



Figure S1. Panels output from STRUcTURE analysis of 1058 genets at 33 sites after removing clonal duplicates. The number of clusters was assumed to be between 2 and 10 (i.e., $K = 2$ to $K = 10$). The panels were output from the CLUMPAK server. The number under each panel corresponds to the site number, as described in Table 1.

Table S1. Population genetic parameters per locus for each site.

Site		Themp030	Themp041	Themp047	Themp048	Themp049	Themp066	Themp103	Themp107	Themp193
B-CNR G = 36	NA	3	2	2	8	1	2	2	2	1
	AR	2.47	2.00	1.73	7.19	1.00	1.96	1.47	1.47	1.00
	PA	0	0	0	0	0	0	0	0	0
	HO	0.389	0.444	0.000	0.889	0.000	0.083	0.028	0.028	0.000
	HE	0.506	0.475	0.054	0.806	0.000	0.129	0.027	0.027	0.000
	FIS	0.231	0.065	1.000***	-0.103	N.A.	0.355*	-0.014	-0.014	N.A.
B-NLP G = 41	NA	5	3	3	12	2	3	2	2	2
	AR	4.77	2.41	2.42	9.06	2.00	2.66	1.42	2.00	2.00
	PA	0	0	0	0	0	0	0	0	0
	HO	0.683	0.268	0.390	0.902	0.244	0.415	0.024	0.634	0.268
	HE	0.656	0.253	0.421	0.835	0.476	0.473	0.024	0.497	0.232
	FIS	-0.040	-0.060	0.073	-0.081	0.488**	0.124***	-0.012	-0.275	-0.155
N-TPL G = 31	NA	3	1	2	13	2	1	2	1	1
	AR	2.54	1.00	2.00	9.40	1.55	1.00	2.00	1.00	1.00
	PA	0	0	0	0	0	0	0	0	0
	HO	0.194	0.000	0.226	0.774	0.032	0.000	0.355	0.000	0.000
	HE	0.203	0.000	0.200	0.776	0.032	0.000	0.367	0.000	0.000
	FIS	0.049*	N.A.	-0.127	0.003	-0.016	N.A.	0.033	N.A.	N.A.
N-BYG G = 17	NA	6	3	3	8	1	2	1	1	1
	AR	6.00	3.00	3.00	8.00	1.00	2.00	1.00	1.00	1.00
	PA	0	0	0	0	0	0	0	0	0
	HO	0.706	0.412	0.235	0.706	0.000	0.294	0.000	0.000	0.000
	HE	0.647	0.348	0.386	0.806	0.000	0.251	0.000	0.000	0.000
	FIS	-0.091	-0.184	0.390*	0.124	N.A.	-0.172	N.A.	N.A.	N.A.
W-AND G = 39	NA	12	2	3	16	2	2	3	2	2
	AR	10.05	2.00	3.00	12.17	2.00	1.69	2.68	1.91	1.91
	PA	0	0	0	0	0	0	0	0	0
	HO	0.897	0.667	0.179	0.923	0.231	0.051	0.282	0.103	0.103
	HE	0.868	0.473	0.624	0.891	0.204	0.050	0.285	0.097	0.097
	FIS	-0.034*	-0.408*	0.712***	-0.036	-0.130	-0.026	0.010	-0.054	-0.054
W-SAN G = 40	NA	14	2	3	13	2	3	2	2	2
	AR	10.43	2.00	3.00	10.69	1.97	2.32	1.99	1.97	1.67
	PA	0	0	0	0	0	0	0	0	0
	HO	0.925	0.250	0.175	0.925	0.150	0.125	0.200	0.150	0.050
	HE	0.862	0.289	0.624	0.871	0.139	0.118	0.180	0.139	0.049
	FIS	-0.073	0.134	0.720***	-0.062	-0.081	-0.055	-0.111	-0.081	-0.026
W-ILM G = 42	NA	10	2	5	13	3	3	2	2	2
	AR	9.24	2.00	3.93	9.21	2.94	2.53	1.96	1.65	2.00
	PA	0	0	0	0	0	0	0	0	0
	HO	0.857	0.476	0.381	0.738	0.286	0.095	0.143	0.048	0.286
	HE	0.831	0.459	0.556	0.782	0.274	0.135	0.133	0.046	0.278
	FIS	-0.031	-0.037	0.315	0.056	-0.045	0.294*	-0.077	-0.024	-0.029
W-CMY G = 39	NA	8	2	3	10	3	4	4	3	2
	AR	6.13	1.91	3.00	7.39	2.83	3.12	3.51	2.44	2.00
	PA	0	0	0	0	0	1	2	0	0
	HO	0.821	0.103	0.410	0.718	0.513	0.667	0.308	0.410	0.513
	HE	0.724	0.097	0.500	0.715	0.447	0.518	0.311	0.346	0.460
	FIS	-0.134	-0.054	0.179	-0.004**	-0.148***	-0.286***	0.012*	-0.185	-0.114
W-MOR G = 44	NA	5	2	3	6	3	2	3	3	2
	AR	4.30	2.00	2.92	4.03	2.39	1.63	2.39	2.38	2.00
	PA	0	0	0	0	0	0	0	0	0
	HO	0.591	0.455	0.568	0.455	0.614	0.045	0.432	0.250	0.455
	HE	0.598	0.397	0.482	0.498	0.471	0.044	0.343	0.238	0.474
	FIS	0.013	-0.146	-0.180	0.088	-0.303	-0.023	-0.258	-0.049	0.041
D-BLT G = 38	NA	9	2	4	5	3	3	1	2	1
	AR	7.47	2.00	3.84	4.83	2.87	2.45	1.00	1.91	1.00
	PA	0	0	0	0	0	0	0	0	0
	HO	0.763	0.605	0.289	0.711	0.158	0.237	0.000	0.053	0.000
	HE	0.770	0.497	0.342	0.736	0.216	0.305	0.000	0.100	0.000
	FIS	0.009***	-0.218	0.155***	0.034	0.268***	0.224	N.A.	0.472**	N.A.
D-MCH G = 37	NA	8	2	3	8	2	2	1	2	2
	AR	5.67	2.00	3.00	6.78	2.00	1.46	1.00	2.00	1.92
	PA	0	0	0	0	0	0	0	0	0
	HO	0.486	0.432	0.054	0.784	0.216	0.027	0.000	0.541	0.054
	HE	0.552	0.456	0.461	0.687	0.456	0.027	0.000	0.497	0.102
	FIS	0.118***	0.051	0.883***	-0.141	0.526**	-0.014	N.A.	-0.088	0.471**
D-HNR G = 22	NA	3	2	3	6	2	1	1	2	2
	AR	3.00	2.00	3.00	5.32	1.95	1.00	1.00	1.99	1.99
	PA	0	0	0	0	0	0	0	0	0
	HO	0.727	0.227	0.136	0.636	0.091	0.000	0.000	0.136	0.136

D-LMB	He	0.633	0.491	0.505	0.614	0.087	0.000	0.000	0.127	0.127
	Fis	−0.148	0.537*	0.730***	−0.037	−0.048	N.A.	N.A.	−0.073	−0.073
	NA	7	2	2	4	2	3	2	2	2
	Ar	6.90	2.00	1.99	3.96	2.00	2.89	2.00	2.00	1.96
	PA	0	0	0	0	0	0	0	0	0
E-PNT	Ho	0.808	0.308	0.000	0.769	0.115	0.231	0.500	0.500	0.115
	He	0.717	0.260	0.142	0.676	0.174	0.322	0.464	0.375	0.109
	Fis	−0.126	−0.182	1.000***	−0.138	0.336	0.284***	−0.078	−0.333	−0.061
	NA	4	2	2	4	2	2	1	3	1
	Ar	3.99	2.00	2.00	2.92	2.00	2.00	1.00	2.93	1.00
E-CGB	PA	0	0	0	0	0	0	0	0	0
	Ho	0.611	0.417	0.056	0.139	0.000	0.528	0.000	1.000	0.000
	He	0.700	0.389	0.444	0.132	0.198	0.497	0.000	0.549	0.000
	Fis	0.127	−0.072	0.875***	−0.050	1.000***	−0.063	N.A.	−0.820***	N.A.
	NA	12	2	4	4	2	3	1	2	2
E-BAC	Ar	8.59	2.00	3.42	3.24	2.00	2.42	1.00	2.00	1.42
	PA	0	0	0	0	0	0	0	0	0
	Ho	0.732	0.341	0.146	0.195	0.171	0.415	0.000	0.976	0.024
	He	0.792	0.283	0.658	0.223	0.232	0.441	0.000	0.500	0.024
	Fis	0.076	−0.206	0.777***	0.124	0.265	0.059	N.A.	−0.952***	−0.012
E-SSB	NA	5	1	2	4	1	3	1	2	1
	Ar	4.68	1.00	2.00	3.70	1.00	3.00	1.00	2.00	1.00
	PA	0	0	0	0	0	0	0	0	0
	Ho	0.400	0.000	0.000	0.400	0.000	0.650	0.000	0.900	0.000
	He	0.466	0.000	0.420	0.368	0.000	0.635	0.000	0.495	0.000
E-BLM	Fis	0.142	N.A.	1.000***	−0.088***	N.A.	−0.024	N.A.	−0.818***	N.A.
	NA	8	2	2	9	3	4	2	3	2
	Ar	7.53	2.00	2.00	7.44	2.63	3.91	1.92	3.00	1.92
	PA	0	0	0	0	0	0	0	0	0
	Ho	0.750	0.250	0.000	0.667	0.042	0.500	0.000	0.958	0.083
P-HND	He	0.787	0.278	0.375	0.574	0.119	0.595	0.080	0.609	0.080
	Fis	0.047	0.100	1.000***	−0.162	0.650***	0.159	1.000***	−0.575***	−0.043
	NA	6	2	2	8	1	3	1	2	1
	Ar	4.95	2.00	1.57	7.09	1.00	2.99	1.00	2.00	1.00
	PA	0	0	0	0	0	0	0	0	0
P-PPB	Ho	0.633	0.400	0.033	0.867	0.000	0.600	0.000	0.667	0.000
	He	0.641	0.444	0.033	0.770	0.000	0.572	0.000	0.498	0.000
	Fis	0.011**	0.100	−0.017	−0.126	N.A.	−0.050	N.A.	−0.339	N.A.
	NA	22	2	3	13	2	4	2	3	1
	Ar	15.60	2.00	3.00	9.68	2.00	3.28	1.45	2.42	1.00
V-UNB	PA	8	0	0	0	0	1	0	0	0
	Ho	0.921	0.395	0.026	0.763	0.263	0.553	0.026	0.184	0.000
	He	0.912	0.422	0.608	0.745	0.465	0.527	0.026	0.169	0.000
	Fis	−0.010	0.065	0.957***	−0.024	0.435**	−0.048***	−0.013	−0.088	N.A.
	NA	2	2	1	3	1	3	2	1	1
V-STN	Ar	−	−	−	−	−	−	−	−	−
	PA	0	0	0	0	0	0	0	0	0
	Ho	−	−	−	−	−	−	−	−	−
	He	−	−	−	−	−	−	−	−	−
	Fis	−	−	−	−	−	−	−	−	−
V-SII	NA	13	3	4	7	2	3	1	3	2
	Ar	10.82	2.52	3.78	5.59	2.00	3.00	1.00	2.53	1.96
	PA	0	0	0	0	0	0	0	0	0
	Ho	0.813	0.219	0.313	0.750	0.031	0.375	0.000	0.500	0.125
	He	0.859	0.198	0.629	0.686	0.195	0.631	0.000	0.480	0.117
V-BTY	Fis	0.054	−0.106	0.503***	−0.094***	0.840***	0.406*	N.A.	−0.042	−0.067
	NA	9	2	3	13	2	3	2	3	2
	Ar	7.64	2.00	2.88	10.08	1.75	2.94	1.99	3.00	2.00
	PA	0	0	0	0	0	0	0	0	0
	Ho	0.824	0.206	0.029	0.765	0.059	0.382	0.206	0.824	0.265
G = 32	He	0.797	0.271	0.502	0.792	0.057	0.443	0.185	0.625	0.230
	Fis	−0.033	0.241	0.941***	0.034	−0.030	0.137	−0.115	−0.319***	−0.153
	NA	10	2	4	7	2	4	2	3	2
	Ar	8.92	2.00	3.92	5.57	1.46	3.42	1.85	2.46	1.98
	PA	0	0	0	0	0	0	0	0	0
G = 36	Ho	0.865	0.108	0.135	0.432	0.027	0.351	0.081	0.649	0.162
	He	0.855	0.193	0.545	0.558	0.027	0.396	0.078	0.447	0.149
	Fis	−0.012**	0.439**	0.752***	0.225	−0.014	0.113	−0.042	−0.452*	−0.088
	NA	6	3	3	8	1	4	2	3	3
	Ar	5.70	2.42	2.99	6.13	1.00	2.79	1.40	2.93	2.76
G = 43	PA	0	0	0	0	0	0	0	0	1
	Ho	0.488	0.070	0.000	0.651	0.000	0.465	0.023	0.744	0.186

V-ALB G = 41	<i>H_E</i>	0.688	0.111	0.411	0.643	0.000	0.470	0.023	0.511	0.211
	<i>F_{IS}</i>	0.290***	0.372***	1.000***	-0.013	N.A.	0.010	-0.012	-0.457**	0.119
	<i>N_A</i>	10	3	3	13	2	2	1	3	2
	<i>A_R</i>	7.84	2.42	2.66	8.33	1.81	2.00	1.00	2.94	2.00
	<i>P_A</i>	0	0	0	0	0	0	0	0	0
V-PAB G = 37	<i>H_O</i>	0.756	0.488	0.000	0.659	0.024	0.341	0.000	0.707	0.390
	<i>H_E</i>	0.781	0.441	0.522	0.682	0.070	0.493	0.000	0.534	0.343
	<i>F_{IS}</i>	0.032	-0.107	1.000***	0.035**	0.654***	0.307*	N.A.	-0.325*	-0.139
	<i>N_A</i>	12	3	3	9	2	3	2	3	2
	<i>A_R</i>	9.29	2.71	3.00	7.18	2.00	2.99	1.46	2.96	2.00
V-TCL G = 22	<i>P_A</i>	0	0	0	0	0	0	1	0	0
	<i>H_O</i>	0.703	0.432	0.135	0.838	0.054	0.405	0.027	0.649	0.514
	<i>H_E</i>	0.812	0.349	0.489	0.738	0.497	0.456	0.027	0.561	0.428
	<i>F_{IS}</i>	0.135	-0.238	0.724***	-0.135	0.891***	0.111	-0.014	-0.157	-0.199
	<i>N_A</i>	3	2	1	1	1	3	1	2	1
V-GUI G = 36	<i>A_R</i>	2.77	2.00	1.00	1.00	1.00	2.77	1.00	2.00	1.00
	<i>P_A</i>	0	0	0	0	0	0	0	0	0
	<i>H_O</i>	0.273	0.273	0.000	0.000	0.000	0.227	0.000	0.773	0.000
	<i>H_E</i>	0.274	0.351	0.000	0.000	0.000	0.206	0.000	0.474	0.000
	<i>F_{IS}</i>	0.004	0.224	N.A.	N.A.	N.A.	-0.106	N.A.	-0.630**	N.A.
M-OPL G = 30	<i>N_A</i>	6	2	2	4	1	5	2	2	1
	<i>A_R</i>	5.65	2.00	2.00	3.73	1.00	4.19	2.00	2.00	1.00
	<i>P_A</i>	0	0	0	0	0	0	1	0	0
	<i>H_O</i>	0.611	0.500	0.139	0.611	0.000	0.500	0.611	0.500	0.000
	<i>H_E</i>	0.681	0.444	0.435	0.665	0.000	0.449	0.498	0.401	0.000
M-LGD G = 31	<i>F_{IS}</i>	0.102	-0.125	0.681***	0.081	N.A.	-0.112	-0.226	-0.246	N.A.
	<i>N_A</i>	9	2	4	2	2	2	1	2	2
	<i>A_R</i>	6.65	2.00	3.82	2.00	1.92	1.82	1.00	2.00	2.00
	<i>P_A</i>	0	0	0	0	0	0	0	0	0
	<i>H_O</i>	0.700	0.433	0.067	0.467	0.033	0.067	0.000	1.000	0.400
M-RIZ G = 31	<i>H_E</i>	0.707	0.473	0.651	0.420	0.095	0.064	0.000	0.500	0.391
	<i>F_{IS}</i>	0.010***	0.083	0.898***	-0.111	0.649***	-0.034	N.A.	-1.000***	-0.023
	<i>N_A</i>	9	3	4	11	4	2	2	4	2
	<i>A_R</i>	6.99	2.80	3.55	8.93	3.96	2.00	1.55	3.35	2.00
	<i>P_A</i>	0	0	0	1	0	0	1	0	0
M-BAT G = 17	<i>H_O</i>	0.613	0.323	0.355	0.935	0.290	0.387	0.032	1.000	0.258
	<i>H_E</i>	0.704	0.323	0.541	0.806	0.637	0.350	0.032	0.545	0.271
	<i>F_{IS}</i>	0.130***	0.000	0.344*	-0.16	0.544***	-0.107	-0.016	-0.836***	0.046
	<i>N_A</i>	9	4	5	10	2	3	2	3	2
	<i>A_R</i>	7.95	3.76	4.01	8.82	1.91	2.55	1.55	3.00	1.99
M-SAG G = 22	<i>P_A</i>	0	1	0	0	0	0	0	0	0
	<i>H_O</i>	0.548	0.097	0.194	0.581	0.097	0.742	0.032	0.968	0.194
	<i>H_E</i>	0.739	0.335	0.564	0.796	0.092	0.505	0.032	0.608	0.175
	<i>F_{IS}</i>	0.258	0.711***	0.657**	0.271**	-0.050	-0.469*	-0.016	-0.591***	-0.107
	<i>N_A</i>	5	2	2	6	2	2	1	2	2
M-SAG G = 22	<i>A_R</i>	5.00	2.00	2.00	6.00	2.00	2.00	1.00	2.00	2.00
	<i>P_A</i>	0	0	0	0	0	0	0	0	0
	<i>H_O</i>	0.824	0.529	0.059	0.941	0.059	0.529	0.000	0.471	0.824
	<i>H_E</i>	0.715	0.389	0.327	0.785	0.057	0.493	0.000	0.498	0.484
	<i>F_{IS}</i>	-0.153*	-0.360	0.820***	-0.198	-0.030	-0.074	N.A.	0.056	-0.700**
M-SAG G = 22	<i>N_A</i>	9	2	2	7	1	4	2	3	2
	<i>A_R</i>	8.31	1.95	2.00	6.93	1.00	3.77	1.95	3.00	1.77
	<i>P_A</i>	0	0	0	0	0	0	1	0	0
	<i>H_O</i>	0.773	0.091	0.000	0.727	0.000	0.682	0.091	0.818	0.045
	<i>H_E</i>	0.782	0.087	0.351	0.736	0.000	0.588	0.087	0.642	0.044
M-SAG G = 22	<i>F_{IS}</i>	0.012	-0.048	1.000***	0.011	N.A.	-0.160	-0.048	-0.275***	-0.023

G is the number of multilocus genotypes, including identical genotypes resulting from sexual reproduction by chance. *N_A* is the number of alleles. *A_R* is allelic richness. *P_A* is the number of private alleles. *H_O* and *H_E* are observed and expected heterozygosities. *F_{IS}* is the inbreeding coefficient. The probability of deviation from Hardy-Weinberg equilibrium was calculated in *F_{IS}* (**P* < 0.05, ***P* < 0.01, ****P* < 0.001).

Table S2. Characteristics of nine polymorphic microsatellite loci used in this study: locus name, repeat motif, forward and reverse primer sequences, allele size range, combination of loci for multiplex PCR, fluorescent label and GenBank accession number.

Locus	Repeat motif	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')	Size range (bp)	Multiplex (fluorescent)	Accession No.
Themp030	(AC)6(AG)13	ACACACACACACAGAGAGAGAG	ACAAGTGCTGCAGGGATGACA	94–165	A (NED)	AB688099
Themp041	(AC)8(TC)6	AATTCGTGGATGCCTCGCTT	U19-ATTCTTAAGGAGAGGTCATGG	368–377	A (FAM)	AB688100
Themp047	(AC)6(AG)5	ACACACACACACAGAGAGAGAG	CATCTTATGATCCATCCATGTGG	113–121	B (FAM)	AB688101
Themp048	(AC)6(AG)13	ACACACACACACAGAGAGAGAG	CAACAATTCATTCACCTCCTCCC	147–199	B (FAM)	AB688102
Themp049	(AC)6(AG)7	ACACACACACACAGAGAGAGAG	CCACGTGATTGTTAGTATAGG	255–261	B (FAM)	AB688103
Themp066	(AC)9AT(AG)14	GTGCGATGGAAAGAGTAGAC	U19-TCTATATTCAGAGTACGTGCC	284–306	A (FAM)	AB688104
Themp103	(AC)6(AG)10	ACACACACACACAGAGAGAGAG	GTCCTACACGTTGTAGTCATCG	93–127	C (VIC)	AB688105
Themp107	(AC)6(AG)6	ACACACACACACAGAGAGAGAG	TCAACGCCTTTGGTGACATCC	140–146	C (VIC)	AB688106
Themp193	(AC)8	AAGTCAGGTGCTACGAGAGTG	U19-CACAGTGGGTCTTTTTCCTTG	144–154	A (FAM)	AB688107

Details of primers are provided in Matsuki et al. [32].

Table S3. Pairwise F_{ST} values (below diagonal) and geographic distance (km) (above diagonal) between sites.

	B- CNR	B- NLP	N- TPL	N- BYG	W- AND	W- SAN	W- ILM	W- CMY	W- MOR	D- BLT	D- MCH	D- HNR	D- LMB	E- PNT	E- CGB	E- BAC	E- SSB	E- BLM	P- HND	V- UNB	V- STN	V- SII	V- BTY	V- ALB	V- PAB	V- TCL	V- GUI	M- OPL	M- LGD	M- RIZ	M- BAT	M- SAG
B-CNR		15.1	236.8	256.6	501.6	493.2	507.1	656.0	665.8	778.0	776.6	779.0	786.5	521.4	687.5	852.2	897.5	762.1	1229.9	945.3	1116.9	1270.1	1243.2	1226.1	1152.1	1072.2	1129.8	1353.9	1341.0	1324.2	1561.6	1587.1
B-NLP	0.245		224.5	241.5	486.7	478.2	492.1	641.6	651.4	764.3	763.0	765.3	772.9	508.2	674.7	842.3	887.4	750.6	1215.4	932.7	1104.7	1258.3	1231.6	1214.9	1141.3	1062.7	1121.1	1343.3	1330.3	1312.7	1551.4	1576.9
N-TPL	0.371	0.349		152.7	307.5	303.4	320.0	437.1	445.9	546.3	544.8	547.1	553.9	287.0	451.2	624.8	669.2	526.8	1007.9	708.7	880.2	1034.0	1007.6	991.9	919.3	847.7	911.2	1122.0	1108.7	1088.9	1331.4	1357.0
N-BYG	0.132	0.163	0.306		252.2	242.1	254.5	418.9	429.4	558.3	557.3	559.7	569.2	324.5	492.1	712.8	754.5	593.4	988.0	746.6	925.4	1085.8	1062.6	1054.3	988.0	936.9	1008.6	1191.2	1177.1	1145.1	1403.6	1429.4
W-AND	0.133	0.171	0.278	0.083		13.7	21.7	174.8	185.7	328.0	327.6	330.0	341.2	180.2	301.4	567.6	601.5	425.6	736.2	531.1	711.2	874.7	855.4	855.9	799.1	780.4	863.4	998.2	983.2	937.5	1210.6	1236.2
W-SAN	0.132	0.148	0.274	0.071	0.026		17.1	187.7	198.6	341.4	341.1	343.4	354.8	190.5	314.7	580.2	614.4	438.6	747.0	544.7	724.8	888.4	869.0	869.6	812.7	793.4	876.3	1011.8	996.8	951.1	1224.2	1249.9
W-ILM	0.128	0.171	0.319	0.086	0.033	0.073		182.9	193.9	338.8	338.5	340.9	352.5	201.6	318.6	586.7	620.0	443.9	736.5	543.6	723.3	887.0	868.2	869.9	814.2	798.2	881.8	1012.5	997.4	950.2	1224.7	1250.3
W-CMY	0.350	0.286	0.491	0.318	0.216	0.248	0.233		10.9	158.0	158.1	160.4	172.6	181.7	179.6	453.4	478.7	305.8	573.9	365.3	543.5	707.2	689.8	694.9	644.4	647.1	735.4	838.5	823.2	771.2	1049.5	1074.9
W-MOR	0.352	0.315	0.480	0.331	0.203	0.226	0.222	0.106		147.6	147.7	150.0	162.2	186.8	174.4	447.0	471.7	299.6	564.3	355.0	533.0	696.7	679.5	684.8	634.7	639.1	727.6	828.5	813.2	760.7	1039.3	1064.8
D-BLT	0.325	0.262	0.470	0.257	0.159	0.145	0.196	0.160	0.155		2.5	2.9	15.5	260.3	127.7	341.9	356.4	206.1	473.9	207.6	385.5	549.3	531.9	537.9	490.6	509.1	600.2	681.8	666.5	613.2	892.2	917.6
D-MCH	0.281	0.209	0.458	0.267	0.183	0.202	0.186	0.175	0.196	0.217		2.4	14.7	258.6	125.3	339.8	354.5	203.8	475.9	207.3	385.5	549.2	531.7	537.5	489.8	507.7	598.7	681.4	666.0	613.1	891.8	917.2
D-HNR	0.568	0.386	0.667	0.513	0.423	0.433	0.440	0.370	0.469	0.437	0.429		12.7	260.8	126.6	339.1	353.5	203.7	474.1	205.1	383.2	547.0	529.5	535.4	487.8	506.2	597.3	679.3	663.9	610.8	889.7	915.1
D-LMB	0.469	0.374	0.567	0.441	0.315	0.340	0.342	0.201	0.238	0.290	0.310	0.522		267.2	126.3	328.8	342.4	195.4	471.3	192.8	371.2	535.0	517.3	522.9	475.1	493.9	585.0	666.7	651.4	598.7	877.2	902.6
E-PNT	0.429	0.299	0.537	0.355	0.289	0.290	0.314	0.342	0.366	0.381	0.300	0.395	0.466		169.3	402.2	440.4	271.4	728.9	427.2	603.6	762.5	738.6	729.8	664.0	622.7	700.7	867.1	852.9	821.0	1079.7	1105.5
E-CGB	0.455	0.276	0.552	0.381	0.327	0.301	0.352	0.315	0.368	0.343	0.326	0.323	0.440	0.081		275.6	304.4	128.4	595.9	258.3	434.3	593.8	570.6	564.1	501.9	480.0	565.0	703.7	689.1	653.1	916.5	942.3
E-BAC	0.546	0.341	0.632	0.443	0.355	0.343	0.381	0.392	0.420	0.412	0.405	0.421	0.516	0.102	0.093		45.8	147.6	678.8	258.1	337.4	452.0	420.0	389.3	309.1	224.4	298.5	505.0	493.1	493.7	709.9	735.3
E-SSB	0.411	0.224	0.517	0.305	0.232	0.197	0.271	0.236	0.266	0.210	0.271	0.325	0.351	0.149	0.086	0.116		176.5	660.2	244.3	301.3	408.8	376.4	344.3	263.7	182.7	261.9	459.2	447.2	449.0	664.4	689.8
E-BLM	0.441	0.317	0.575	0.388	0.255	0.302	0.289	0.261	0.329	0.335	0.307	0.317	0.436	0.251	0.278	0.311	0.263		613.8	211.3	360.6	508.4	481.2	465.5	395.4	355.0	438.0	598.9	585.1	562.1	810.6	836.4
P-HND	0.260	0.175	0.404	0.189	0.105	0.092	0.136	0.180	0.194	0.121	0.218	0.349	0.273	0.242	0.215	0.278	0.135	0.224		421.3	415.5	487.6	501.2	549.2	573.3	701.0	780.9	653.4	640.0	541.0	802.8	822.0
V-UNB	0.383	0.198	0.482	0.272	0.234	0.202	0.250	0.254	0.297	0.230	0.266	0.237	0.351	0.177	0.114	0.144	0.047	0.239	0.136		180.3	343.7	324.8	330.7	288.6	340.6	432.5	474.7	459.3	406.6	684.6	710.0
V-STN	0.429	0.260	0.507	0.334	0.275	0.268	0.299	0.285	0.329	0.298	0.311	0.288	0.415	0.205	0.175	0.149	0.133	0.197	0.204	0.104		163.8	148.0	167.3	161.5	288.4	365.5	307.9	292.2	227.9	511.6	536.5
V-SII	0.462	0.281	0.553	0.404	0.347	0.312	0.370	0.351	0.379	0.352	0.355	0.370	0.437	0.271	0.192	0.259	0.162	0.368	0.274	0.157	0.214		34.1	86.4	160.7	316.6	360.0	168.1	153.8	66.1	354.2	378.3
V-BTY	0.455	0.322	0.553	0.404	0.314	0.309	0.337	0.394	0.393	0.396	0.380	0.396	0.475	0.225	0.236	0.220	0.221	0.292	0.281	0.203	0.191	0.130		55.7	126.7	282.9	328.6	165.2	149.8	82.6	363.8	388.6
V-ALB	0.374	0.237	0.481	0.296	0.220	0.205	0.255	0.216	0.259	0.221	0.259	0.233	0.345	0.168	0.127	0.177	0.071	0.159	0.126	0.078	0.130	0.192	0.196		82.4	232.8	273.6	144.1	128.6	105.4	354.9	380.5
V-PAB	0.352	0.173	0.450	0.281	0.189	0.198	0.216	0.262	0.264	0.265	0.249	0.329	0.343	0.196	0.204	0.225	0.165	0.188	0.124	0.154	0.170	0.265	0.220	0.127		157.3	214.8	203.5	189.7	187.8	415.6	441.4
V-TCL	0.634	0.483	0.744	0.629	0.474	0.494	0.484	0.490	0.503	0.563	0.519	0.589	0.599	0.349	0.369	0.420	0.410	0.440	0.423	0.378	0.339	0.283	0.127	0.354	0.368		92.4	306.7	298.0	332.8	497.5	522.2
V-GUI	0.440	0.318	0.520	0.401	0.352	0.362	0.366	0.381	0.437	0.437	0.358	0.398	0.485	0.312	0.311	0.355	0.315	0.358	0.349	0.294	0.282	0.222	0.238	0.299	0.331	0.333		304.0	299.6	359.9	467.2	490.1
M-OPL	0.452	0.306	0.537	0.379	0.293	0.284	0.323	0.355	0.343	0.350	0.310	0.386	0.449	0.215	0.228	0.260	0.211	0.314	0.267	0.208	0.244	0.255	0.232	0.185	0.183	0.429	0.359		15.7	113.5	212.9	238.6
M-LGD	0.401	0.233	0.486	0.321	0.235	0.236	0.264	0.300	0.308	0.298	0.266	0.294	0.358	0.160	0.178	0.195	0.156	0.212	0.179	0.152	0.170	0.236	0.181	0.122	0.089	0.362	0.307	0.107		101.7	227.6	253.3
M-RIZ	0.377	0.205	0.475	0.279	0.224	0.190	0.255	0.252	0.297	0.226	0.282	0.224	0.371	0.178	0.108	0.160	0.072	0.176	0.122	0.062	0.110	0.180	0.187	0.034	0.129	0.380	0.296	0.172	0.100		288.2	312.2
M-BAT	0.421	0.215	0.522	0.303	0.232	0.217	0.269	0.211	0.267	0.211	0.289	0.324	0.343	0.292	0.233	0.300	0.103	0.284	0.172	0.112	0.187	0.232	0.292	0.095	0.184	0.511	0.356	0.266	0.195	0.117		25.8
M-SAG	0.415	0.222	0.502	0.289	0.229	0.197	0.264	0.269	0.318	0.215	0.323	0.353	0.390	0.279	0.210	0.249	0.089	0.314	0.171	0.103	0.166	0.208	0.257	0.126	0.212	0.491	0.327	0.271	0.187	0.110	0.078	

All P_s = 0.001 in pairwise F_{ST} . P-PPB was removed due to the low sample size after removal of clonal replicates.

Table S4. Pairwise migration rates for 32 sites using BayesAss.

In	From																																
	B-CNR	B-NLP	N-TPL	N-BYG	W-AND	W-SAN	W-ILM	W-CMY	W-MOR	D-BLT	D-MCH	D-HNR	D-LMB	E-PNT	E-CGB	E-BAC	E-SSB	E-BLM	P-HND	V-UNB	V-STN	V-SII	V-BTY	V-ALB	V-PAB	V-TCL	V-GUI	M-OPL	M-LGD	M-RIZ	M-BAT	M-SAG	
B-CNR	0.843	0.005	0.006	0.005	0.005	0.007	0.006	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	
B-NLP	0.011	0.841	0.005	0.005	0.005	0.006	0.006	0.005	0.006	0.006	0.006	0.004	0.005	0.007	0.005	0.004	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.004	0.005
N-TPL	0.019	0.006	0.815	0.005	0.005	0.010	0.006	0.005	0.006	0.006	0.006	0.005	0.005	0.006	0.005	0.005	0.006	0.006	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005
N-BYG	0.113	0.007	0.007	0.674	0.007	0.011	0.017	0.007	0.007	0.007	0.007	0.007	0.006	0.007	0.006	0.007	0.007	0.006	0.007	0.006	0.007	0.006	0.007	0.007	0.007	0.007	0.006	0.007	0.006	0.006	0.006	0.006	0.008
W-AND	0.011	0.005	0.006	0.004	0.672	0.183	0.010	0.004	0.005	0.004	0.004	0.004	0.005	0.004	0.005	0.004	0.005	0.004	0.004	0.004	0.004	0.004	0.005	0.004	0.004	0.004	0.005	0.004	0.004	0.005	0.004	0.004	0.004
W-SAN	0.028	0.006	0.007	0.005	0.005	0.807	0.008	0.005	0.005	0.006	0.007	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.008	0.005	0.005	0.005	0.006	0.010	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.008
W-ILM	0.056	0.005	0.006	0.005	0.005	0.014	0.785	0.006	0.006	0.007	0.011	0.005	0.005	0.005	0.005	0.004	0.004	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.004	0.005	0.004	0.004	0.005	0.004	0.004	0.004	0.005
W-CMY	0.005	0.005	0.005	0.004	0.005	0.005	0.005	0.823	0.022	0.007	0.008	0.005	0.006	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.008
W-MOR	0.005	0.006	0.004	0.004	0.004	0.005	0.005	0.006	0.853	0.005	0.006	0.004	0.005	0.005	0.004	0.004	0.004	0.005	0.005	0.005	0.004	0.005	0.007	0.005	0.005	0.004	0.004	0.005	0.004	0.004	0.005	0.005	0.005
D-BLT	0.005	0.005	0.005	0.005	0.005	0.006	0.005	0.006	0.009	0.835	0.010	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.004	0.005	0.005	0.005	0.006	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005
D-MCH	0.006	0.005	0.005	0.005	0.005	0.006	0.006	0.005	0.007	0.006	0.837	0.005	0.005	0.005	0.005	0.005	0.005	0.008	0.006	0.005	0.005	0.005	0.005	0.006	0.006	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005
D-HNR	0.007	0.006	0.006	0.006	0.006	0.006	0.007	0.006	0.006	0.006	0.006	0.805	0.006	0.007	0.006	0.006	0.006	0.007	0.006	0.006	0.006	0.006	0.006	0.009	0.006	0.006	0.006	0.007	0.006	0.006	0.006	0.006	
D-LMB	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.007	0.008	0.007	0.006	0.006	0.814	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.007	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	
E-PNT	0.005	0.005	0.006	0.005	0.005	0.009	0.005	0.005	0.005	0.005	0.006	0.005	0.005	0.837	0.005	0.005	0.005	0.006	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005
E-CGB	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.005	0.004	0.004	0.004	0.197	0.672	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.004	0.005	0.005	0.004	0.004	0.005	0.004	0.004	0.004	0.004	0.005
E-BAC	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.144	0.007	0.673	0.006	0.006	0.006	0.006	0.007	0.006	0.006	0.007	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.007
E-SSB	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.052	0.013	0.006	0.673	0.007	0.006	0.006	0.007	0.006	0.006	0.009	0.007	0.006	0.006	0.007	0.006	0.006	0.006	0.006	0.092
E-BLM	0.005	0.005	0.005	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.007	0.005	0.005	0.005	0.824	0.006	0.005	0.006	0.006	0.006	0.008	0.006	0.005	0.006	0.006	0.006	0.006	0.006	0.005	0.006
P-HND	0.008	0.005	0.005	0.005	0.005	0.009	0.007	0.007	0.006	0.013	0.007	0.005	0.005	0.007	0.005	0.005	0.005	0.012	0.806	0.006	0.009	0.005	0.005	0.009	0.006	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.007
V-UNB	0.005	0.005	0.005	0.005	0.005	0.005	0.006	0.005	0.006	0.007	0.007	0.010	0.006	0.037	0.006	0.005	0.005	0.006	0.006	0.696	0.009	0.005	0.006	0.010	0.005	0.005	0.005	0.006	0.005	0.005	0.005	0.006	0.095
V-STN	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.007	0.006	0.006	0.006	0.006	0.005	0.019	0.006	0.005	0.005	0.025	0.006	0.005	0.772	0.005	0.006	0.014	0.006	0.005	0.005	0.006	0.005	0.005	0.005	0.005	0.027
V-SII	0.005	0.006	0.005	0.005	0.005	0.006	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.008	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.834	0.011	0.006	0.005	0.005	0.006	0.006	0.005	0.005	0.005	0.005	
V-BTY	0.005	0.004	0.005	0.005	0.005	0.005	0.005	0.004	0.004	0.005	0.004	0.004	0.005	0.005	0.004	0.004	0.005	0.005	0.004	0.005	0.005	0.010	0.845	0.009	0.005	0.004	0.005	0.007	0.004	0.004	0.005	0.006	
V-ALB	0.005	0.005	0.005	0.005	0.005	0.007	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.006	0.005	0.004	0.004	0.009	0.006	0.005	0.005	0.005	0.005	0.836	0.007	0.005	0.005	0.006	0.005	0.005	0.005	0.010	
V-PAB	0.006	0.006	0.005	0.005	0.005	0.006	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.010	0.005	0.005	0.005	0.008	0.007	0.005	0.006	0.005	0.005	0.014	0.819	0.005	0.005	0.008	0.005	0.005	0.005	0.007	
V-TCL	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.143	0.006	0.006	0.674	0.006	0.006	0.006	0.006	0.006	0.006	
V-GUI	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.010	0.005	0.005	0.005	0.841	0.005	0.005	0.005	0.005	0.005	
M-OPL	0.006	0.006	0.006	0.005	0.005	0.006	0.006	0.006	0.005	0.005	0.006	0.005	0.005	0.006	0.005	0.006	0.006	0.006	0.005	0.005	0.006	0.006	0.007	0.007	0.006	0.006	0.005	0.827	0.005	0.005	0.005	0.006	
M-LGD	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.006	0.005	0.006	0.005	0.005	0.005	0.007	0.005	0.005	0.005	0.005	0.005	0.118	0.022	0.005	0.005	0.038	0.678	0.005	0.005	0.005	
M-RIZ	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.005	0.008	0.008	0.005	0.005	0.010	0.005	0.006	0.005	0.006	0.005	0.159	0.005	0.005	0.005	0.005	0.005	0.672	0.005	0.007	
M-BAT	0.007	0.007	0.007	0.006	0.007	0.006	0.006	0.007	0.007	0.007	0.007	0.006	0.007	0.008	0.007	0.007	0.006	0.009	0.007	0.006	0.007	0.007	0.007	0.007	0.007	0.007	0.007	0.007	0.007	0.674	0.125		
M-SAG	0.006	0.006	0.006	0.006	0.006	0.007	0.007	0.006	0.006	0.007	0.006	0.006	0.006	0.011	0.006	0.006	0.006	0.007	0.007	0.007	0.008	0.009	0.006	0.008	0.006	0.006	0.006	0.006	0.006	0.006	0.007	0.793	

High migration rates (more than 0.1) are highlighted in gray cells. P-PPB was removed due to the low sample size after removal of clonal replicates.