SUPPLEMENTAL MATERIAL

Table S1. Landscape variables compiled. The original spatial resolution is presented

Variable	Source	Format	Spatial resolution	Temporal coverage	Provider
Climate[1]	Worldclim	Grid	1 km^2	1950-2000	Worldclim (Hijmans et al. 2005 [Int. J. Climatology])
Planted crops[2]	U.S. National Agriculture Statistics Service Cropland Data 2012	Grid	30 m^2	2012	U.S. Department of Agriculture, National Agriculture Statistics Service, Cropland Data 2012
Elevation	Global 30 Arc-Second Elevation (GTOPO30)	Grid	1km^2	N/A	U.S. Geological Survey, GTOPO30
Landcover	Moderate Resolution Imaging Spectroradiometer (MODIS MCD12Q1)	Grid	500 m^2	January 2012	U.S. National Aeronautics and Space Administration, Land Processes Distributed Active Archive Center U.S. Geological Survey, Earth Resources Observation and Science Center
Population density	U.S. Census Bureau	Vector	N/A	2010	U.S. Census Bureau Center for International Earth Science Information Network, Columbia University
Roads	Digital Chart of the World	Vector	N/A	Unknown	DIVA-GIS
Soils[1]	International Soil Reference and Information Center (ISRIC)	Grid	1 km^2	N/A	ISRIC World Soil Information Database

1. Variables in these datasets were summarized through the use of principal component analyses (PCAs), of which we retained the first component (Table S2).
2. For manageability, this original data were aggregated into broader crops categories following Food and Agriculture Organization (FAO)'s Indicative Crop Classification Version 1.0 (World Programme for the Census of Agriculture 2010)

Table S2. Loadings of separate principal component analyses (PCA) on 19 climatic and 8 soil variables, resepectively. Only the loadings of the first two principal components and their cumulative variance explained are shown, as these are the synthetic variable used in all landscape analyses. Loadings above the 75th percentile absolute value are highlighted in bold.

Climate PCA			Soil PCA		
Variable	PC1	PC2	Variable	PC1	PC2
Annual mean temperature	**0.297**	**0.274**	Bulk density of the fine earth fraction	0.016	**0.631**
Mean diurnal range	0.132	-0.065	Cation exchange capacity	0.438	-0.224
Isothermality	0.277	-0.013	Clay content	0.263	-0.140
Temperature seasonality	**-0.292**	-0.015	Percent of fraction over 2mm	-0.095	-0.646
Maximum temperature of warmest month	0.156	0.231	Soil organic carbon content	-0.021	-0.093
Minimum temperature of coldest month	**0.312**	0.226	pH	**0.521**	0.293
Temperature annual range	-0.199	-0.037	Silt content	**0.492**	-0.069
Mean temperature of wettest quarter	-0.104	0.556	Sand content	-0.464	0.123
Mean temperature of driest quarter	**0.411**	-0.160			
Mean temperature of warmest quarter	0.207	**0.299**			
Mean temperature of coldest quarter	**0.338**	0.233			
Annual precipitation	0.162	-0.202			
Precipitation of wettest month	0.237	-0.139			
Precipitation of driest month	0.114	-0.229			
Precipitation seasonality	-0.013	**0.298**			
Precipitation of wettest quarter	0.221	-0.112			
Precipitation of driest quarter	0.118	-0.222			
Precipitation of	0.112	0.094			

warmest quarter					
Precipitation of driest quarter	0.251	**-0.261**			
Cumulative variance		**78.84%**			**78.29%**

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Table S3. Sampled localities included in the analyses. In addition to geographic coordinates and sample size for the microsatellite (n SSR) and SNP (n SNP) datasets, expected (He), observed heterozygosity (Ho), and estimated effective population size (Ne) are provided. Localities with both SNP and SSR dataset (in bold) have SSR-based estimates on top of SNP-based estimates.

Locality	State	Longitude	Latitude	n SSR	n SNP	He	Ho	Ne
39	IN	-85.742262	39.988984	23	-	0.312	0.373	20.8
36	IN	-85.503826	40.565608	28	-	0.297	0.316	24.1
35	IN	-85.770156	39.853945	24	-	0.324	0.273	19.7
2	NC	-77.927484	34.595714	24	-	0.300	0.316	21.3
4	NC	-79.125602	34.556672	22	-	0.294	0.269	13.4
10	NC	-78.039309	34.983161	26	10	0.339 0.252	0.292 0.242	16.1 9.5
14	NC	-77.917121	35.424763	16	10	0.269 0.306	0.248 0.277	10.9 9.5
19	NC	-78.70899	34.508193	8	-	0.299	0.334	3.7
21	NC	-77.877314	35.369816	11	-	0.222	0.285	9.1
29	NC	-78.738897	34.705135	19	-	0.301	0.282	11.4
40	OH	-83.847252	41.284684	16	-	0.252	0.358	16
54	OH	-85.548739	40.255337	10	-	0.305	0.319	7.5
38	OH	-83.407431	39.515447	25	-	0.304	0.307	22.7
34	OH	-83.910189	39.44316	8	-	0.306	0.280	6.4
5	SC	-79.909072	33.859875	14	-	0.222	0.265	13.1
8	SC	-79.991259	34.297195	28	-	0.294	0.239	17
12	SC	-79.865313	34.145812	27	10	0.276 0.291	0.255 0.278	18.8 9.6
15	SC	-79.073735	34.104209	33	-	0.297	0.253	23.3
17	SC	-79.272908	34.159155	15	-	0.315	0.289	10
28	SC	-80.377715	34.097917	18	-	0.303	0.281	9.3
1	TN	-85.903419	35.775237	–	10	0.314	0.283	9.2
20	TN	-85.777871	35.830692	13	-	0.244	0.305	10.9
48	TN	-87.35373	35.31653	–	10	0.245	0.240	9.5
23	TN	-86.62955	35.067905	34	-	0.313	0.307	21.7
26	TN	-85.951902	35.533413	12	10	0.258 0.210	0.322 0.207	7.6 9.6
46	TN	-86.17985	35.536019	12	-	0.269	0.308	9.1
31	TN	-85.846379	35.608482	16	-	0.358	0.384	11.1
32	TN	-86.225509	35.099356	12	10	0.239 0.236	0.261 0.209	10.6 9.4
30	TN	-85.945003	35.31105	15	-	0.298	0.293	12.2

44	VA	-78.797088	38.285415	14	-	0.341	0.400	4.8
42	VA	-78.662516	38.373523	25	10	0.238 0.235	0.191 0.266	13.2 9.6
41	VA	-78.472921	38.636343	23	-	0.346	0.290	12.7
43	VA	-78.553156	36.886448	26	-	0.275	0.223	16.5

Table S4. Genetic diversity estimates for localities with both SSR and SNP data. Standard error is presented in parentheses

Estimate	SSRc	SNPc
Mean He	0.249 (0.030)	0.255 (0.001)
Mean Ho	0.272 (0.022)	0.246 (0.01)
Mean Ne	12.867 (1.658)	9.540 (0.09)
F_{ST}	0.103 (0.012)	0.144 (0.005)

Table S5. Analysis of Molecular Variance (AMOVA) of localities with both SSR and SNP data. The contribution of spatial clusters (regions), localities, and individuals is shown. For comparison, results from an AMOVA analysis with no region category defined are presented in parentheses underneath.

Effect	F-statistic	Variance explained		F-value		P-value	
		SSRc	SNPc	SSRc	SNPc	SSRc	SNPc
Regions	F_{RT}	12.87 %	0.00%	0.129	-0.007	0.001	0.759
Localities	F_{SR}	4.86% (16.15%)	14.63% (36.08%)	0.056	0.146	0.001	0.001
Individuals (among)	F_{ST}	39.88 % (40.65%)	23.07% (17.23%)	0.177 (0.161)	0.140 (0.361)	0.001 (0.001)	0.001 (0.001)
Individuals (within)	F_{IS}	42.39% (43.20%)	62.30% (46.69%)	0.485 (0.485)	0.270 (0.270)	0.001 (0.001)	0.001 (0.001)
Total	F_{IT}	100% (100%)	100% (100%)	0.576 (0.568)	0.373 (0.533)	0.001 (0.001)	0.001 (0.001)

Table S6. Summary of additional landscape genetic models. To assess the robustness of our results to the method employed, in addition to Multiple Regression on Distance Matrices (MRDM) we run separate simple and partial dbRDA (distance-based Redundancy Analysis Legendre & Anderson, 1999[1])—the latter uses the geographic distance between populations as a covariate to account for the null model of concurrent increase in cumulative resistance with geographic distance. In these models we also used effective population size as a predictor to assess the effects of local environmental conditions on population differentiation. We opted for dbRDA instead of the most commonly used Mantel test given the statistical issues of the latter (Guillot & Rousset, 2013[2]; Ruafaste & Rousset, 2001[3]). We run dbRDA using the package vegan (Oksanen et al. 2015[4]) in R and assessed significance with 9999 permutations.

Feature	**dbRDA**		**partial-dbRDA**	
	SSR	**SNP**	**SSR**	**SNP**
Intrinsic variables				
Geographic distance	1.234 (0.247)	2.503 (0.206)	—	—
Population size (Ne)	1.390 (0.311)	0.265 (0.755)	1.805 (0.117)	0.320 (0.770)
Natural environment variables				
Climate PC1	**1.454** (0.030)	1.513 (0.324)	**1.402** (0.036)	1.031 (0.493)
Climate PC2	1.199 (0.242)	4.957 (0.163)	1.298 (0.194)	4.702 (0.142)
Elevation	1.236 (0.208)	1.369 (0.387)	1.195 (0.194)	1.256 (0.148)
Soil PC1	**1.599** (0.030)	3.847 (0.163)	1.315 (0.131)	2.644 (0.255)
Soil PC2	0.848 (0.614)	3.110 (0.163)	1.421 (0.131)	5.758 (0.142)
Human-impact variables				
Crops	0.819 (0.947)	2.484 (0.206)	0.836 (0.880)	1.270 (0.432)
Landcover	1.272 (0.135)	3.392 (0.194)	1.249 (0.194)	4.423 (0.318)
Population density	**1.656** (0.030)	3.808 (0.166)	1.401* (0.099)	2.873 (0.191)

1. Legendre, P., & Anderson, M. J. (1999). Distance-based redundancy analysis: Testing multispecies responses in multifactorial ecological experiments. Ecological Monographs, 69, 1–24.

2. Guillot, G., & Rousset, F. (2013). Dismantling the Mantel tests. Methods in Ecology and Evolution, 4, 336–344.

3. Raufaste, N., & Rousset, F. (2001). Are Partial Mantel Tests Adequate? Evolution, 55, 1703–1705.

4. Oksanen, J., Blanchet, F. G., Kindt, R., Legendre, P., Minchin, P. R., O'Hara, R. B., … Helene, W. (2015). vegan: community ecology package. Retrieved from http://cran.r792project.org/package=vegan

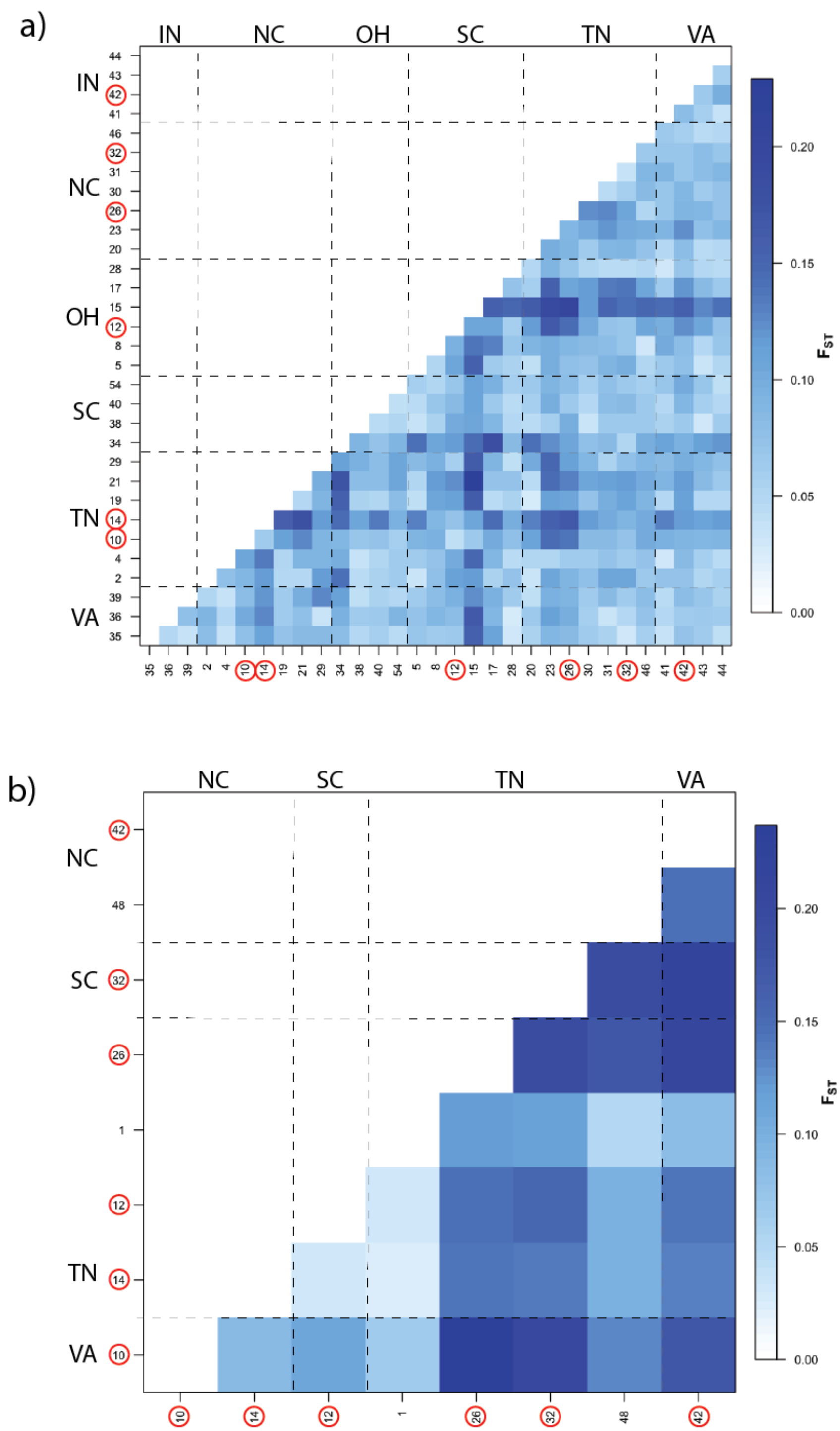

Figure S1. Pairwise F_{ST} values between sampled localities. F_{ST} matrices for both SSR (A) and SNP (B) datasets are shown. Localities with both SSR and SNP datasets are encircled in red. Locality numbers follow Fig. 1.

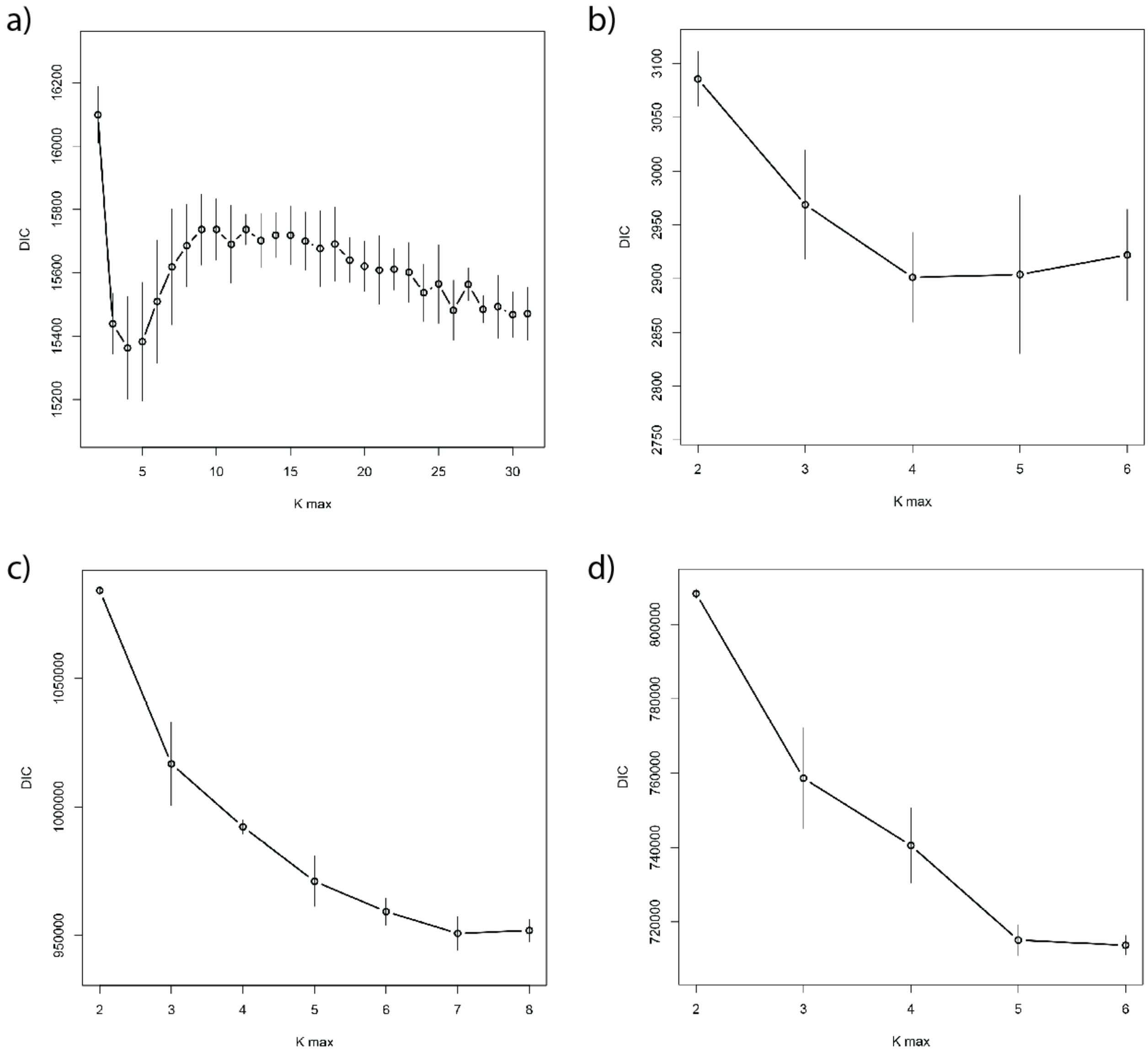

Figure S2. K selection for TESS models. DIC plotted as a function of maximum number of groups allowed (K) for the SSR (a), SNP (a), SSRc (c), and SNPc (d) datasets. Each dot corresponds to the average DIC value computed over 10 replicate runs with its standard deviation shown as error bars.

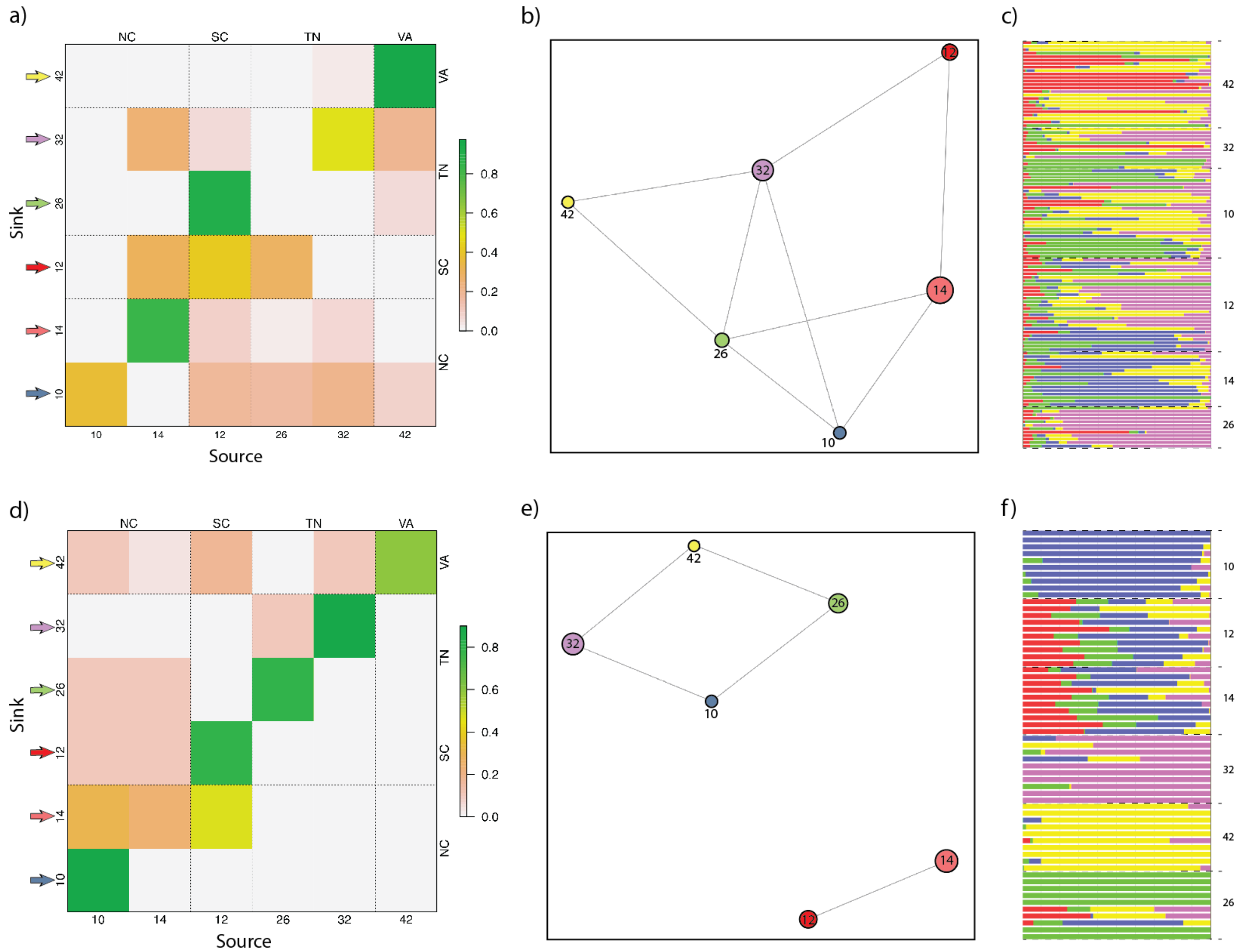

Figure S3. Inferred population connectivity for localities with both SSR and SNP data. The estimated origin of individuals for each sampled locality (i.e., sink) is depicted according to the locality they were inferred to have originated from (source) (a, d). The color of each cell in these plots depicts the proportion of individuals in the sink population that were estimated to be recent immigrants from each locality along the x-axis. Cells on the minor diagonal correspond to the proportion of native individuals. Pruned conditional genetic networks (b, e) and posterior estimates of admixture proportion identified by TESS analysis (c, f) are also displayed. The top row shows SSR-based results, the bottom shows the SNP-based results. Locality numbers follow Fig. 1. Localities shared between SSR and SNP datasets are denoted by unique colors in all panels.

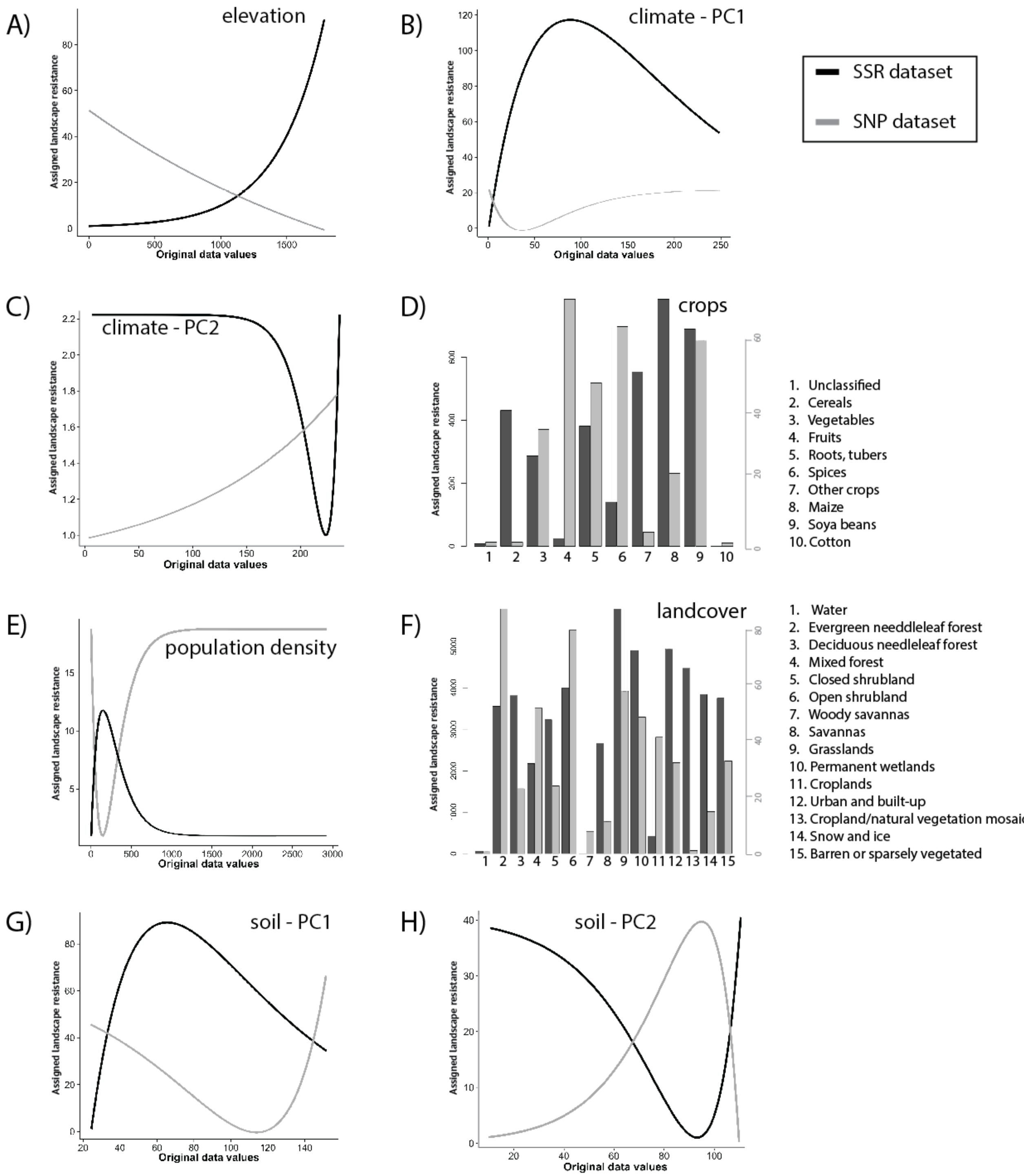

Figure S4. Optimal landscape resistance transformations. Transformations for both SSR and SNP datasets for continuous and categorical variables are shown.

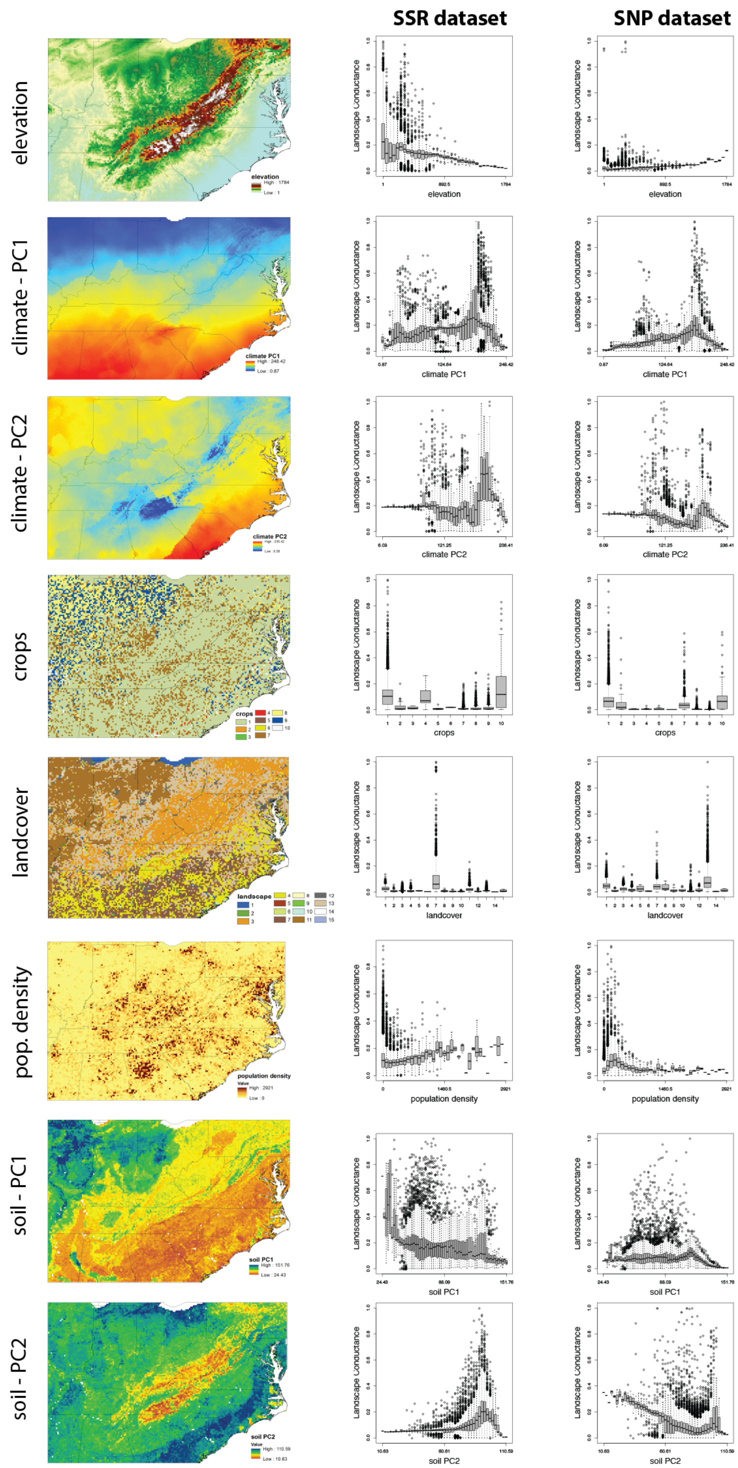

Figure S5. Landscape layers included in the analyses and corresponding landscape conductance. The association between each landscape variable (leftmost column) and their inferred effect on the ease of migration (i.e., conductivity; right columns) is depicted.