

Supplemental Information for:

Comparing methods for detecting multilocus adaptation with multivariate genotype-environment associations

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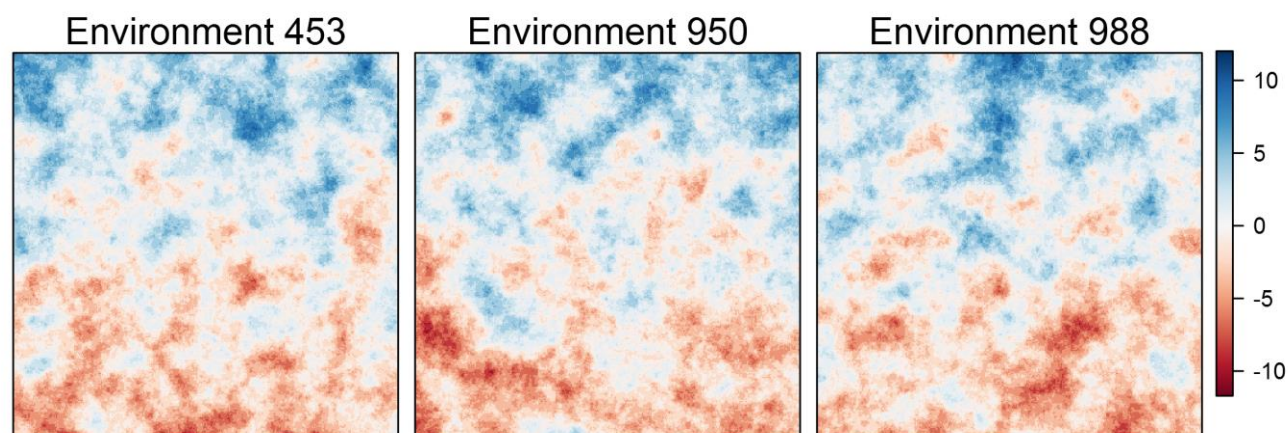


Figure S1. The three environmental surfaces used as replicates from Lotterhos & Whitlock (2015). Colors represent values of the environment.

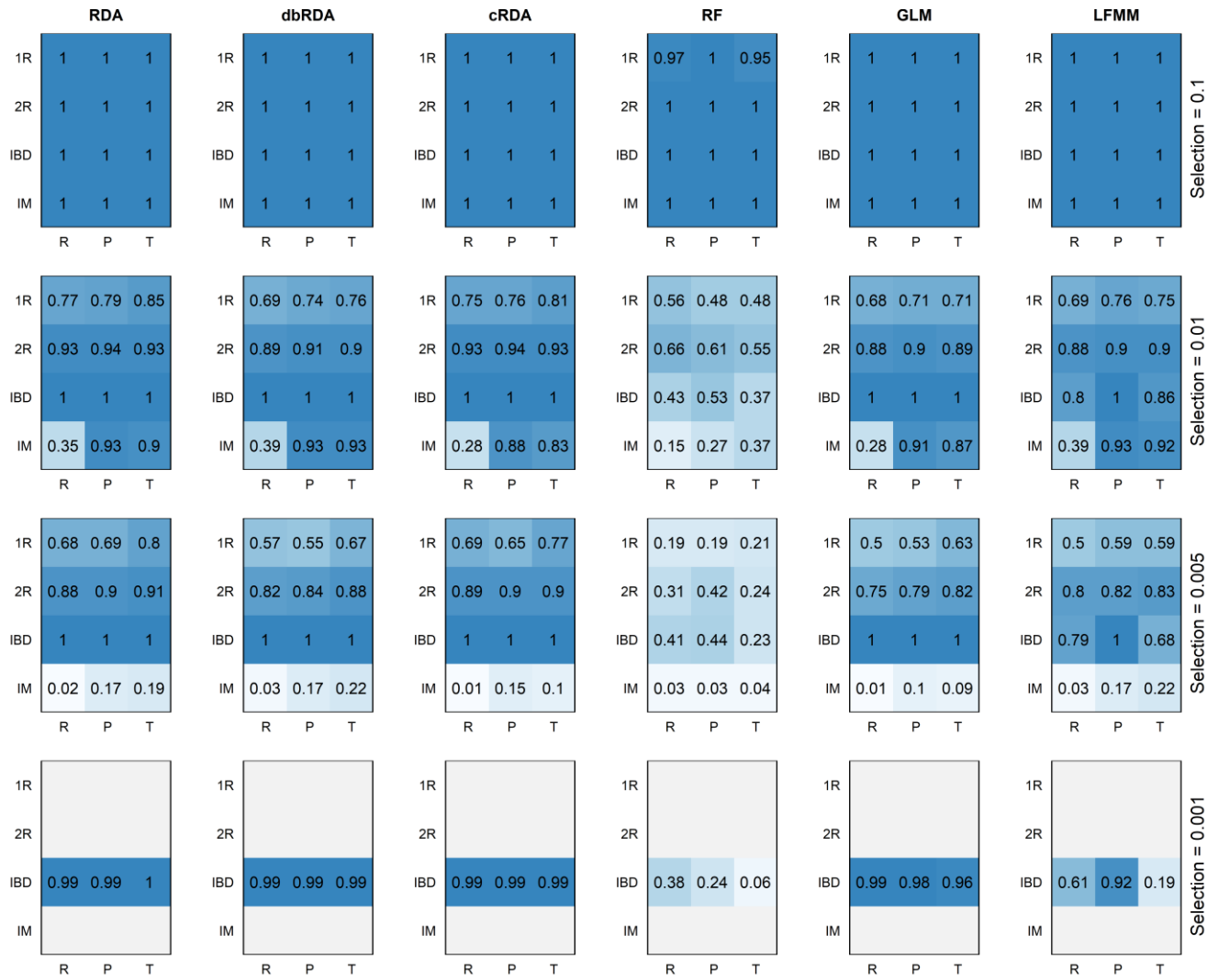


Figure S2. Average power (from empirical p -values) for different levels of selection (rows) from six methods (columns) using a sample size of 6 individuals per deme. Each method shows results for different sampling strategies (R = random, P = pairs, T = transects) and demographies (1R and 2R = refugial expansion, IBD = equilibrium isolation by distance, IM = equilibrium island model). Only the IBD demography included very weak selection ($s=0.001$).

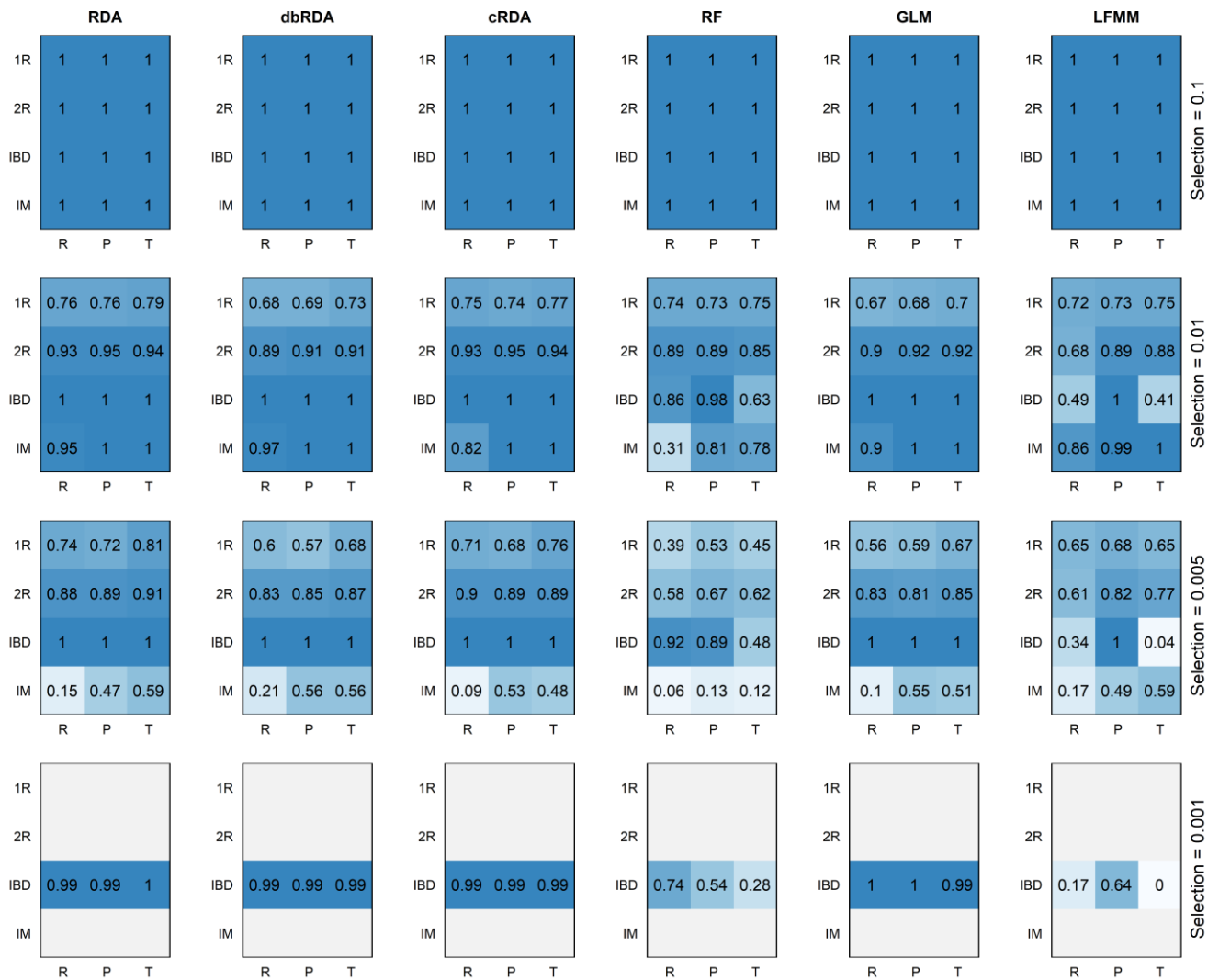


Figure S3. Average power (from empirical p -values) for different levels of selection (rows) from six methods (columns) using a sample size of 20 individuals per deme. NOTE: this figure reproduces Figure 4 from the main text, but includes the addition of Random Forest results for comparison. Each method shows results for different sampling strategies (R = random, P = pairs, T = transects) and demographies (1R and 2R = refugial expansion, IBD = equilibrium isolation by distance, IM = equilibrium island model). Only the IBD demography included very weak selection ($s=0.001$).

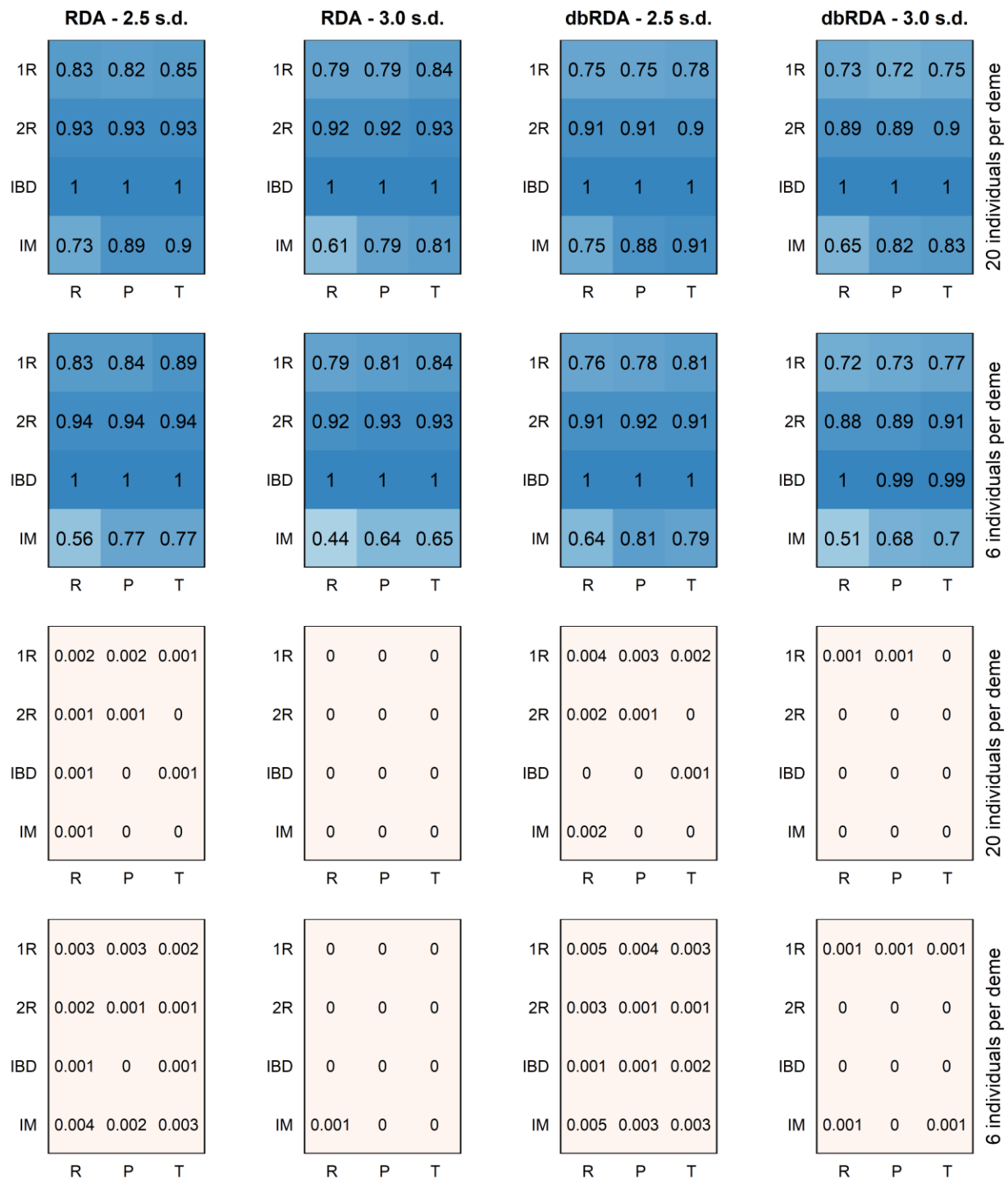


Figure S4. Average true positive (top two rows, in blue) and false positive (bottom two rows, in red) rates for constrained ordinations using ± 2.5 and 3.0 SD cutoffs. Each method and cutoff shows results for different sampling strategies (R = random, P = pairs, T = transects), demographies (1R and 2R = refugial expansion, IBD = equilibrium isolation by distance, IM = equilibrium island model), and sample sizes (rows).

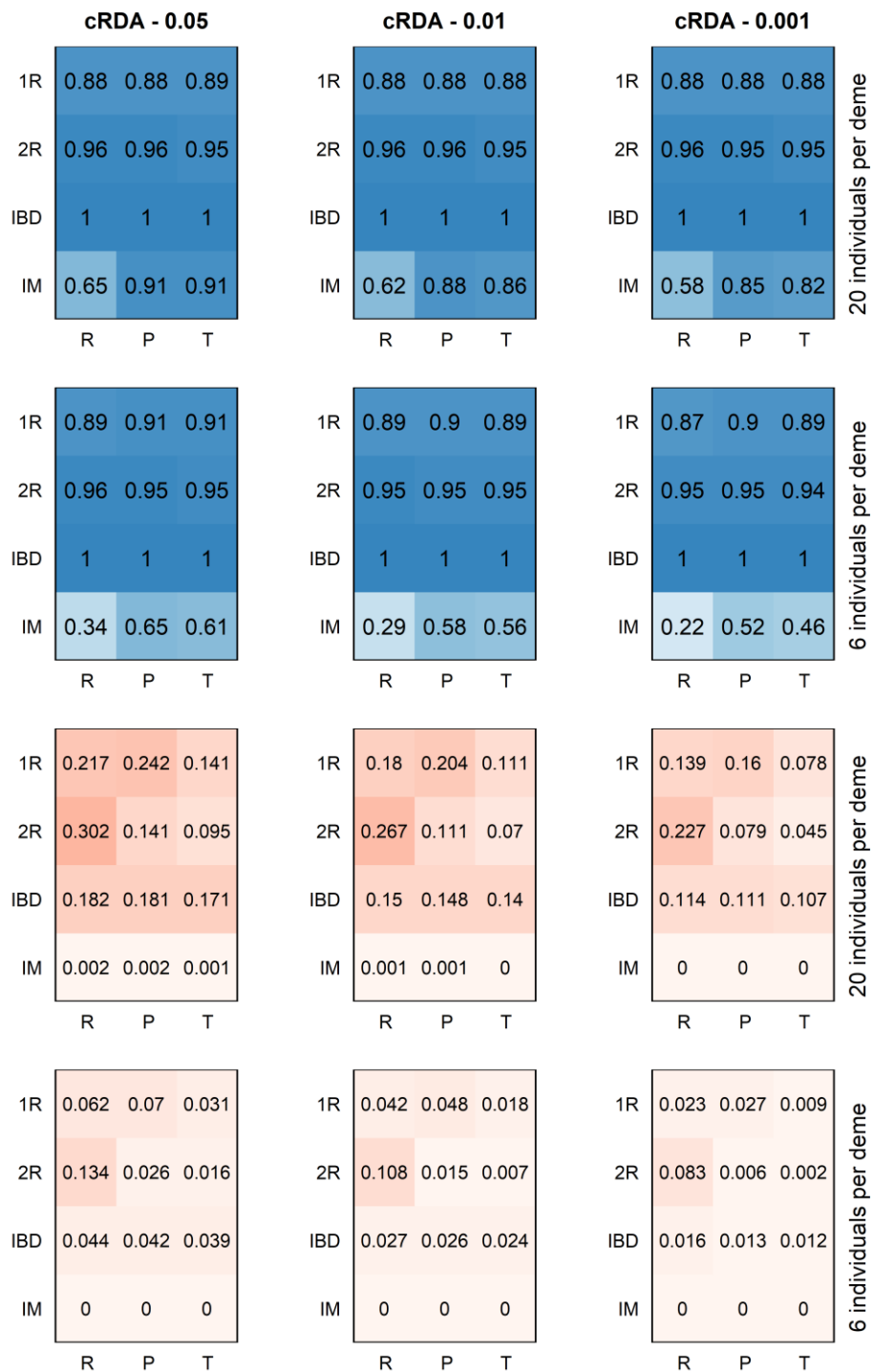


Figure S5. Average true positive (top two rows, in blue) and false positive (bottom two rows, in red) rates for cRDA using SNP-component correlation cutoffs of $\alpha = 0.05$, 0.01 , and 0.001 . Each cutoff shows results for different sampling strategies (R = random, P = pairs, T = transects), demographies (1R and 2R = refugial expansion, IBD = equilibrium isolation by distance, IM = equilibrium island model), and sample sizes (rows).

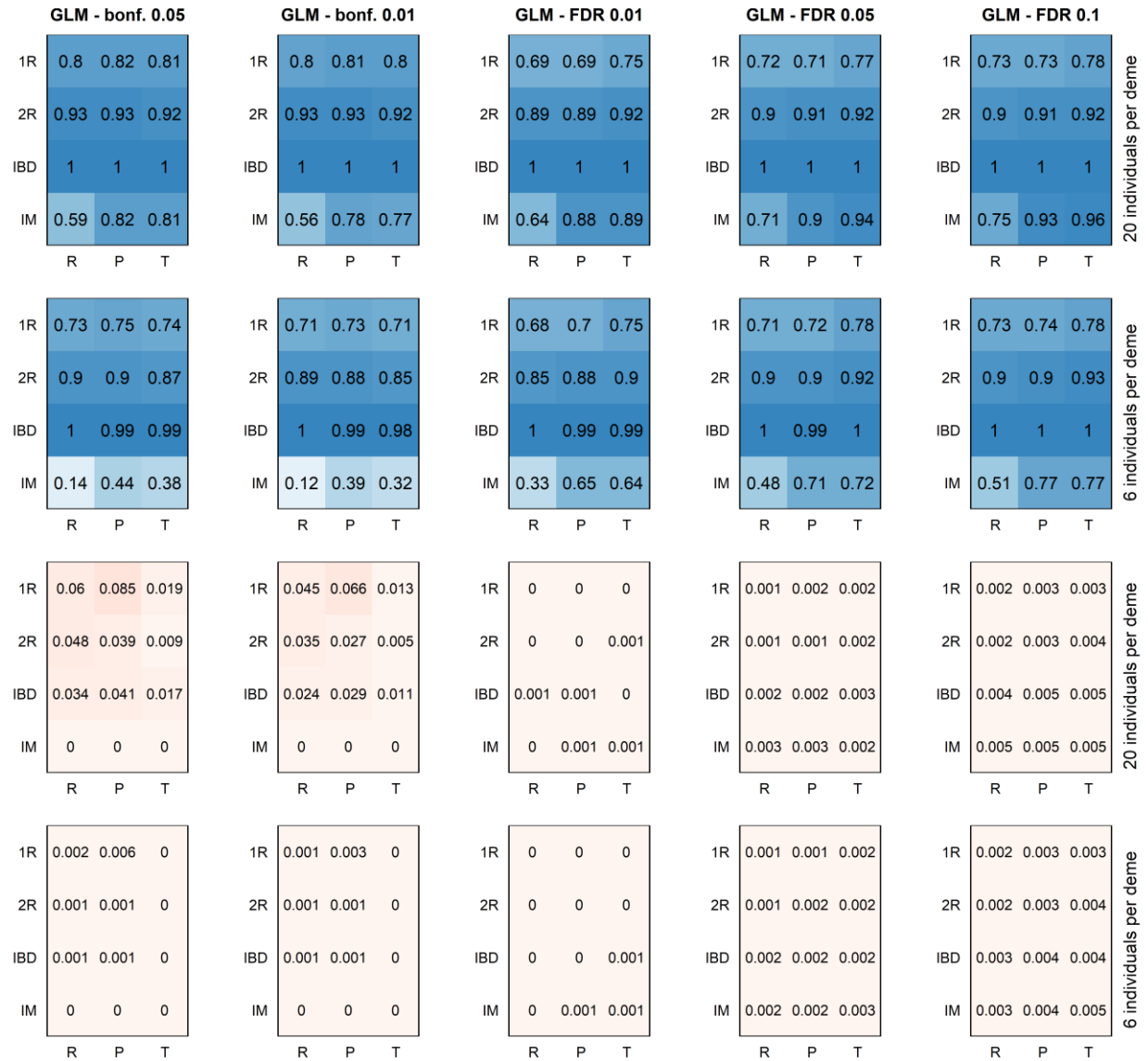


Figure S6. Average true positive (top two rows, in blue) and false positive (bottom two rows, in red) rates for GLM using Bonferroni-corrected cutoffs of 0.05 and 0.01, and false discovery rate (FDR) cutoffs of 0.01, 0.05, and 0.1. FDR results should be evaluated in the context of the corresponding genomic inflation factors (Table S1) to assess model calibration. Each cutoff shows results for different sampling strategies (R = random, P = pairs, T = transects), demographies (1R and 2R = refugial expansion, IBD = equilibrium isolation by distance, IM = equilibrium island model), and sample sizes (rows).

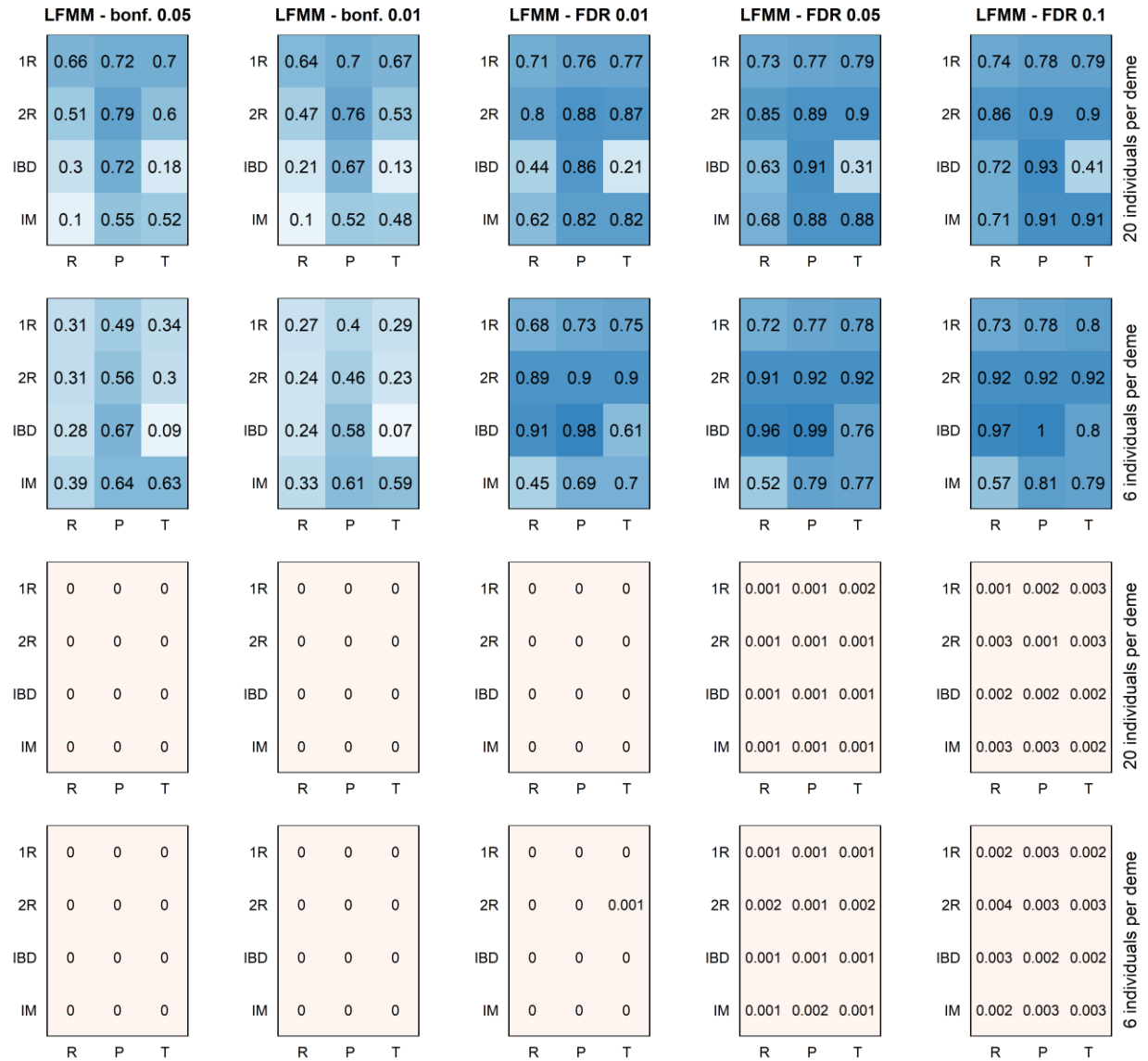


Figure S7. Average true positive (top two rows, in blue) and false positive (bottom two rows, in red) rates for LFMM using Bonferroni-corrected cutoffs of 0.05 and 0.01, and false discovery rate (FDR) cutoffs of 0.01, 0.05, and 0.1. FDR results should be evaluated in the context of the corresponding genomic inflation factors (Table S1) to assess model calibration. Each cutoff shows results for different sampling strategies (R = random, P = pairs, T = transects), demographies (1R and 2R = refugial expansion, IBD = equilibrium isolation by distance, IM = equilibrium island model), and sample sizes (rows).

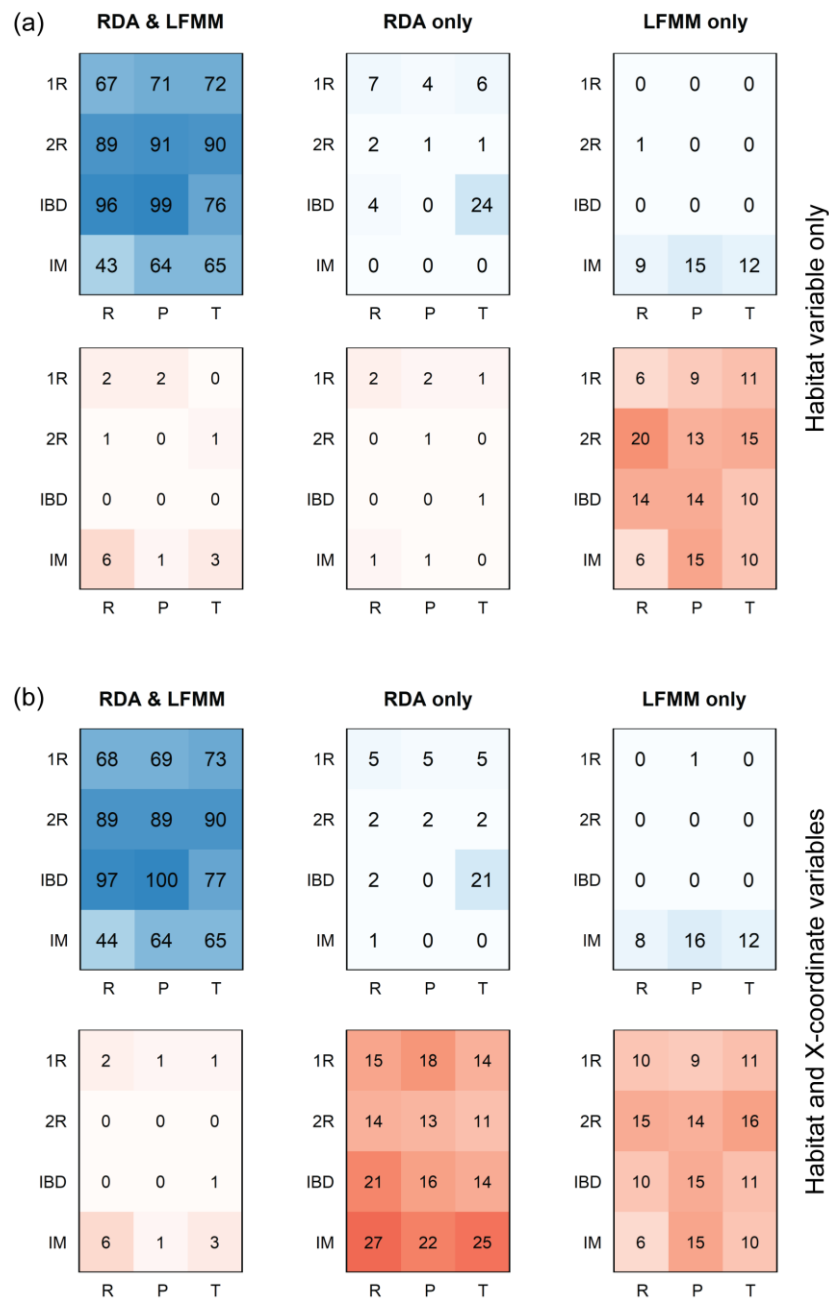


Figure S8. Average counts of true positive (top rows of a and b, in blue) and false positive (bottom rows of a and b, in red) detections for two methods, RDA and LFMM, using their best cutoffs and a sample size of 6 individuals per deme. The first column shows the average number of loci detected by both methods. The second and third columns show the average number of detections that are unique to RDA and LFMM, respectively. (a) Results for GEAs using Habitat as the only predictor. (b) Results for GEAs using Habitat and the (uninformative) X-coordinate predictor. Results are presented for different sampling strategies (R = random, P = pairs, T = transects), demographies (1R and 2R = refugial expansion, IBD = equilibrium isolation by distance, IM = equilibrium island model), and sample sizes (rows).

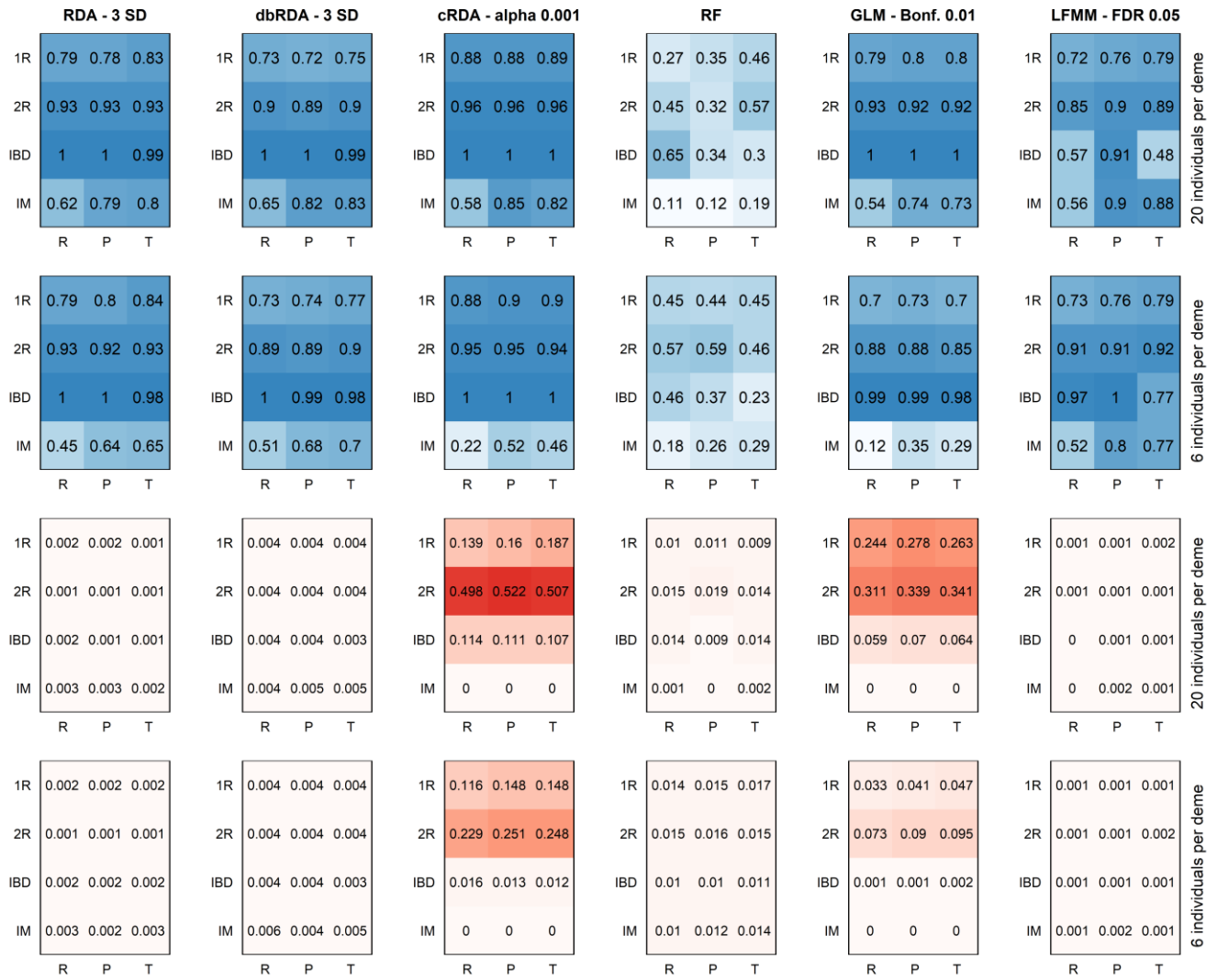


Figure S9. Average true positive (top two rows, in blue) and false positive (bottom two rows, in red) rates from six methods (columns) using the habitat and uninformative x-coordinate predictors and the best cutoff for each method. Each method shows results for different sampling strategies (R = random, P = pairs, T = transects), demographies (1R and 2R = refugial expansion, IBD = equilibrium isolation by distance, IM = equilibrium island model), and sample sizes (rows).

Table S1: Parameters from generalized linear model (GLM) and latent factor mixed model (LFMM) runs: genomic inflation factors (GIF) for GLM and LFMM, and K for LFMM.

Demo- graphy	Sampling Design	Envir. Surface	6 individuals per deme			20 individuals per deme		
			GLM GIF	LFMM K	LFMM GIF	GLM GIF	LFMM K	LFMM GIF
1R	R	453	2.30	5	0.51	6.55	5	1.17
1R	R	950	1.81	5	0.45	4.69	5	1.02
1R	R	988	1.64	5	0.42	4.31	5	1.19
1R	P	453	1.92	5	0.43	5.25	5	1.02
1R	P	950	2.68	5	0.63	7.80	5	1.20
1R	P	988	2.04	5	0.49	5.64	5	1.08
1R	T	453	1.36	5	0.41	3.23	5	0.98
1R	T	950	1.41	5	0.36	3.44	5	1.07
1R	T	988	1.13	5	0.33	2.53	5	0.64
2R	R	453	1.70	5	0.31	4.44	5	0.50
2R	R	950	1.46	5	0.25	3.50	5	0.65
2R	R	988	2.19	5	0.27	5.94	5	0.60
2R	P	453	1.33	5	0.27	3.39	5	0.70
2R	P	950	1.58	5	0.35	3.97	5	0.69
2R	P	988	1.99	5	0.27	5.43	5	0.79
2R	T	453	1.11	5	0.23	2.41	5	0.57
2R	T	950	1.25	5	0.26	2.84	5	0.67
2R	T	988	0.98	5	0.18	2.10	5	0.42
IBD	R	453	1.75	4	0.40	4.59	4	1.16
IBD	R	950	1.42	4	0.35	3.34	4	1.12
IBD	R	988	1.41	4	0.34	3.48	4	0.95
IBD	P	453	1.67	4	0.36	4.45	4	1.20
IBD	P	950	1.73	4	0.42	4.45	4	1.12
IBD	P	988	1.50	4	0.36	3.83	4	0.95
IBD	T	453	1.46	4	0.48	3.67	4	1.37
IBD	T	950	1.19	4	0.32	2.72	4	1.09
IBD	T	988	1.18	4	0.35	2.65	4	0.86
IM	R	453	0.72	1	1.12	1.10	4	0.22
IM	R	950	0.69	1	1.13	1.05	4	0.20
IM	R	988	0.70	1	1.13	1.10	4	0.16
IM	P	453	0.71	1	1.16	1.11	2	0.56
IM	P	950	0.70	1	1.12	1.06	2	0.53
IM	P	988	0.69	1	1.11	1.06	2	0.52
IM	T	453	0.68	1	1.09	1.06	2	0.54
IM	T	950	0.69	1	1.10	1.06	2	0.59
IM	T	988	0.69	1	1.09	1.04	2	0.62

Table S2: RF results averaged across environments for true and false positive rates using no correction for population structure and two different approaches to correcting for population structure: using ancestry values to correct the habitat predictor only, and using ancestry values to correct both the genotypes and habitat predictor.

Demo- graphy	Sampling Design	True Positive Rates					
		6 individuals per deme			20 individuals per deme		
		No correction	Habitat corrected	Genotypes & Habitat corrected	No correction	Habitat corrected	Genotypes & Habitat corrected
1R	R	0.43	0.46	0.16	0.60	0.63	0.14
1R	P	0.40	0.43	0.15	0.67	0.66	0.14
1R	T	0.41	0.44	0.15	0.64	0.68	0.15
2R	R	0.53	0.55	0.13	0.75	0.77	0.16
2R	P	0.57	0.53	0.17	0.80	0.83	0.17
2R	T	0.45	0.52	0.14	0.75	0.78	0.18
IBD	R	0.44	0.45	0.09	0.83	0.91	0.09
IBD	P	0.40	0.46	0.13	0.75	0.86	0.18
IBD	T	0.23	0.26	0.08	0.45	0.54	0.09
IM	R	0.19	0.20	0.20	0.26	0.34	0.07
IM	P	0.23	0.31	0.31	0.51	0.56	0.08
IM	T	0.28	0.26	0.26	0.49	0.52	0.06

Demo- graphy	Sampling Design	False Positive Rates					
		6 individuals per deme			20 individuals per deme		
		No correction	Habitat corrected	Genotypes & Habitat corrected	No correction	Habitat corrected	Genotypes & Habitat corrected
1R	R	0.005	0.006	0.008	0.009	0.011	0.004
1R	P	0.004	0.006	0.006	0.013	0.011	0.004
1R	T	0.006	0.004	0.006	0.008	0.011	0.008
2R	R	0.005	0.004	0.006	0.008	0.008	0.009
2R	P	0.006	0.005	0.005	0.012	0.012	0.010
2R	T	0.005	0.005	0.007	0.012	0.012	0.010
IBD	R	0.004	0.004	0.006	0.010	0.013	0.014
IBD	P	0.005	0.006	0.009	0.014	0.016	0.019
IBD	T	0.006	0.004	0.007	0.008	0.008	0.016
IM	R	0.006	0.005	0.005	0.009	0.009	0.027
IM	P	0.006	0.007	0.007	0.009	0.012	0.024
IM	T	0.007	0.004	0.004	0.009	0.009	0.028

Table S3: LFMM results averaged across environments for power (from empirical p -values) and true and false positive rates (from 0.05 FDR cutoff) using K and K-1. GIF is the genomic inflation factor. For the 6 individual IM demography scenarios the best value of K was 1, so no reduction in K was tested for these cases.

		6 individuals per deme								
Demo-graphy	Sampling Design	K	GIF K	GIF K-1	Emp P K	Emp P K-1	TPR K	TPR K-1	FPR K	FPR K-1
1R	R	5	0.46	0.89	0.64	0.65	0.72	0.73	0.001	0.001
1R	P	5	0.52	1.23	0.71	0.68	0.77	0.75	0.001	0.001
1R	T	5	0.36	0.68	0.71	0.70	0.78	0.79	0.001	0.001
2R	R	5	0.28	0.41	0.85	0.83	0.91	0.91	0.002	0.002
2R	P	5	0.29	0.47	0.87	0.88	0.92	0.92	0.001	0.001
2R	T	5	0.22	0.35	0.88	0.87	0.92	0.90	0.002	0.002
IBD	R	4	0.36	0.78	0.72	0.64	0.96	0.91	0.001	0.001
IBD	P	4	0.38	0.73	0.96	0.96	0.99	0.98	0.001	0.002
IBD	T	4	0.38	0.68	0.51	0.35	0.76	0.63	0.001	0.002

		20 individuals per deme								
Demo-graphy	Sampling Design	K	GIF K	GIF K-1	Emp P K	Emp P K-1	TPR K	TPR K-1	FPR K	FPR K-1
1R	R	5	1.13	2.62	0.72	0.68	0.73	0.73	0.001	0.001
1R	P	5	1.10	4.04	0.74	0.68	0.77	0.73	0.001	0.002
1R	T	5	0.89	1.61	0.73	0.72	0.79	0.78	0.002	0.001
2R	R	5	0.59	1.14	0.68	0.68	0.85	0.88	0.001	0.002
2R	P	5	0.73	1.53	0.87	0.86	0.89	0.91	0.001	0.001
2R	T	5	0.55	0.87	0.84	0.88	0.90	0.91	0.001	0.001
IBD	R	4	1.08	1.44	0.34	0.32	0.63	0.69	0.001	0.001
IBD	P	4	1.09	1.65	0.84	0.84	0.91	0.96	0.001	0.002
IBD	T	4	1.11	1.53	0.15	0.30	0.31	0.52	0.001	0.001
IM	R	4	0.19	0.41	0.54	0.45	0.68	0.55	0.001	0.001
IM	P	2	0.54	1.70	0.75	0.80	0.88	0.94	0.001	0.002
IM	T	2	0.58	1.71	0.80	0.79	0.88	0.94	0.001	0.002

Table S4: LFMM results for power (from empirical p -values) and true and false positive rates (from 0.05 FDR cutoff) using K and K-1. GIF is the genomic inflation factor. For the 6 individual IM demography scenarios the best value of K was 1, so no reduction in K was tested for these cases.

Demo- graphy	Sampling Design	Envir. Surface	6 individuals per deme								
			K	GIF K	GIF K-1	Emp P K	Emp P K-1	TPR K	TPR K-1	FPR K	FPR K-1
1R	R	453	5	0.51	1.06	0.66	0.67	0.78	0.80	0.001	0.002
1R	R	950	5	0.45	0.94	0.62	0.65	0.68	0.70	0.001	0.001
1R	R	988	5	0.42	0.66	0.64	0.64	0.69	0.68	0.000	0.001
1R	P	453	5	0.43	0.88	0.76	0.75	0.82	0.82	0.001	0.001
1R	P	950	5	0.63	1.71	0.71	0.70	0.76	0.74	0.001	0.001
1R	P	988	5	0.49	1.10	0.66	0.59	0.72	0.68	0.001	0.001
1R	T	453	5	0.41	0.90	0.75	0.75	0.85	0.86	0.001	0.001
1R	T	950	5	0.36	0.63	0.67	0.65	0.71	0.71	0.001	0.002
1R	T	988	5	0.33	0.52	0.70	0.69	0.78	0.78	0.001	0.001
2R	R	453	5	0.31	0.46	0.92	0.91	0.94	0.94	0.003	0.002
2R	R	950	5	0.25	0.41	0.86	0.86	0.91	0.91	0.002	0.002
2R	R	988	5	0.27	0.35	0.79	0.74	0.89	0.88	0.002	0.002
2R	P	453	5	0.27	0.45	0.87	0.88	0.93	0.92	0.001	0.002
2R	P	950	5	0.35	0.56	0.88	0.90	0.93	0.93	0.001	0.001
2R	P	988	5	0.27	0.40	0.87	0.87	0.90	0.90	0.002	0.001
2R	T	453	5	0.23	0.38	0.90	0.89	0.95	0.93	0.002	0.002
2R	T	950	5	0.26	0.40	0.87	0.88	0.90	0.90	0.002	0.002
2R	T	988	5	0.18	0.27	0.88	0.85	0.90	0.88	0.001	0.001
IBD	R	453	4	0.40	0.81	0.99	0.99	1.00	0.99	0.001	0.001
IBD	R	950	4	0.35	0.83	0.79	0.58	0.97	0.91	0.002	0.002
IBD	R	988	4	0.34	0.72	0.39	0.34	0.91	0.83	0.001	0.001
IBD	P	453	4	0.36	0.70	0.98	0.98	0.99	0.99	0.001	0.002
IBD	P	950	4	0.42	0.81	0.99	0.99	0.99	0.99	0.002	0.002
IBD	P	988	4	0.36	0.68	0.92	0.92	1.00	0.97	0.002	0.001
IBD	T	453	4	0.48	0.83	0.63	0.44	0.74	0.58	0.001	0.001
IBD	T	950	4	0.32	0.66	0.68	0.25	0.87	0.69	0.002	0.002
IBD	T	988	4	0.35	0.55	0.21	0.36	0.68	0.63	0.001	0.003

Table S4 (continued)

Demo- graphy	Sampling Design	Envir. Surface	20 individuals per deme								
			K	GIF K	GIF K-1	Emp P K	Emp P K-1	TPR K	TPR K-1	FPR K	FPR K-1
1R	R	453	5	1.17	2.85	0.77	0.73	0.79	0.78	0.001	0.002
1R	R	950	5	1.02	3.05	0.65	0.65	0.66	0.68	0.001	0.002
1R	R	988	5	1.19	1.96	0.74	0.67	0.75	0.74	0.000	0.001
1R	P	453	5	1.02	2.89	0.83	0.77	0.85	0.78	0.001	0.001
1R	P	950	5	1.20	5.53	0.70	0.67	0.71	0.69	0.002	0.002
1R	P	988	5	1.08	3.70	0.69	0.61	0.76	0.72	0.001	0.002
1R	T	453	5	0.98	2.15	0.78	0.78	0.85	0.86	0.001	0.001
1R	T	950	5	1.07	1.61	0.65	0.64	0.70	0.71	0.001	0.001
1R	T	988	5	0.64	1.08	0.76	0.73	0.82	0.78	0.003	0.001
2R	R	453	5	0.50	1.73	0.90	0.90	0.92	0.94	0.002	0.002
2R	R	950	5	0.65	0.93	0.82	0.85	0.88	0.89	0.001	0.001
2R	R	988	5	0.60	0.77	0.33	0.29	0.74	0.81	0.001	0.003
2R	P	453	5	0.70	1.29	0.88	0.87	0.89	0.92	0.001	0.001
2R	P	950	5	0.69	1.78	0.87	0.84	0.90	0.90	0.001	0.001
2R	P	988	5	0.79	1.53	0.86	0.86	0.88	0.90	0.001	0.002
2R	T	453	5	0.57	0.99	0.85	0.91	0.90	0.94	0.001	0.001
2R	T	950	5	0.67	1.11	0.87	0.87	0.89	0.88	0.001	0.001
2R	T	988	5	0.42	0.51	0.80	0.86	0.90	0.92	0.001	0.002
IBD	R	453	4	1.16	1.61	0.62	0.73	0.84	0.93	0.000	0.000
IBD	R	950	4	1.12	1.54	0.30	0.13	0.76	0.75	0.001	0.001
IBD	R	988	4	0.95	1.17	0.09	0.11	0.30	0.39	0.001	0.001
IBD	P	453	4	1.20	1.57	0.82	0.77	0.89	0.96	0.000	0.002
IBD	P	950	4	1.12	1.85	0.86	0.99	0.95	0.99	0.002	0.002
IBD	P	988	4	0.95	1.54	0.83	0.76	0.90	0.92	0.002	0.001
IBD	T	453	4	1.37	1.90	0.15	0.23	0.19	0.38	0.000	0.000
IBD	T	950	4	1.09	1.30	0.15	0.48	0.42	0.65	0.001	0.002
IBD	T	988	4	0.86	1.39	0.16	0.18	0.33	0.53	0.002	0.001
IM	R	453	4	0.22	0.50	0.61	0.41	0.68	0.48	0.001	0.000
IM	R	950	4	0.20	0.40	0.45	0.51	0.61	0.57	0.000	0.001
IM	R	988	4	0.16	0.34	0.57	0.42	0.74	0.60	0.003	0.001
IM	P	453	2	0.56	1.71	0.80	0.86	0.88	0.95	0.001	0.002
IM	P	950	2	0.53	1.72	0.87	0.86	0.88	0.95	0.000	0.001
IM	P	988	2	0.52	1.68	0.58	0.67	0.87	0.92	0.003	0.002
IM	T	453	2	0.54	1.69	0.83	0.92	0.91	0.98	0.001	0.001
IM	T	950	2	0.59	1.73	0.76	0.76	0.84	0.91	0.002	0.002
IM	T	988	2	0.62	1.70	0.82	0.69	0.89	0.93	0.001	0.002

Table S5: Change in power (from empirical *p*-values) and true and false positive rates (from cutoffs) for RDA using three different approaches for partialling out population structure. There are no MEM corrections for the IM demography, which has no significant spatial structure. Ancestry corrections apply only to 20 individual runs, where $K \neq 1$.

Demo- graphy	Sampling Design	Envir. Surface	Change in power (empirical <i>p</i> -values)					
			6 individuals per deme			20 individuals per deme		
			Ancestry	MEMs uncorr. Hab.	All retained MEMs	Ancestry	MEMs uncorr. Hab.	All retained MEMs
1R	R	453	-0.63	-0.73	-0.78	-0.33	-0.28	-0.63
1R	R	950	-0.49	-0.53	-0.70	-0.46	-0.12	-0.57
1R	R	988	-0.59	-0.74	-0.68	-0.38	NA	-0.67
1R	P	453	-0.51	-0.63	-0.62	-0.17	-0.01	-0.38
1R	P	950	-0.61	-0.47	-0.73	-0.38	-0.16	-0.38
1R	P	988	-0.56	-0.57	-0.58	-0.13	-0.22	-0.42
1R	T	453	-0.51	-0.58	-0.92	-0.08	-0.05	-0.89
1R	T	950	-0.42	-0.47	-0.73	-0.25	-0.11	-0.57
1R	T	988	-0.44	-0.55	-0.71	-0.14	-0.19	-0.70
2R	R	453	-0.82	-0.92	-0.95	-0.52	-0.48	-0.89
2R	R	950	-0.78	-0.66	-0.91	-0.60	-0.09	-0.72
2R	R	988	-0.81	-0.81	-0.77	-0.78	NA	-0.78
2R	P	453	-0.88	-0.60	-0.80	-0.77	-0.06	-0.45
2R	P	950	-0.93	-0.33	-0.92	-0.70	-0.04	-0.75
2R	P	988	-0.79	-0.29	-0.77	-0.73	-0.15	-0.50
2R	T	453	-0.78	-0.28	-0.94	-0.44	-0.05	-0.91
2R	T	950	-0.77	-0.58	-0.80	-0.62	-0.06	-0.75
2R	T	988	-0.74	-0.29	-0.72	-0.56	-0.05	-0.57
IBD	R	453	-1.00	-1.00	-1.00	-0.95	-0.93	-1.00
IBD	R	950	-0.92	-0.92	-0.99	-0.92	-0.83	-0.95
IBD	R	988	-0.93	-0.93	-0.99	-0.93	NA	-0.93
IBD	P	453	-0.93	-0.92	-0.93	-0.93	-0.34	-0.87
IBD	P	950	-0.98	-0.17	-0.98	-0.92	-0.49	-0.90
IBD	P	988	-0.93	-0.18	-0.93	-0.93	-0.54	-0.93
IBD	T	453	-0.93	-0.84	-0.93	-0.93	-0.69	-0.93
IBD	T	950	-0.93	-0.92	-0.99	-0.93	-0.75	-0.93
IBD	T	988	-0.93	-0.91	-0.93	-0.93	-0.91	-0.92
IM	R	453	-	-	-	-0.55	-	-
IM	R	950	-	-	-	-0.56	-	-
IM	R	988	-	-	-	-0.59	-	-
IM	P	453	-	-	-	-0.76	-	-
IM	P	950	-	-	-	-0.81	-	-
IM	P	988	-	-	-	-0.66	-	-
IM	T	453	-	-	-	-0.93	-	-
IM	T	950	-	-	-	-0.79	-	-
IM	T	988	-	-	-	-0.69	-	-

Table S5 (continued)

Demo- graphy	Sampling Design	Envir. Surface	Change in TPR (cutoffs)					
			6 individuals per deme			20 individuals per deme		
			Ancestry	MEMs uncorr. Hab.	All retained MEMs	Ancestry	MEMs uncorr. Hab.	All retained MEMs
1R	R	453	-0.53	-0.60	-0.75	-0.21	-0.22	-0.46
1R	R	950	-0.48	-0.32	-0.70	-0.31	-0.04	-0.43
1R	R	988	-0.39	-0.62	-0.67	-0.15	-0.81	-0.57
1R	P	453	-0.35	-0.54	-0.63	-0.09	-0.02	-0.30
1R	P	950	-0.52	-0.28	-0.58	-0.24	-0.08	-0.28
1R	P	988	-0.41	-0.48	-0.62	-0.15	-0.09	-0.28
1R	T	453	-0.29	-0.44	-0.91	-0.07	-0.05	-0.76
1R	T	950	-0.37	-0.32	-0.65	-0.19	-0.07	-0.45
1R	T	988	-0.18	-0.24	-0.70	-0.03	-0.05	-0.68
2R	R	453	-0.72	-0.82	-0.95	-0.41	-0.26	-0.80
2R	R	950	-0.62	-0.48	-0.89	-0.24	-0.03	-0.49
2R	R	988	-0.79	-0.78	-0.77	-0.79	-0.92	-0.59
2R	P	453	-0.75	-0.48	-0.69	-0.56	-0.02	-0.28
2R	P	950	-0.73	-0.22	-0.77	-0.34	-0.03	-0.34
2R	P	988	-0.72	-0.14	-0.63	-0.57	-0.13	-0.31
2R	T	453	-0.68	-0.09	-0.84	-0.32	-0.05	-0.79
2R	T	950	-0.67	-0.35	-0.69	-0.58	-0.04	-0.54
2R	T	988	-0.64	-0.25	-0.61	-0.38	-0.05	-0.48
IBD	R	453	-0.97	-0.93	-0.99	-0.93	-0.92	-0.96
IBD	R	950	-0.92	-0.91	-0.95	-0.92	-0.58	-0.92
IBD	R	988	-0.93	-0.93	-0.93	-0.93	-1.00	-0.93
IBD	P	453	-0.93	-0.91	-0.91	-0.93	-0.29	-0.76
IBD	P	950	-0.92	-0.10	-0.92	-0.87	-0.40	-0.87
IBD	P	988	-0.93	-0.12	-0.93	-0.93	-0.36	-0.93
IBD	T	453	-0.93	-0.63	-0.93	-0.93	-0.54	-0.90
IBD	T	950	-0.93	-0.87	-0.93	-0.92	-0.57	-0.89
IBD	T	988	-0.93	-0.79	-0.93	-0.93	-0.78	-0.91
IM	R	453	-	-	-	-0.60	-	-
IM	R	950	-	-	-	-0.52	-	-
IM	R	988	-	-	-	-0.61	-	-
IM	P	453	-	-	-	-0.77	-	-
IM	P	950	-	-	-	-0.78	-	-
IM	P	988	-	-	-	-0.78	-	-
IM	T	453	-	-	-	-0.80	-	-
IM	T	950	-	-	-	-0.77	-	-
IM	T	988	-	-	-	-0.79	-	-

Table S5 (continued)

Demo- graphy	Sampling Design	Envir. Surface	Change in FPR (cutoffs)					
			6 individuals per deme			20 individuals per deme		
			Ancestry	MEMs uncorr. Hab.	All retained MEMs	Ancestry	MEMs uncorr. Hab.	All retained MEMs
1R	R	453	0.0016	0.0018	0.0016	0.0012	0.0007	0.0018
1R	R	950	0.0017	0.0011	0.0016	0.0002	0.0000	0.0013
1R	R	988	0.0014	0.0013	0.0026	0.0009	-0.0001	0.0015
1R	P	453	0.0008	0.0018	0.0014	0.0009	0.0000	0.0008
1R	P	950	0.0013	0.0017	0.0026	0.0005	0.0006	0.0015
1R	P	988	0.0008	0.0011	0.0020	0.0000	0.0007	0.0010
1R	T	453	0.0005	0.0016	0.0029	0.0001	0.0000	0.0017
1R	T	950	0.0008	0.0009	0.0018	0.0004	0.0004	0.0013
1R	T	988	0.0008	0.0005	0.0017	0.0005	0.0004	0.0015
2R	R	453	0.0017	0.0016	0.0027	0.0012	0.0007	0.0017
2R	R	950	0.0019	0.0015	0.0022	0.0012	0.0004	0.0017
2R	R	988	0.0026	0.0012	0.0020	0.0021	-0.0002	0.0011
2R	P	453	0.0017	0.0013	0.0019	0.0016	0.0003	0.0010
2R	P	950	0.0027	0.0011	0.0021	0.0016	0.0003	0.0019
2R	P	988	0.0021	0.0004	0.0018	0.0013	0.0003	0.0011
2R	T	453	0.0014	0.0008	0.0017	0.0007	0.0000	0.0024
2R	T	950	0.0024	0.0005	0.0028	0.0018	0.0003	0.0016
2R	T	988	0.0019	0.0011	0.0017	0.0010	0.0002	0.0011
IBD	R	453	0.0024	0.0022	0.0025	0.0023	0.0017	0.0026
IBD	R	950	0.0025	0.0019	0.0022	0.0020	0.0008	0.0020
IBD	R	988	0.0031	0.0030	0.0029	0.0025	0.0000	0.0027
IBD	P	453	0.0024	0.0021	0.0019	0.0027	0.0003	0.0016
IBD	P	950	0.0020	0.0003	0.0029	0.0022	0.0009	0.0021
IBD	P	988	0.0028	0.0004	0.0033	0.0027	0.0014	0.0023
IBD	T	453	0.0024	0.0013	0.0012	0.0018	0.0010	0.0028
IBD	T	950	0.0024	0.0021	0.0025	0.0016	0.0015	0.0012
IBD	T	988	0.0019	0.0019	0.0014	0.0012	0.0013	0.0012
IM	R	453	-	-	-	0.0021	-	-
IM	R	950	-	-	-	0.0020	-	-
IM	R	988	-	-	-	0.0022	-	-
IM	P	453	-	-	-	0.0021	-	-
IM	P	950	-	-	-	0.0021	-	-
IM	P	988	-	-	-	0.0016	-	-
IM	T	453	-	-	-	0.0028	-	-
IM	T	950	-	-	-	0.0029	-	-
IM	T	988	-	-	-	0.0026	-	-

Table S6: Percent variance explained for Random Forest models.

Demography	Design	Env	PVE: 6 ind./deme	PVE: 20 ind./deme
1R	R	453	0.86	0.85
1R	R	950	0.81	0.80
1R	R	988	0.81	0.79
1R	P	453	0.88	0.87
1R	P	950	0.90	0.88
1R	P	988	0.88	0.88
1R	T	453	0.83	0.82
1R	T	950	0.87	0.86
1R	T	988	0.82	0.80
2R	R	453	0.85	0.84
2R	R	950	0.80	0.80
2R	R	988	0.81	0.79
2R	P	453	0.87	0.86
2R	P	950	0.90	0.88
2R	P	988	0.89	0.88
2R	T	453	0.83	0.82
2R	T	950	0.86	0.86
2R	T	988	0.82	0.80
IBD	R	453	0.85	0.84
IBD	R	950	0.81	0.79
IBD	R	988	0.81	0.79
IBD	P	453	0.88	0.86
IBD	P	950	0.89	0.88
IBD	P	988	0.89	0.88
IBD	T	453	0.85	0.83
IBD	T	950	0.84	0.84
IBD	T	988	0.82	0.80
IM	R	453	0.83	0.82
IM	R	950	0.85	0.83
IM	R	988	0.81	0.80
IM	P	453	0.88	0.87
IM	P	950	0.91	0.89
IM	P	988	0.88	0.88
IM	T	453	0.86	0.85
IM	T	950	0.88	0.86
IM	T	988	0.85	0.85

Table S7: Correlations between habitat and x- and y-coordinates of demes; average and maximum trend in neutral markers; average and maximum levels of local adaptation.

Demo- graphy	De- sign	Env	Correlations:		Neutral trend: 6 indiv./deme		Neutral trend: 20 indiv./deme		Local adaptation: 6 indiv./deme		Local adaptation: 20 indiv./deme	
			Hab. and X	Hab. and Y	Avg.	Max.	Avg.	Max.	Avg	Max.	Avg.	Max.
1R	R	453	0.00	0.65	0.11	0.61	0.20	0.79	0.49	0.76	0.55	0.80
1R	R	950	0.05	0.63	0.11	0.63	0.20	0.80	0.37	0.68	0.42	0.70
1R	R	988	0.03	0.55	0.11	0.64	0.20	0.80	0.36	0.65	0.42	0.67
1R	P	453	0.00	0.84	0.12	0.64	0.21	0.80	0.52	0.80	0.57	0.80
1R	P	950	0.00	0.69	0.13	0.68	0.22	0.83	0.52	0.83	0.56	0.83
1R	P	988	-0.11	0.70	0.12	0.62	0.21	0.82	0.44	0.83	0.50	0.84
1R	T	453	0.13	0.82	0.13	0.67	0.23	0.84	0.42	0.70	0.46	0.71
1R	T	950	0.12	0.83	0.12	0.68	0.22	0.84	0.38	0.73	0.42	0.76
1R	T	988	-0.14	0.78	0.12	0.60	0.21	0.80	0.36	0.70	0.41	0.73
2R	R	453	0.00	0.65	0.14	0.71	0.25	0.83	0.55	0.74	0.62	0.75
2R	R	950	0.05	0.63	0.13	0.70	0.24	0.83	0.45	0.67	0.51	0.68
2R	R	988	0.03	0.55	0.14	0.69	0.25	0.83	0.42	0.68	0.49	0.70
2R	P	453	0.00	0.84	0.14	0.70	0.25	0.85	0.58	0.80	0.64	0.81
2R	P	950	0.00	0.69	0.14	0.76	0.26	0.85	0.61	0.83	0.66	0.84
2R	P	988	-0.11	0.70	0.15	0.73	0.26	0.84	0.54	0.83	0.61	0.84
2R	T	453	0.13	0.82	0.15	0.80	0.27	0.91	0.49	0.71	0.55	0.73
2R	T	950	0.12	0.83	0.14	0.70	0.26	0.87	0.45	0.74	0.51	0.76
2R	T	988	-0.14	0.78	0.14	0.70	0.26	0.82	0.41	0.71	0.48	0.71
IBD	R	453	0.00	0.65	0.06	0.42	0.11	0.58	0.61	0.72	0.65	0.74
IBD	R	950	0.05	0.63	0.06	0.43	0.10	0.59	0.48	0.68	0.52	0.69
IBD	R	988	0.03	0.55	0.06	0.41	0.10	0.56	0.44	0.68	0.48	0.69
IBD	P	453	0.00	0.84	0.06	0.43	0.11	0.56	0.63	0.81	0.68	0.82
IBD	P	950	0.00	0.69	0.07	0.44	0.11	0.63	0.68	0.83	0.72	0.83
IBD	P	988	-0.11	0.70	0.06	0.41	0.10	0.57	0.60	0.83	0.64	0.84
IBD	T	453	0.13	0.82	0.07	0.47	0.12	0.63	0.43	0.71	0.46	0.71
IBD	T	950	0.12	0.83	0.06	0.56	0.10	0.69	0.42	0.71	0.46	0.72
IBD	T	988	-0.14	0.78	0.07	0.41	0.11	0.58	0.35	0.69	0.37	0.69
IM	R	453	0.00	0.65	0.02	0.25	0.02	0.22	0.17	0.74	0.26	0.79
IM	R	950	0.05	0.63	0.02	0.18	0.02	0.20	0.16	0.76	0.24	0.82
IM	R	988	0.03	0.55	0.02	0.25	0.02	0.28	0.18	0.72	0.26	0.77
IM	P	453	0.00	0.84	0.02	0.17	0.02	0.18	0.26	0.82	0.38	0.87
IM	P	950	0.00	0.69	0.02	0.20	0.02	0.22	0.27	0.85	0.40	0.87
IM	P	988	-0.11	0.70	0.02	0.20	0.02	0.20	0.26	0.82	0.39	0.86
IM	T	453	0.13	0.82	0.02	0.21	0.02	0.18	0.25	0.76	0.38	0.81
IM	T	950	0.12	0.83	0.02	0.19	0.02	0.21	0.24	0.82	0.36	0.84
IM	T	988	-0.14	0.78	0.02	0.27	0.02	0.22	0.25	0.80	0.37	0.83

Table S8: Parameters from cRDA runs: number of axes retained by the parallel analysis criterion, and component axes significantly correlated with the constrained ordination axis. Results shown for all selection strengths and simulation data with weak selection only.

Demo- graphy	De- sign	Env	All selection strengths				Weak selection only			
			6 ind.		20ind		6 ind.		20ind	
			Ret. axes	Signif. Comp.	Ret. axes	Signif. Comp.	Ret. axes	Signif. Comp.	Ret. axes	Signif. Comp.
1R	R	453	540	2	1800	2	540	3	0	0
1R	R	950	540	2	1800	2	540	2	1800	0
1R	R	988	540	2	1800	2	540	2	1800	9
1R	P	453	540	2	1800	2	540	2	0	0
1R	P	950	540	2	1800	2	540	2	1800	2
1R	P	988	540	2	1800	2	540	2	1800	8, 11, 1300
1R	T	453	540	2	1800	2	540	3	1800	7, 995, 1421
1R	T	950	540	2	1800	2	540	3	1800	1277
1R	T	988	540	2	1800	2	540	2	1800	7, 9
2R	R	453	540	2	1800	2	540	2	1800	1, 2
2R	R	950	540	2	1800	2	540	1, 2	1800	1, 2
2R	R	988	540	1, 2	1800	1, 2	540	1, 2	1800	1, 1348
2R	P	453	540	2	1800	2	540	2	1800	2
2R	P	950	540	2	1800	2	540	2	1800	2
2R	P	988	540	2	1800	2	540	1, 2	1800	1, 2
2R	T	453	540	2	1800	2	540	2	1800	2
2R	T	950	540	2	1800	2	540	2	1800	1, 2
2R	T	988	540	2	1800	2	540	2	1800	2
IBD	R	453	540	1	1800	1	540	1	1800	1
IBD	R	950	540	1	1800	1	540	1	1800	1
IBD	R	988	540	1	1800	1	540	1	1800	1
IBD	P	453	540	1	1800	1	540	1	1800	1
IBD	P	950	540	1	1800	1	540	1	1800	1
IBD	P	988	540	1	1800	1	540	1	1800	1
IBD	T	453	540	1	1800	1	540	1	1800	1
IBD	T	950	540	1	1800	1	540	1	1800	1
IBD	T	988	540	1	1800	1	540	1	1800	1
IM	R	453	540	1	1800	1	0	0	0	0
IM	R	950	540	1	1800	1	0	0	1800	137, 1254
IM	R	988	540	1	1800	1	0	0	1800	47
IM	P	453	540	1	1800	1	0	0	1800	3, 1726
IM	P	950	540	1	1800	1	0	0	1800	1, 370, 402, 462, 494, 1521
IM	P	988	540	1	1800	1	0	0	1800	2, 66, 207, 1295, 1385
IM	T	453	540	1	1800	1	0	0	1800	3, 891, 1311, 1559, 1785
IM	T	950	540	1	1800	1	0	0	1800	5, 1600
IM	T	988	540	1	1800	1	540	125	1800	1, 845, 1219, 1681