Supplemental Figures and Tables

Using genotype-environment associations to identify multilocus local adaptation

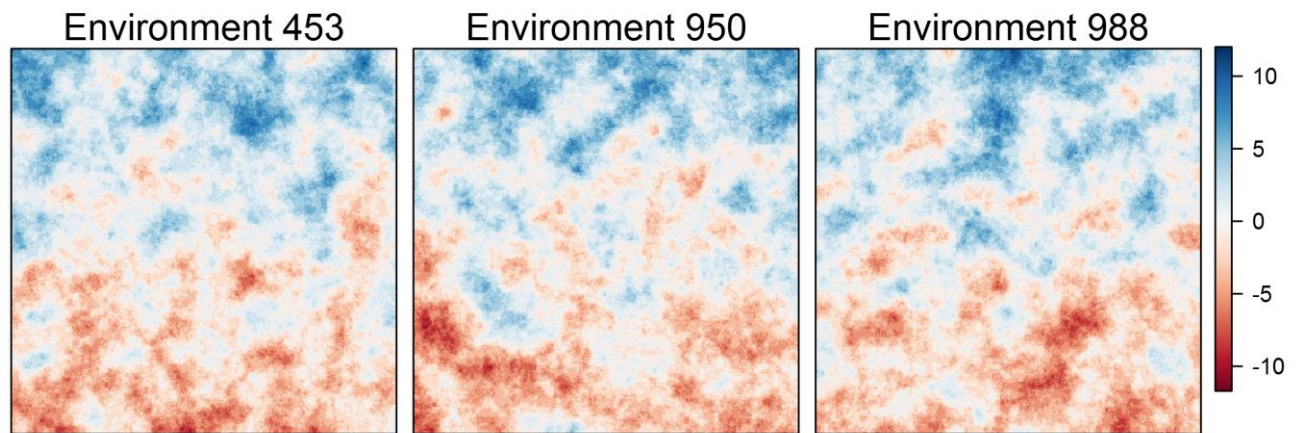Brenna R. Forester, Jesse R. Lasky, Helene H. Wagner, Dean L. Urban

Figure S1. The three environmental surfaces used as replicates from Lotterhos & Whitlock (2015). Colors represent values of the environment.
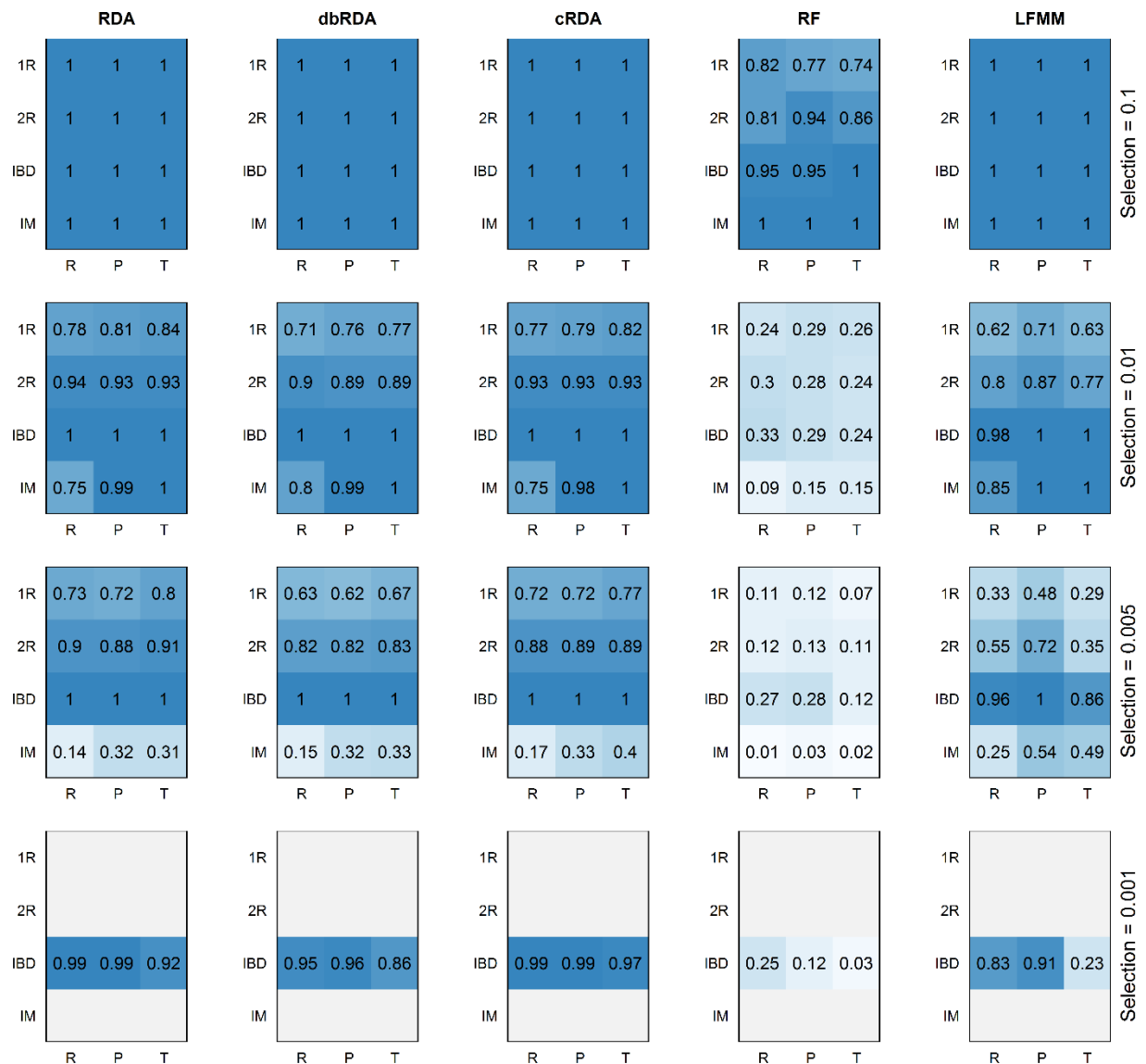
Figure S2. Average true positive rates for different levels of selection (rows) from five methods (columns) using locus rankings and a sample size of 6 individuals per deme. Each method shows results for different sampling strategies (R = random, P = pairs, T = transects) and demographies (1R and 2R = 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 true positive rates for different levels of selection (rows) from five methods (columns) using the best cutoff for each method and 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 S4. Average true positive rates for different levels of selection (rows) from five methods (columns) using the best cutoff for each method and a sample size of 20 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).
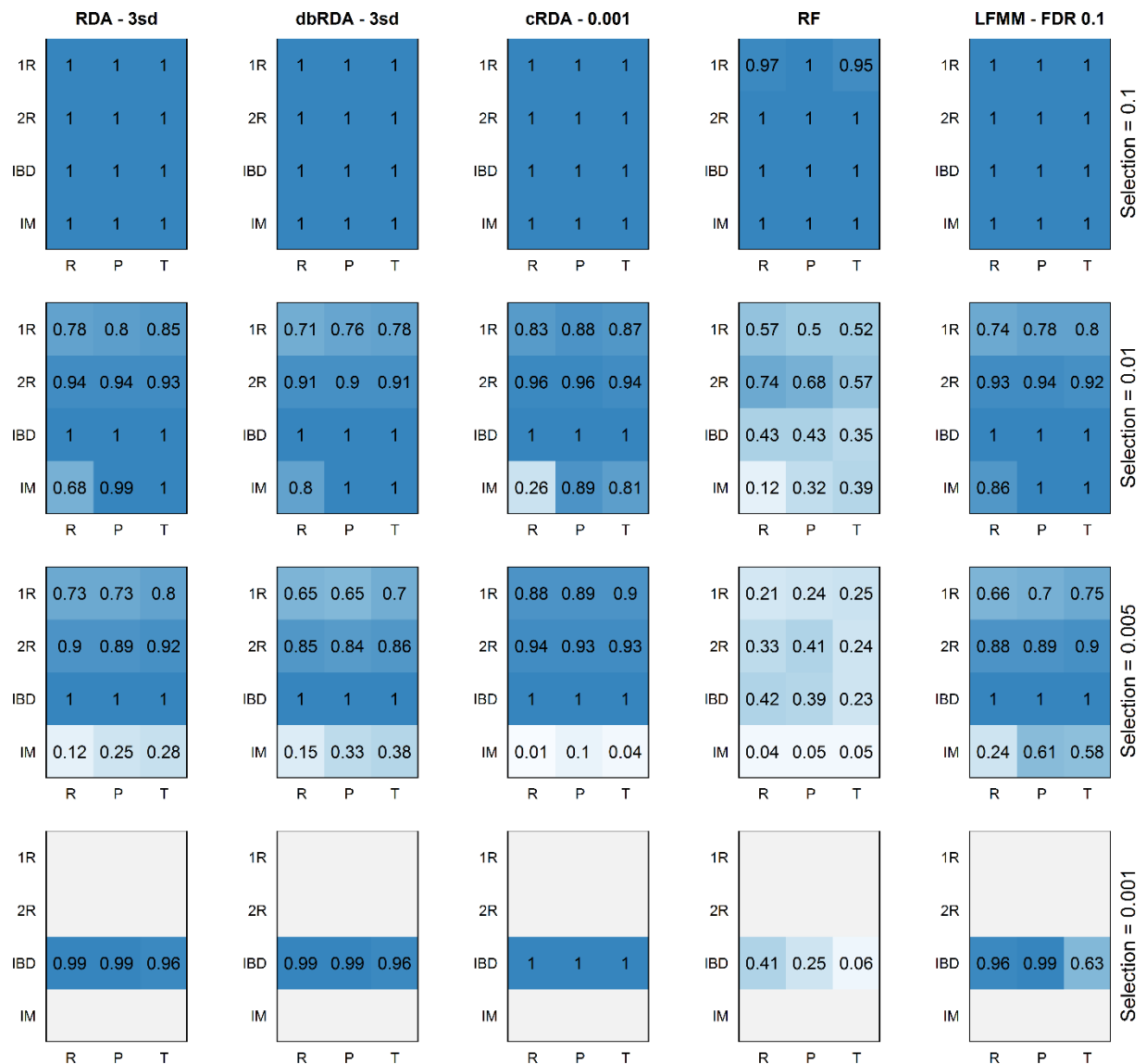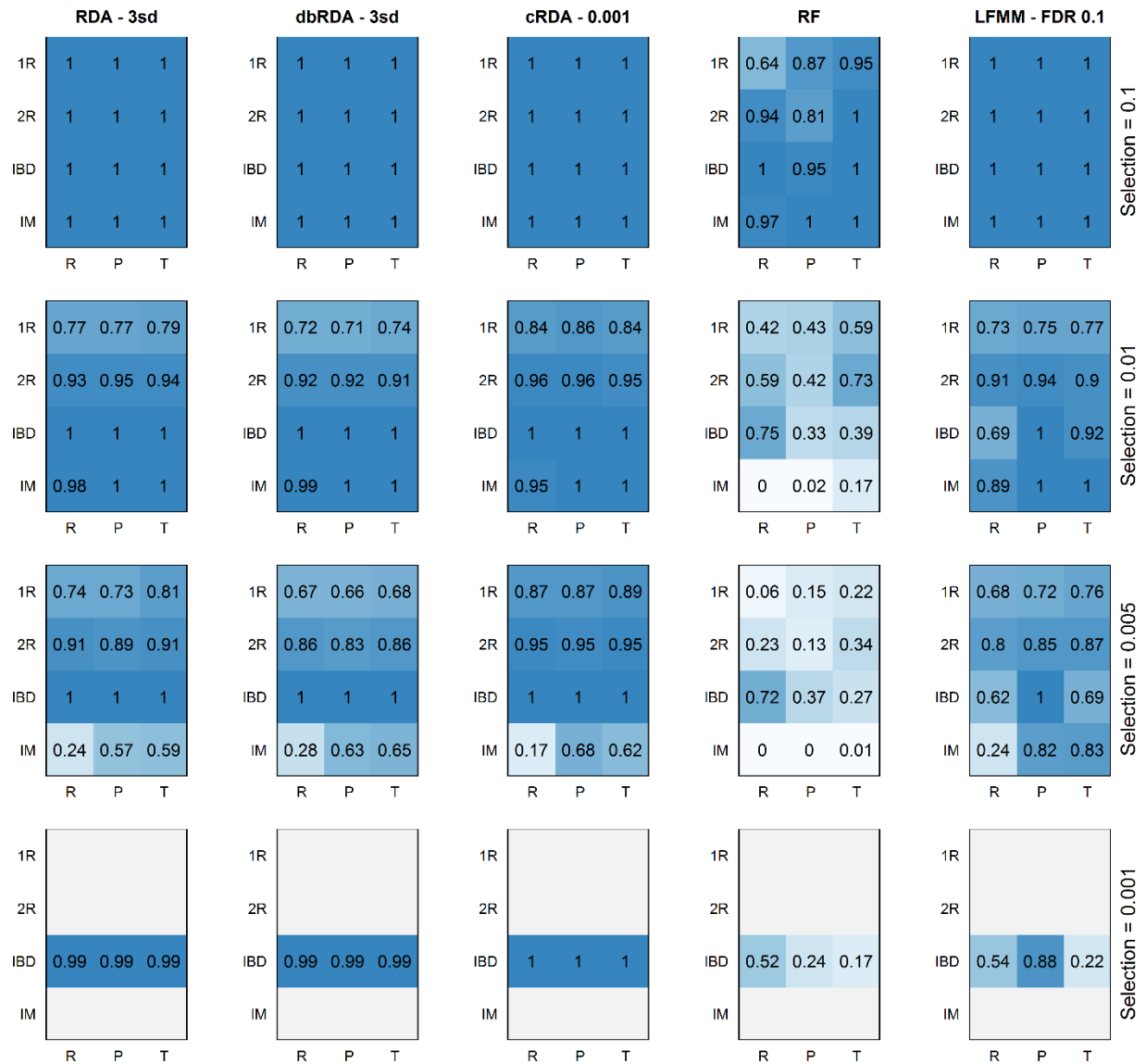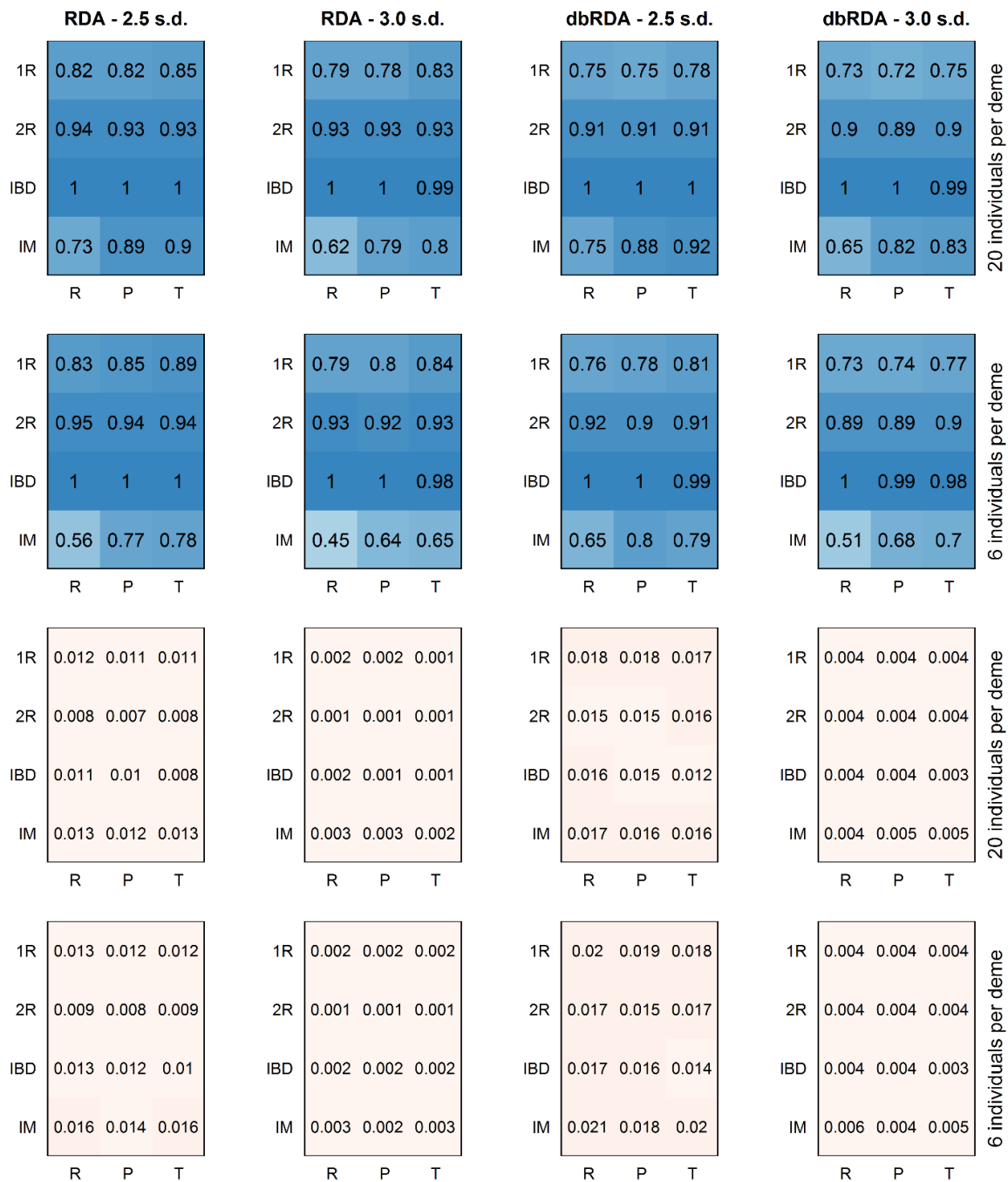
RDA - 2.5 s.d. (20 individuals per deme)

	R	P	T
1R	0.82	0.82	0.85
2R	0.94	0.93	0.93
IBD	1	1	1
IM	0.73	0.89	0.9

RDA - 3.0 s.d. (20 individuals per deme)

	R	P	T
1R	0.79	0.78	0.83
2R	0.93	0.93	0.93
IBD	1	1	0.99
IM	0.62	0.79	0.8

dbRDA - 2.5 s.d. (20 individuals per deme)

	R	P	T
1R	0.75	0.75	0.78
2R	0.91	0.91	0.91
IBD	1	1	1
IM	0.75	0.88	0.92

dbRDA - 3.0 s.d. (20 individuals per deme)

	R	P	T
1R	0.73	0.72	0.75
2R	0.9	0.89	0.9
IBD	1	1	0.99
IM	0.65	0.82	0.83

RDA - 2.5 s.d. (6 individuals per deme)

	R	P	T
1R	0.83	0.85	0.89
2R	0.95	0.94	0.94
IBD	1	1	1
IM	0.56	0.77	0.78

RDA - 3.0 s.d. (6 individuals per deme)

	R	P	T
1R	0.79	0.8	0.84
2R	0.93	0.92	0.93
IBD	1	1	0.98
IM	0.45	0.64	0.65

dbRDA - 2.5 s.d. (6 individuals per deme)

	R	P	T
1R	0.76	0.78	0.81
2R	0.92	0.9	0.91
IBD	1	1	0.99
IM	0.65	0.8	0.79

dbRDA - 3.0 s.d. (6 individuals per deme)

	R	P	T
1R	0.73	0.74	0.77
2R	0.89	0.89	0.9
IBD	1	0.99	0.98
IM	0.51	0.68	0.7

RDA - 2.5 s.d. (20 individuals per deme, false positive)

	R	P	T
1R	0.012	0.011	0.011
2R	0.008	0.007	0.008
IBD	0.011	0.01	0.008
IM	0.013	0.012	0.013

RDA - 3.0 s.d. (20 individuals per deme, false positive)

	R	P	T
1R	0.002	0.002	0.001
2R	0.001	0.001	0.001
IBD	0.002	0.001	0.001
IM	0.003	0.003	0.002

dbRDA - 2.5 s.d. (20 individuals per deme, false positive)

	R	P	T
1R	0.018	0.018	0.017
2R	0.015	0.015	0.016
IBD	0.016	0.015	0.012
IM	0.017	0.016	0.016

dbRDA - 3.0 s.d. (20 individuals per deme, false positive)

	R	P	T
1R	0.004	0.004	0.004
2R	0.004	0.004	0.004
IBD	0.004	0.004	0.003
IM	0.004	0.005	0.005

RDA - 2.5 s.d. (6 individuals per deme, false positive)

	R	P	T
1R	0.013	0.012	0.012
2R	0.009	0.008	0.009
IBD	0.013	0.012	0.01
IM	0.016	0.014	0.016

RDA - 3.0 s.d. (6 individuals per deme, false positive)

	R	P	T
1R	0.002	0.002	0.002
2R	0.001	0.001	0.001
IBD	0.002	0.002	0.002
IM	0.003	0.002	0.003

dbRDA - 2.5 s.d. (6 individuals per deme, false positive)

	R	P	T
1R	0.02	0.019	0.018
2R	0.017	0.015	0.017
IBD	0.017	0.016	0.014
IM	0.021	0.018	0.02

dbRDA - 3.0 s.d. (6 individuals per deme, false positive)

	R	P	T
1R	0.004	0.004	0.004
2R	0.004	0.004	0.004
IBD	0.004	0.004	0.003
IM	0.006	0.004	0.005

Figure S5. Average true positive (blue) and false positive (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).
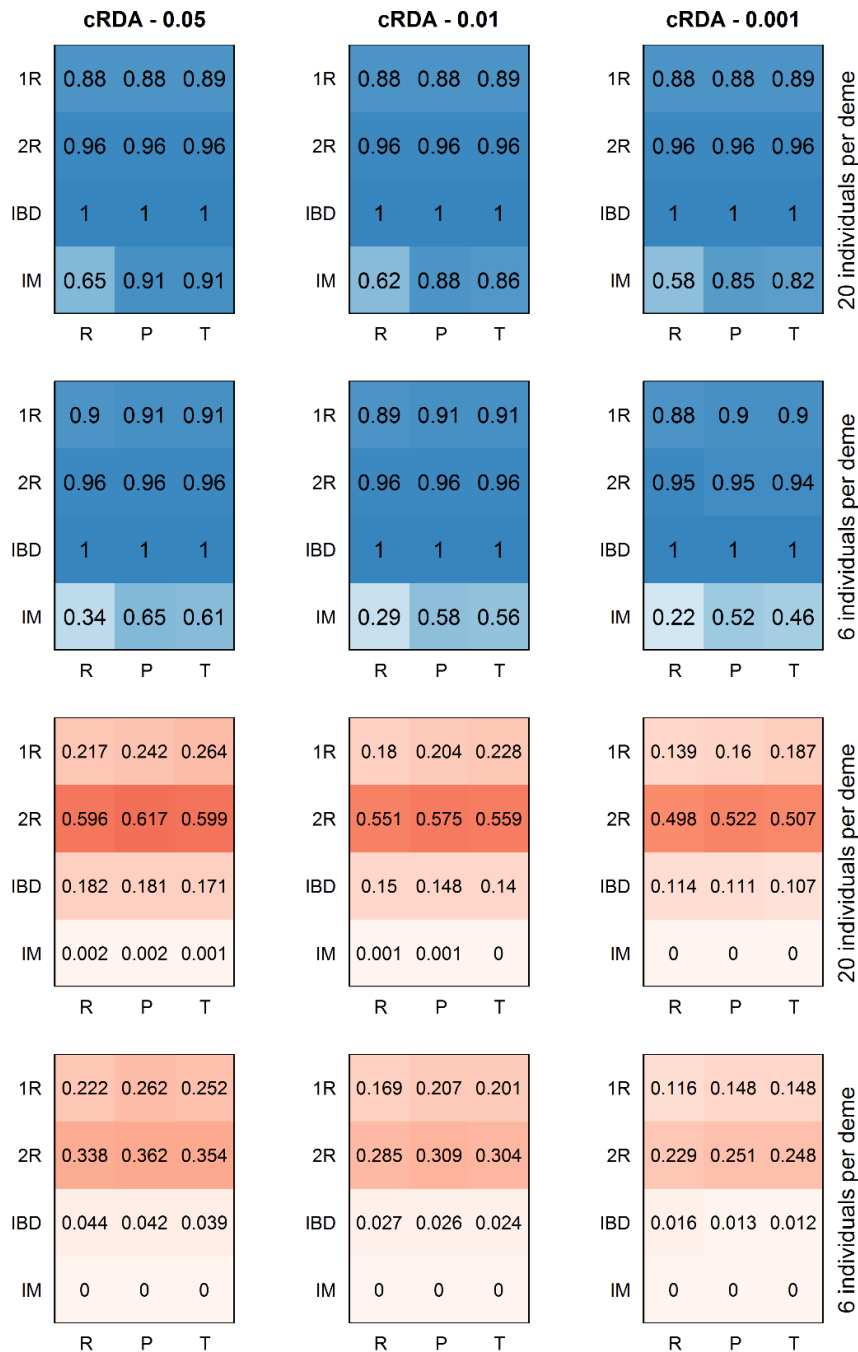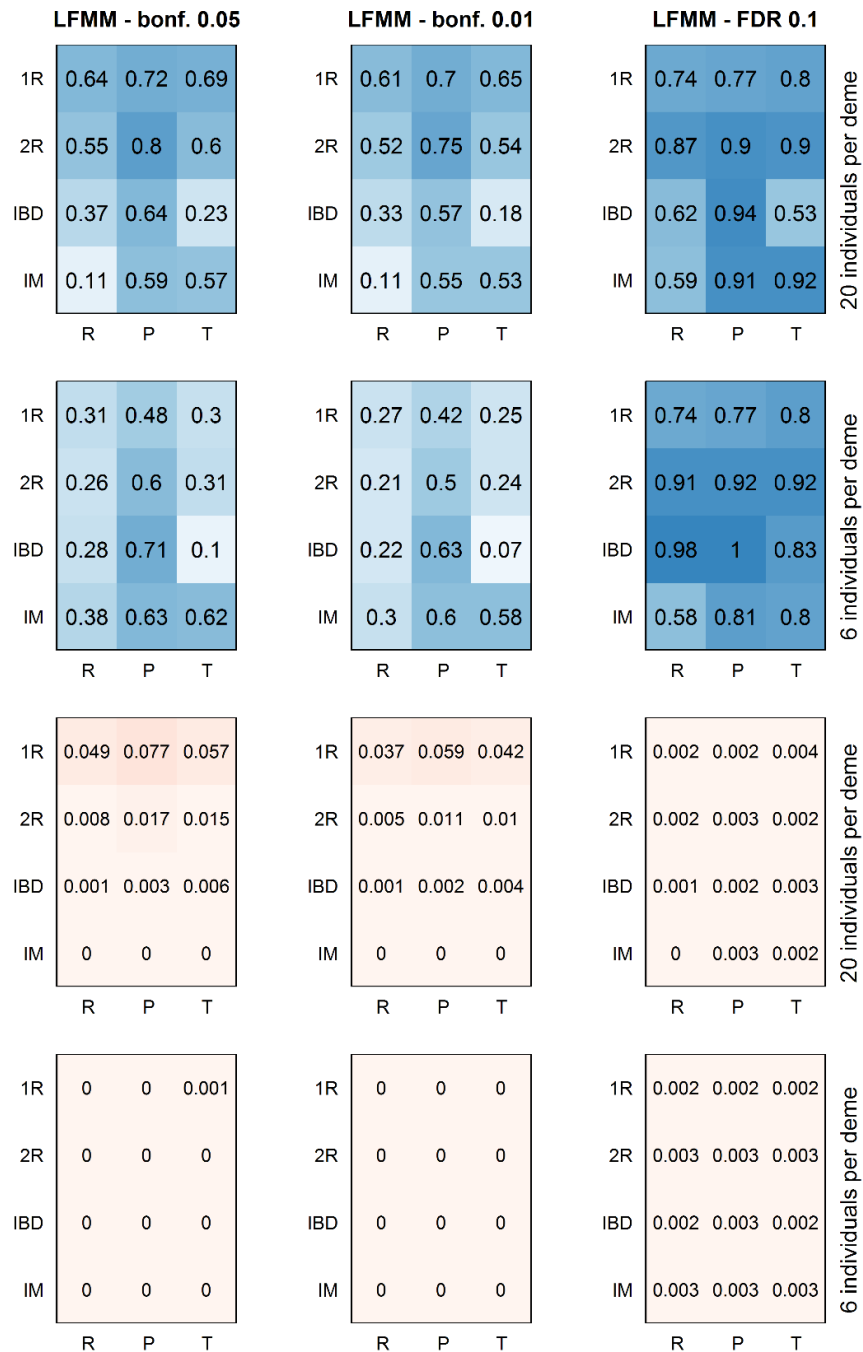
Figure S6. Average true positive (blue) and false positive (red) rates for cRDA using SNP-component correlation cutoffs of alpha = 0.05, 0.01, and 0.001. Each cutoff shows results for different sampling strategies (R = random, P = pairs, T = transects), demographies (1R and 2R = refugial expansion, IBD = equilibrium isolation by distance, IM = equilibrium island model), and sample sizes (rows).
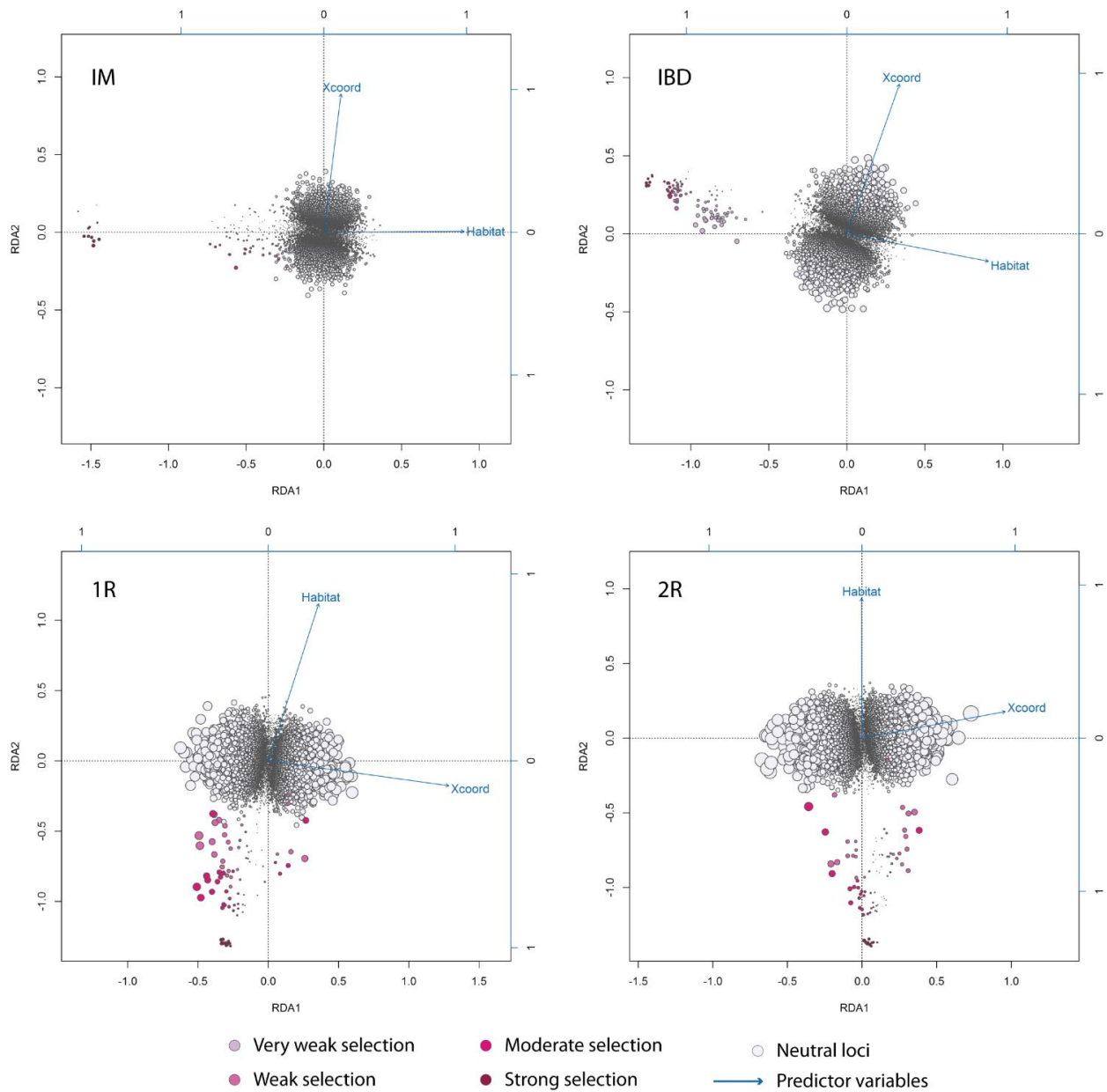
Figure S7. Average true positive (blue) and false positive (red) rates for LFMM using Bonferroni-corrected cutoffs of 0.05 and 0.01, and a false discovery rate cutoff of 0.1. Each cutoff shows results for different sampling strategies (R = random, P = pairs, T = transects), demographies (1R and 2R = refugial expansion, IBD = equilibrium isolation by distance, IM = equilibrium island model), and sample sizes (rows)

Figure S8. Redundancy analysis plots showing loci with point size scaled by their correlation with the spurious X-coordinate variable ("Xcoord"), and correlation of predictor variables with the constrained RDA axes (arrows). Plots are shown for an equilibrium island model (IM), equilibrium isolation by distance model (IBD), and non-equilibrium one- and two- refugial expansion models (1R and 2R) for paired sampling (6 individuals/deme) on environmental surface "453".
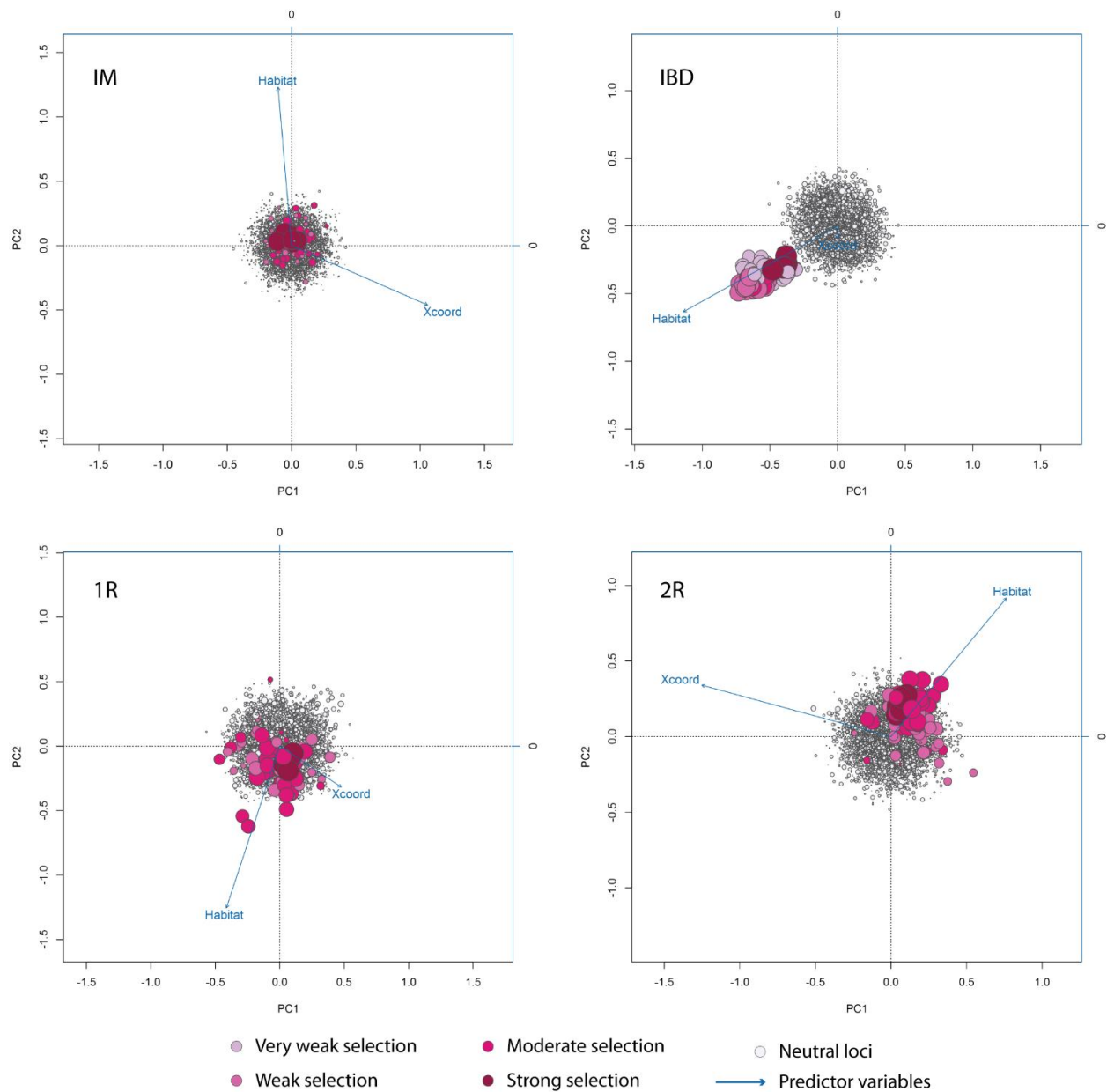
Figure S9. Plots of the first two unconstrained (PC) axes from redundancy analysis showing loci with point size scaled by their correlation with the driving environmental variable ("Habitat"), and correlation of predictor variables with the unconstrained PC axes (arrows). Plots are shown for an equilibrium island model (IM), equilibrium isolation by distance model (IBD), and non-equilibrium one- and two- refugial expansion models (1R and 2R) for paired sampling (6 individuals/deme) on environmental surface "453".
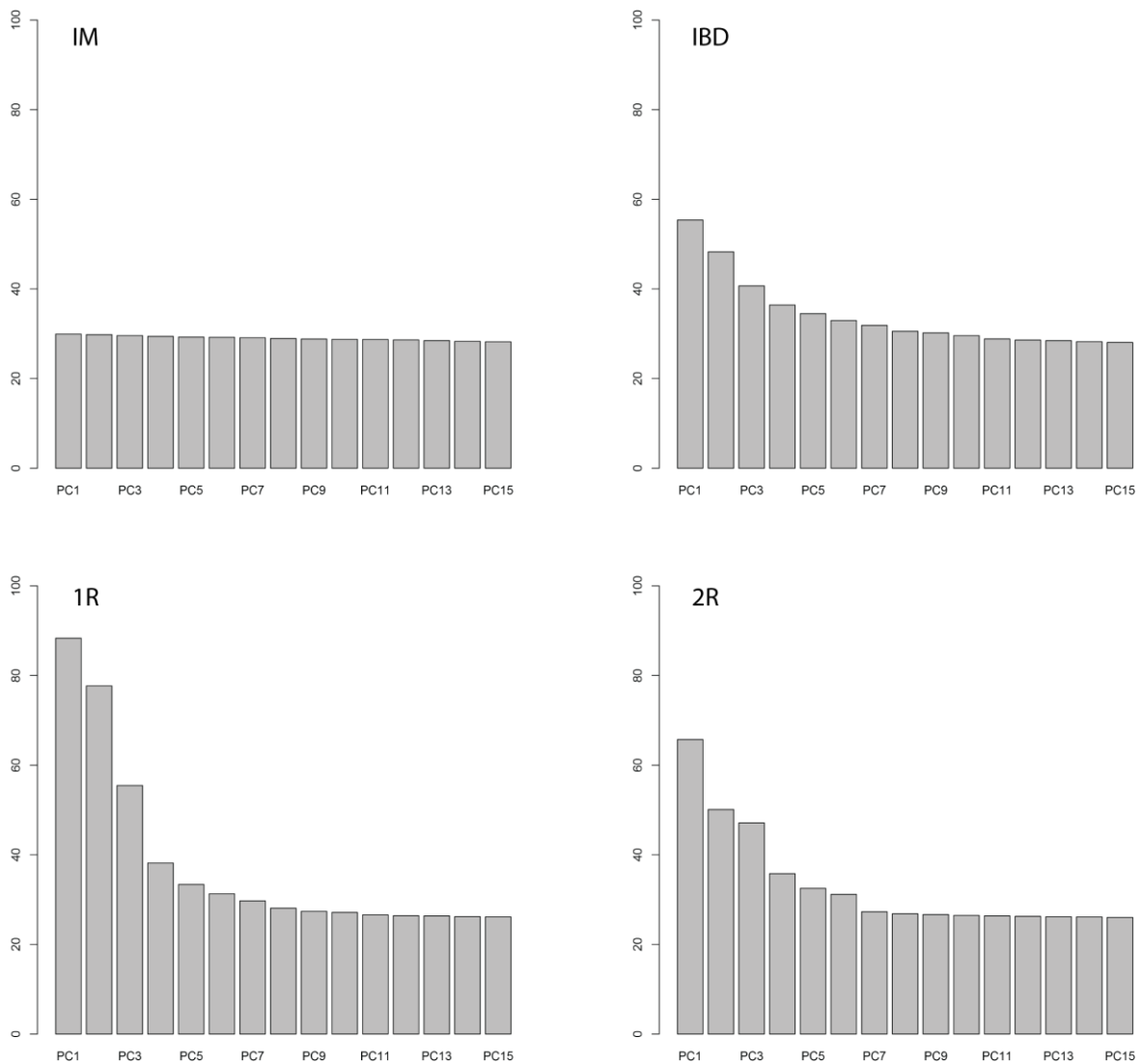
Figure S10. Screeplots of the eigenvalues for the first 15 (of 537 total) unconstrained (PC) axes from redundancy analysis. All screeplots use the same y-axis scale. Plots are shown for an equilibrium island model (IM), equilibrium isolation by distance model (IBD), and non-equilibrium one- and two- refugial expansion models (1R and 2R) for paired sampling (6 individuals/deme) on environmental surface "453".

Table S1: Parameters from latent factor mixed model runs: values of K and genomic inflation factors (GIF) for habitat and x-coordinate predictors.

Demography	Sampling Design	Envir. Surface	6 individuals per deme			20 individuals per deme		
			K	GIFh	GIFx	K	GIFh	GIFx
1R	R	453	5	0.52	1.45	5	1.12	5.42
1R	R	950	5	0.43	1.42	5	0.98	5.19
1R	R	988	5	0.40	1.35	5	1.07	5.37
1R	P	453	5	0.45	1.26	5	0.86	6.70
1R	P	950	5	0.67	1.47	5	1.26	8.32
1R	P	988	5	0.48	1.30	5	1.00	6.97
1R	T	453	5	0.38	1.72	5	0.89	7.45
1R	T	950	5	0.40	1.53	5	0.88	5.61
1R	T	988	5	0.33	1.31	5	0.64	5.83
2R	R	453	5	0.31	1.02	5	0.81	2.46
2R	R	950	5	0.23	1.10	5	0.57	2.93
2R	R	988	5	0.27	1.00	5	0.64	2.96
2R	P	453	5	0.30	1.39	5	0.62	2.98
2R	P	950	5	0.38	1.24	5	0.59	4.27
2R	P	988	5	0.29	1.11	5	0.71	4.01
2R	T	453	5	0.27	1.60	5	0.54	4.46
2R	T	950	5	0.28	1.48	5	0.71	3.06
2R	T	988	5	0.18	1.36	5	0.42	2.85
IBD	R	453	4	0.37	0.61	4	1.13	2.05
IBD	R	950	4	0.37	0.60	4	1.27	2.02
IBD	R	988	4	0.39	0.59	4	1.07	1.94
IBD	P	453	4	0.40	0.62	4	0.97	1.97
IBD	P	950	4	0.44	0.78	4	1.10	2.67
IBD	P	988	4	0.39	0.65	4	1.01	2.23
IBD	T	453	4	0.46	0.88	4	1.26	2.85
IBD	T	950	4	0.34	0.66	4	0.75	2.68
IBD	T	988	4	0.38	0.68	4	0.97	2.50
IM	R	453	1	1.14	1.14	4	0.27	0.30
IM	R	950	1	1.13	1.15	4	0.22	0.29
IM	R	988	1	1.13	1.12	4	0.25	0.30
IM	P	453	1	1.16	1.05	2	0.58	0.85
IM	P	950	1	1.12	1.07	2	0.61	0.72
IM	P	988	1	1.13	1.08	2	0.65	0.91
IM	T	453	1	1.09	1.06	2	0.65	0.85
IM	T	950	1	1.11	1.06	2	0.73	0.87
IM	T	988	1	1.09	1.11	2	0.60	0.88

Table S2: Correlations between habitat and x- and y-coordinates of demes for each simulation; average and maximum trend in neutral markers; average and maximum levels of local adaptation.

Demo-graphy	De-sign	Env	Correlations: Habitat and X	Correlations: Habitat and Y	Neutral trend: 6 indiv./deme Avg.	Neutral trend: 6 indiv./deme Max.	Neutral trend: 20 indiv./deme Avg.	Neutral trend: 20 indiv./deme Max.	Local adaptation: 6 indiv./deme Avg.	Local adaptation: 6 indiv./deme Max.	Local adaptation: 20 indiv./deme Avg.	Local adaptation: 20 indiv./deme 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 S3: Detection rates (using locus rankings) for simulation scenarios (6 individuals sampled per deme) with and without correction for population structure.

Demo-graphy	De-sign	Env	True Positive Rates								False Positive Rates							
			RDA	RDA corr	db RDA	db RDA corr	cRDA	cRDA corr	RF	RF corr	RDA	RDA corr	db RDA	db RDA corr	cRDA	cRDA corr	RF	RF corr
1R	R	453	0.82	0.81	0.73	0.72	0.78	0.78	0.29	0.09	0.18	0.19	0.27	0.28	0.22	0.22	0.71	0.91
1R	R	950	0.75	0.74	0.70	0.71	0.75	0.75	0.24	0.09	0.25	0.26	0.30	0.29	0.25	0.25	0.76	0.91
1R	R	988	0.80	0.80	0.71	0.69	0.80	0.80	0.26	0.11	0.20	0.20	0.29	0.31	0.20	0.20	0.74	0.38
1R	P	453	0.83	0.84	0.76	0.75	0.85	0.85	0.26	0.17	0.17	0.16	0.24	0.25	0.15	0.15	0.74	0.83
1R	P	950	0.79	0.79	0.74	0.75	0.76	0.76	0.30	0.10	0.21	0.21	0.26	0.25	0.24	0.24	0.70	0.90
1R	P	988	0.76	0.76	0.67	0.67	0.74	0.74	0.24	0.10	0.24	0.24	0.33	0.33	0.26	0.26	0.76	0.90
1R	T	453	0.90	0.91	0.80	0.78	0.87	0.87	0.26	0.13	0.10	0.09	0.20	0.22	0.13	0.13	0.74	0.87
1R	T	950	0.76	0.79	0.71	0.71	0.76	0.76	0.23	0.12	0.24	0.21	0.29	0.29	0.24	0.24	0.77	0.88
1R	T	988	0.86	0.88	0.75	0.74	0.83	0.83	0.22	0.12	0.14	0.12	0.25	0.26	0.17	0.17	0.78	0.88
2R	R	453	0.94	0.94	0.90	0.89	0.94	0.94	0.30	0.10	0.06	0.06	0.10	0.11	0.06	0.06	0.70	0.90
2R	R	950	0.93	0.93	0.88	0.88	0.90	0.90	0.31	0.14	0.07	0.07	0.12	0.12	0.10	0.10	0.69	0.86
2R	R	988	0.91	0.88	0.85	0.81	0.91	0.91	0.22	0.09	0.09	0.12	0.15	0.19	0.09	0.09	0.78	0.91
2R	P	453	0.92	0.93	0.86	0.87	0.92	0.92	0.28	0.18	0.08	0.07	0.14	0.13	0.08	0.08	0.72	0.82
2R	P	950	0.93	0.93	0.89	0.89	0.93	0.93	0.32	0.12	0.07	0.07	0.11	0.11	0.07	0.07	0.68	0.88
2R	P	988	0.90	0.91	0.86	0.86	0.91	0.91	0.26	0.12	0.10	0.09	0.14	0.14	0.09	0.09	0.74	0.88
2R	T	453	0.95	0.95	0.89	0.89	0.94	0.94	0.33	0.15	0.05	0.05	0.11	0.11	0.06	0.06	0.67	0.85
2R	T	950	0.91	0.91	0.87	0.86	0.90	0.90	0.21	0.10	0.09	0.09	0.13	0.14	0.10	0.10	0.79	0.90
2R	T	988	0.93	0.92	0.87	0.86	0.92	0.92	0.21	0.10	0.07	0.08	0.13	0.14	0.08	0.08	0.79	0.90
IBD	R	453	1.00	1.00	0.98	0.98	1.00	1.00	0.27	0.07	0.00	0.00	0.02	0.02	0.00	0.00	0.73	0.93
IBD	R	950	0.98	0.98	0.97	0.96	0.99	0.99	0.31	0.06	0.02	0.02	0.03	0.04	0.01	0.01	0.69	0.94
IBD	R	988	1.00	1.00	0.98	0.98	1.00	1.00	0.37	0.08	0.00	0.00	0.02	0.02	0.00	0.00	0.63	0.92
IBD	P	453	0.99	0.99	0.98	0.98	1.00	1.00	0.27	0.10	0.01	0.01	0.02	0.02	0.00	0.00	0.73	0.90
IBD	P	950	0.99	0.99	0.98	0.98	0.99	0.99	0.28	0.08	0.01	0.01	0.02	0.02	0.01	0.01	0.72	0.92
IBD	P	988	1.00	1.00	0.99	0.99	1.00	1.00	0.21	0.09	0.00	0.00	0.01	0.01	0.00	0.00	0.79	0.91
IBD	T	453	0.94	0.94	0.94	0.94	1.00	1.00	0.14	0.07	0.06	0.06	0.06	0.06	0.00	0.00	0.86	0.93
IBD	T	950	0.97	0.96	0.90	0.93	0.98	0.98	0.24	0.11	0.03	0.04	0.10	0.07	0.02	0.02	0.76	0.89
IBD	T	988	0.98	0.96	0.97	0.97	0.98	0.98	0.10	0.07	0.02	0.04	0.03	0.03	0.02	0.02	0.90	0.93
IM	R	453	0.50	NA	0.51	NA	0.49	NA	0.19	0.21	0.50	NA	0.49	NA	0.51	NA	0.81	0.79
IM	R	950	0.44	NA	0.47	NA	0.46	NA	0.10	0.14	0.56	NA	0.53	NA	0.54	NA	0.90	0.86
IM	R	988	0.51	NA	0.54	NA	0.54	NA	0.15	0.15	0.49	NA	0.46	NA	0.46	NA	0.85	0.85
IM	P	453	0.66	NA	0.66	NA	0.73	NA	0.20	0.30	0.34	NA	0.34	NA	0.27	NA	0.80	0.69
IM	P	950	0.67	NA	0.67	NA	0.68	NA	0.18	0.22	0.33	NA	0.33	NA	0.32	NA	0.82	0.78
IM	P	988	0.68	NA	0.68	NA	0.61	NA	0.19	0.18	0.32	NA	0.32	NA	0.39	NA	0.81	0.82
IM	T	453	0.70	NA	0.70	NA	0.69	NA	0.19	0.26	0.30	NA	0.30	NA	0.31	NA	0.81	0.74
IM	T	950	0.63	NA	0.65	NA	0.72	NA	0.16	0.16	0.37	NA	0.35	NA	0.28	NA	0.84	0.84
IM	T	988	0.67	NA	0.69	NA	0.73	NA	0.20	0.30	0.33	NA	0.31	NA	0.27	NA	0.80	0.70

Table S4: Detection rates (using locus rankings) for simulation scenarios (20 individuals sampled per deme) with and without correction for population structure.

Demo-graphy	De-sign	Env	True Positive Rates								False Positive Rates							
			RDA	RDA corr	db RDA	db RDA corr	cRDA	cRDA corr	RF	RF corr	RDA	RDA corr	db RDA	db RDA corr	cRDA	cRDA corr	RF	RF corr
1R	R	453	0.80	0.80	0.74	0.74	0.85	0.85	0.17	0.10	0.20	0.20	0.26	0.26	0.15	0.15	0.83	0.90
1R	R	950	0.74	0.74	0.68	0.68	0.76	0.76	0.21	0.11	0.26	0.26	0.32	0.32	0.24	0.24	0.79	0.89
1R	R	988	0.81	0.80	0.73	0.72	0.82	0.82	0.24	0.13	0.19	0.20	0.27	0.28	0.18	0.18	0.76	0.88
1R	P	453	0.83	0.84	0.76	0.76	0.86	0.86	0.30	0.22	0.17	0.16	0.24	0.24	0.14	0.14	0.70	0.78
1R	P	950	0.74	0.75	0.70	0.70	0.77	0.77	0.19	0.10	0.26	0.25	0.30	0.30	0.23	0.23	0.81	0.90
1R	P	988	0.78	0.78	0.68	0.68	0.79	0.79	0.23	0.18	0.22	0.22	0.32	0.32	0.21	0.21	0.77	0.82
1R	T	453	0.88	0.88	0.78	0.78	0.85	0.85	0.33	0.16	0.12	0.12	0.22	0.22	0.15	0.15	0.67	0.84
1R	T	950	0.78	0.78	0.69	0.69	0.79	0.79	0.37	0.18	0.22	0.22	0.31	0.31	0.21	0.21	0.63	0.82
1R	T	988	0.85	0.85	0.73	0.73	0.84	0.84	0.32	0.14	0.15	0.15	0.27	0.27	0.16	0.16	0.68	0.86
2R	R	453	0.93	0.94	0.90	0.89	0.93	0.93	0.43	0.21	0.07	0.06	0.10	0.11	0.07	0.07	0.57	0.79
2R	R	950	0.91	0.91	0.88	0.88	0.88	0.88	0.28	0.11	0.09	0.09	0.12	0.12	0.12	0.12	0.72	0.89
2R	R	988	0.93	0.93	0.86	0.86	0.91	0.91	0.16	0.09	0.07	0.07	0.14	0.14	0.09	0.09	0.84	0.91
2R	P	453	0.93	0.93	0.88	0.87	0.91	0.91	0.33	0.23	0.07	0.07	0.12	0.13	0.09	0.09	0.67	0.77
2R	P	950	0.91	0.91	0.87	0.87	0.91	0.91	0.25	0.19	0.09	0.09	0.13	0.13	0.09	0.09	0.75	0.81
2R	P	988	0.93	0.93	0.87	0.87	0.91	0.91	0.07	0.16	0.07	0.07	0.13	0.13	0.09	0.09	0.93	0.84
2R	T	453	0.95	0.95	0.89	0.89	0.92	0.92	0.39	0.19	0.05	0.05	0.11	0.11	0.08	0.08	0.61	0.81
2R	T	950	0.89	0.89	0.86	0.86	0.89	0.89	0.28	0.12	0.11	0.11	0.14	0.14	0.11	0.11	0.72	0.88
2R	T	988	0.95	0.95	0.89	0.89	0.93	0.93	0.23	0.08	0.05	0.05	0.11	0.11	0.07	0.07	0.77	0.92
IBD	R	453	1.00	1.00	0.98	0.98	1.00	1.00	0.29	0.12	0.00	0.00	0.02	0.02	0.00	0.00	0.71	0.88
IBD	R	950	0.99	0.99	0.98	0.98	0.99	0.99	0.22	0.10	0.01	0.01	0.02	0.02	0.01	0.01	0.78	0.90
IBD	R	988	1.00	1.00	0.99	0.99	1.00	1.00	0.24	0.11	0.00	0.00	0.01	0.01	0.00	0.00	0.76	0.89
IBD	P	453	1.00	1.00	0.98	0.98	1.00	1.00	0.16	0.08	0.00	0.00	0.02	0.02	0.00	0.00	0.84	0.92
IBD	P	950	0.99	0.99	0.98	0.98	0.99	0.99	0.39	0.21	0.01	0.01	0.02	0.02	0.01	0.01	0.61	0.79
IBD	P	988	1.00	1.00	0.99	0.99	1.00	1.00	0.30	0.16	0.00	0.00	0.01	0.01	0.00	0.00	0.70	0.84
IBD	T	453	0.98	0.98	0.96	0.96	1.00	1.00	0.28	0.07	0.02	0.02	0.04	0.04	0.00	0.00	0.72	0.93
IBD	T	950	0.98	0.98	0.96	0.96	0.99	0.99	0.29	0.12	0.02	0.02	0.04	0.04	0.01	0.01	0.71	0.88
IBD	T	988	0.99	0.99	0.98	0.97	1.00	1.00	0.09	0.12	0.01	0.01	0.02	0.03	0.00	0.00	0.91	0.88
IM	R	453	0.64	NA	0.64	NA	0.72	NA	0.09	0.08	0.36	NA	0.36	NA	0.28	NA	0.91	0.92
IM	R	950	0.61	NA	0.62	NA	0.66	NA	0.08	0.07	0.39	NA	0.38	NA	0.34	NA	0.92	0.93
IM	R	988	0.68	NA	0.68	NA	0.66	NA	0.09	0.07	0.32	NA	0.32	NA	0.34	NA	0.91	0.93
IM	P	453	0.77	NA	0.75	NA	0.92	NA	0.10	0.08	0.23	NA	0.25	NA	0.08	NA	0.90	0.92
IM	P	950	0.80	NA	0.79	NA	0.86	NA	0.12	0.09	0.20	NA	0.21	NA	0.14	NA	0.88	0.91
IM	P	988	0.77	NA	0.79	NA	0.85	NA	0.09	0.06	0.23	NA	0.21	NA	0.15	NA	0.91	0.94
IM	T	453	0.80	NA	0.79	NA	0.93	NA	0.10	0.07	0.20	NA	0.21	NA	0.07	NA	0.90	0.93
IM	T	950	0.77	NA	0.73	NA	0.84	NA	0.10	0.08	0.23	NA	0.27	NA	0.16	NA	0.90	0.92
IM	T	988	0.80	NA	0.77	NA	0.71	NA	0.16	0.10	0.20	NA	0.23	NA	0.29	NA	0.84	0.90

Table S5: Parameters from cRDA runs: number of axes retained by the parallel analysis criterion, and component axes significantly correlated with constrained ordination axes. Data are shown for all selection strengths (full simulation data set) and simulation data with weak selection only.

Demo-graphy	De-sign	Env	Retained axes		All selection strengths		Weak selection only	
			6 ind.	20 ind.	Signficant components: 6 ind.	Signficant components: 20 ind.	Signficant components: 6 ind.	Signficant components: 20 ind.
1R	P	453	540	1800	2,1	2	1,2	NA
1R	P	950	540	1800	2,1	2	2,1	2
1R	P	988	540	1800	1,2	2	1,2	8,11,1300
1R	R	453	540	1800	2,1	2	1,3	NA
1R	R	950	540	1800	1,2	2	2,1	NA
1R	R	988	540	1800	2,1	2	1,2	9
1R	T	453	540	1800	2,1	2,1	1,3	1,7,995,1421
1R	T	950	540	1800	1,2	2	1,3	8
1R	T	988	540	1800	2,1	2	2,1	7,9
2R	P	453	540	1800	1,2	2,1	2,1	1,2
2R	P	950	540	1800	1,2	1,2	1,2	1,2
2R	P	988	540	1800	1,2	2,1	1,2	2,1
2R	R	453	540	1800	1,2	2,1	1,2	2,1
2R	R	950	540	1800	1,2	1,2	1,2	1,2
2R	R	988	540	1800	2,1	2,1	1,2	11,348
2R	T	453	540	1800	1,2	1,2	1,2	2,1
2R	T	950	540	1800	2,1	1,2	1,2	1,2
2R	T	988	540	1800	2,1	2,1	1,2	1,2
IBD	P	453	540	1800	1	1	1	1
IBD	P	950	540	1800	1,2	1	1	1
IBD	P	988	540	1800	1	1	2,1	1
IBD	R	453	540	1800	1	1	2,1	1
IBD	R	950	540	1800	1	1	1	1
IBD	R	988	540	1800	1	1	1	1
IBD	T	453	540	1800	1	1	1	1
IBD	T	950	540	1800	183,1	1	1	1
IBD	T	988	540	1800	263,1	1	1	1
IM	P	453	540	1800	1	1	NA	31,726
IM	P	950	540	1800	1	1	NA	13,704,024, 624,941,500
IM	P	988	540	1800	235,1	1	NA	2,66,207,1295,270
IM	R	453	540	1800	1	1	NA	NA
IM	R	950	540	1800	1	1	NA	1,371,254
IM	R	988	540	1800	1	1	NA	47
IM	T	453	540	1800	1	1	NA	3,891,131, 115,591,780
IM	T	950	540	1800	1	1	NA	NA
IM	T	988	540	1800	1	935,1	NA	184,512,191,681

Table S6: Percent variance explained for uncorrected and corrected Random Forest models.

Demography	Design	Env	6 individuals sampled per deme			
			Uncorrected		Corrected	
			PVE: Habitat	PVE: Xcoord	PVE: Habitat	PVE: Xcoord
1R	R	453	0.86	0.85	0.87	0.98
1R	R	950	0.81	0.84	0.85	0.98
1R	R	988	0.81	0.86	0.85	0.98
1R	P	453	0.88	0.87	0.88	0.97
1R	P	950	0.90	0.88	0.88	0.98
1R	P	988	0.88	0.87	0.89	0.98
1R	T	453	0.83	0.91	0.86	0.99
1R	T	950	0.87	0.89	0.89	0.99
1R	T	988	0.82	0.88	0.86	0.99
2R	R	453	0.85	0.87	0.88	0.97
2R	R	950	0.80	0.86	0.82	0.98
2R	R	988	0.81	0.86	0.85	0.98
2R	P	453	0.87	0.88	0.87	0.96
2R	P	950	0.90	0.89	0.87	0.97
2R	P	988	0.89	0.88	0.88	0.96
2R	T	453	0.83	0.91	0.87	0.98
2R	T	950	0.86	0.90	0.91	0.98
2R	T	988	0.82	0.88	0.89	0.97
IBD	R	453	0.86	0.67	0.86	0.96
IBD	R	950	0.81	0.65	0.81	0.96
IBD	R	988	0.80	0.64	0.82	0.96
IBD	P	453	0.88	0.66	0.86	0.97
IBD	P	950	0.89	0.71	0.86	0.96
IBD	P	988	0.89	0.66	0.88	0.97
IBD	T	453	0.84	0.73	0.85	0.99
IBD	T	950	0.84	0.66	0.87	0.97
IBD	T	988	0.82	0.66	0.85	0.98
IM	R	453	0.83	0.41	0.83	0.39
IM	R	950	0.85	0.39	0.83	0.39
IM	R	988	0.81	0.40	0.81	0.36
IM	P	453	0.88	0.42	0.88	0.38
IM	P	950	0.91	0.38	0.90	0.36
IM	P	988	0.88	0.39	0.88	0.37
IM	T	453	0.86	0.36	0.85	0.35
IM	T	950	0.88	0.40	0.87	0.36
IM	T	988	0.85	0.38	0.85	0.36