Table S3.2: Haplotype-based tests of selection comparing high outlier populations identified for climate-PC1 (Scotland, France, Corsica) vs core climate-PC1 populations, with the results focused on candidate SNPs associated with climate-PC1. For each candidate SNP, the SNP identifier (SNP), chromosome (Chr) and base position (BP) are given, with table row shading indicating distinct genomic regions. Average Bayes Factor (BF) values > 10 indicate association to climate, estimated over 3 runs of the BayPass Auxiliary model from the GEA analysis in Chapter 2. Alongside XP-EHH and Rsb output test values are reported for comparisons between identified outlier climate-PC1 populations (Scotland, France, Corsica) and core PC1 populations. SNPs exceeding XP-EHH or Rsb values of 4.0 are regarded as significant and shown in bold. Annotated genes within 100kbp of the potential SNP showing local adaptation signatures to the closest part of the coding region of the gene are listed. Follow up haplotype-based tests were later run to test whether signatures of selection were confined to one or multiple populations, in this case with Scotland tested independently from the geographically discrete France and Corsica populations.

SNP	Chr	BP	Mean BF	Core Allele	Outlier Allele	XP-EHH	Rsb	XP-EHH	Rsb	XP-EHH	Rsb	Nearest Gene (kbp)
High PC1 Populations						All outliers		Scotland		France & Corsica		
AX-100958411	1	7,518,315	**38.3**	T	C	3.82	**4.77**	2.04	3.24	3.18	3.41	ATP6AP2 (0.2), MED14 (14.8)
AX-100661901	1	77,737,574	19.6	G	G	**4.13**	**5.58**	**9.39**	**5.46**	0.73	1.19	LOC107205061 (4.5), LOC107205040 (10.6), VSTM5 (14.9), MED17 (24.7), C11orf54 (36.8)
AX-100430005	2	99,275,394	19.4	C	T	**5.61**	**6.71**	**4.26**	2.09	**4.56**	**6.64**	GNAL (11.5)
AX-100260562	3	26,891,280	**37.7**	-	-	1.79	**4.80**	**7.95**	**6.25**	0.20	0.22	-
AX-100623282	3	26,906,594	21.2	-	-	2.51	**4.32**	**8.34**	**6.24**	-0.58	0.07	-
AX-100879265	3	26,910,322	16.1	T	C	3.81	**9.11**	**9.10**	**6.25**	0.26	1.49	-
AX-100212698	3	27,095,579	16.4	A	G	1.92	**4.61**	**7.90**	**6.86**	-1.96	2.02	LRFN2 (54.6)
AX-100568531	3	95,360,440	16.1	C	C	2.85	**6.29**	0.78	1.90	2.90	**6.18**	EIPR1 (0)
AX-100245354	3	95,362,016	13.6	G	G	2.98	**6.60**	0.94	2.13	2.93	**6.29**	EIPR1 (0)
AX-100566910	4	45,986,689	16.8	T	G	2.71	**4.95**	**5.78**	**5.52**	0.41	1.54	NSUN7 (0), APBB2 (12.8), RBM47 (47.5)
AX-100626511	30	32,286,754	17.9	T	G	0.36	**4.94**	**4.05**	**5.56**	0.60	1.48	LLPH (12.6), HMGA2 (47.2)
AX-100233920	30	64,188,067	14.0	-	**-**	**5.35**	2.15	2.77	1.00	3.40	0.72	-

Table S3.3: Haplotype-based tests of selection comparing low outlier populations identified for climate-PC1 (Finland, Estonia, Russia) vs core climate-PC1 populations, with the results focused on candidate SNPs associated with climate-PC1 (Table details as given for S.Table 1). Subsequent haplotype-based tests were then run to test whether signatures of selection were confined to one geographical region or multiple regions, in this case with the two Finnish populations tested as geographically discrete from the combined Estonia and Russia populations.

SNP	Chr	BP	Mean BF	Core Allele	Outlier Allele	XP-EHH	Rsb	XP-EHH	Rsb	XP-EHH	Rsb	Nearest Gene (kbp)
Low PC1 Populations						All outliers		Finland		Estonia & Russia		
AX-100714706	1	83,214,308	**27.4**	-	-	**4.08**	2.75	3.89	1.65	2.37	2.66	-
AX-100381328	3	28,495,580	18.0	G	G	**6.88**	**9.83**	**6.03**	**8.35**	3.87	**6.11**	PLB1 (0), PPP1CB (36.0)
AX-100125376	3	28,714,949	19.3	G	G	**5.86**	2.20	**5.07**	1.44	3.25	1.32	TTC7A (0)
AX-100479507	3	28,881,614	15.4	C	T	**5.58**	**5.59**	**5.01**	**4.87**	2.64	2.81	TTC7A (0), MCFD2 (11.5)
AX-100310214	3	101,282,641	17.3	-	-	**4.12**	2.21	NA	1.22	2.83	1.71	-
AX-100116579	4	45,894,683	14.9	G	G	3.55	**6.30**	**4.27**	**7.11**	0.84	1.80	APBB2 (0)

Table S3.4: Haplotype-based tests of selection comparing high outlier populations identified for climate-PC2 (Spain, France and Corsica) vs core climate-PC2 populations, with the results focused on candidate SNPs associated with climate-PC2 (Table details as given for S.Table 1). Subsequent haplotype-based tests were then run to test whether signatures of selection were confined to one geographical region or multiple regions, in this case with the Spain population as a distinct outlier on the PC2 axis, was tested independently from the combined France and Corsica populations.

SNP	Chr	BP	Mean BF	Core allele	Outlier allele	XP-EHH	Rsb	XP-EHH	Rsb	XP-EHH	Rsb	Nearest Gene (kbp)
High PC2 Populations						All outliers		Spain		France & Corsica		
AX-100813154	5	20,608,707	**33.99**	-	-	**5.19**	0.58	NA	NA	**4.25**	0.27	-
AX-100488537	30	30,282,383	14.27	-	-	2.25	**4.27**	3.11	**4.46**	1.34	2.70	-
AX-100244814	30	58,759,725	16.67	A	G	2.28	**4.04**	1.50	2.23	2.71	**4.52**	MRPS33 (0), LOC107204196 (14.8), BRAF (18.3)
AX-100806969	36	26,922,633	13.30	A	A	1.34	**5.05**	1.86	3.87	1.90	**5.72**	JAK2 (0), RCL1 (43.7)
AX-100954514	36	26,965,165	18.41	T	A	**4.67**	3.67	**5.45**	2.37	1.52	1.49	JAK2 (0), LOC107215974 (28.9), PLGRKT (38.5)
AX-100109545	36	26,969,805	13.27	A	A	3.68	**4.27**	**4.53**	3.10	1.07	1.74	JAK2 (0), LOC107215974 (24.3), PLGRKT (33.8)
AX-100946076	36	26,970,397	17.86	T	T	**4.19**	3.26	**4.76**	2.36	1.50	1.26	JAK2 (0), LOC107215974 (23.7), PLGRKT (33.2)
AX-100229753	36	26,976,609	12.86	C	C	**4.64**	1.94	NA	NA	2.28	0.59	JAK2 (0), LOC107215974 (17.5), PLGRKT (27.0)

Table S3.5: Haplotype-based tests of selection comparing low outlier populations identified for climate-PC2 (Scotland, Switzerland, Seewisen Germany) vs core climate-PC2 populations, with the results focused on candidate SNPs associated with climate-PC2 (Table details as given for S.Table 1). Subsequent haplotype-based tests were then run to test whether signatures of selection were confined to one geographical region or multiple regions, in this case with the Scotland population geographically distinct from the combined Switzerland and Germany populations.

SNP	Chr	BP	Mean BF	Core allele	Outlier allele	XP-EHH	Rsb	XP-EHH	Rsb	XP-EHH	Rsb	Nearest Gene (kbp)
Low PC2 Populations						All outliers		Scotland		Switzerland & Germany		
AX-100110584	1	57,164,548	13.25	-	-	1.14	**4.02**	1.60	2.55	0.67	2.79	-
AX-100609544	1	105,069,332	10.79	G	G	**4.14**	2.21	2.63	0.43	3.63	2.64	ROBO1 (0)
AX-100459612	3	25,920,756	12.36	A	G	**4.59**	**7.68**	**5.74**	**5.08**	2.33	3.43	SRBD1 (0)
AX-100460780	3	25,925,802	**24.02**	C	T	**4.09**	**7.44**	**5.57**	**5.04**	1.86	3.17	SRBD1 (0)
AX-100333849	3	25,931,865	13.69	G	A	**4.73**	**10.27**	**6.34**	**6.45**	1.60	3.13	SRBD1 (0)
AX-100807975	3	25,962,716	18.73	G	T	**4.72**	**4.11**	**5.80**	2.98	1.51	2.17	SRBD1 (0)
AX-100592584	3	25,997,114	13.37	G	G	1.65	**5.65**	3.53	3.99	1.25	2.73	SRBD1 (0)
AX-100617706	3	26,000,833	10.80	C	A	2.36	**6.34**	3.76	**4.39**	1.67	2.92	SRBD1 (0), PRKCE (49.8)
AX-100053712	3	26,617,245	16.42	G	A	2.12	**4.00**	**6.08**	**4.32**	-0.99	-1.15	CRIPT (16.0), PIGF (23.8), RHOQ (42.8)
AX-100599526	4	41,856,879	**27.91**	T	T	1.81	**6.40**	3.14	3.46	1.51	3.37	EXOC1 (0), CEP135 (23.3)
AX-100690978	5	21,629,221	**20.05**	T	G	1.06	**4.31**	**5.06**	**4.67**	0.30	-1.35	CD82 (73.4), ALX4 (82.8)
AX-100234338	5	21,629,745	13.86	T	A	1.02	**4.05**	**5.05**	**4.82**	0.20	-1.34	CD82 (72.9), ALX4 (83.3)
AX-100498169	11	16,154,834	15.71	-	-	3.88	**4.13**	3.69	2.86	1.57	2.13	-

Table S3.6: Haplotype-based tests of selection comparing high outlier populations identified for climate-PC3 (Germany, Switzerland and Corsica) vs core climate-PC3 populations, with the results focused on candidate SNPs associated with climate-PC3 (Table details as given for S.Table 1). Subsequent haplotype-based tests were then run to test whether signatures of selection were confined to one geographical region or multiple regions, in this case with Corsica as a distinct outlier in PC3 space tested independently from the combined Switzerland and Germany populations.

SNP	**Chr**	**BP**	**Mean BF**	**Core allele**	**Outlier allele**	**XP-EHH**	**Rsb**	**XP-EHH**	**Rsb**	**XP-EHH**	**Rsb**	**Nearest Gene (kbp)**
High PC3 Populations						All Outliers		Corsica		Switzerland & Germany		
AX-100461181	1	22,290,752	**32.68**	-	-	3.70	**4.09**	3.39	2.99	2.38	2.57	-
AX-100562724	2	40,186,867	12.73	C	C	**4.43**	1.23	NA	NA	**4.87**	2.62	RBMS3 (0)
AX-100702409	6	14,874,111	12.94	G	G	**4.24**	3.42	1.74	0.83	3.64	3.11	PANK1 (0), SLC16A12 (24.9), KIF20B (28.3)
AX-100781085	6	14,879,335	12.68	A	A	**4.39**	3.11	1.70	0.91	3.86	2.66	PANK1 (0), KIF20B (23.1), SLC16A12 (30.2)
AX-100186023	12	1,951,293	13.65	A	A	**4.00**	2.57	1.59	0.51	3.31	2.22	ATP2B2 (0)

Table S3.7: Haplotype-based tests of selection comparing low outlier populations identified for climate-PC3 (Sweden and Cambridge and Oxford, UK) vs core climate-PC3 populations, with the results focused on candidate SNPs associated with climate-PC3 (Table details as given for S.Table 1). Subsequent haplotype-based tests were then run to test whether signatures of selection were confined to one geographical region or multiple regions, in this case with Sweden tested distinct from the two UK populations.

SNP	Chr	BP	Mean BF	Core allele	Outlier allele	XP-EHH	Rsb	XP-EHH	Rsb	XP-EHH	Rsb	Nearest Gene (kbp)
Low PC3 Populations						All outliers		Cambridge, UK & Oxford, UK		Sweden		
AX-100191975	1	25,451,983	12.44	C	C	-1.55	**4.05**	-0.016	3.77	-1.54	2.89	MCF2L (0), F7 (17.6), F10 (25.5)
AX-100681217	2	46,317,558	13.11	A	C	**6.00**	**9.04**	**7.54**	**10.36**	0.47	1.39	HERPUD2 (28.0)
AX-100450881	2	46,321,777	13.13	C	C	**4.92**	**4.84**	**5.27**	**6.33**	1.93	1.10	HERPUD2 (23.8)
AX-100379572	2	129,919,204	11.25	T	C	2.28	**4.79**	3.35	**5.56**	-0.0069	0.58	VPS13B (0)
AX-100271597	2	136,082,831	**48.95**	T	C	**4.27**	**10.15**	**4.27**	**10.15**	-0.96	-0.24	TRPS1 (0)
AX-100647140	2	136,083,734	**46.11**	G	A	**5.41**	**7.65**	**8.42**	**8.34**	-0.67	-0.25	TRPS1 (0)
AX-100611187	2	136,084,949	**48.02**	A	G	**5.49**	**5.16**	**8.36**	**6.40**	-0.52	-0.73	TRPS1 (0)
AX-100471209	2	136,089,569	**21.93**	C	T	2.57	**7.59**	**5.60**	**9.38**	-0.57	-1.37	TRPS1 (0)
AX-100831970	2	136,091,965	**23.78**	T	T	2.56	**7.47**	**5.34**	**9.61**	-0.73	-0.89	TRPS1 (0)
AX-100449257	2	136,134,403	**27.67**	T	T	1.88	**9.01**	3.50	**9.50**	-1.36	2.20	TRPS1 (0)
AX-100293521	2	136,162,421	**21.96**	G	A	2.21	**8.45**	**4.38**	**9.45**	-0.57	0.67	TRPS1 (0)
AX-100334051	2	136,162,978	**30.08**	G	A	1.88	**8.76**	**4.09**	**9.84**	-0.66	0.74	TRPS1 (0)
AX-100824331	2	136,185,085	17.97	G	A	**6.35**	**9.63**	**9.31**	**10.60**	0.38	0.82	TRPS1 (0)
AX-100532629	2	136,185,927	**23.50**	T	C	3.56	**13.85**	**6.94**	**15.04**	0.11	1.33	TRPS1 (0)
AX-100386254	3	38,558,688	**21.11**	T	C	**5.29**	**6.17**	**4.76**	**4.97**	1.29	1.90	PDE10A (85.9)
AX-100117479	3	38,559,130	13.00	-	-	**5.32**	**4.63**	**4.76**	3.77	1.39	1.21	PDE10A (85.4)
AX-100994796	15	10,634,483	**27.12**	A	A	**4.31**	1.59	**4.17**	1.00	2.09	1.06	RNF185 (0), LIMK2 (5.2), HNF1A (16.4), PIK3IP1 (37.8)
AX-100465268	4A	12,124,142	14.63	G	T	2.35	**5.92**	3.77	**6.89**	0.20	0.45	ACSL4 (0), NXT2 (24.1), COL4A5 (129.8)
AX-100844877	4A	12,152,707	13.88	C	T	2.97	**5.47**	**4.32**	**6.03**	0.41	1.27	ACSL4 (15.1), COL4A5 (158.4)

Table S3.8: Haplotype-based tests of selection comparing high outlier populations identified for climate-PC4 (Vieland NL, Corsica and Sweden) vs core climate-PC4 populations, with the results focused on candidate SNPs associated with climate-PC4 (Table details as given for S.Table 1). Subsequent haplotype-based tests were then run to test whether signatures of selection were confined to one geographical region or multiple regions, in this case the Netherlands population was identified as a distinct outlier in PC4 space and was tested independently from the combined Corsica and Sweden populations.

SNP	Chr	BP	Mean BF	Core allele	Outlier allele	XP-EHH	Rsb	XP-EHH	Rsb	XP-EHH	Rsb	Nearest Gene (kbp)
High PC4 Populations						All Outliers		Vieland_NL		Corsica & Sweden		
AX-100217751	2	25,955,554	13.02	-	-	**4.05**	2.20	0.077	0.014	-1.79	-0.69	-
AX-100908692	3	42,395,148	16.19	T	T	**4.33**	2.97	-0.078	-0.22	-1.37	0.10	EXOC8 (4.7), EGLN1 (12.2), RHOU (35.4)
AX-100460058	5	8,497,380	**29.65**	-	-	**4.25**	3.54	2.63	-0.15	**4.75**	0.75	-

Table S3.9: Haplotype-based tests of selection comparing low outlier populations identified for climate-PC4 (Spain, Switzerland, Belgium) vs core climate-PC4 populations, with the results focused on candidate SNPs associated with climate-PC4 (Table details as given for S.Table 1). Subsequent haplotype-based tests were then run to test whether signatures of selection were confined to one geographical region or multiple regions, in this case Spain was identified as a distinct outlier in PC4 space and was tested independently from the combined Switzerland and Belgium populations.

SNP	**Chr**	**BP**	**Mean BF**	**Core allele**	**Outlier allele**	**XP-EHH**	**Rsb**	**XP-EHH**	**Rsb**	**XP-EHH**	**Rsb**	**Nearest Gene (kbp)**
Low PC4 Populations						All Outliers		Spain		Switzerland & Belgium		
AX-100510880	1	43,087,208	12.75	**-**	**-**	**4.40**	2.66	-1.24	-0.80	-0.99	-0.26	-
AX-100312107	2	75,788,400	**20.21**	A	A	0.48	**4.53**	0.09	0.42	-0.29	0.97	CDH18 (0)
AX-100915012	2	129,447,141	18.93	C	C	2.23	**4.59**	-0.05	-1.84	0.50	-1.41	STK3 (0)
AX-100817387	3	27,563,410	12.45	-	-	3.66	**4.89**	-3.09	-6.86	**4.87**	**5.63**	-
AX-100460058	5	8,497,380	**29.65**	**-**	**-**	**4.72**	-0.14	**4.99**	2.38	0.46	0.27	-
AX-100523182	15	8,303,211	**33.05**	C	T	2.21	**4.47**	0.96	1.09	-0.62	-0.76	PI4KA (11.6), SERPIND1 (36.9)
AX-100780977	15	8,308,275	**25.54**	G	G	1.45	**5.16**	0.64	-0.03	-0.05	-0.71	PI4KA (6.6), SERPIND1 (31.8)
AX-100258669	36	24,097,058	17.57	A	G	1.43	**4.27**	-0.38	-0.68	0.80	-0.29	-