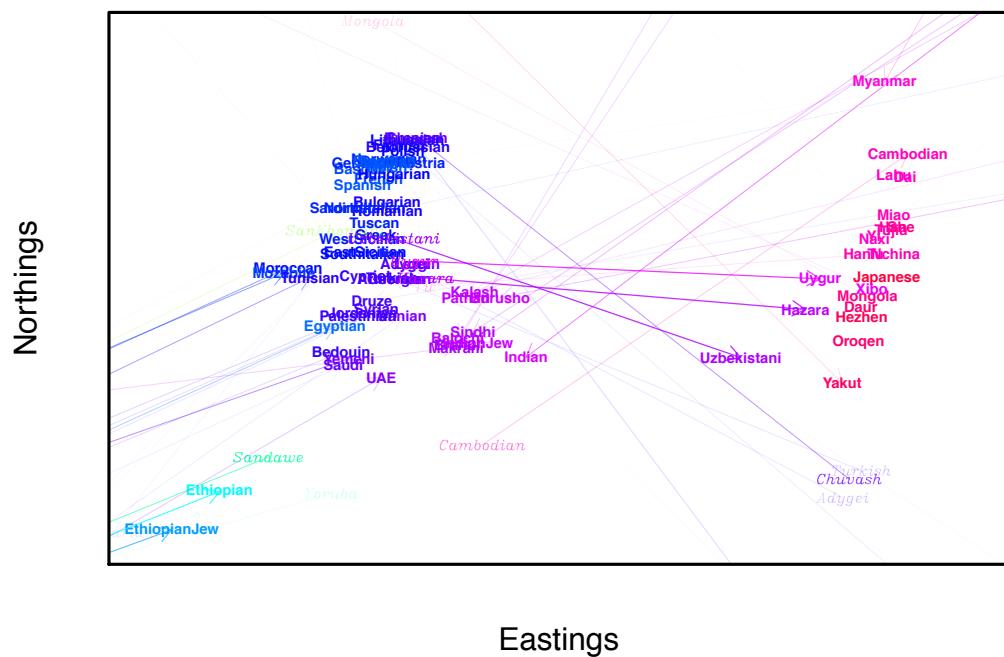


(b) Close-up of Eurasian populations

Figure S19. Map of human populations from a different SpaceMix analysis (“Real.Prior1” – inferred with admixture), using real geographic coordinates as population location priors. a) complete map; b) close-up of Eurasian populations



(a) Inferred map of human populations



(b) Close-up of Eurasian populations

Figure S20. Map of human populations from another SpaceMix analysis (“Real_Prior2”, inferred with admixture), using real geographic coordinates as population location priors. a) complete map; b) close-up of Eurasian populations

PCA map of human samples

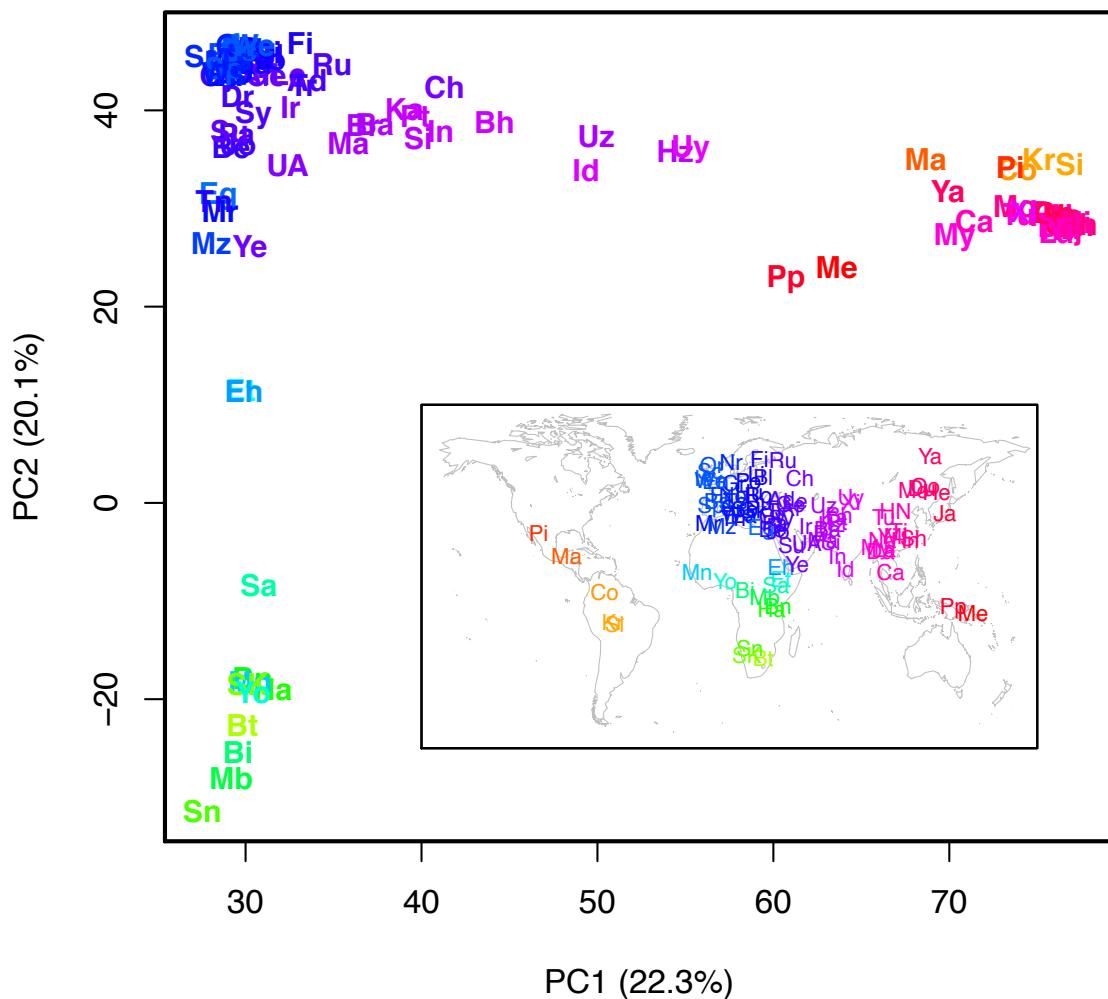


Figure S21. PCA map of human samples used in SpaceMix analyses. The PC coordinates have undergone a full Procrustes transformation around the actual sampling coordinates (shown in the inset map).

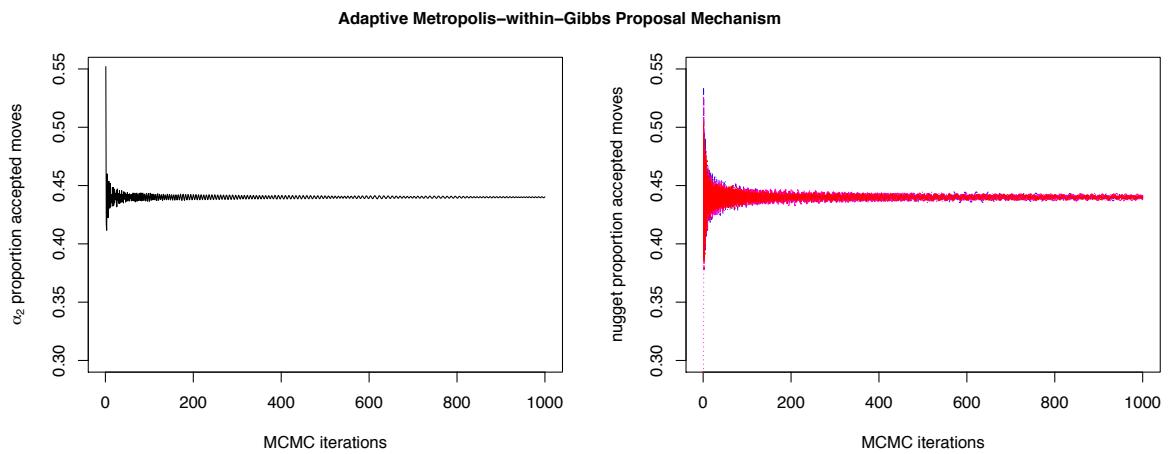


Figure S22. Example parameter acceptance proportions for the α_2 parameter and the nugget parameter, η , using the adaptive Metropolis-within-Gibbs proposal mechanism.

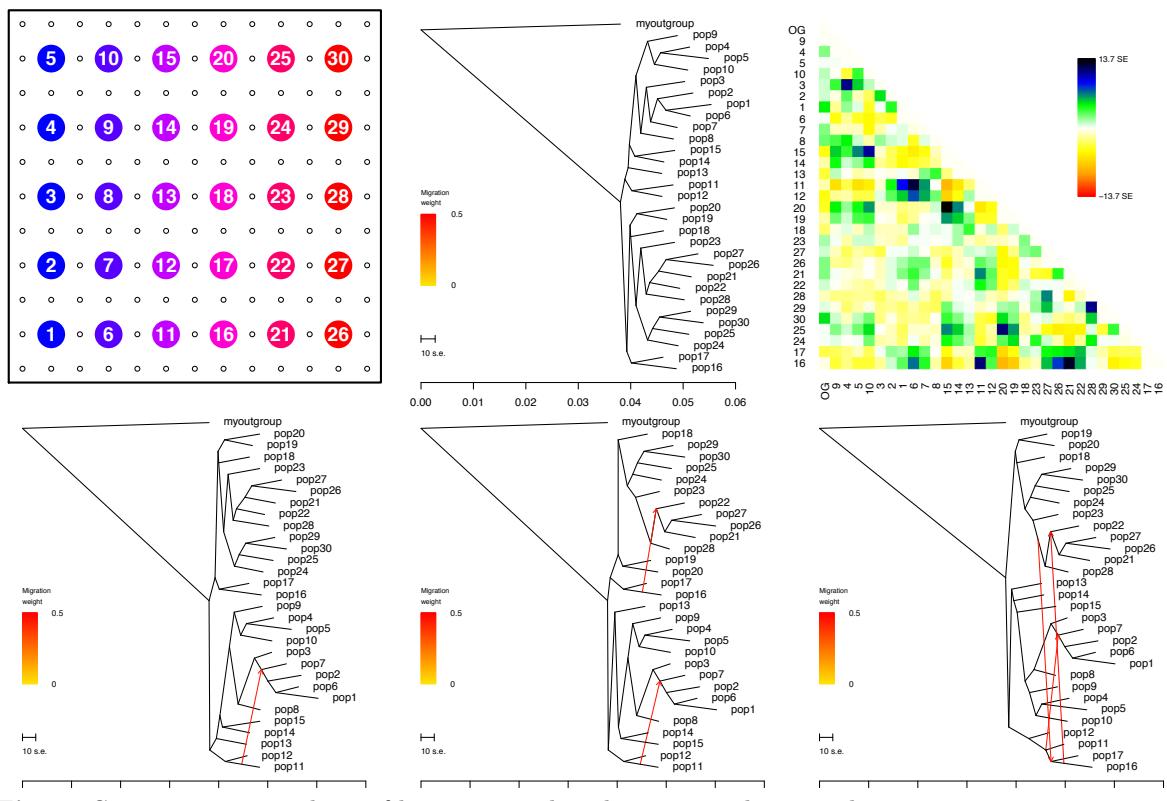


Figure S23. TreeMix analysis of lattice spatial coalescent simulation. The tree, residual covariance matrix, and first three migration admixture arrows are shown

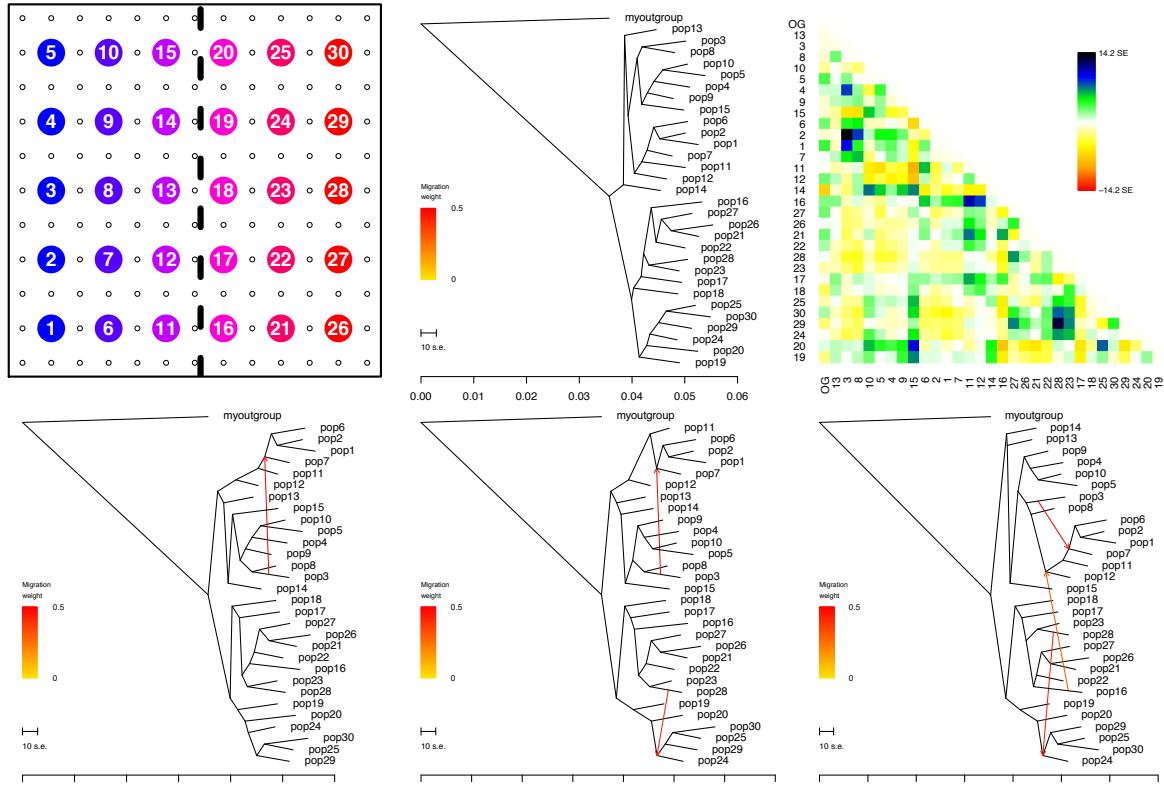


Figure S24. TreeMix analysis of lattice spatial coalescent simulation with a barrier..

The tree, residual covariance matrix, and first three migration admixture arrows are shown

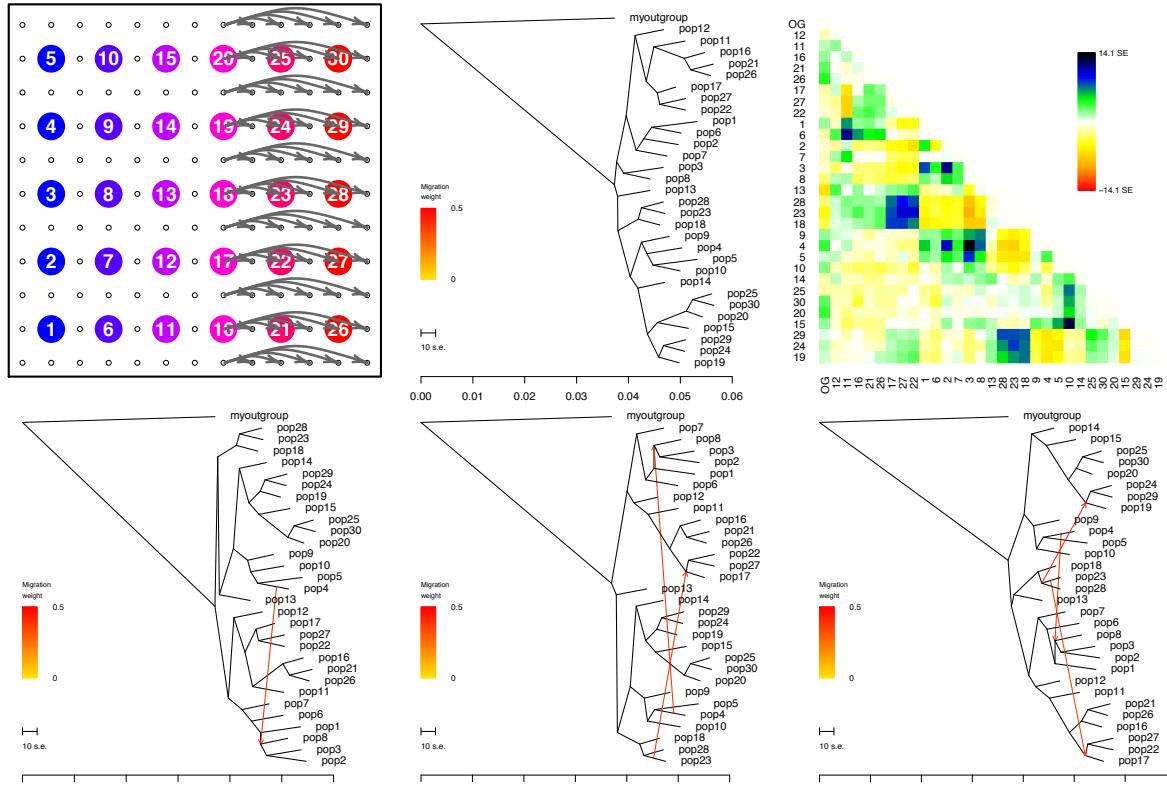


Figure S25. TreeMix analysis of lattice spatial coalescent simulation with an expansion event. The tree, residual covariance matrix, and first three migration admixture arrows are shown

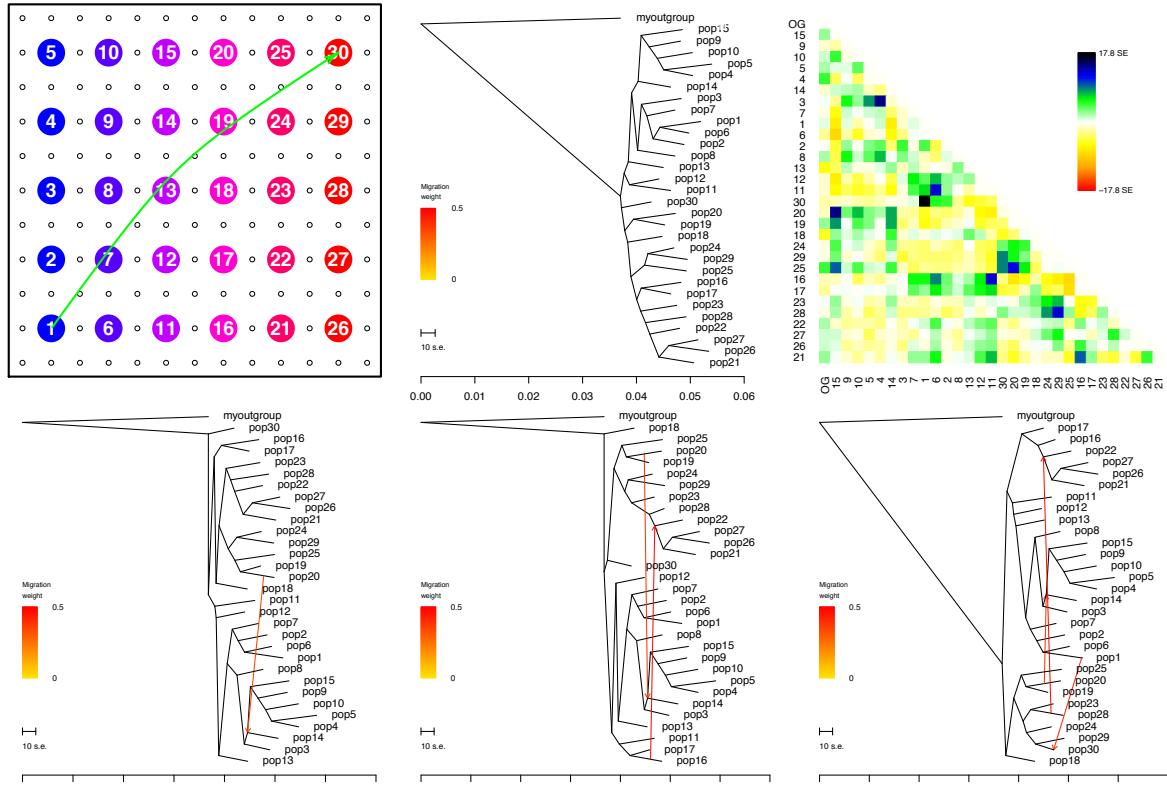


Figure S26. TreeMix analysis of lattice spatial coalescent simulation with a long-range admixture event. The tree, residual covariance matrix, and first three migration admixture arrows are shown

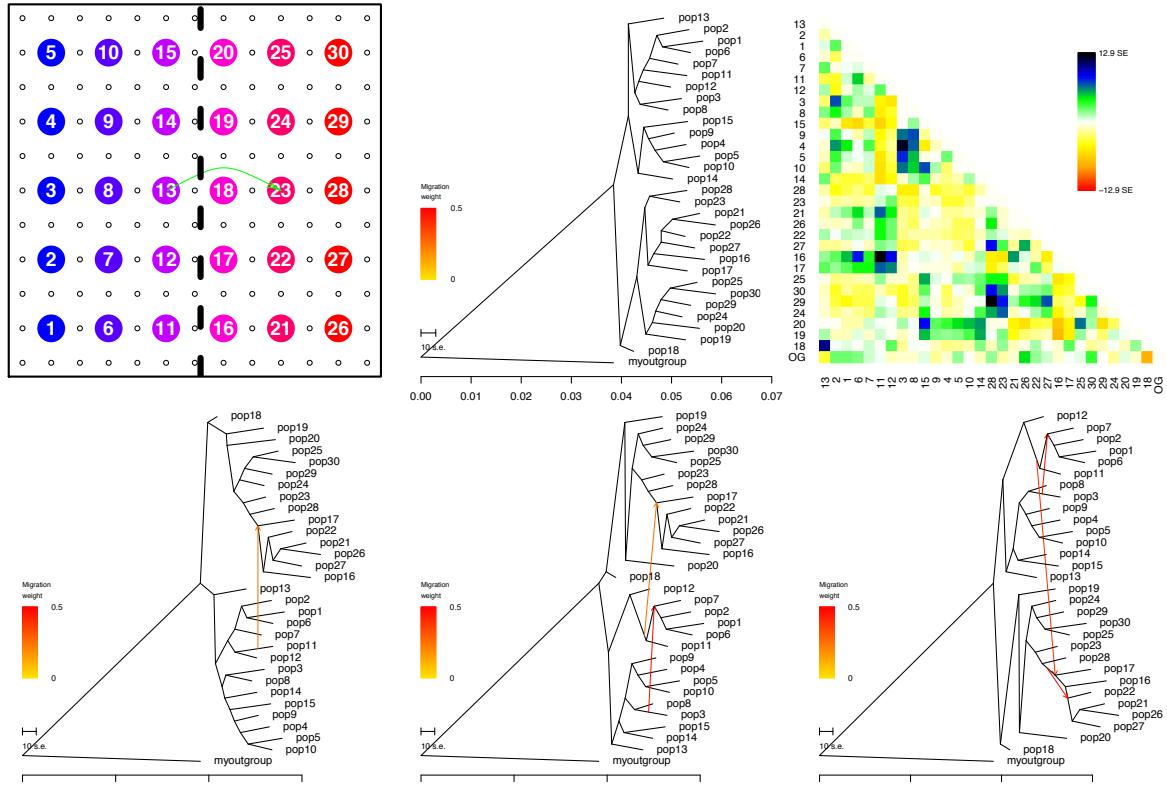


Figure S27. TreeMix analysis of lattice spatial coalescent simulation with a barrier and short-range admixture event. The tree, residual covariance matrix, and first three migration admixture arrows are shown

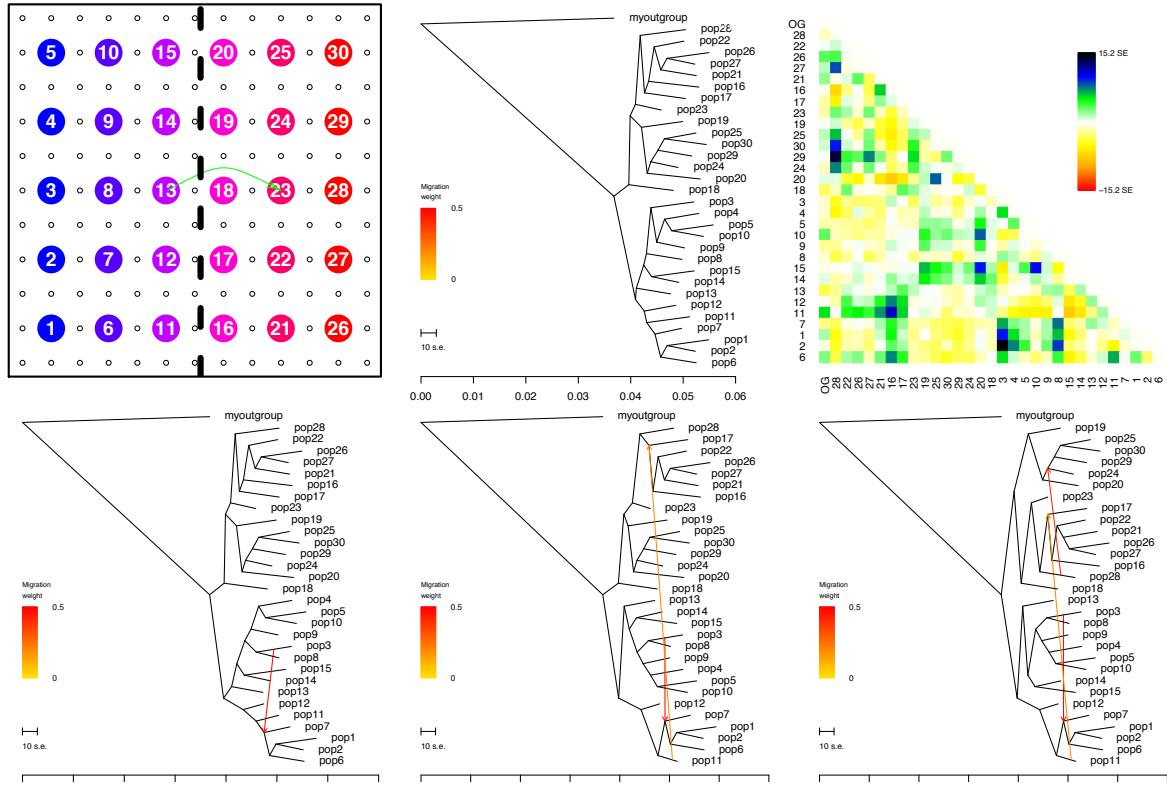


Figure S28. TreeMix analysis of lattice spatial coalescent simulation with a barrier and mid-range admixture event. The tree, residual covariance matrix, and first three migration admixture arrows are shown

Sample	Subspecies	Longitude	Latitude
Vir-YK1	<i>Viridanus</i>	60.60	60.60
Vir-YK11	<i>Viridanus</i>	60.60	60.60
Vir-YK3	<i>Viridanus</i>	60.60	60.60
Vir-YK4	<i>Viridanus</i>	60.60	60.60
Vir-YK5	<i>Viridanus</i>	60.60	60.60
Vir-YK6	<i>Viridanus</i>	60.60	60.60
Vir-YK7	<i>Viridanus</i>	60.60	60.60
Vir-YK9	<i>Viridanus</i>	60.60	60.60
Vir-AB1	<i>Viridanus</i>	89.50	89.50
Vir-AB2	<i>Viridanus</i>	89.50	89.50
Vir-STv1	<i>Viridanus</i>	92.60	92.60
Vir-STv2	<i>Viridanus</i>	92.60	92.60
Vir-STv3	<i>Viridanus</i>	92.60	92.60
Vir-TL1	<i>Viridanus</i>	87.60	87.60
Vir-TL10	<i>Viridanus</i>	87.60	87.60
Vir-TL11	<i>Viridanus</i>	87.60	87.60
Vir-TL12	<i>Viridanus</i>	87.60	87.60
Vir-TL2	<i>Viridanus</i>	87.60	87.60
Vir-TL3	<i>Viridanus</i>	87.60	87.60
Vir-TL4	<i>Viridanus</i>	87.60	87.60
Vir-TL5	<i>Viridanus</i>	87.60	87.60
Vir-TL7	<i>Viridanus</i>	87.60	87.60
Vir-TL8	<i>Viridanus</i>	87.60	87.60
Vir-TL9	<i>Viridanus</i>	87.60	87.60
Vir-AA1	<i>Viridanus</i>	74.48	74.48
Vir-AA10	<i>Viridanus</i>	74.48	74.48
Vir-AA11	<i>Viridanus</i>	74.48	74.48
Vir-AA3	<i>Viridanus</i>	74.48	74.48
Vir-AA4	<i>Viridanus</i>	74.48	74.48
Vir-AA5	<i>Viridanus</i>	74.48	74.48
Vir-AA6	<i>Viridanus</i>	74.48	74.48
Vir-AA7	<i>Viridanus</i>	74.48	74.48
Vir-AA8	<i>Viridanus</i>	74.48	74.48
Vir-AA9	<i>Viridanus</i>	74.48	74.48
Ni-TU1	<i>Nitidus</i>	42.00	42.00
Ni-TU2	<i>Nitidus</i>	42.00	42.00
Lud-PKA8	<i>Ludlowi</i>	73.69	73.69
Lud-PKA10	<i>Ludlowi</i>	73.69	73.69
Lud-PKB1	<i>Ludlowi</i>	73.61	73.61
Lud-PKB2	<i>Ludlowi</i>	73.61	73.61
Lud-PKB4	<i>Ludlowi</i>	73.61	73.61
Lud-PKB5	<i>Ludlowi</i>	73.61	73.61
Lud-KS1	<i>Ludlowi</i>	75.19	75.19
Lud-KS2	<i>Ludlowi</i>	75.19	75.19
Lud-KL6	<i>Ludlowi</i>	76.37	76.37
Lud-KL7	<i>Ludlowi</i>	76.37	76.37
Lud-KL1	<i>Ludlowi</i>	76.37	76.37
Lud-PA1	<i>Ludlowi</i>	76.97	76.97
Lud-PA2	<i>Ludlowi</i>	76.97	76.97
Lud-ML2	<i>Ludlowi</i>	76.43	76.43
Lud-MN1	<i>Ludlowi</i>	77.16	77.16
Lud-MN12	<i>Ludlowi</i>	77.16	77.16
Lud-MN3	<i>Ludlowi</i>	77.16	77.16
Lud-MN5	<i>Ludlowi</i>	77.16	77.16
Lud-MN8	<i>Ludlowi</i>	77.16	77.16
Lud-MN9	<i>Ludlowi</i>	77.16	77.16
Tro-LN1	<i>Trochilooides</i>	85.50	85.50
Tro-LN10	<i>Trochilooides</i>	85.50	85.50
Tro-LN11	<i>Trochilooides</i>	85.50	85.50
Tro-LN12	<i>Trochilooides</i>	85.50	85.50
Tro-LN14	<i>Trochilooides</i>	85.50	85.50
Tro-LN16	<i>Trochilooides</i>	85.50	85.50
Tro-LN18	<i>Trochilooides</i>	85.50	85.50
Tro-LN19	<i>Trochilooides</i>	85.50	85.50
Tro-LN2	<i>Trochilooides</i>	85.50	85.50
Tro-LN20	<i>Trochilooides</i>	85.50	85.50
Tro-LN3	<i>Trochilooides</i>	85.50	85.50
Tro-LN4	<i>Trochilooides</i>	85.50	85.50
Tro-LN6	<i>Trochilooides</i>	85.50	85.50
Tro-LN7	<i>Trochilooides</i>	85.50	85.50
Tro-LN8	<i>Trochilooides</i>	85.50	85.50
Obs-EM1	<i>Obscuratus</i>	103.30	103.30
Obs-XN1	<i>Obscuratus</i>	102.00	102.00
Obs-XN2	<i>Obscuratus</i>	102.00	102.00
Obs-XN3	<i>Obscuratus</i>	102.00	102.00
Obs-XN5	<i>Obscuratus</i>	102.00	102.00
Plu-BK2	<i>Plumbeitarus</i>	104.90	104.90
Plu-BK3	<i>Plumbeitarus</i>	104.90	104.90
Plu-AN1	<i>Plumbeitarus</i>	102.50	102.50
Plu-AN2	<i>Plumbeitarus</i>	102.50	102.50
Plu-IL1	<i>Plumbeitarus</i>	95.50	95.50
Plu-IL2	<i>Plumbeitarus</i>	95.50	95.50
Plu-IL4	<i>Plumbeitarus</i>	95.50	95.50
Plu-ST1	<i>Plumbeitarus</i>	92.60	92.60
Plu-ST12	<i>Plumbeitarus</i>	92.60	92.60
Plu-ST3	<i>Plumbeitarus</i>	92.60	92.60
Plu-UY1	<i>Plumbeitarus</i>	94.10	94.10
Plu-UY2	<i>Plumbeitarus</i>	94.10	94.10
Plu-UY3	<i>Plumbeitarus</i>	94.10	94.10
Plu-UY4	<i>Plumbeitarus</i>	94.10	94.10
Plu-UY5	<i>Plumbeitarus</i>	94.10	94.10
Plu-UY6	<i>Plumbeitarus</i>	94.10	94.10
Plu-SL1	<i>Plumbeitarus</i>	91.00	91.00
Plu-SL2	<i>Plumbeitarus</i>	91.00	91.00
Plu-TA1	<i>Plumbeitarus</i>	92.00	92.00

Table S1. Subspecies and geographic meta-data for greenish warbler individuals included in analysis

	Population	Longitude	Latitude	Mean	Sample Size
1	BantuSouthAfrica	28.00	-26.00	15.99	
2	SanKhomani	18.10	-24.60	59.96	
3	SanNamibia	20.00	-21.50	9.99	
4	Hadza	33.10	-4.50	5.93	
5	BantuKenya	37.00	-3.00	21.99	
6	MbutiPygmy	29.00	1.00	25.98	
7	BiakaPygmy	17.00	4.00	41.97	
8	Sandawe	35.70	6.20	55.94	
9	Yoruba	5.00	8.00	41.98	
10	Ethiopian	38.70	9.00	37.70	
11	Mandenka	-12.00	12.00	43.98	
12	EthiopianJew	38.70	14.10	22.00	
13	Egyptian	26.80	30.80	24.00	
14	Mozabite	3.00	32.00	57.98	
15	Moroccan	-5.50	33.60	49.97	
16	Tunisian	9.80	35.60	24.00	
17	Ireland	-8.20	53.40	14.00	
18	Scottish	-4.20	56.50	12.00	
19	Spanish	-3.70	40.50	67.95	
20	Welsh	-3.70	52.60	8.00	
21	Orcadian	-3.00	59.00	29.99	
22	English	-0.80	52.00	12.00	
23	Basque	0.00	43.00	47.99	
24	French	2.00	46.00	55.97	
25	Norwegian	8.50	60.50	35.99	
26	Sardinian	9.00	40.00	55.98	
27	NorthItalian	9.70	45.70	23.99	
28	GermanyAustria	10.50	51.20	8.00	
29	Tuscan	11.00	43.00	16.00	
30	WestSicilian	12.50	38.00	20.00	
31	EastSicilian	16.10	37.00	20.00	
32	SouthItalian	16.90	39.50	35.96	
33	Polish	19.10	51.90	31.99	
34	Hungarian	19.50	47.20	40.00	
35	Greek	21.80	39.10	39.99	
36	Lithuanian	23.90	55.20	20.00	
37	Romanian	25.00	45.90	28.00	
38	Bulgarian	25.50	42.70	35.99	
39	Finnish	25.70	61.90	4.00	
40	Belorussian	28.00	53.70	16.00	
41	Bedouin	33.50	31.00	89.98	
42	Cypriot	33.50	35.50	24.00	
43	Palestinian	35.00	33.50	91.95	
44	Turkish	35.20	39.00	34.00	
45	Druze	37.00	32.00	83.96	
46	Jordanian	37.00	30.00	40.00	
47	Adygei	39.00	44.00	33.99	
48	Syrian	39.00	34.80	32.00	
49	Russian	40.00	61.00	49.98	
50	Georgian	44.60	41.80	39.99	
51	Armenian	45.00	40.10	31.99	
52	Saudi	45.10	23.90	20.00	
53	Lezgin	47.50	43.00	35.96	
54	Yemeni	48.50	15.60	13.99	
55	Chuvash	50.20	53.20	34.00	
56	Iranian	53.70	32.40	39.99	
57	UAE	54.40	24.50	27.98	
58	Makrani	64.00	26.00	49.99	
59	Uzbekistani	64.60	41.40	29.99	
60	Brahui	65.00	29.00	49.98	
61	Balochi	67.00	31.00	47.99	
62	Sindhi	69.00	25.00	47.99	
63	Hazara	69.50	33.00	43.98	
64	Kalash	71.00	36.00	45.99	
65	Pathan	72.50	34.00	43.99	
66	IndianJew	72.90	19.00	16.00	
67	Burusho	74.00	37.00	49.98	
68	Indian	77.60	13.00	25.97	
69	Uygur	81.00	44.00	20.00	
70	Xibo	81.00	43.00	17.99	
71	Myanmar	96.00	21.90	5.99	
72	Dai	99.00	21.00	19.98	
73	Naxi	100.00	26.00	15.99	
74	Lahu	101.00	22.00	16.00	
75	Tu	101.00	36.00	20.00	
76	Yi	103.00	28.00	20.00	
77	Cambodian	105.00	12.00	19.98	
78	HanNchina	108.00	39.00	20.00	
79	Miao	108.00	28.00	19.99	
80	Tujia	110.00	29.00	20.00	
81	Han	114.00	26.00	67.96	
82	Mongola	119.00	48.00	20.00	
83	She	119.00	27.00	19.99	
84	Daur	124.00	49.00	17.99	
85	Oroqen	126.00	50.00	18.00	
86	Yakut	129.00	63.00	49.98	
87	Hezhen	133.00	47.00	16.00	
88	Japanese	138.00	38.00	55.97	
89	Papuan	143.00	-4.00	33.97	
90	Melanesian	155.00	-6.00	19.99	
91	Pima	-108.00	29.00	27.99	
92	Maya	-91.00	19.00	41.97	
93	Colombian	-68.00	3.00	13.99	
94	Karitiana	-63.00	-10.00	27.99	
95	Surui	-62.00	-11.00	16.00	

Table S2. sample size and geographic meta-data for human samples included in analysis