Supplementary online figures for the manuscript "Weak founder effects but significant spatial genetic imprint of recent contraction and expansion of European beech populations", by Tonya A. Lander Etienne K Klein, Anne Roig, and Sylvie Oddou-Muratorio.

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Figure S1: Location of the studied plots in the climatic space explored by European beech over its distribution range.

The climatic space is represented as the variation of temperature and summer precipitation over beech distribution area, extracted for the SAFRAN database for the period 1958-2015 (collected on a 8 km2 grid represented by grey dots). Each black triangle represents the average climate recorded since 2007 with HOBO weather stations for the plot W_257-2 (N1, 1020 m), W_N2 (N2, 1140 m) and W_384 (N4, 1340 m a.s.l.).



Table S1: Geographical location and information on the 71 sampled plots.

N : number of sampled trees. Ng: number of genet kept for analyses. Long and Lat: the longitude and latitude in Lambert 93 coordinate system. Alti: altitude (in m). Age: estimated maximal age of the stand. MaxCirc and MinCirc: maximal and minimal circumference (in mm) within the plot. distNE, distNW, distSE, distSW: weighted least-cost distances (in m) from each plot to the North-East, North-West, South-East and South-West refuges, respectively.

Plot	Region	Ν	Ng	Long	Lat	Alti	Age	Max	Min	distNE	distNW	distSE	distSW
								Circ	Circ				
E_132	NE_REF	30	30	883758	6344256	1396	189	1310	230	148.8	3192.1	3022.1	1317.0
E_168	NE_REF	30	30	884283	6343887	1457	153	2443	274	17.1	3591.6	1434.1	690.7
E_170	NE_REF	26	26	884639	6343902	1309	219	1510	391	80.1	4628.3	1412.6	875.3
E_184	NE_REF	29	29	884627	6343710	1396	150	1339	277	43.9	4264.5	1214.0	725.5
E_186	NE_REF	30	30	884989	6343713	1321	199	1416	310	1.2	5198.4	1194.8	675.3
E_188	NE_REF	30	30	885338	6343708	1294	212	1199	273	52.1	6087.5	964.2	858.7
E_191	NE_REF	30	30	885847	6343703	1208	129	981	151	7.7	7078.5	880.1	952.9
E_203	NE_REF	21	21	885527	6343534	1319	155	1676	278	21.4	5743.6	642.3	681.6
E_21	NE_REF	30	30	882548	6345846	1219	123	2680	260	0.2	251.6	6605.9	2801.0
E_217	NE_REF	30	29	884984	6343361	1513	197	470	260	30.6	4757.1	722.1	377.5
E_224	NE_REF	30	30	886208	6343354	1289	212	1491	254	73.6	6761.6	697.0	641.9
E_243	NE_REF	30	30	885501	6343177	1529	150	1042	302	1.2	4877.5	468.7	377.9
E_28	NE_REF	30	30	882736	6345610	1165	282	2102	243	32.1	333.1	6251.2	2199.5
E_61	NE_REF	30	29	882699	6344960	1494	102	1855	316	86.3	553.9	4273.9	1568.1
E_76	NE_REF	31	30	883247	6344771	1386	162	2495	218	15.8	1657.1	4793.2	1460.2
E_91	NE_REF	30	30	883604	6344602	1339	181	1300	183	243.4	2177.7	3246.4	1683.5
W_10	NW_REF	29	29	881142	6346187	1172	116	2676	235	987.1	1.8	7073.9	2902.8
W_122	NW_REF	7	7	879278	6346550	1051	NA	1605	282	3104.2	94.7	6346.3	4622.8
W_142	NW_REF	29	29	880280	6346261	1163	92	1320	333	1572.0	120.0	5632.4	3399.2
W_164	NW_REF	27	27	880552	6346204	1211	80	1618	314	1183.0	11.5	7170.2	2905.9
W_206	NW_REF	24	20	879222	6345806	1058	75	1381	165	2997.2	14.9	6459.8	2983.1
W_221	NW_REF	40	39	880002	6345770	1282	210	1367	319	2066.7	182.3	5587.2	2686.0
W_229	NW_REF	41	41	879984	6345695	1314	180	2030	316	2293.9	42.8	6087.5	3203.2
W_257-1	NW_REF	33	31	878775	6345394	1065	75	1051	175	2813.4	16.5	5832.9	2739.1
W_257-2	NW_REF	184	40	878659	6345401	1032	112	1425	183	3094.0	159.7	5581.5	2445.2
W_260	NW_REF	30	30	879079	6345428	1085	133	1550	331	2925.1	1.7	5794.5	3121.1
W_263	NW_REF	42	39	879686	6345423	1181	75	793	277	3139.8	33.8	5315.6	2610.2
W_313	NW_REF	30	30	878740	6344921	1109	65	931	161	2600.6	0.6	5290.3	1804.1
W_362-1	NW_REF	40	39	878814	6344870	1159	122	1543	315	2533.9	13.6	5136.1	1597.2
W_362-2	NW_REF	42	39	878966	6344911	1175	65	1068	271	2381.3	0.8	5448.6	1649.0
W_384	NW_REF	296	40	879342	6344728	1363	126	884	70	1513.4	0.2	4672.4	1722.9
W_415	NW_REF	13	13	878137	6344665	1139	65	1030	234	3174.5	305.0	6412.1	2544.7
W_429	NW_REF	13	13	879924	6344587	1567	65	378	161	807.1	94.6	3795.4	1021.7
W 435	NW REF	40	40	879429	6344477	1482	179	1267	325	1115.3	102.1	4531.2	1148.6
W_484	NW_REF	36	33	878733	6344250	1372	65	686	174	1324.9	276.0	4919.3	1385.8
W A	NW REF	29	28	880752	6345722	1351	221	2890	366	1735.5	131.3	4221.4	2068.7
W B	NW REF	30	30	880476	6345675	1361	220	4100	350	2308.2	27.2	4638.1	2681.0
W C	NW REF	30	29	879955	6344974	1396	258	1979	265	1229.8	13.3	5205.9	1760.1
W D	NW REF	12	12	881049	6346353	1000	NA	1830	382	1309.2	49.4	6684.5	2920.8
W N2	NW REF	99	40	878998	6345235	1195	NA	977	357	3569.6	11.1	5243.4	2604.5
W N3	NW REF	31	30	879113	6344863	1226	NA	1560	322	2503.1	23.1	5105.1	1895.1
S_1101	S_REF	30	30	884063	6342071	1427	156	1609	391	1686.0	3126.1	1141.6	1.1

S_1225	S_REF	30	30	882580	6341859	1345	210	1618	421	1676.3	2958.2	1541.7	27.0
S_1250	S_REF	30	29	886364	6341702	1423	191	1260	375	717.3	5736.7	0.1	915.4
S_5	S_REF	30	29	886616	6342311	1517	120	1169	388	413.5	5204.1	2.9	707.5
S_901	S_REF	30	30	881199	6343020	1454	221	1431	387	1210.5	1280.7	3269.4	8.8
S_905	S_REF	30	30	881977	6342722	1430	199	1165	482	1716.2	2168.0	2837.6	4.8
S_985	S_REF	30	30	882618	6342836	1503	183	1623	465	1077.9	1838.0	2086.9	5.7
E_1217	NE_EXP	30	30	890082	6341948	1224	156	2179	347	1440.7	10837.0	2207.7	3170.6
E_1231	NE_EXP	30	30	891475	6342079	1289	105	1121	381	1762.8	11408.3	2016.1	3169.8
E_256	NE_EXP	7	7	887791	6343152	1231	218	1613	430	90.3	8747.3	626.4	1382.2
E_259	NE_EXP	30	30	888297	6343149	1338	135	528	253	316.7	9188.5	926.9	1643.6
E_267	NE_EXP	30	30	886805	6343030	1419	243	1201	284	42.1	7261.0	325.3	862.6
E_274	NE_EXP	30	30	888655	6342801	1305	194	2067	295	417.9	8792.6	982.3	1787.0
E_68	NE_EXP	30	30	890769	6340854	1099	134	1700	441	2574.7	9611.4	2311.9	3760.4
E_940	NE_EXP	30	30	890389	6342743	1198	173	968	295	2091.2	10271.3	1848.3	2891.5
E_979	NE_EXP	30	30	891629	6342749	1024	187	1223	390	4112.8	12373.3	2944.5	3878.4
E_980	NE_EXP	30	29	892943	6342699	993	220	1620	270	5123.1	11439.5	4123.5	5024.3
E_E	NE_EXP	11	10	888405	6343898	983	NA	1520	645	427.6	9055.7	1348.1	2406.4
E_1755	NE_EXP	30	30	888023	6340224	1238	118	1621	443	1567.7	7494.8	1000.6	2484.5
S_1	S_EXP	30	29	882615	6337726	895	NA	932	83	3349.0	3879.3	1794.0	1360.1
S_1332	S_EXP	30	30	884976	6341206	1321	158	1295	360	1449.2	5192.0	302.7	437.4
S_1727	S_EXP	30	29	886026	6340302	1223	148	1455	315	1773.3	4891.5	46.6	1043.5
S_1739	S_EXP	30	30	882784	6340206	1103	93	741	300	1709.0	3144.7	1226.8	587.4
S_1832	S_EXP	30	30	883779	6339938	1119	222	2650	528	1988.1	4162.1	796.5	1356.8
S_1913	S_EXP	30	30	886787	6339439	1203	93	1202	300	2216.3	5731.4	782.8	1734.0
S_2007	S_EXP	30	29	882583	6339011	979	95	864	290	2097.7	3514.9	2072.4	930.2
S_2046	S_EXP	30	30	886361	6338618	1096	232	1437	360	2561.4	5767.5	775.0	1520.6
S_23	S_EXP	19	19	887210	6341512	1406	NA	1502	530	1050.9	7630.7	63.3	1598.1
S_3	S_EXP	20	20	885981	6339608	1204	NA	1168	356	2066.3	5641.6	385.5	1260.3
S_93	S_EXP	30	30	885546	6338720	1121	NA	2410	210	2037.8	5205.6	751.3	1512.3

Figure S2: Variation of altitude, age, tree size and distance to refugia among the five studied regions.

S_REF and NE_REF have a significantly higher altitude; NW_REF has a significantly lower age; NE_REF and NW_REF have a significantly lower minimal circumference; variations in maximal circumference were not significant. Logically, plots from NW_REF region are closer from NE refuge axis, plots from NE_REF region are closer from NW refugia axis, and plots from S_REF region are closer from SW refugia.



Table S2: Diversity parameters and Bayesian assignments of the 71 plots

Clust: name of the cluster the plot was assigned with STRUCTURE/TESS (with its corresponding p-value, p_{val}); **Na**: number of alleles; **Ar**: allelic richness; **Ho**: observed heterozygosity; **He**: expected heterozygosity; **difHe** : difference in He between the old and young cohort (in %); **difAr** : difference in Ar between the old and young cohort (in %); **F**_{IS}: inbreeding coefficient. p_{Hdef} : probability of heterozygote deficiency; p_{Hexc} : probability of heterozygote excess; βwt : genetic differentiation from the entire pool; **Sp** : intensity of spatial genetic structure, (with its corresponding p-value, p_{Sp})

Plot	Clust	p _{val}	Na	Ar	Но	Не	difHe	DifAr	Fis	р _{Hdef}	р _{нехс}	βwt	Sp	p _{Sp}
North West Refuge (NW_REF)														
W_10	C2	0.65	71	4.08	0.68	0.66	3.0	-2.8	-0.013	NS	NS	0.046	0.031	*
W_122	C1	0.68	55	3.82	0.62	0.62	-27.5	-13.5	0.081	NS	NS	0.050	0.062	*
W_142	C1	0.77	82	4.47	0.67	0.67	-4.7	-4.0	0.014	NS	NS	0.032	0.009	*
W_164	C1	0.68	76	4.16	0.66	0.65	-4.8	0.4	0.001	NS	NS	0.062	0.023	NS
W_206	C1	0.75	73	4.44	0.7	0.7	4.3	0.8	0.031	NS	NS	-0.024	0.020	*
W_221	C1	0.88	86	4.45	0.74	0.7	2.9	2.6	-0.047	NS	*	-0.005	0.005	NS
W_229	C1	0.71	86	4.67	0.75	0.71	6.9	6.3	-0.033	NS	NS	-0.027	0.015	*
W_257-1	C1	0.76	75	4.35	0.69	0.69	0.0	0.0	0.025	NS	NS	0.002	0.028	*
W_257-2	C1	0.86	81	4.39	0.69	0.69	8.7	3.5	0.007	NS	NS	0.007	0.026	*
W_260	C1	0.84	79	4.32	0.7	0.7	-1.5	4.6	0.014	NS	NS	-0.013	0.004	NS
W_263	C1	0.73	82	4.43	0.7	0.7	4.3	3.8	0.012	NS	NS	-0.001	0.011	*
W_313	C1	0.93	81	4.43	0.66	0.68	-3.1	-1.2	0.046	NS	NS	0.014	0.023	*
W_362-1	C1	0.93	76	4.34	0.71	0.67	1.5	1.9	-0.037	NS	NS	0.033	0.030	*
W_362-2	C1	0.82	81	4.28	0.7	0.68	-9.7	-6.7	-0.005	NS	NS	0.017	0.029	*
W_384	C1	0.87	91	4.66	0.7	0.7	-2.9	-2.7	0.02	NS	NS	-0.009	0.009	*
W_415	C1	0.77	62	3.91	0.61	0.61	-40.9	-28.9	0.041	NS	NS	0.100	0.081	*
W_429	C1	0.49	62	3.99	0.72	0.65	7.8	5.3	-0.072	NS	NS	0.045	0.033	NS
W_435	C1	0.61	79	4.36	0.67	0.67	-4.6	-8.2	0.013	NS	NS	0.033	0.001	NS
W_484	C1	0.86	79	4.55	0.69	0.69	-1.5	1.1	0.011	NS	NS	0.005	0.012	*
W_A	C2	0.77	71	4.39	0.73	0.71	-4.4	-3.9	-0.015	NS	NS	-0.020	0.018	*
W_B	C1	0.69	76	4.39	0.67	0.67	-3.1	-4.9	0.011	NS	NS	0.039	0.041	*
W_C	C2	0.64	70	4.27	0.7	0.68	-1.5	1.5	-0.022	NS	NS	0.022	0.042	*
W_D	C1	0.80	60	3.99	0.74	0.65	3.1	3.6	-0.092	NS	*	0.030	-0.007	NS
W_N2	C1	0.74	83	4.42	0.71	0.69	2.9	2.7	-0.016	NS	NS	0.011	0.015	*
W_N3	C1	0.65	77	4.36	0.71	0.7	2.9	0.8	-0.005	NS	NS	-0.005	0.007	NS
Mean			75.8	4.32	0.69	0.68	-2.5	-1.5	-0.001			0.018	0.023	
						North	East Ref	uge (NE	_REF)					
E_132	C1	0.47	82	4.44	0.65	0.65	-1.6	-0.4	0.017	NS	NS	0.062	0.015	*
E_168	C1	0.61	82	4.68	0.76	0.71	-2.9	-1.5	-0.048	NS	*	-0.027	-0.004	NS
E_170	C1	0.74	70	4.35	0.69	0.67	3.0	0.8	-0.006	NS	NS	0.023	-0.012	NS
E_184	C1	0.72	75	4.44	0.72	0.7	0.0	4.5	-0.008	NS	NS	-0.008	-0.004	NS
E_186	C1	0.85	78	4.44	0.71	0.68	4.4	3.9	-0.029	NS	NS	0.014	0.002	NS
E_188	C1	0.61	75	4.33	0.67	0.67	-4.7	-2.4	0.011	NS	NS	0.036	0.016	NS
E_191	C1	0.64	74	4.14	0.61	0.62	1.6	2.8	0.033	NS	NS	0.099	0.029	*
E_203	C2	0.69	67	4.2	0.73	0.65	29.2	15.6	-0.096	NS	*	0.057	0.025	*
E_21	C1	0.74	74	4.28	0.64	0.65	-3.2	-3.3	0.044	NS	NS	0.056	0.030	*
E_217	C1	0.60	75	4.31	0.65	0.64	-20.8	-16.2	-0.006	NS	NS	0.077	0.059	*
E_224	C1	0.56	74	4.23	0.63	0.65	6.2	-0.4	0.045	NS	NS	0.068	0.035	*
E_243	C2	0.70	81	4.52	0.68	0.66	-1.6	0.0	-0.011	NS	NS	0.052	0.003	*

E_28	C1	0.77	73	4.39	0.72	0.69	4.3	1.9	-0.025	NS	NS	0.007	0.009	NS
E_61	C2	0.87	71	4.25	0.7	0.68	3.0	-2.0	-0.016	NS	NS	0.023	0.032	*
E_76	C2	0.59	72	4.26	0.68	0.66	0.0	2.0	-0.024	NS	NS	0.051	0.009	NS
E_91	C1	0.76	84	4.45	0.72	0.68	5.9	7.3	-0.047	NS	NS	0.024	0.000	NS
Mean			75.4	4.36	0.69	0.67	1.4	0.8	-0.010			0.038	0.015	
						Sou	uth Refu	ge (S_RE	F)					
S_1101	C2	0.79	82	4.49	0.64	0.67	-6.1	0.8	0.108	NS	NS	0.019	0.028	*
S_1225	C2	0.55	70	4.24	0.68	0.66	4.5	-1.6	-0.017	NS	NS	0.049	0.027	*
S_1250	C2	0.83	67	4.06	0.71	0.64	9.9	0.5	-0.078	NS	*	0.060	0.065	*
S_5	C2	0.56	71	4.04	0.63	0.64	1.6	-0.4	0.03	NS	NS	0.073	0.018	*
S_901	C1	0.60	68	3.92	0.64	0.65	0.0	-8.3	0.05	NS	NS	0.050	0.014	NS
S_905	C2	0.82	69	3.78	0.66	0.63	-1.6	-7.4	-0.026	NS	NS	0.083	0.027	*
S_985	C2	0.77	81	4.48	0.73	0.7	-9.2	-8.0	-0.017	NS	NS	-0.016	0.041	*
Mean			72.6	4.14	0.67	0.66	-0.1	-3.5	0.007			0.045	0.032	
	1	T	1	1	Ν	lorth E	ast Expa	nsion (N	E_EXP)	r	T	1	1	T
E_1217	C1	0.76	71	4.08	0.72	0.67	4.5	5.5	-0.048	NS	NS	0.026	0.043	*
E_1231	C3	0.88	82	4.54	0.6	0.62	3.2	-0.9	0.057	*	NS	0.101	0.008	NS
E_256	C2	0.76	52	3.84	0.69	0.63	3.3	0.8	-0.021	NS	NS	0.038	-0.038	NS
E_259	C1	0.59	75	4.4	0.7	0.68	4.4	4.6	-0.02	NS	NS	0.022	0.005	NS
E_267	C2	0.79	76	4.27	0.68	0.66	4.5	2.3	-0.014	NS	NS	0.051	0.011	NS
E_274	C2	0.48	76	4.52	0.69	0.68	-4.6	-1.6	-0.001	NS	NS	0.015	0.000	NS
E_68	C1	0.50	72	3.87	0.63	0.64	33.8	13.4	0.043	NS	NS	0.072	0.020	NS
E_940	C1	0.59	71	4.25	0.66	0.67	1.5	-2.4	0.035	NS	NS	0.027	0.022	NS
E_979	C1	0.57	75	4.36	0.64	0.68	-7.8	-4.0	0.076	*	NS	0.018	0.024	NS
E_980	C1	0.76	70	4.24	0.68	0.7	0.0	-3.6	0.042	NS	NS	-0.013	0.014	NS
E_E	C1	0.69	60	4.05	0.74	0.65	3.1	5.1	-0.087	NS	NS	0.027	0.068	*
E_1755	C3	0.65	93	5.11	0.71	0.7	7.0	3.3	0.002	NS	NS	-0.013	-0.001	NS
Mean			72.8	4.29	0.68	0.67	4.4	1.9	0.005			0.031	0.015	
		T	1	T	-	Sout	h Expans	sion (S_E	XP)	Γ.	-	1	1	T
S_1	C1	0.60	71	4.39	0.65	0.68	-1.5	0.4	0.058	*	NS	0.018	0.003	NS
S_1332	C2	0.90	70	4.14	0.71	0.67	7.4	0.0	-0.02	NS	NS	0.008	0.020	NS
S_1727	C3	0.48	77	4.59	NA	0.72	-4.3	-4.4	0.062	*	NS	0.010	0.013	NS
S_1739	C1	0.50	73	4.41	0.69	0.62	-18.3	-3.9	-0.096	NS	*	0.102	0.007	NS
S_1832	C2	0.80	72	4.34	0.67	0.65	-1.6	4.7	-0.005	NS	NS	0.058	0.021	*
S_1913	C3	0.90	84	4.63	0.63	0.65	-3.2	-3.2	0.044	NS	NS	0.062	-0.001	NS
S_2007	C2	0.56	66	3.86	0.66	0.61	0.0	-2.3	-0.045	NS	NS	0.108	0.048	*
S_2046	C1	0.76	58	3.1	NA	0.62	-1.6	0.0	0.033	NS	NS	0.072	0.018	NS
S_23	C3	0.79	77	4.56	0.64	0.63	6.3	-0.8	0.009	NS	NS	0.078	0.019	NS
S_3	C3	0.89	76	4.57	0.67	0.66	-8.1	-6.0	0.022	NS	NS	0.033	-0.005	NS
S_93	C1	0.74	76	4.39	0.67	0.69	2.9	-1.2	0.041	NS	NS	0.011	0.033	*
Mean			72.7	4.27	0.67	0.65	-2.0	-1.5	0.009			0.051	0.016	

Table S3: Hierarchical analysis of genetic variation at 12 microsatellite loci for 2042 beech individuals distributed in 71 plots (lev2-pop) nested within 5 regions (lev1-reg).

The variance components estimated with *hierfstat* for each hierarchical level are displayed for each locus and overall.

			I	I
Locus	lev1-reg	lev2-pop	Ind	Error
FS1-15	-0.0001	0.0318	0.0129	0.8208
FS3-04	0.0026	0.0132	-0.0268	0.5003
sfc0007-2	0.0017	0.0217	0.0166	0.7470
sfc0018	0.0002	0.0186	0.0578	0.6607
sfc0036	0.0002	0.0233	0.0015	0.6595
sfc1143	0.0004	0.0228	-0.0227	0.8159
csolfagus-5	0.0020	0.0186	0.0164	0.7181
csolfagus-6	-0.0001	0.0230	-0.0049	0.8370
csolfagus-25	0.0013	0.0135	-0.0083	0.5365
csolfagus-29	-0.0002	0.0152	-0.0146	0.5488
csolfagus-31	0.0037	0.0216	-0.0253	0.7530
mfs7	0.0051	0.0202	-0.0017	0.6286
overall	0.0168	0.2435	0.0009	8.2260

Figure S3: Pairwise genetic differentiation among plots, displayed as the matrix of pairwise F_{ST} among plots (a) and F_{ST} -based trees of plots based on a neighbor-joining algorithm (b) and on a hierarchical cluster algorithm (c).

The green oval on plot (b) and (c) correspond to the six plots assigned to the C3 cluster by STRUCTURE/TESS.

(a)







Figure S4: Detailed results of STRUCTURE analyses with population identifier as a prior information.

(a) Variation in the log-probability of data (L(K)) and of the statistics ΔK with K ; (b) Individual probability to belong to each cluster for K=3 and K=6 (c) Spatial interpolates of the admixture coefficients estimated for K=6 (d) Coefficients of membership of plots for K=3 and K=6 (e) Maps of the proportion of each cluster at each plot position for K=3 and K=6.

(a)















0.8

- 0.6

- 0.4

- 0.2

0.0

1.0

- 0.8

- 0.6

- 0.4

0.2







```
(d) K=3
```



(d) K=6



(d) K=6 (end)



(e) K=3







Figure S5: Detailed results of STRUCTURE analyses without population identifier as a prior information.

(a) Variation in the log-probability of data (L(K)) and of the statistics ΔK with K ; (b) Individual probability to belong to each cluster for K=3 (c) Spatial interpolates of the admixture coefficients estimated for K=3 (d) Coefficients of membership of plots for K=3.

(a)















0.50

0.45 0.40

0.35

0.30







Figure S6: Detailed results of TESS output

(a) Variation in DIC with K ; (b) Spatial interpolates of the admixture coefficients estimated for different K values (c) Coefficients of membership of plots for K=2, K=3 and K=6











1.2

- 1.0

- 0.8

- 0.6

- 0.4

0.2













K=6





K=2, Coeff. of membership of plots to Cluster 1







K=6, Coeff. of membership of plots to Cluster 1



K=6, Coeff. of membership of plots to Cluster 4

Figure S7: Comparison of EEMS results for the three independent analyses (corresponding to 400, 600 or 800 demes)

(A) Posterior probability trace



(B) Effective migration surface, as represented by posterior migration rates on the log10 scale



(C) Effective diversity surface, as represented by posterior diversity rates q on the log10 scale

