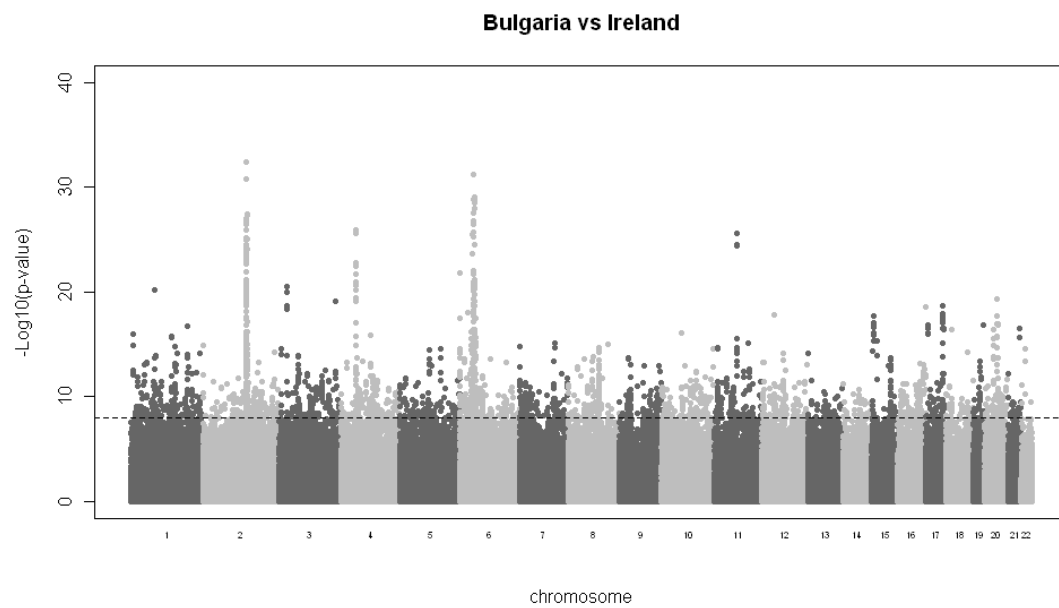
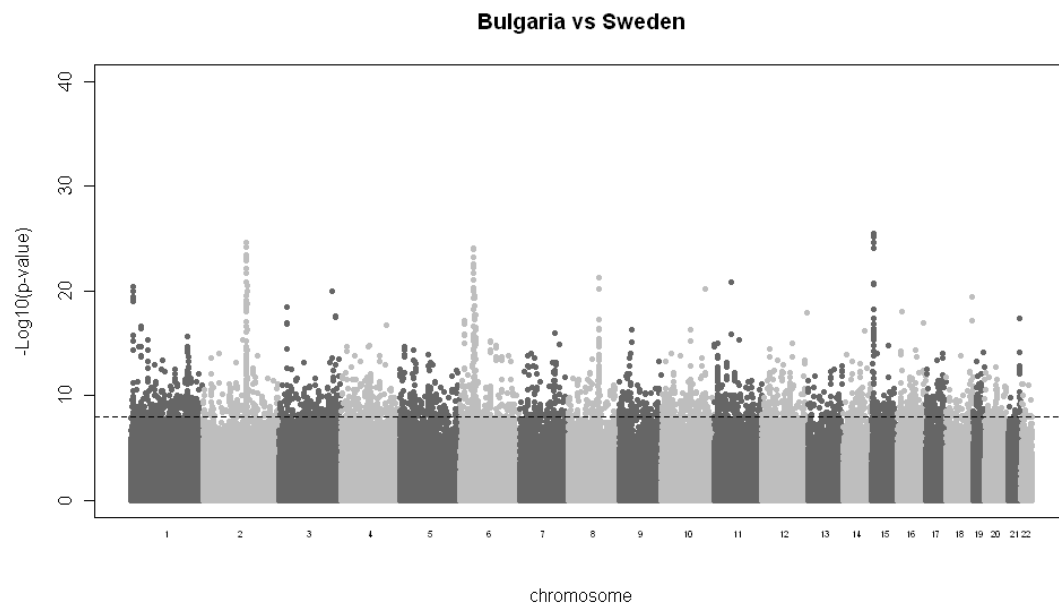


Supplementary Figure 1. Significance of all pair-wise population comparisons vs genomic position with the scaled down sample sizes.

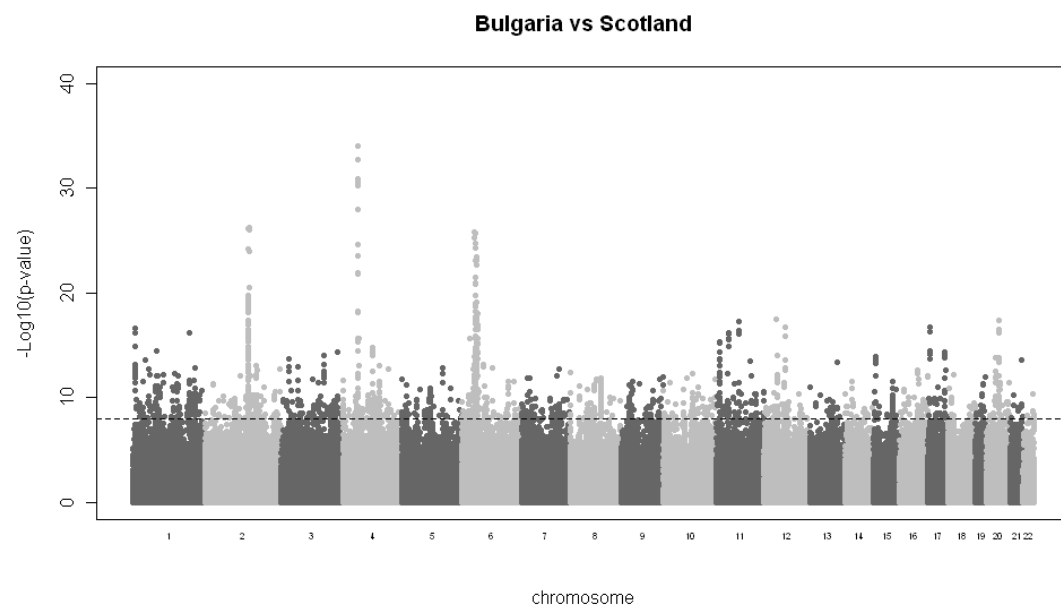
A.



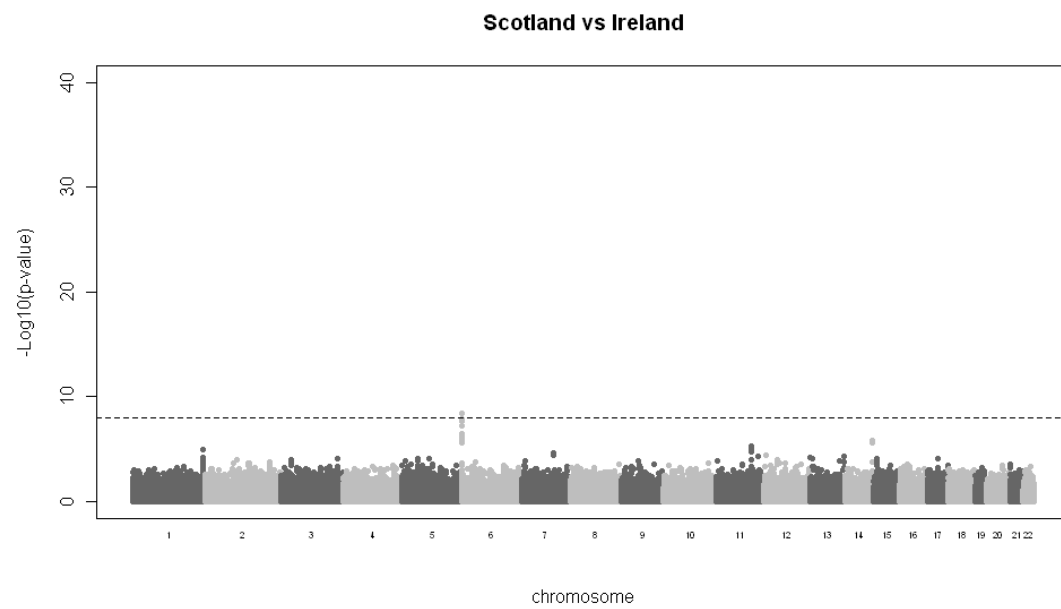
B.



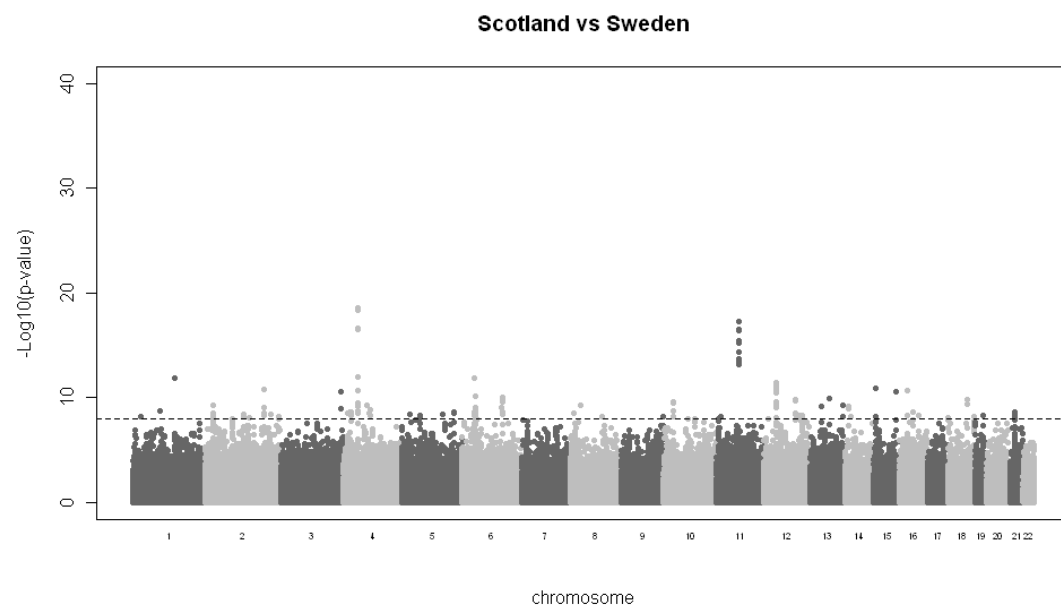
C.



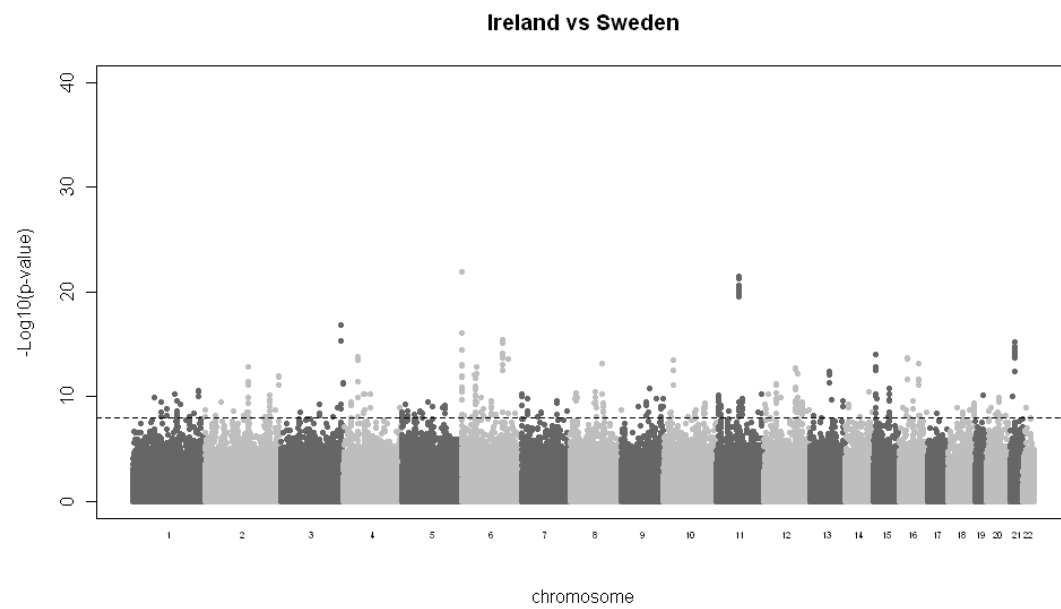
D.



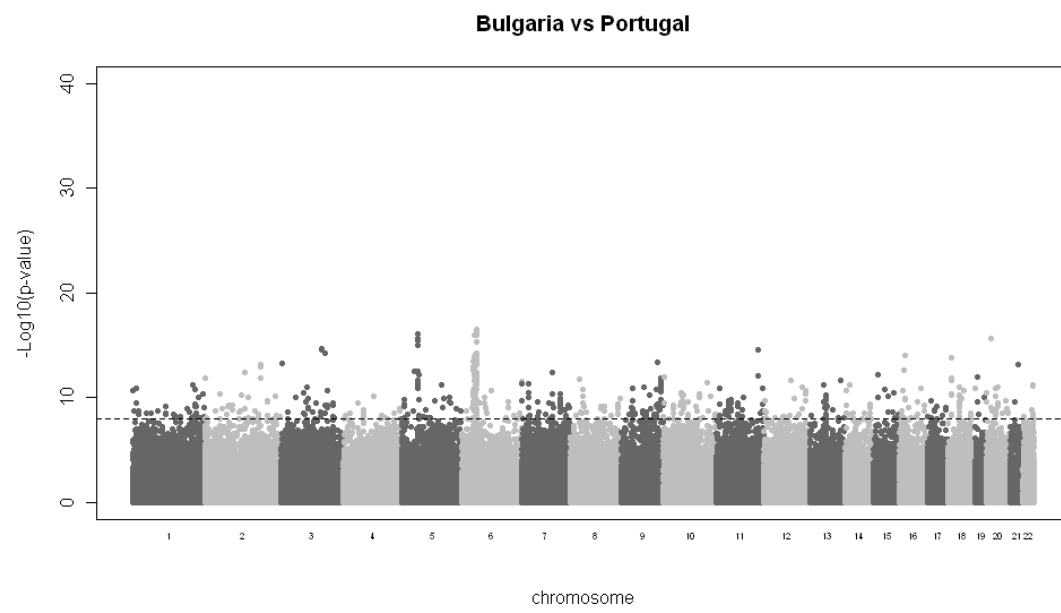
E.



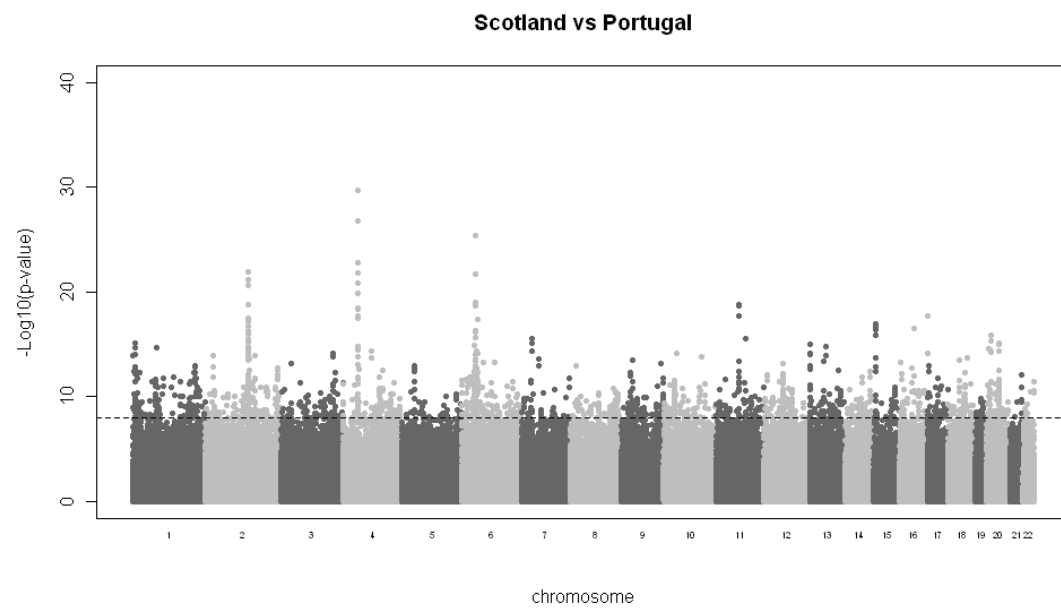
F.



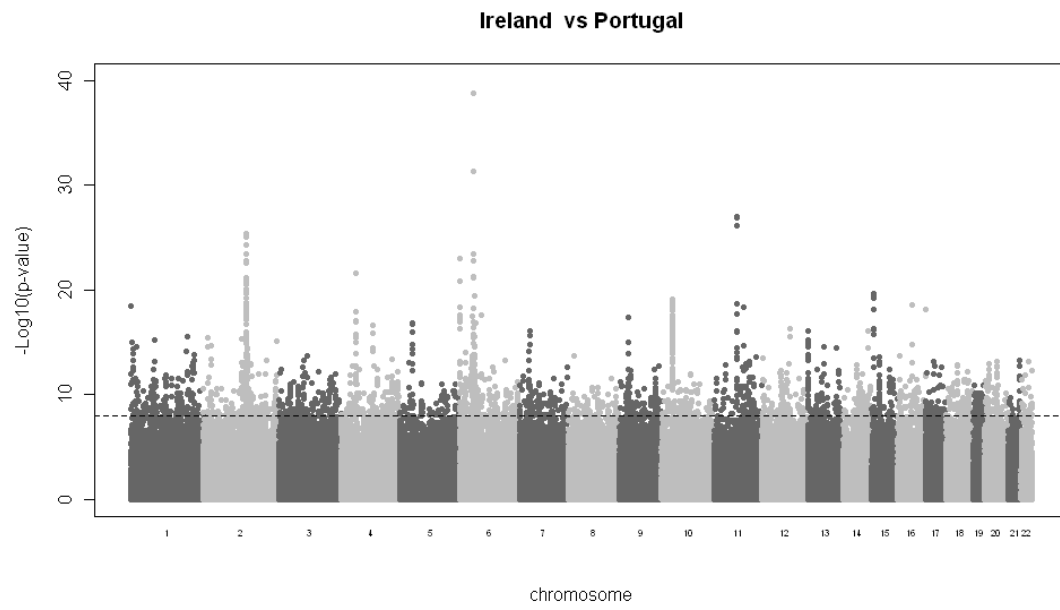
G.



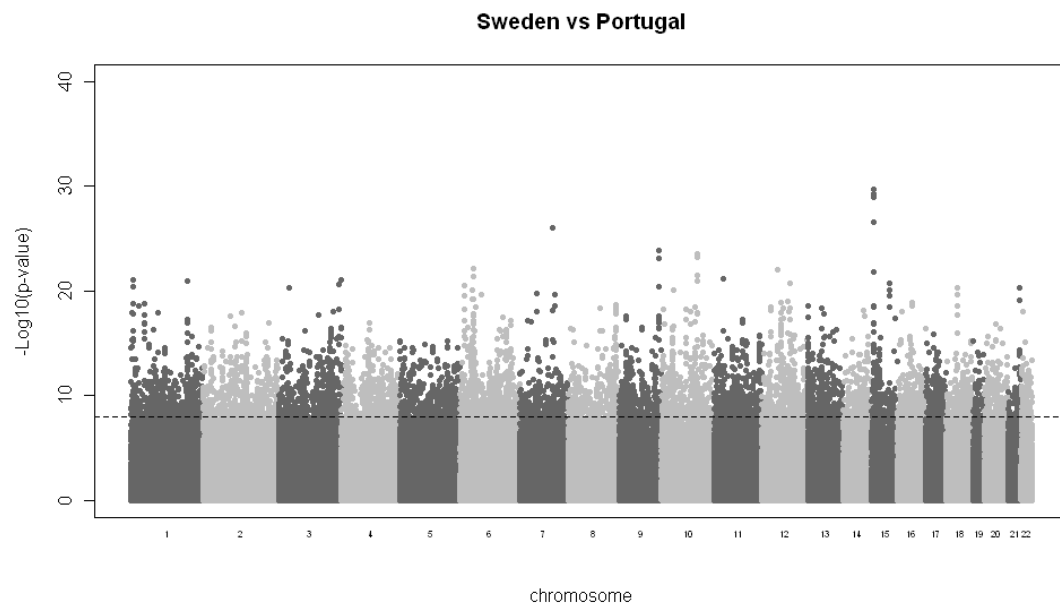
H.



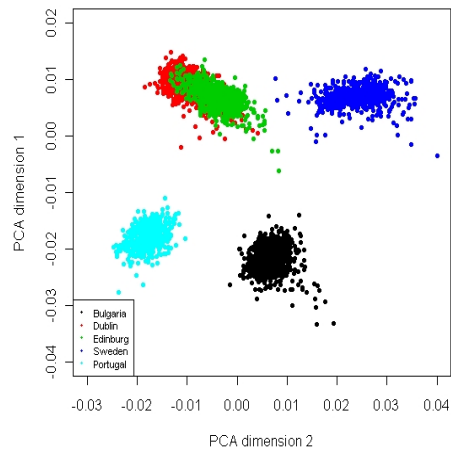
I.



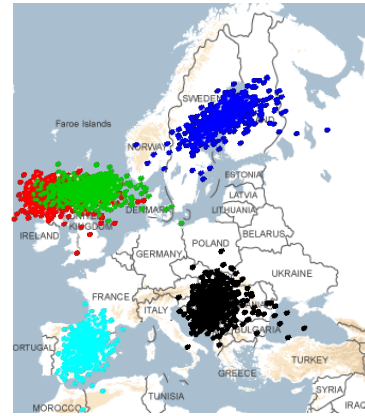
J.



Supplementary Figure 2. Principal component analysis performed on 101532 SNPs with r^2 smaller or equal 0.5 merged with the map of Europe (<http://www.multimap.com>).

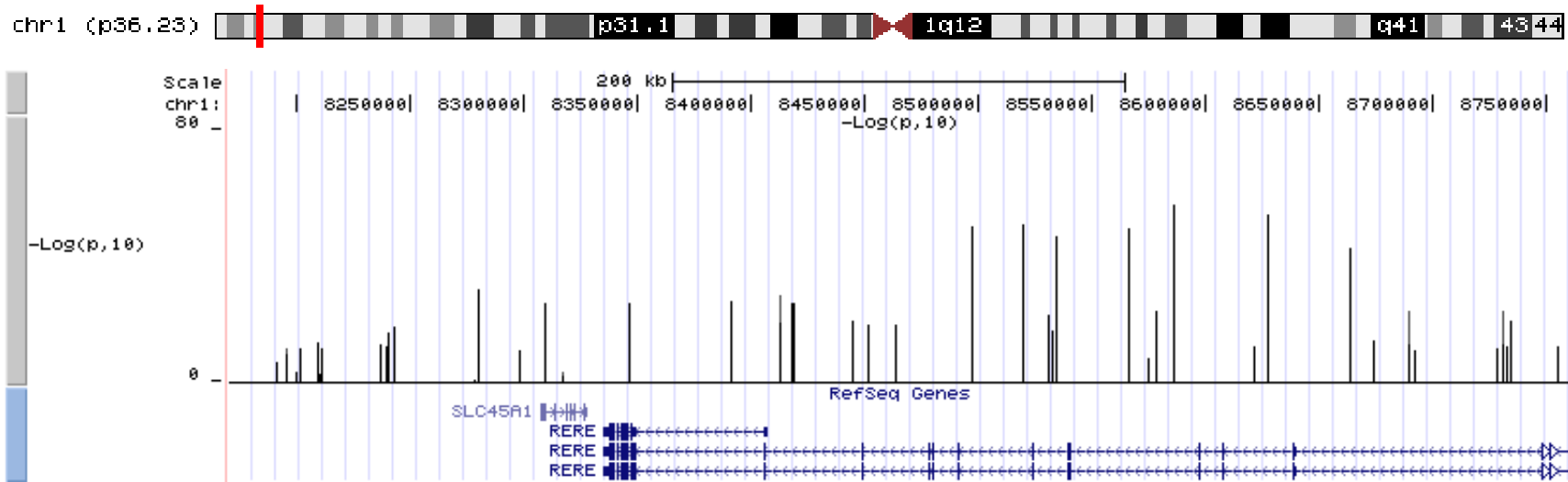


a.

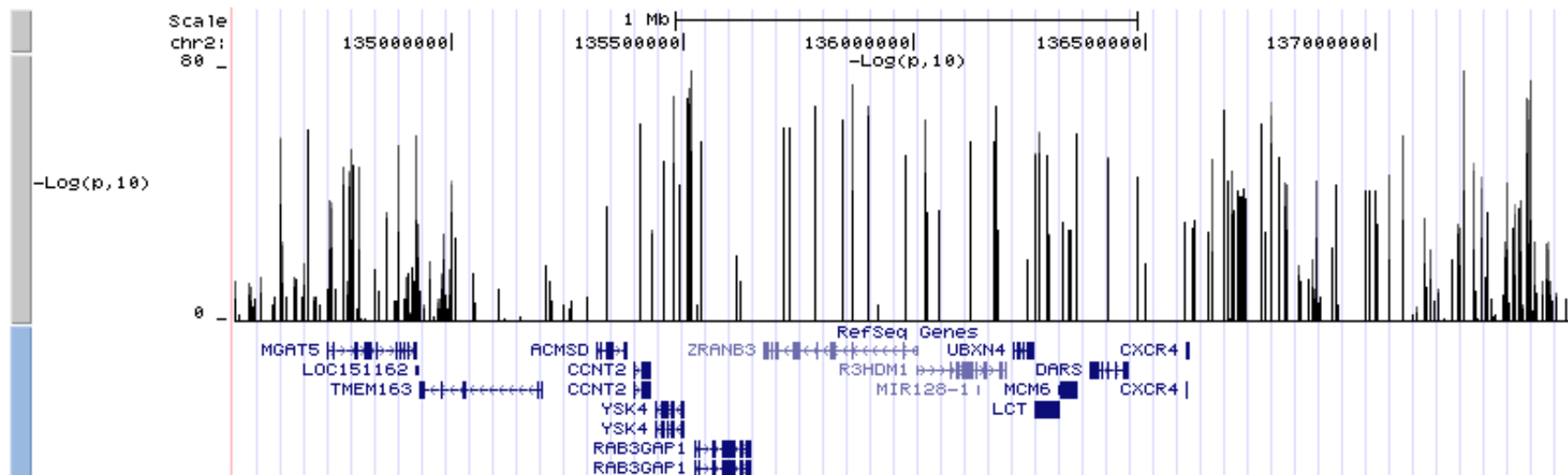


b.

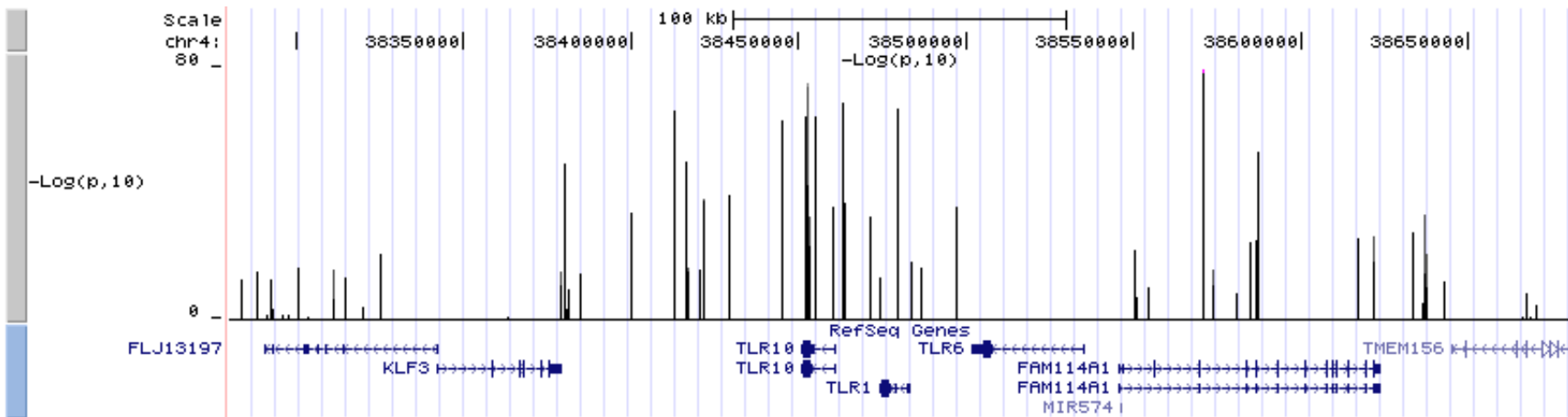
Supplementary Figure 3. Genetic region around 11 top-ranked loci. Vertical bars indicate the strength of the stratification for each SNP, on a scale of 0 - 80 for the $-\log(p,10)$.



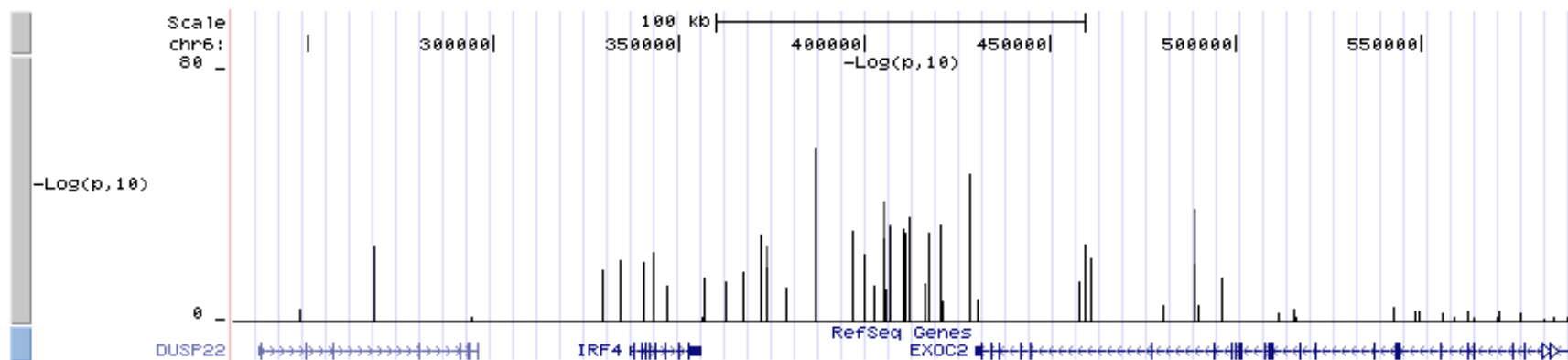
chr2 (q21.2-q22.1)

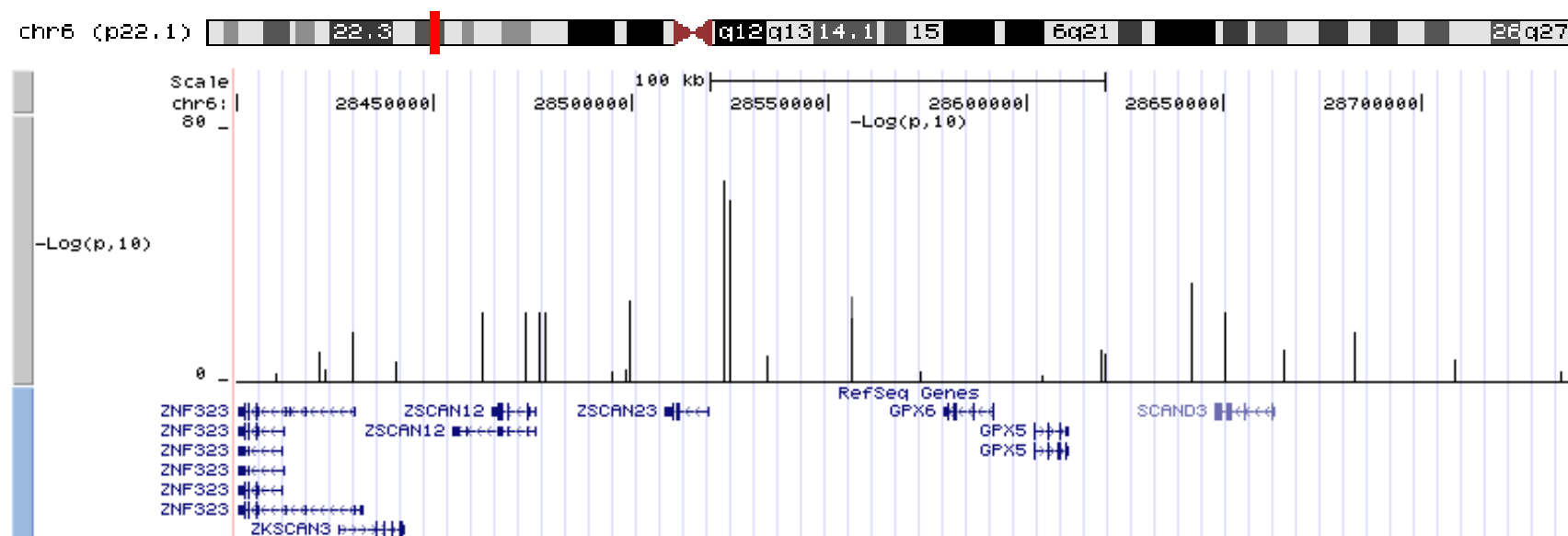


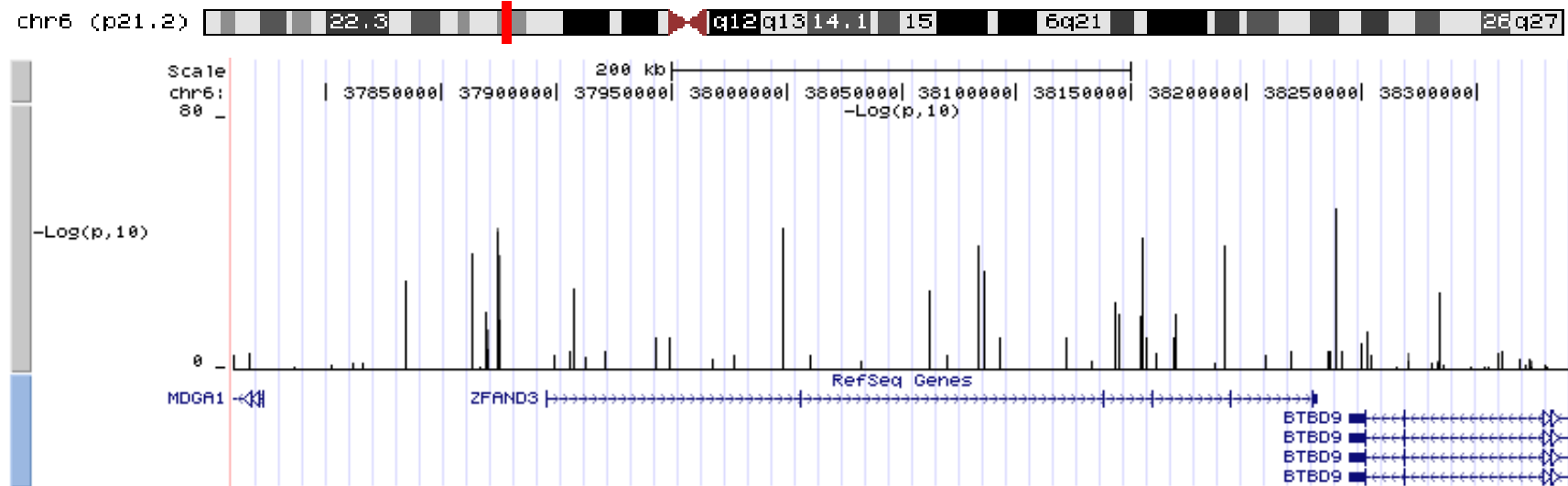
chr4 (p14) 11.13 q12 24 q25 q26 28.3



chr6 (p25.3) 22.3 q12 q13 q14.1 15 6q21 26 q27

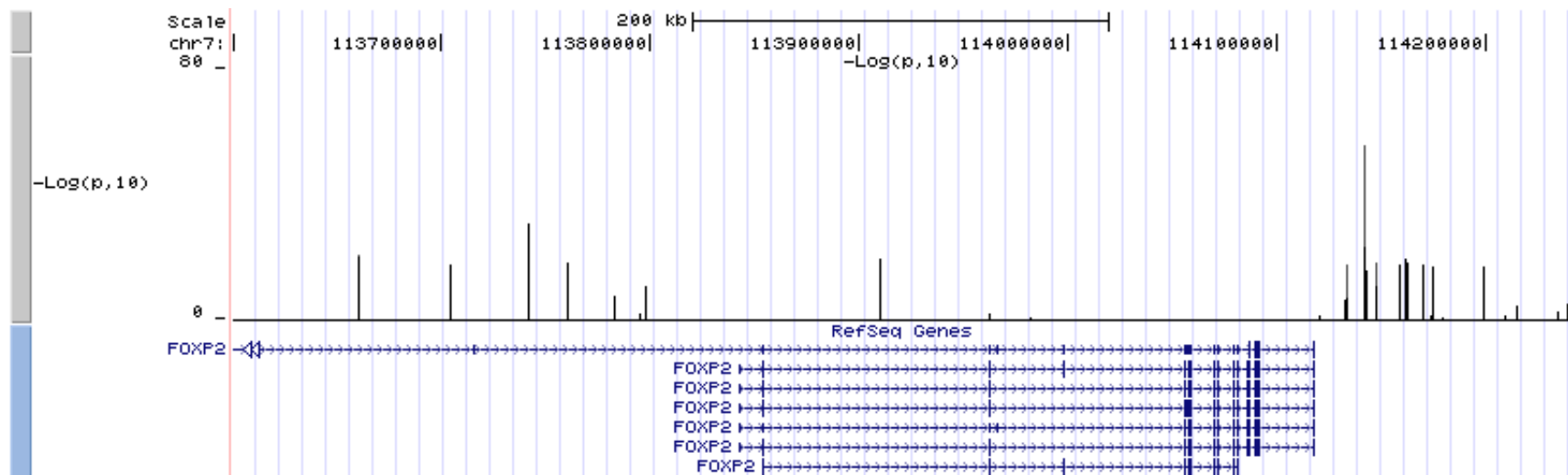




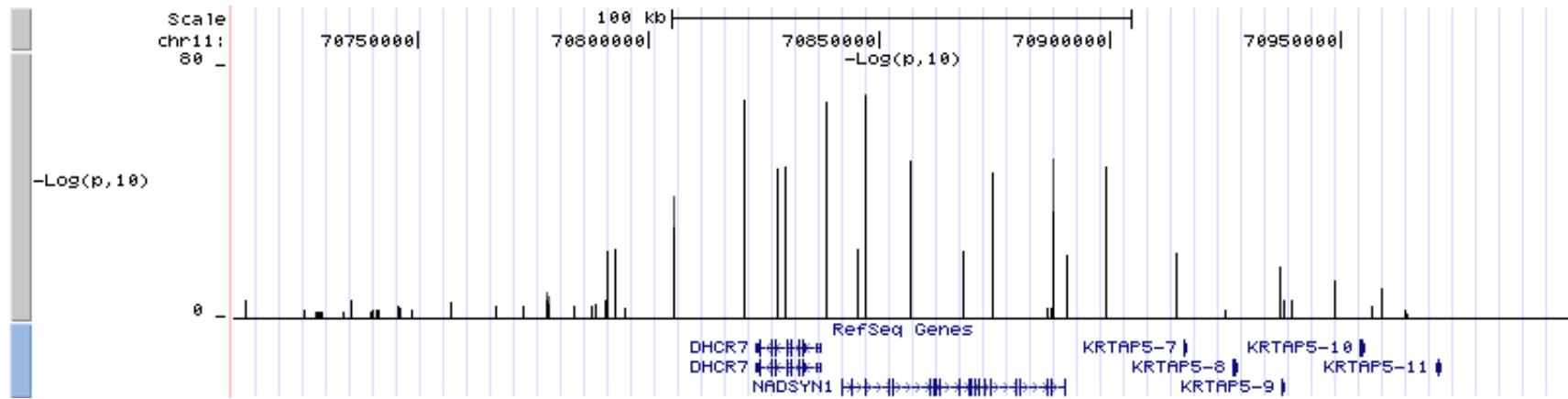


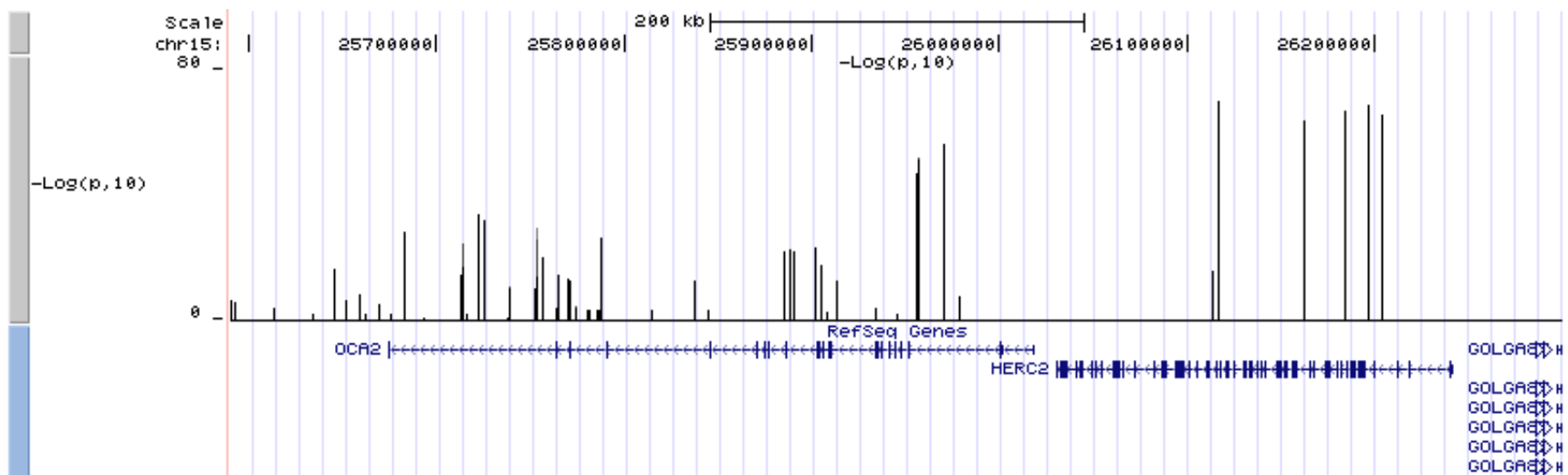


21.11 31.1 33 q34 35



chr11 (q13.4) p15.4 p13 p12 q14.1 q21 q22.3 25





chr20 (q11.22) 20p13 p12.3 12.2 20p12.1 11.23 11.21 20q12 q13.12 13.13 20q13.2 q13.33

