Online Supplementary Tables and Figures

For the article: "Genetic signatures of divergent selection in European beech (Fagus sylvatica L.) are associated with the variation in temperature and precipitation across its distribution range"

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Table S1: Coordinates, country of origin and climatic characteristics of the 64 populations

We extracted the 19 bioclimatic variables from the WordClim 1.4 database (30 seconds resolution) over the period 1950-2000 and computed their average values. **MAT**: Mean Annual Temperature (°C) ; **TDR**: Mean diurnal range (°C); **isoT**: Isothermality (MAT/TAR ×100), **Tseas**: Temperature Seasonality (CV) ; **MaxTWarm**: Max Temperature of Warmest Period (°C); **MaxTCold**: Min Temperature of Coldest Period (°C); **TAR**: Temperature Annual Range (MaxTWarm-MaxTCold; °C); **MeanTWet**: Mean Temperature of Wettest Quarter (°C); **MeanTdry**: Mean Temperature of Driest Quarter (°C); **MeanTwarm**: Mean Temperature of Warmest Quarter (°C) ; **MeanTcold**: Mean Temperature of Coldest Quarter (°C); **MAP**: Annual Precipitation (mm); **Pwet**: Precipitation of Wettest Period (mm); **Pdry**: Precipitation of Driest Period (mm); **Pseas**: Precipitation Seasonality (CV); **PwetQ**: Precipitation of Wettest Quarter (mm); **PdryQ**: Precipitation of Driest Quarter (mm); **PwarmQ**: Precipitation of Warmest Quarter (mm); **PcoldQ**: Precipitation of Coldest Quarter (mm)

Population	Long (°)	Lat (°)	Country	MAT	TDR	isoT	Tseas	MaxTWarm	MaxTCold	TAR	MeanTWet	MeanTdry	MeanTwarm	MeanTcold	MAP	Pwet	Pdry	Pseas	PwetQ	PdryQ	PwarmQ	PcoldQ
BG_58	25.5	42.6	BG	10.7	10.2	31.7	805.1	27.7	-4.3	32	15.1	16.3	20.5	0.6	609	72	38	22.6	194	123	161	141
BG_BN	23.3	41.9	BG	3.9	9.1	33.4	665.0	18.6	-8.5	27.1	6.5	9.3	12.0	-4.1	693	73	33	21.9	205	120	165	190
BG_VT	23.3	42.6	BG	5.0	9.0	32.6	691.1	19.6	-8.1	27.7	8.1	10.5	13.3	-3.6	679	80	39	22.5	218	130	190	160
BG-156	23.1	43.2	BG	8.2	9.5	31.8	751.6	23.7	-6.1	29.8	15.3	-0.1	17.1	-1.4	669	84	42	25.6	229	133	200	140
BG-157	23.1	43.2	BG	10.1	9.9	31.8	783.2	26.3	-4.8	31.1	17.7	1.5	19.4	0.1	643	79	41	24.5	216	129	186	135
BG-158	24.4	42.8	BG	6.8	9.3	31.5	753.0	22.3	-7.4	29.7	14.1	-1.8	15.9	-2.6	700	93	41	28.0	245	139	216	146
BG-16	23.7	41.5	BG	8.0	9.6	33.2	714.3	23.6	-5.2	28.8	0.9	13.6	16.7	-0.8	607	64	30	21.8	180	108	142	164
BIH_Bih	16.0	44.7	BIH	8.5	8.8	31.5	712.2	23.9	-4.2	28.1	4.6	16.6	17.1	-0.5	1187	140	78	20.8	392	248	259	305
BIH_Cja	17.5	43.5	BIH	4.9	7.0	28.8	648.7	18.6	-5.6	24.2	1.8	12.6	13.0	-2.8	1159	133	78	18.3	364	242	259	307
BIH_Din	16.6	44.0	BIH	6.2	7.4	28.8	677.3	20.4	-5.1	25.5	2.8	14.1	14.6	-2.1	1153	139	74	22.7	383	233	253	310

Population	Long (°)	Lat (°)	Country	MAT	TDR	isoT	Tseas	MaxTWarm	MaxTCold	TAR	MeanTWet	MeanTdry	MeanTwarm	MeanTcold	MAP	Pwet	Pdry	Pseas	PwetQ	PdryQ	PwarmQ	PcoldQ
DE_07	7.8	48.0	DE	10.3	8.4	32.2	670.9	24.9	-1.2	26.1	18.5	3.3	18.5	2.1	891	111	52	25.5	297	172	297	172
DE_08	10.1	51.6	DE	7.8	8.3	33.7	638.0	21	-3.7	24.7	15.5	0.6	15.5	-0.2	769	87	49	19.1	245	158	245	177
DE_09	11.8	48.9	DE	7.7	8.5	30.8	720.1	22.5	-5	27.5	16.3	3.3	16.3	-1.4	747	93	42	29.5	269	138	269	146
DK_21	9.6	54.9	DK	8.2	6.0	27.6	604.6	19.7	-2	21.7	9.3	3.2	15.6	1.0	774	86	41	22.9	241	136	211	175
DK_24	10.2	55.3	DK	7.9	6.1	27.8	607.1	19.9	-2.2	22.1	9.0	2.9	15.4	0.9	644	70	36	20.9	195	115	180	144
DK_26	10.7	55.2	DK	8.0	5.1	24.1	611.0	19.3	-1.7	21	9.4	2.6	15.5	0.9	605	66	34	21.2	180	107	173	118
DK_32	9.4	54.5	DK	8.3	6.5	28.8	615.2	20.5	-1.9	22.4	15.4	3.4	15.9	1.0	844	92	46	24.0	258	145	238	194
DK_33	11.3	54.8	DK	8.2	5.1	23.1	629.0	19.3	-2.8	22.1	15.7	2.6	15.9	0.8	606	65	35	18.8	181	116	176	122
DK_37	10.2	56.1	DK	7.6	6.7	27.3	632.5	19.9	-4.6	24.5	8.5	2.4	15.4	0.1	616	65	34	22.7	191	107	172	119
ES_15	-0.9	42.8	ES	8.9	9.8	39.5	558.1	22.7	-2.2	24.9	3.2	15.9	15.9	2.3	994	107	55	16.6	290	199	199	272
ES_16	-3.5	41.1	ES	9.0	10.7	37.4	649.1	25.9	-2.6	28.5	10.6	17.5	17.5	1.8	578	68	23	27.1	176	92	92	148
FR_10	2.7	48.4	FR	10.7	8.7	36.1	595.9	24.2	0	24.2	16.4	7.0	18.0	3.3	668	64	46	8.5	178	147	170	166
FR_12	5.0	46.0	FR	10.9	9.3	34.0	667.2	25.9	-1.3	27.2	15.8	4.1	19.1	2.6	822	83	55	15.3	232	172	220	172
FR_13	4.6	44.2	FR	12.5	10.0	35.8	646.7	28.1	0.2	27.9	13.1	20.6	20.6	4.7	792	103	34	25.8	263	147	147	189
FR_AIG	3.6	44.1	FR	7.0	8.8	36.2	563.3	20.8	-3.6	24.4	11.7	1.0	14.1	0.5	913	91	57	14.3	250	203	219	215
FR_ARG	0.7	43.0	FR	10.3	9.7	38.5	585.1	24	-1.2	25.2	12.3	4.4	17.5	3.2	919	95	61	14.2	265	202	234	207
FR_AUB	2.6	45.1	FR	5.9	9.2	38.4	552.7	19.3	-4.6	23.9	7.6	-0.1	12.7	-0.6	1014	113	66	15.6	290	214	271	234
FR_CHI	-0.4	46.1	FR	12.0	8.9	38.4	552.7	24.7	1.6	23.1	6.1	18.8	18.8	5.2	838	98	46	22.7	277	165	165	249
FR_CIR	-0.3	44.4	FR	12.6	10.6	41.7	564.0	26.4	1.1	25.3	6.5	19.5	19.5	5.6	931	105	53	18.0	286	191	191	268
FR_COL	3.0	46.2	FR	9.4	9.9	38.8	590.5	23.4	-2	25.4	14.9	5.5	16.7	2.2	772	93	47	23.0	238	147	228	160
FR_FOU	-1.2	48.4	FR	10.6	8.1	39.0	495.0	22.2	1.4	20.8	5.5	16.6	16.6	4.6	768	86	49	18.0	239	163	163	217
FR_HES	2.0	50.4	FR	10.0	6.8	33.7	519.7	21	0.9	20.1	11.2	6.2	16.4	3.7	667	80	41	19.6	209	134	167	166
FR_LAG	2.9	49.6	FR	10.0	8.4	36.0	566.6	22.8	-0.4	23.2	10.7	6.3	16.9	3.0	651	63	44	10.3	178	138	169	159

Population	Long (°)	Lat (°)	Country	MAT	TDR	isoT	Tseas	MaxTWarm	MaxTCold	TAR	MeanTWet	MeanTdry	MeanTwarm	MeanTcold	MAP	Pwet	Pdry	Pseas	PwetQ	PdryQ	PwarmQ	PcoldQ
FR_LEO	5.2	44.9	FR	6.0	8.5	33.4	617.3	20	-5.4	25.4	2.7	13.4	13.7	-1.5	1109	105	71	10.8	299	253	258	273
FR_PAI	-0.3	44.7	FR	12.5	10.3	41.5	557.7	26.1	1.3	24.8	6.5	19.3	19.3	5.6	924	103	53	18.5	286	188	188	266
FR_ROL	-1.4	43.3	FR	11.2	9.2	40.3	511.2	23.8	1	22.8	5.9	17.4	17.6	5.1	1305	157	67	21.8	421	249	255	395
GB_01	-4.8	57.3	GB	6.9	6.5	34.1	475.0	17.1	-1.9	19	2.3	9.0	13.1	1.4	1402	169	75	29.5	478	228	267	433
GB_02	-3.0	54.3	GB	8.8	6.9	35.6	482.2	19.4	-0.1	19.5	6.2	10.9	14.8	3.0	1014	109	58	23.7	324	189	234	267
GB_03	-2.7	51.8	GB	9.8	7.0	36.3	467.5	20.6	1.3	19.3	5.2	6.2	15.7	4.4	795	84	52	16.7	242	170	177	220
GR_OX	21.4	39.2	GR	12.5	11.0	36.2	694.9	29.6	-0.7	30.3	5.7	21.2	21.2	4.2	930	141	21	51.2	379	87	87	362
GR_PO	23.0	41.2	GR	12.2	10.3	33.1	768.9	29	-2	31	4.2	21.2	21.6	2.8	491	58	27	22.4	148	90	105	128
GR_TP	21.6	40.4	GR	6.6	10.3	34.8	690.7	23.1	-6.6	29.7	-0.4	14.8	15.1	-1.8	788	94	39	27.2	259	126	133	229
IT_16	7.6	45.6	IT	-0.2	6.1	28.1	575.9	11.5	-10.3	21.8	1.3	7.0	7.0	-6.7	1726	160	130	7.1	459	411	411	431
IT_18	11.8	43.8	IT	10.1	7.0	28.2	659.2	24.1	-0.8	24.9	6.7	18.4	18.4	2.4	886	109	47	22.8	288	165	165	218
IT_19	10.9	45.8	IT	5.6	7.3	28.4	663.7	19.6	-6.1	25.7	13.6	-2.4	13.8	-2.4	752	94	30	37.6	261	96	258	96
IT_19P	9.5	44.5	IT	6.6	5.7	25.1	618.1	19.2	-3.6	22.8	7.8	-0.2	14.3	-0.6	980	120	58	23.1	325	202	208	207
IT_20	16.6	39.0	IT	14.1	6.8	30.2	583.7	26.8	4.4	22.4	11.9	21.4	21.5	7.6	932	143	18	58.5	394	67	95	363
IT_32	12.6	43.1	IT	11.1	7.4	28.8	670.6	25.6	0	25.6	12.2	19.6	19.6	3.3	905	108	52	20.4	287	191	191	207
IT_R	15.0	37.8	IT	9.8	6.2	26.5	641.5	23.2	-0.1	23.3	7.2	18.0	18.0	2.7	667	91	16	49.3	258	60	60	235
PL_115	20.6	49.5	PL	4.6	8.7	30.0	743.2	19.3	-9.7	29	13.5	-4.0	13.5	-4.8	934	137	43	42.1	377	143	377	150
PL_117	16.9	50.3	PL	6.8	8.4	30.9	707.4	21.1	-6.2	27.3	15.2	-1.1	15.2	-2.2	639	91	28	48.2	271	86	271	89

Population	Long (°)	Lat (°)	Country	MAT	TDR	isoT	Tseas	MaxTWarm	MaxTCold	TAR	MeanTWet	MeanTdry	MeanTwarm	MeanTcold	MAP	Pwet	Pdry	Pseas	PwetQ	PdryQ	PwarmQ	PcoldQ
PL_121	15.6	52.2	PL	8.8	7.8	27.1	780.1	23.9	-4.7	28.6	18.1	0.1	18.1	-1.1	560	70	29	28.9	196	94	196	109
PL_66	23.4	50.3	PL	7.1	8.2	27.5	799.8	22.4	-7.4	29.8	16.5	-2.0	16.5	-3.1	627	87	29	40.6	245	93	245	98
PL_68	14.6	53.0	PL	8.6	7.8	27.9	757.7	23.3	-4.6	27.9	17.6	0.1	17.6	-1.1	551	69	30	26.2	188	99	188	110
PL_69	20.0	49.3	PL	5.2	9.1	30.8	749.5	20.2	-9.3	29.5	14.0	-3.4	14.0	-4.4	1040	166	44	48.2	442	141	442	147
RO_CA	24.7	45.3	RO	6.4	9.8	32.0	769.4	21.6	-8.9	30.5	14.0	-2.2	15.5	-3.5	764	115	39	42.8	311	120	299	123
RO_DB	22.3	44.6	RO	10.4	9.4	31.0	798.6	26.8	-3.6	30.4	18.2	1.8	19.8	0.2	658	90	41	28.0	232	124	213	135
RO_GH	25.9	47.5	RO	6.5	9.4	30.2	820.1	22.1	-9.1	31.2	14.8	-4.0	16.2	-4.0	657	107	28	54.2	293	87	283	87
RO_SC	23.1	46.0	RO	7.3	9.2	32.1	731.6	22.1	-6.5	28.6	14.4	-1.0	16.0	-2.0	770	118	40	41.6	309	123	297	132
SE_04	11.7	57.9	SE	7.3	6.2	25.9	686.8	19.8	-4.3	24.1	12.7	1.6	15.7	-1.0	695	81	36	27.2	231	115	194	149
SE_05	14.3	55.6	SE	7.7	5.5	24.8	636.0	19.7	-2.4	22.1	15.3	2.2	15.7	0.4	591	64	33	21.1	180	105	168	139
SE_25	11.6	58.3	SE	6.9	6.0	24.9	687.8	19.6	-4.5	24.1	12.1	1.2	15.5	-1.3	746	86	39	26.5	244	125	207	162
SE_28	14.6	56.1	SE	7.3	6.0	26.0	650.6	20.1	-3	23.1	15.0	1.9	15.6	-0.2	610	69	35	21.6	188	110	174	144
SK_23	19.1	48.6	SK	8.7	10.7	32.7	803.5	25.4	-7.2	32.6	18.0	0.0	18.0	-1.8	681	85	41	24.2	220	124	220	137

*Country : BG= Bulgaria; BIH= Bosnia and Herzegovina; DE= Germany; DK= Denmark; ES= Spain; FR=France; GB= Great Britain; IT=Italy; PL=Poland; RO= Romania; SE= Sweden; SK= Slovakia.

Table S2: Diversity parameters and cluster assignments of the 64 populations.

q1, q2, q2: q-values for the assignation to cluster C1, C2, C3 (respectively green, red and blue on Fig. 2) using DAPC; **n:** number of genotyped individuals; **Na:** mean number of alleles; **Ar:** allelic richness; **%polloc:** percentage of polymorphic loci; **He:** expected heterozygosity; **Ho:** observed heterozygosity; **F_{IS}:** inbreeding coefficient. **βwt** : genetic differentiation from the entire pool.

Population	q1	q2	q3	n	Na	Ar	%polloc	H_E	H_0	F_{IS}	$β_{WT}$
BG_156	0.15	0.19	0.66	4	1.67	1.51	67	0.287	0.277	0.005	0.102
BG_157	0.42	0.10	0.47	4	1.71	1.56	71	0.306	0.297	-0.001	0.039
BG_158	0.12	0.18	0.70	3	1.67	1.56	67	0.316	0.333	-0.100	-0.007
BG_16	0.05	0.06	0.88	4	1.65	1.51	65	0.265	0.272	-0.045	0.162
BG_58	0.06	0.12	0.83	4	1.71	1.57	71	0.310	0.298	0.003	0.032
BG_BN	0.12	0.12	0.76	8	1.83	1.59	83	0.298	0.313	-0.045	0.057
BG_VT	0.05	0.06	0.89	7	1.77	1.56	77	0.288	0.291	-0.011	0.093
BIH_Bih	0.29	0.07	0.64	8	1.75	1.56	75	0.291	0.327	-0.116	0.078
BIH_Cja	0.11	0.06	0.83	7	1.75	1.56	75	0.295	0.304	-0.047	0.070
BIH_Din	0.14	0.09	0.77	8	1.77	1.55	77	0.280	0.291	-0.026	0.115
DE_07	0.52	0.37	0.11	9	1.81	1.6	81	0.306	0.307	-0.008	0.037
DE_08	0.74	0.10	0.16	10	1.81	1.58	81	0.302	0.309	-0.007	0.047
DE_09	0.65	0.11	0.24	10	1.83	1.59	83	0.300	0.289	0.030	0.058
DK_21	0.80	0.15	0.05	4	1.72	1.58	72	0.319	0.318	-0.022	-0.006
DK_24	0.79	0.12	0.09	4	1.73	1.58	73	0.318	0.347	-0.106	-0.019
DK_26	0.85	0.08	0.07	4	1.67	1.52	67	0.302	0.262	0.092	0.065
DK_32	0.73	0.16	0.11	4	1.69	1.53	69	0.294	0.286	-0.004	0.076
DK_33	0.86	0.06	0.09	4	1.68	1.56	68	0.298	0.316	-0.080	0.053
DK_37	0.82	0.08	0.10	4	1.71	1.59	71	0.319	0.339	-0.083	-0.012
ES_15	0.10	0.84	0.06	10	1.84	1.6	84	0.297	0.299	-0.001	0.065
ES_16	0.07	0.78	0.15	10	1.85	1.6	85	0.297	0.289	0.022	0.065
FR_10	0.40	0.43	0.17	10	1.85	1.6	85	0.301	0.312	-0.027	0.050
FR_12	0.26	0.66	0.08	9	1.83	1.62	83	0.316	0.305	0.029	0.005
FR_13	0.52	0.37	0.12	8	1.82	1.6	82	0.304	0.298	0.026	0.045
FR_AIG	0.09	0.63	0.28	8	1.82	1.61	82	0.307	0.304	0.002	0.034
FR_ARG	0.07	0.84	0.09	8	1.86	1.62	86	0.307	0.316	-0.028	0.031
FR_AUB	0.11	0.76	0.13	8	1.86	1.62	86	0.313	0.313	0.002	0.015
FR_CHI	0.07	0.68	0.25	8	1.84	1.62	84	0.306	0.326	-0.052	0.033
FR_CIR_B	0.14	0.74	0.13	8	1.86	1.61	86	0.322	0.311	0.016	-0.011
FR_COL	0.18	0.71	0.12	8	1.87	1.65	87	0.322	0.337	-0.041	-0.018
FR_FOU	0.33	0.44	0.22	8	1.85	1.62	85	0.314	0.328	-0.029	0.006
FR_HES	0.39	0.45	0.17	8	1.83	1.65	83	0.327	0.336	-0.027	-0.034
FR_LAG	0.38	0.44	0.18	8	1.81	1.61	81	0.301	0.313	-0.035	0.049
FR_LEO	0.14	0.74	0.12	8	1.85	1.64	85	0.319	0.318	-0.003	-0.006
FR_PAI	0.11	0.80	0.09	8	1.86	1.62	86	0.312	0.307	0.021	0.017
FR_ROL	0.05	0.91	0.04	8	1.80	1.55	80	0.290	0.283	0.016	0.087

Population	q1	q2	q3	n	Na	Ar	%polloc	H_E	H_0	F_{IS}	β_{WT}
GB_01	0.35	0.49	0.16	10	1.85	1.61	85	0.307	0.282	0.062	0.038
GB_02	0.50	0.44	0.06	9	1.83	1.59	83	0.295	0.307	-0.028	0.068
GB_03	0.49	0.42	0.09	9	1.85	1.6	85	0.301	0.306	-0.011	0.050
GR_OX	0.09	0.08	0.83	7	1.80	1.59	80	0.306	0.296	0.013	0.042
GR_PO	0.06	0.06	0.88	7	1.80	1.57	81	0.296	0.282	0.035	0.073
GR_TP	0.05	0.06	0.90	5	1.73	1.54	73	0.291	0.302	-0.042	0.081
IT_16	0.36	0.28	0.36	4	1.76	1.59	76	0.317	0.321	-0.031	-0.001
IT_18	0.29	0.07	0.64	6	1.73	1.54	73	0.285	0.301	-0.061	0.098
IT_19	0.63	0.12	0.25	6	1.77	1.58	77	0.292	0.315	-0.070	0.074
IT_20	0.04	0.07	0.90	9	1.80	1.56	80	0.280	0.290	-0.033	0.116
IT_32	0.25	0.15	0.61	5	1.73	1.57	73	0.307	0.312	-0.032	0.030
IT_P	0.46	0.10	0.45	4	1.69	1.54	69	0.293	0.281	0.005	0.082
IT_R	0.03	0.06	0.91	5	1.63	1.49	63	0.251	0.289	-0.136	0.195
PL_115	0.49	0.23	0.28	4	1.62	1.48	62	0.248	0.293	-0.167	0.201
PL_117	0.50	0.07	0.43	4	1.71	1.57	71	0.296	0.308	-0.056	0.062
PL_121	0.78	0.07	0.15	4	1.71	1.57	71	0.301	0.327	-0.097	0.041
PL_66	0.61	0.07	0.32	4	1.70	1.55	70	0.302	0.293	-0.003	0.054
PL_68	0.59	0.14	0.27	4	1.75	1.59	75	0.310	0.317	-0.045	0.021
PL_69	0.61	0.08	0.31	4	1.71	1.59	71	0.317	0.330	-0.060	-0.006
RO_CA	0.22	0.09	0.69	8	1.79	1.59	79	0.307	0.320	-0.034	0.057
RO_DB	0.29	0.06	0.65	8	1.81	1.61	81	0.305	0.309	-0.014	0.029
RO_GH	0.14	0.10	0.76	7	1.82	1.59	82	0.287	0.272	0.047	0.039
RO_SC	0.41	0.06	0.53	8	1.78	1.56	78	0.300	0.294	0.010	0.099
SE_04	0.87	0.09	0.05	10	1.76	1.57	76	0.285	0.285	0.000	0.103
SE_05	0.90	0.05	0.06	10	1.83	1.61	83	0.300	0.308	-0.025	0.055
SE_25	0.84	0.10	0.06	3	1.63	1.52	63	0.287	0.297	-0.071	0.090
SE_28	0.83	0.06	0.11	4	1.69	1.55	69	0.294	0.290	-0.011	0.074
SK_23	0.57	0.10	0.33	7	1.77	1.58	77	0.304	0.319	-0.042	0.037

Figure S1: Patterns of population structure and admixture inferred by Discriminant Analysis of Principal Components (DAPC)

(a) Variation in the Bayesian Information Criterion (BIC) with the possible number of clusters

(b) PCA on allelic frequencies

(c) Geographical distribution of the frequency of each cluster in each population. Each point correspond to one individual. We used a simple jitter around population coordinates to avoid superposition.
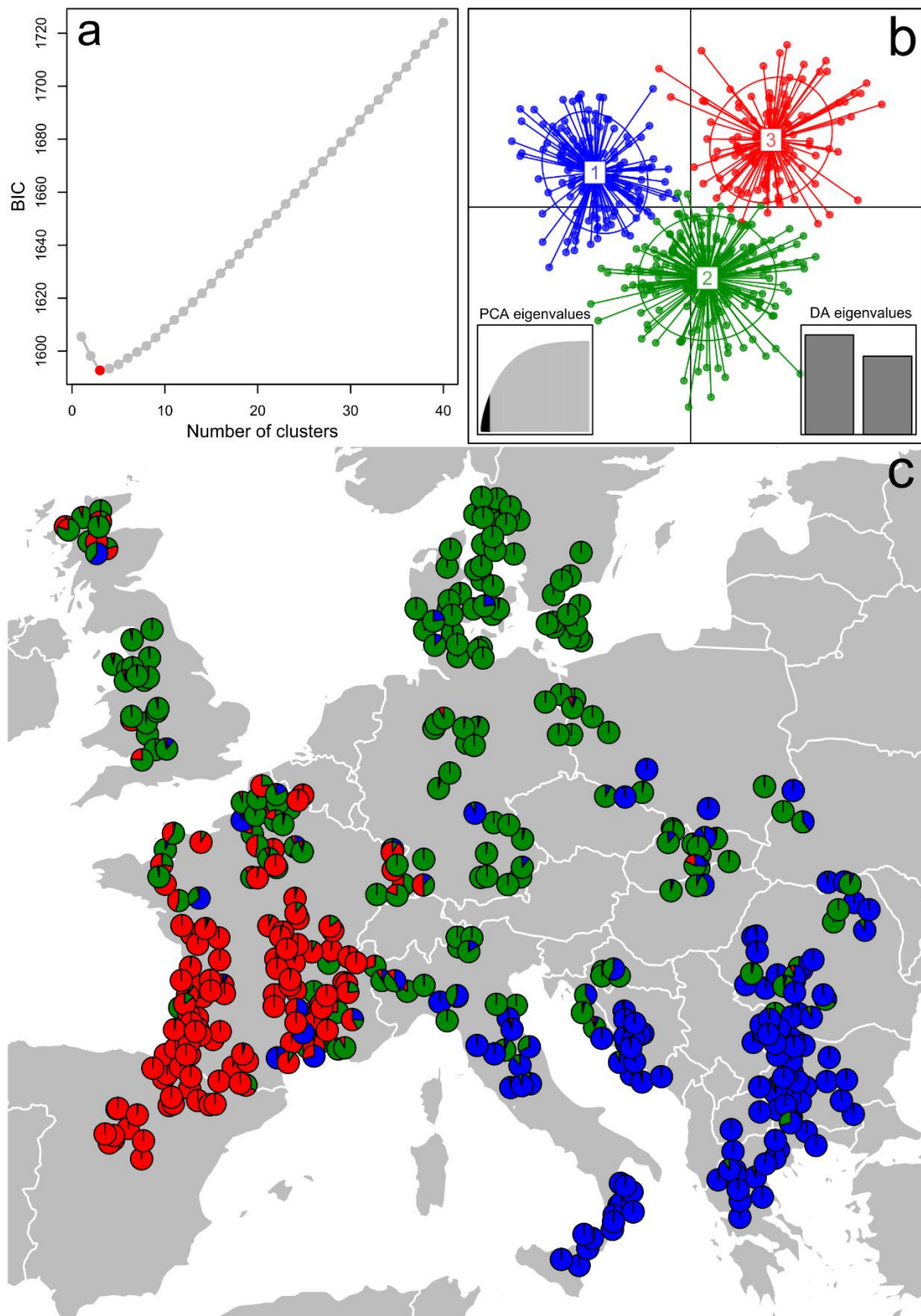
Figure S2: Variation of genetic diversity and differentiation among populations assigned to different genetic clusters.

Boxplots were used to visualize the variation in (a) expected heterozygosity, He, (b) percentage of polymorphic loci,%polloc and (c) genetic differentiation relative to the entire pool,β_{WT}, between the three inferred genetic clusters. These analyses were run on the 47 populations assigned to the green (16), red (12) and blue clusters as defined by STRUCTURE and DAPC. We used Tukey test to compare means of each variable among each pairs of clusters.
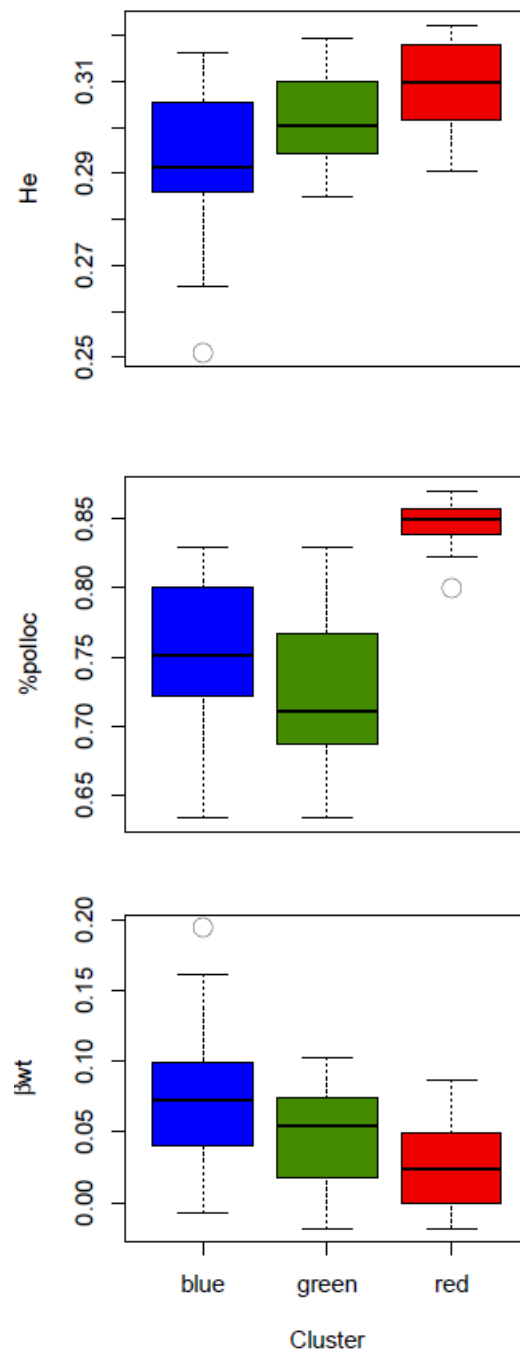
Figure S3: Patterns of variation in the percentage of polymorphic SNPs within a population for the two different SNP arrays used in this study.

The first array of SNP markers ("KASP array"), developed by Lalagüe et al. (2014), was based on the genotyping of one population south-eastern France, while the second array of SNP markers ("Sequenom Array"), developed for this study, was based on a larger number of populations representative of beech distribution range. The fraction of polymorphic loci displayed below for each SNP array and their combination suggests that that diversity patterns do not markedly differ between the two arrays.
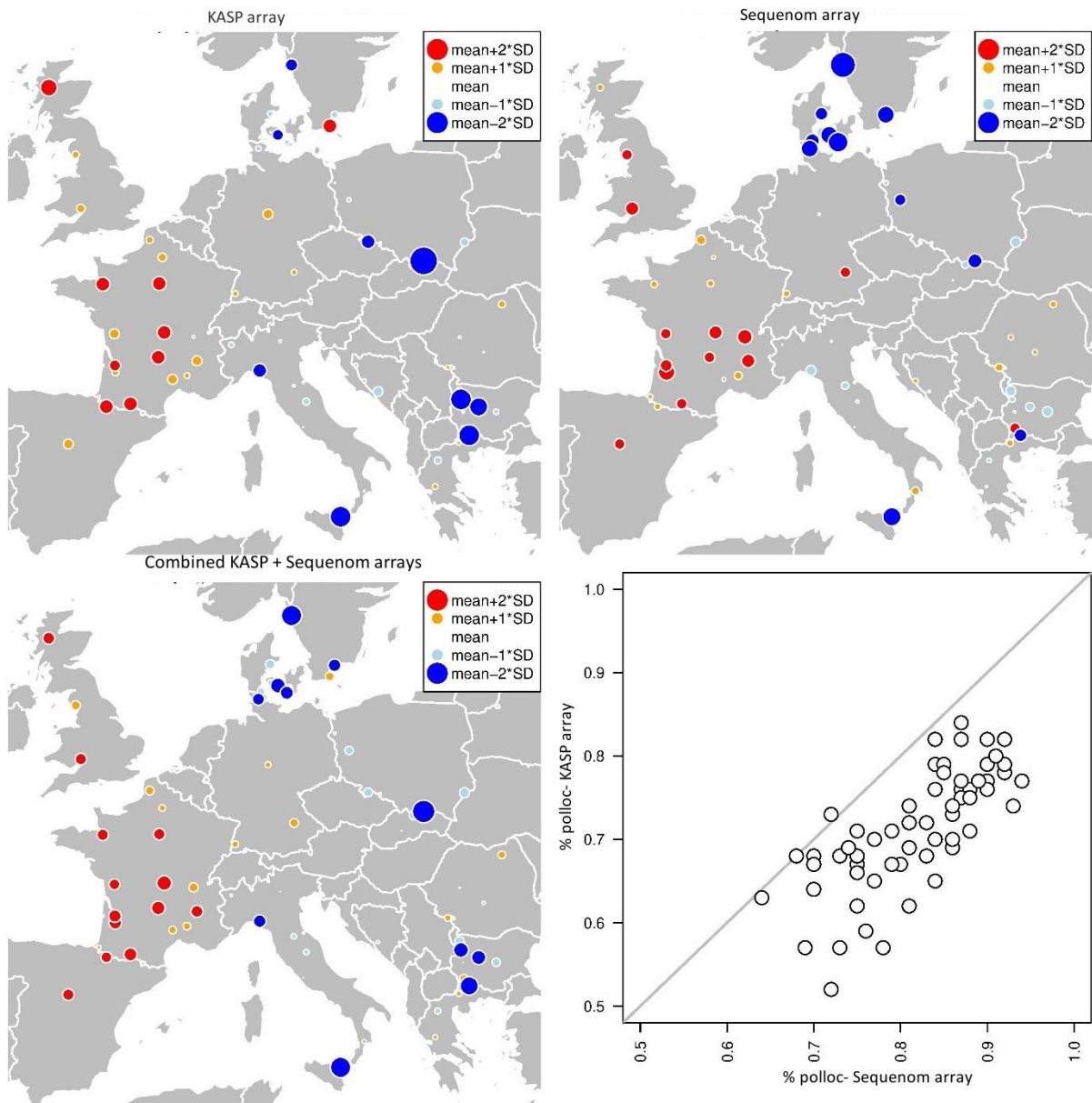
Table S3: Signal of isolation by distance (IBD) on genetic differentiation between all populations, and between populations belonging to each cluster.

nPop/nIndiv: number of populations/individuals considered in the SGS analyses; **blog:** slope of the regression of $F_{ST}/1-F_{ST}$ values against logarithm of distance with its standard error (**se**); **bmin, bmax:** distribution envelope of blog values under the hypothesis of complete spatial randomness; **p-value** associated to the one-sided test with H1 $blog_{observed} > blog_{expected}$.

Group	nPop	nIndiv	blog	se	bmin	bmax	pvalue
Blue cluster	29	117	0.0192	0.0043	-0.0140	0.0153	0.0056
Red cluster	20	99	0.0030	0.0057	-0.0093	0.0095	0.2685
Green cluster	36	142	0.0079	0.0024	-0.0086	0.0094	0.05
All populations	64	430	0.0266	0.0021	-0.0030	0.0033	0

Figure S4: Patterns of spatial genetic structure among all the 64 studied populations (black) and within each DAPC-defined cluster (in red, blue and green).

The values of genetic differentiation (measured by $F_{ST}/1-F_{ST}$ values) are plotted for each distance class against the logarithm of geographic distance between populations. Bars represent standard error at 95% level within each distance class
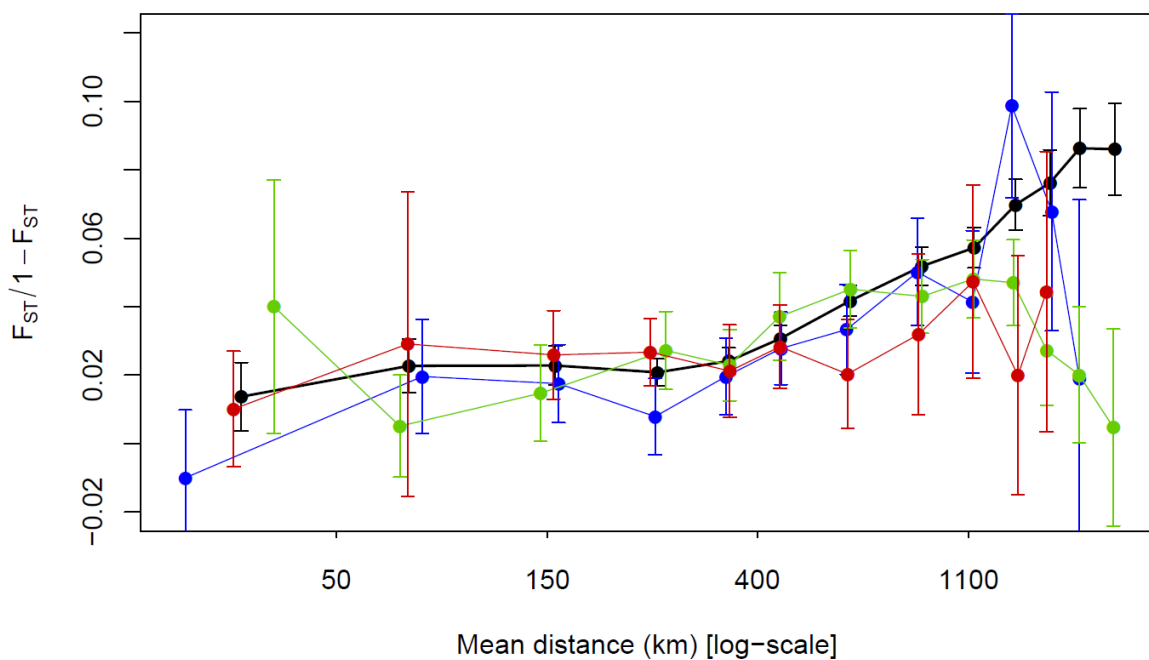
Table S4: Outlier SNPs detected with a)PCAdapt and b)LEA.

p-value: p-value of PCAdapt/LEA test statistic. **pBonf**: p-value corrected for multiple comparisons using Bonferroni approach; **pBH**: p-value corrected for multiple comparisons using Benjamini-Hochberg approach; **q-value**: direct (unbiased) estimate of the False Discovery Rate (FDR) associated with pBH; **localFDR**: Empirical Bayesian posterior probability that the null is true conditional on the observed p-value; **nfp** : Expected number of false positives as based on q-value

We show only outlier SNPs (ie, those having q-value associated with an expected number of false positives, nfp, equal to zero).

(a) *pcadapt*

SNP	p-value	pBonf	pBH	q-value	localFDR
QB_c13549-857	$9.52 \cdot 10^{-5}$	0.0172	0.0172	0.0172	0.0762

(b) *lea*

SNP	p-value	pBonf	pBH	q-value	localFDR
154_1_251	0.000090	0.0243	0.0243	0.0243	0.0272
QB_c13549-857	0.000262	0.0708	0.0354	0.0354	0.0466
QB_c10512-206	0.000493	0.1330	0.0443	0.0443	0.0651
154_1_715	0.001005	0.2714	0.0603	0.0603	0.0956
154_1_845	0.001116	0.3015	0.0603	0.0603	0.1012

Table S5: Outlier SNPs detected with *lfmm*.

β: lfmm test statistic for the correlation between environmental variable and allelic frequencies; **p-value**: p-value of the regression model. **q-value**: direct (unbiased) estimate of the False Discovery Rate (FDR) associated with p-value; **lFDR**: Empirical Bayesian posterior probability that the null is true conditional on the observed p-value; **CLIM**: synthetic climatic variable from PCA on climatic variables.

We show only outlier SNPs (ie, those having q-value associated with an expected number of false positives, nfp, equal to zero).

SNP	β	p.value	q.value	lFDR	CLIM
QB_c10517-841	0.179	0.000	0.033	0.033	Temp1
39_225	-0.180	0.001	0.033	0.040	Temp1
QB_c15642-205	-0.164	0.001	0.033	0.050	Temp1
21_243	-0.162	0.001	0.033	0.052	Temp1
150_2_924	0.167	0.001	0.033	0.054	Temp1
SB_c15868-233	0.164	0.001	0.033	0.055	Temp1
91_2_1441	0.155	0.003	0.065	0.081	Temp1
QB_c10512-206	-0.176	0.000	0.004	0.006	Temp2
150_2_924	-0.199	0.000	0.004	0.008	Temp2
21_243	0.188	0.000	0.004	0.008	Temp2
52_1_246	0.185	0.000	0.009	0.015	Temp2
154_2_371	0.175	0.000	0.015	0.023	Temp2
154_1_845	-0.148	0.001	0.018	0.029	Temp2
QB_c15913-902	-0.162	0.001	0.023	0.038	Temp2
QB_c6167-1062	0.165	0.001	0.023	0.040	Temp2
92_352	0.159	0.001	0.027	0.049	Temp2
QB_c15913-724	0.160	0.002	0.027	0.052	Temp2
ctrlfagus_c13215-830	0.156	0.002	0.027	0.054	Temp2
QB_c17017-1048	0.155	0.002	0.027	0.055	Temp2
142_143	0.154	0.002	0.029	0.060	Temp2
50_232	-0.215	0.000	0.010	0.008	Temp3
92_352	-0.205	0.000	0.011	0.013	Temp3
QB_c13152-130	-0.190	0.000	0.015	0.023	Temp3
27_485	-0.186	0.000	0.015	0.024	Temp3
7_186	0.192	0.000	0.015	0.026	Temp3
QB_c10512-206	0.161	0.000	0.016	0.031	Temp3
SB_c5654-1048	-0.169	0.001	0.017	0.035	Temp3
ctrlfagus_c15935-232	0.166	0.001	0.022	0.046	Temp3
QB_c13130-798	-0.177	0.001	0.022	0.048	Temp3
150_2_924	0.171	0.001	0.026	0.057	Temp3
154_2_371	0.168	0.002	0.032	0.067	Temp3
66_698	0.206	0.000	0.005	0.013	Precip1
QB_c13152-130	0.178	0.000	0.013	0.038	Precip1
133_306	-0.147	0.001	0.056	0.099	Precip1

19_206	-0.153	0.001	0.056	0.106	Precip1
SB_c13339-608	-0.193	0.000	0.029	0.021	Precip2
SB_c968-192	0.080	0.001	0.053	0.034	Precip2
SB_c968-1354	-0.108	0.001	0.053	0.045	Precip2
155_2_911	-0.152	0.001	0.053	0.048	Precip2
SB_c968-719	-0.073	0.002	0.053	0.053	Precip2
QB_c10517-414	0.147	0.002	0.053	0.053	Precip2
SB_c968-935	0.075	0.002	0.053	0.059	Precip2
QB_c13406-208	-0.147	0.002	0.053	0.061	Precip2
SB_c7640-125	0.153	0.002	0.053	0.061	Precip2
129_685	0.250	0.000	0.000	0.000	Precip3
21_243	0.229	0.000	0.000	0.000	Precip3
QB_c10517-414	-0.216	0.000	0.000	0.000	Precip3
150_2_924	-0.227	0.000	0.000	0.000	Precip3
91_2_1441	-0.212	0.000	0.000	0.002	Precip3
148_1_1411	-0.213	0.000	0.000	0.002	Precip3
91_2_57	0.199	0.000	0.001	0.005	Precip3
SB_c15868-233	-0.197	0.000	0.001	0.005	Precip3
154_2_371	0.198	0.000	0.001	0.006	Precip3
68_277	-0.185	0.000	0.002	0.011	Precip3
92_352	0.166	0.001	0.010	0.033	Precip3
SB_c13643-626	-0.159	0.001	0.019	0.049	Precip3
154_1_845	-0.138	0.002	0.020	0.054	Precip3
62_1_148	-0.153	0.002	0.021	0.058	Precip3
154_1_715	-0.134	0.002	0.021	0.059	Precip3
QB_c10512-206	-0.127	0.003	0.025	0.069	Precip3

Table S6: Outlier SNPs detected with *SamBada*.

G: genotype; **D:** log-likelihood ratio test statistic deriving from the comparison among the null and alternative model for the *i-th* genotype; β_{clim}: Regression coefficient linking the climatic variable with the i-th genotype frequency; **p-value**: p-value associated with the log-likelihood test statistic D; **q-value**: direct (unbiased) estimate of the False Discovery Rate (FDR) associated with p-value; **IFDR**: Empirical Bayesian posterior probability that the null is true conditional on the observed p-value; **Clim**: synthetic climatic variable from PCA on climatic variables. We show only outlier SNPs (ie, those having q-value associated with an expected number of false positives, nfp, equal to zero).

SNP	G	D	β_{clim}	β_{DAPC1}	β_{DAPC2}	p.value	q.value	IFDR	OR_env	Clim
154_1_251	CC	16.54	0.34	-0.30	-0.30	0.000	0.028	0.042	1.40	Temp1
QB_c10460-202	GG	12.99	-0.23	0.35	0.35	0.000	0.076	0.073	0.79	Temp1
91_2_1441	GT	12.30	0.30	-0.04	-0.04	0.000	0.076	0.084	1.35	Temp1
154_1_845	TT	11.90	0.33	-0.46	-0.46	0.001	0.076	0.092	1.39	Temp1
154_1_390	GG	11.66	-0.19	0.06	0.06	0.001	0.076	0.097	0.83	Temp1
52_1_246	TT	22.04	0.28	0.10	0.10	0.000	0.002	0.005	1.32	Temp2
ctrlfagus_c13215-830	GG	16.64	0.31	0.07	0.07	0.000	0.013	0.022	1.36	Temp2
52_1_246	AT	16.44	-0.24	-0.06	-0.06	0.000	0.013	0.024	0.79	Temp2
150_2_924	TT	15.45	0.23	-0.03	-0.03	0.000	0.013	0.034	1.26	Temp2
21_243	TT	15.26	-0.24	-0.02	-0.02	0.000	0.013	0.036	0.79	Temp2
154_2_371	CC	15.07	0.24	0.15	0.15	0.000	0.013	0.039	1.28	Temp2
QB_c15913-902	GG	12.93	-0.21	-0.18	-0.18	0.000	0.032	0.084	0.81	Temp2
133_306	CC	12.82	0.33	-0.44	-0.44	0.000	0.032	0.088	1.39	Temp2
133_306	CT	11.67	-0.32	0.38	0.38	0.001	0.053	0.121	0.72	Temp2
50_232	AA	22.70	0.47	-0.24	-0.24	0.000	0.001	0.005	1.60	Temp3
50_232	AG	16.51	-0.39	0.11	0.11	0.000	0.015	0.039	0.68	Temp3
QB_c10512-206	AA	14.57	-0.48	-0.67	-0.67	0.000	0.028	0.059	0.62	Temp3
SB_c6451-300	AA	12.07	-0.52	-0.57	-0.57	0.001	0.074	0.092	0.59	Temp3
92_352	TT	11.82	0.33	0.15	0.15	0.001	0.074	0.096	1.40	Temp3
QB_c7172-467	TT	14.46	-0.25	-0.02	-0.02	0.000	0.088	0.075	0.78	Precip1
133_306	CC	11.68	-0.21	-0.49	-0.49	0.001	0.111	0.116	0.81	Precip1
66_698	CT	11.43	0.31	0.02	0.02	0.001	0.111	0.123	1.36	Precip1
66_698	TT	11.43	-0.31	-0.02	-0.02	0.001	0.111	0.123	0.73	Precip1
129_685	AA	22.81	-0.53	0.08	0.08	0.000	0.001	0.002	0.59	Precip3
21_243	TT	18.82	-0.50	0.05	0.05	0.000	0.003	0.009	0.61	Precip3
150_2_924	TT	16.35	0.43	-0.09	-0.09	0.000	0.008	0.018	1.54	Precip3
SB_c13339-608	CC	14.13	0.62	-0.01	-0.01	0.000	0.017	0.028	1.85	Precip3
SB_c13429-427	AA	14.00	0.60	0.07	0.07	0.000	0.017	0.028	1.82	Precip3
91_2_1441	TT	12.62	0.69	-0.07	-0.07	0.000	0.030	0.036	1.99	Precip3
91_2_1441	GT	11.80	-0.67	0.06	0.06	0.001	0.040	0.043	0.51	Precip3
134_2_834	AA	11.43	-0.73	0.43	0.43	0.001	0.042	0.046	0.48	Precip3
21_243	CC	11.24	0.53	0.07	0.07	0.001	0.042	0.049	1.70	Precip3

Table S7: Test for isolation by distance (IBD) and isolation by environment (IBE) based on variance partitioning and pRDA

For both sets of 218 putatively neutral SNPs (Neutral) and 52 outliers (Outliers), we first estimated the portions of variance (adjusted R^2) in the genetic structure explained by spatial ("Spat"), climatic ("Clim"), and joint spatio-climatic ("ClimSpat") structure (table A). We retained a variable number of principal coordinates in the PCoA analyses, explaining from 60 to 80% of total variance in genetic structure ("PCoA Explained Variance"). Significance of the variance components (Clim|Spat: of the climatic component when spatial component was accounted for; Spat|Clim: of the spatial component when climatic component was accounted for) was tested through ANOVA-like permutation test for partial redundancy analysis (pRDA), with result reported as F- and P-values.

Secondly, instead of a Climatic effect we considered distinct Temperature ("Temp") and Precipitation ("Prec") effects (Table B) for the set of 52 outliers and for the case where 80% of the total variance in genetic structure was explained. In this analysis,

A- Temperature and Precipitation effects combined

Data	PCoA Explained Variance	Variance	partitioning			pRDA		
		Clim	ClimSpat	Spatial	Resid	Component	F-value	p-value
Neutral	80%	0.01	0.25	0.16	0.58	Clim|Spat	$F_{6,52}=1.1688$	p=0.1641
						Spat|Clim	$F_{5,52}=4.1193$	p<0.0001
Outliers		0.03	0.32	0.14	0.51	Clim|Spat	$F_{6,52}=1.6504$	p=0.0058
						Spat|Clim	$F_{5,52}=4.0076$	p<0.0001
Neutral	70%	0.02	0.28	0.18	0.53	Clim|Spat	$F_{6,52}=1.2933$	p=0.0876
						Spat|Clim	$F_{5,52}=4.8415$	p<0.0001
Outliers		0.04	0.36	0.15	0.46	Clim|Spat	$F_{6,52}=1.7775$	p=0.0074
						Spat|Clim	$F_{5,52}=4.794$	p<0.0001
Neutral	60%	0.01	0.33	0.18	0.47	Clim|Spat	$F_{6,52}=1.2728$	p=0.1377
						Spat|Clim	$F_{5,52}=5.3762$	p<0.0001
Outliers		0.03	0.41	0.17	0.39	Clim|Spat	$F_{6,52}=1.6672$	p=0.0230
						Spat|Clim	$F_{5,52}=5.8495$	p<0.0001

B- **Distinct Temperature and Precipitation effects instead of a combined Climatic effect**

Data	PCoA Explained Variance	Variance partitioning		pRDA		
				Component	F-value	p-value
Outliers	**80%**	Temp	0.01	Temp|Prec,Spat	$F_{3,57}=7.9543$	$p<0.0001$
		Prec	0.01	Prec|Temp,Spat	$F_{3,57}=3.1206$	$p=0.0003$
		Spat	0.14	Spat|Temp,Prec	$F_{5,55}=5.364$	$p<0.0001$
		TempPrec	0.01		NA	
		TempSpat	0.21		NA	
		PrecSpat	0.06		NA	
		TempPrecSpat	0.05		NA	
		Residuals	0.51		NA	

NA: the interaction effects cannot be tested in pRDA.

Figure S5: Respective contributions of climatic and spatial structure to the genetic structure.

These Venn diagram summarize the portions of variance (adjusted R²) in the genetic structure explained by spatial and climatic effect for both sets of 218 putatively neutral SNPs (Neutral) and 52 outliers (Outliers). In left column, the effects of Temperature and Precipitation were considered together ("Climate" effect) while they were separated in right column. The intersections illustrate the contribution of joint effects, but note that this intersection is not equivalent to an interaction in an ANOVA for instance, and relates to the portion explained by effects which cannot be disentangled from each other.
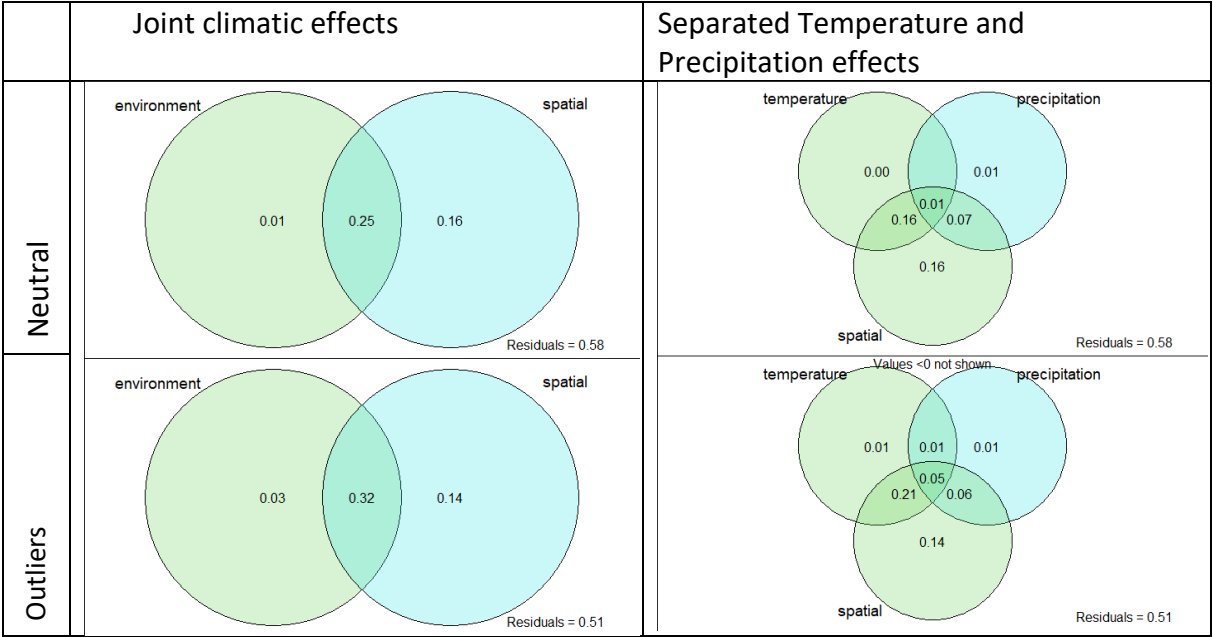
Table S8: Convergence with previous studies investigation genomic signature of selection at SNP loci.

For each previous study based on SNP markers, we give: N_{pop} = the number of studied populations/plots, with their location and sampling design. N_{CG}= the number of candidate genes with their origin (**Resource**) and the number of genotyped SNP (N_{SNP}). For each method (PD= population differentiation approach; EA= environmental association analyses; GPA= Genotype-Phenotype association), we list the number of outlier genes; the final column list the number of outlier genes in common with this study (CO).

Study	N_{pop}	Location	Sampling	N_{CG}	Resource	N_{SNP}	Method 1	Outlier genes	Method 2	Outlier genes	CO
Csilléry et al., 2014	4	South-East France	Altitudinal gradient	53	Lalagüe *et al.*, 2014	546	PD	2-4	Epistatic selection	19	6
Pluess et al., 2016	79	Switzerland	Drought gradient	52	Lalagüe *et al.*, 2014	144	EA	19	Logistic regression	19	3
Müller *et al.*, 2015b	6	Northern Germany	Translocation experiment	9	Müller *et al.*, 2015a	46	GPA	6	PD	6	3
Müller *et al.*, 2017	6	Germany	Latitudinal gradient	9	Müller *et al.*, 2015a	46	GPA	5			2
Cuervo-Alarcon *et al.*, 2018	12	Switzerland	Precipitation gradient	24	Lalagüe *et al.*, 2014; Seifert *et al.*, 2012	70	PD	12	EA	21	8
Krajmerová *et al.*, 2017	19	Slovenian glacial refugia	Provenance test	6	Lalagüe *et al.*, 2014; Seifert *et al.*, 2012	46	PD	3	EA	2	1
Cuervo-Alarcon *et al.*, 2021	12	Rhine and Rhône valleys in Switzerland	Precipitation gradients	24	Lalagüe et al., 2014; Seifert *et al.*, 2012	70	GPA	6			

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Csilléry, K., Lalagüe, H., Vendramin, G. G., González-Martínez, S. C., Fady, B., & Oddou-Muratorio, S. (2014). Detecting short spatial scale local adaptation and epistatic selection in climate-related candidate genes in European beech (Fagus sylvatica) populations. *Molecular Ecology*, *23*(19), 4696–4708. doi:10.1111/mec.12902

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