

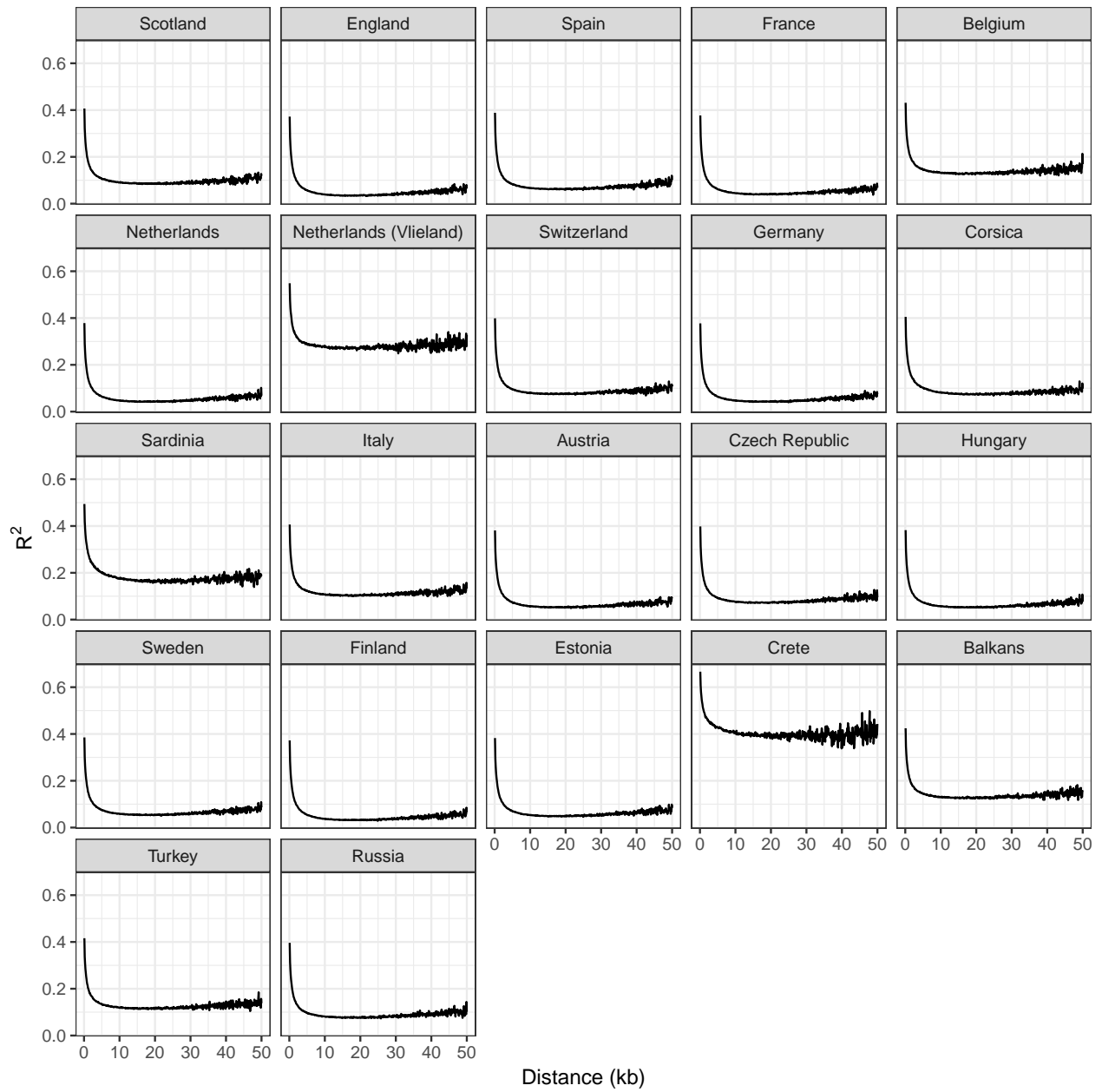
1 **Supplementary material for “The great tit HapMap project: a**
2 **continental-scale analysis of genomic variation in a songbird”**

3 **Table S1** Sampling details for the 29 European great tit populations. “Code” corresponds to labels in Figure
4 1 of the main text.

Code	Population	Region	N	Latitude	Longitude
1	Loch_Lomond_Scotland	Scotland	21	56.108	-4.562
2	Cambridge_UK	England	28	52.198	0.152
3	Wytham_UK	England	48	51.776	-1.303
4	Font_Roja_Spain	Spain	19	38.664	-0.544
5	Mariola_Spain	Spain	21	38.737	-0.658
6	La_Rouviere_France	France	19	43.930	4.235
7	Montpellier_France	France	36	43.098	3.569
8	Antwerp_Belgium	Belgium	15	51.226	4.390
9	Westerheide	Netherlands	50	52.250	5.190
10	Vlieland_NL	Netherlands (Vlieland)	15	53.238	4.932
11	Zurich_Switzerland	Switzerland	22	47.383	8.523
12	Radolfzell_Germany	Germany	18	47.759	8.957
13	Seewisen_Germany	Germany	30	47.978	11.233
14	Pirio_Muro_Corsica	Corsica	27	42.110	9.104
15	Sardinia	Sardinia	9	40.056	9.025
16	Matera_Italy	Italy	5	40.601	16.514
17	Po_Plain_Italy	Italy	8	45.171	9.138
18	Vienna_Austria	Austria	27	48.239	16.347
19	Velky_Kosir_Czech_Republic	Czech Republic	22	49.547	17.062
20	Pilis_Mountains_Hungary	Hungary	28	47.733	18.917
21	Gotland_Sweden	Sweden	32	57.504	18.466
22	Harjavalta_Finland	Finland	44	61.314	22.139
23	Oulu_Finland	Finland	29	65.013	25.468
24	Kilingi-Nõmme_Estonia	Estonia	32	58.150	24.938
25	Crete	Crete	4	35.183	24.960
26	Bulgaria	Balkans	3	42.696	23.328
27	Romania	Balkans	7	46.497	24.582
28	Turkey	Turkey	11	39.464	34.797
29	Zvenigorod_Russia	Russia	17	55.738	36.857

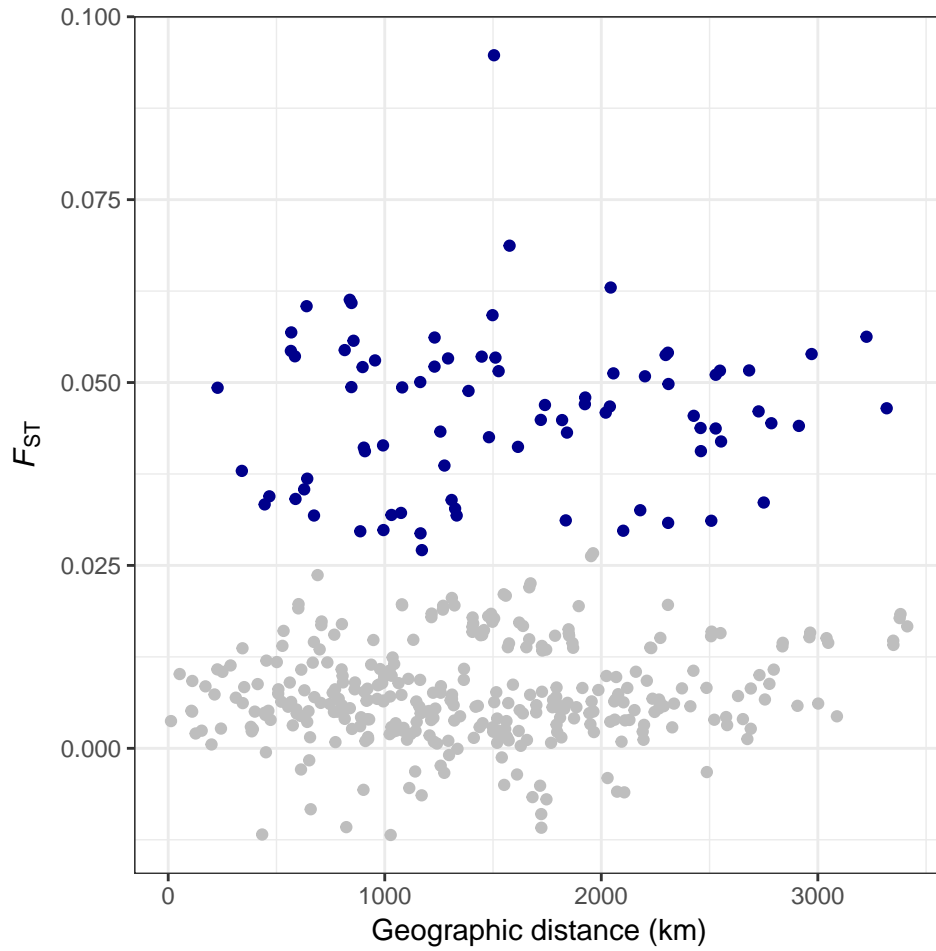
5 **Table S2** Details of outlier F_{ST} regions in European great tit populations. For each region, F_{ST} was calculated for each population versus Turkey.
6 The “number of outliers” represents the number of *populations* in which each region was detected as an outlier. All genes found within 500kb outlier
7 windows are displayed.

Chromosome	Position (MB)	Number of outliers	Outlier comparisons	Genes
2	81.5	12	Austria, Belgium, Czech Republic, Estonia, Finland, France Germany, Hungary, Netherlands, Scotland, Sweden, Switzerland	PADP7, SRDSA1, NSUN2, UBE2QL, MED10
6	18	10	Belgium, Corsica, England, France, Germany, Hungary, Italy Netherlands, Russia, Sweden	RASGEF1A, RET, CSGALNACT2
3	28.5	2	England, Spain	PPP1CB, CALM2, TTC7A, MCFD2
1A	70.5	2	Czech Republic, Russia	CDKN1B
4A	12	2	England, Scotland	COL4A5
6	8	2	Finland, Scotland	SLC18A3, RGR, LRI1, LRI2, CDHR1, GHITM
3	28	1	Spain	MRPL33, RBKS, BRE, FOSL2
1A	48.5	1	Finland	CBX6, CBX7, DNAL4, SUN2, NPTXR, JOSD1, TOMM22, KDELR3, DMC1, GTPBP1, DDX17, CBY1 KCNJ4, THEM184B, CSNK1E, PLA2G6, MAFF, BAIAP2L2, SLC16A8, PICK1, SOX10, MICALL1 EIF3L, ANKRDS4, GCAT, POLR2F
6	7.5	1	Scotland	BMPRI1A, SNGC, MMRN2, GLUD1, FAM35A, GPRIN2, PARG, NCOA4, OGDHL, CHAT
8	7.5	1	Vlieland	-
8	8	1	Belgium	-



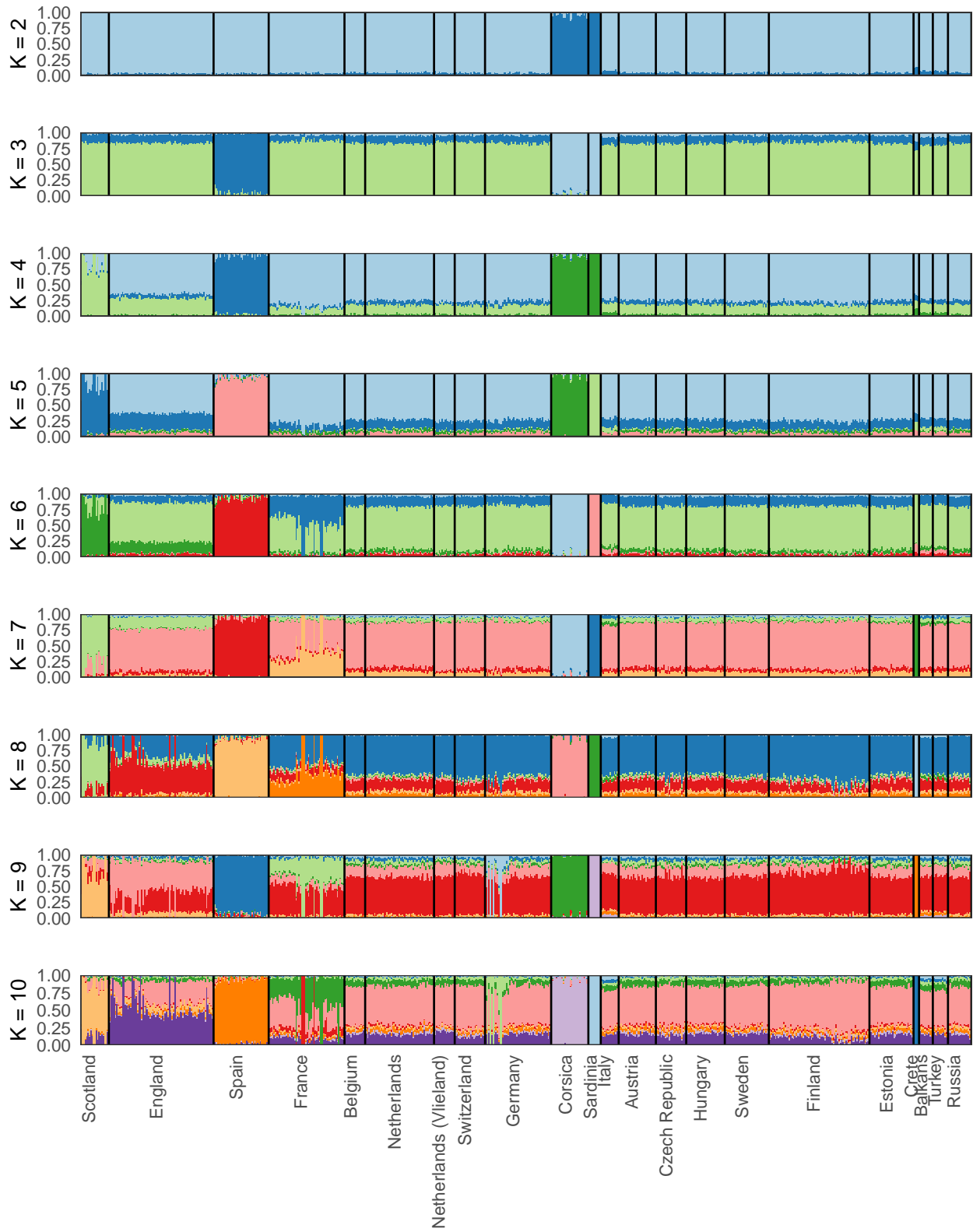
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9 **Figure S1** Linkage disequilibrium in European great tit populations. Lines are means of R^2 values for all
 10 pairs of markers within 100bp distance bins.



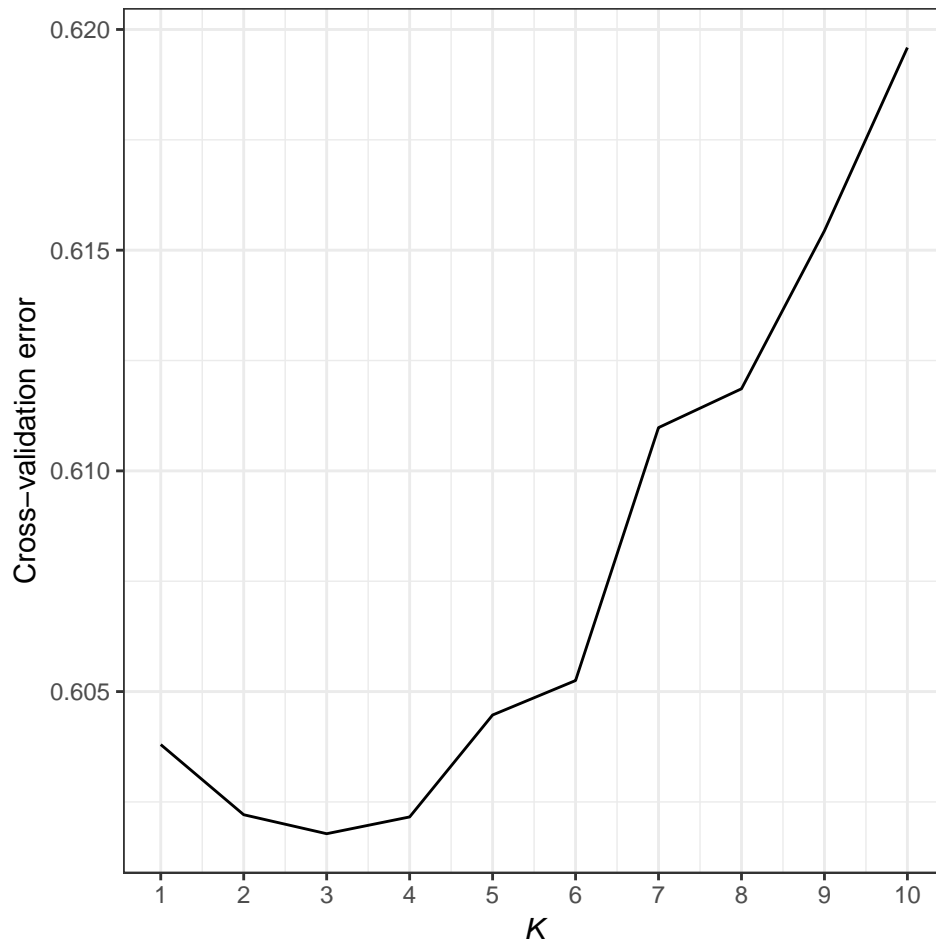
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12 **Figure S2** Pairwise F_{ST} in relation to geographic distance among European great tit populations. Pairwise
13 comparisons involving the island populations of Corsica, Sardinia and Crete are coloured in dark blue.



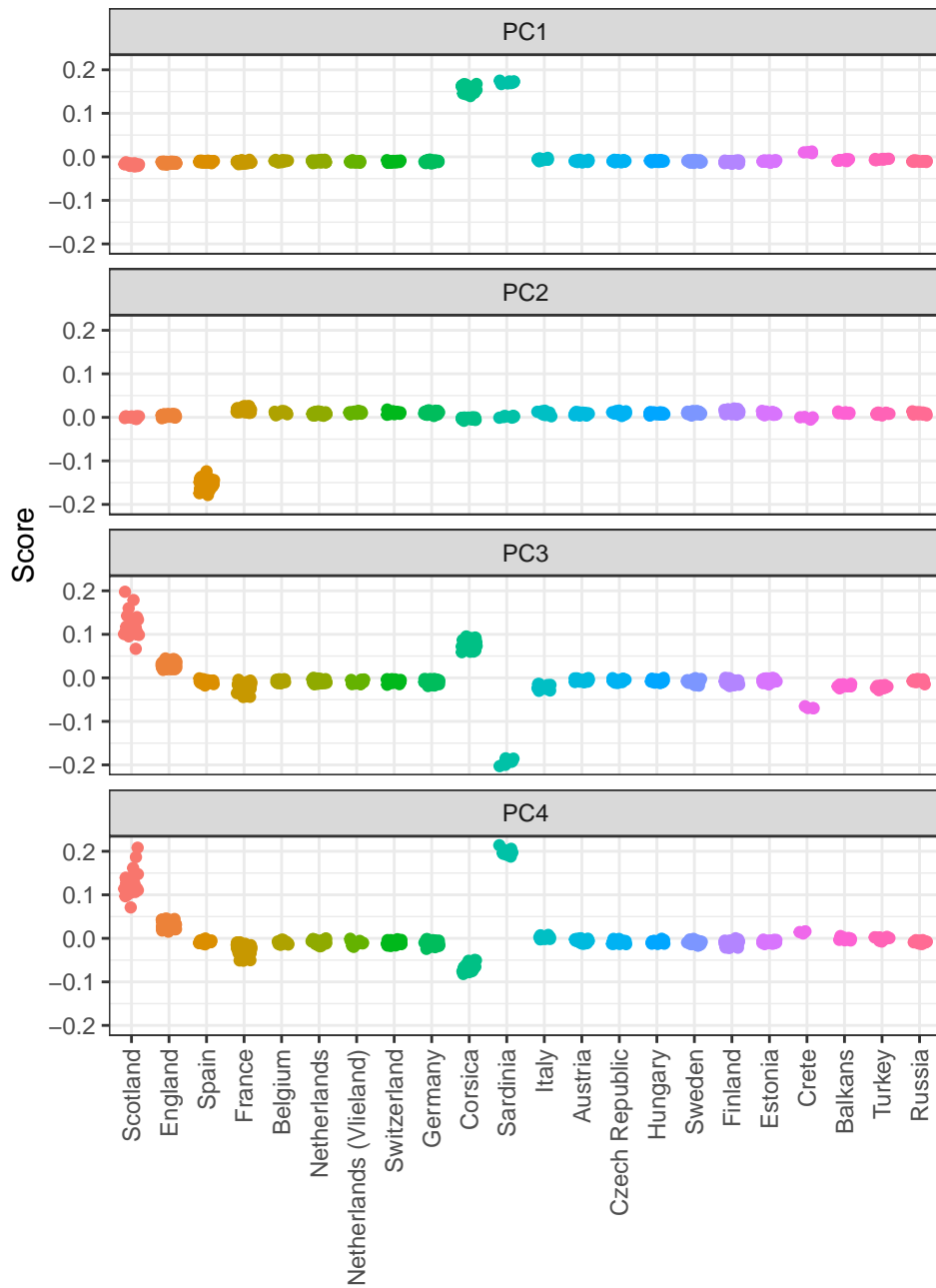
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15 **Figure S3** Admixture analyses at $K = 2$ to 10 in European great tit populations.



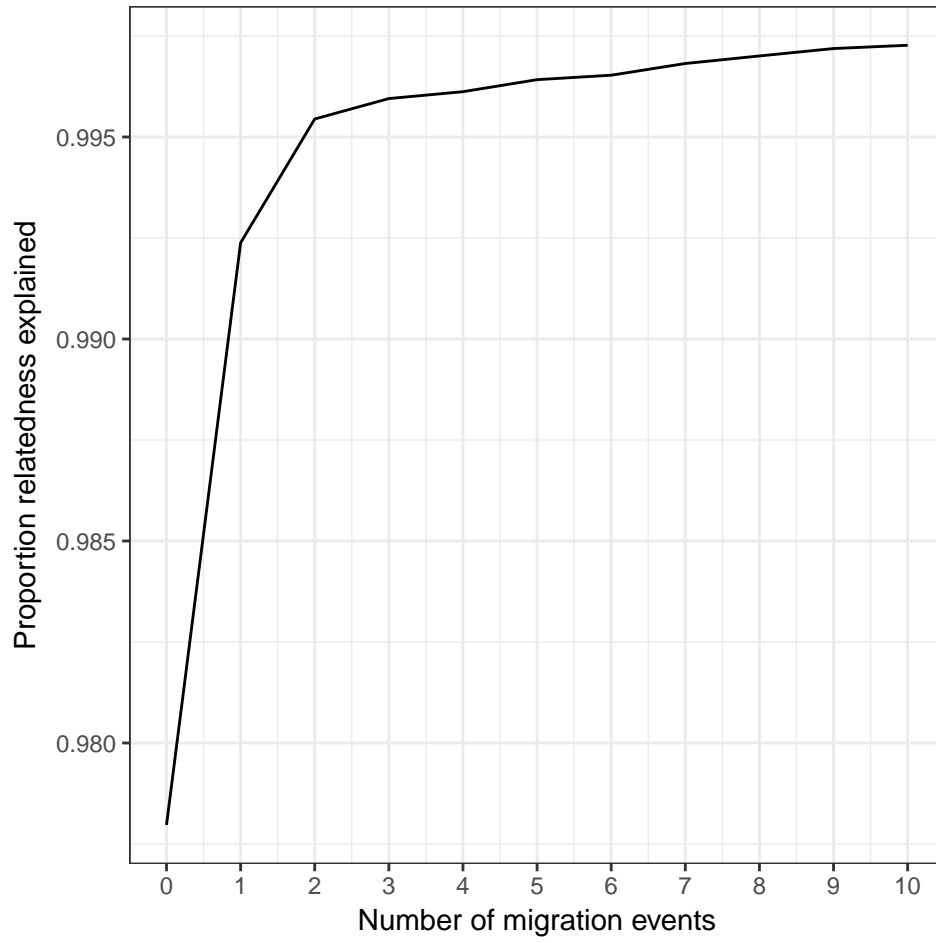
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17 **Figure S4** Cross-validation error from Admixture analyses at $K = 1$ to 10.



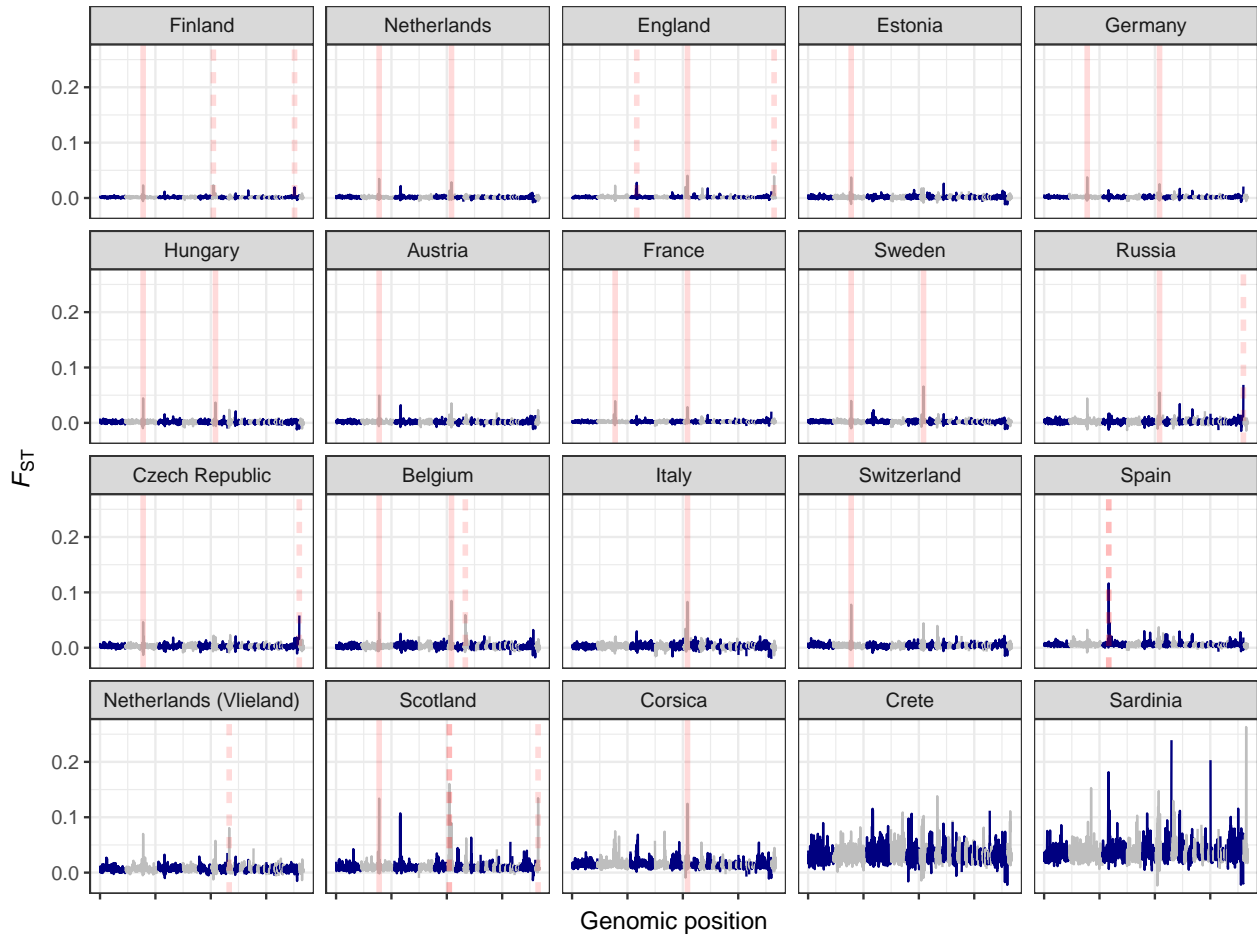
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19 **Figure S5** Results from PCA analysis of European great tit populations.



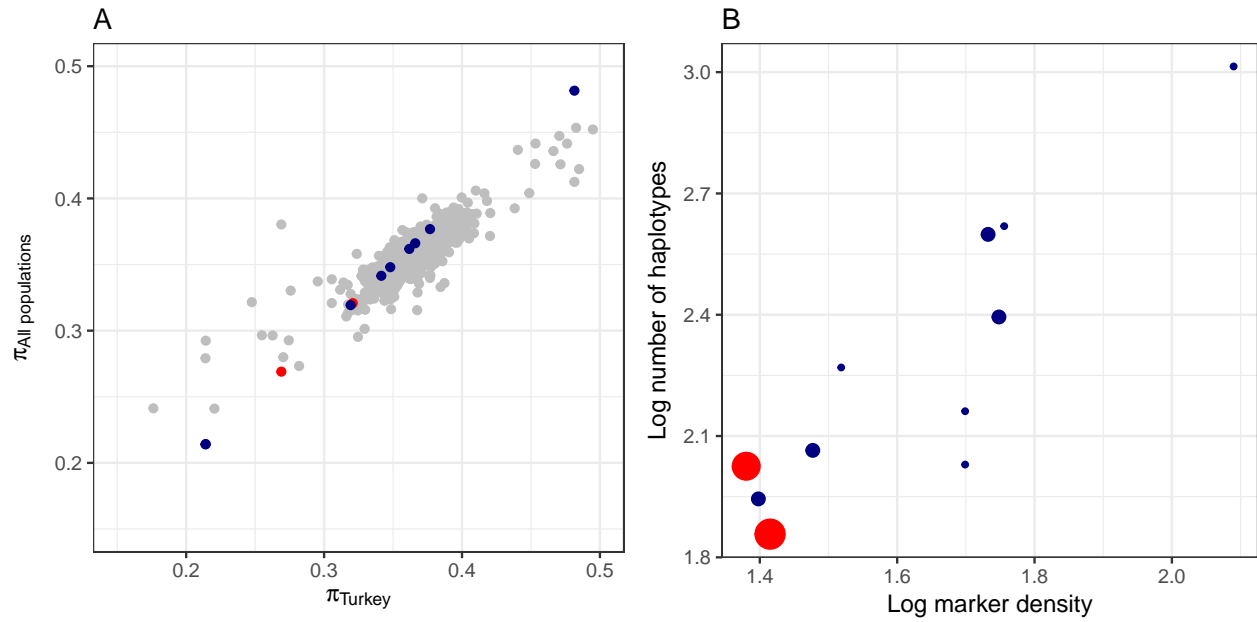
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21 **Figure S6** Proportion of relatedness explained among populations in relation to the number of migration
22 events allowed in TreeMix analyses.



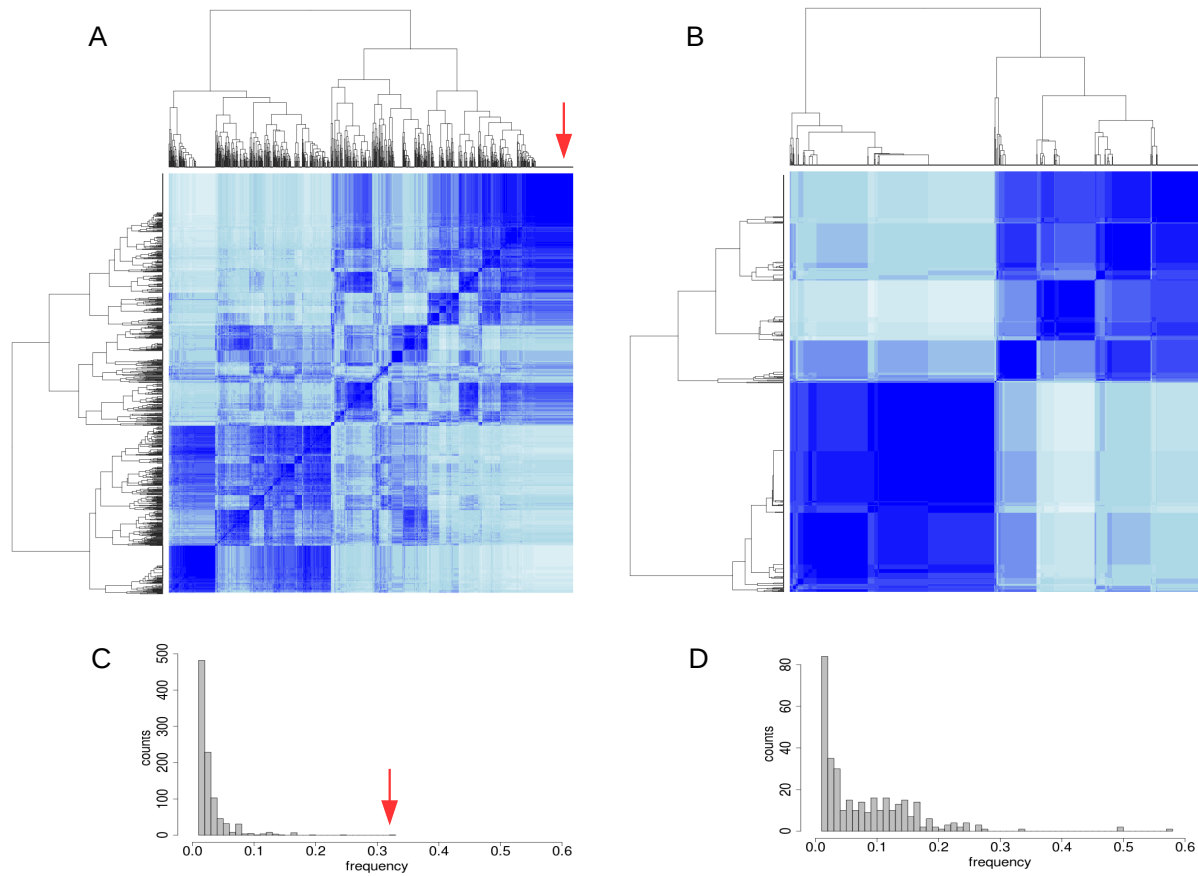
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24 **Figure S7** Landscapes of genomic differentiation in European great tit populations. F_{ST} across the genome
 25 is averaged in 500kb windows, with each panel displaying a pairwise comparison with the proposed refugial
 26 population in Turkey. Red lines represent F_{ST} outliers (windows with mean $zF_{ST} > 10$) shared across more
 27 than two comparisons (solid red lines), or unique to one or two comparisons (dashed red lines).



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29 **Figure S8** Genetic diversity in F_{ST} outlier regions in European great tit populations. Each point is an
 30 outlier window, with point size scaled by the number of populations the outlier was found in - “shared”
 31 haplotypes are coloured red and “unique” haplotypes dark blue (see main text for details). In **A**, Nucleotide
 32 diversity for each window is calculated for the proposed refugial population in Turkey, and plotted against
 33 the mean for all other populations. In **B**, SNP marker density is plotted against haplotype richness for each
 34 region.



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36 **Figure S9** Haplotype structure underlying regions of high differentiation. **A** IBS clustering of all European
 37 haplotypes in the region containing a signal of high differentiation with Turkey specific to the Oulu population.
 38 The red arrow indicates the haplotype at highest frequency in Finland. Colour indicates IBS similarity
 39 (range 0: white - 1: dark blue). **B** IBS clustering of all European haplotypes in the region on chromosome 2
 40 containing a signal of high differentiation with Turkey in multiple populations. **C** Frequency of all identified
 41 haplotypes within each population. The red arrow indicates the high-frequency haplotype within Finland. **D**
 42 Frequency of all identified haplotypes spanning the region on chromosome 2 within each population.