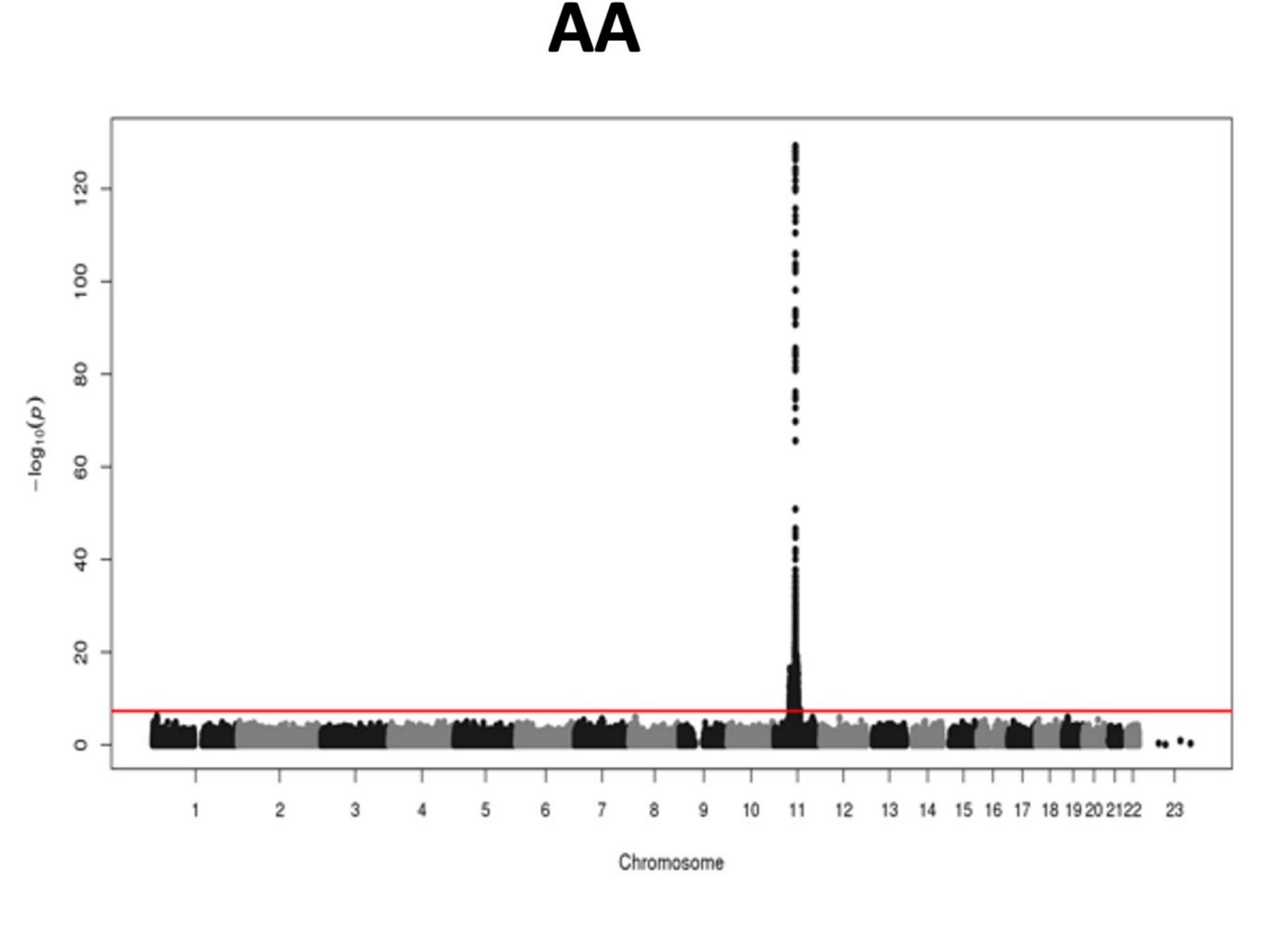
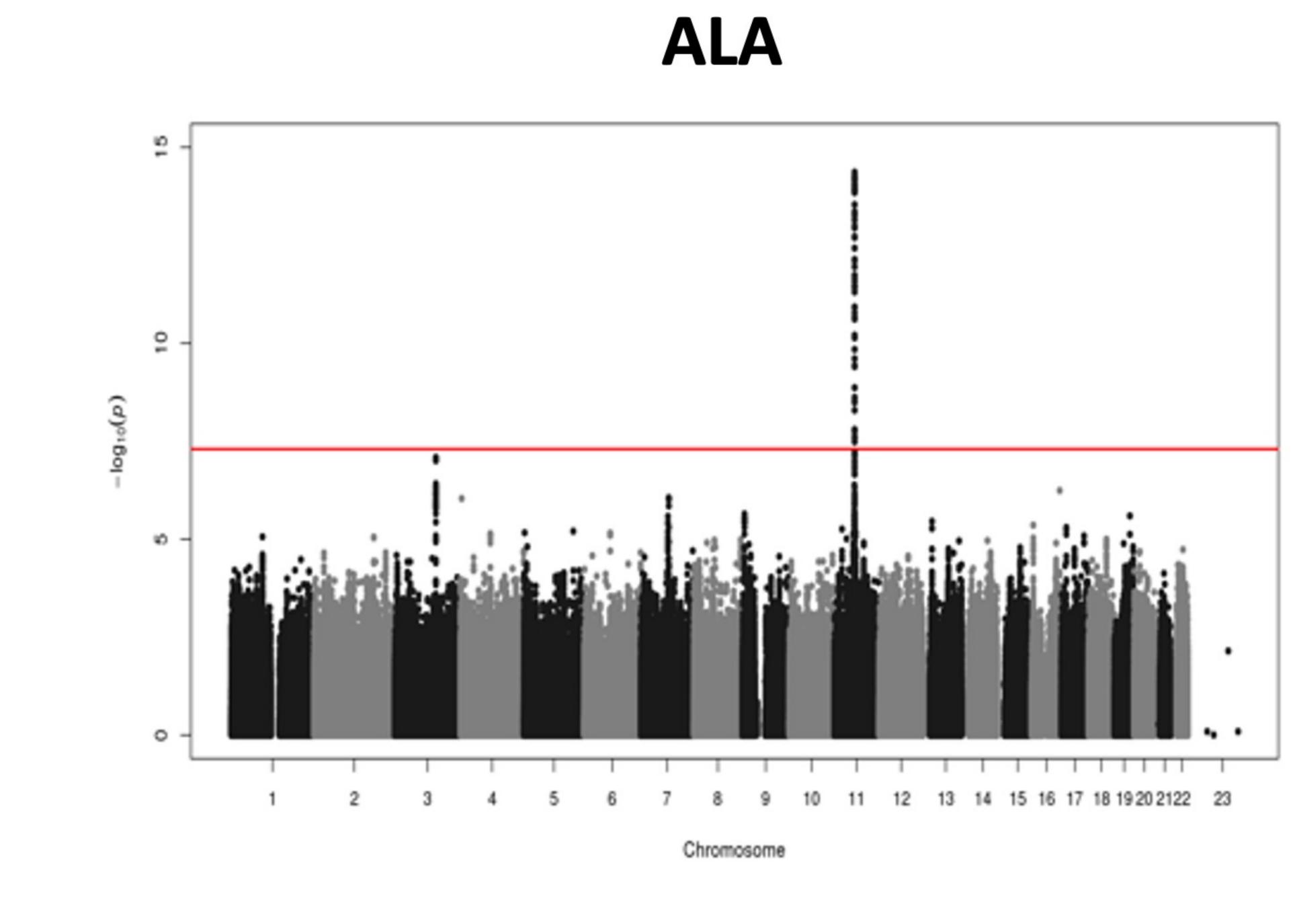
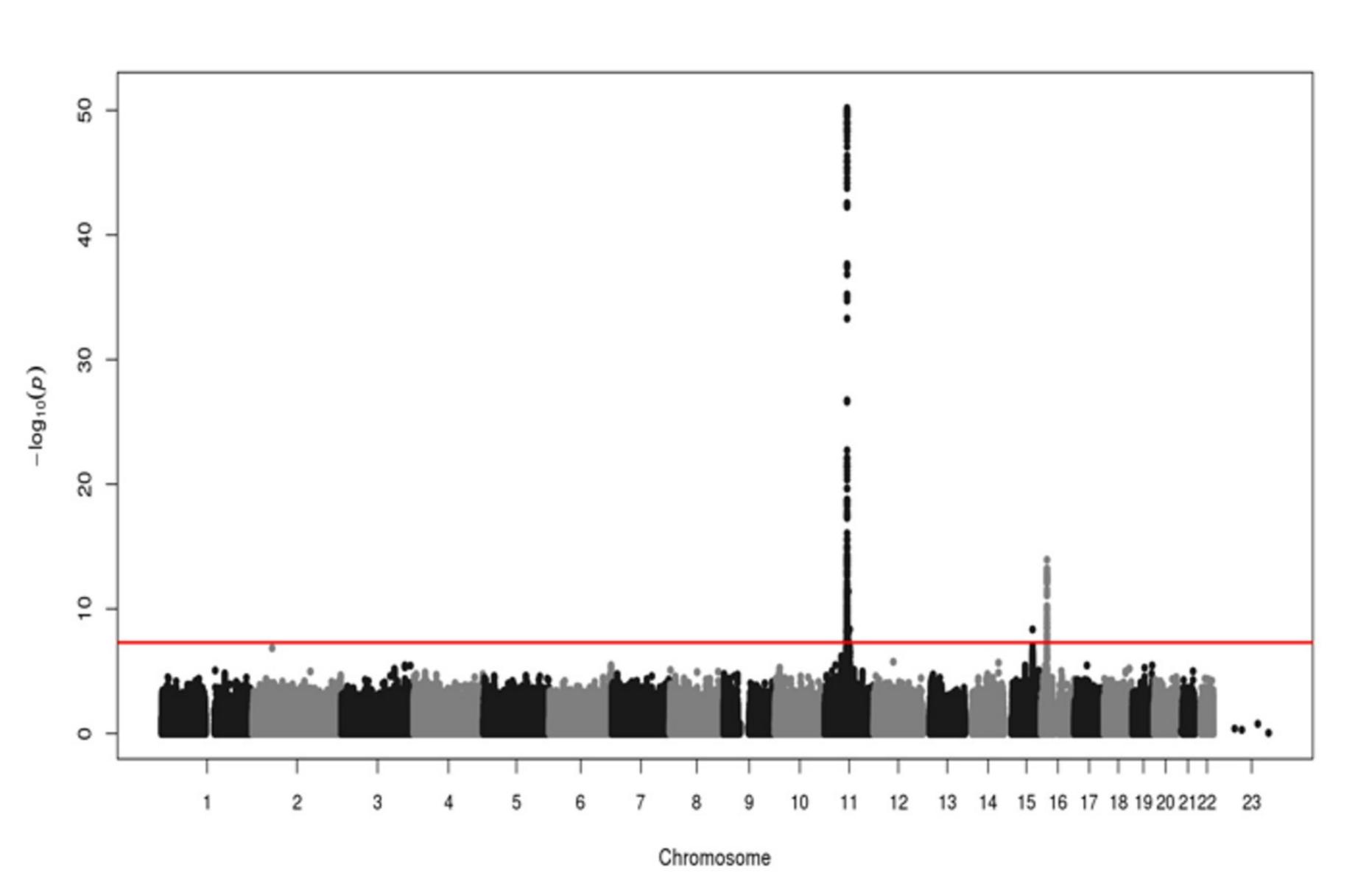
Supplementary Figure 1. Manhattan plot of meta-analysis of GWAS for PUFAs in the Hispanic Americans.

The red line shows the genome-wide significance threshold of $(-\log_{10}(5 \times 10^{-8}))$.

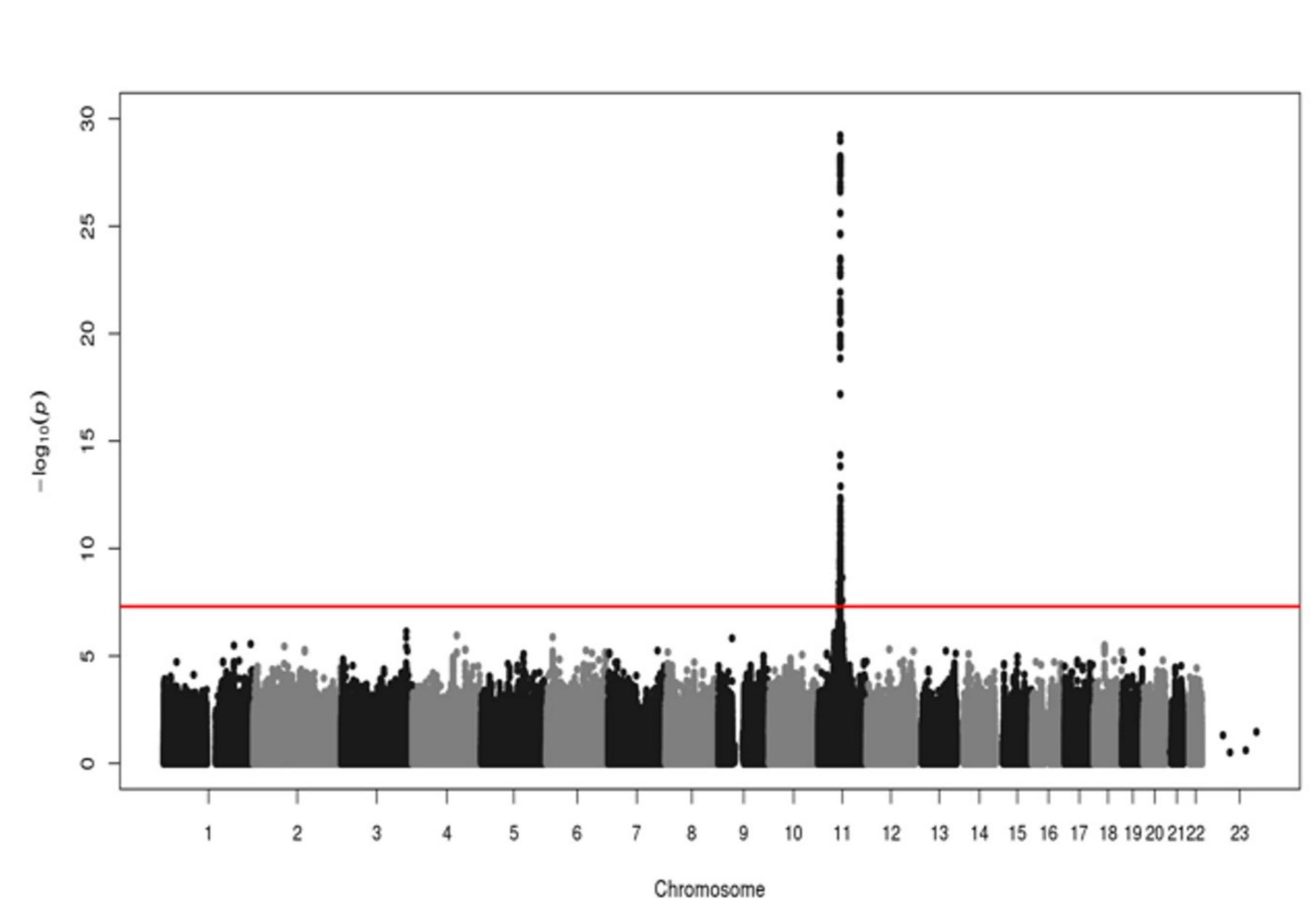




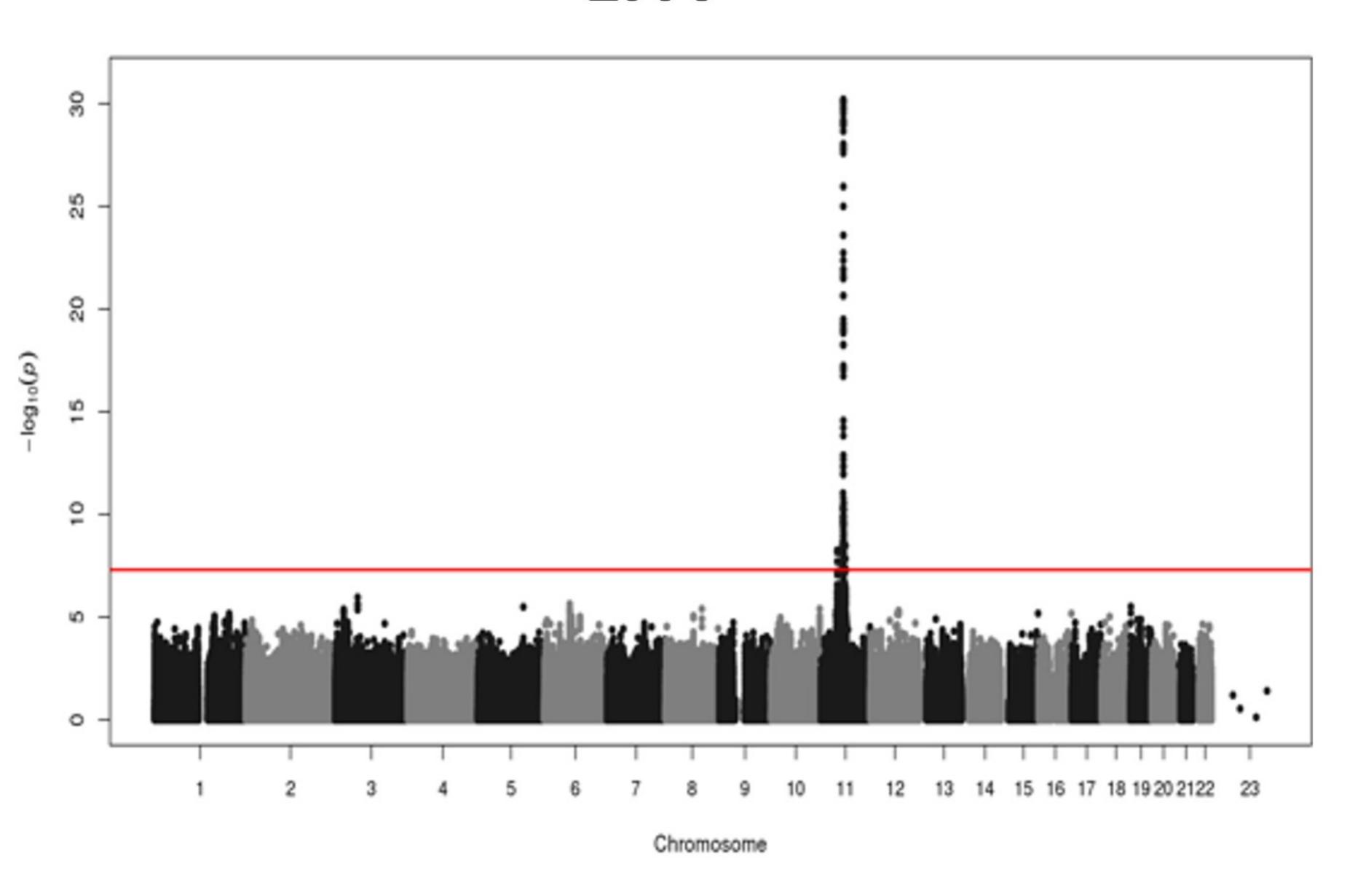




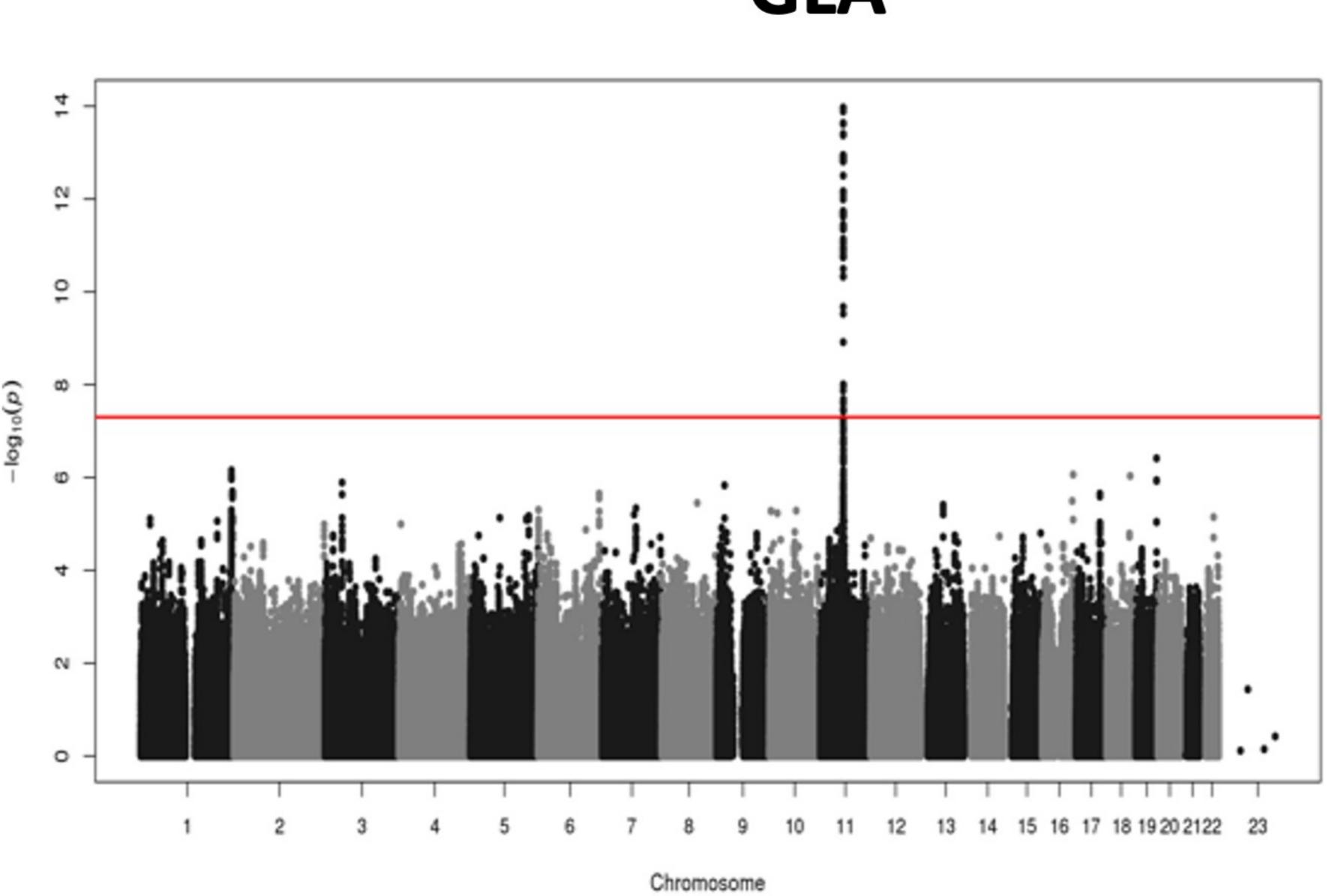




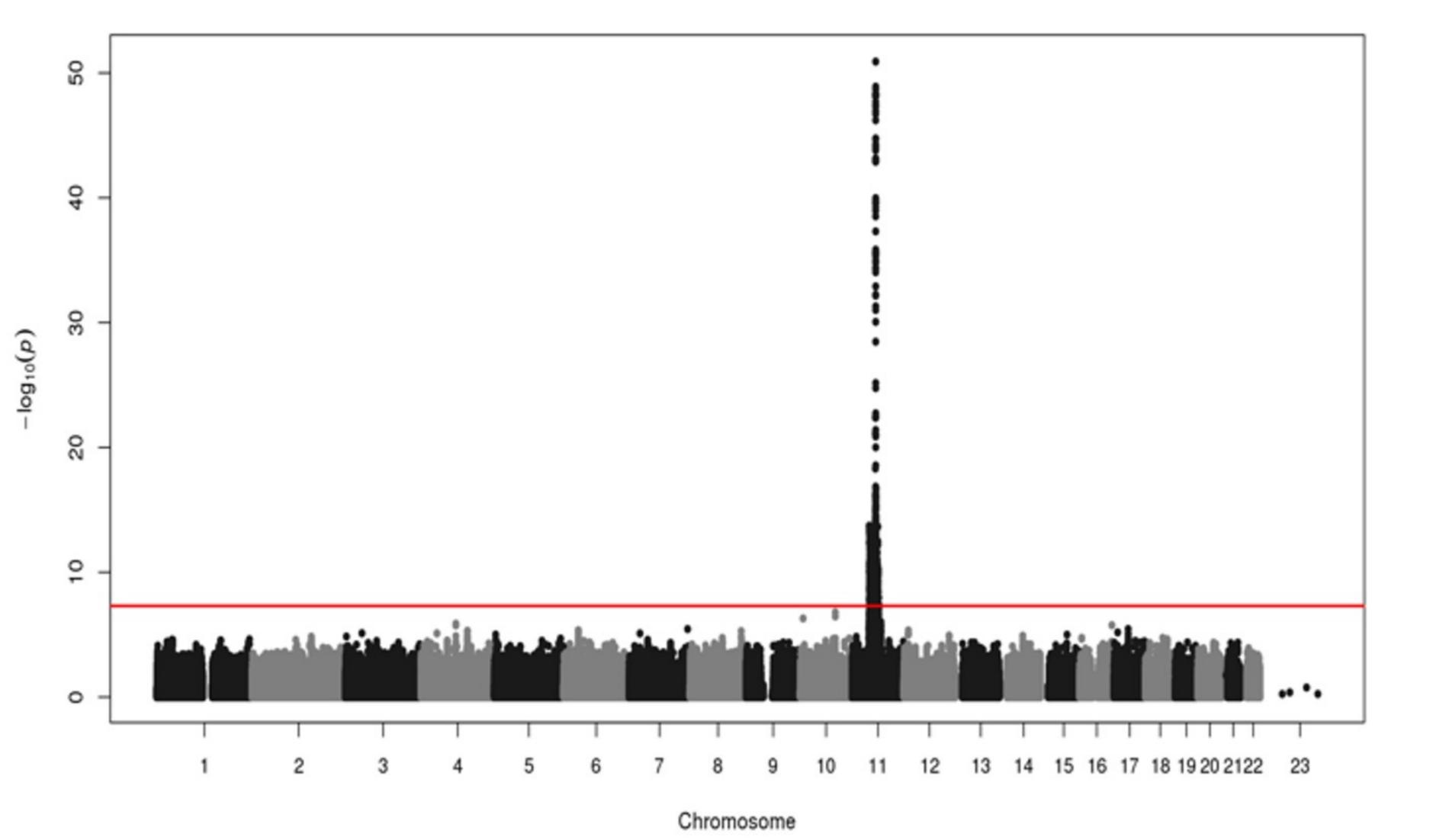
EPA





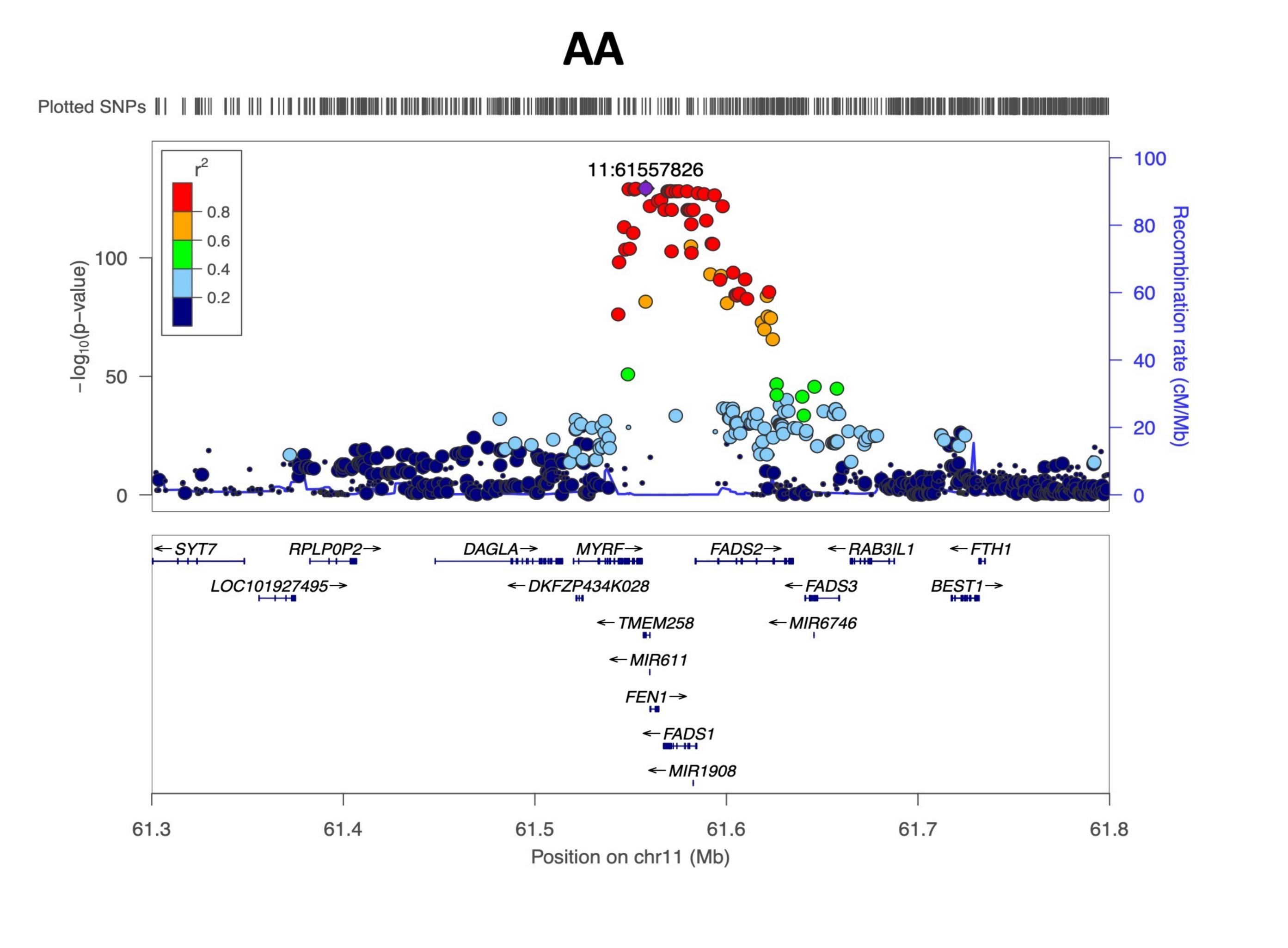


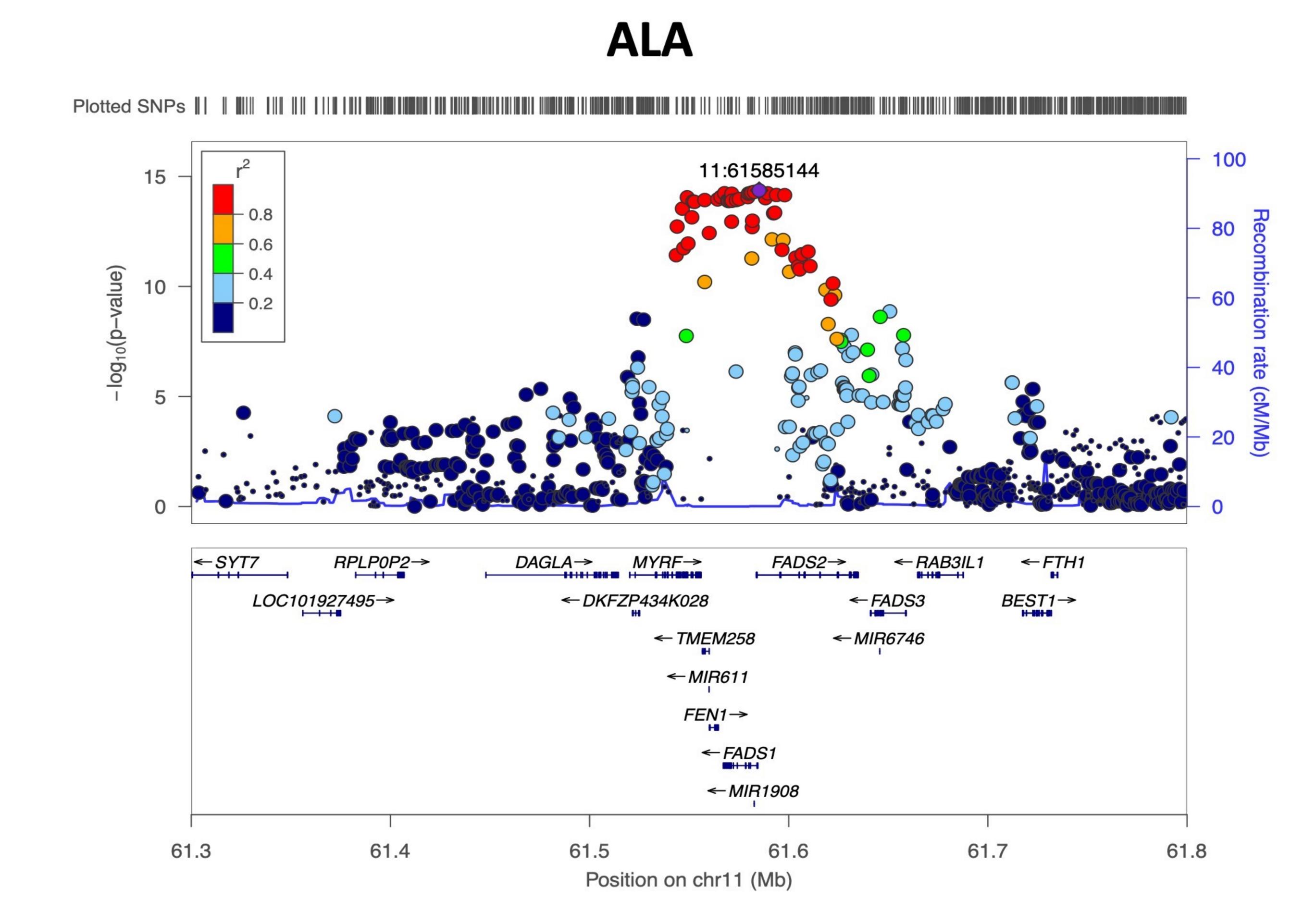
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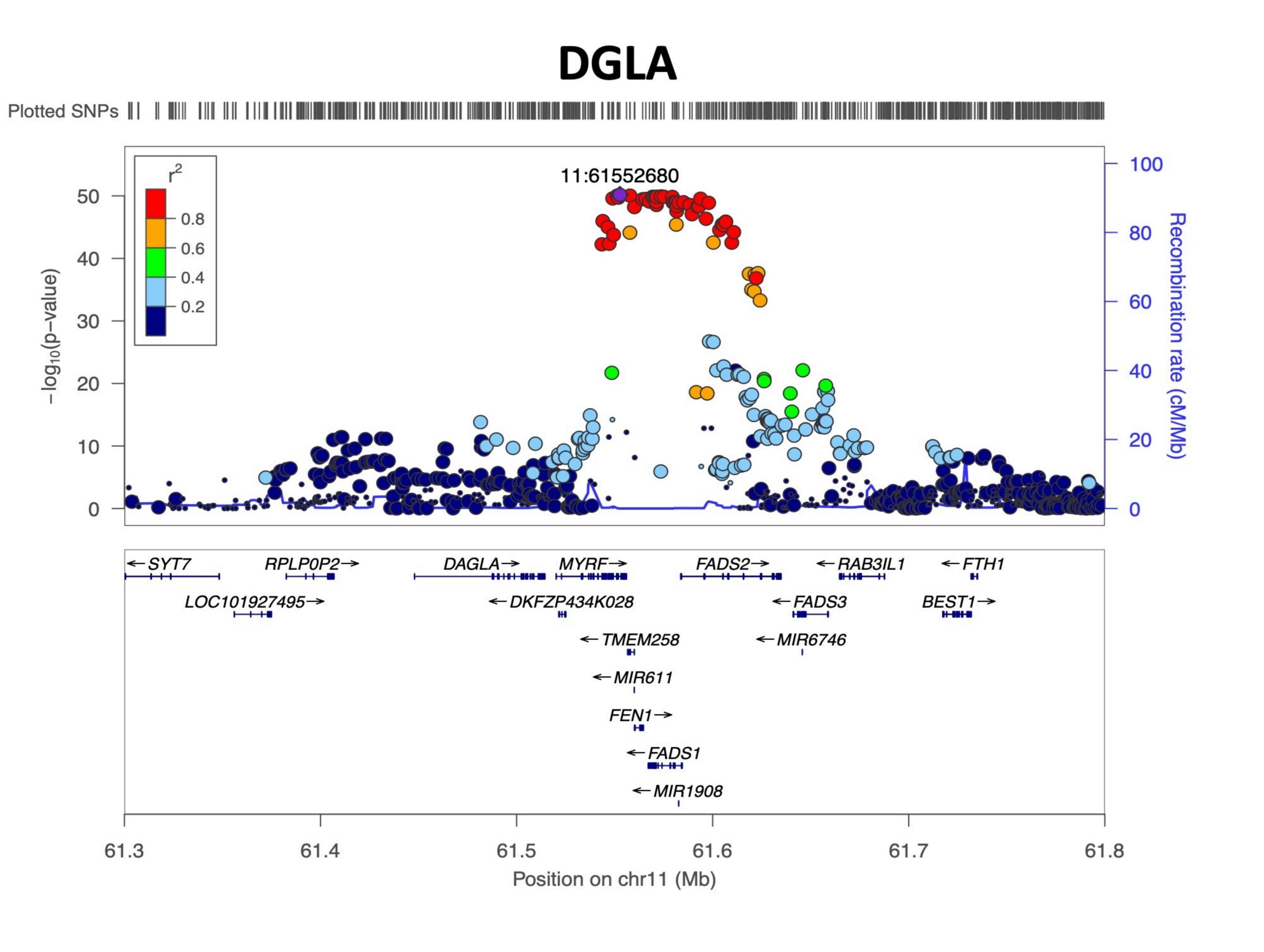


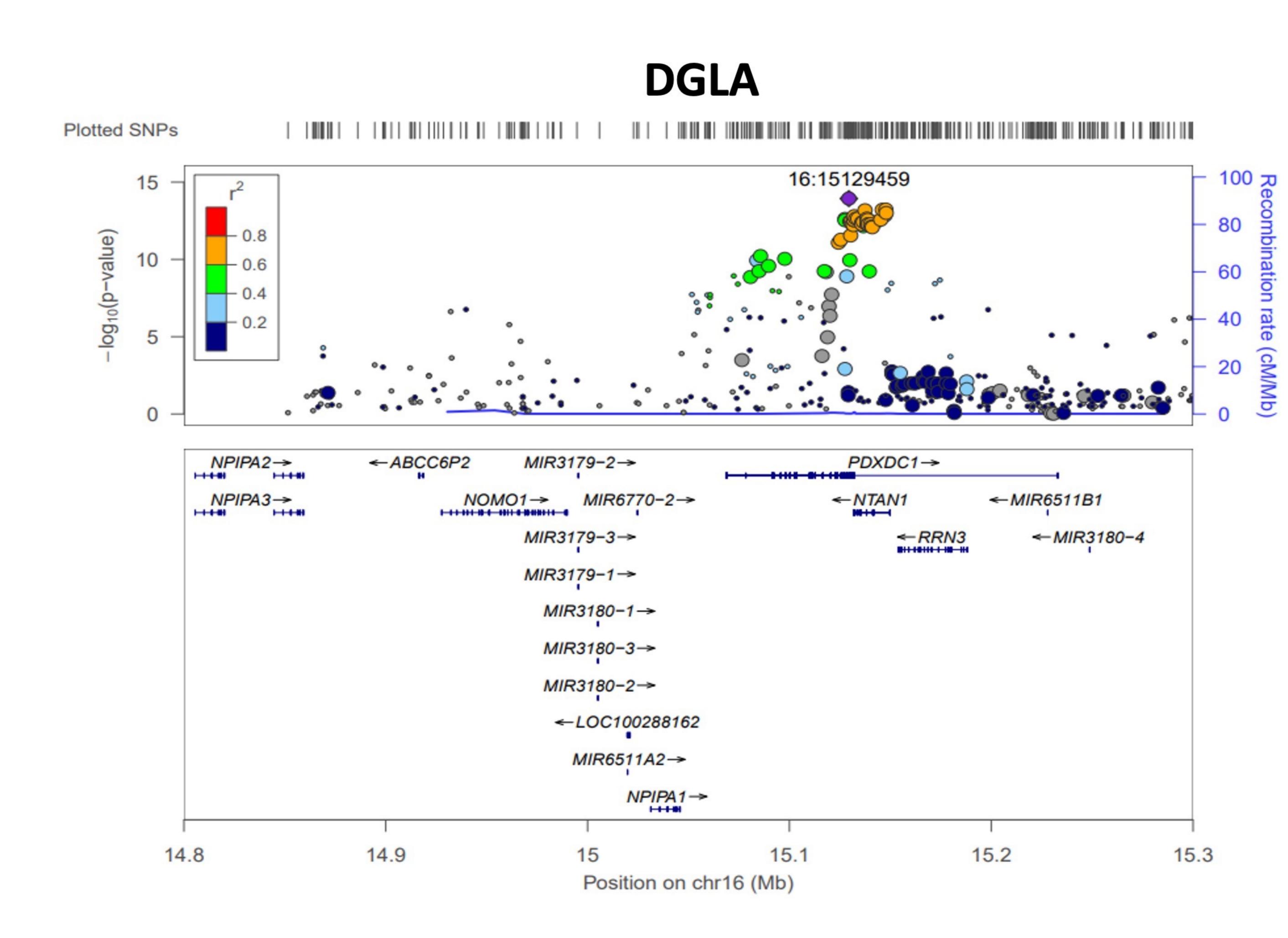
Supplementary Figure 2. Local association plot of most significant for each PUFAs on each chromosome in the Hispanic Americans.

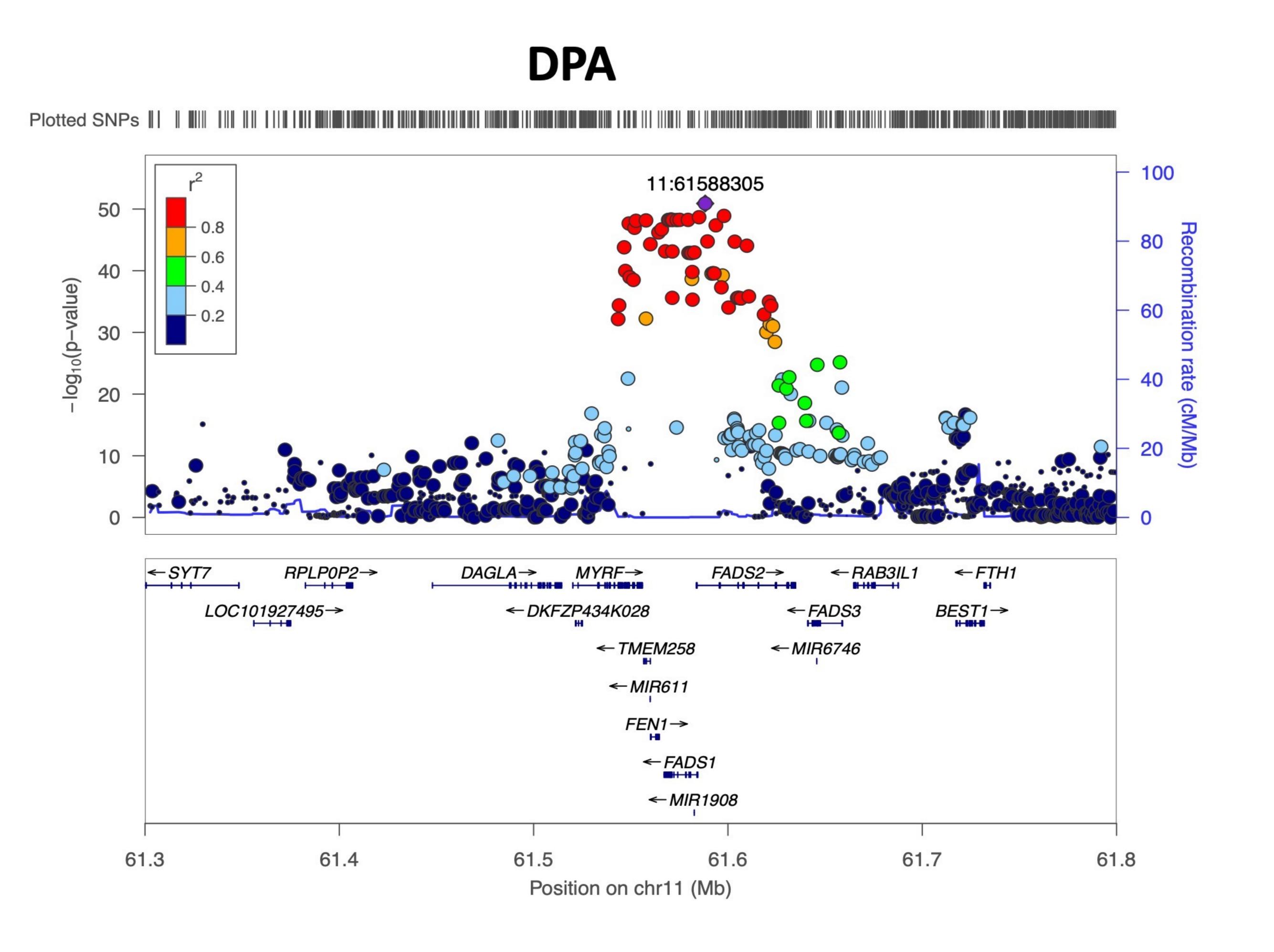
Reference panel used to color LD is 1000 Genomes Ad Mixed American (AMR) and the color scheme is red for strong linkage disequilibrium (LD; r²≥0.8) and blue color for lower LD.

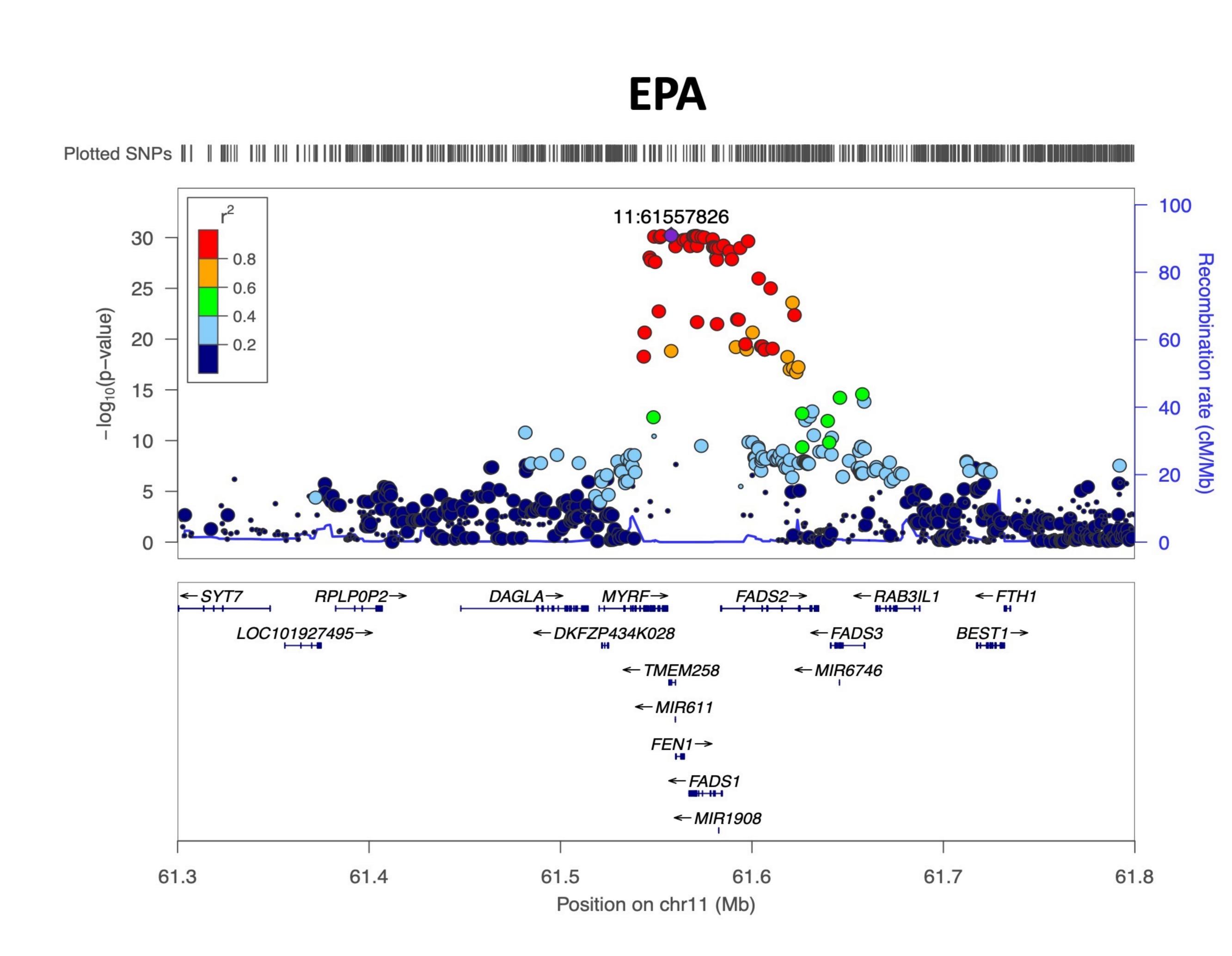


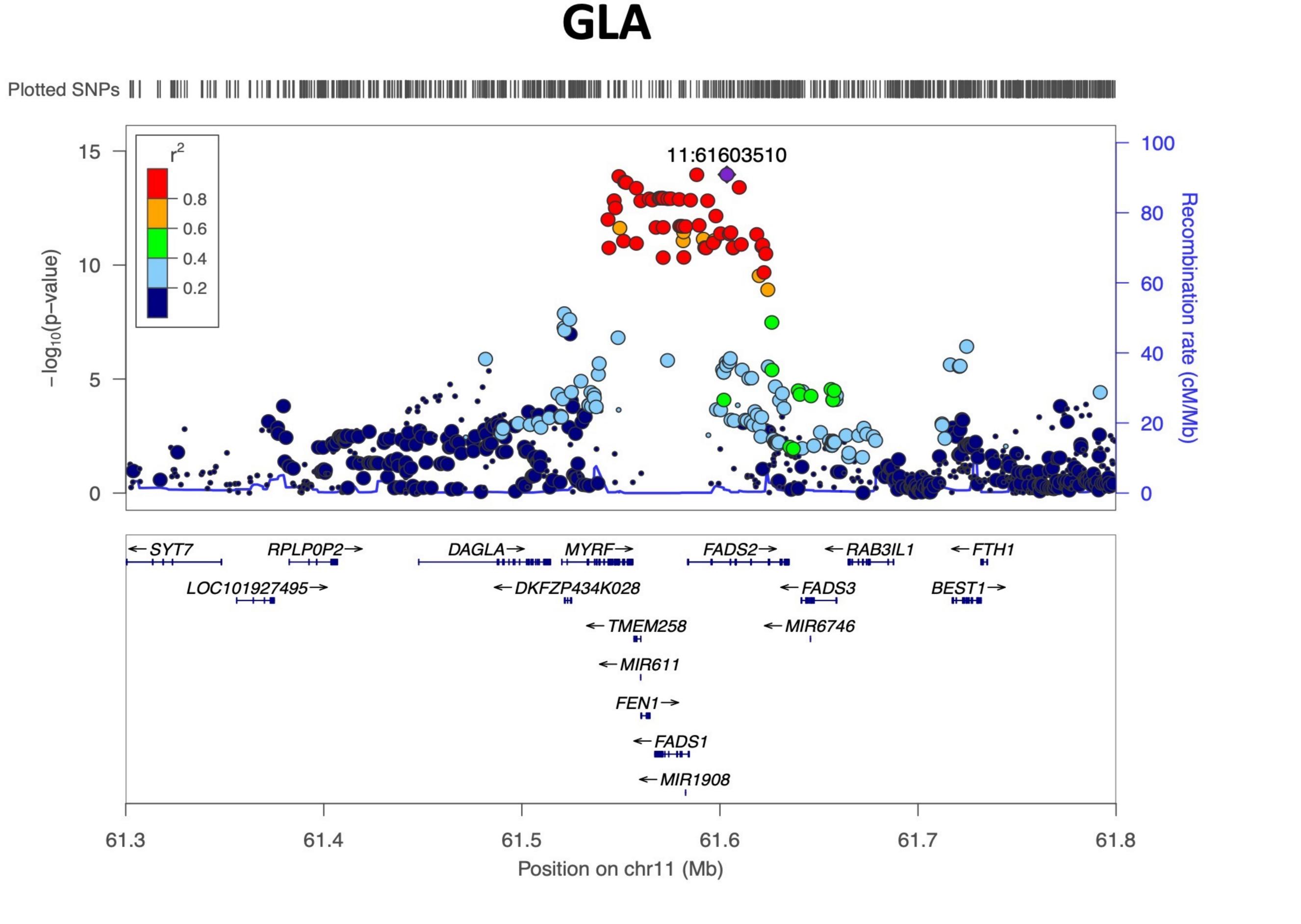


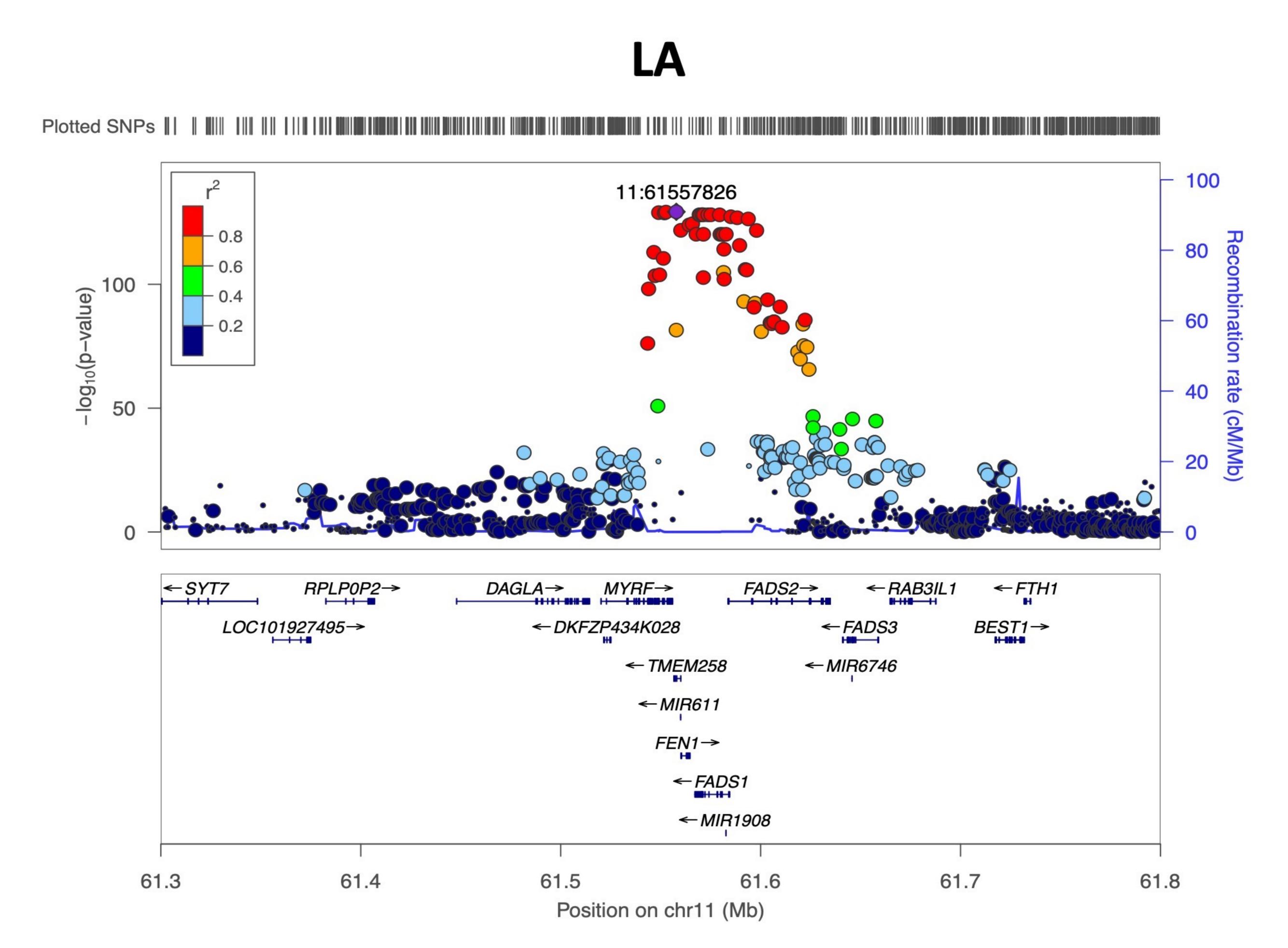




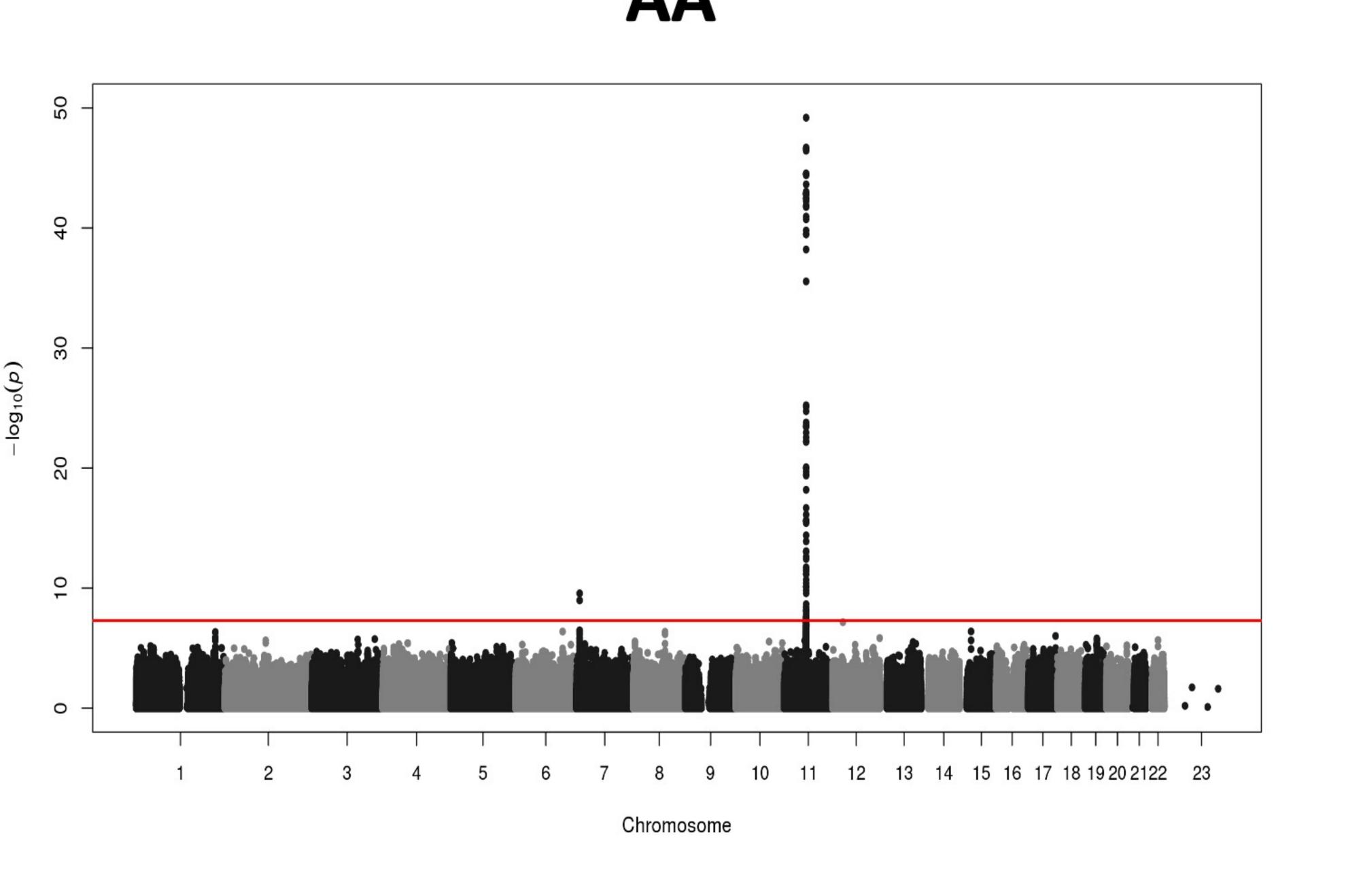


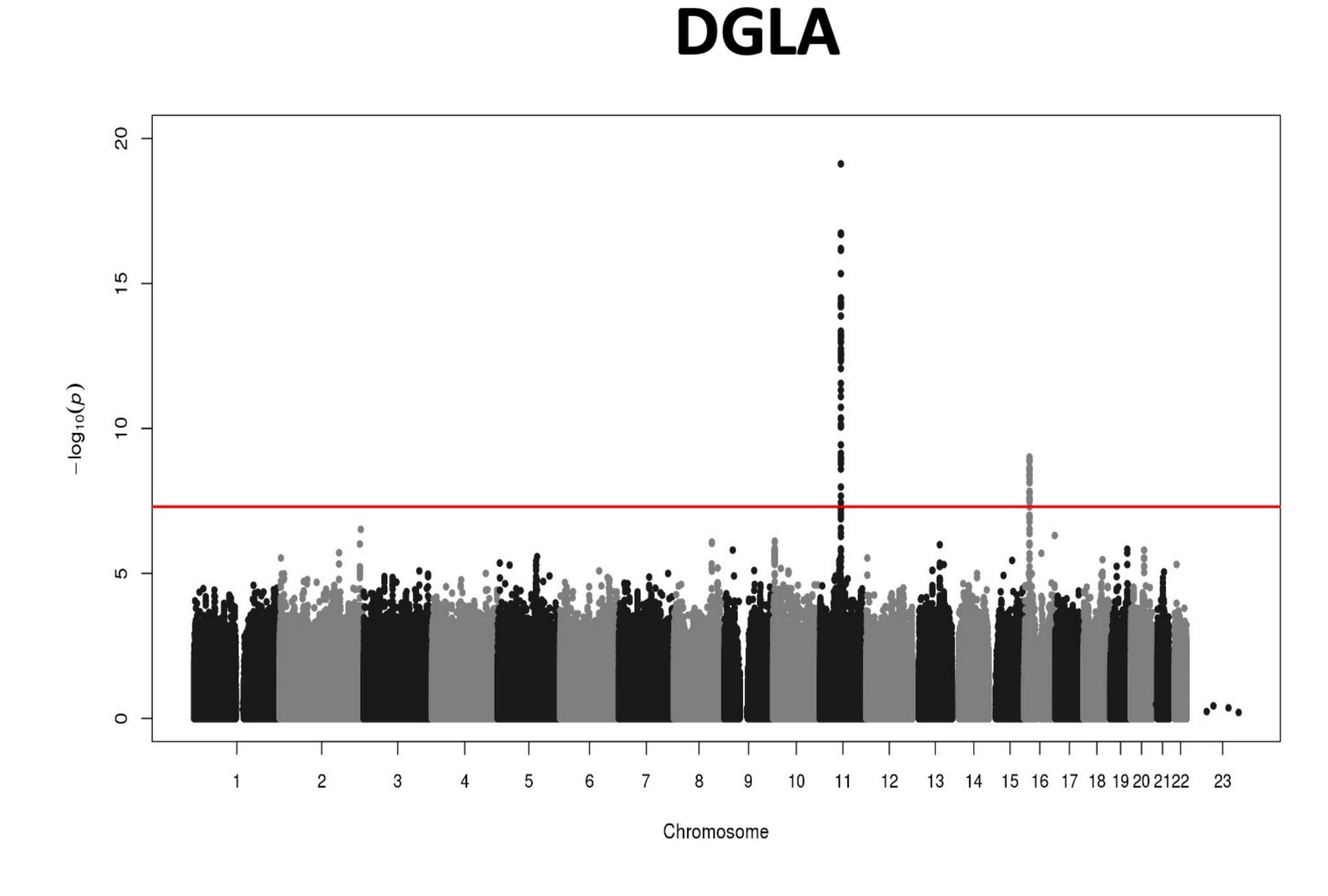


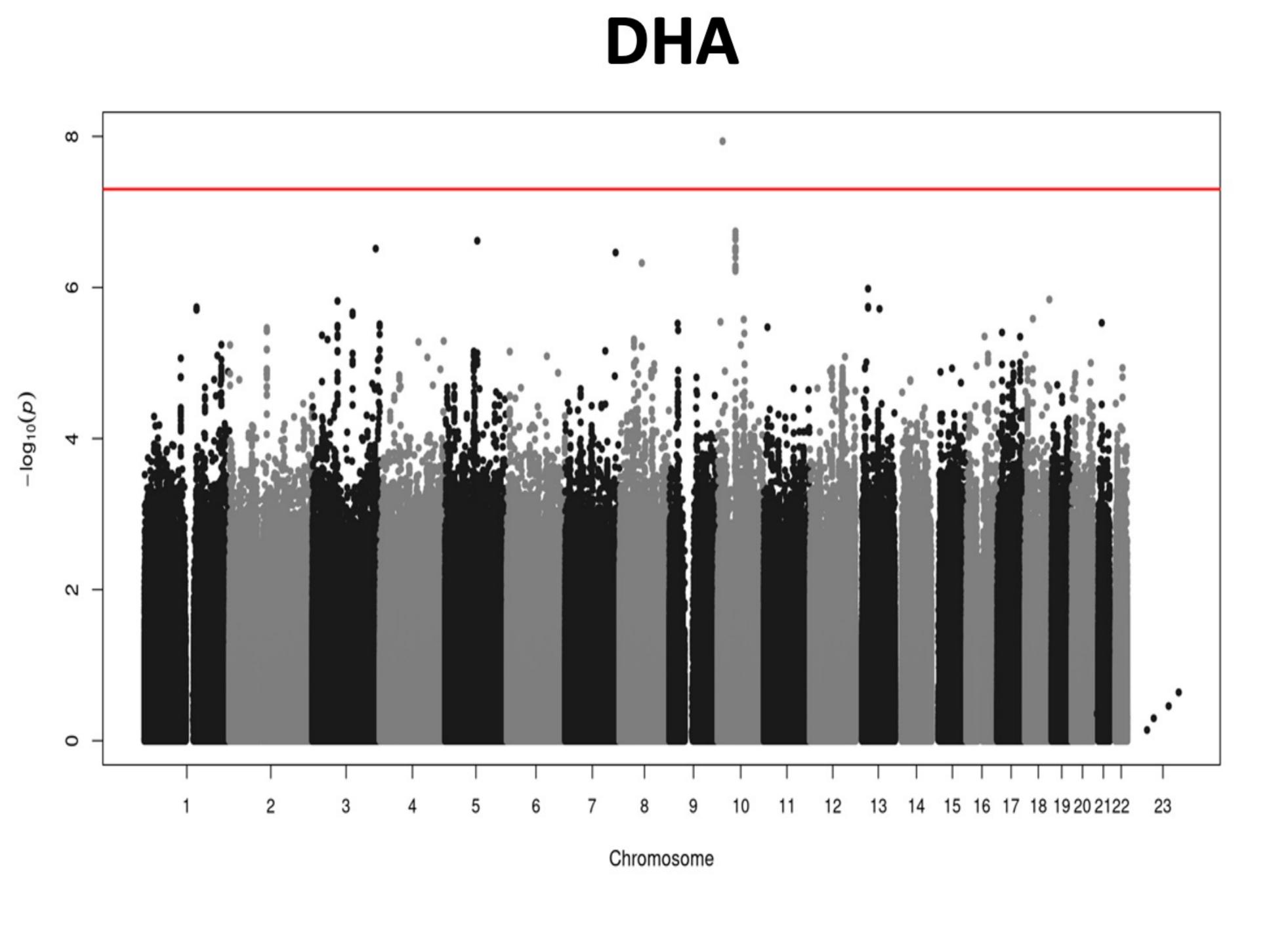


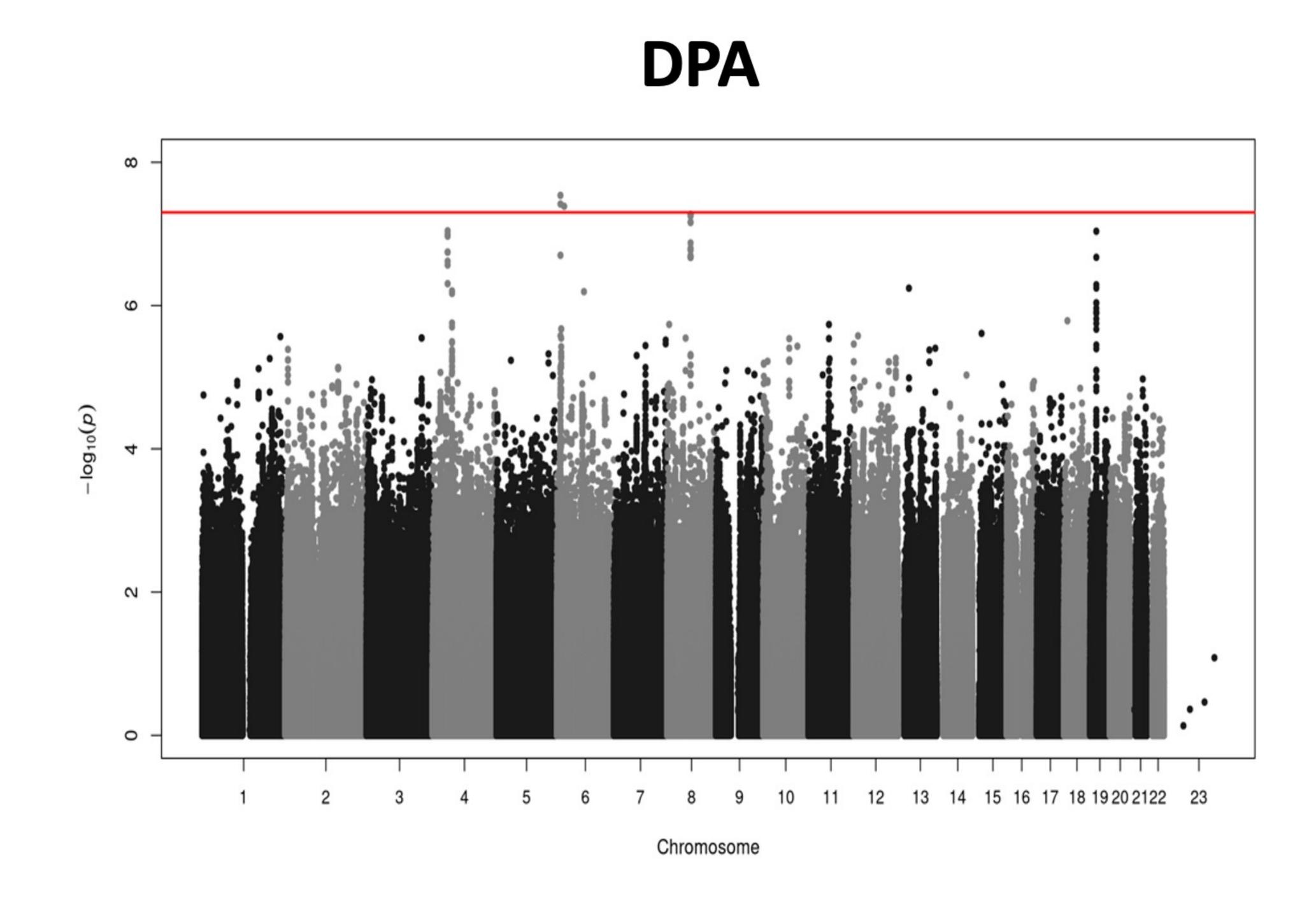


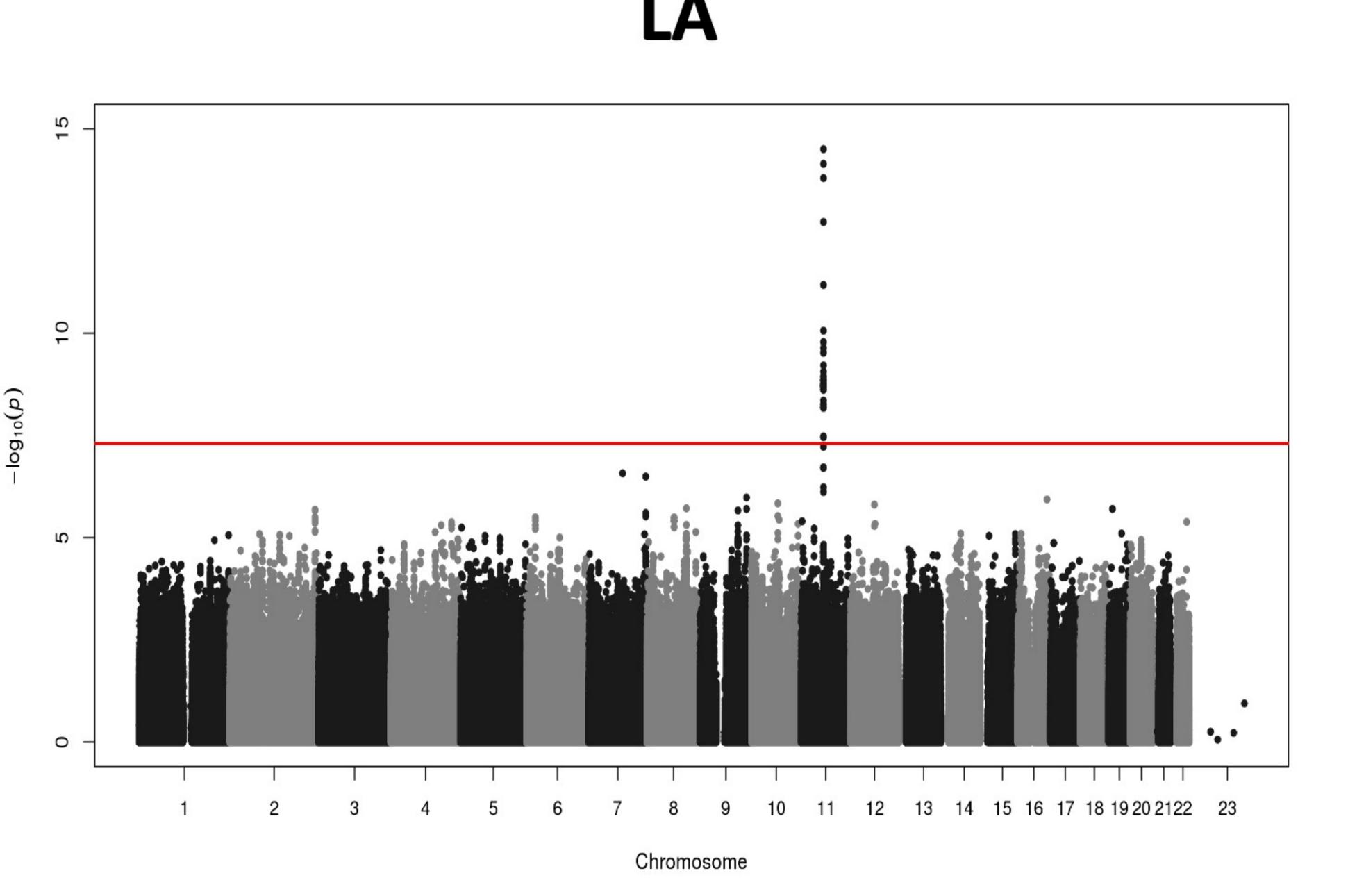
Supplementary Figure 3. Manhattan plot of meta-analysis of GWAS for PUFAs in the African American population. The red line shows the genome-wide significance threshold of $(-\log_{10}(5 \times 10^{-8}))$.











Supplementary Figure 4. Local association plot of most significant for each PUFAs on each chromosome in the African Americans.

Reference panel used to color LD is 1000 Genomes African (AFR) and the color scheme is red for strong linkage disequilibrium (LD; r²≥0.8) and blue color for lower LD.

