Supplementary Material

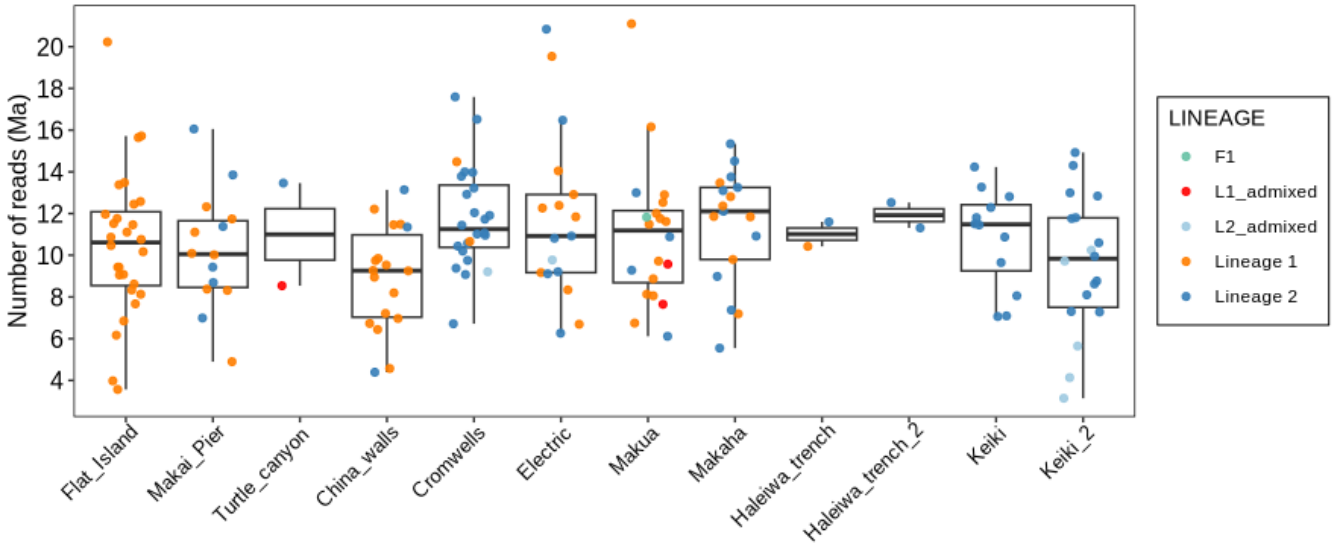

Figure S1. Distribution of per-individual read counts for 174 individuals retained in the final dataset. Individuals are sorted by location and colored by lineage.

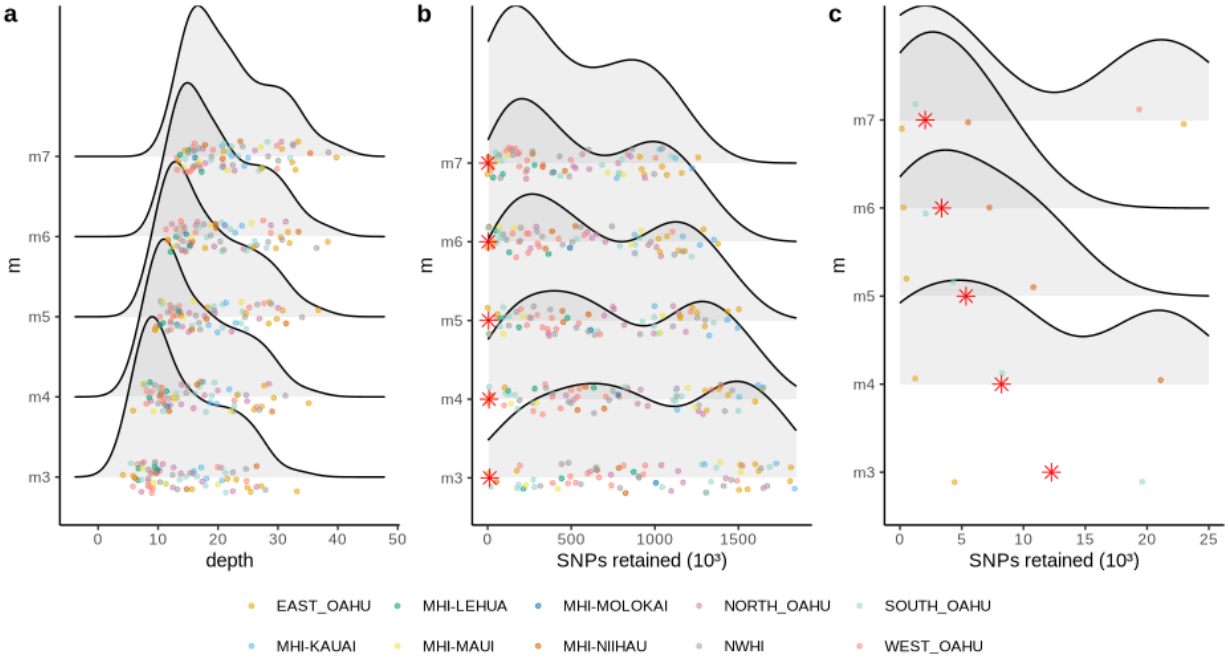

Figure S2. De novo assembly parameters, fine-tuned using a subset of 77 samples spanning the distribution of *A. glomerata* across the Hawaiian archipelago. Dot colors indicate geographic origin, including the Main Hawaiian Islands (MHI: O'ahu with N, S, E, W populations distinguished, Maui, Kaua'i, and Ni'ihau) and samples from the Northwest Hawaiian Islands (NWHI). Fine-tuning of the minimum number of raw reads required to form an allele (m) is shown as (a) m value versus individual depth, (b) m value versus the total number of SNPs retained (10^3), and (c) x-axis truncated at 25,000 SNPs to capture fine-scale variation in the R80 SNP set (loci shared across 80% of samples; red asterisk).

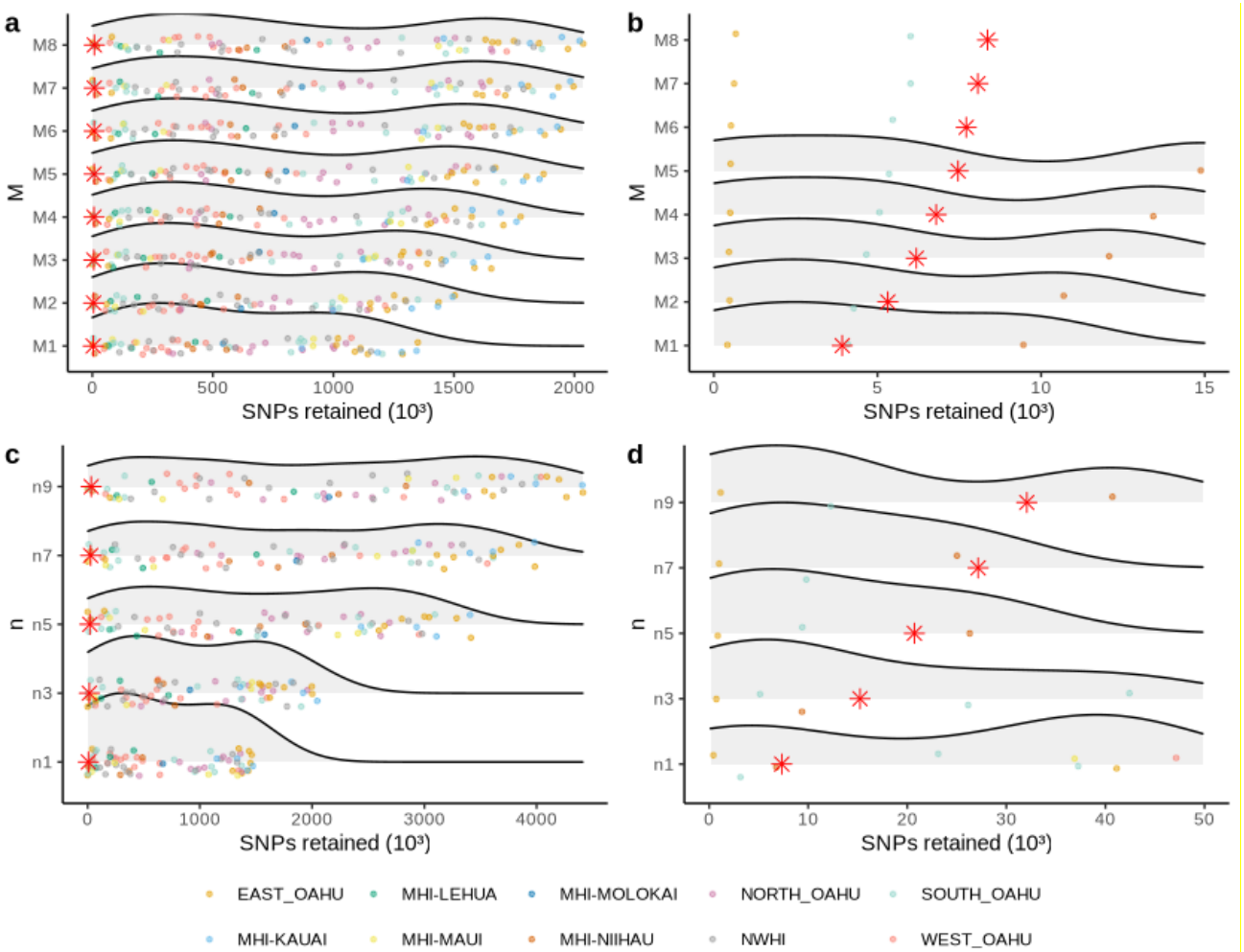

Figure S3. De novo assembly parameters, fine-tuned using a subset of 77 samples spanning the distribution of *A. glomerata* across the Hawaiian archipelago. Dot colors indicate geographic origin, including the Main Hawaiian Islands (MHI: O'ahu with N, S, E, W populations distinguished, Maui, Kaua'i, and Ni'ihau) and samples from the Northwest Hawaiian Islands (NWHI). Panels show the effects of: (a, b) the maximum number of mismatches allowed between putative alleles (M), and (c, d) the maximum number of mismatches allowed between homozygous individuals when building the catalog of loci (n). Panels (b) and (d) have the x-axis truncated to capture fine-scale variation in the R80 SNP set (loci shared across 80% of samples; red asterisk).

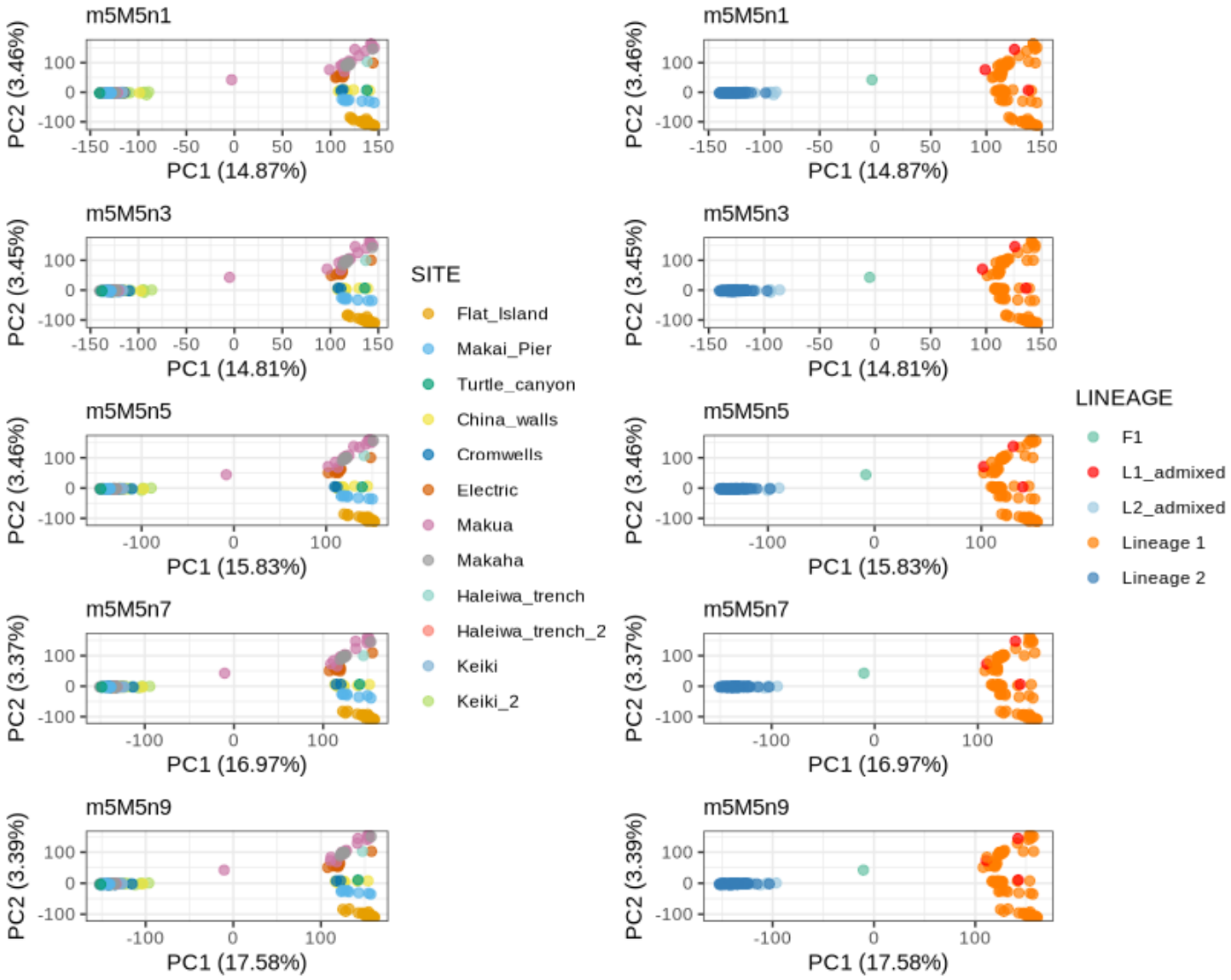

Figure S4. Principal Component Analysis (PCA) showing genetic divergence as a function of the maximum number of mismatches allowed between homozygous individuals when building the catalog of loci (*n*), with *m* and *M* fixed at 5. Principal component analysis (PC1: horizontal axis, PC2: vertical axis) performed on 174 samples retained post-filtering, using 50,000 SNPs randomly sampled from each catalog at *n* = 1, 2, 5, 7, 9. The *n* value for each PCA is indicated at the top of each panel. Left panels show samples colored by O'ahu location, while right panels display lineage assignments based on hybrid inferences.

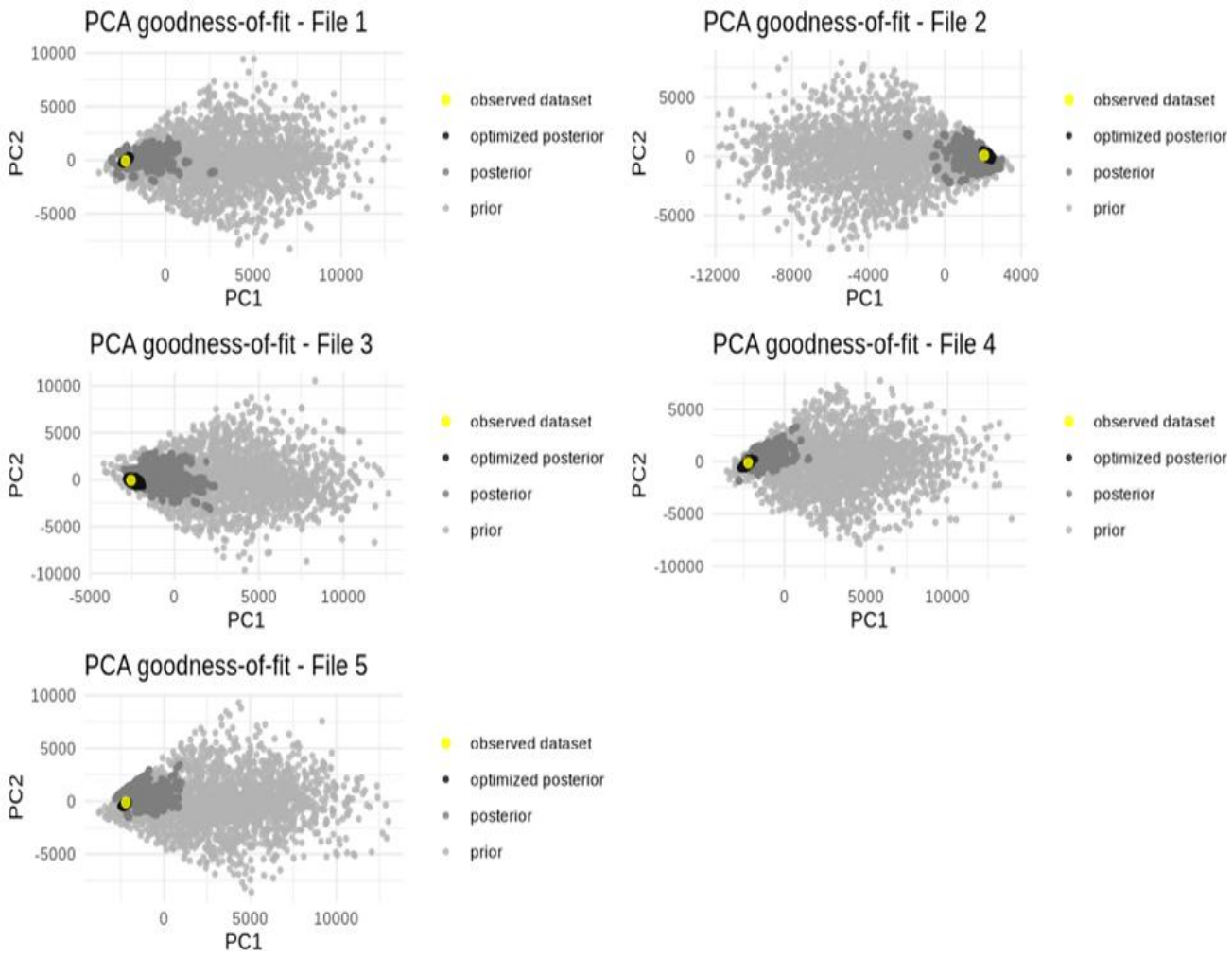

Figure S5. PCA goodness-of-fit DILS for each run showing high consistency between the observed dataset and simulated datasets with optimized posterior.

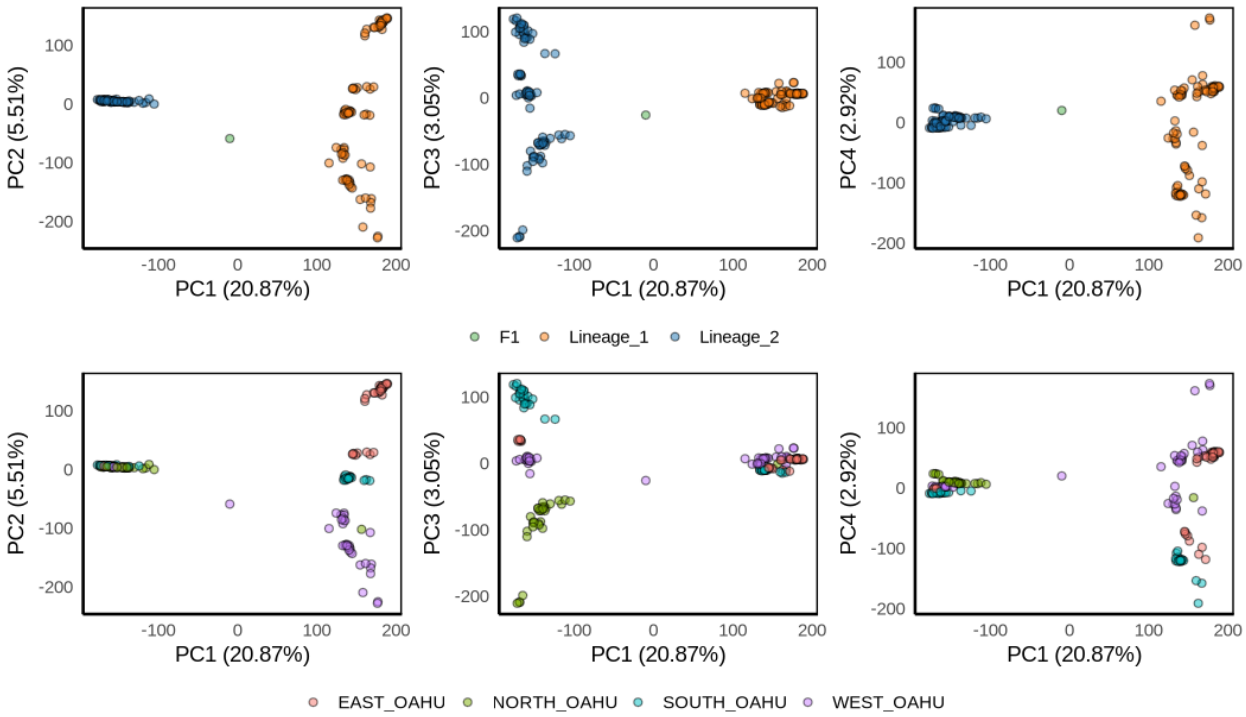

Figure S6. Principal Component Analysis (PCA) showing additional components (PC2, PC3, and PC4). Upper panels: samples are colored by lineage assignment; lower panels: samples are colored by geographic location.

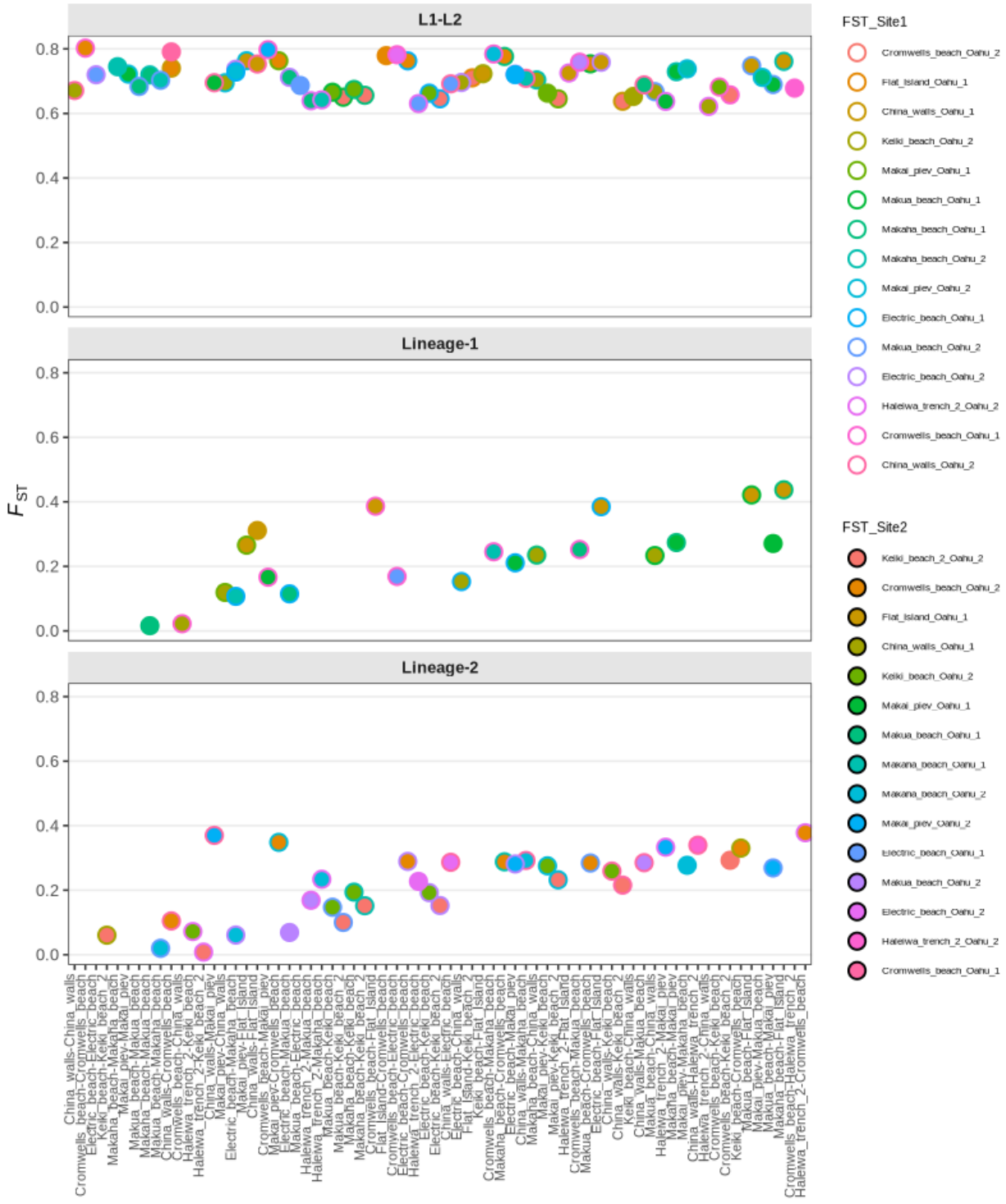

Figure S7. Pairwise F_{ST}, accounting for lineage dissimilarity, with F_{ST} estimated within lineage (Lineage-1 or Lineage-2) or between populations of different lineages (L1-L2). F_{ST} values are ordered by increasing least-cost distance (km).

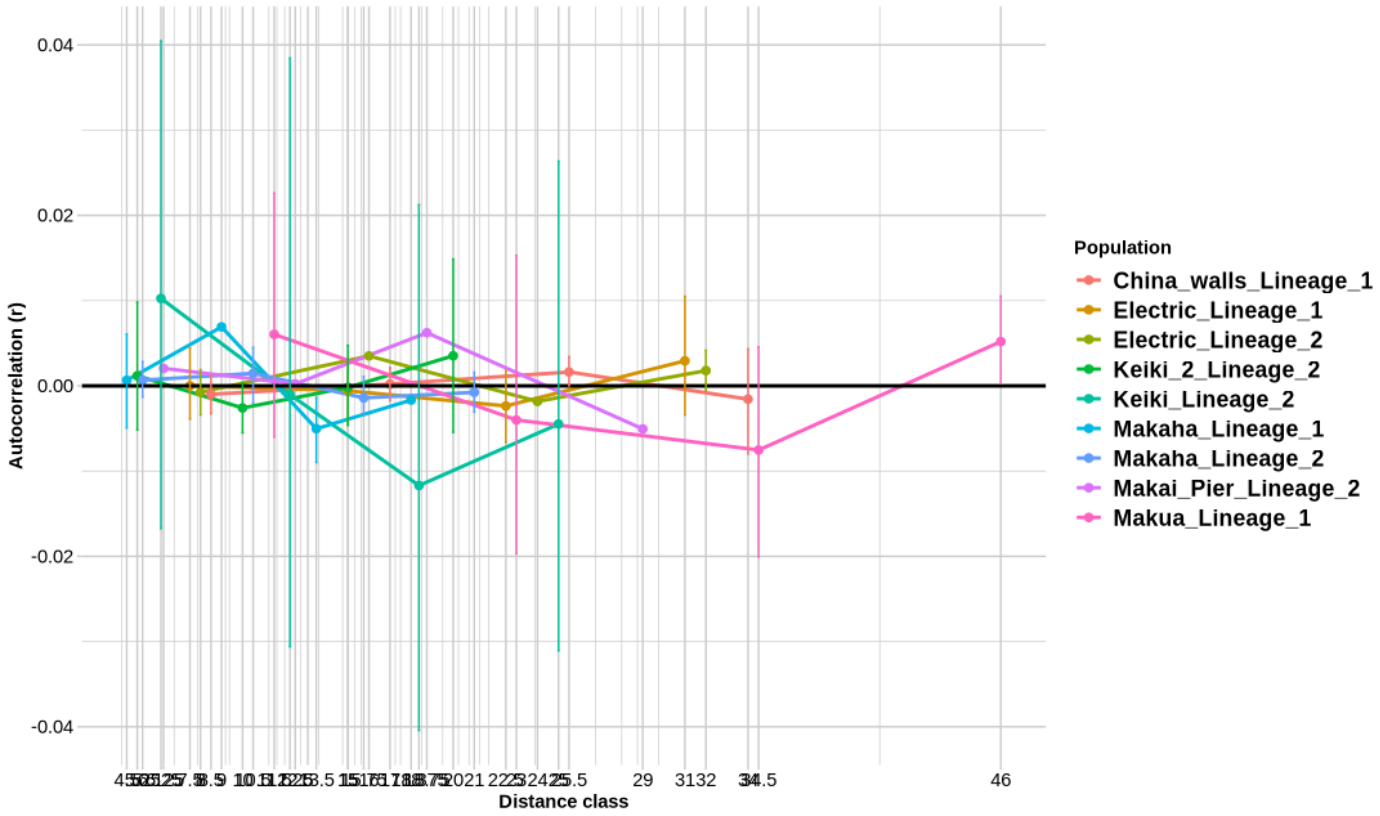

Figure S8. Fine-scale spatial autocorrelation analysis for six transects accounting for lineage dissimilarity.

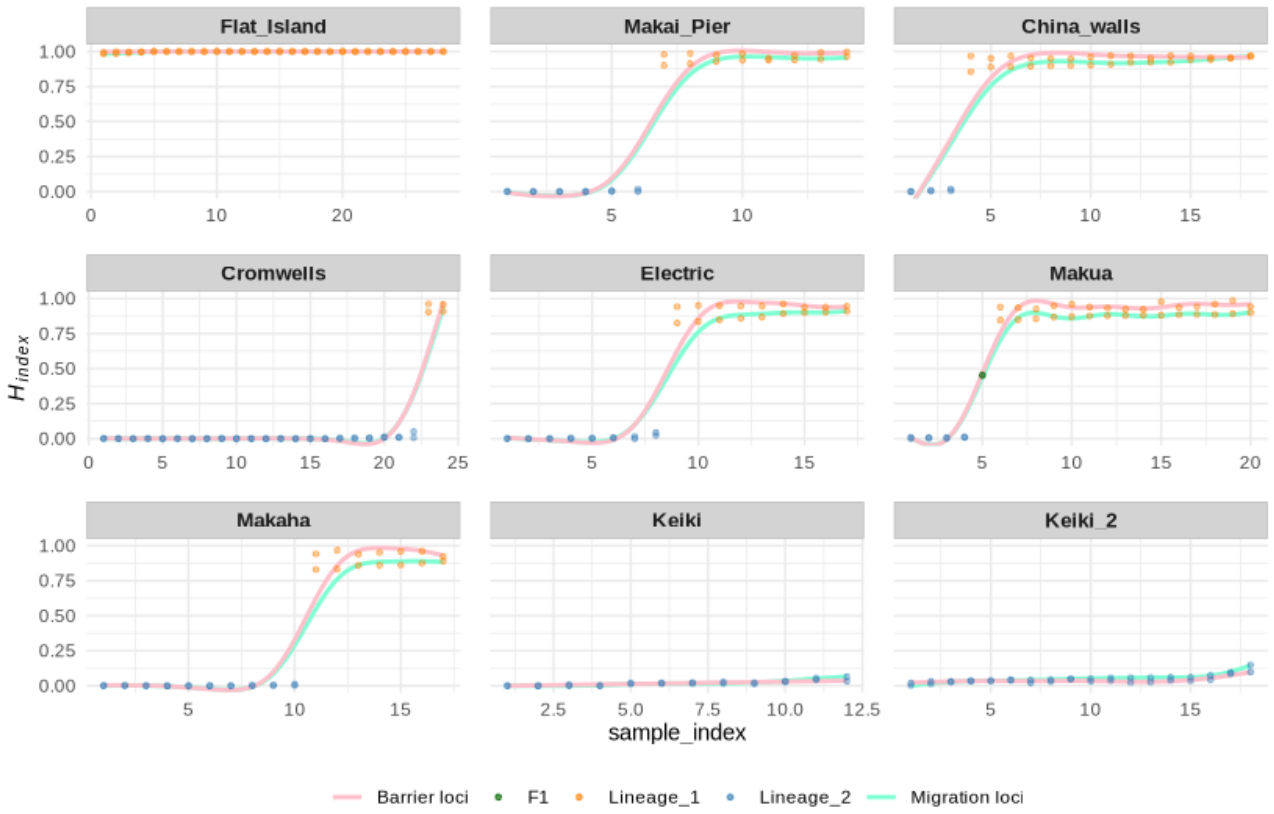

Figure S9. Difference in Hybrid index (H_{index}) between isolated loci (pink) and migration loci (blue) along individuals ordered by H_{index}. Dots represent individual samples, colored by lineage: Lineage 1 (orange), Lineage 2 (blue), and F1 (green). Facets show separate sites that are arranged from the southeastern to the northern part of the island, with western locations in between.

Table S1. Parameters and prior values for DILS analysis.

Type		DILS 2 pop
Parameters	Genomic regions:	noncoding
	max_N_tolerated:	0.2
	nMin:	10
	Lmin:	50
	use jSFS:	yes
	Change in population size:	variable
Priors	μ (per base pair, per generation):	2.76E-07
	Ratio r/μ:	0.5
	Time of split (in number of generation):	min = 0
		max = 1,750,000
	Population size (*Ne*):	min = 0
		max = 500 000
	Migration rates (*4.Ne.m*):	min = 1
		max = 40
	Model for barriers:	bimodal

max_N_tolerated = maximum proportion of missing data in the sequence of a gene for an individual beyond which this sequence is excluded; nMin = minimum number of individuals sequence within lineage for which the gene sequence is not excluded (regarding the number of individuals after filtering with max_N_tolerated); Lmin = minimum number of treatable sites below which a gene is excluded; jSFS = jointed Site Frequency Spectrum – will be used as a summary statistic if set to yes; μ = mutation rate; Ratio r/μ = ratio of recombination (per base pair per generation) over mutation; Time of split = speciation time; Population size = number of diploid individuals within current and ancestral lineages; Migration rate = calculated with 4.Ne.m with m being the fraction of each subpopulation composed of new migrants at each generation.

Table S2. Summary table of lineage and hybrid identity, including the number of samples for each category (n), inference from the complete SNP dataset with Q_1 and Q_2 sNMF ancestry coefficients, and inference with lineage-diagnostics SNPs, with H_{index} and interspecific heterozygosity (Het-inter).

LINEAGE	n	Q1	Q2	H_{index}	Het-inter
Lineage 1	83	0.94	0.06	0.98	0.02
Lineage 2	80	0.03	0.97	0.01	0.01
F1	1	0.45	0.55	0.49	0.86
Admixed lineage 1	3	0.91	0.09	0.97	0.06
Admixed lineage 2	7	0.13	0.87	0.05	0.08

Table S3. Results of Mantel and partial Mantel tests. First, tests between genetic distance matrices and lineage dissimilarity matrices (GENET & LINEAGE), second, tests between genetic distance and transect distance (m) matrices while accounting for lineage dissimilarity (GENET & TRANSECT | LINEAGE).

Test Comparison	Site	Mantel r	P-value
GENET & LINEAGE	China walls	0.996	**0.002**
GENET & TRANSECT | LINEAGE	China walls	0.051	0.271
GENET & LINEAGE	Electric	0.924	**0.001**
GENET & TRANSECT | LINEAGE	Electric	0.002	0.345
GENET & LINEAGE	Makaha	0.997	**0.001**
GENET & TRANSECT | LINEAGE	Makaha	−0.108	0.973
GENET & LINEAGE	Makai pier	0.996	**0.01**
GENET & TRANSECT | LINEAGE	Makai pier	−0.349	0.998
GENET & LINEAGE	Makua	0.941	**0.002**
GENET & TRANSECT | LINEAGE	Makua	0.07	0.194