

Supplementary Material Chapter 3

1 PCA populations

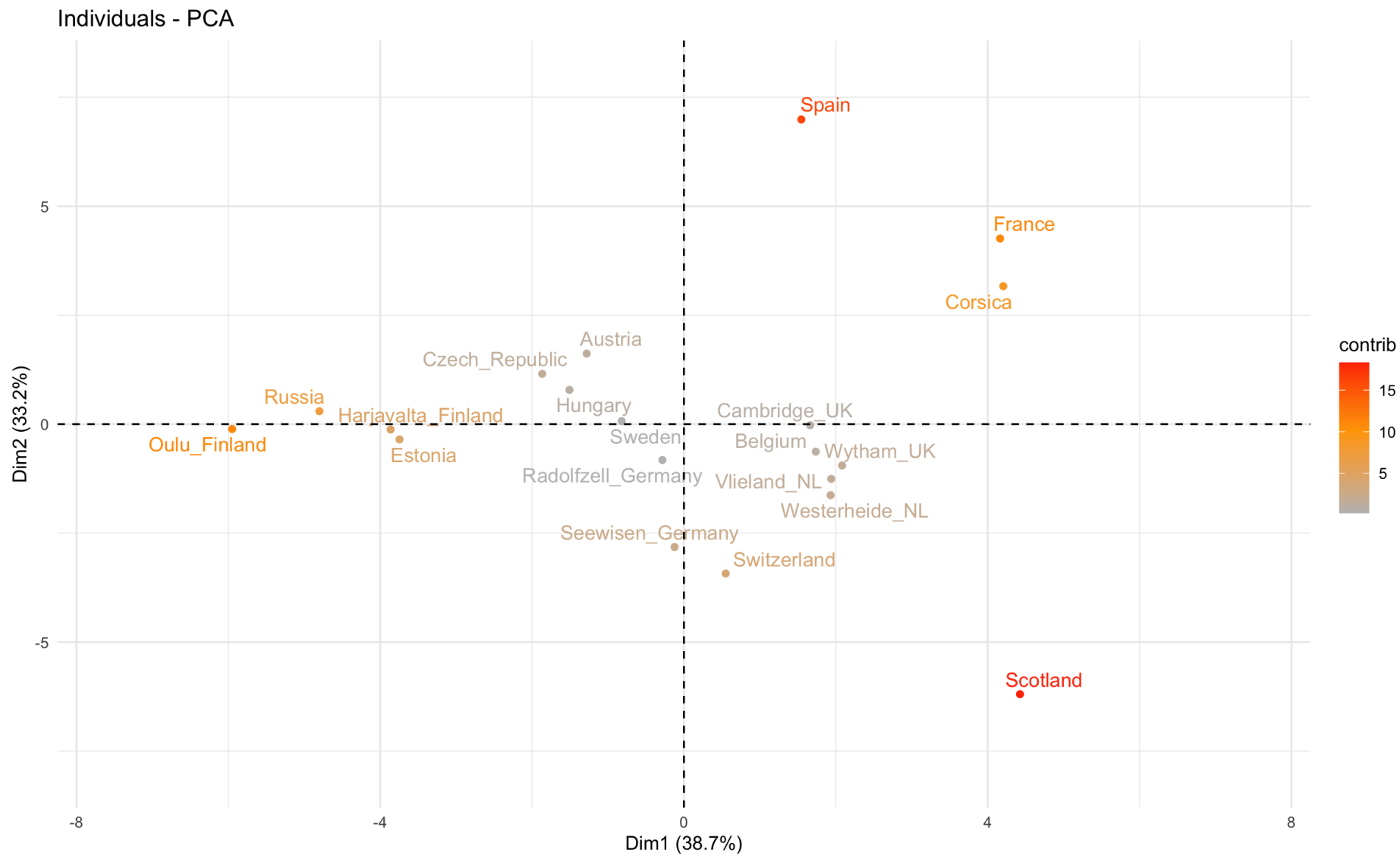


Figure S3.1: Populations factor biplot showing the contribution of each population to climate-PC1 vs. climate-PC2, from PCA of nineteen climate variables for twenty pan-European population locations. Populations with higher contributions are shown dark orange to red.

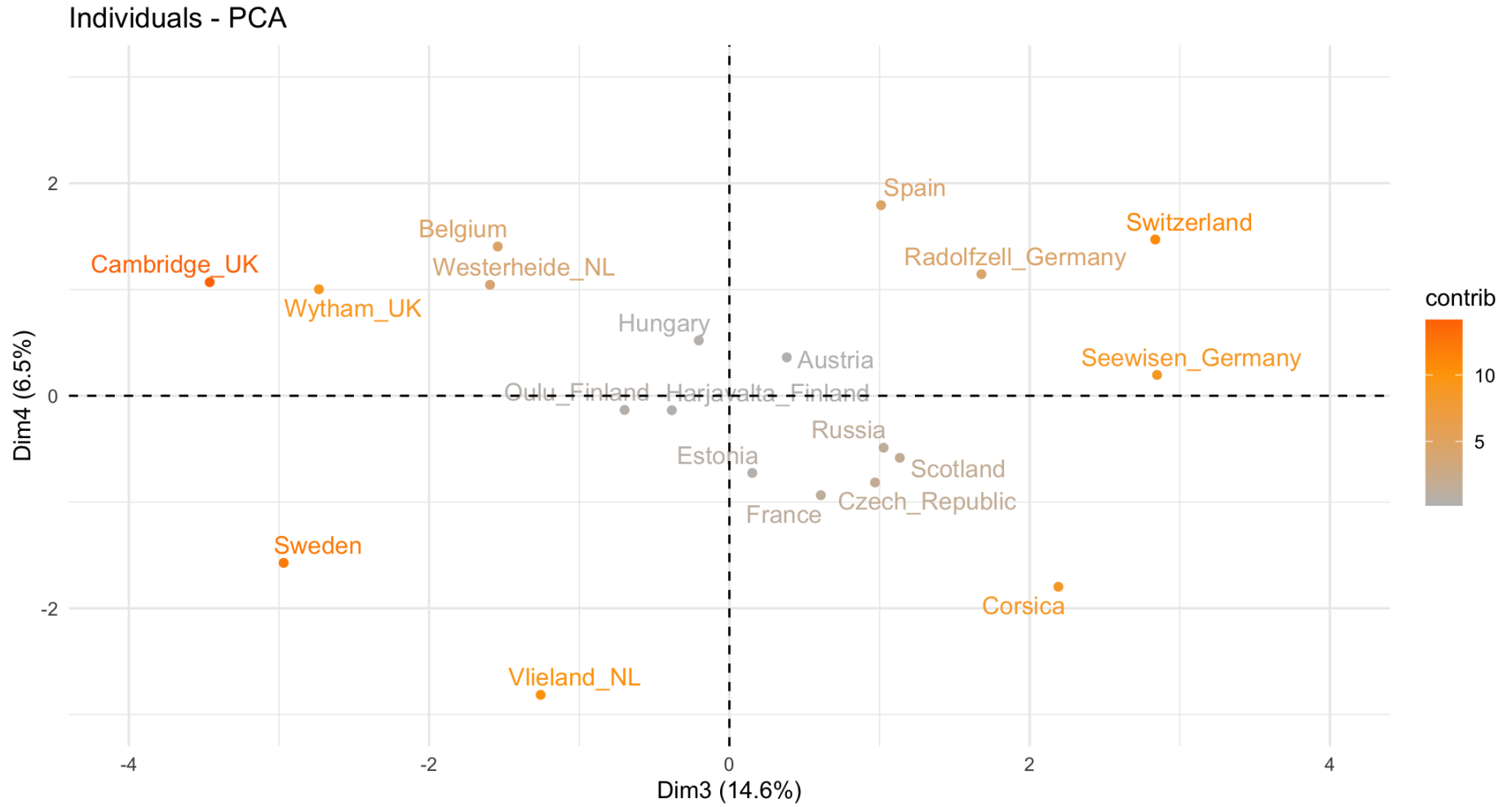


Figure S3.2: Populations factor biplot of climate-PC3 vs. climate-PC4. Plot details as Figure 1.

Table S3.1: The ‘outlier’ populations vs core populations groups are presented, for high (positive outliers) and low (negative outliers), identified from the visualised population contributions to Climate-Principal components one to four (the PCA methodology is described in Chapter 2, and population location co-ordinates are provided there in Table S1).

Population	ClimatePC1	ClimatePC2	ClimatePC3	ClimatePC4
Antwerp Belgium	Core	Core	Core	High
Cambridge United Kingdom	Core	Core	Low	Core
Gotland Sweden	Core	Core	Low	Low
Harjavalta Finland	Low	Core	Core	Core
Loch Lomond Scotland	High	Low	Core	Core
Mariola Spain	Core	High	Core	High
Montpellier France	High	High	Core	Core
Muro Corsica	High	High	High	Low
Oulu Finland	Low	Core	Core	Core
Pilis Mountains Hungary	Core	Core	Core	Core
Radolfzell Germany	Core	Core	Core	Core
Seewisen Germany	Core	Low	High	Core
Tartu Estonia	Low	Core	Core	Core
Velky Kosir Czech Republic	Core	Core	Core	Core
Vienna Austria	Core	Core	Core	Core
Vlieland Netherlands	Core	Core	Core	Low
Westerheide Netherlands	Core	Core	Core	Core
Wytham United Kingdom	Core	Core	Low	Core
Zurich Switzerland	Core	Low	High	High
Zvenigorod Russia	Low	Core	Core	Core

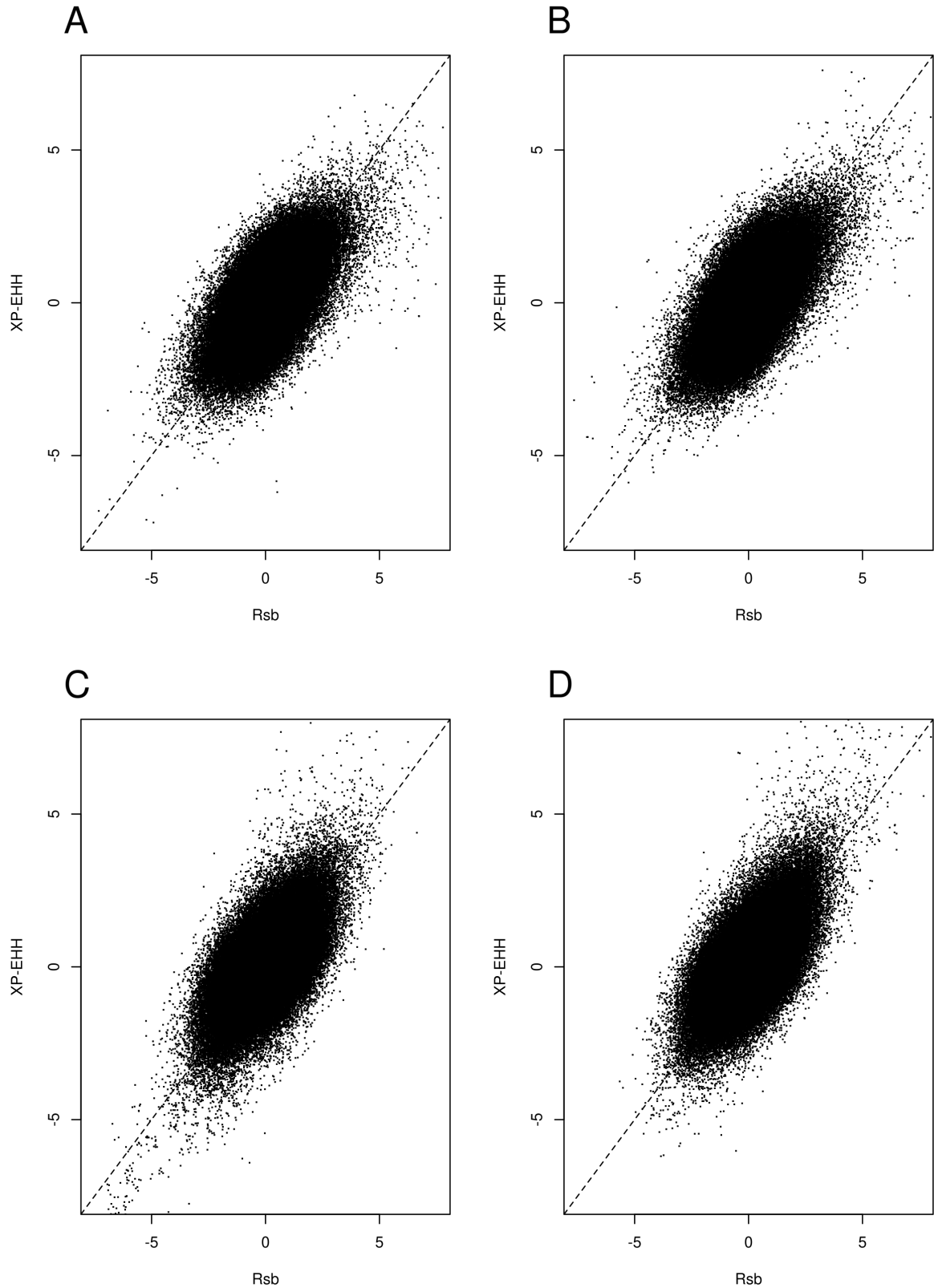


Figure S3.3: Comparison of XP-EHH and Rsb values for indicated vs core populations. Panel A display PC1 high, panel B displays PC1 low, panel C displays PC2 high, panel D displays PC2 low.

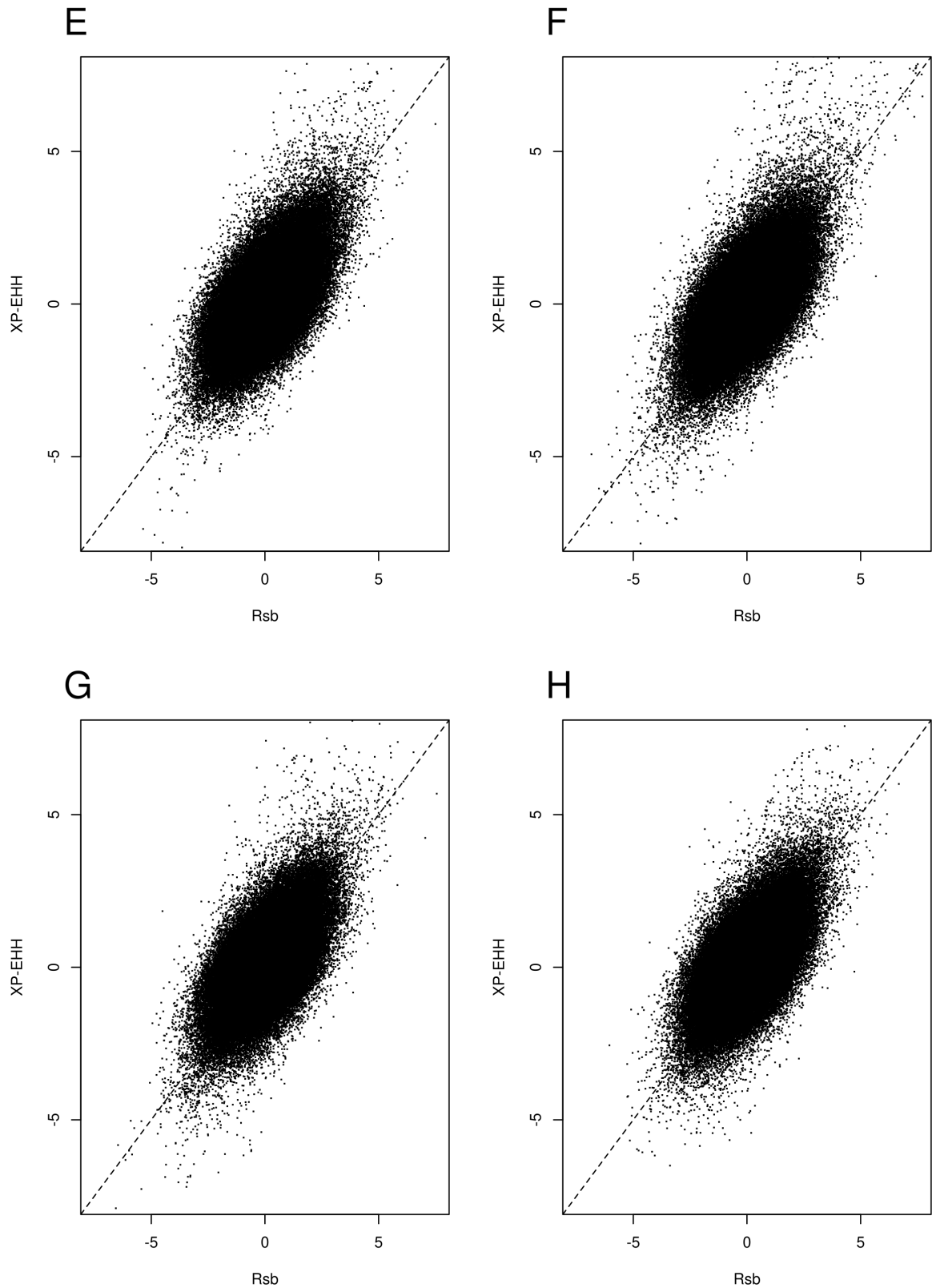


Figure S3.4: Comparison of XP-EHH and Rsb values for indicated vs core populations. Panel E display PC3 high, panel F displays PC3 low, panel G displays PC4 high, panel H displays PC4 low.

2 Extended Haplotype Homozygosity around a site-specific SNP (EHHS) plots with R/Bioconductor package Gviz (Hahne and Ivanek 2016)

2.1 Populations identified with signatures of selective sweeps and associated with PC1

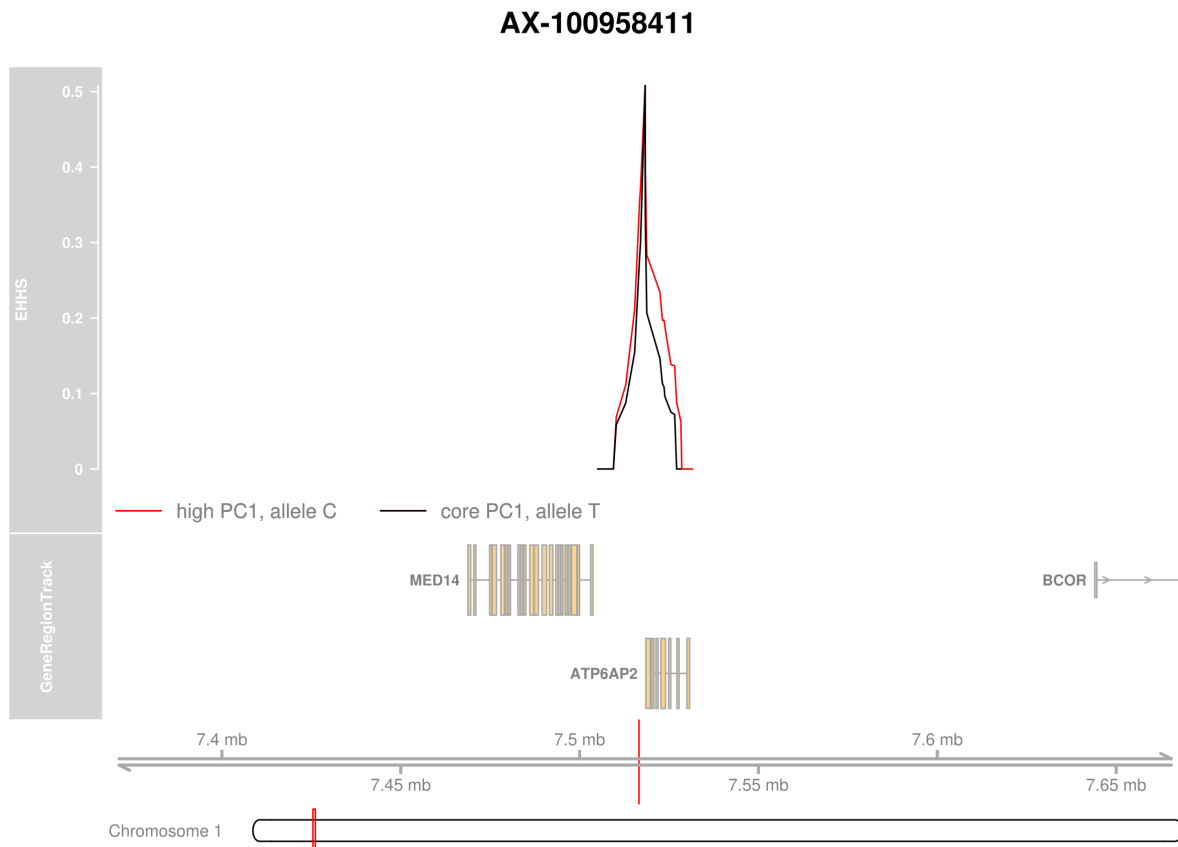


Figure S3.5: A selective sweep identified around focal SNP AX100958411 in the Scotland, France and Corsica populations.

AX-100430005

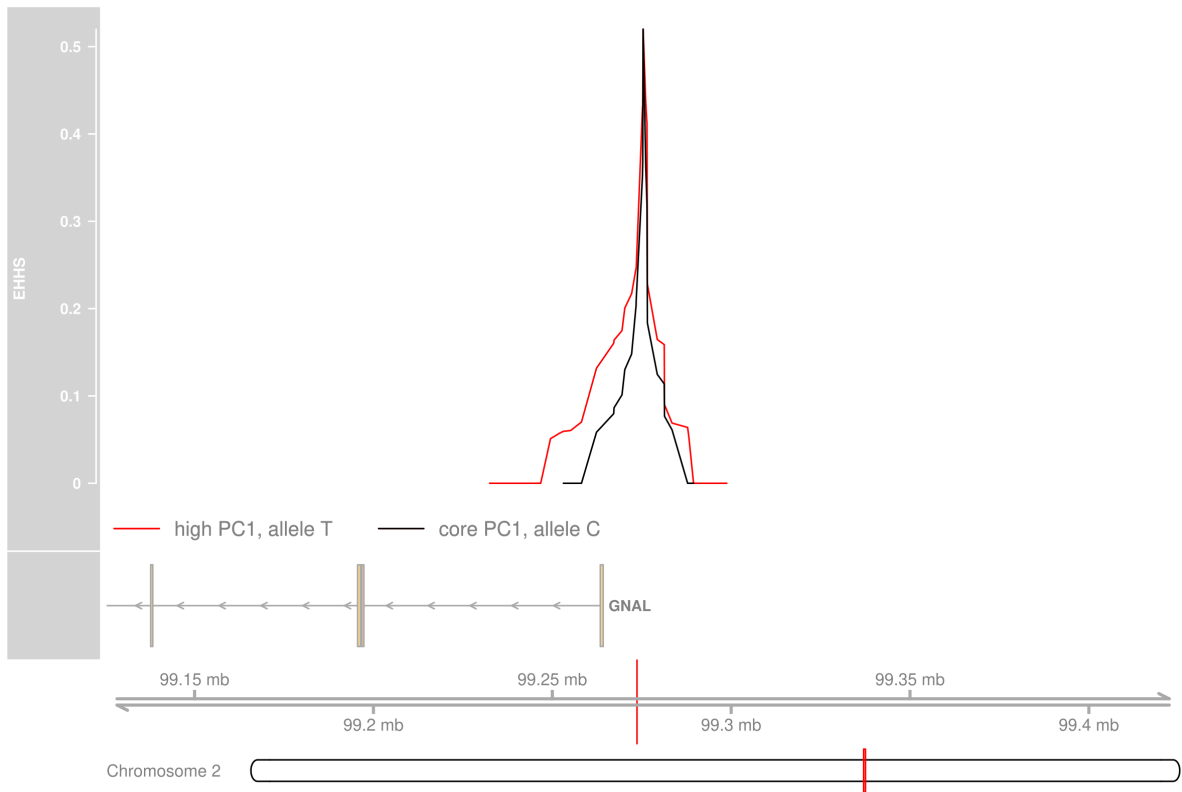


Figure S3.6: A selective sweep identified around focal SNP AX100430005 in the Scotland, France and Corsica populations.

AX-100212698

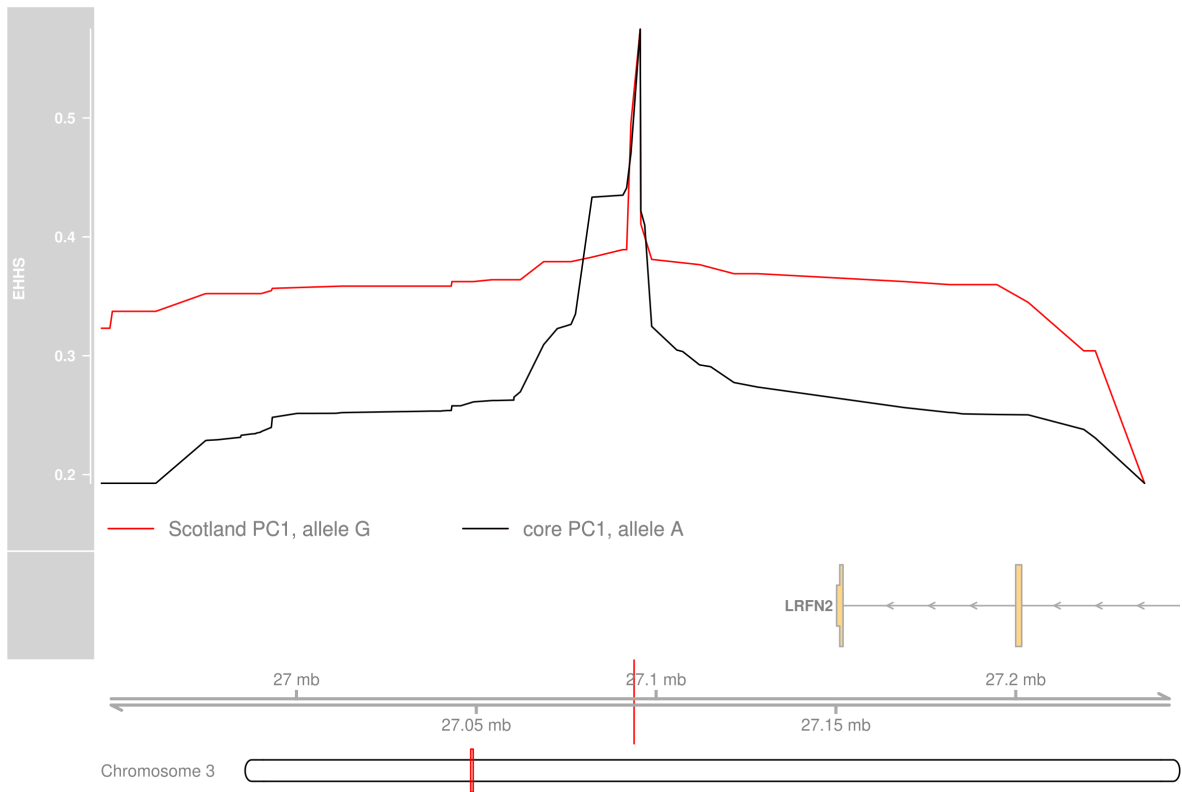


Figure S3.7: A selective sweep identified around focal SNP AX100212698 in the Scotland population.

AX-100566910

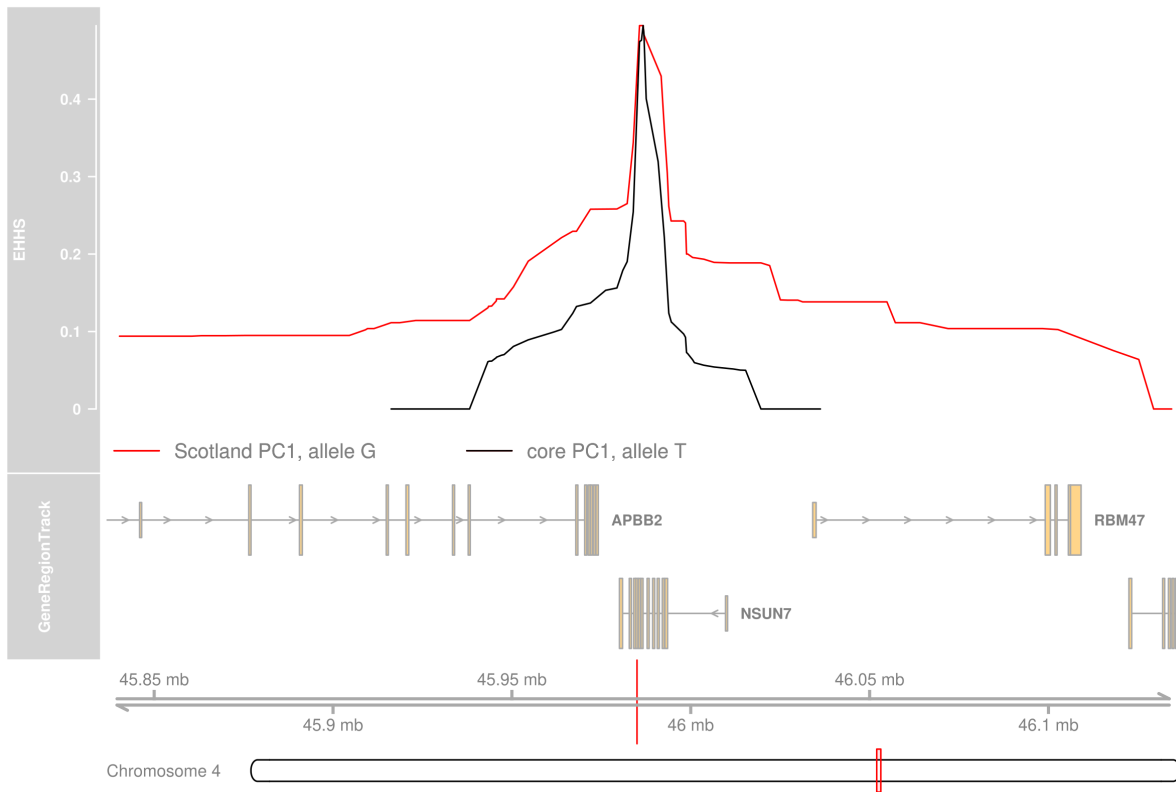


Figure S3.8: A selective sweep identified around focal SNP AX100566910 in the Scotland population.

AX-100626511

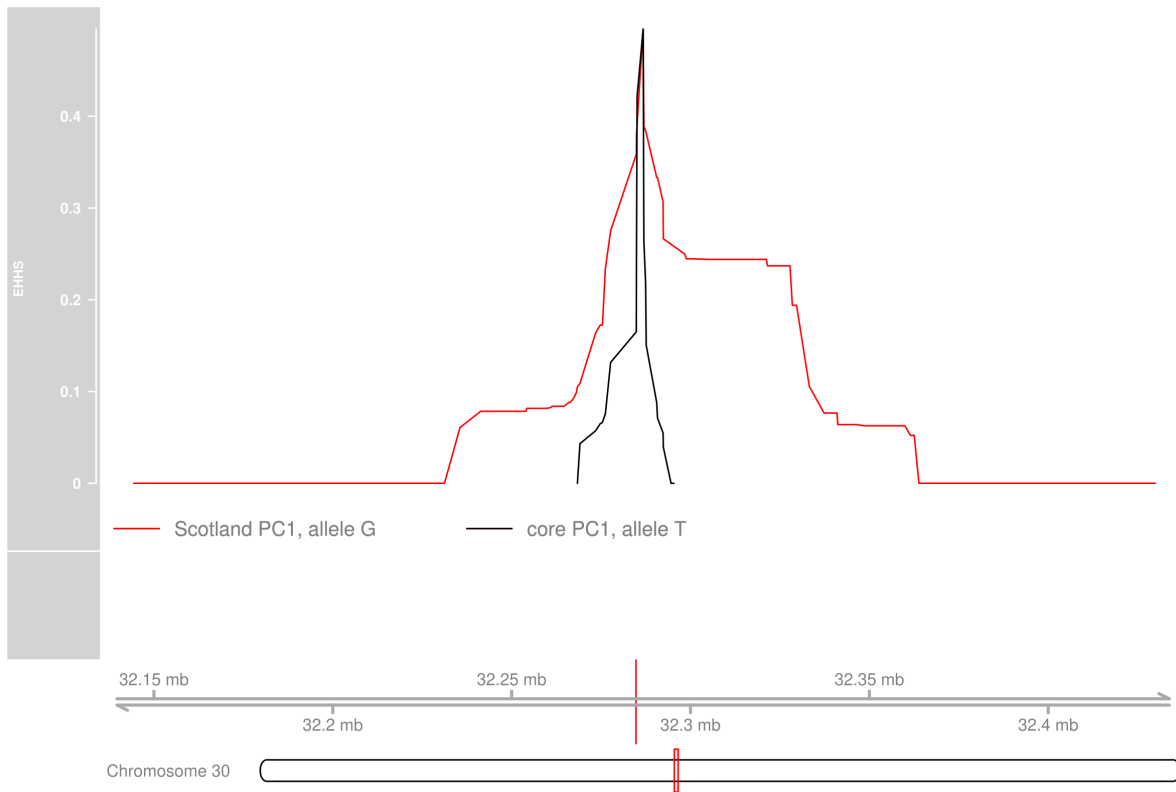


Figure S3.9: A selective sweep identified around focal SNP AX100626511 in the Scotland population.

AX-100479507

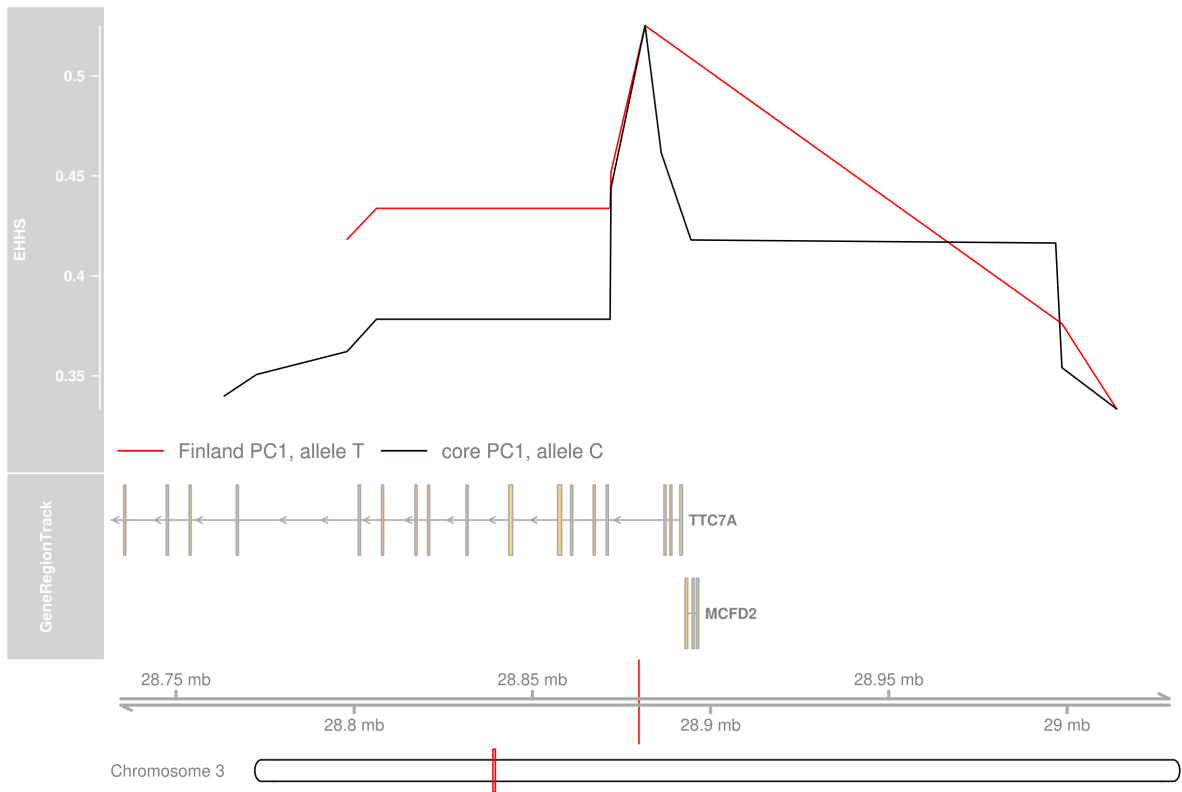


Figure S3.10: A selective sweep identified around focal SNP AX100479507 in the Finland population.

2.2 Populations identified with signatures of selective sweeps and associated with PC2

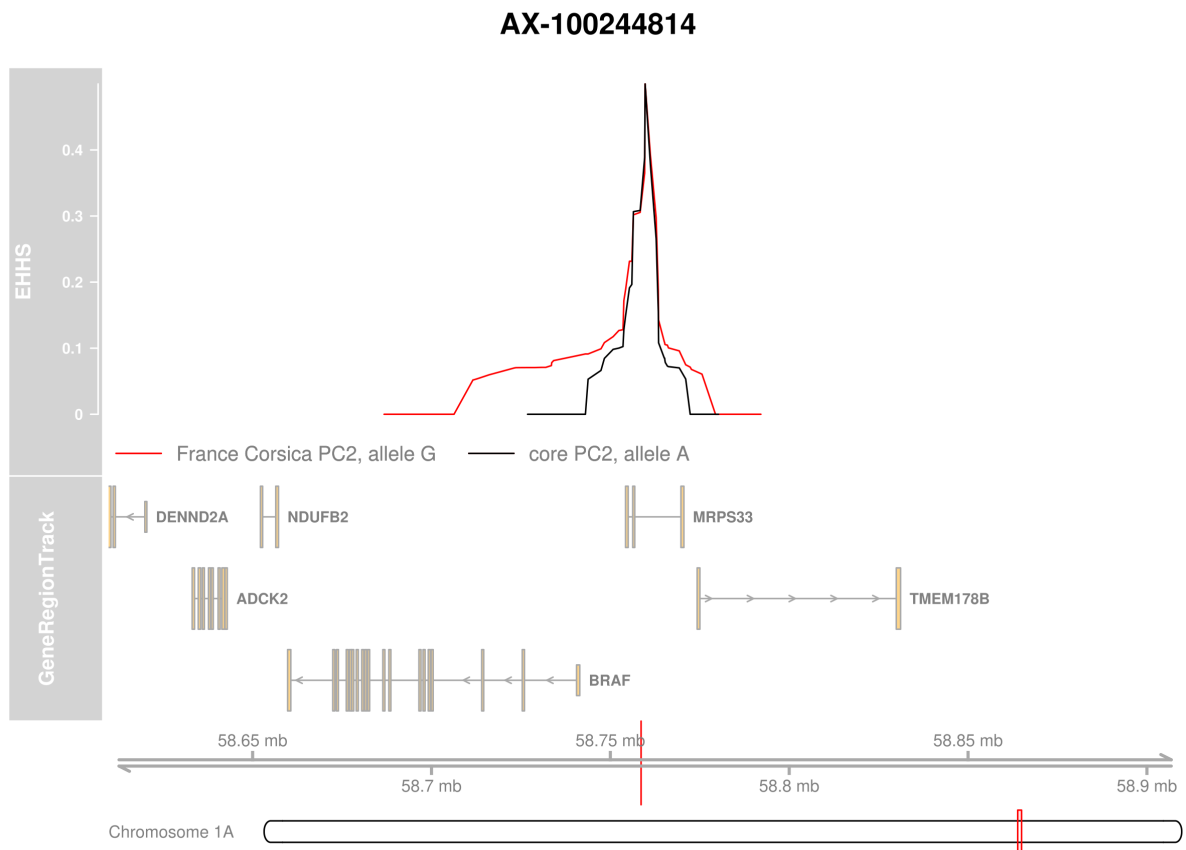


Figure S3.11: A selective sweep identified around focal SNP AX100244814 in the France and Corsica populations.

AX-100954514

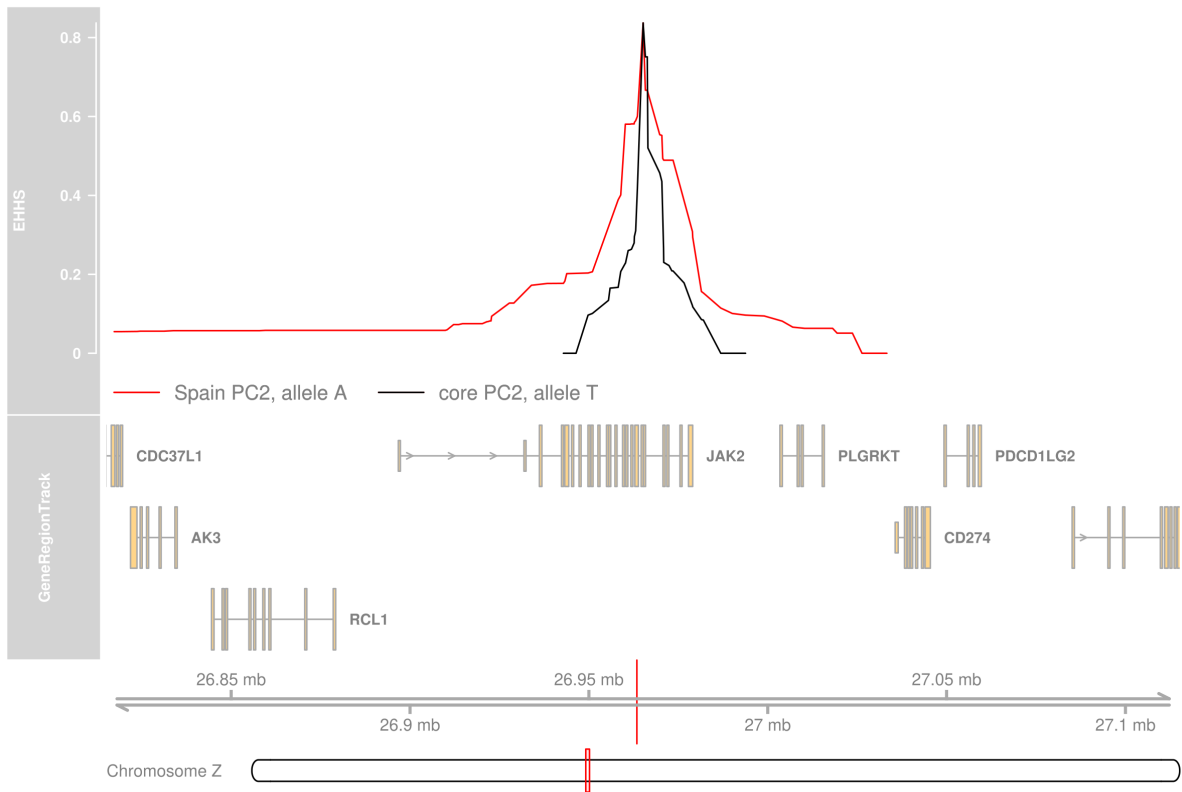


Figure S3.12: A selective sweep identified around focal SNP AX100954514 in the Spain population.

AX-100333849

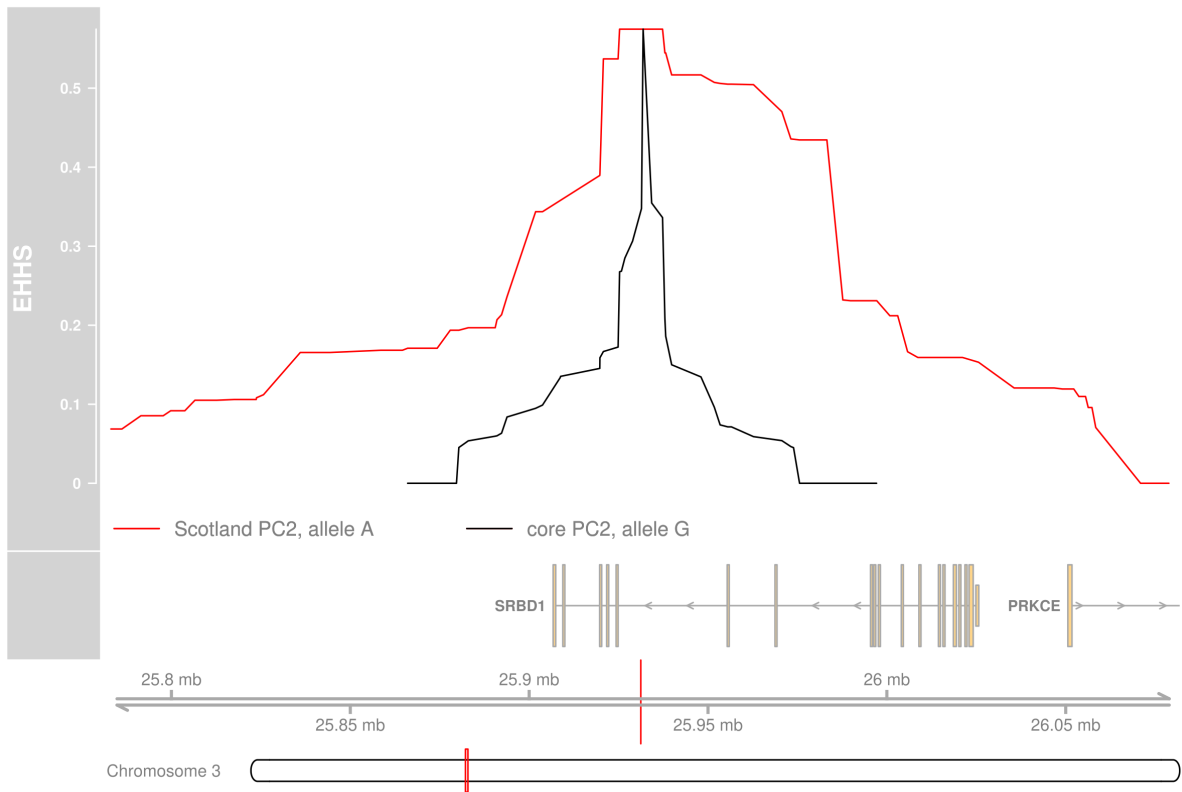


Figure S3.13: A selective sweep identified around focal SNP AX100333849 in the Scotland population.

AX-100053712

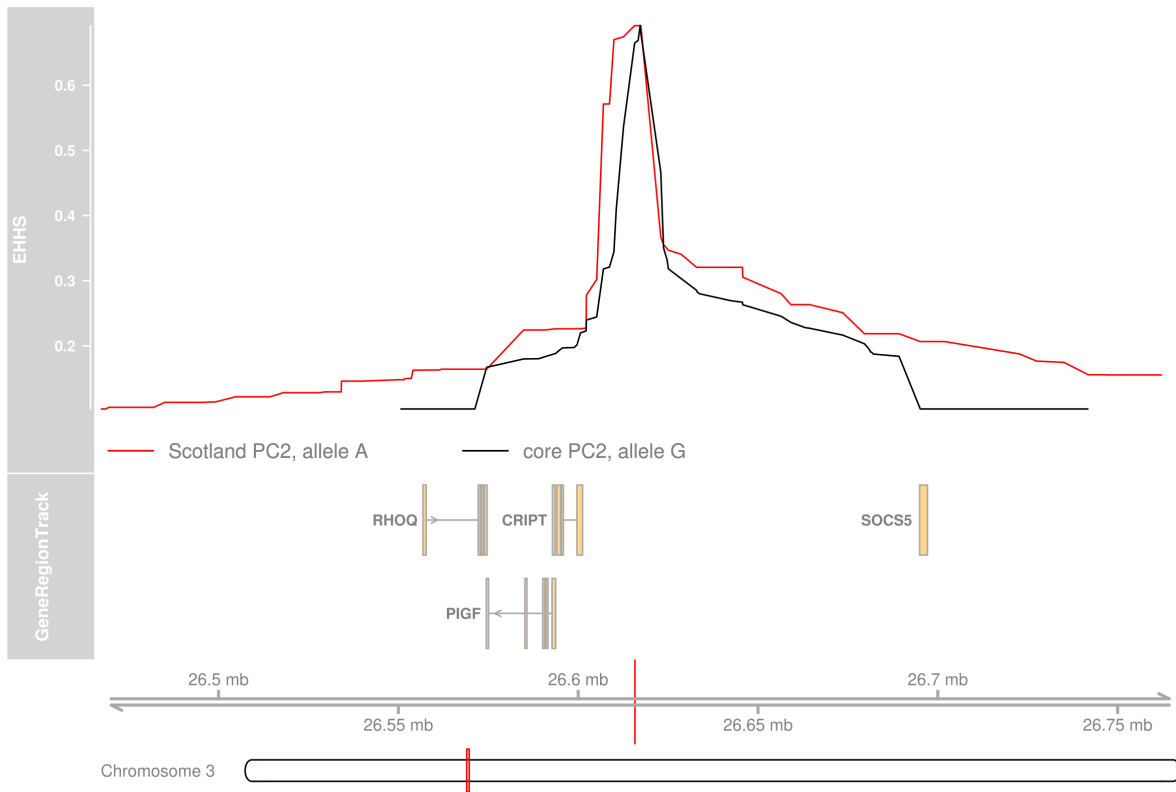


Figure S3.14: A selective sweep identified around focal SNP AX100053712 in the Scotland population.

AX-100690978

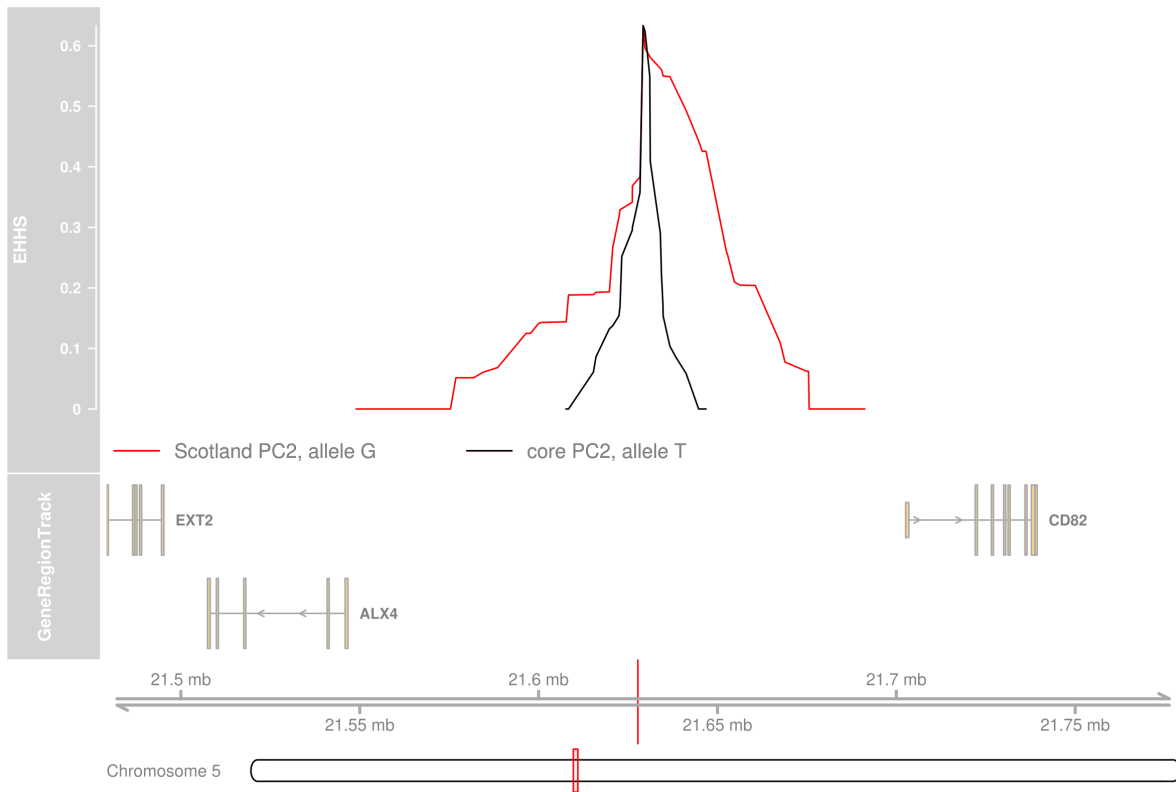


Figure S3.15: A selective sweep identified around focal SNP AX100690978 in the Scotland population.

2.3 Populations identified with signatures of selective sweeps and associated with PC3

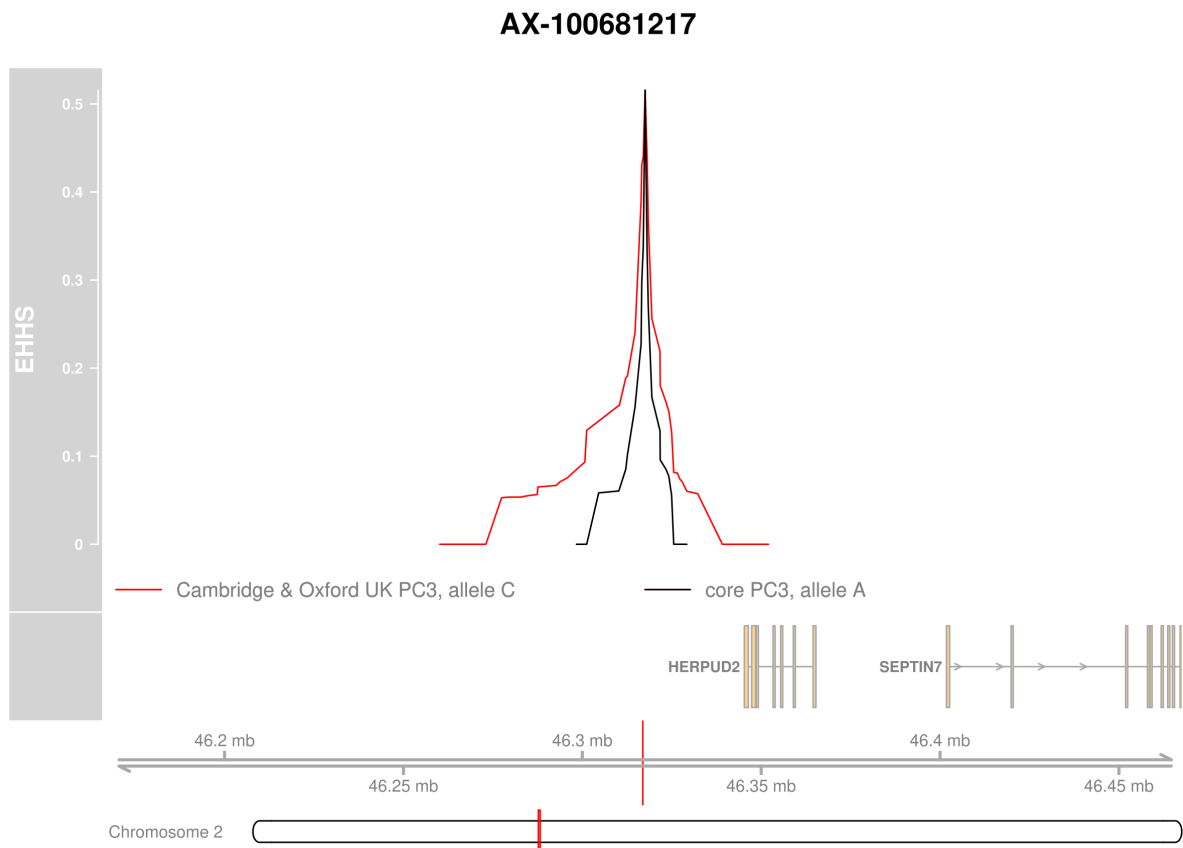


Figure S3.16: A selective sweep identified around focal SNP AX100568531 in the Cambridge and Oxford populations.

AX-100379572

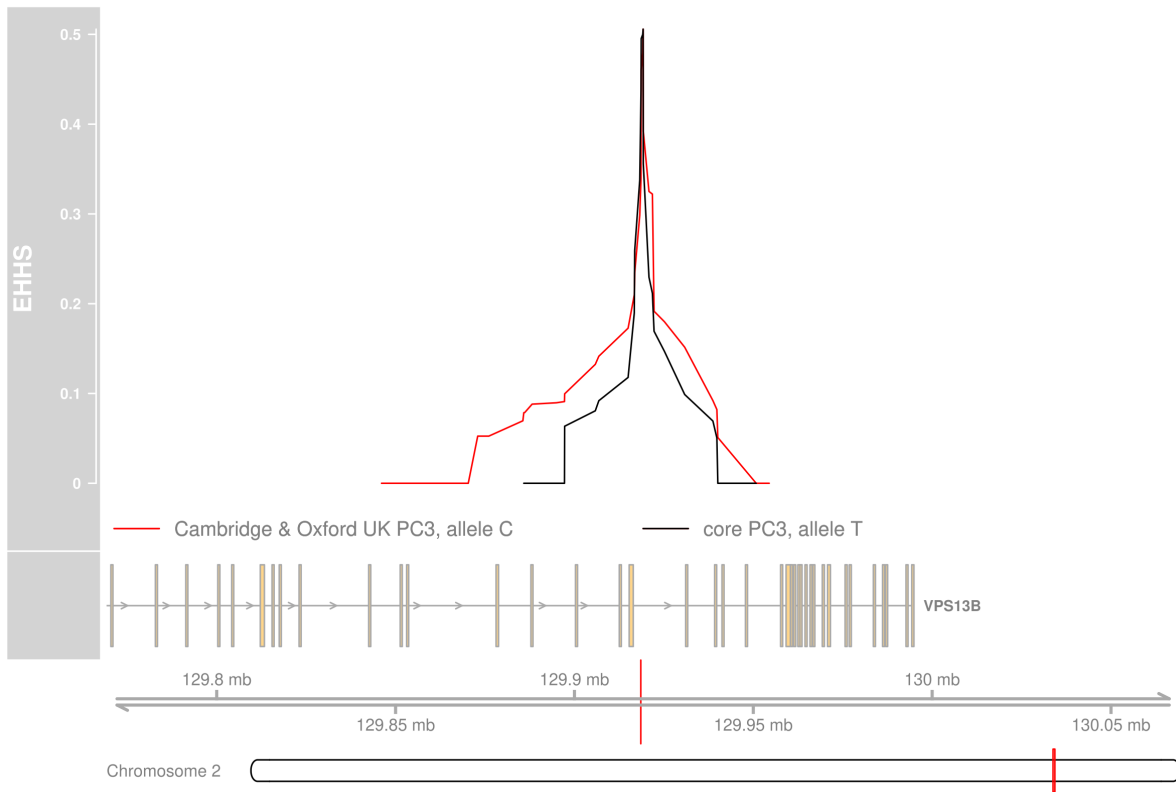


Figure S3.17: A selective sweep identified around focal SNP AX100379572 in the Cambridge and Oxford populations.

AX-100271597

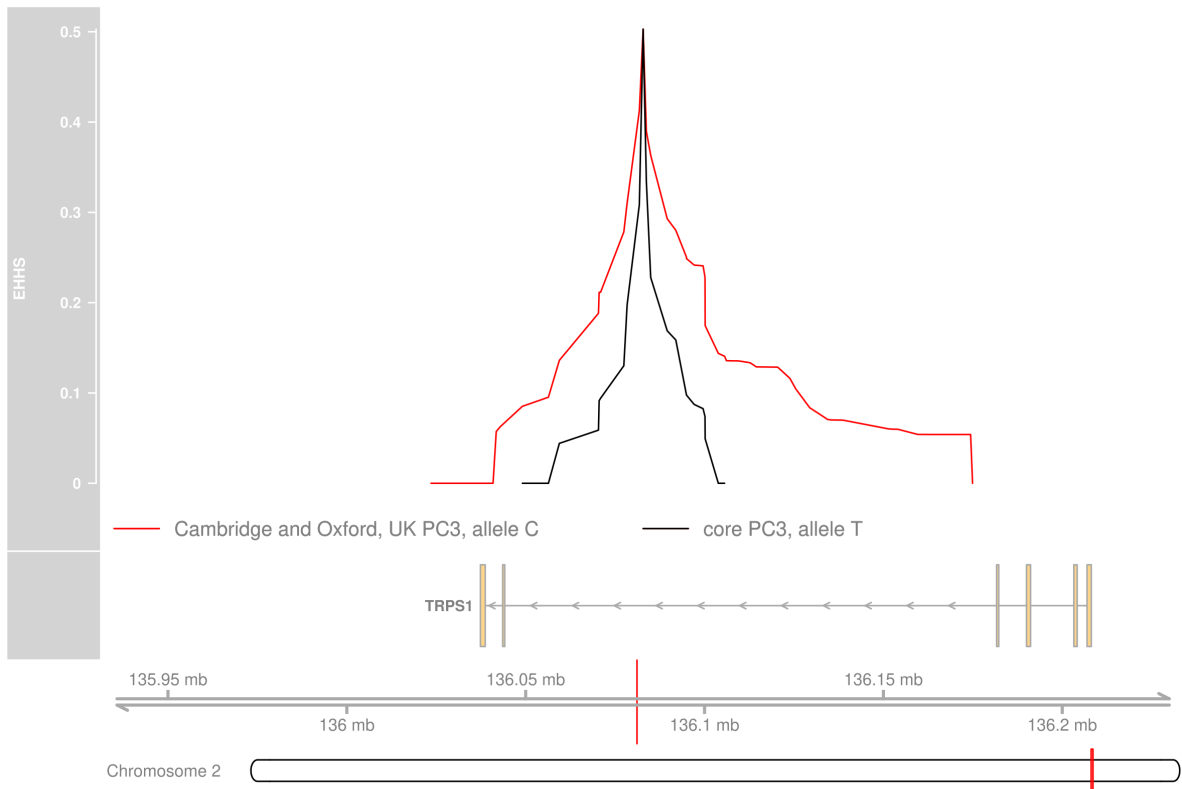


Figure S3.18: A selective sweep identified around focal SNP AX100271597 in the Cambridge and Oxford population.

AX-100386254

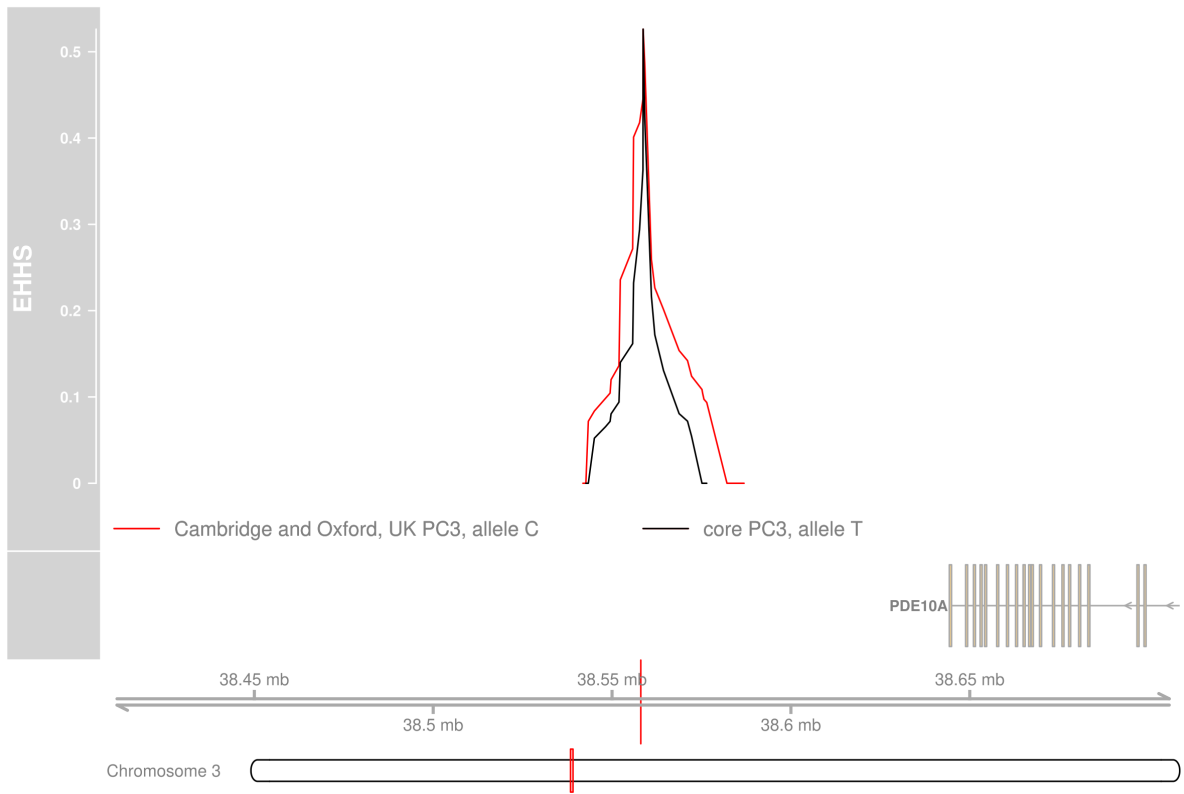


Figure S3.19: A selective sweep identified around focal SNP AXAX-100386254 in the Cambridge and Oxford population.

AX-100844877

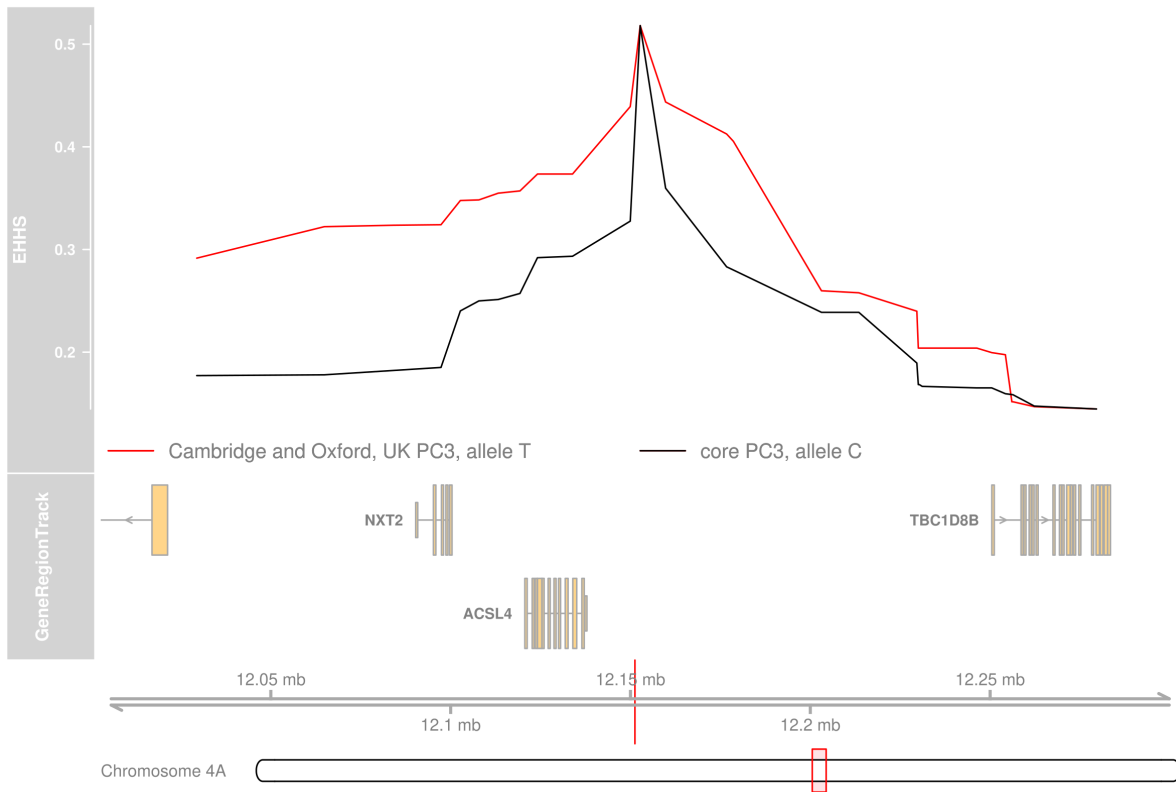


Figure S3.20: A selective sweep identified around focal SNP AX100844877 in the Cambridge and Oxford population.

2.4 Populations identified with signatures of selective sweeps and associated with PC4

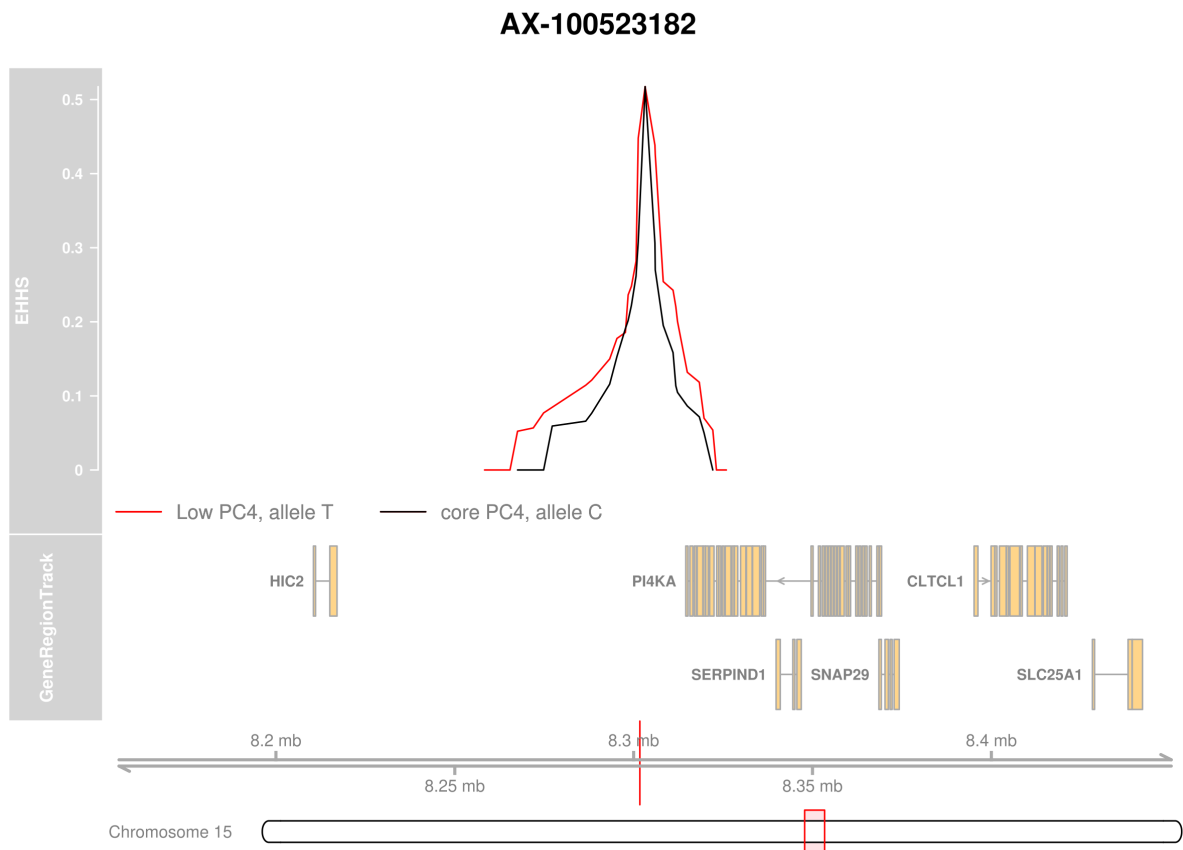


Figure S3.21: A selective sweep identified around focal SNP AX100523182 in the Spain, Switzerland and Belgium populations.

3 References

Hahne, F. and Ivanek, R. (2016). Statistical Genomics: Methods and Protocols. In Mathé E, Davis S (eds.), chapter Visualizing Genomic Data Using Gviz and Bioconductor, 335–351. Springer New York, New York, NY. ISBN 978-1-4939-3578-9, doi: 10.1007/978-1-4939-3578-9_16