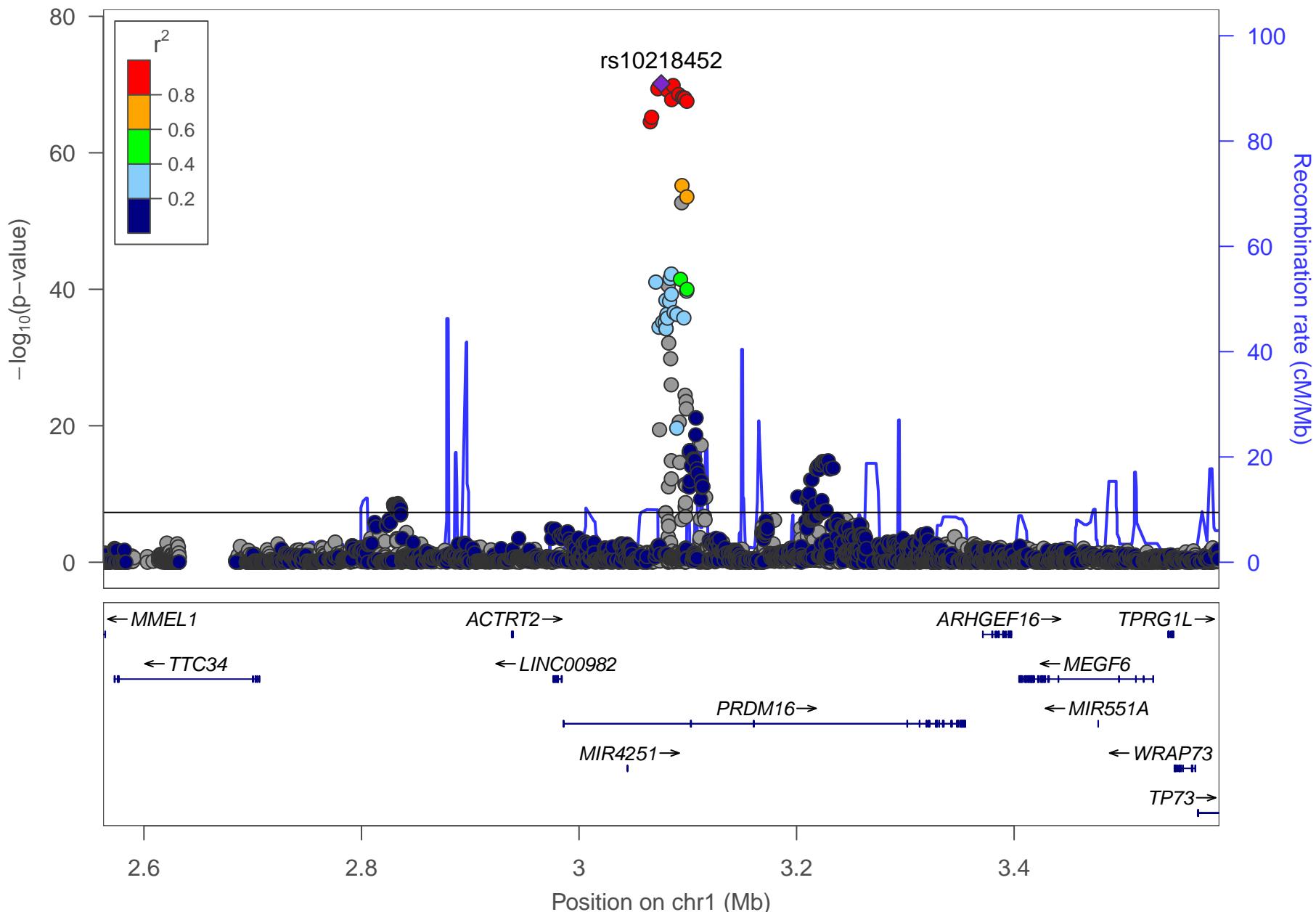
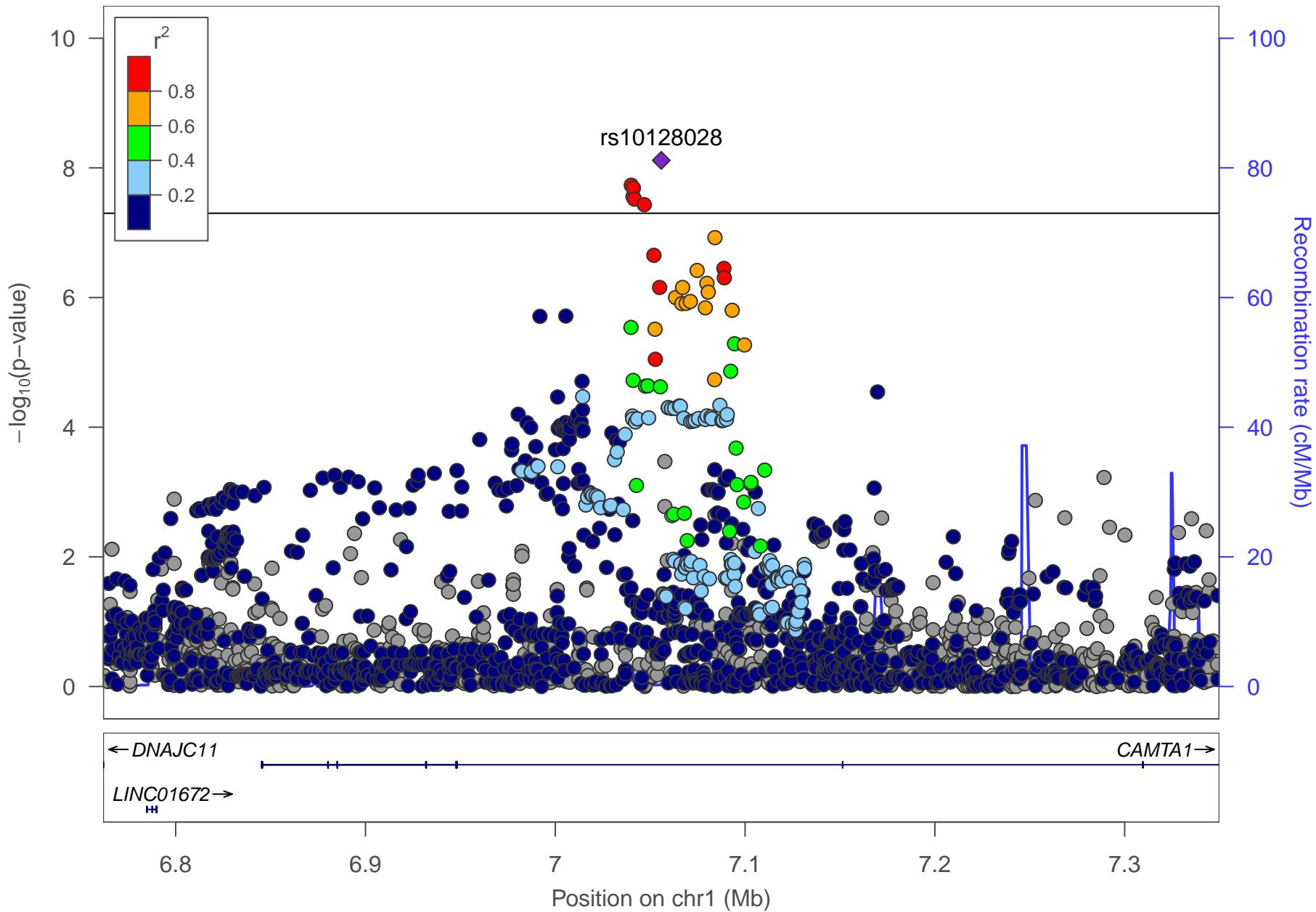
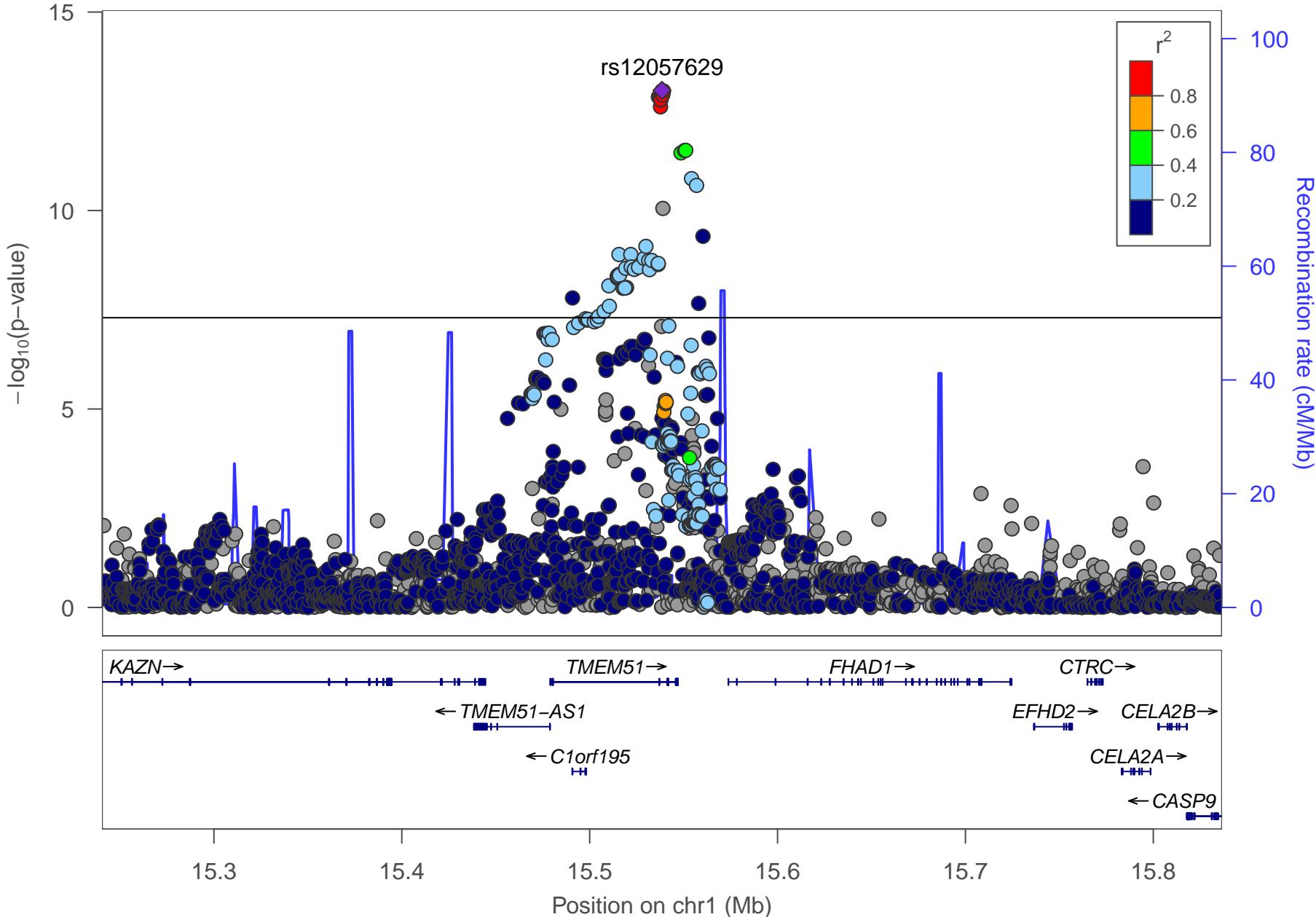


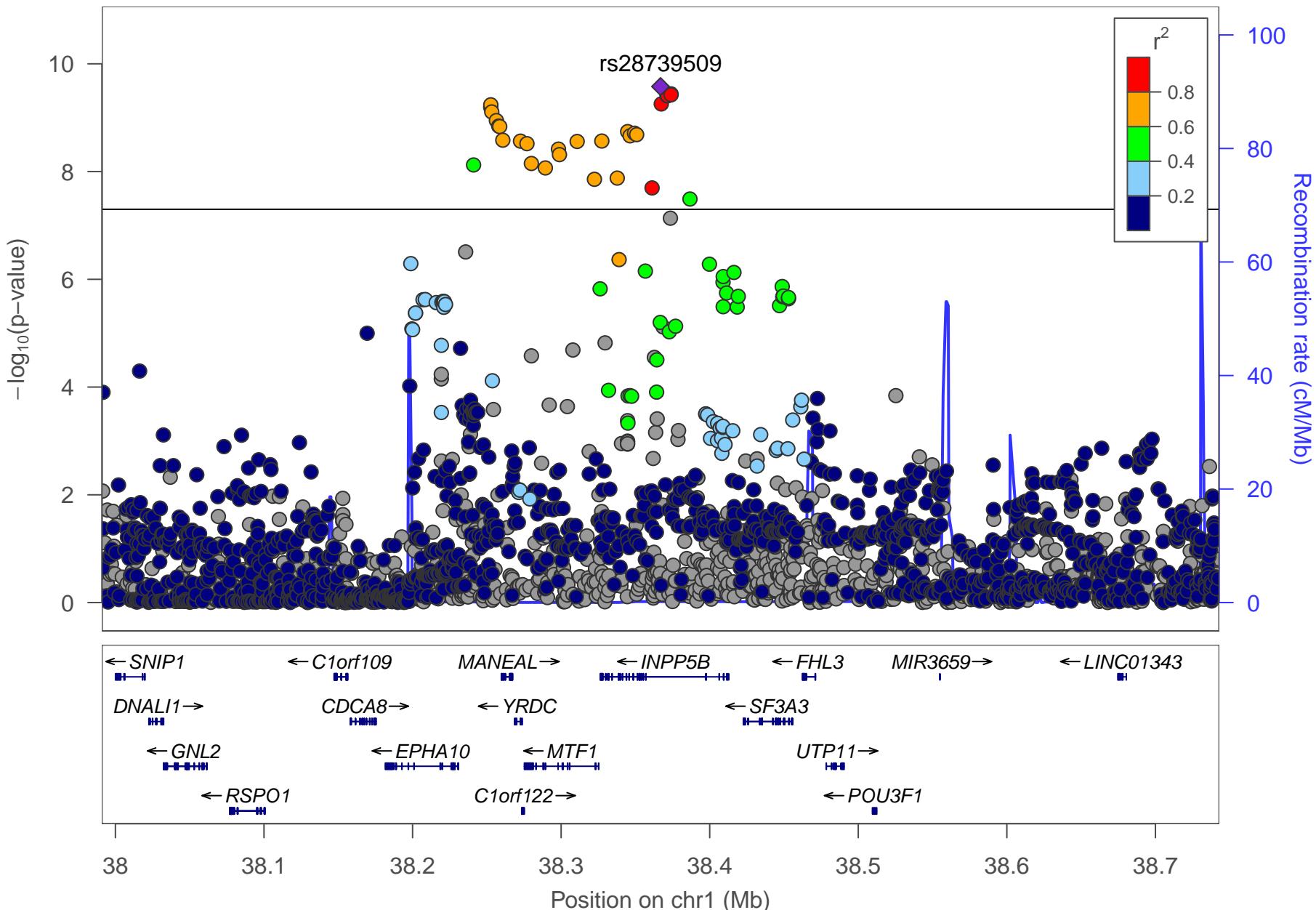
Supplementary Data 1. Regional Locuszoom-plots of the 123 independent migraine risk loci identified from the meta-analysis (N = 873,341; 102,084 cases and 771,257 controls).

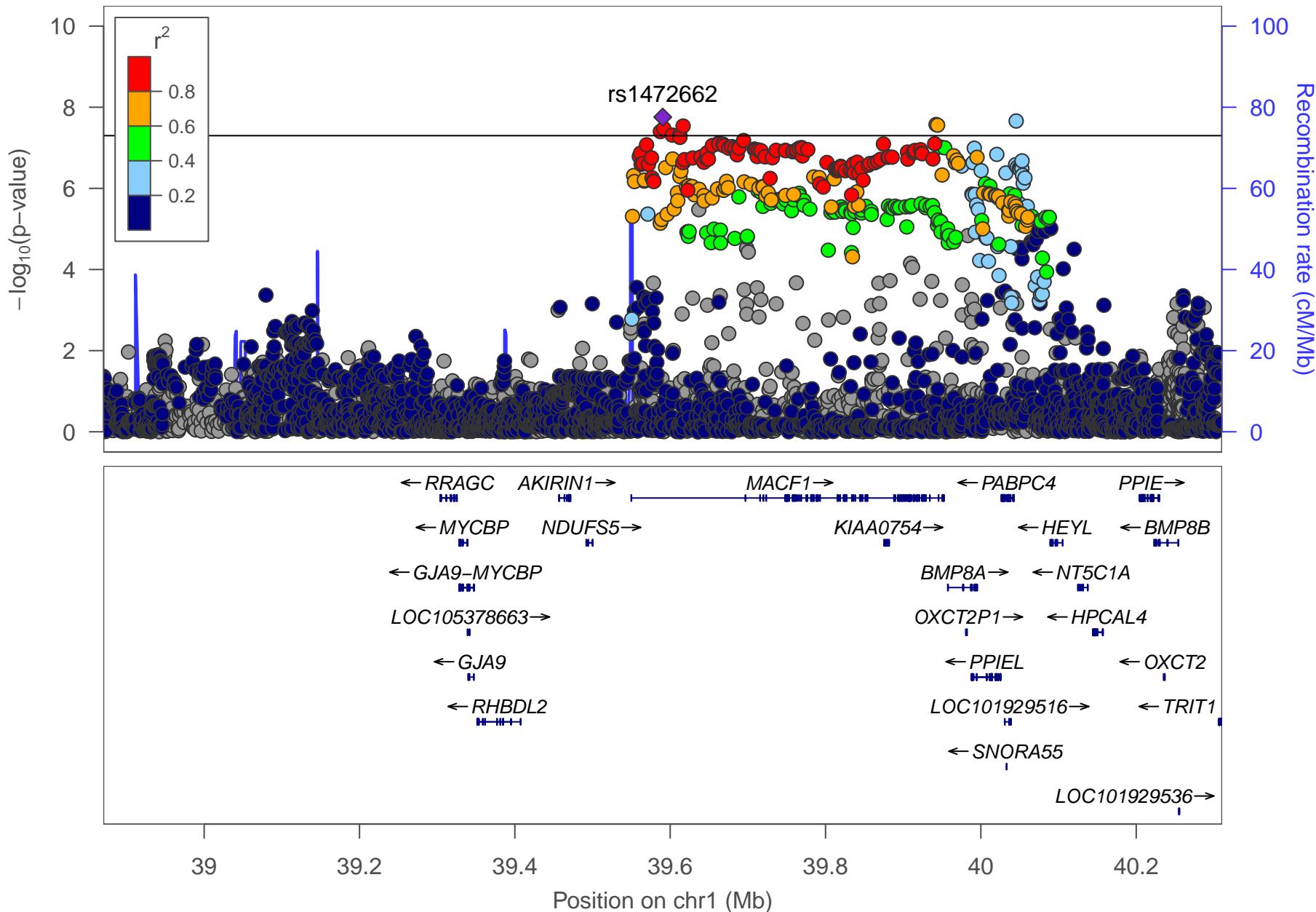
X-axis shows the chromosomal location, and Y-axis shows the strength of the association as uncorrected two-sided negative log₁₀ P-value from the inverse-variance weighted fixed-effects meta-analysis. The squared correlation to the lead variant is shown by colors based on the UK Biobank data for variants that have an effective sample size $\pm 20\%$ of the lead variant's effective sample size. Black horizontal line corresponds to $P = 5 \times 10^{-8}$ and blue line shows the recombination rate.

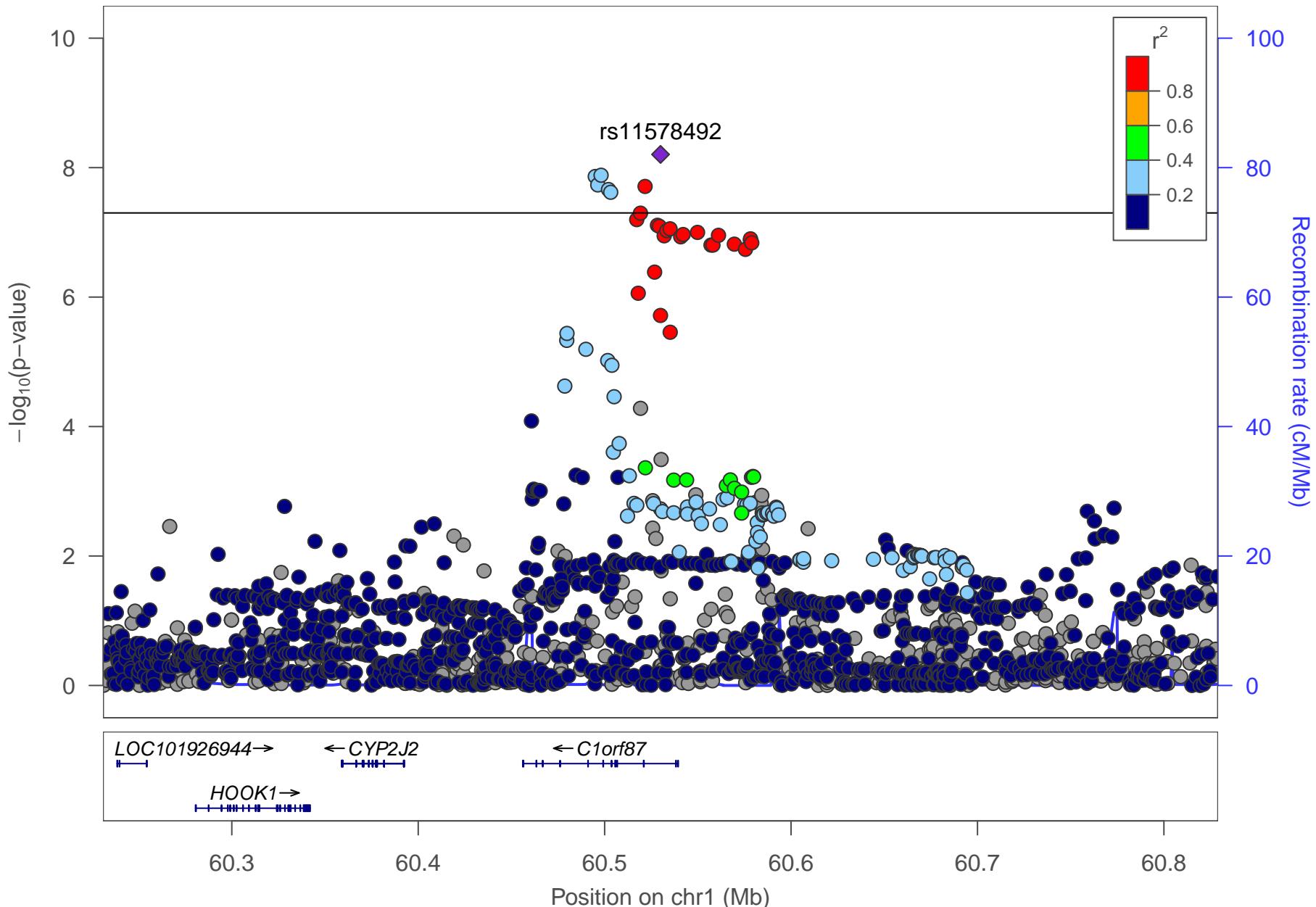


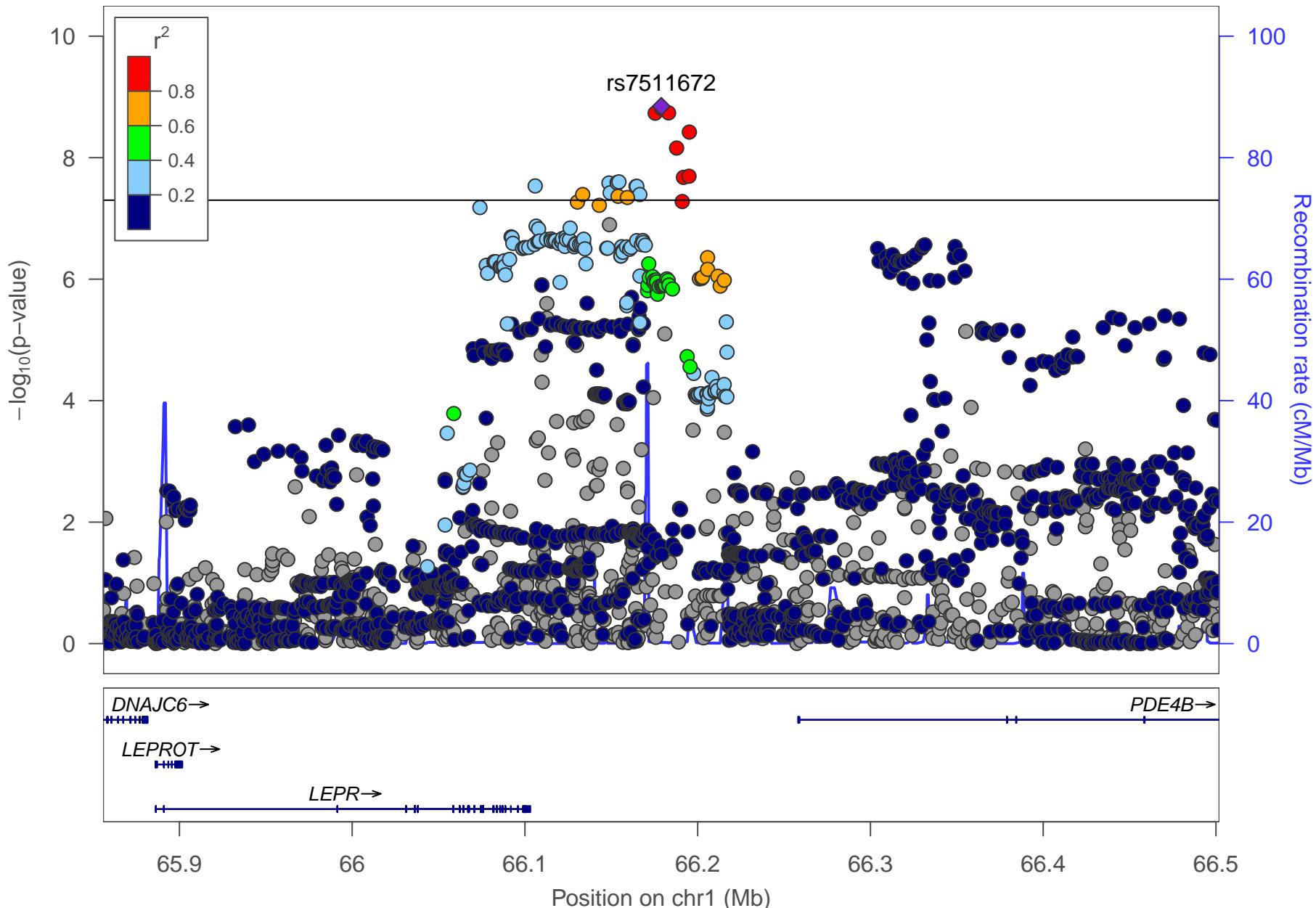


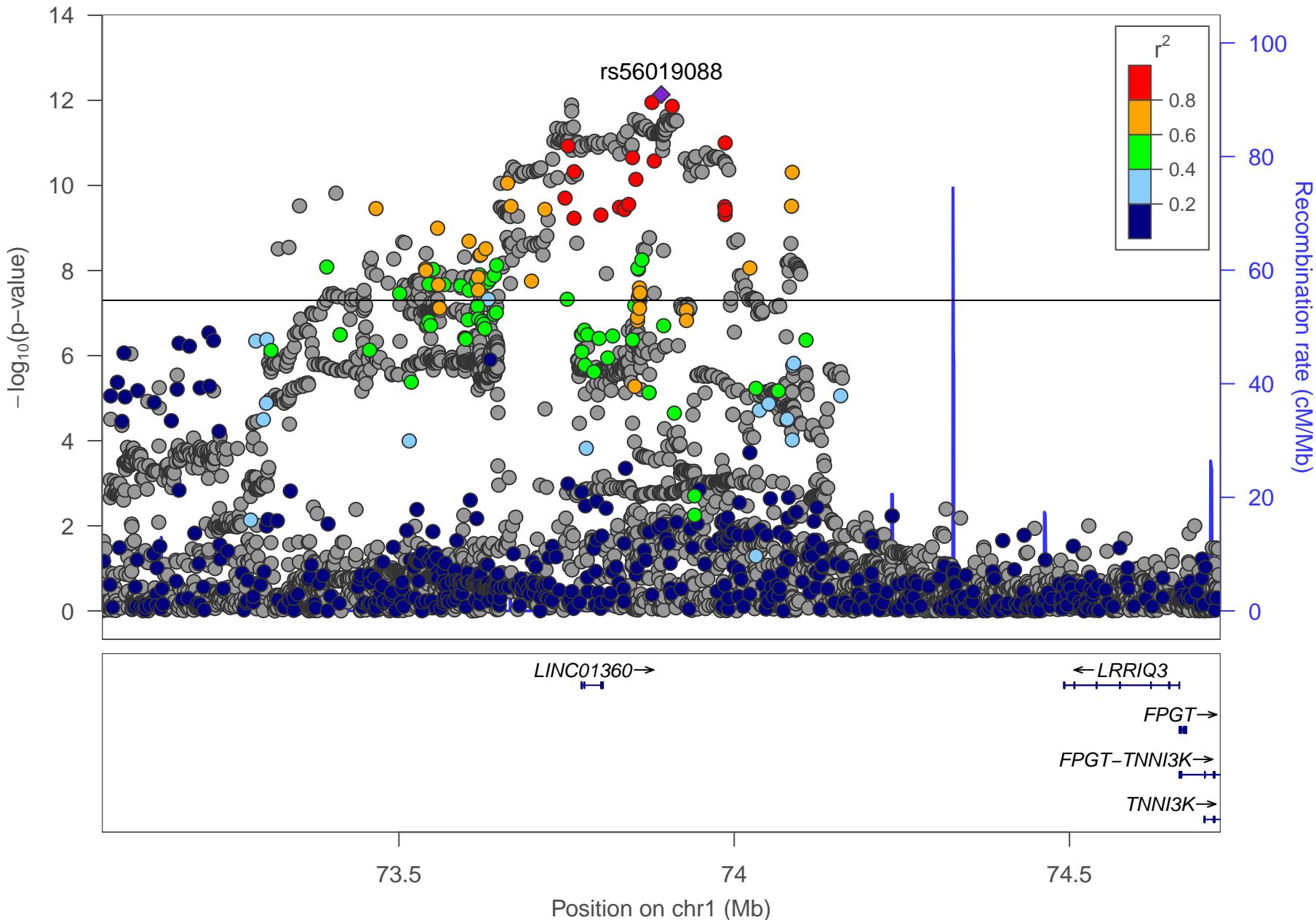


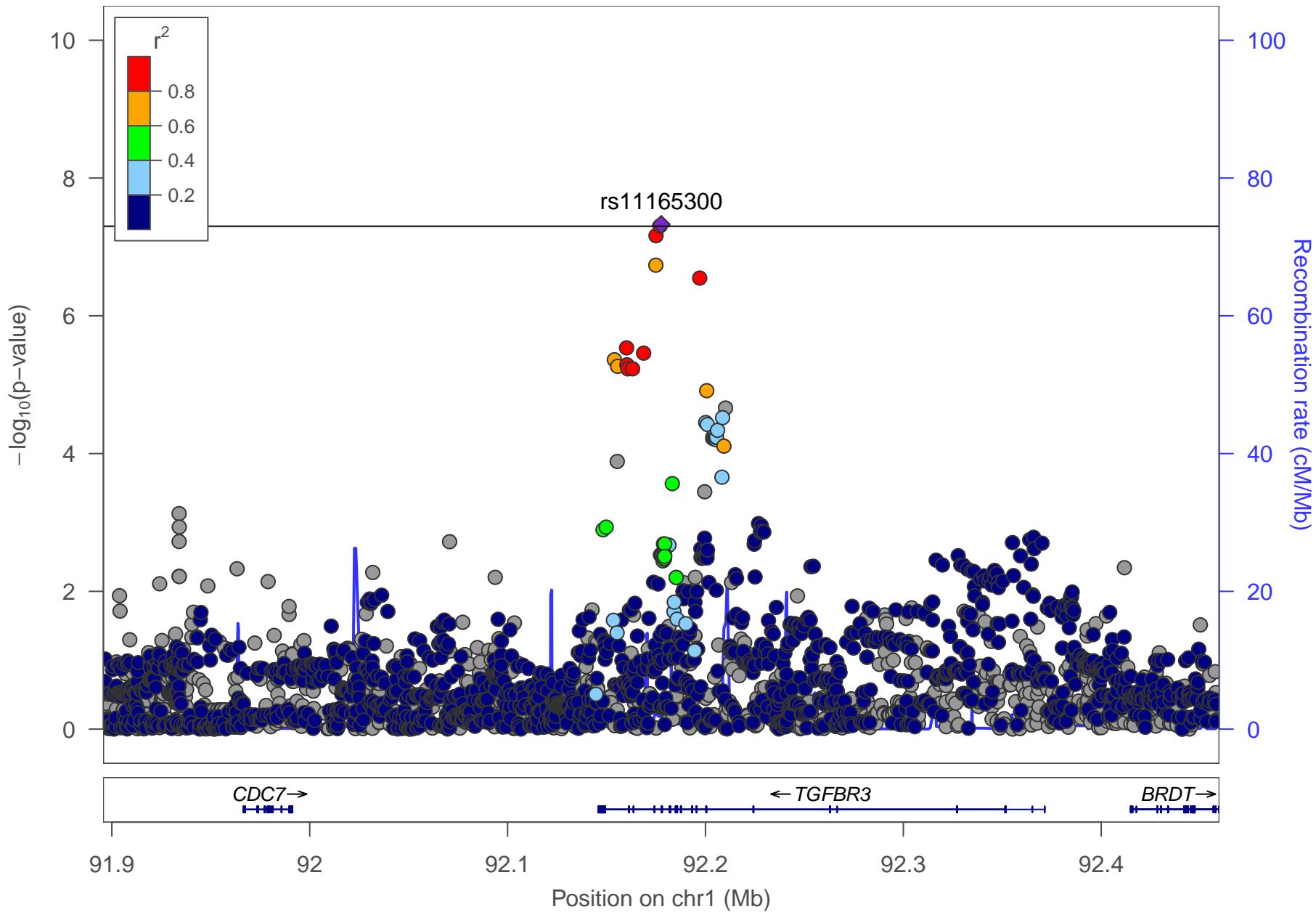


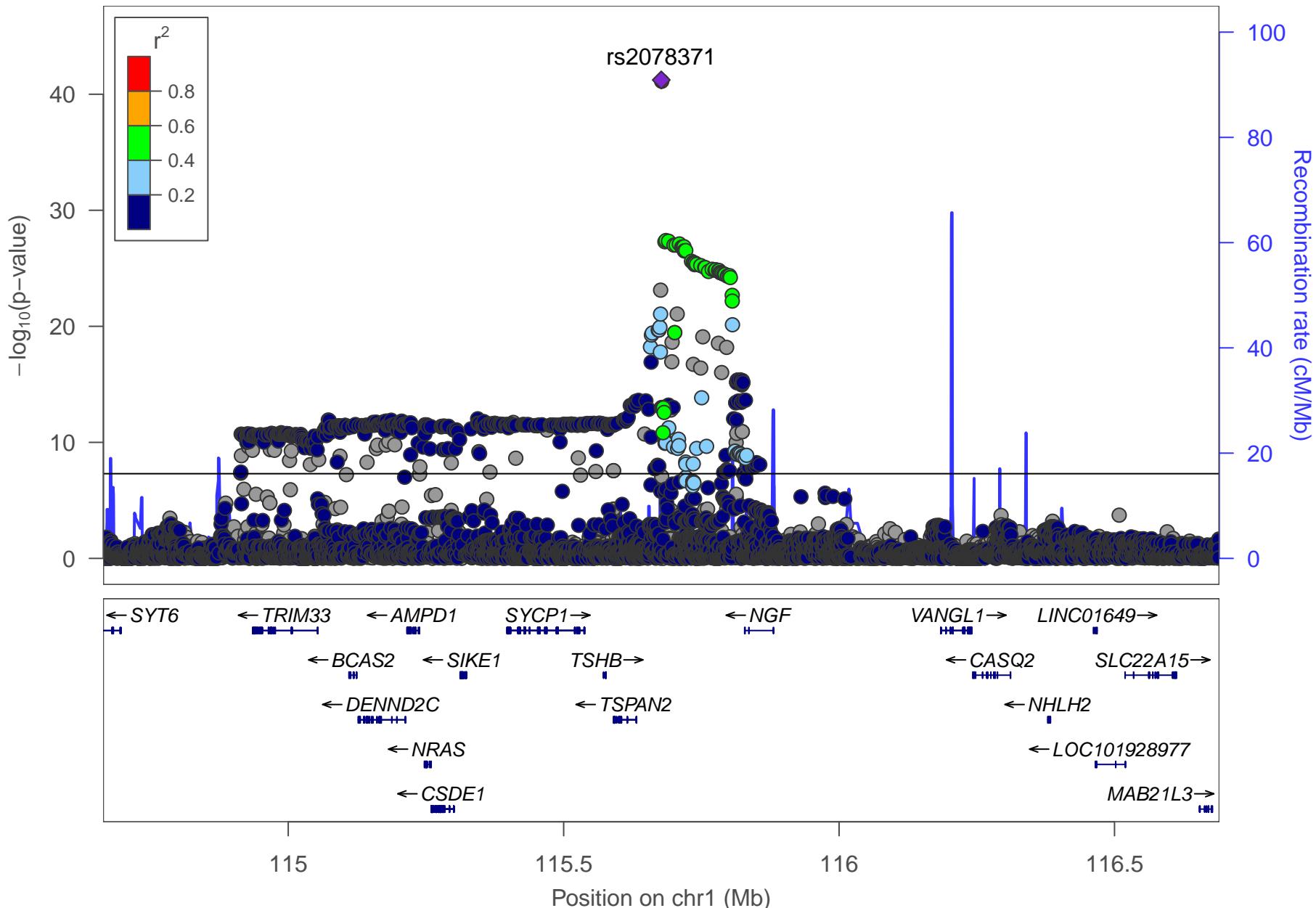


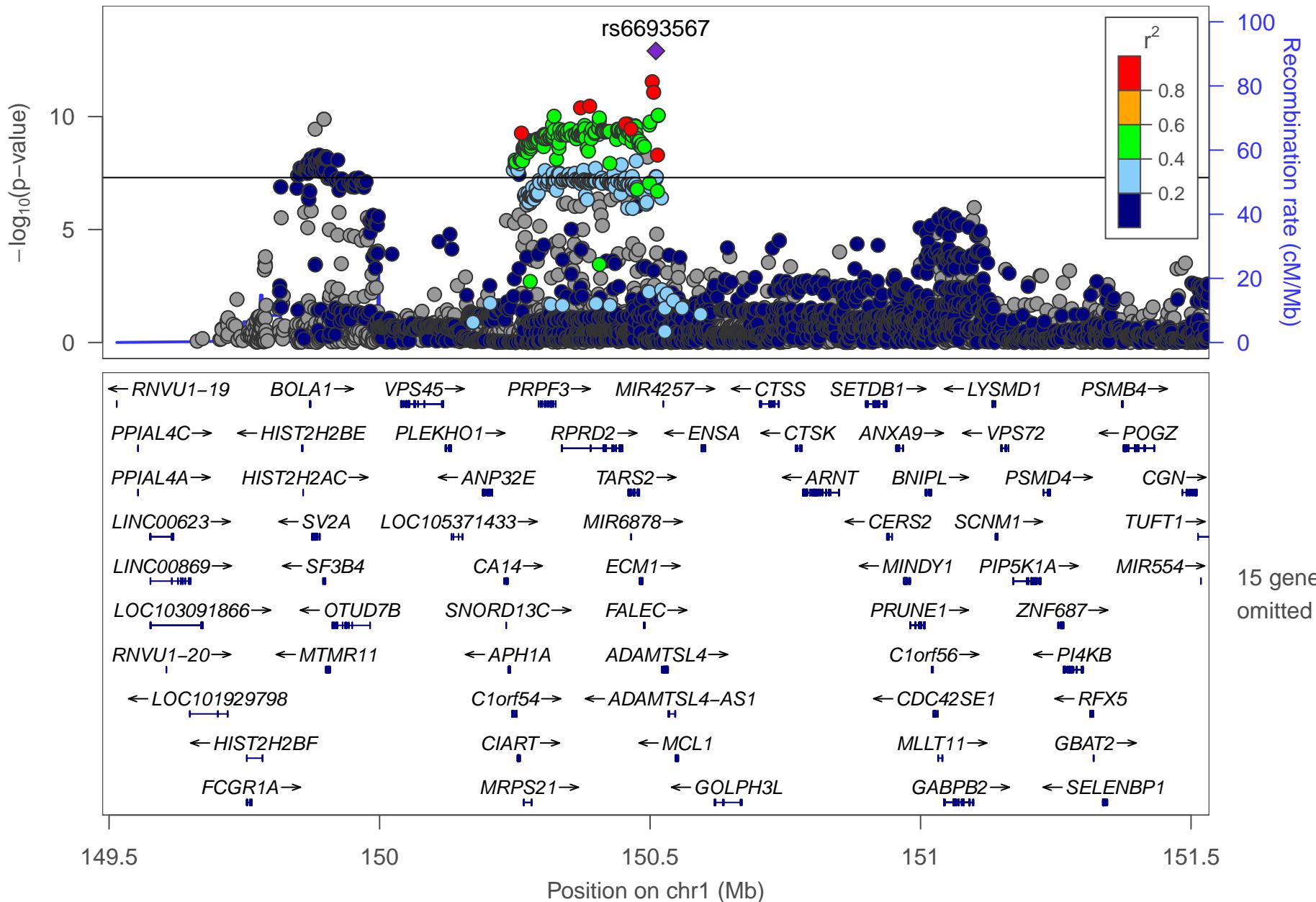


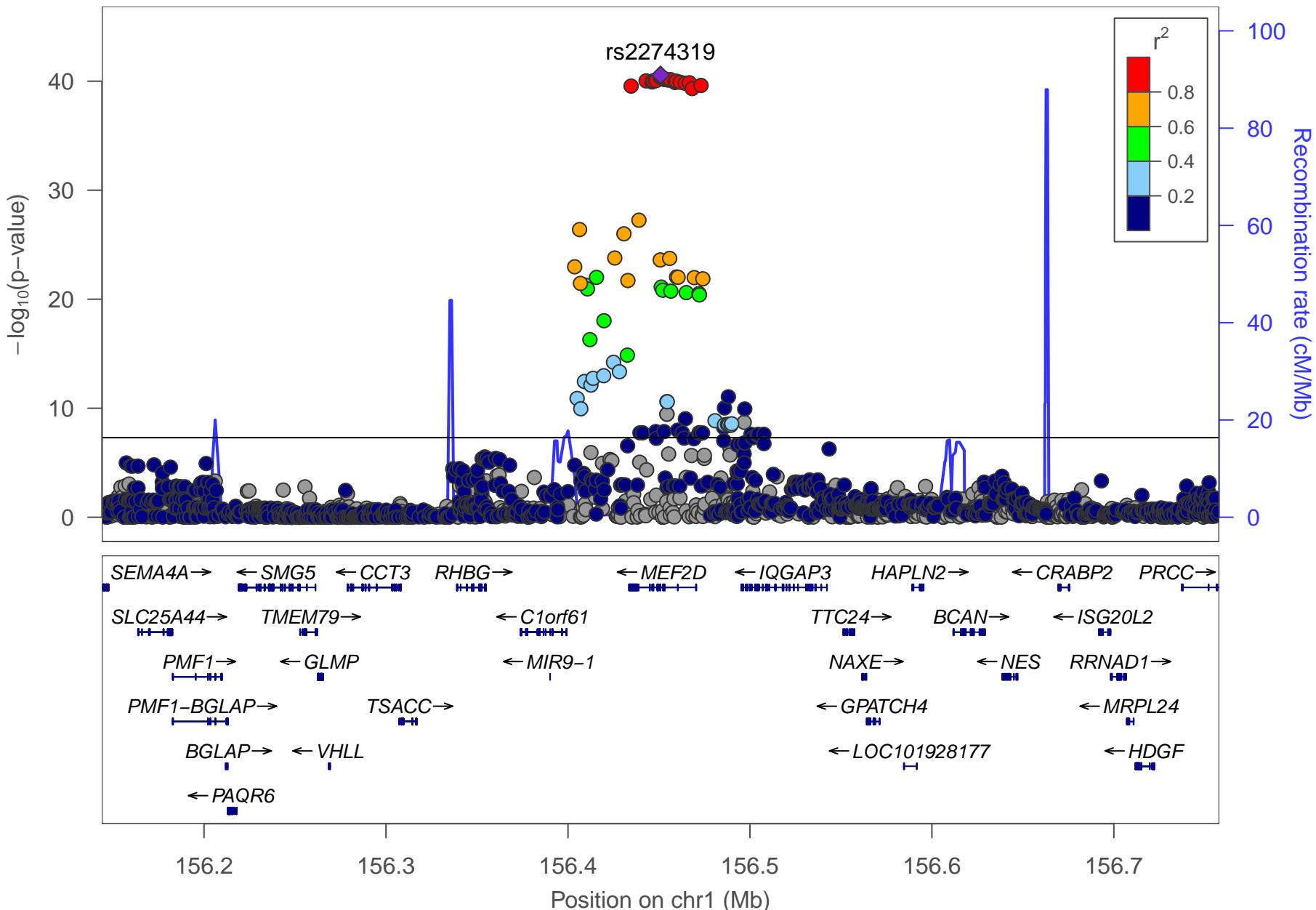


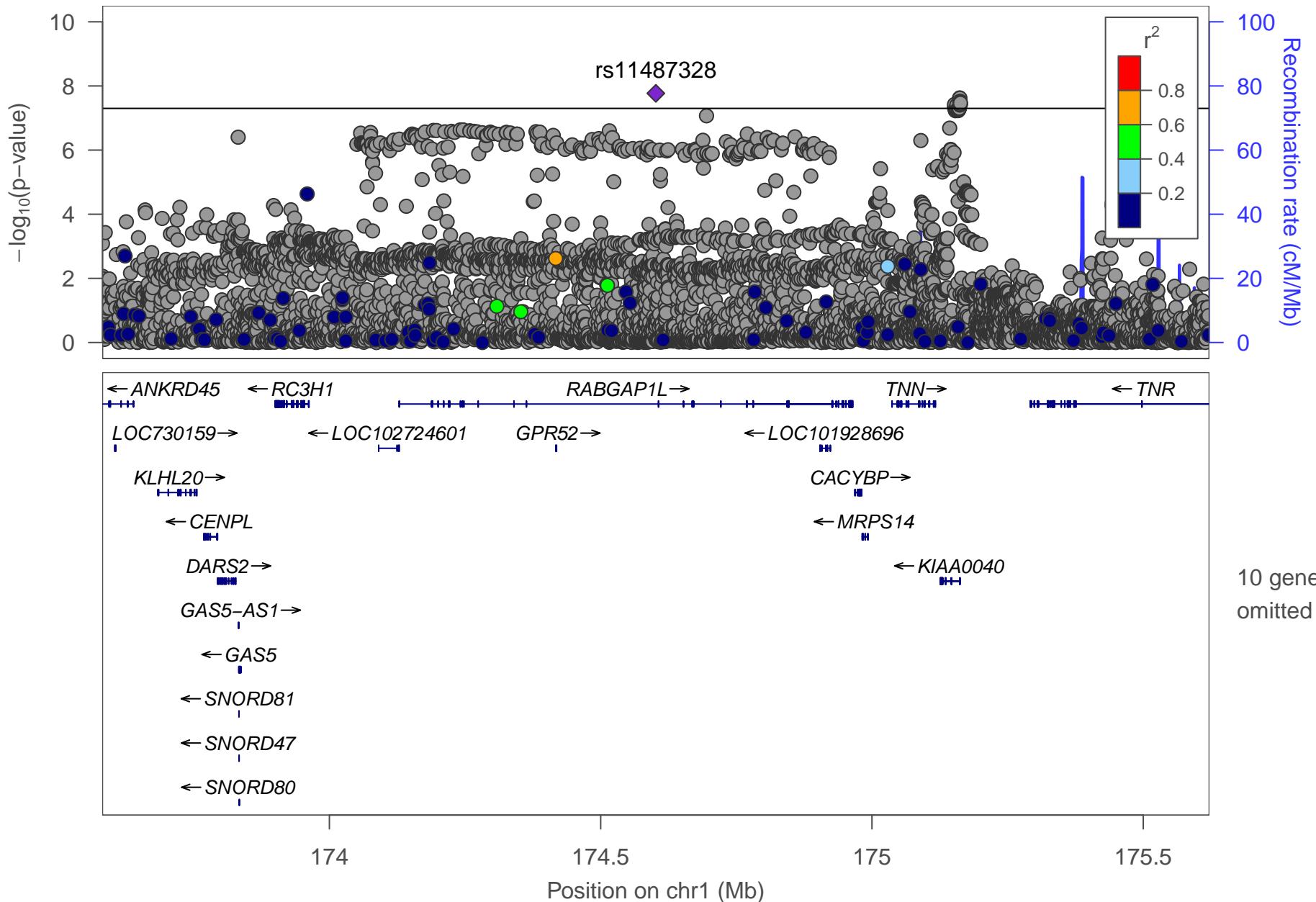


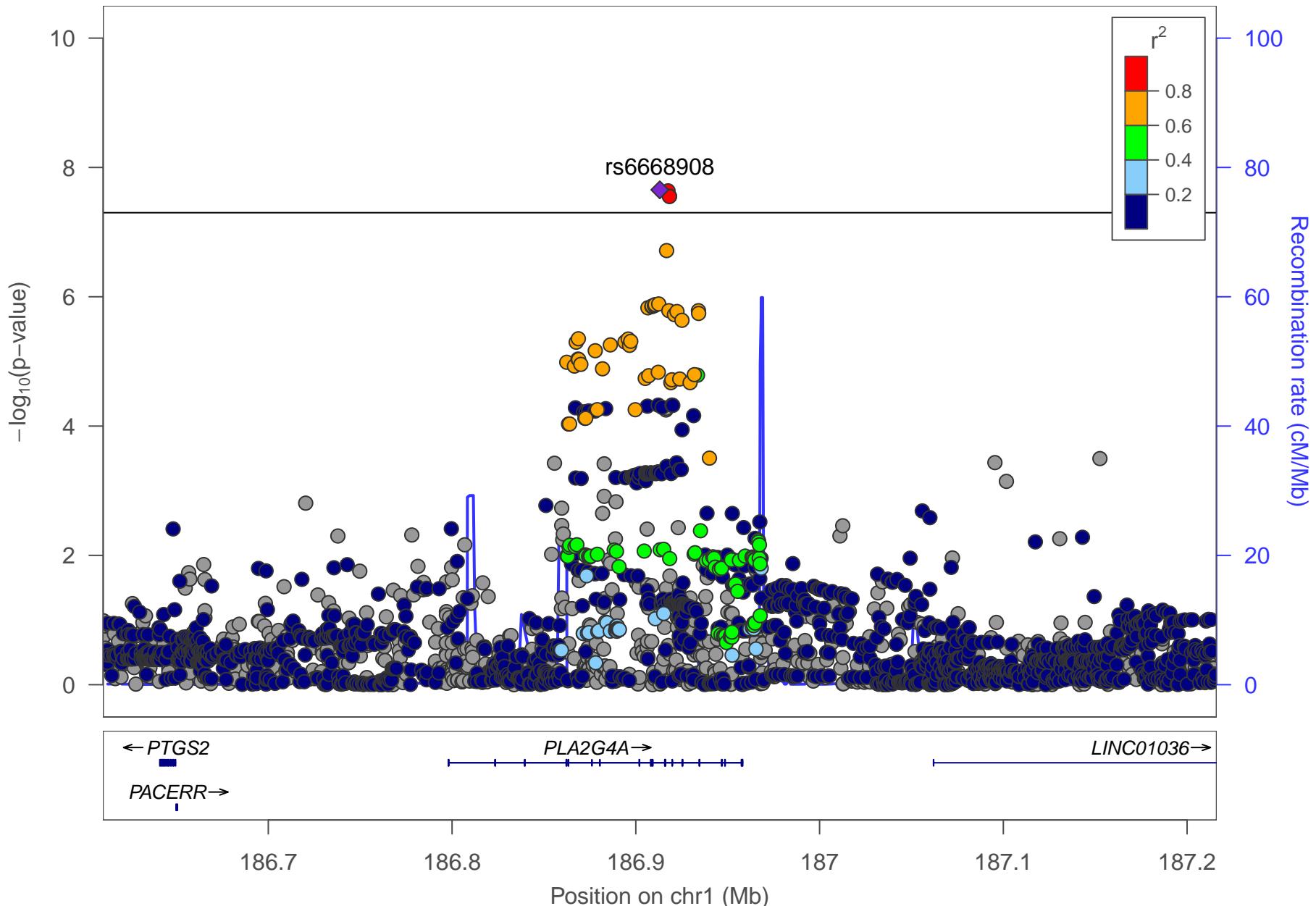


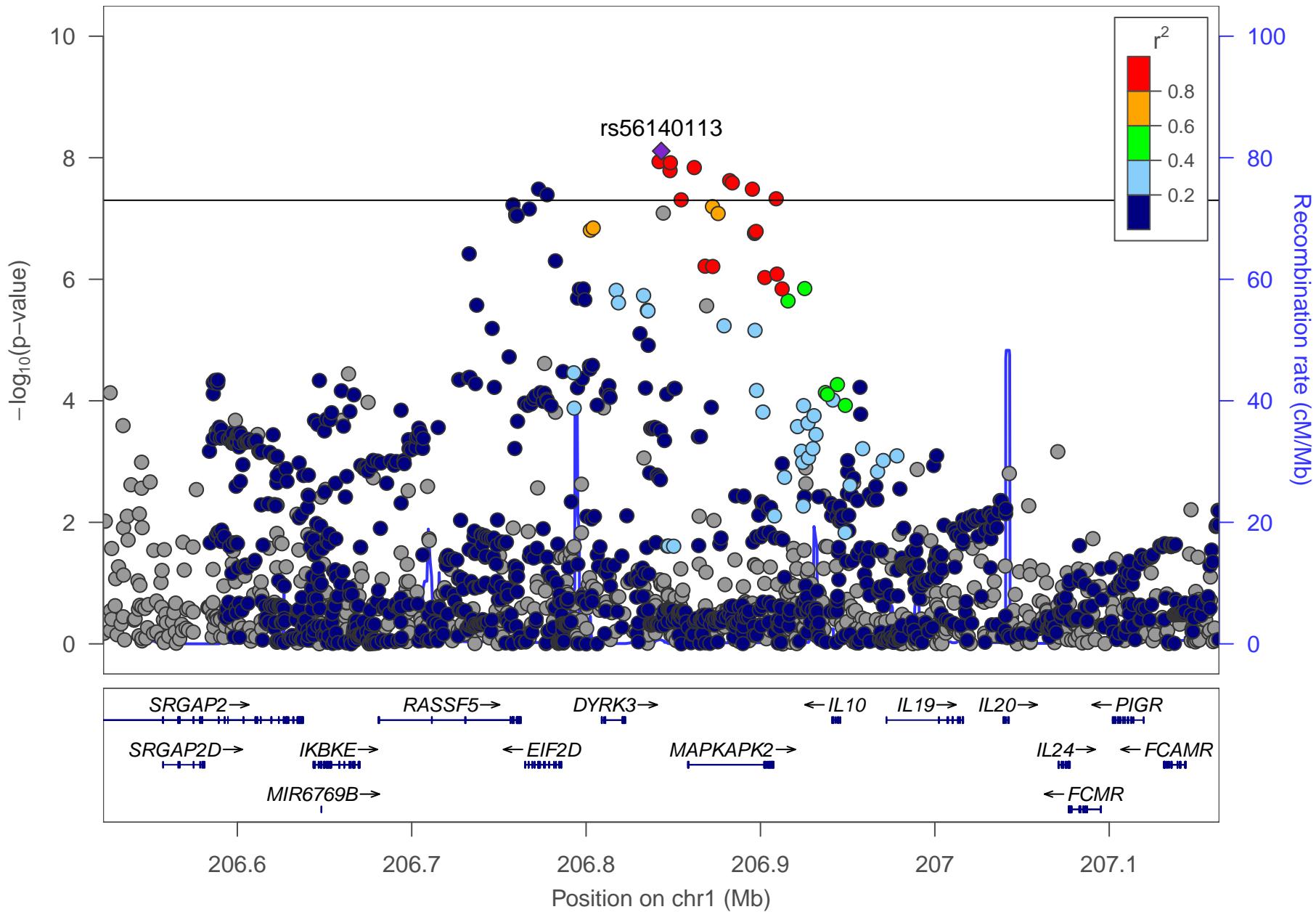


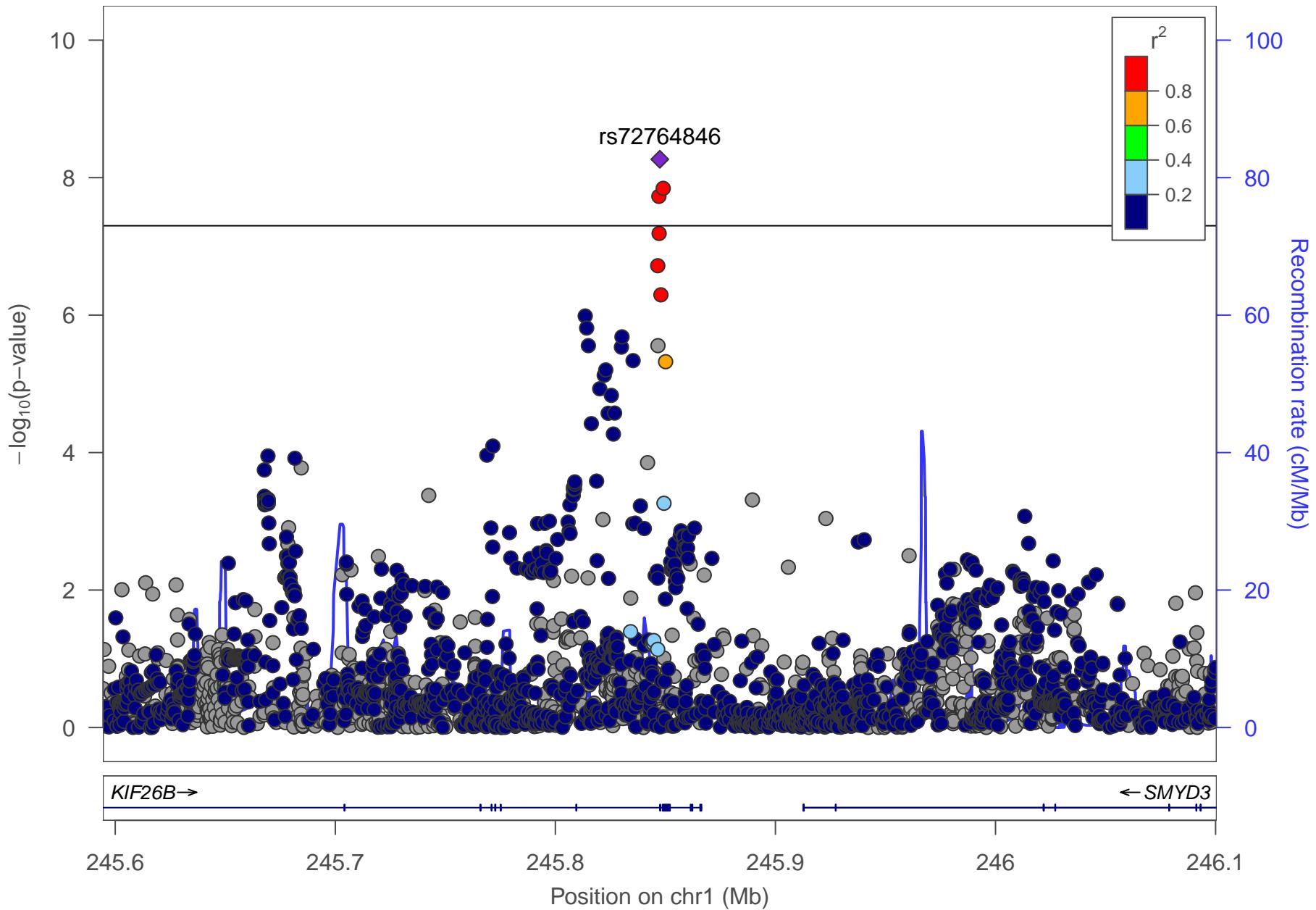


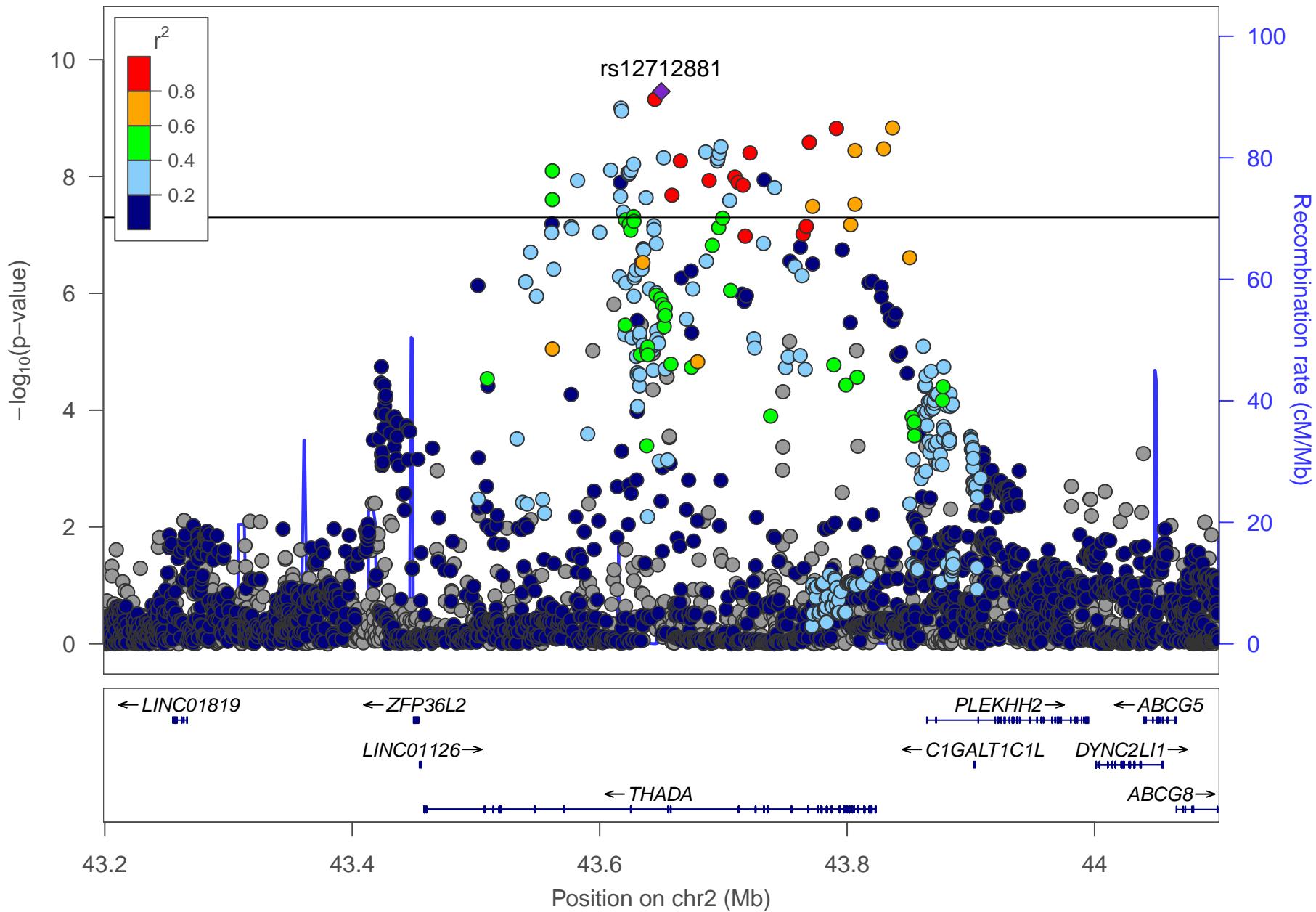


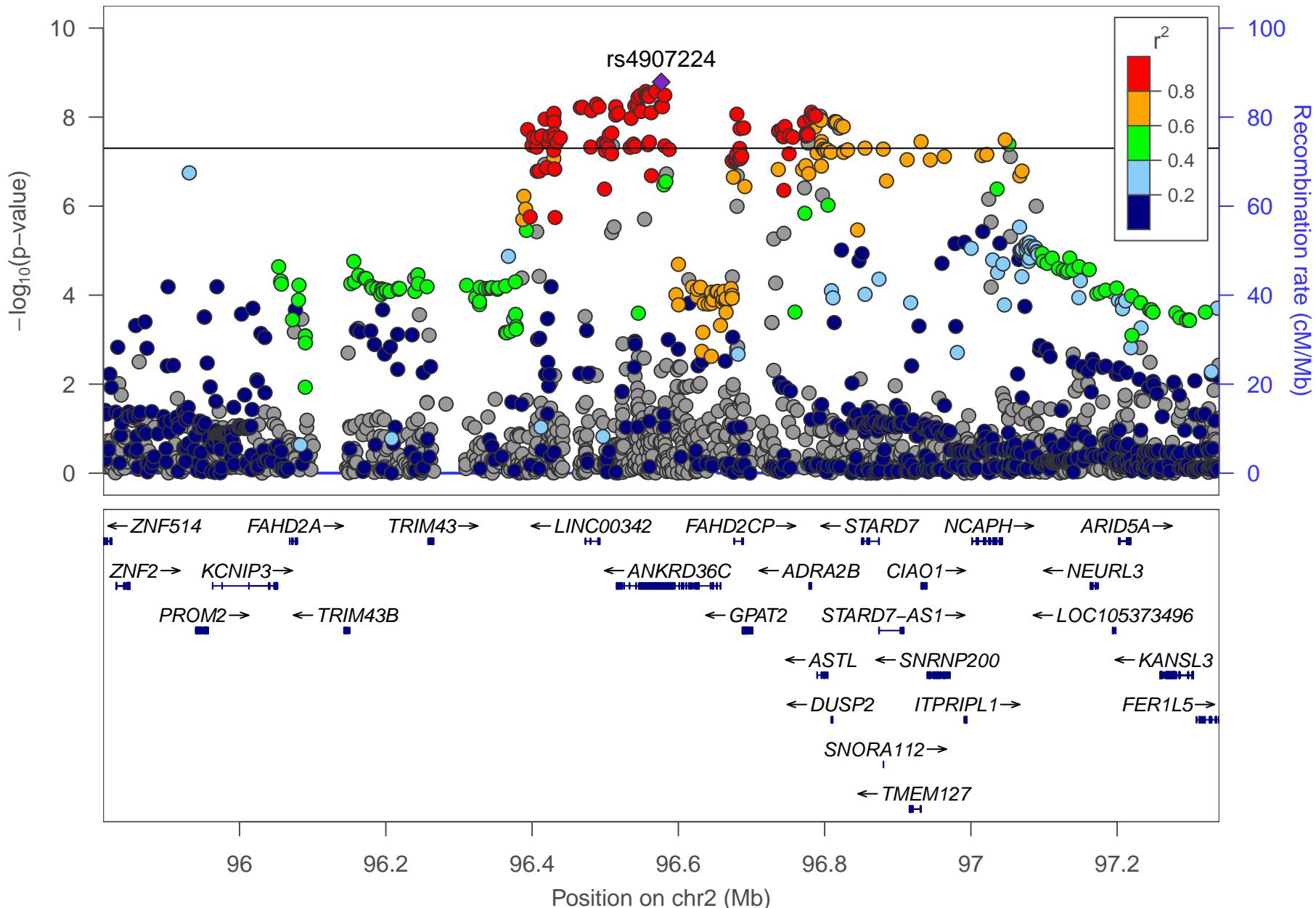


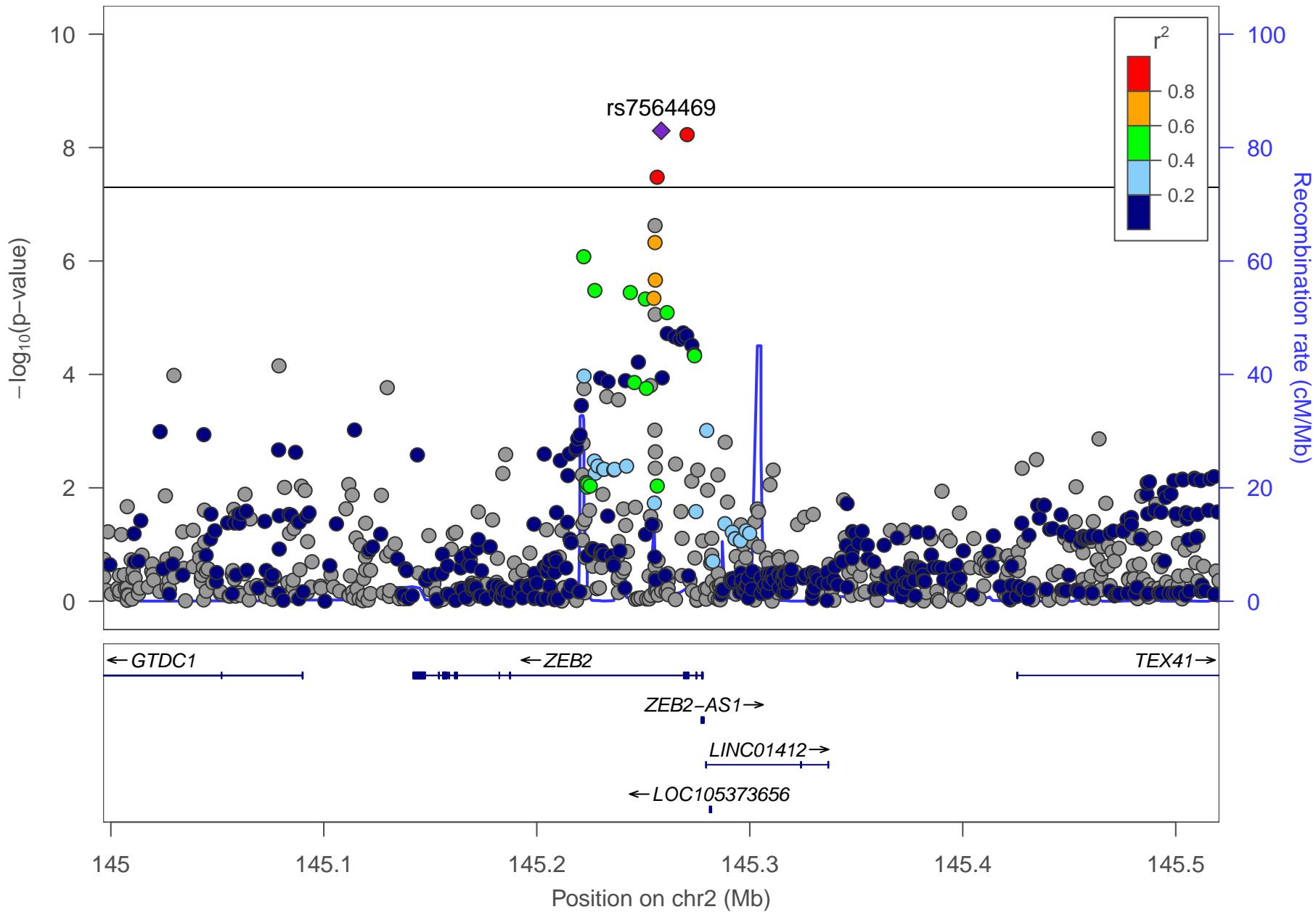


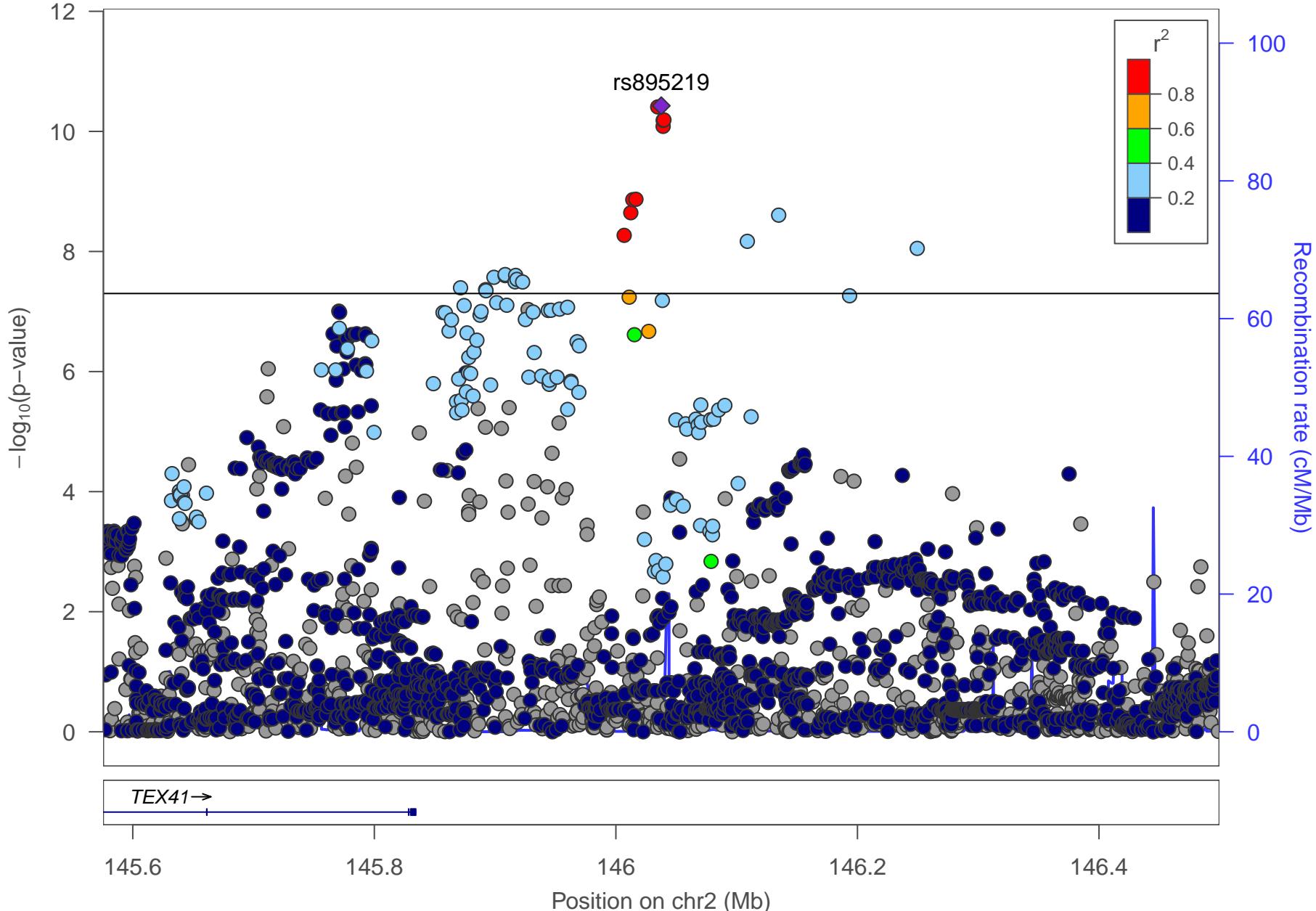


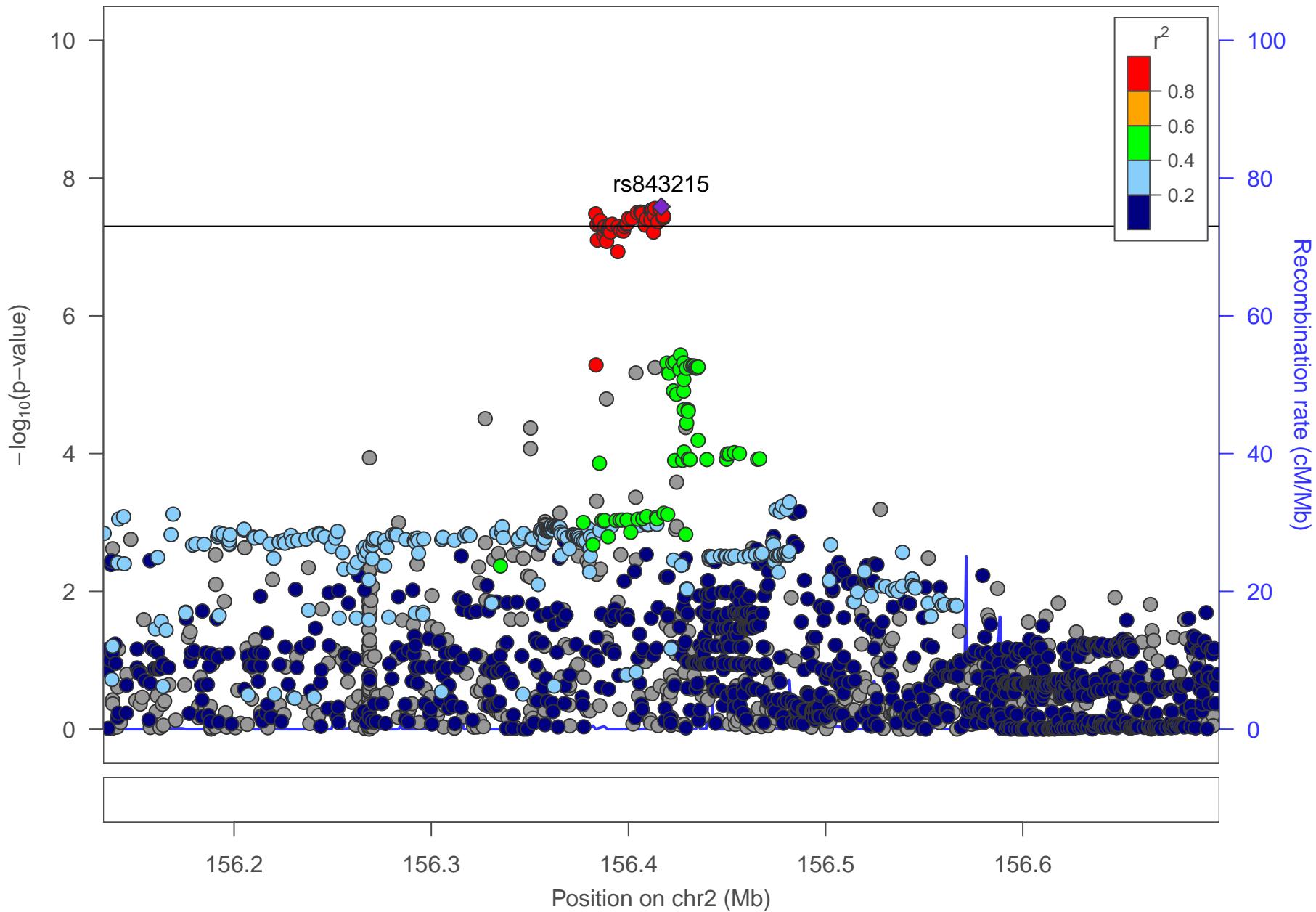


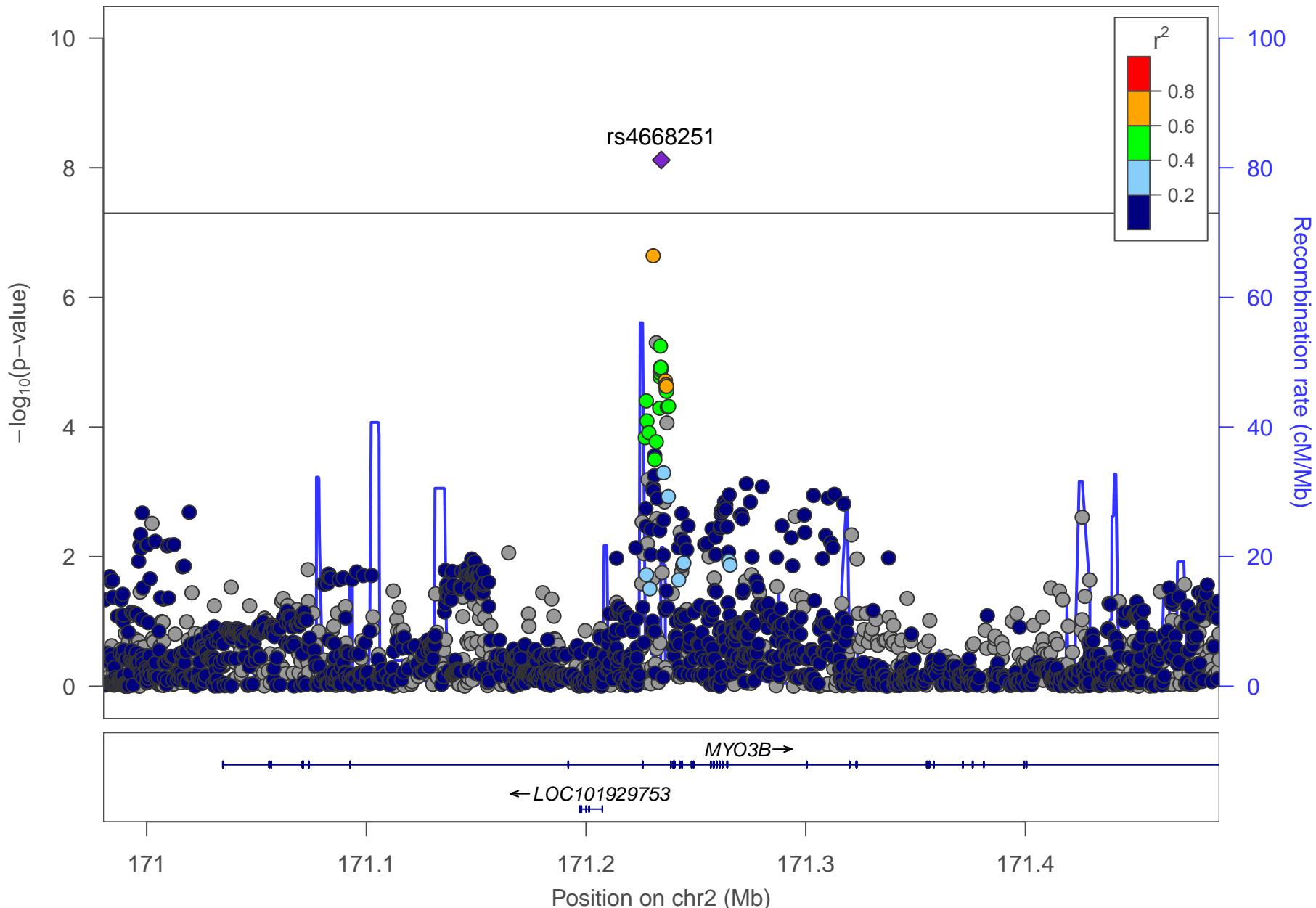


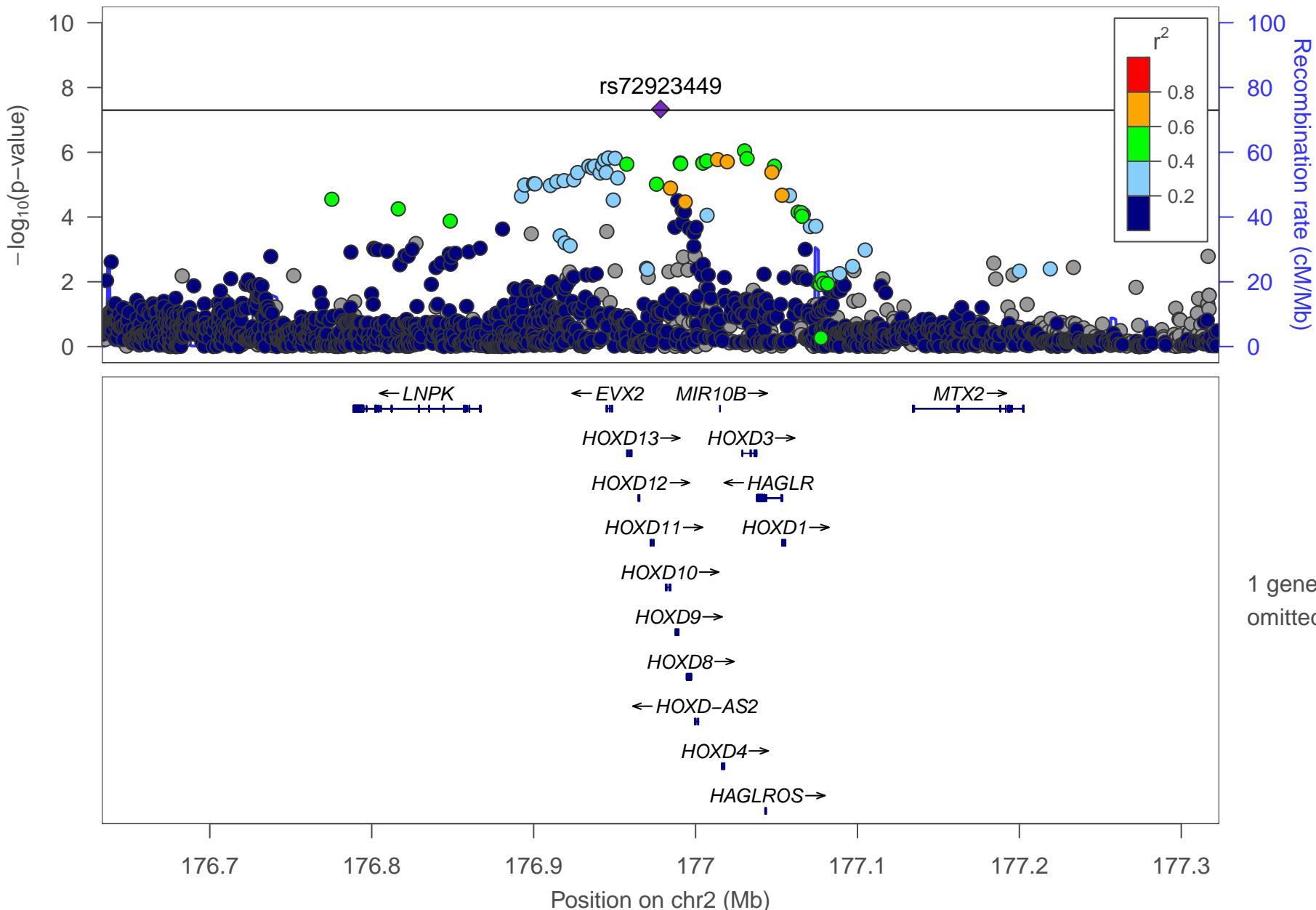


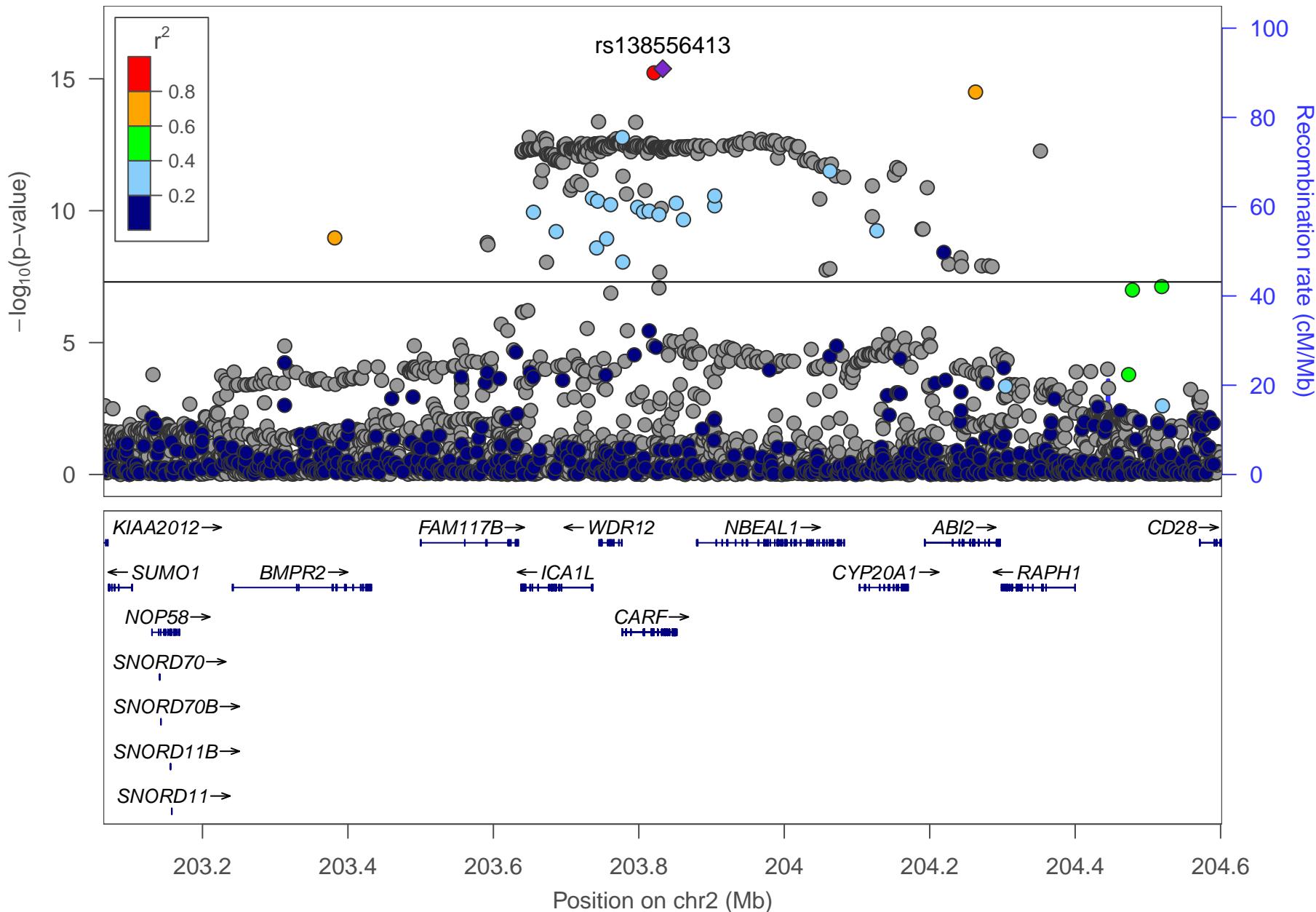


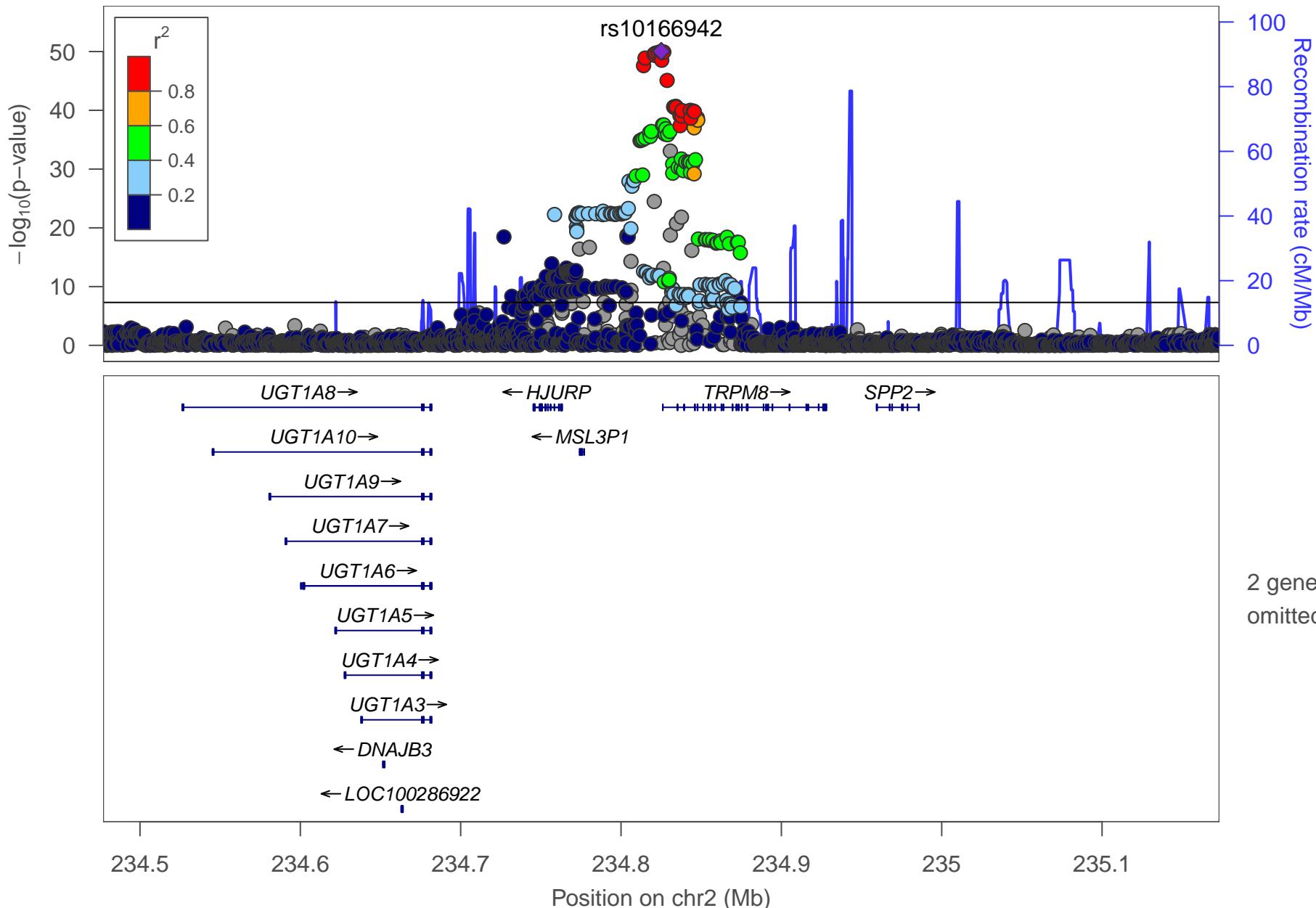


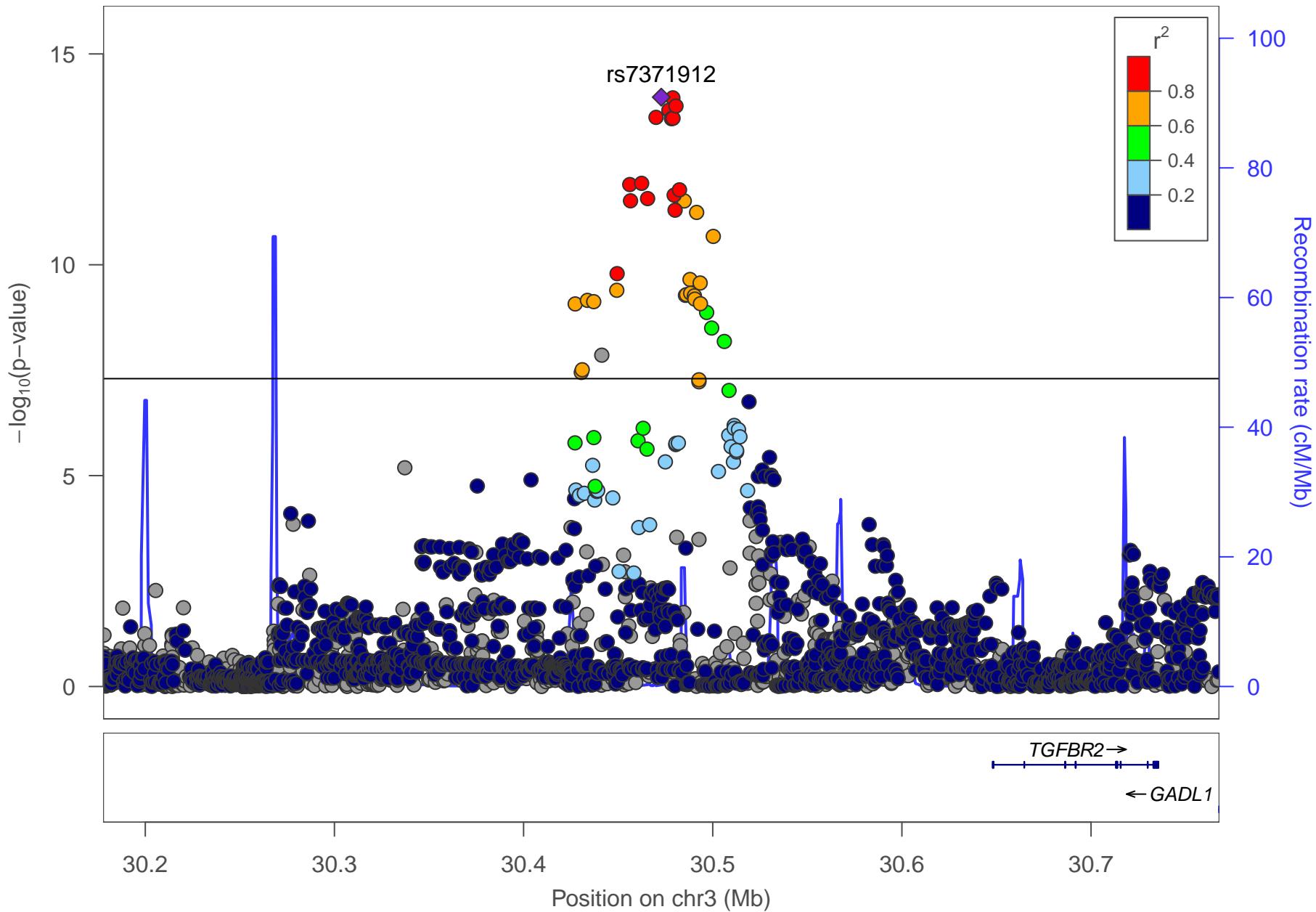


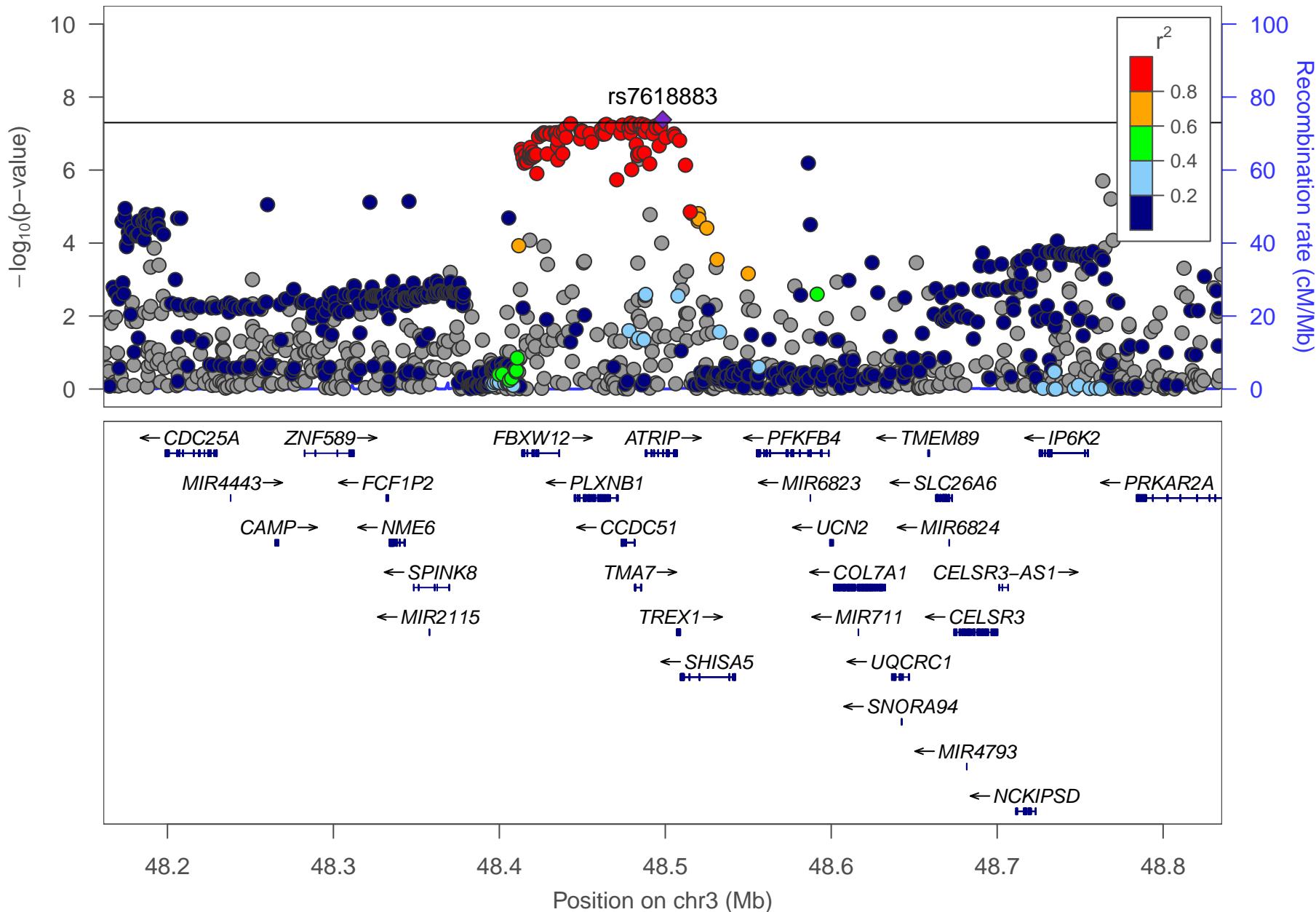


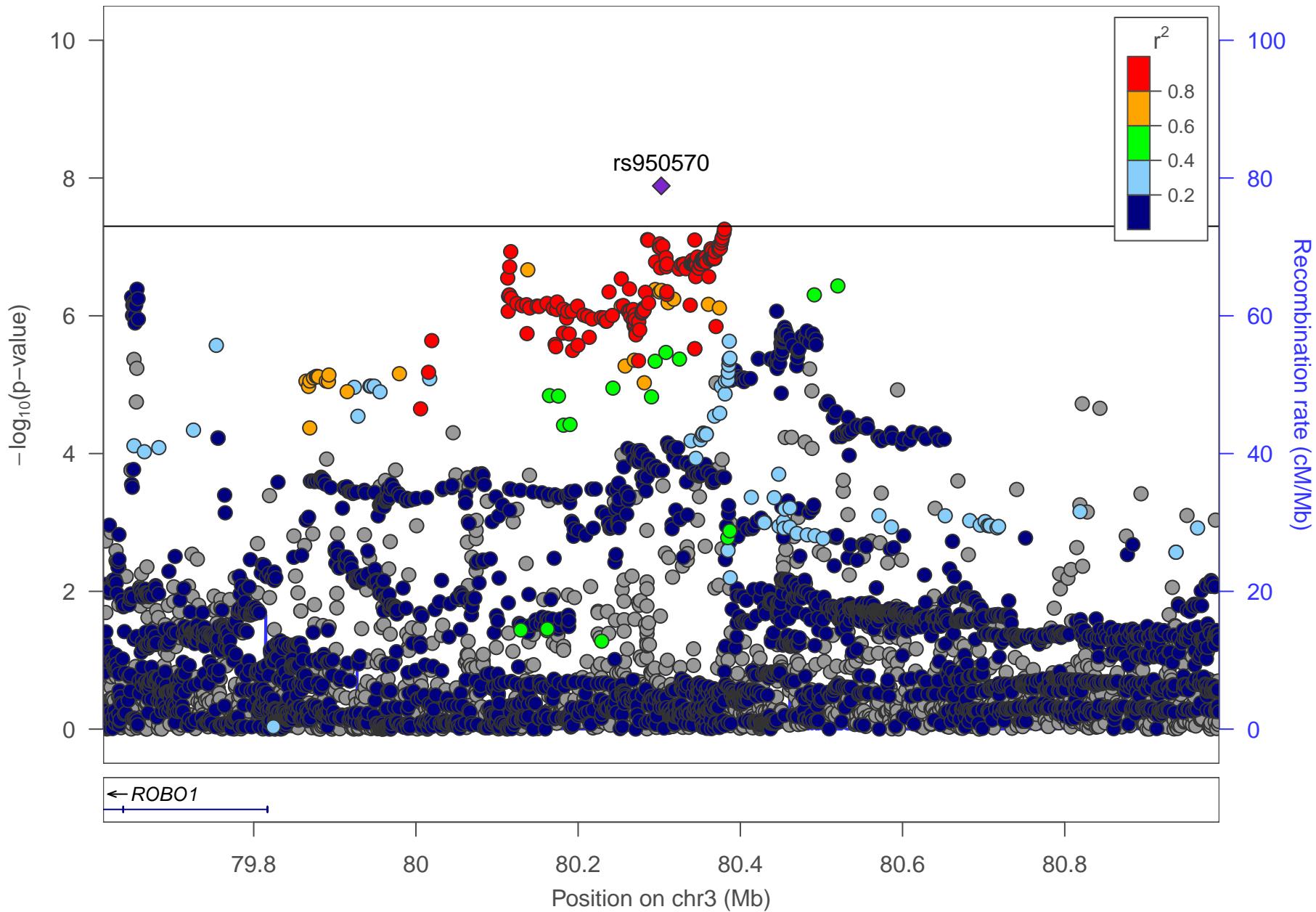


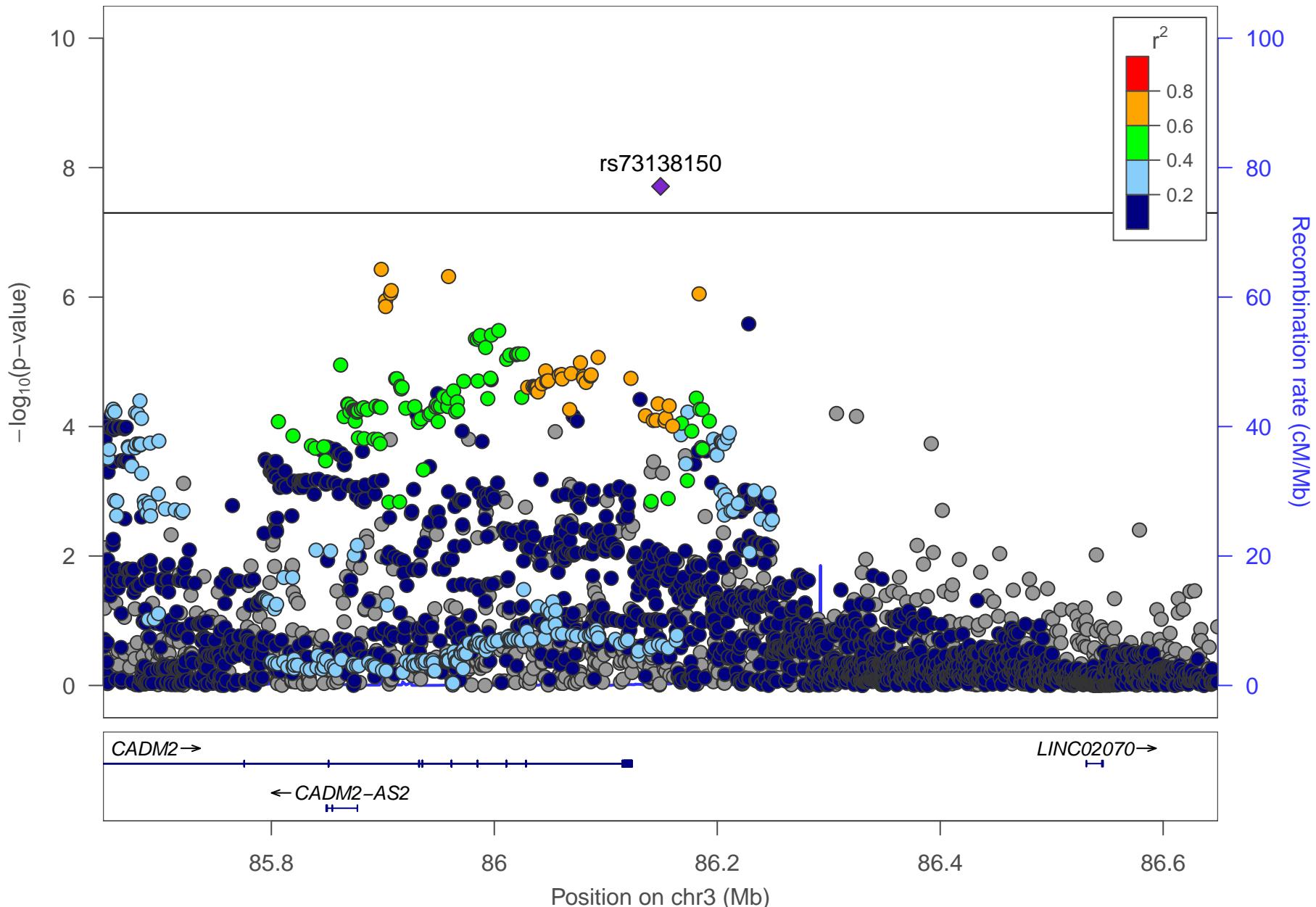


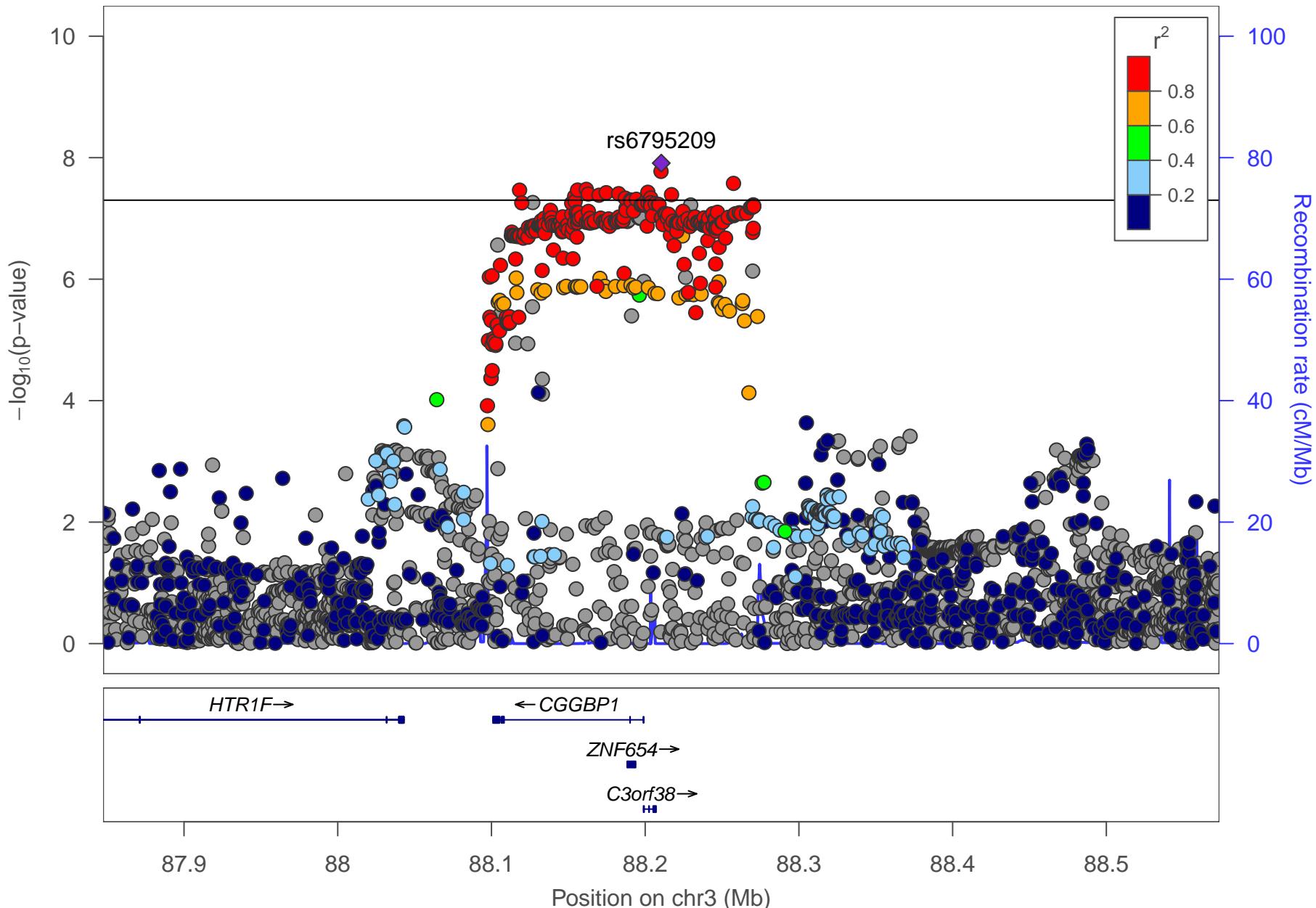


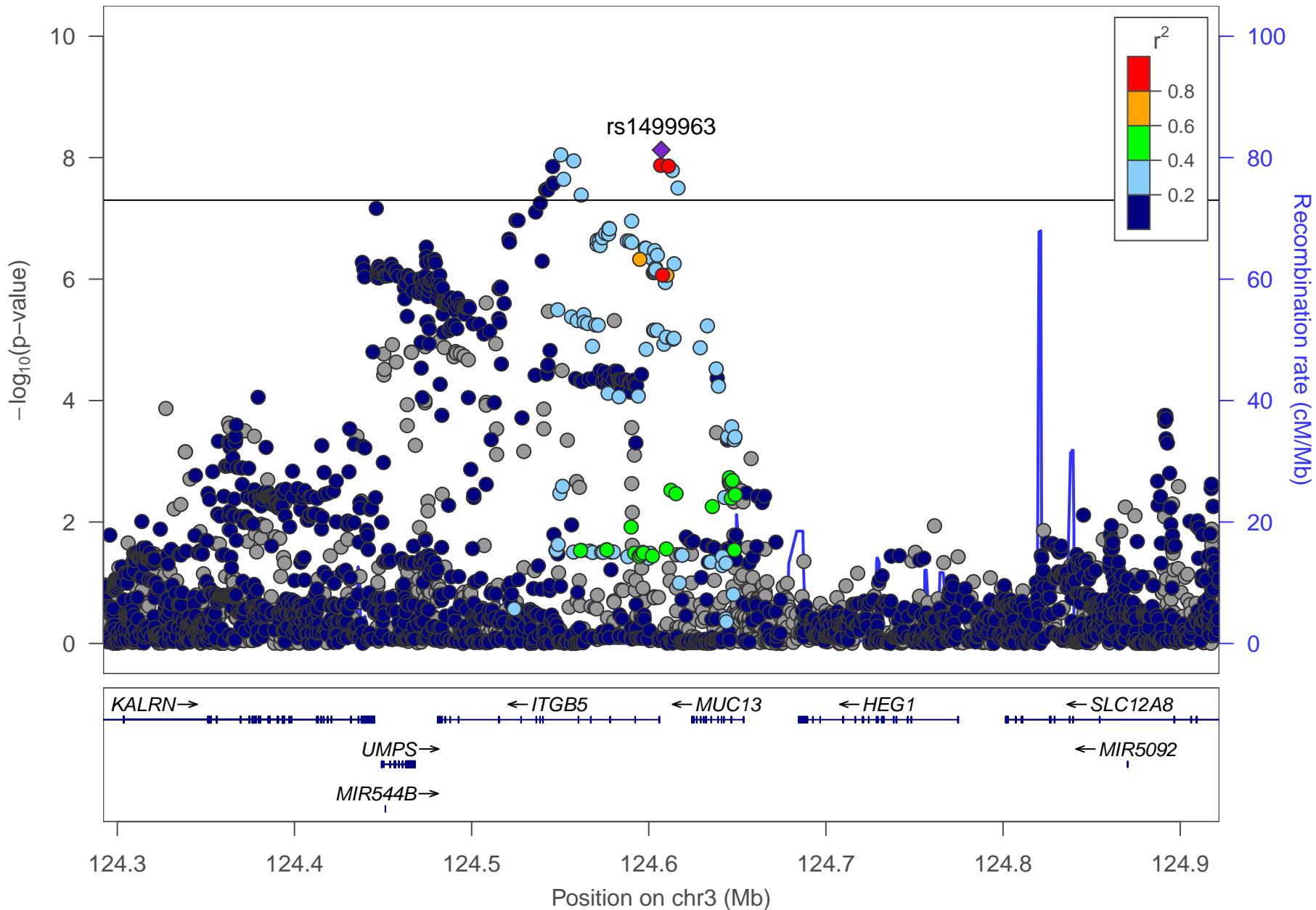


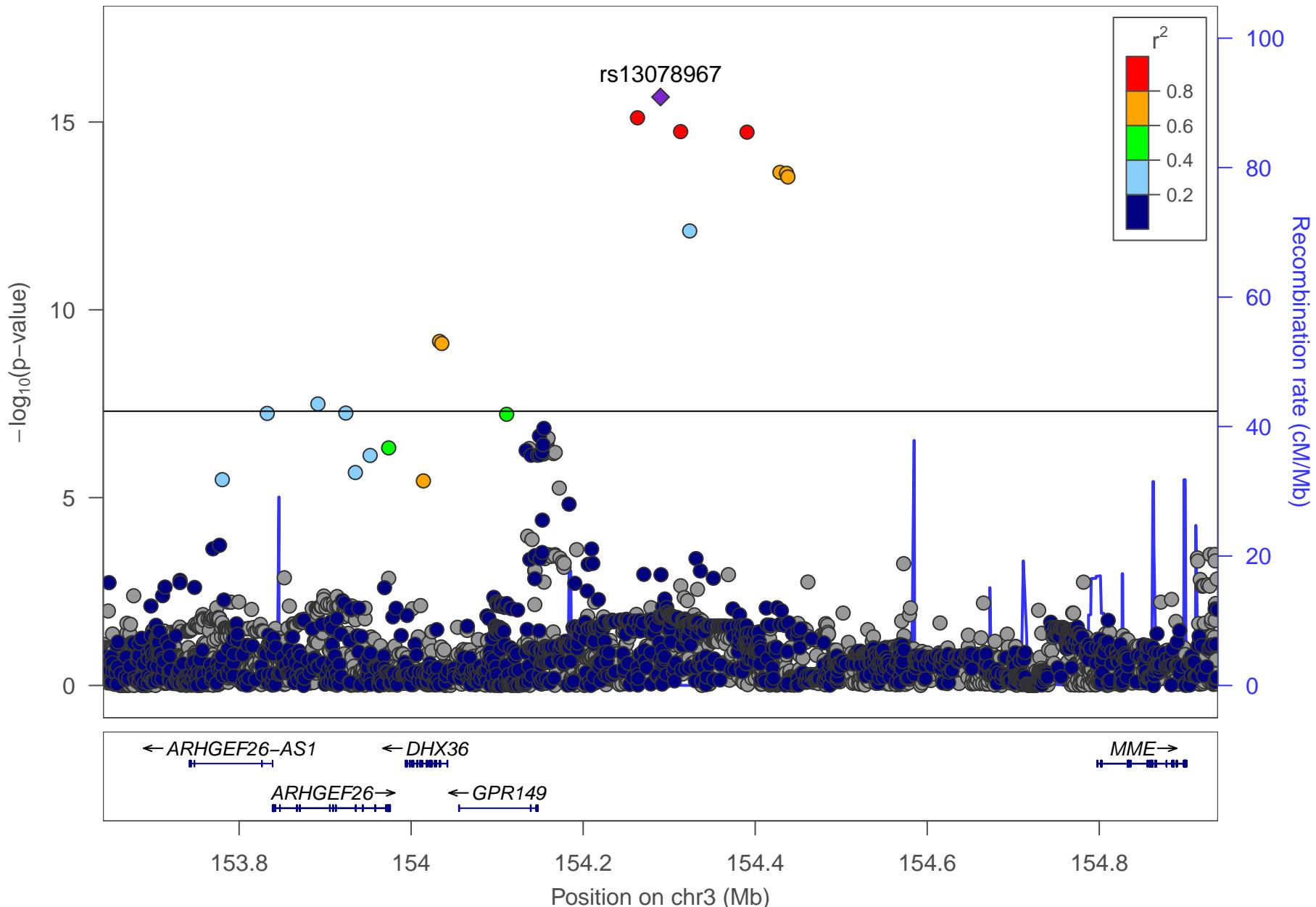


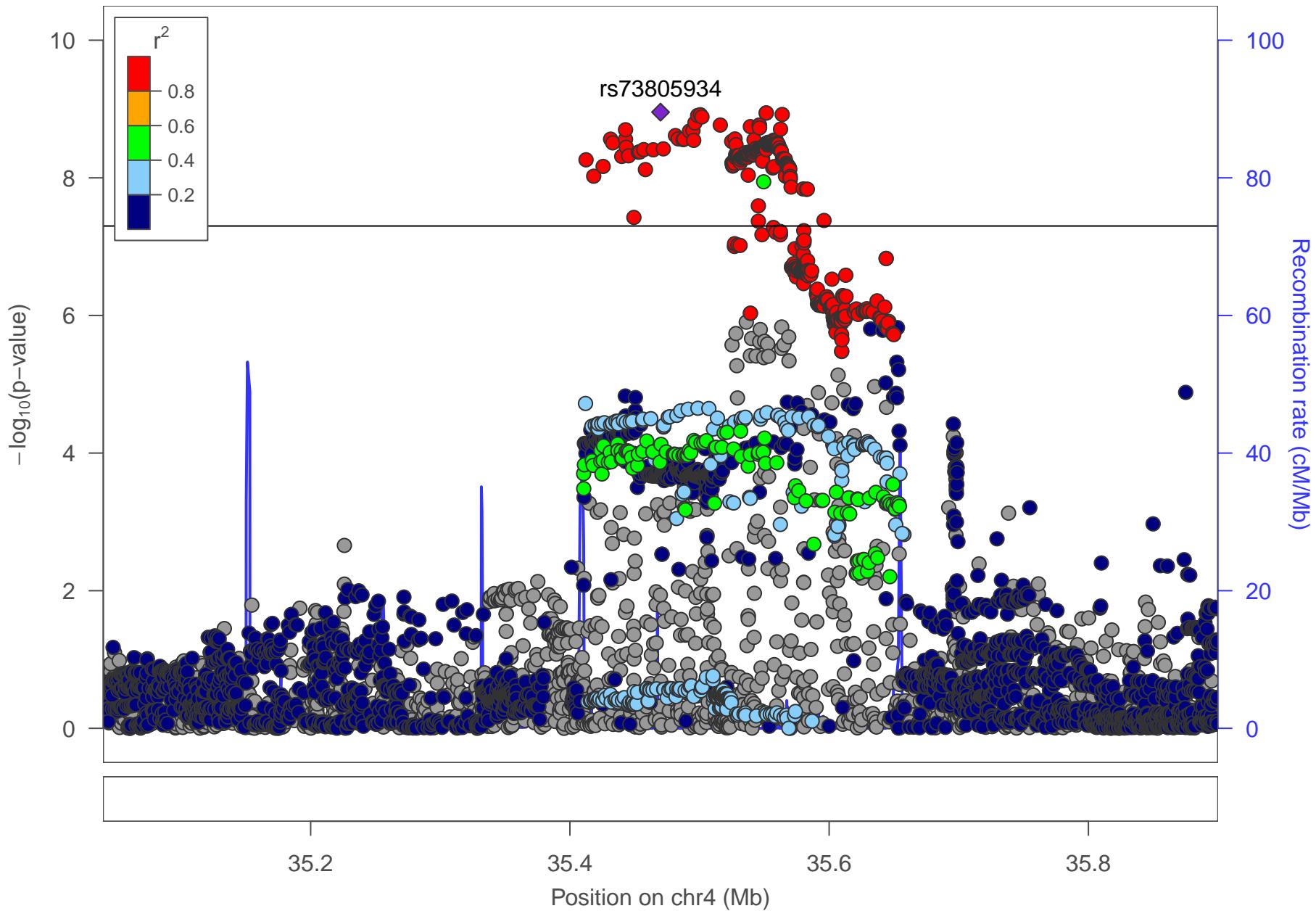


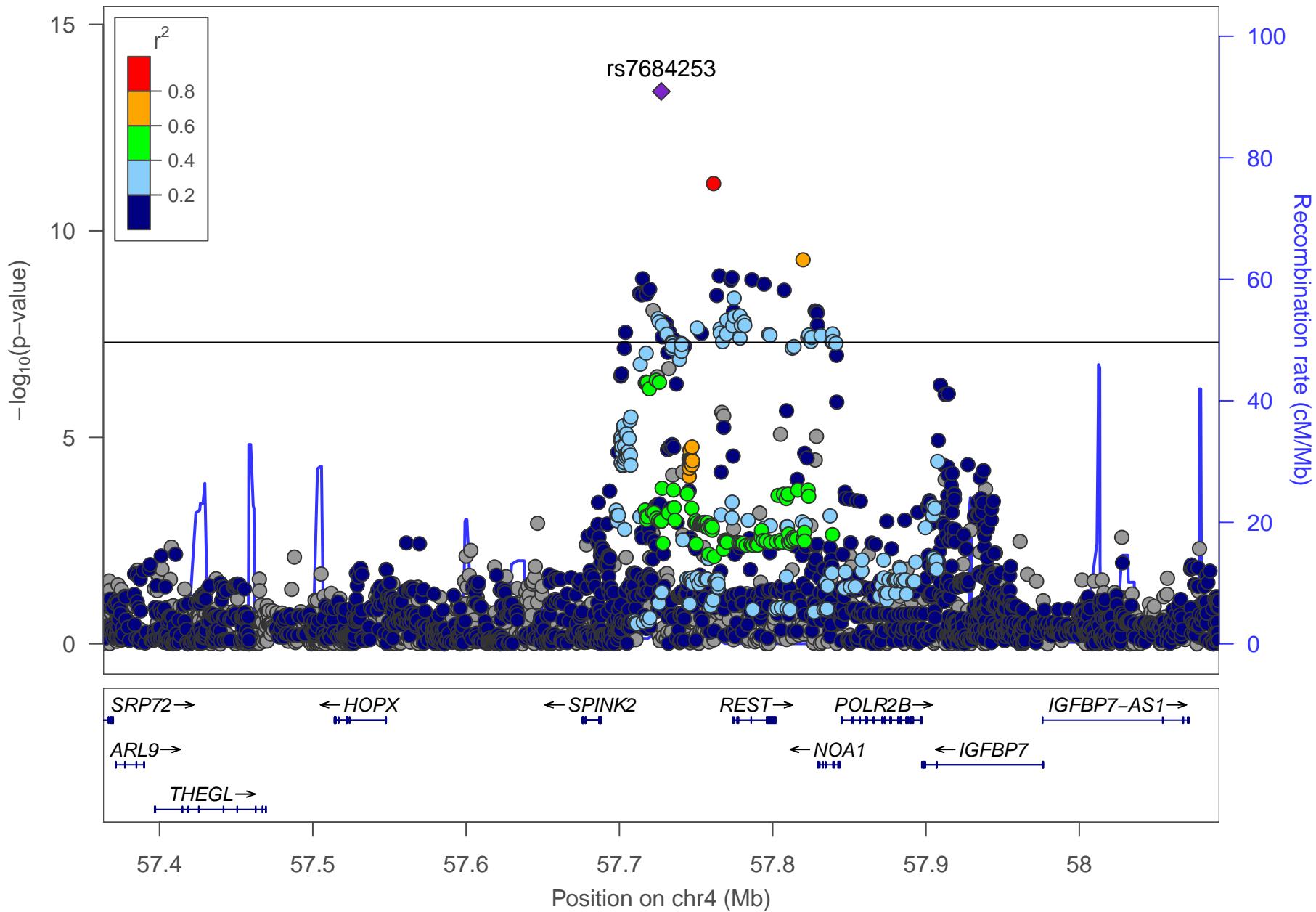


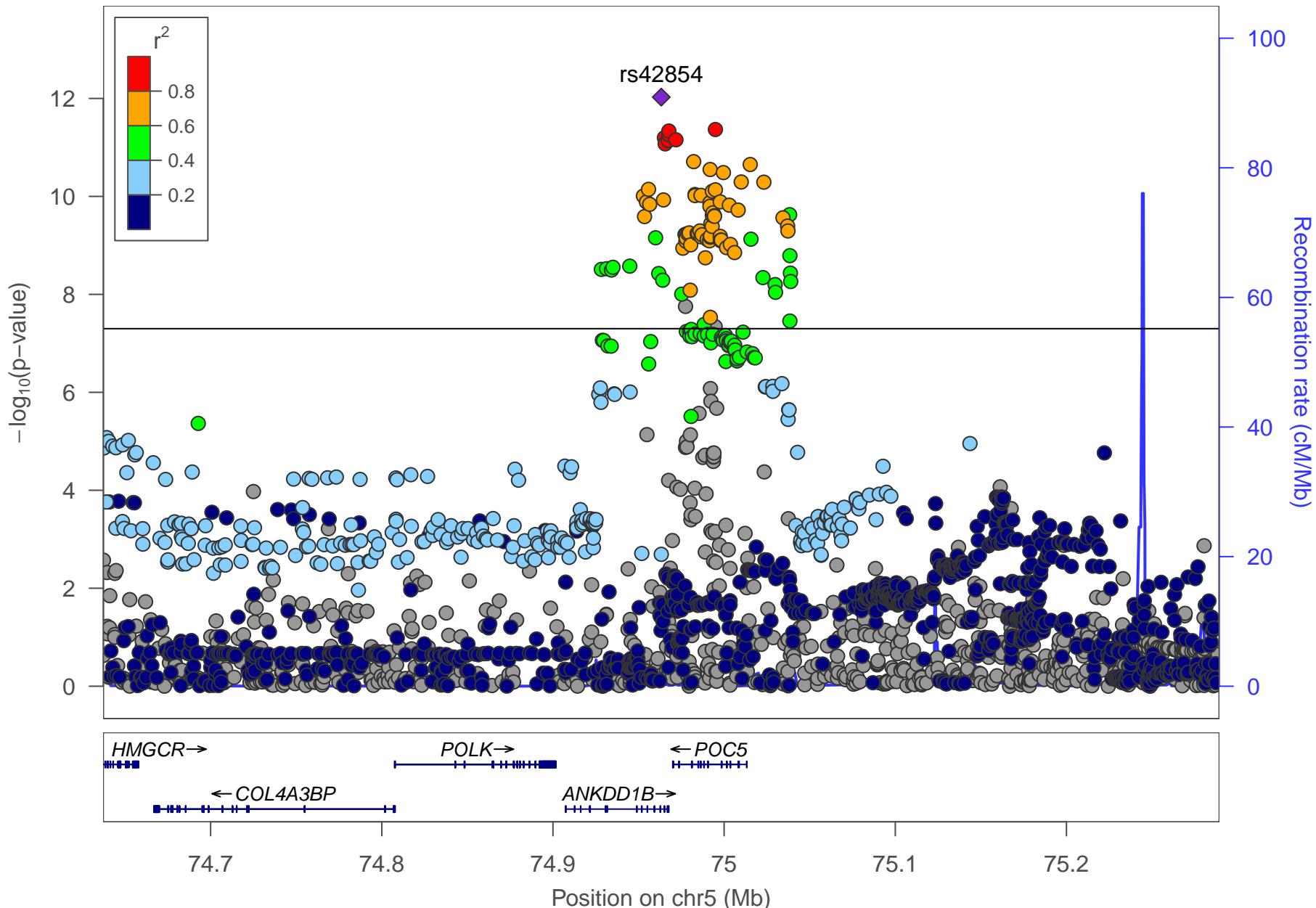


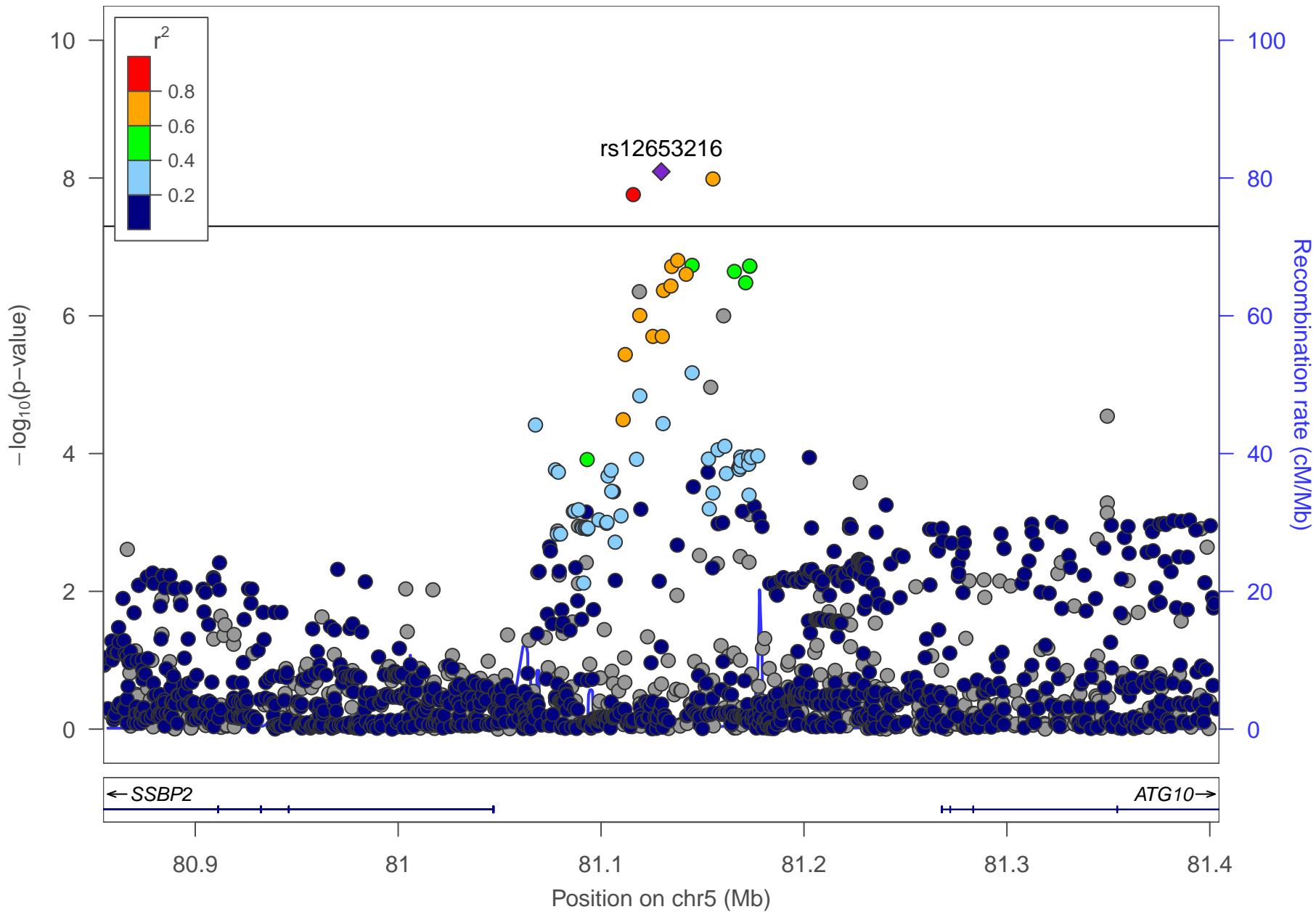


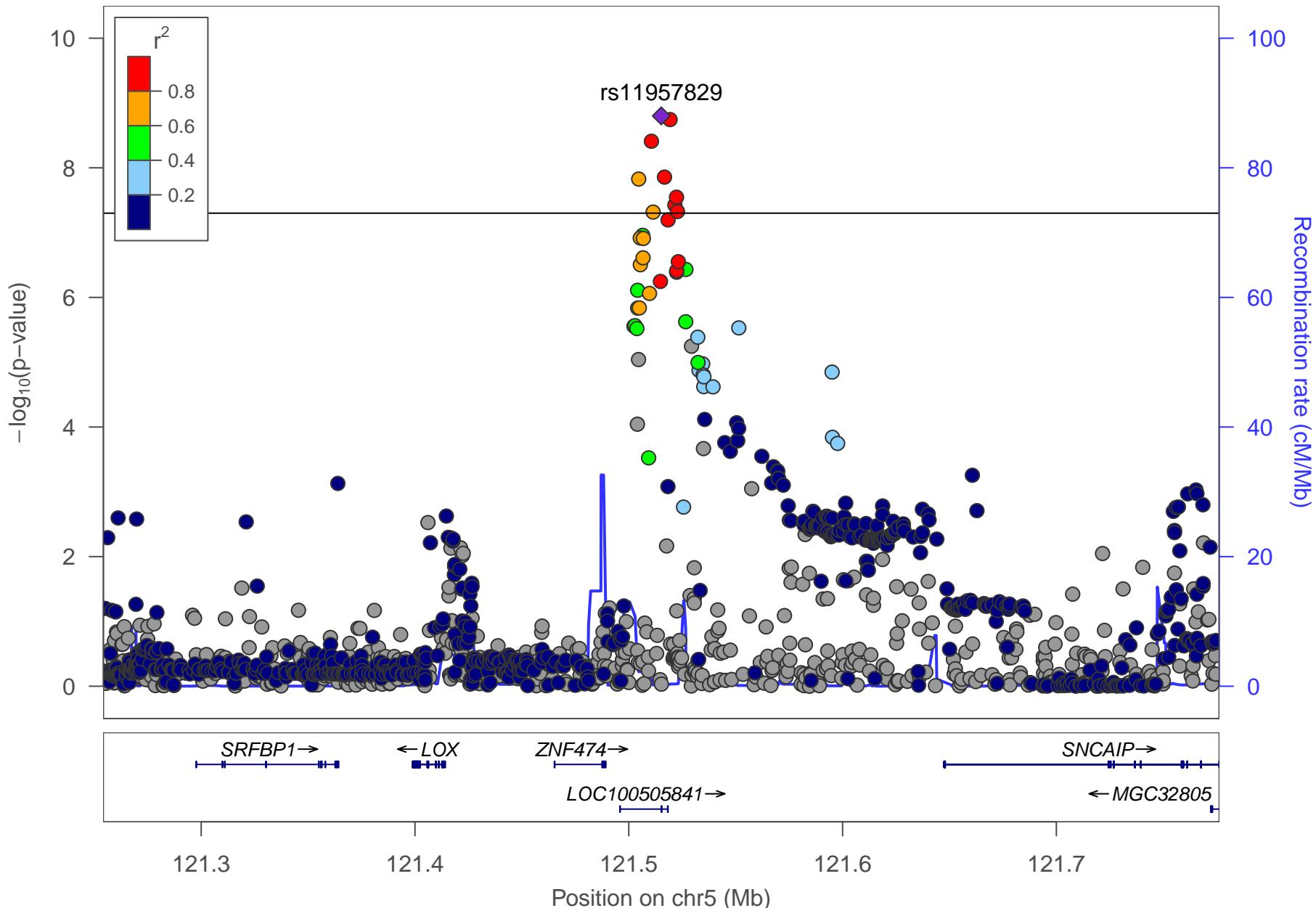


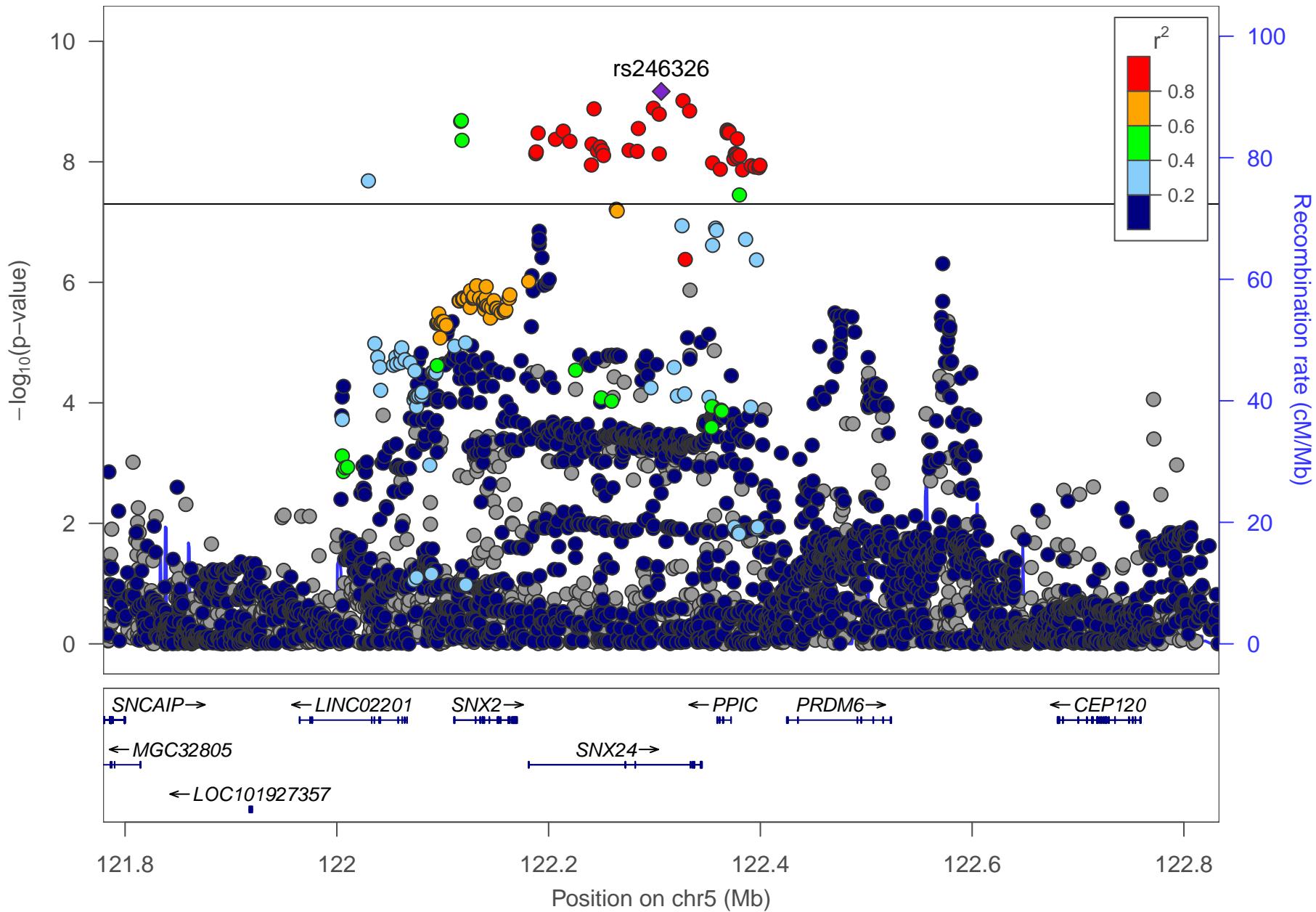


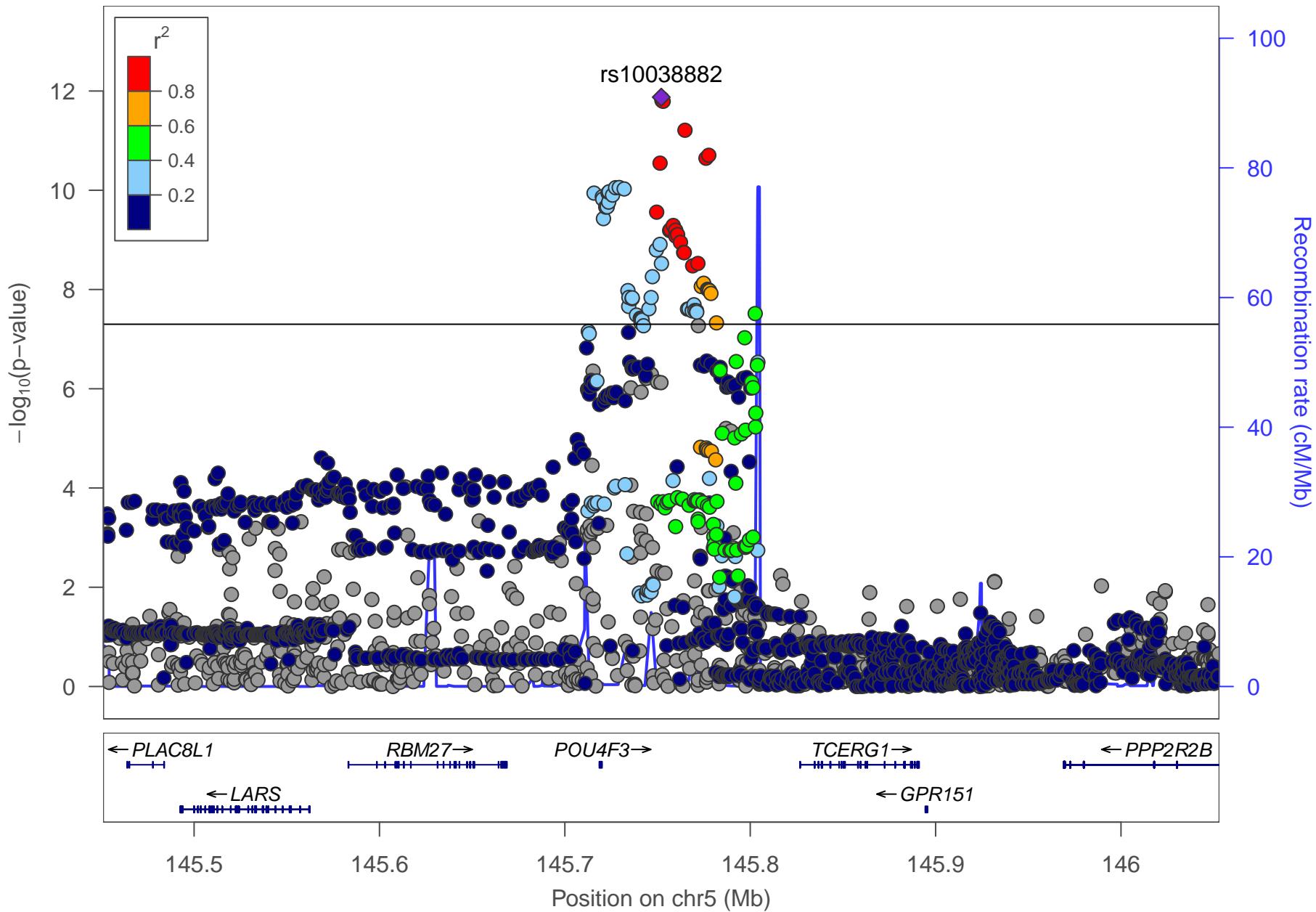


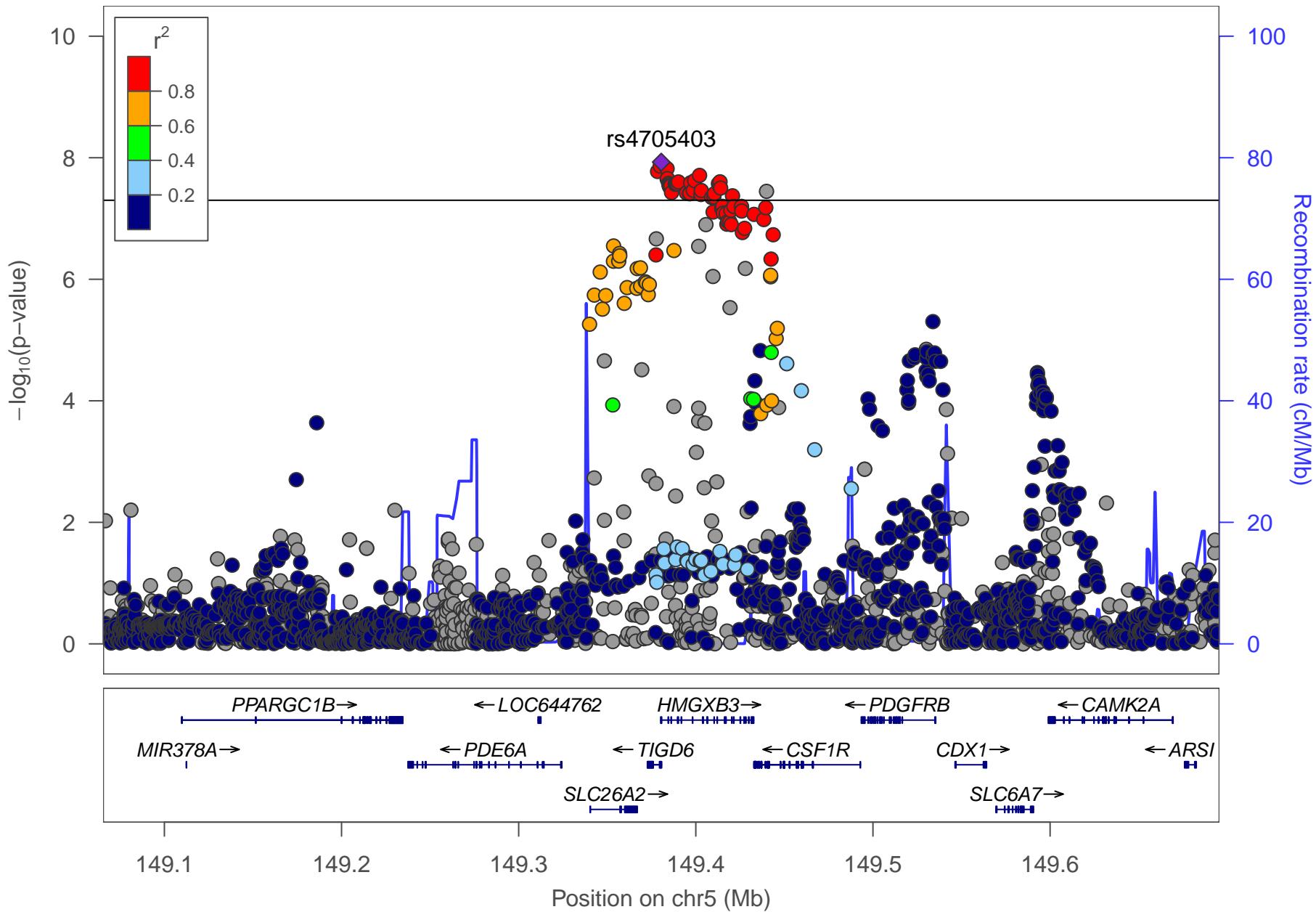


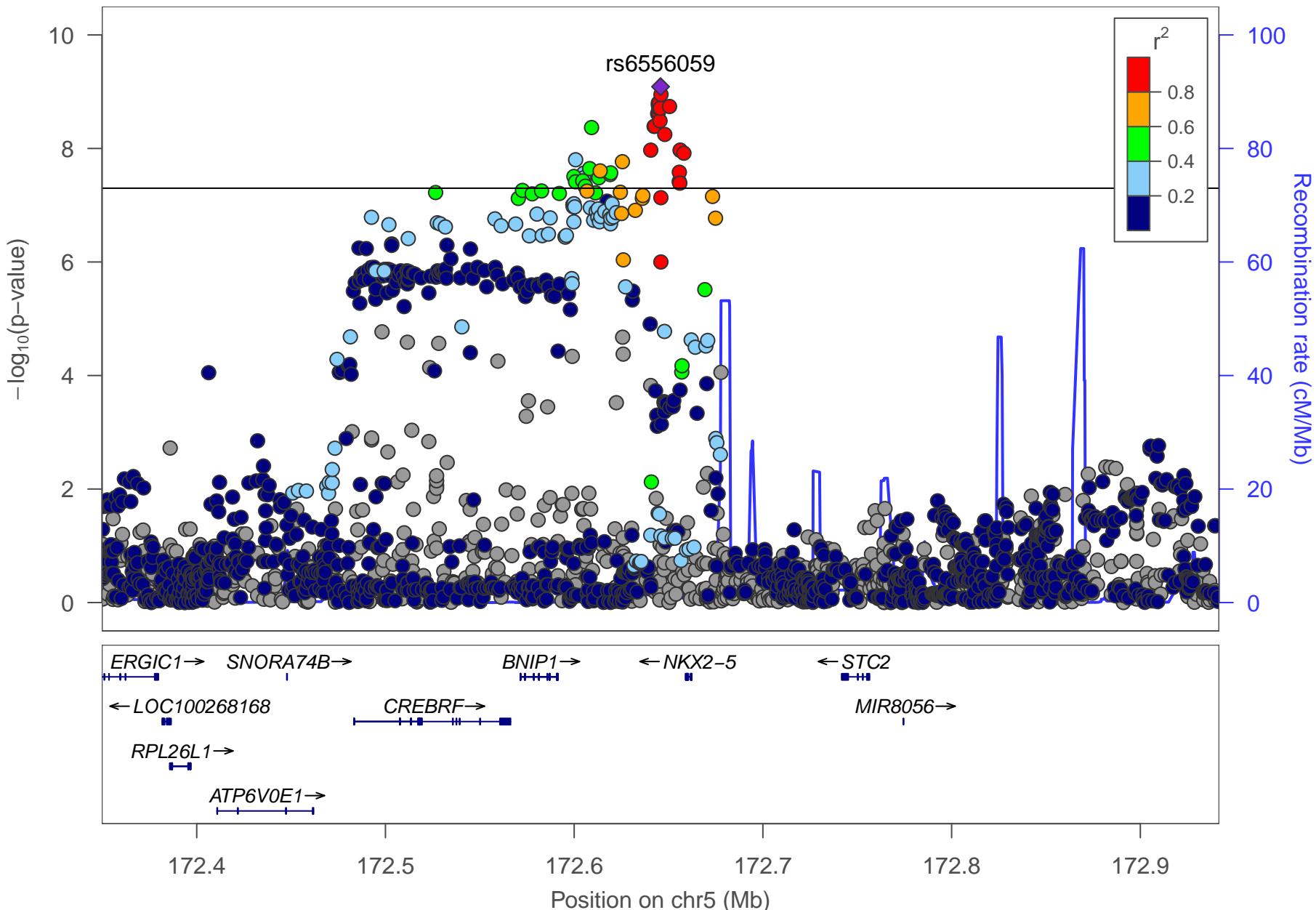


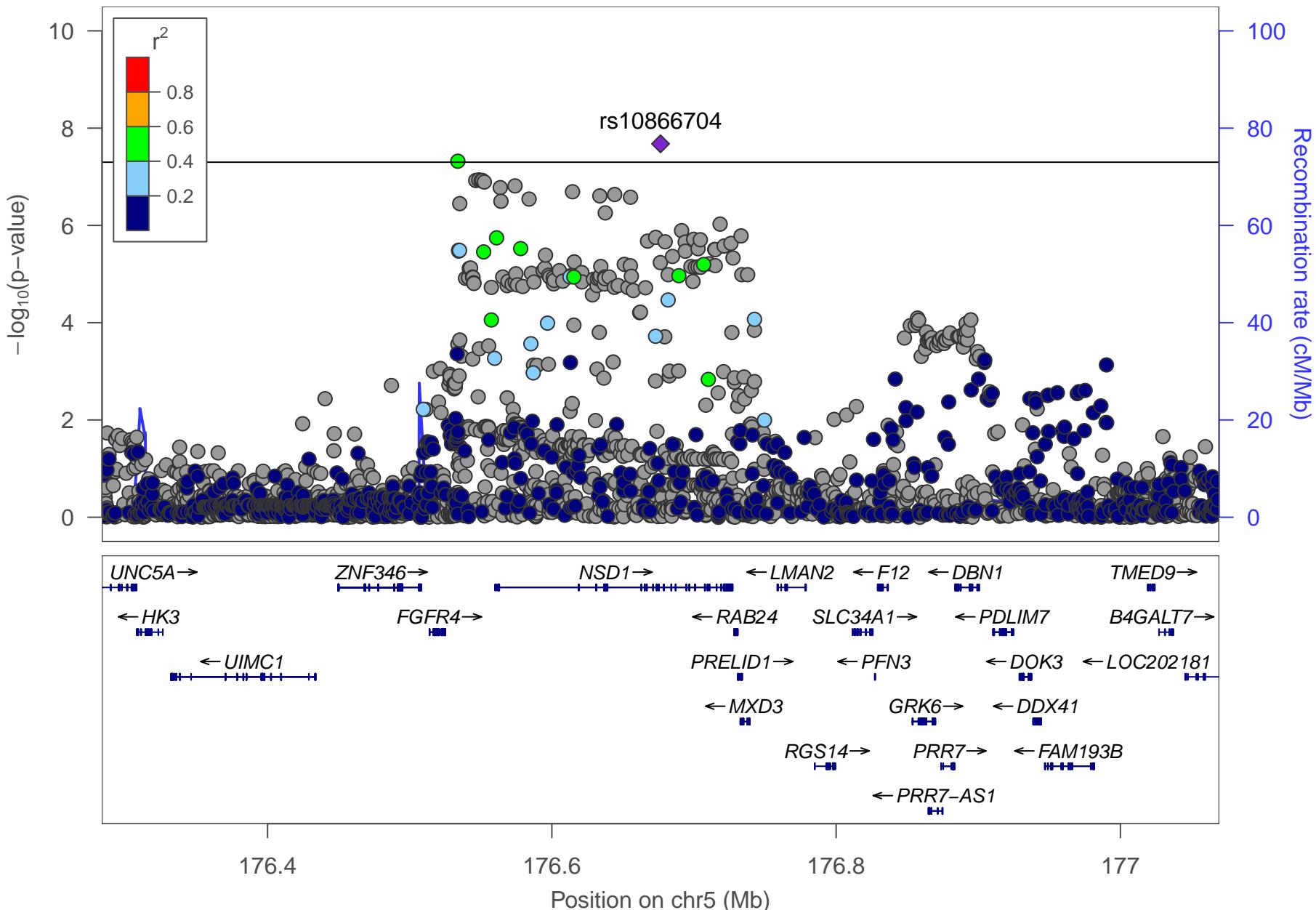


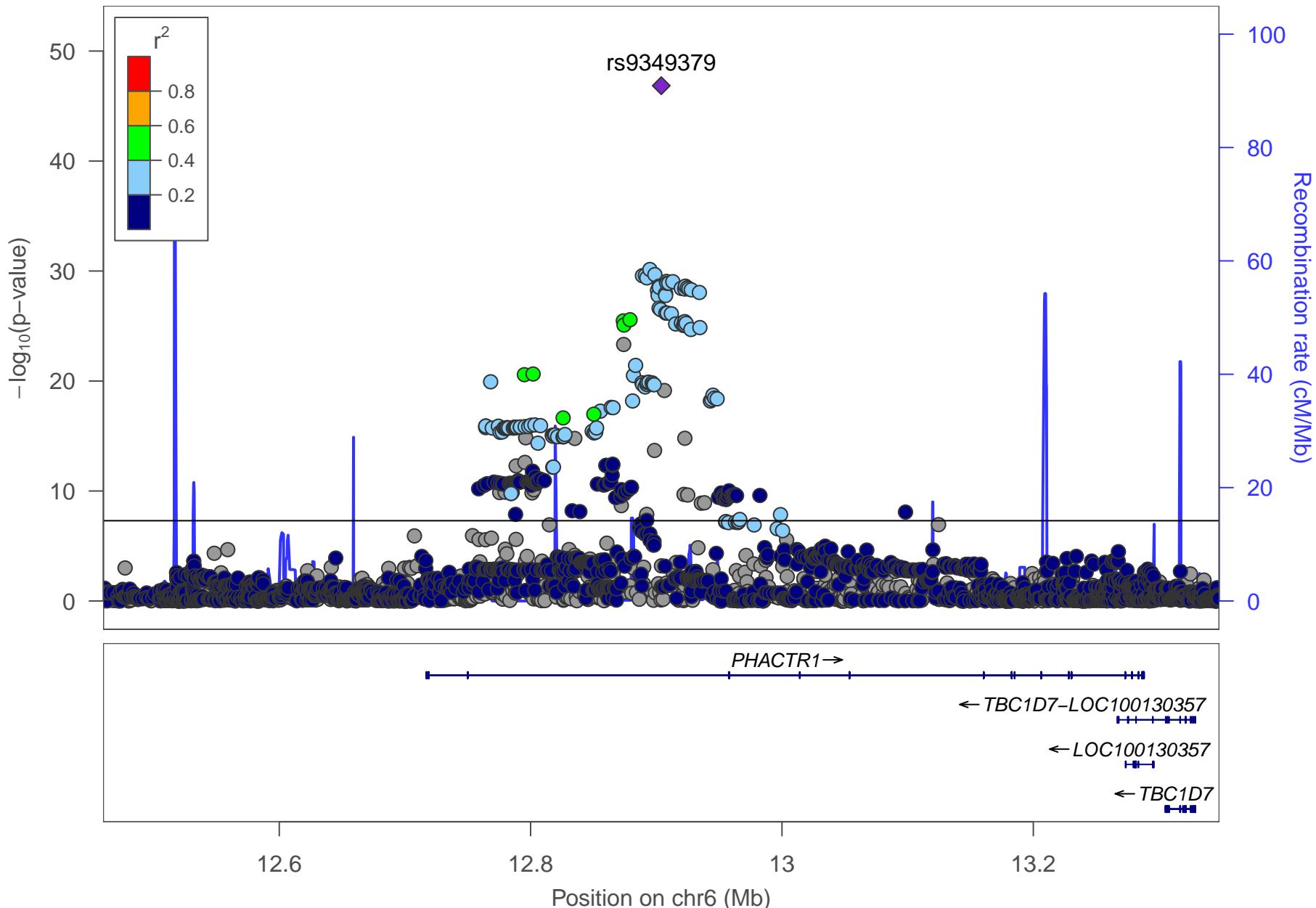


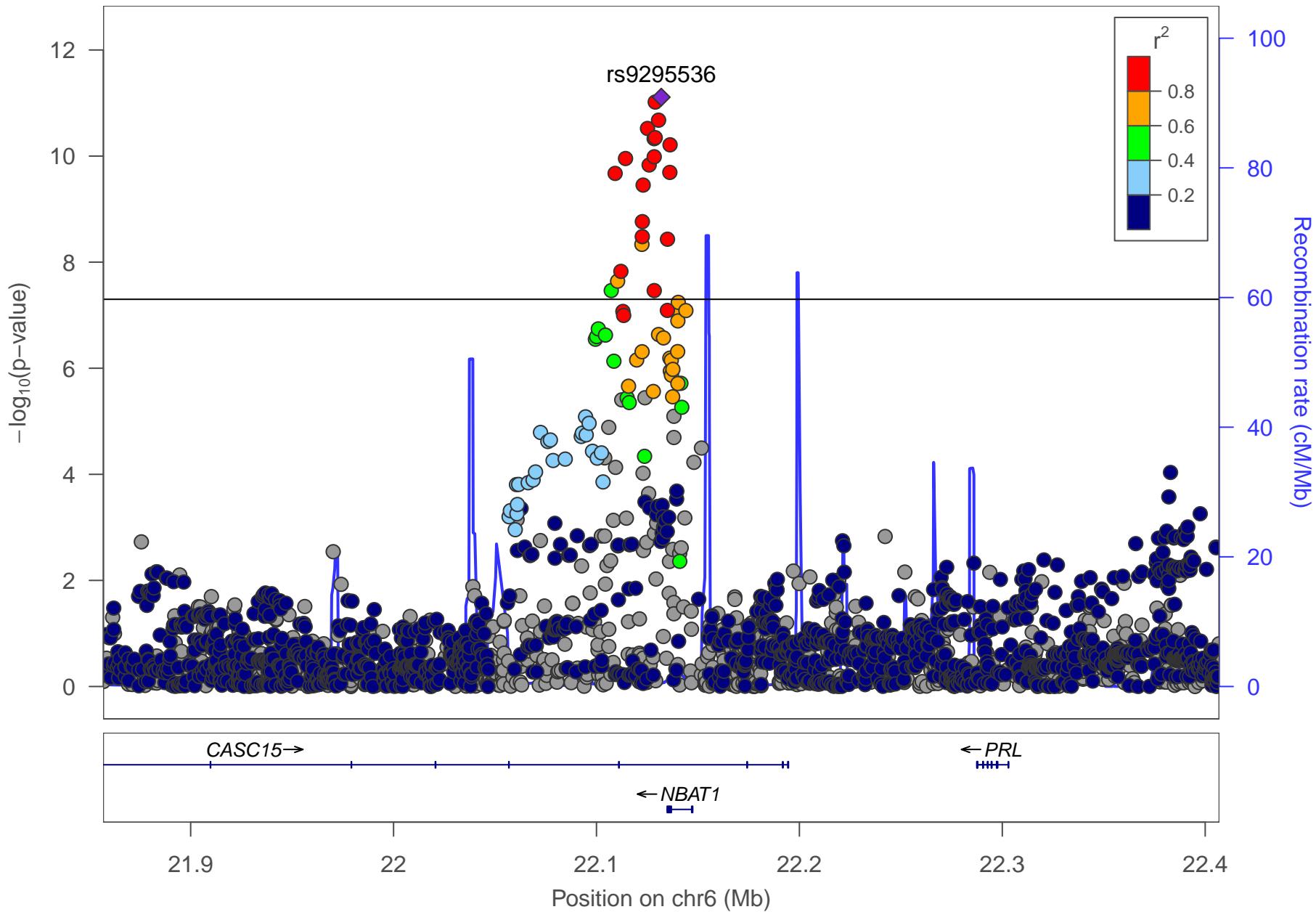


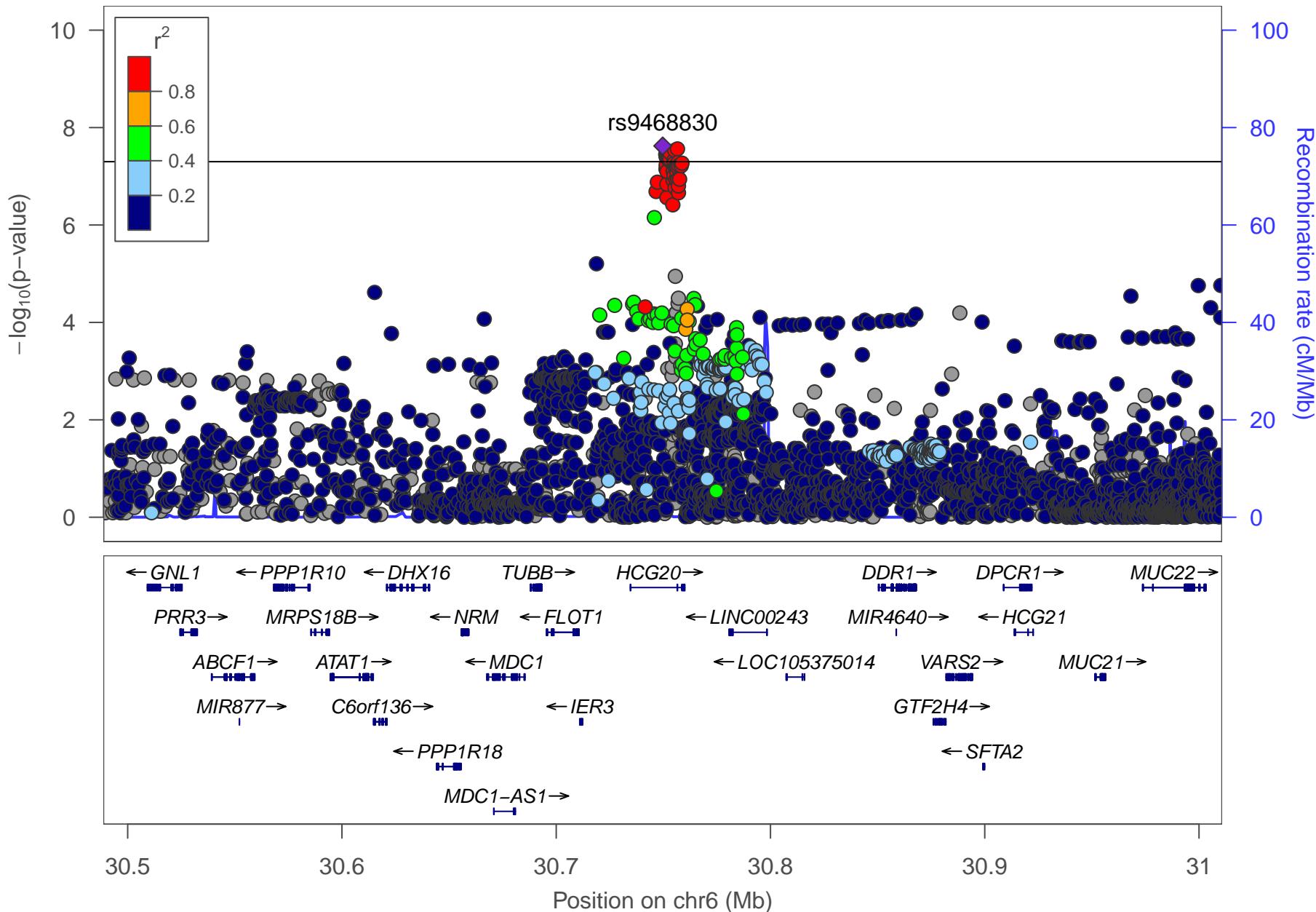


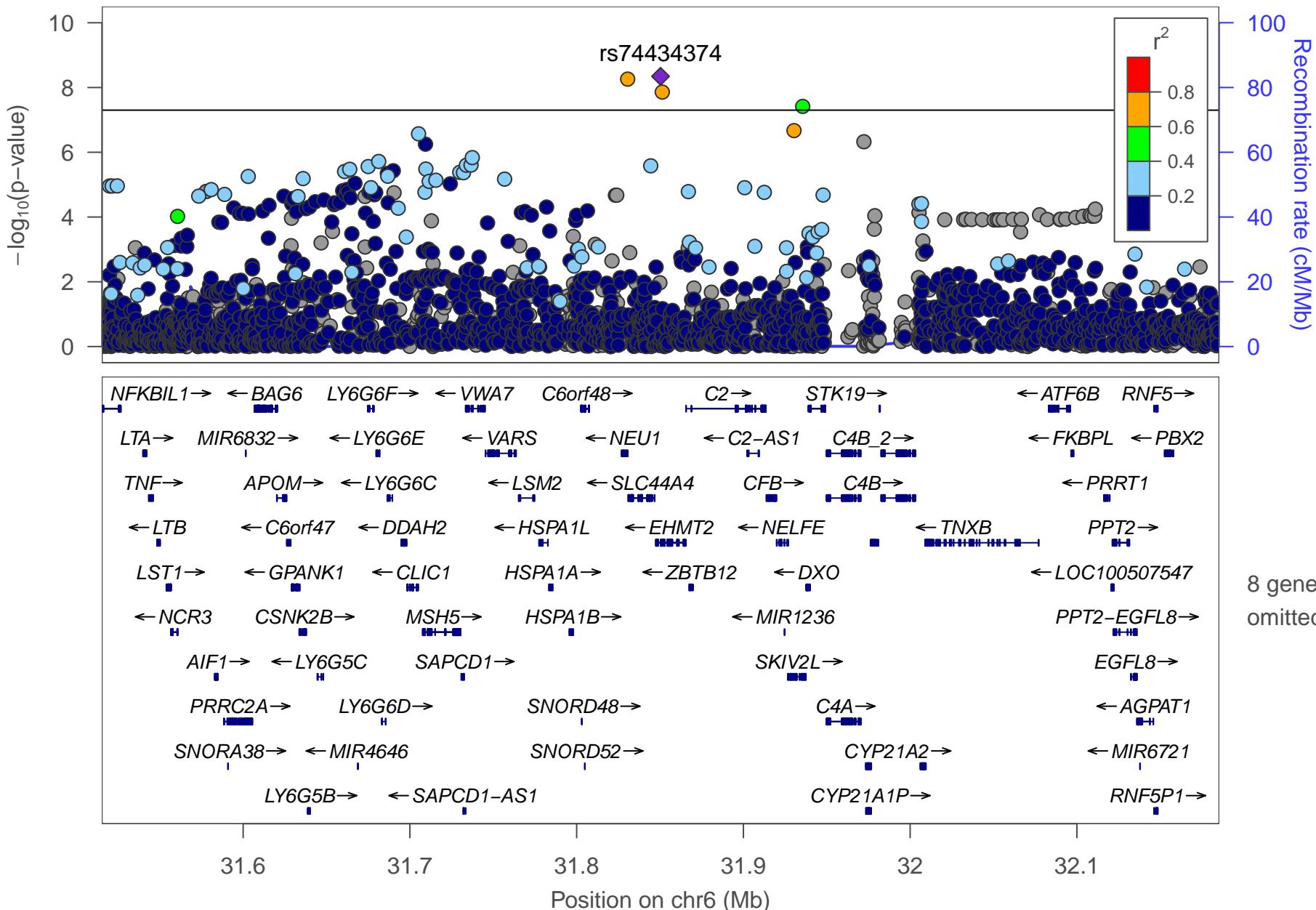


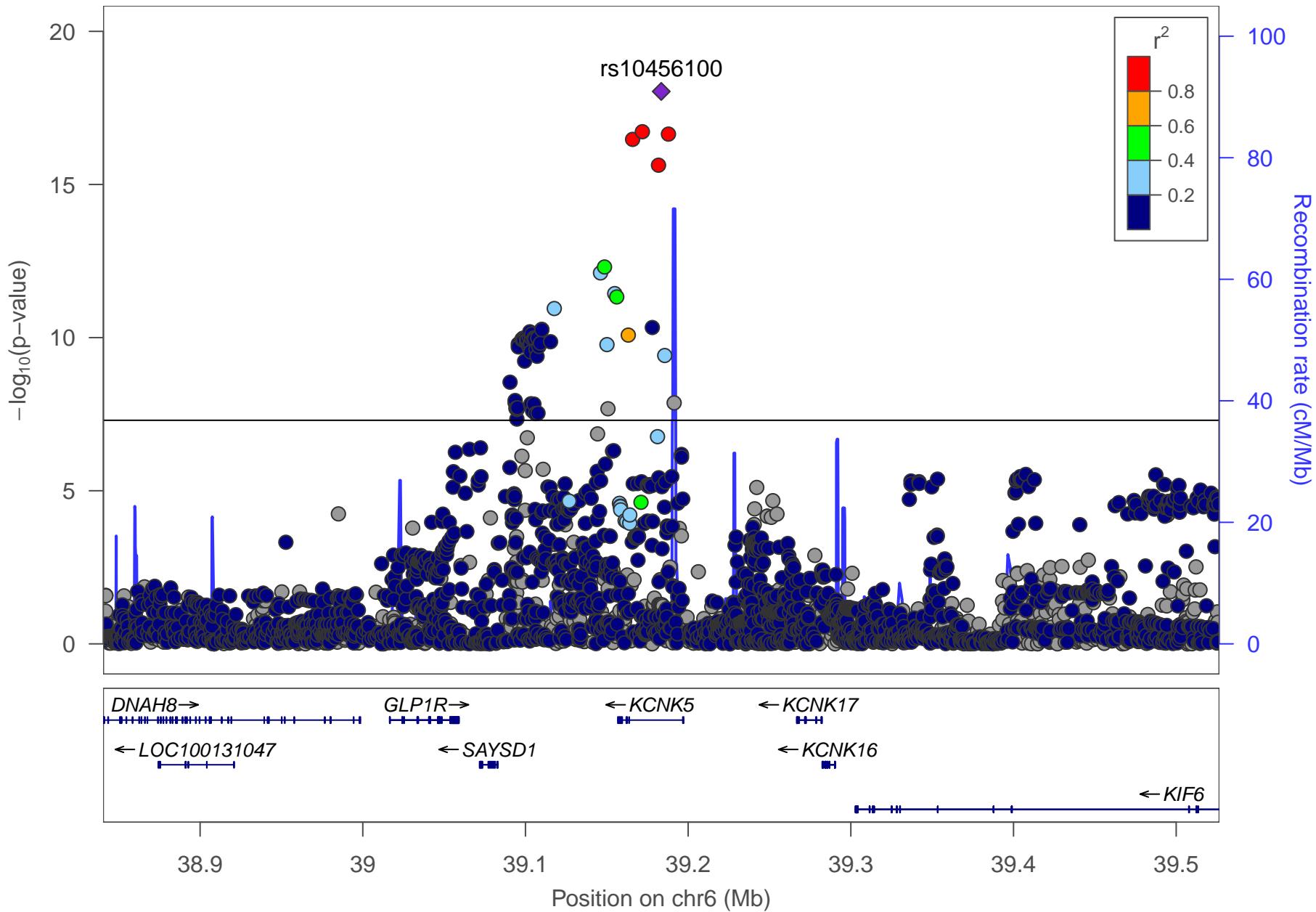


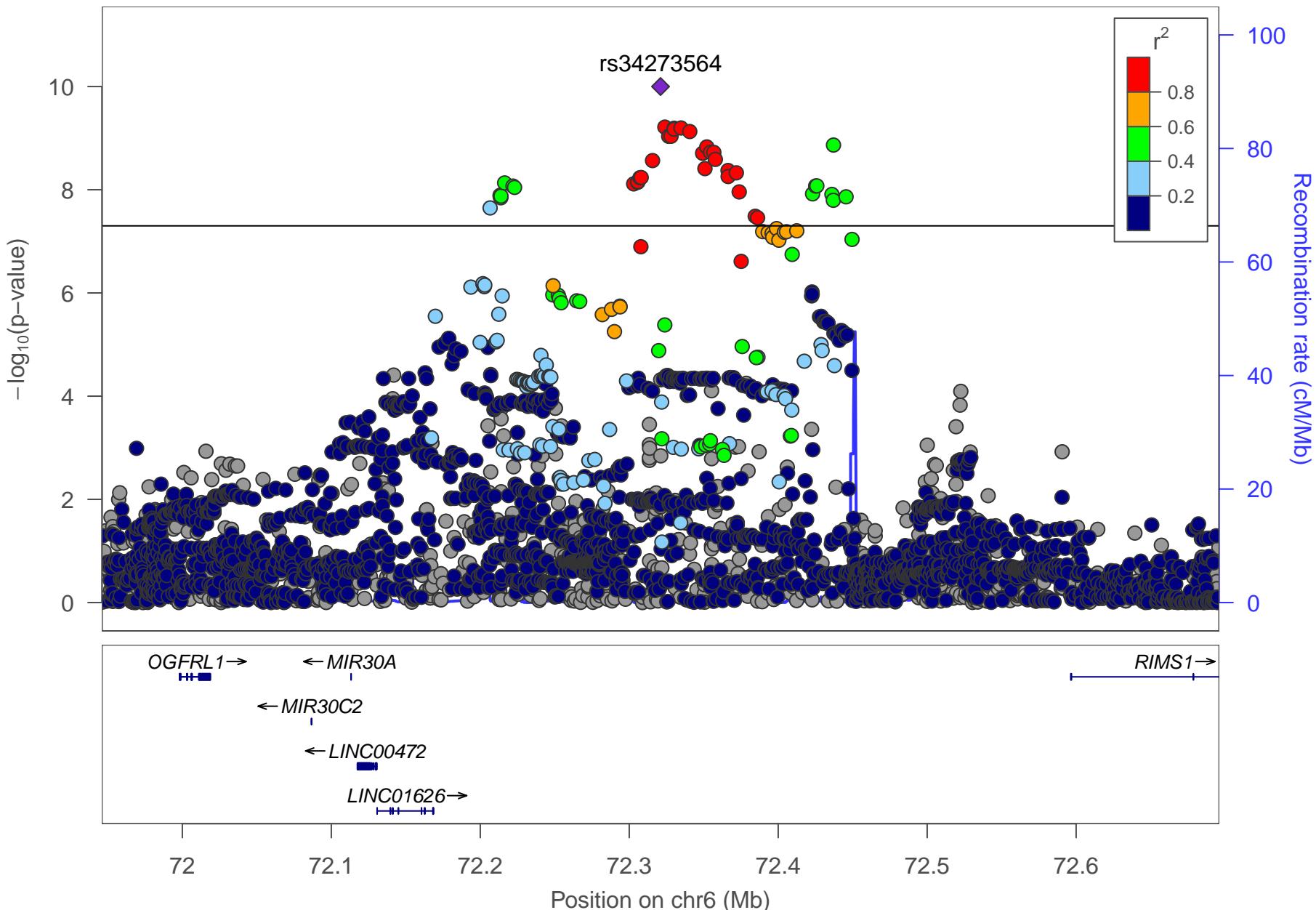


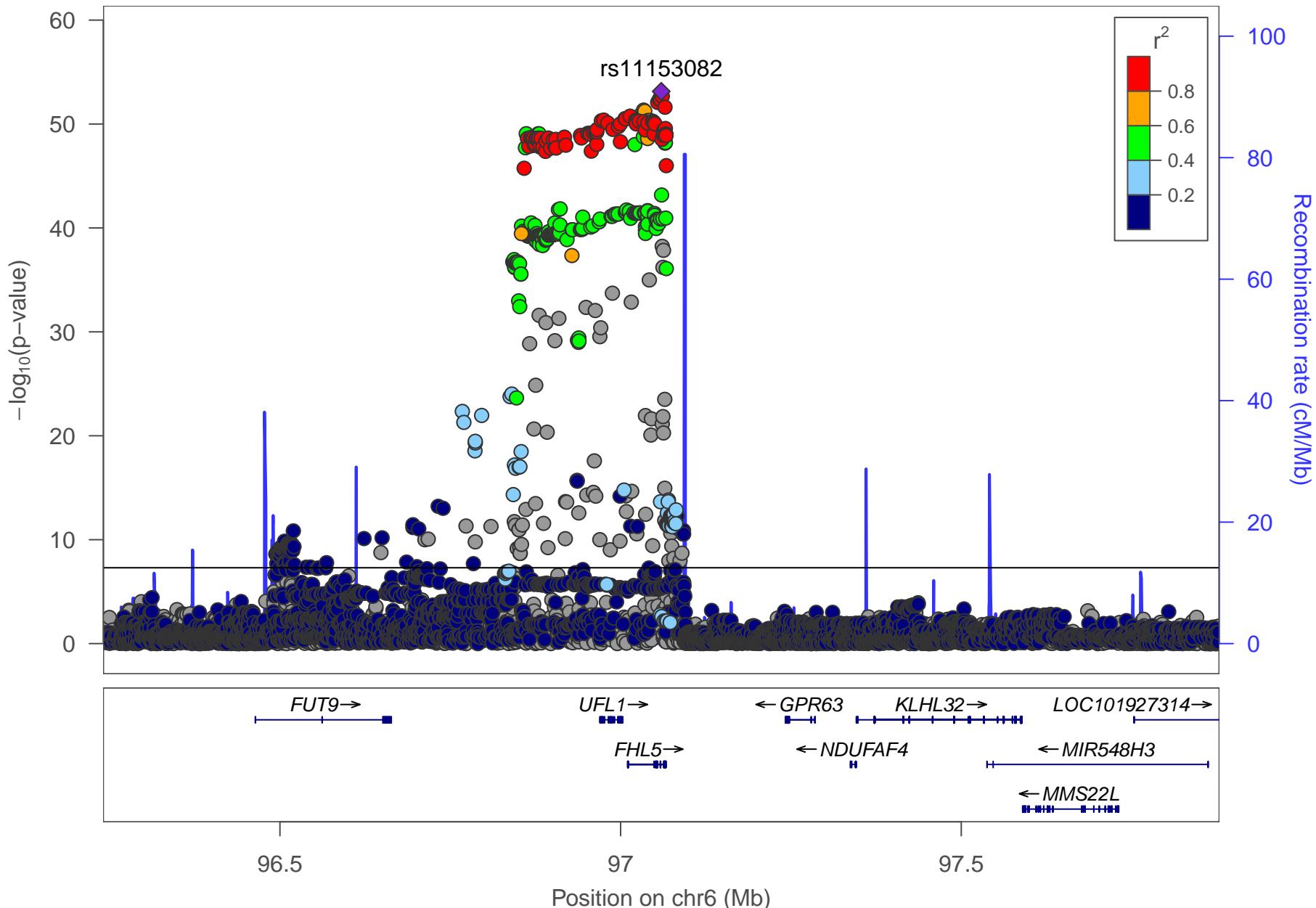


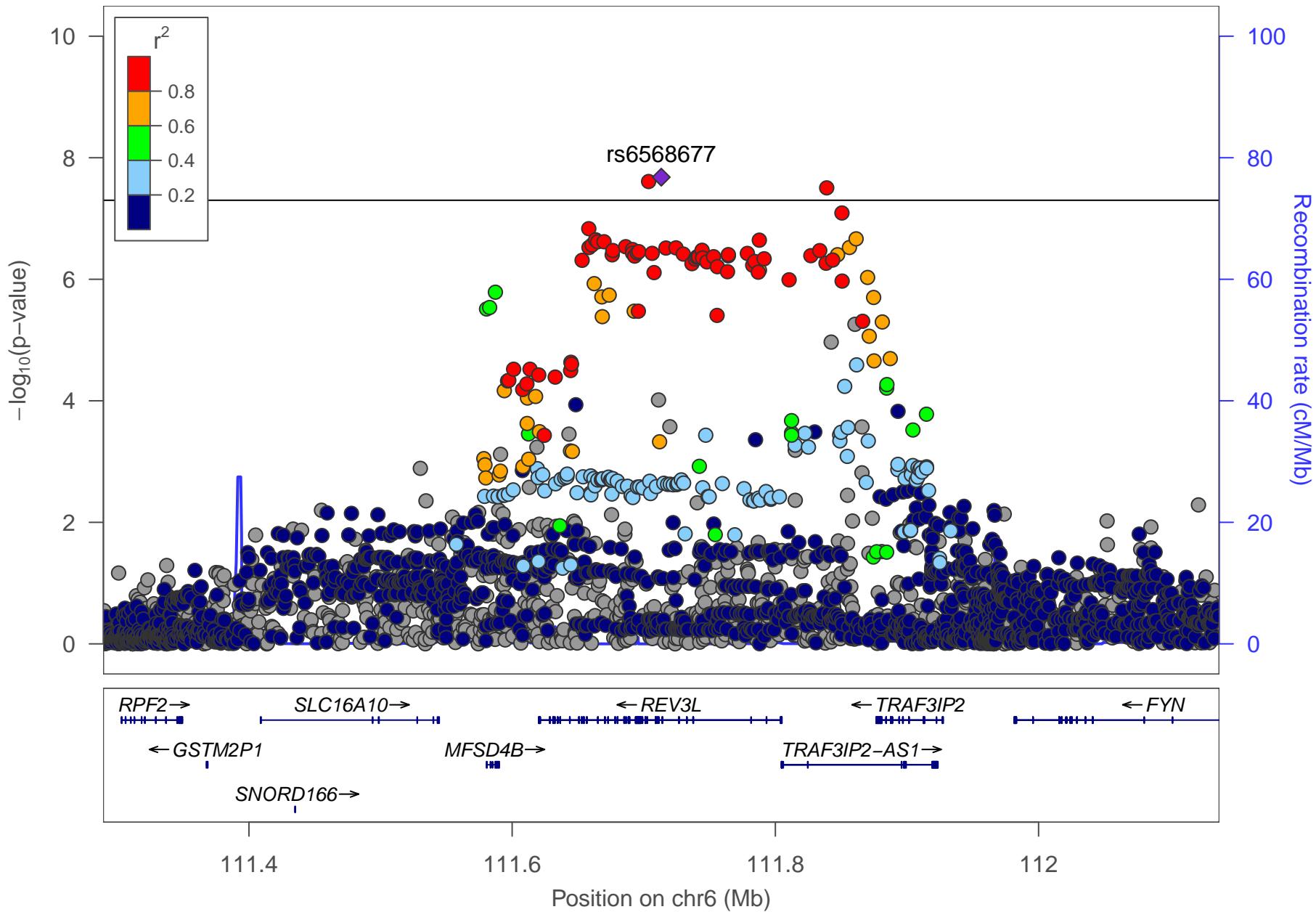


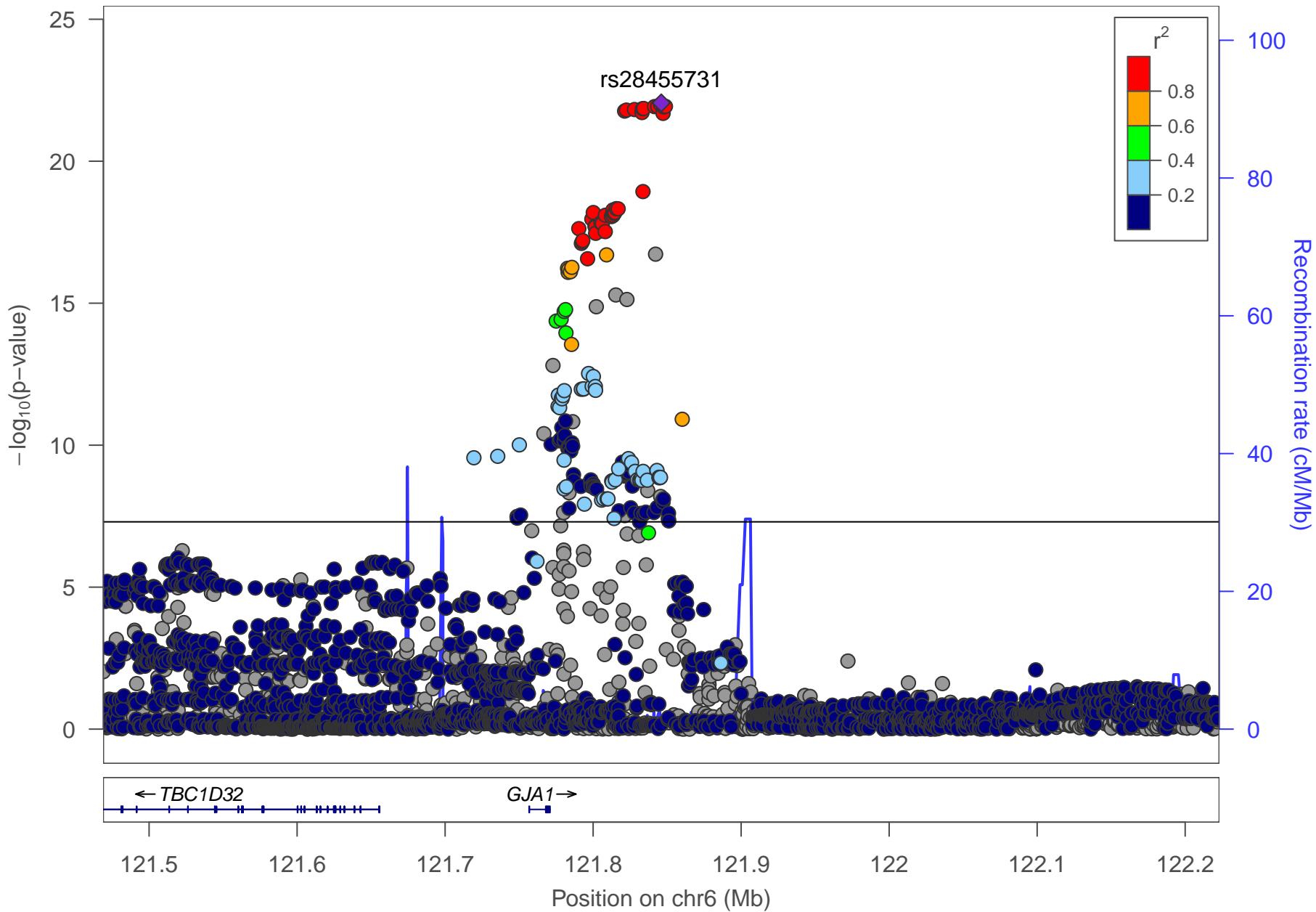


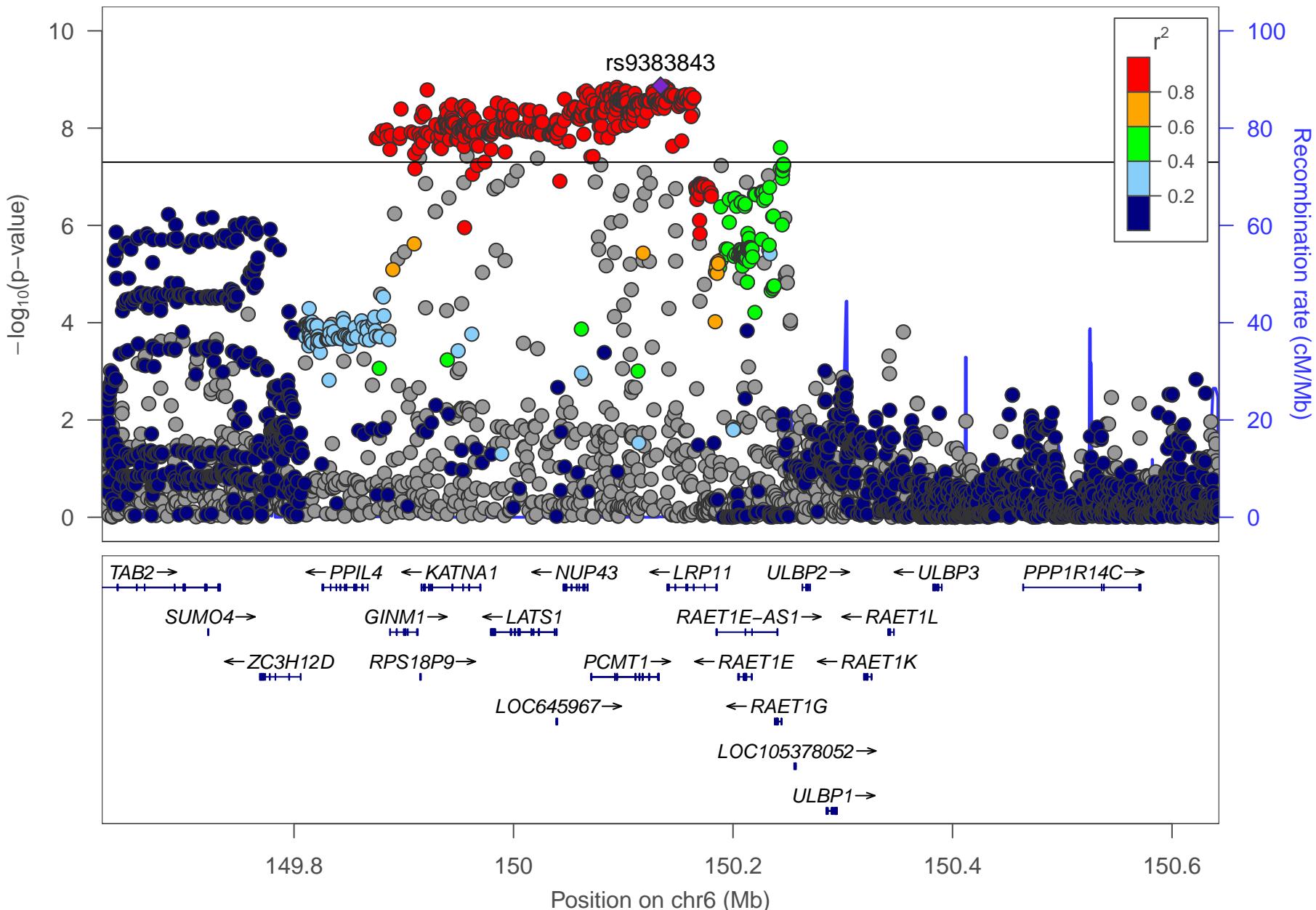


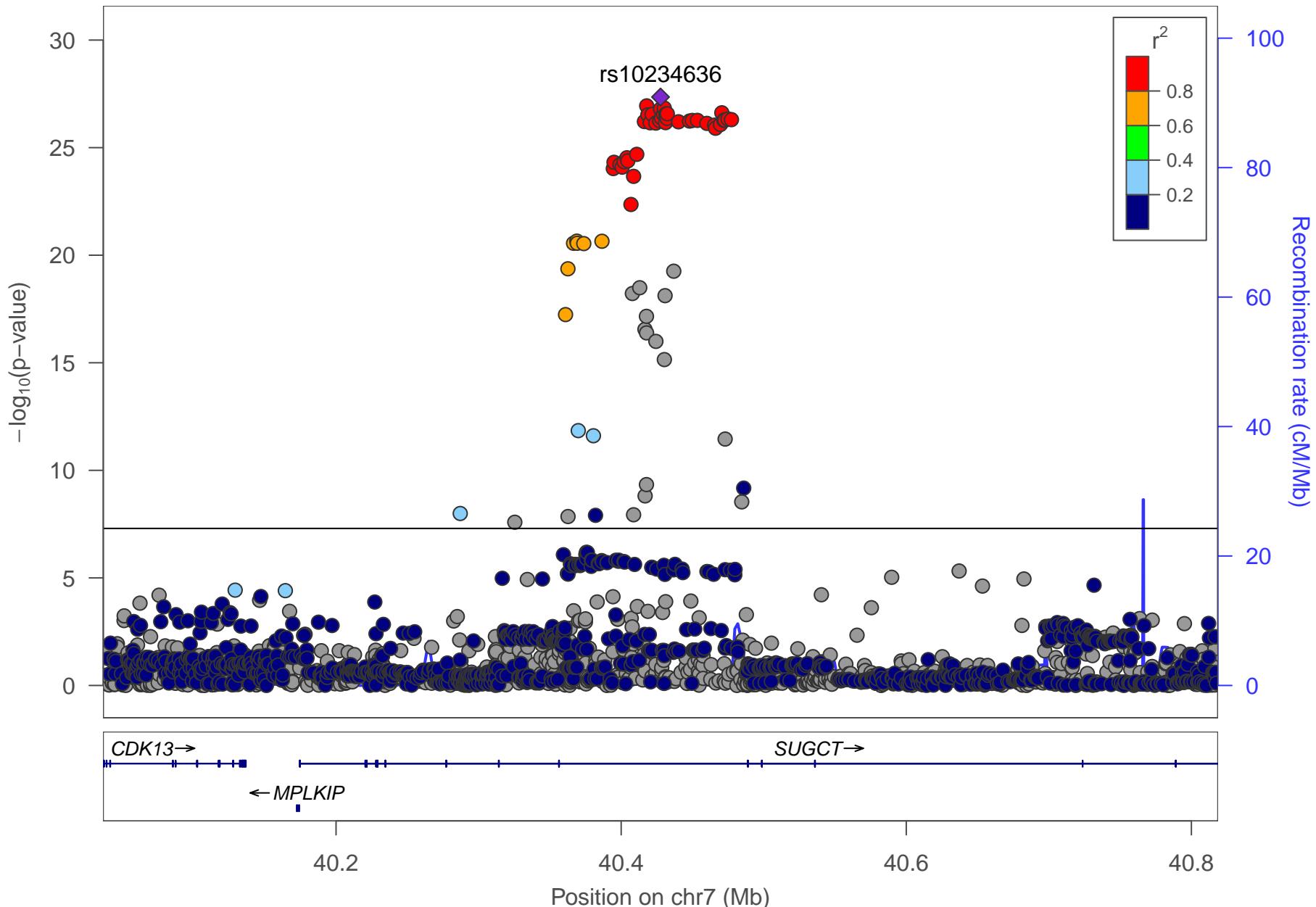


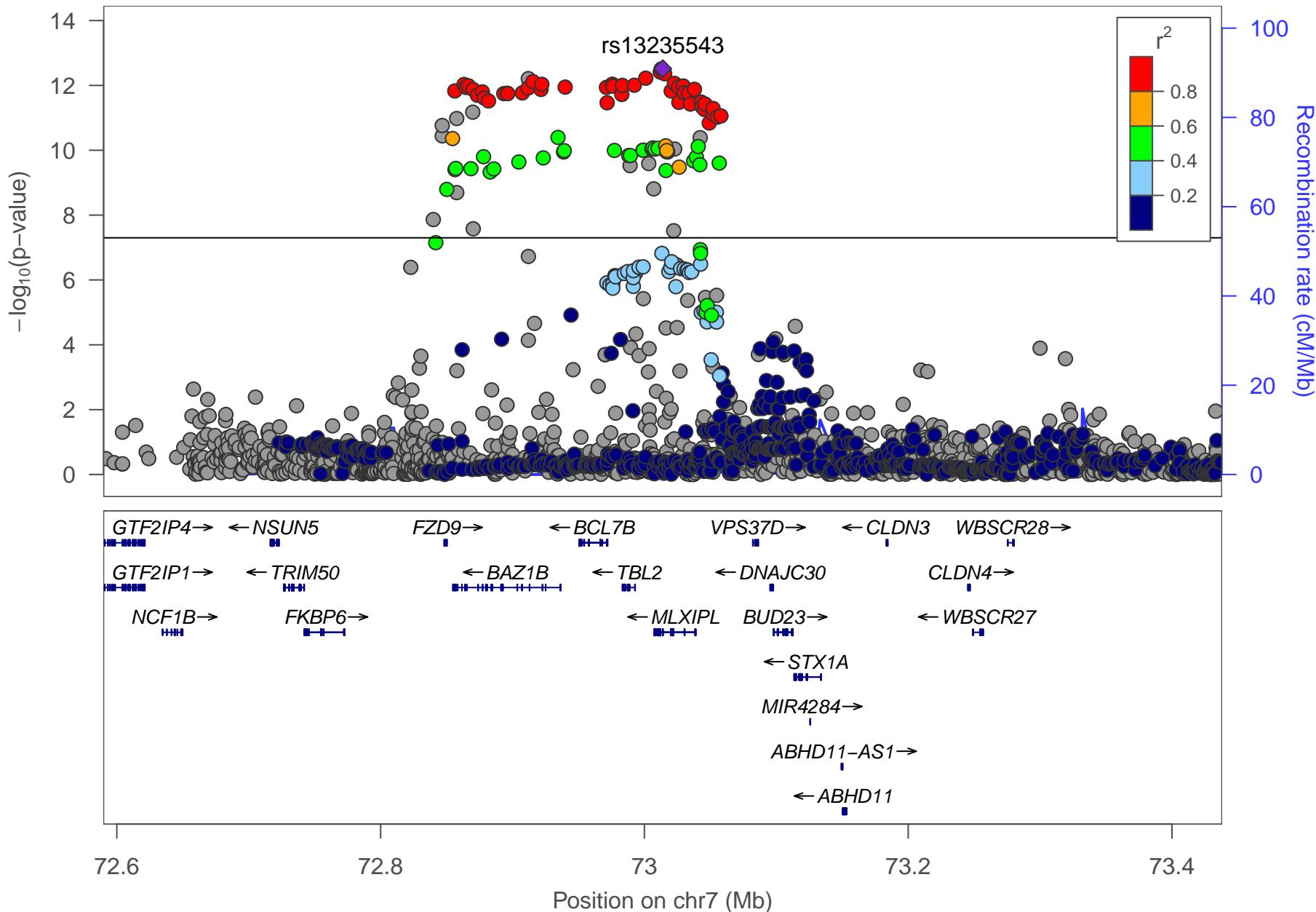


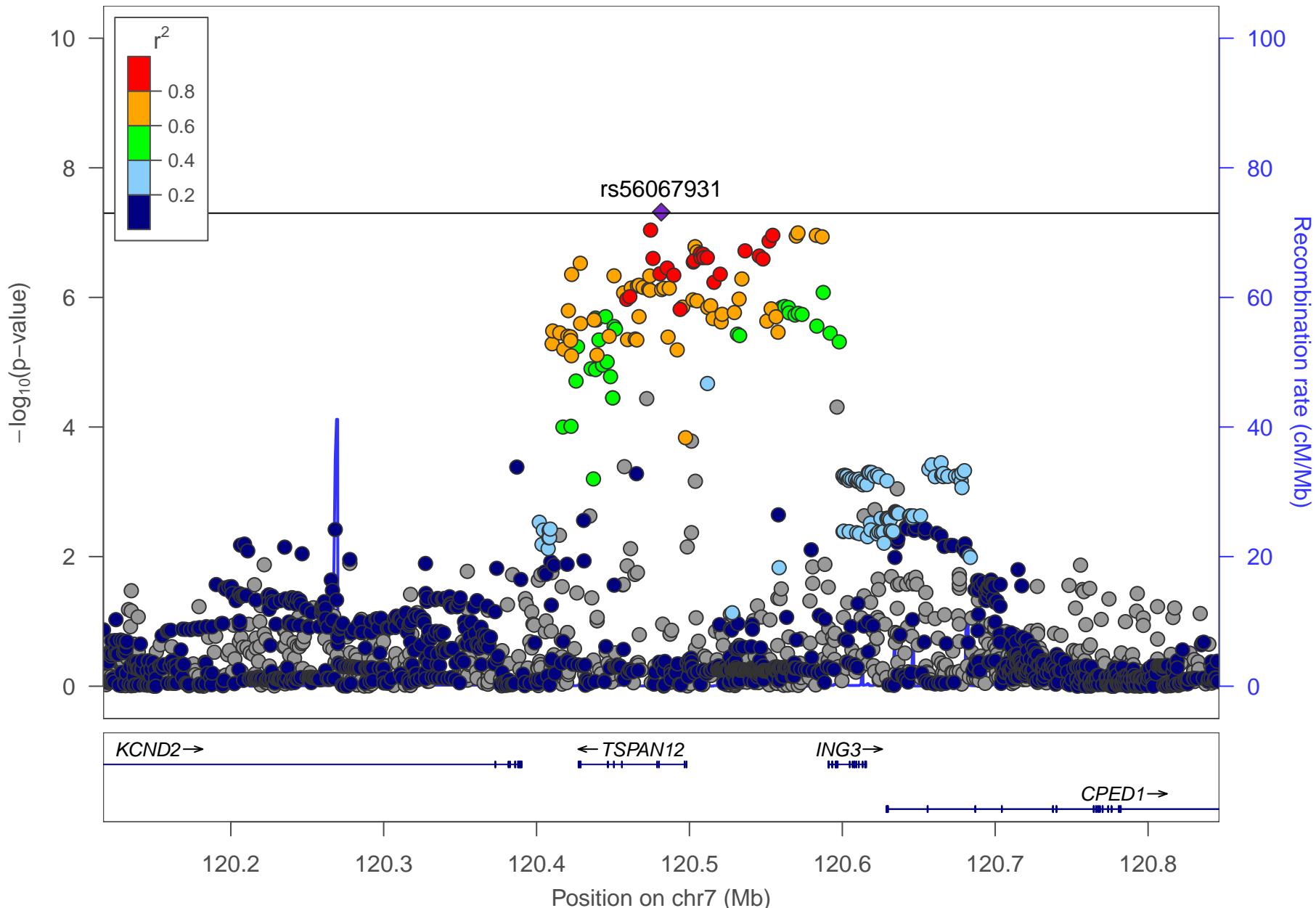


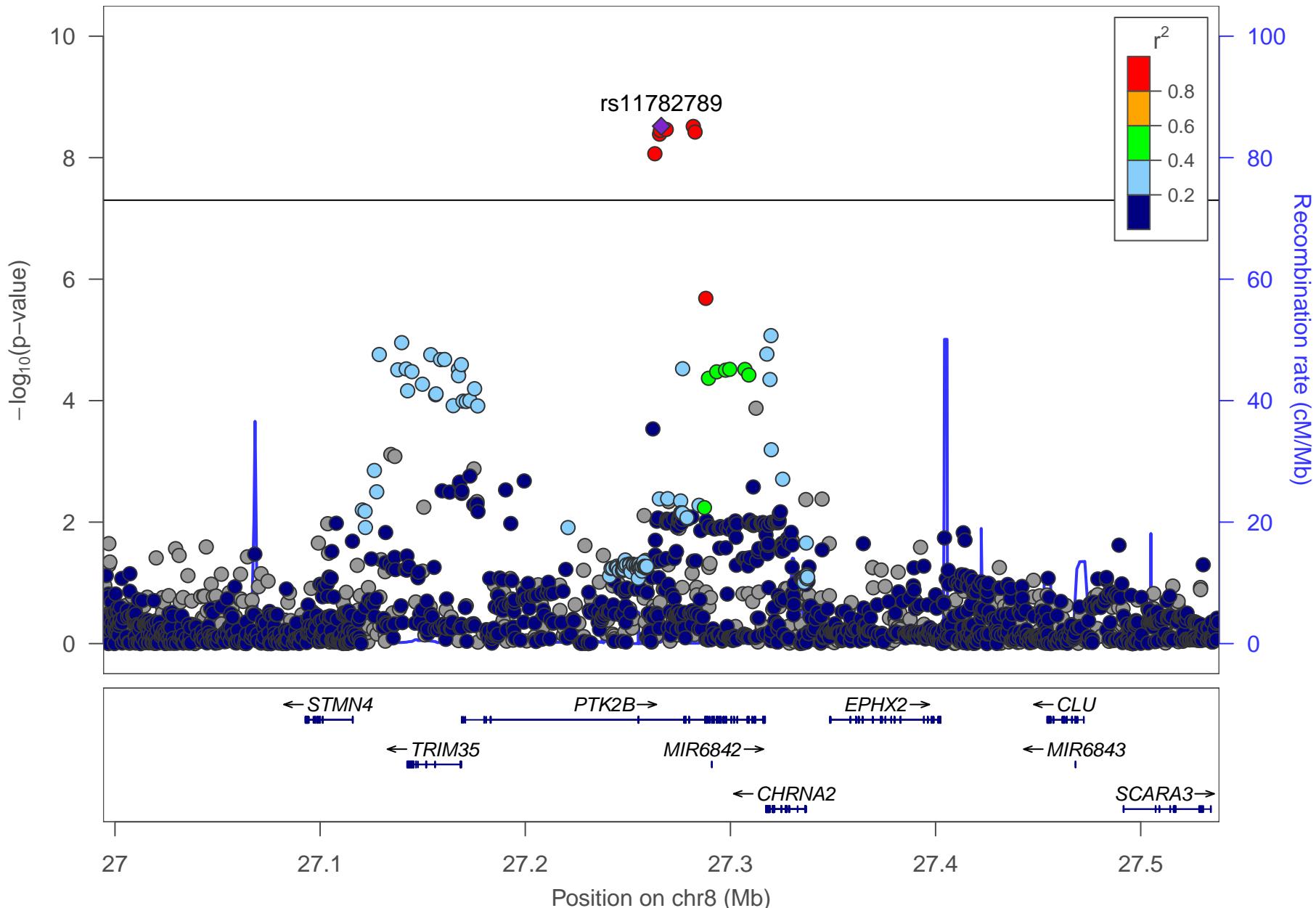


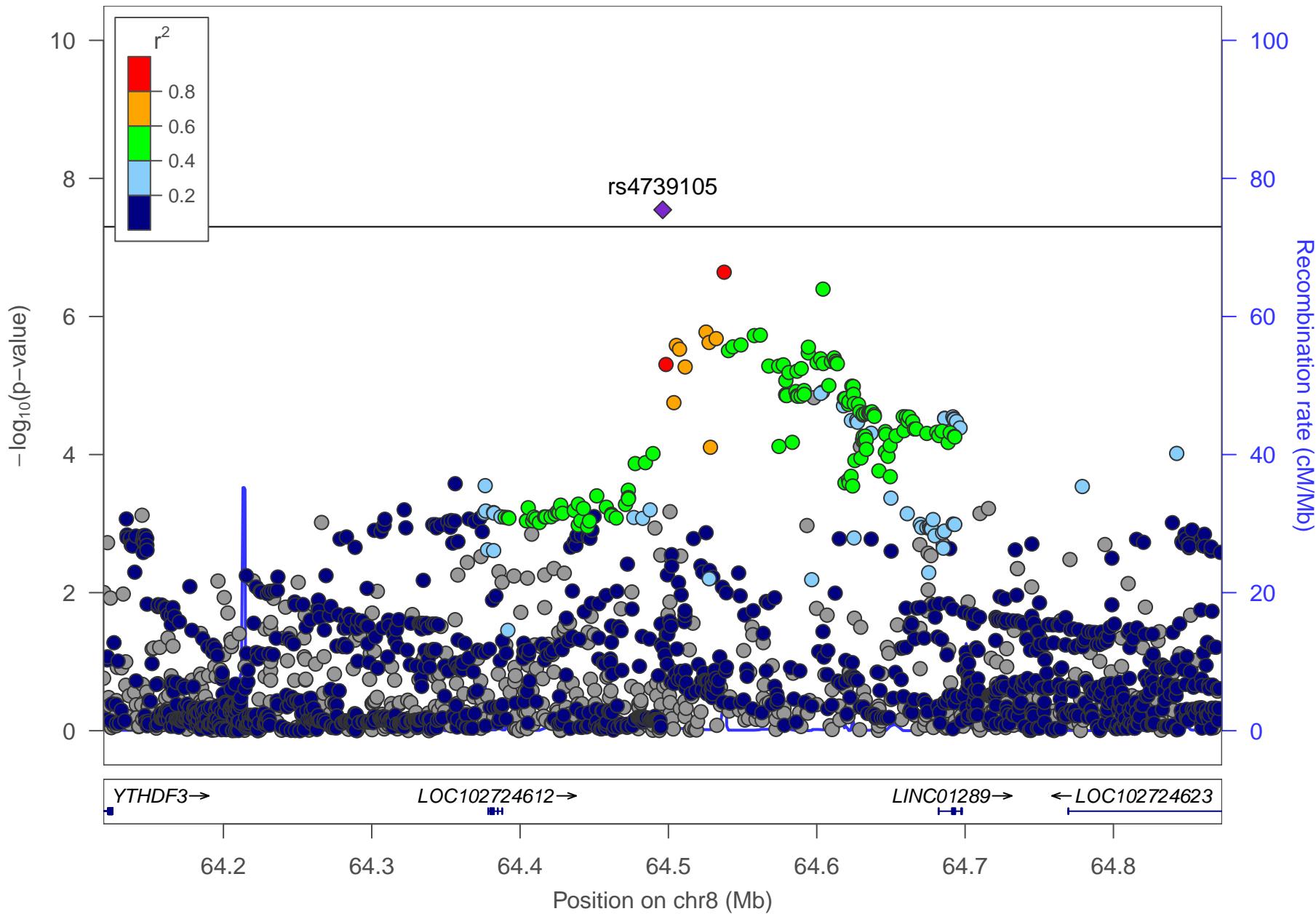


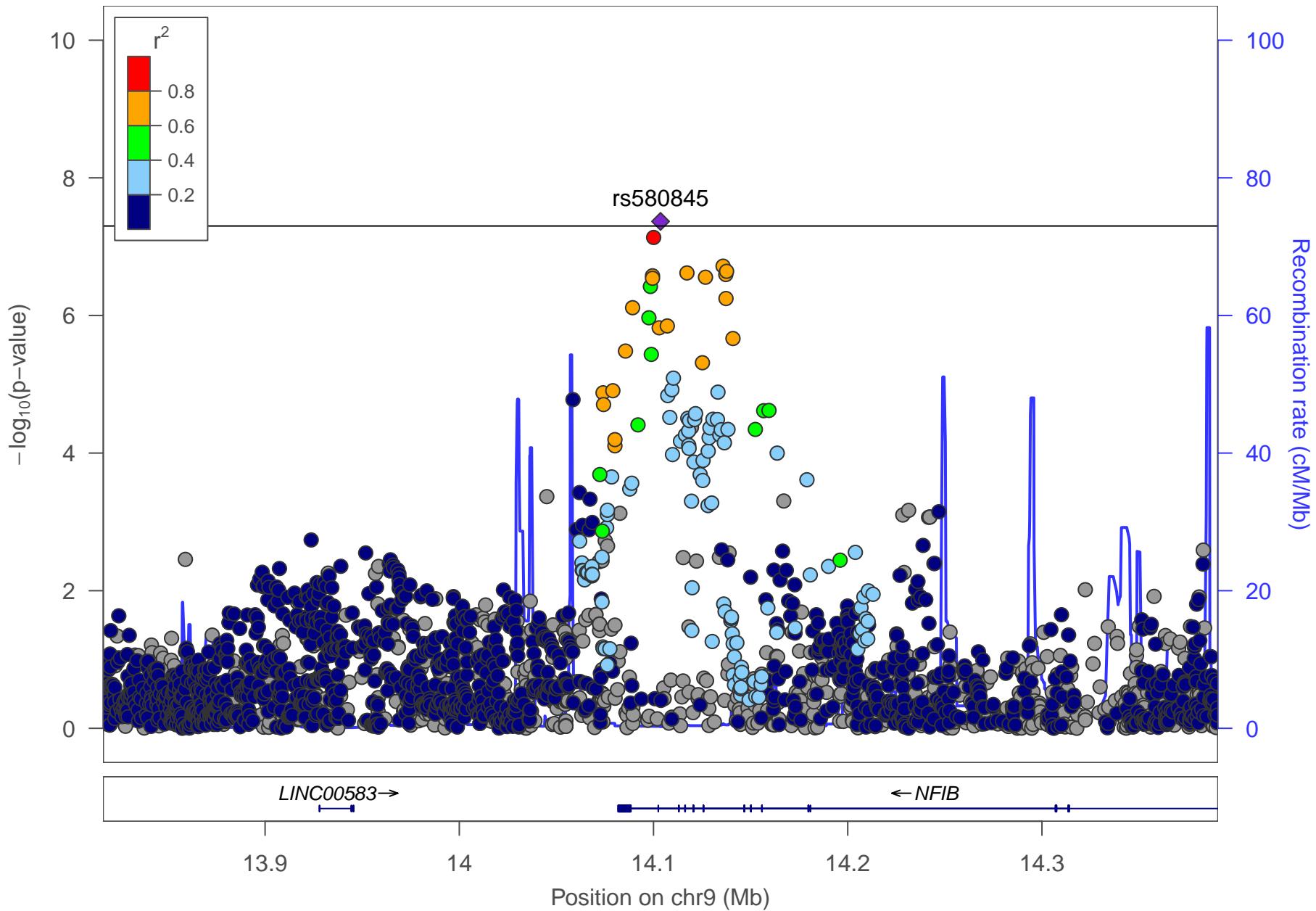


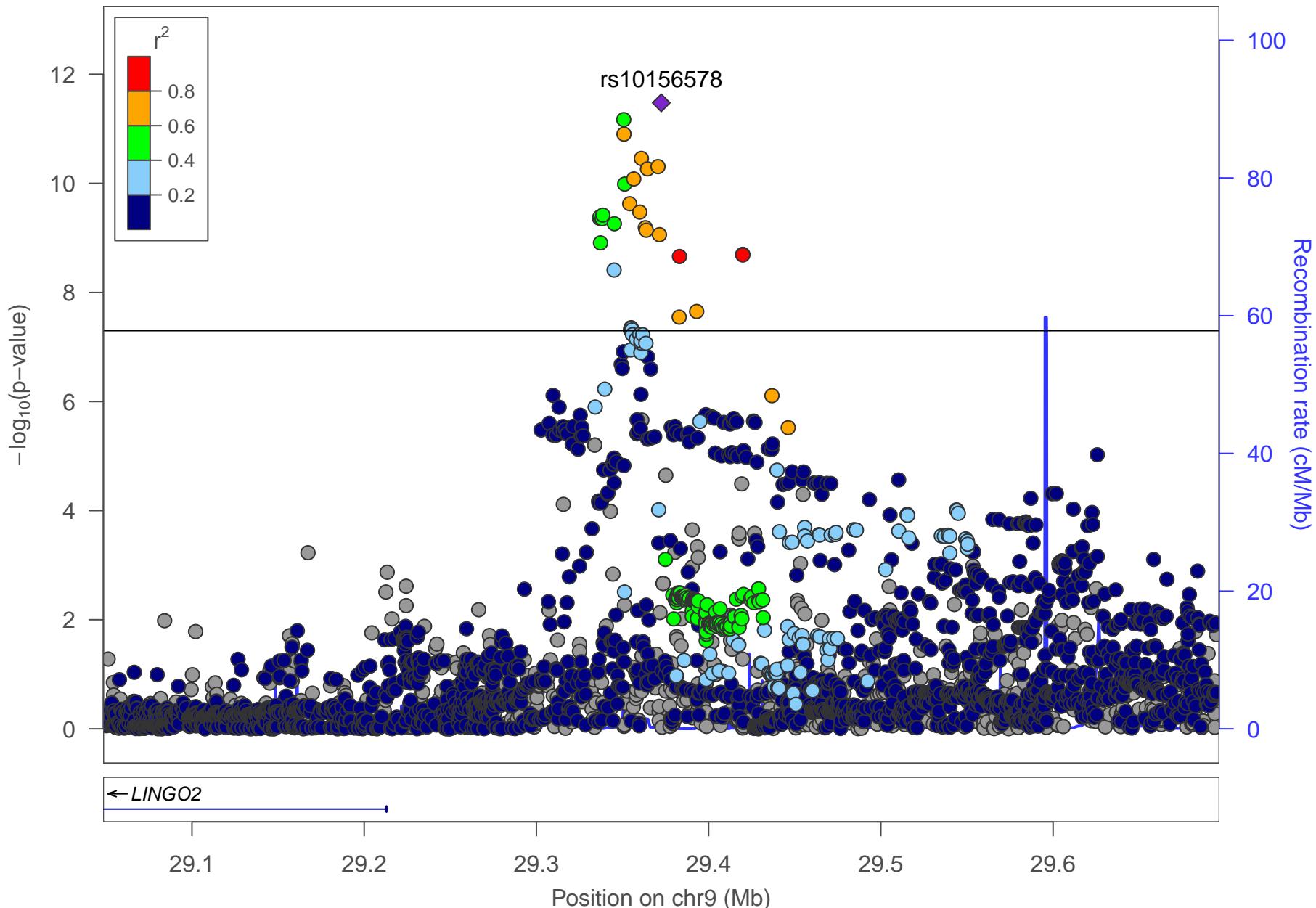


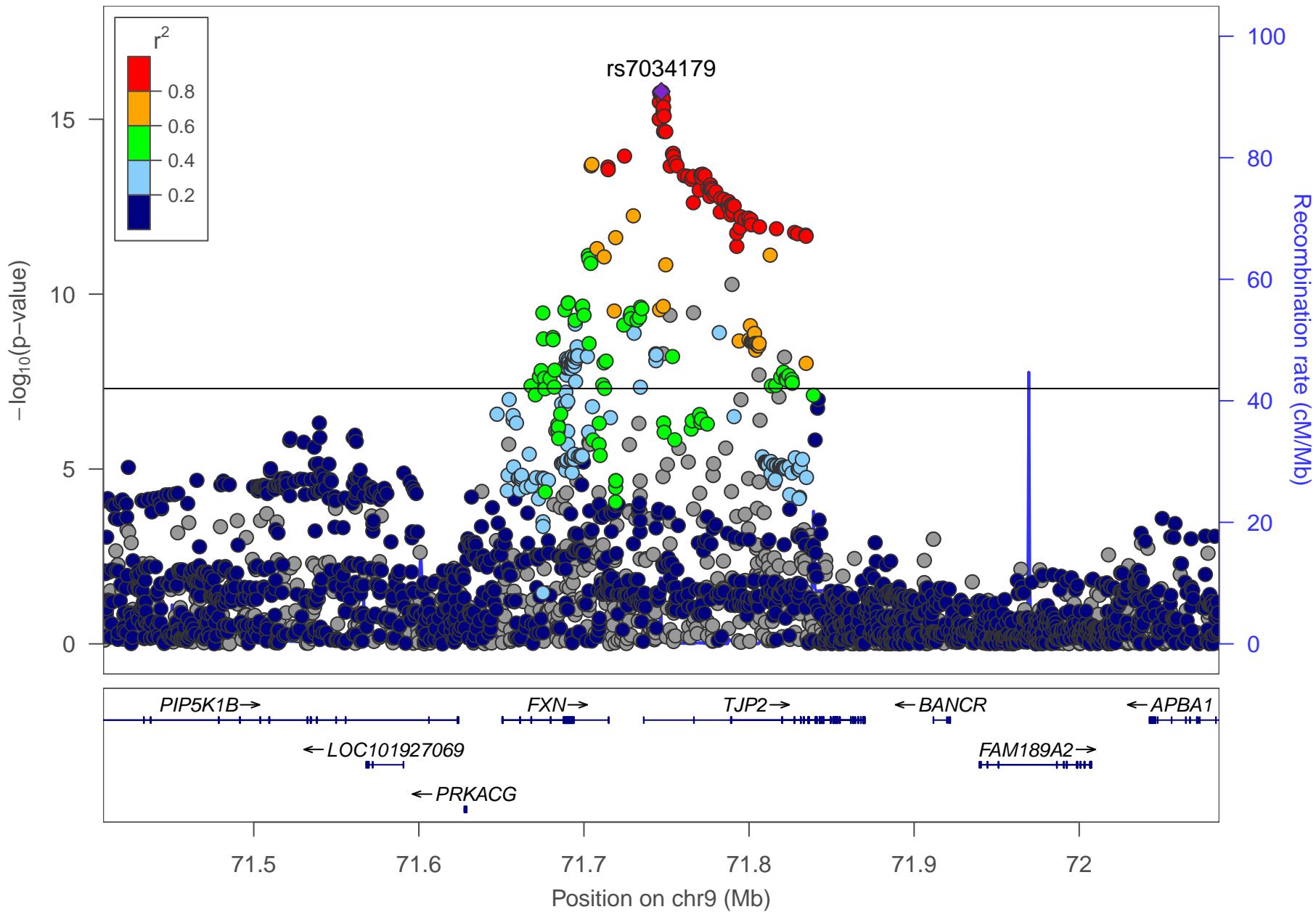


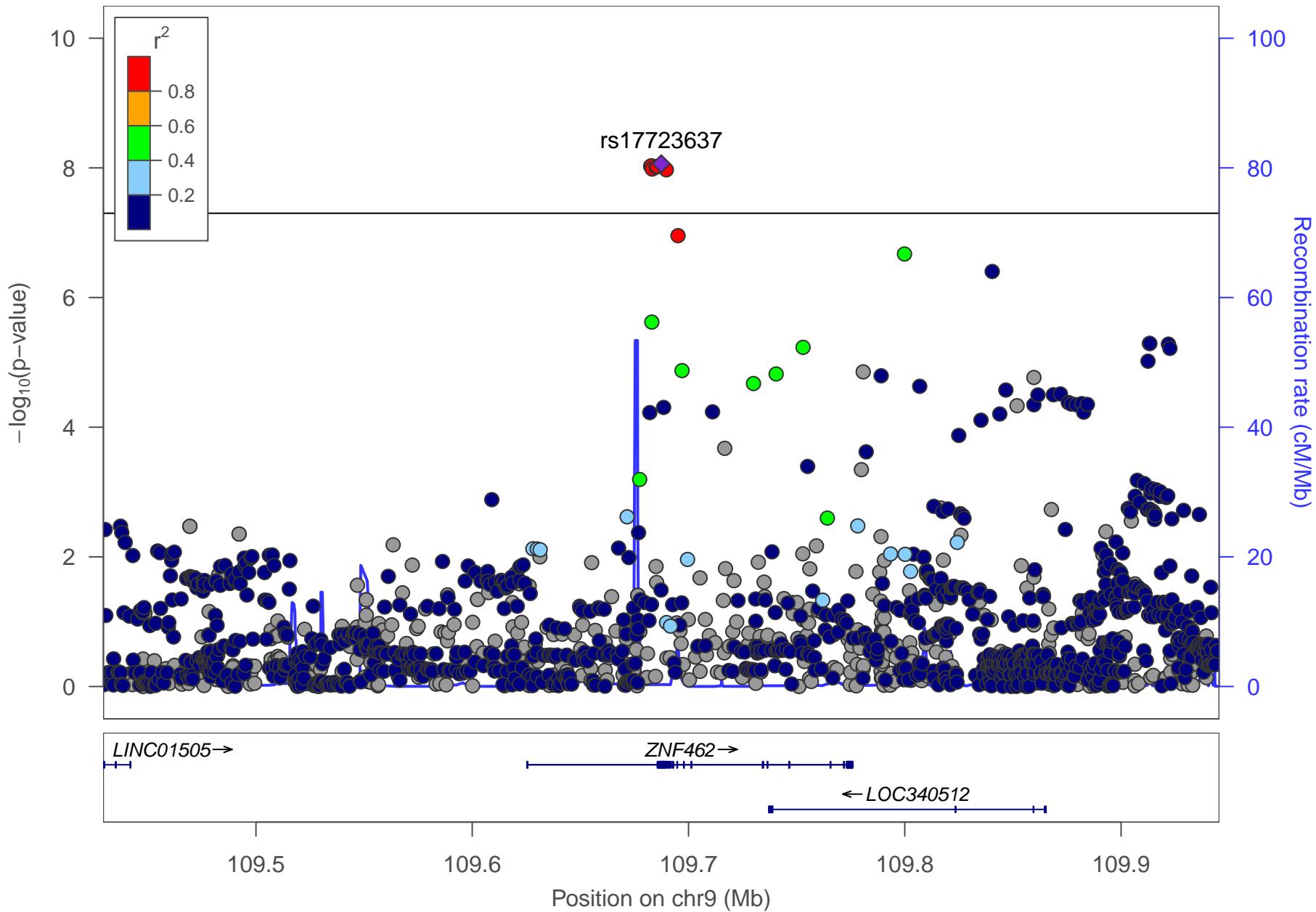


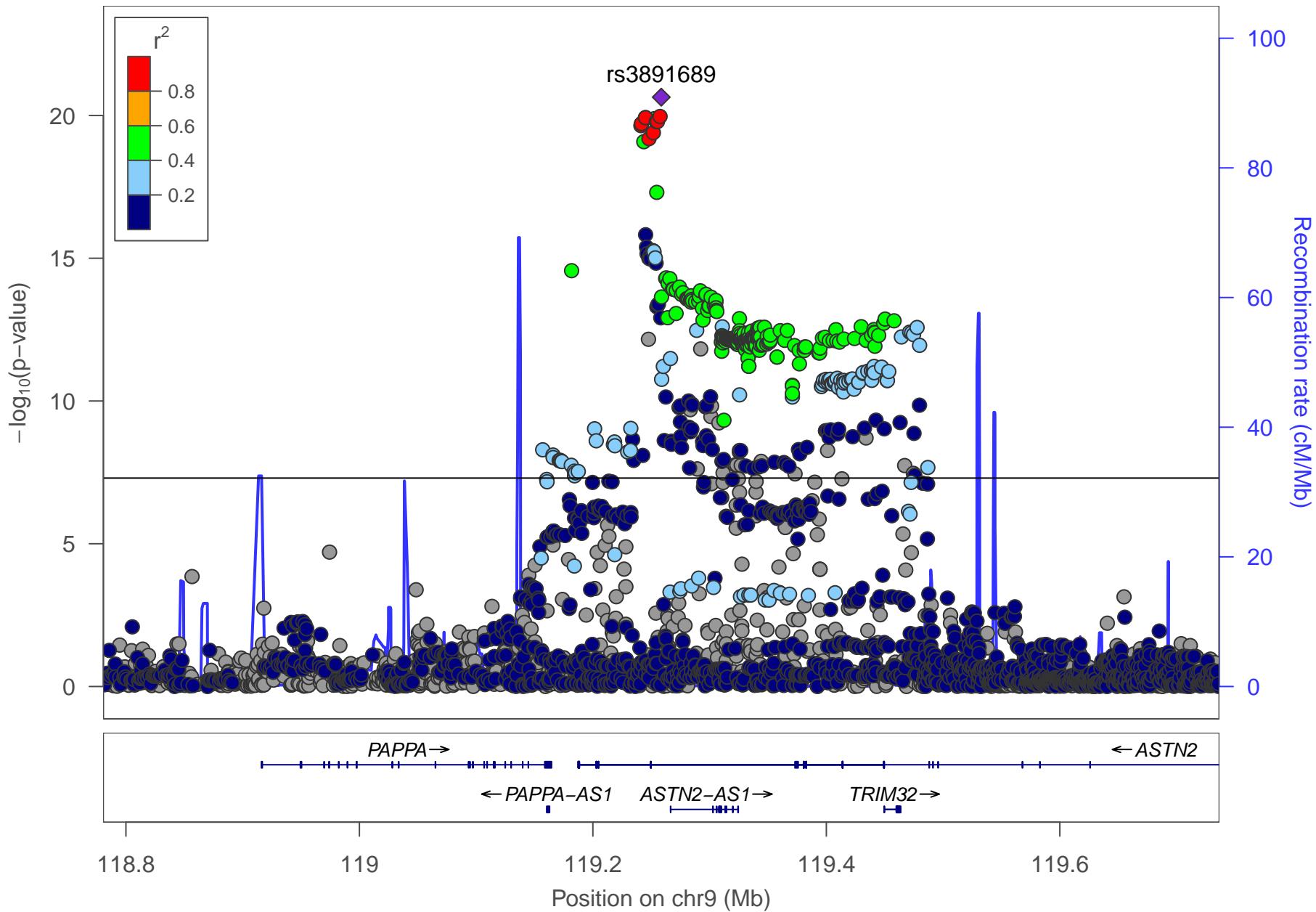


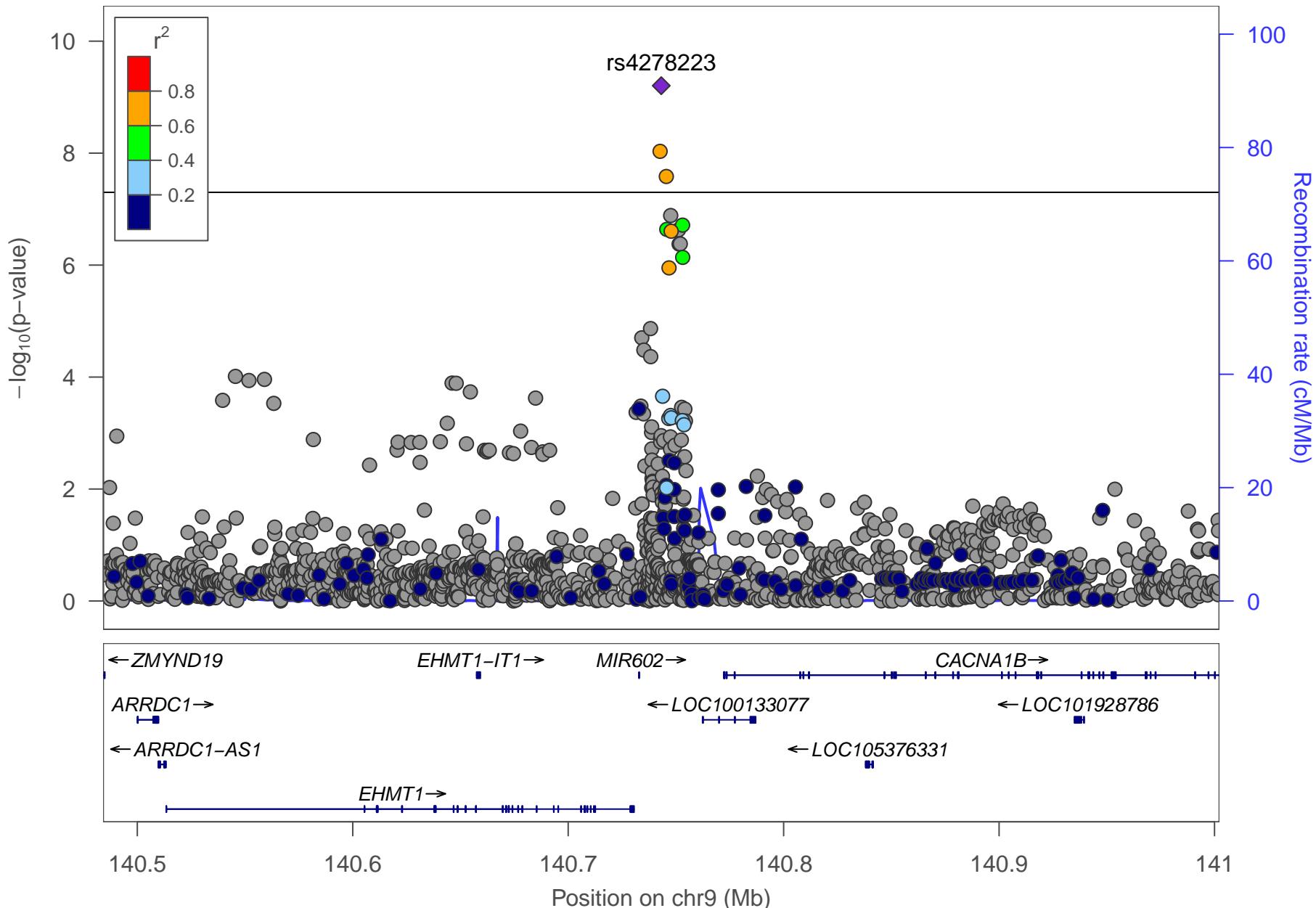


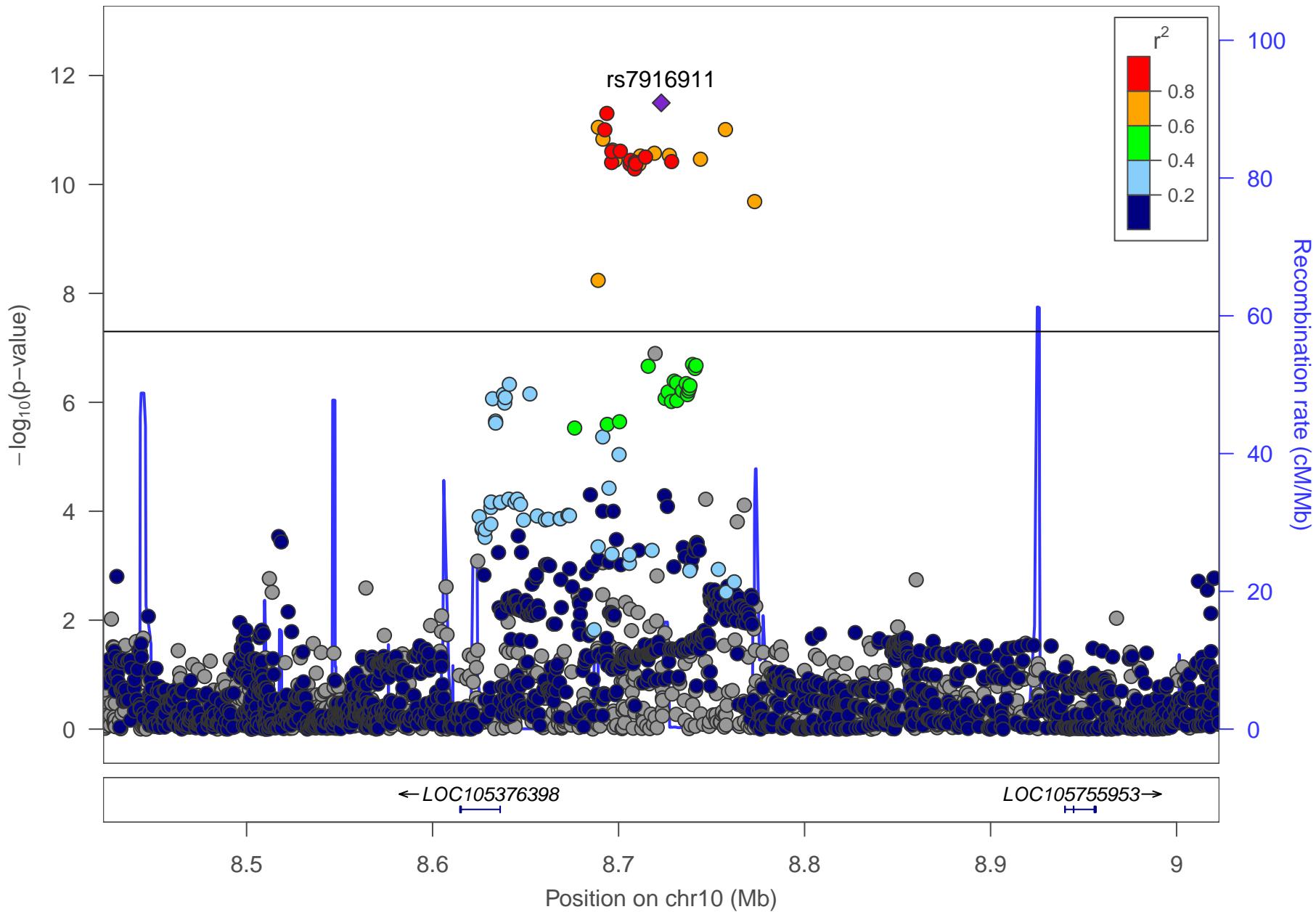


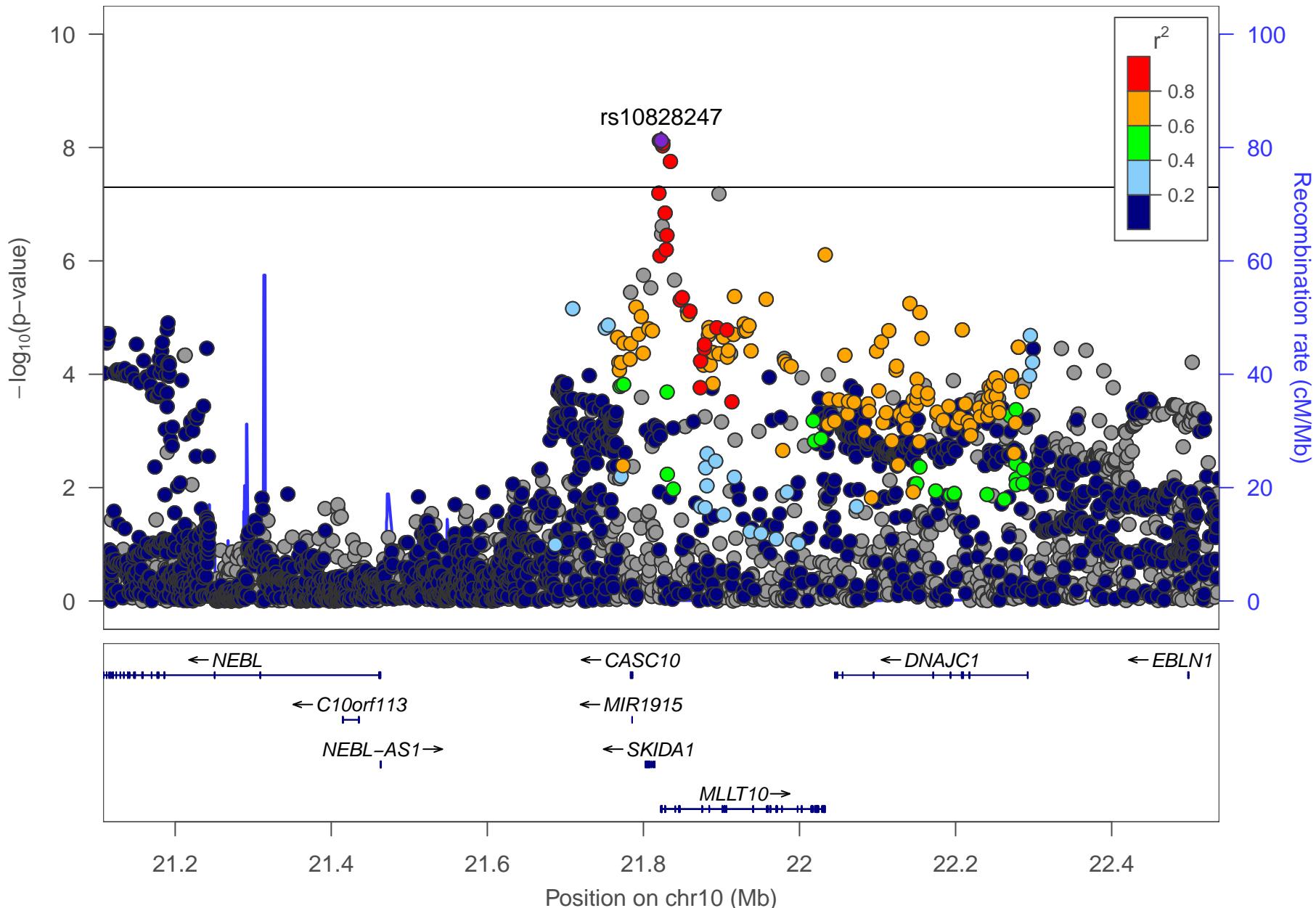


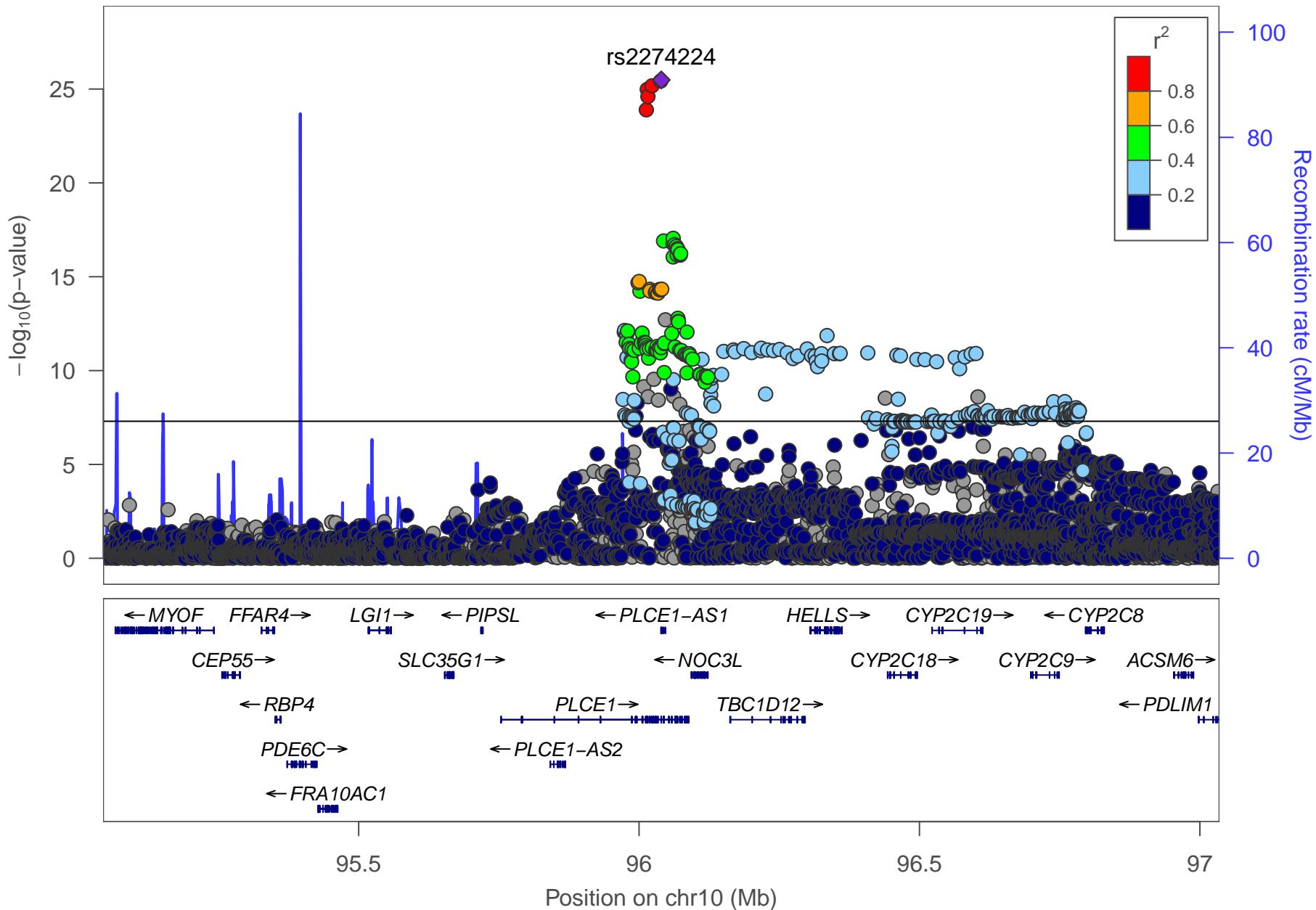


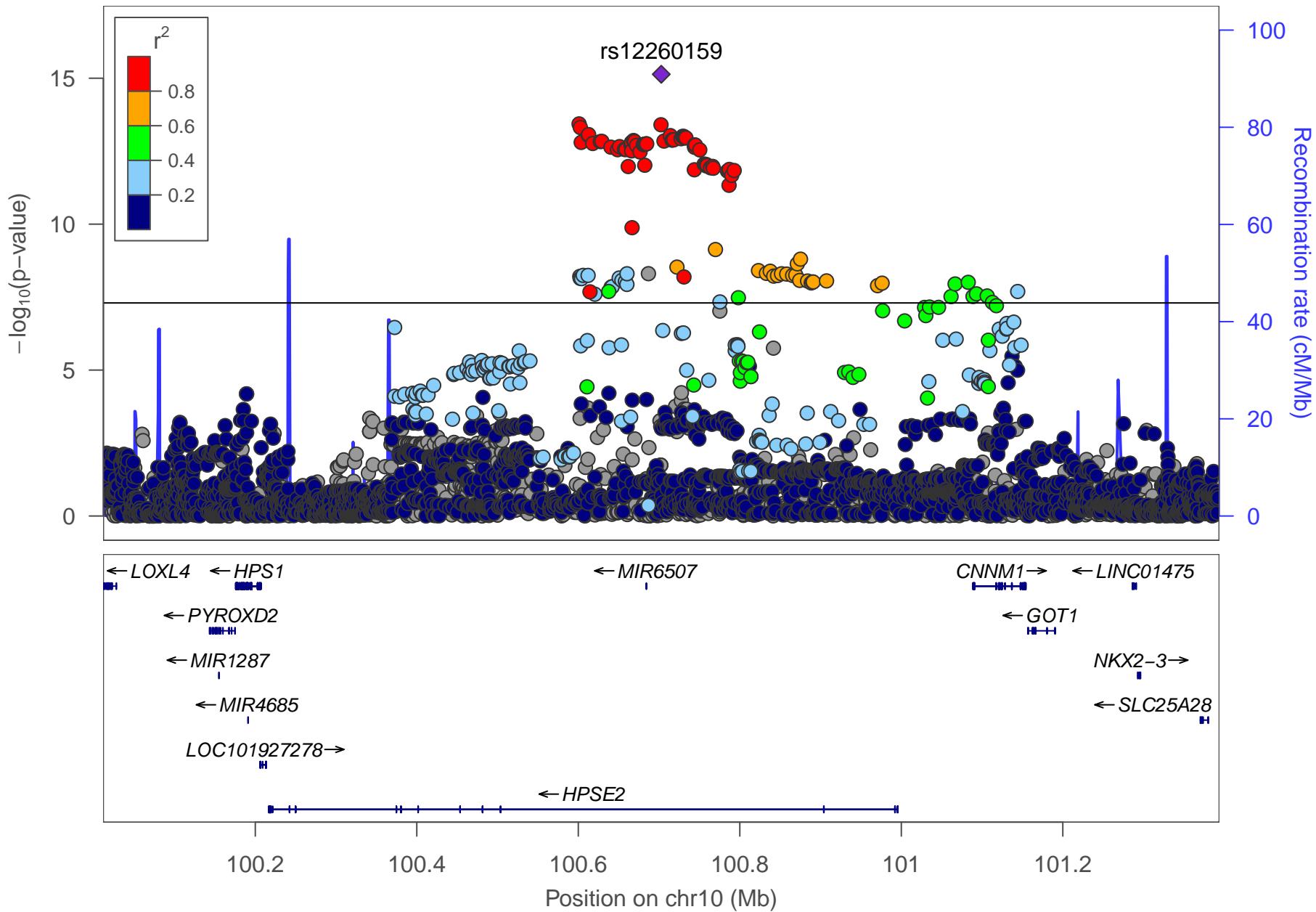


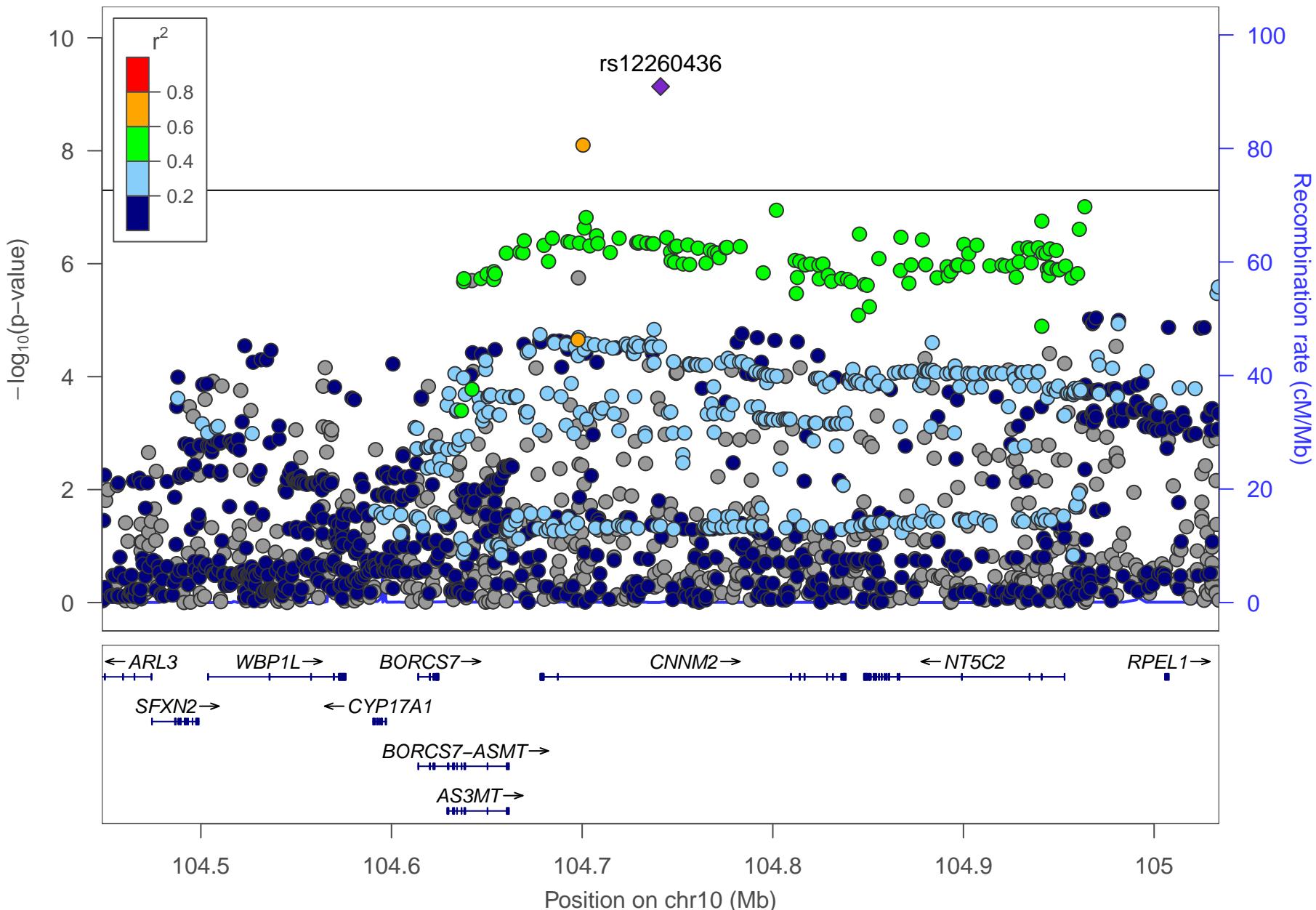


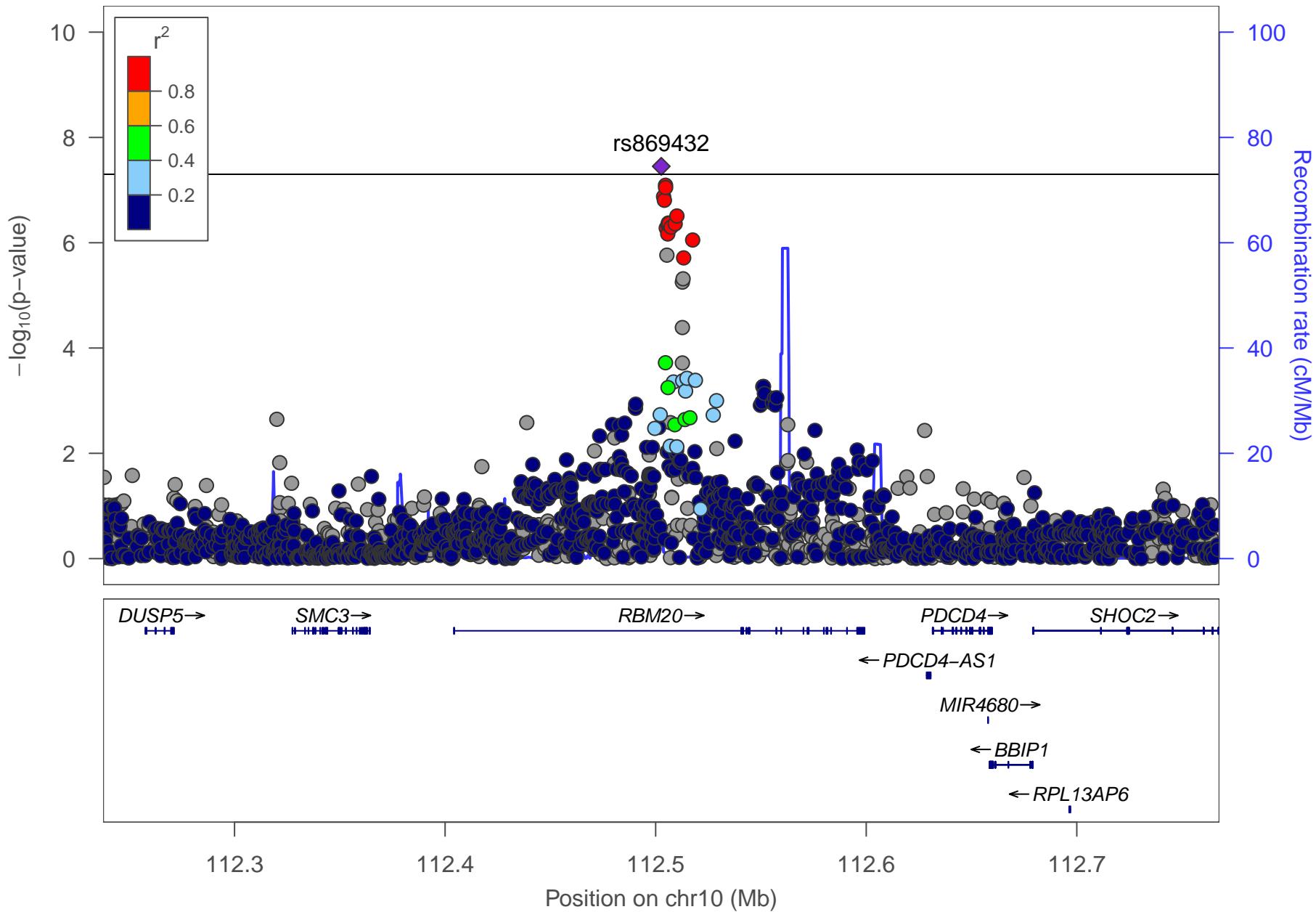


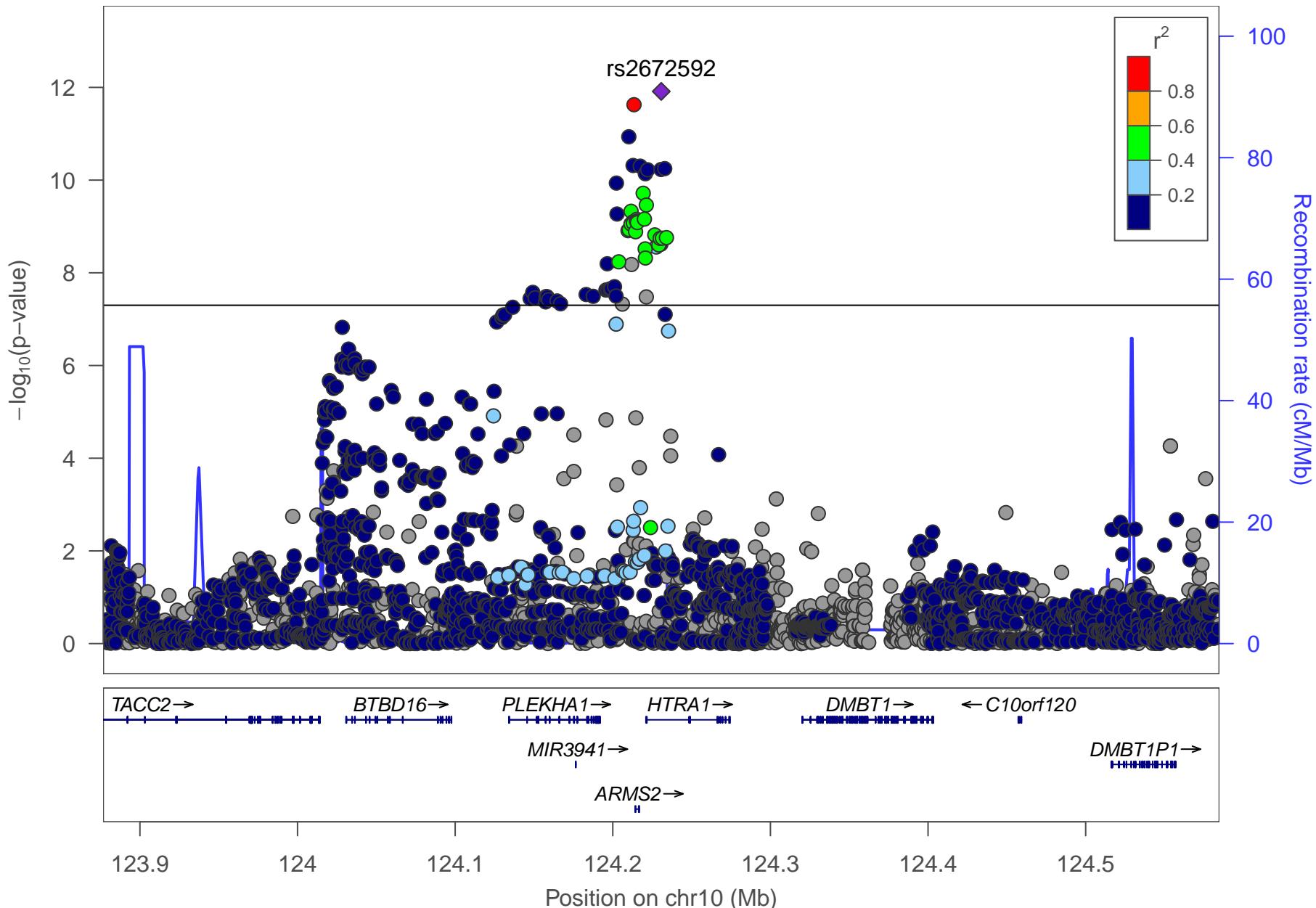


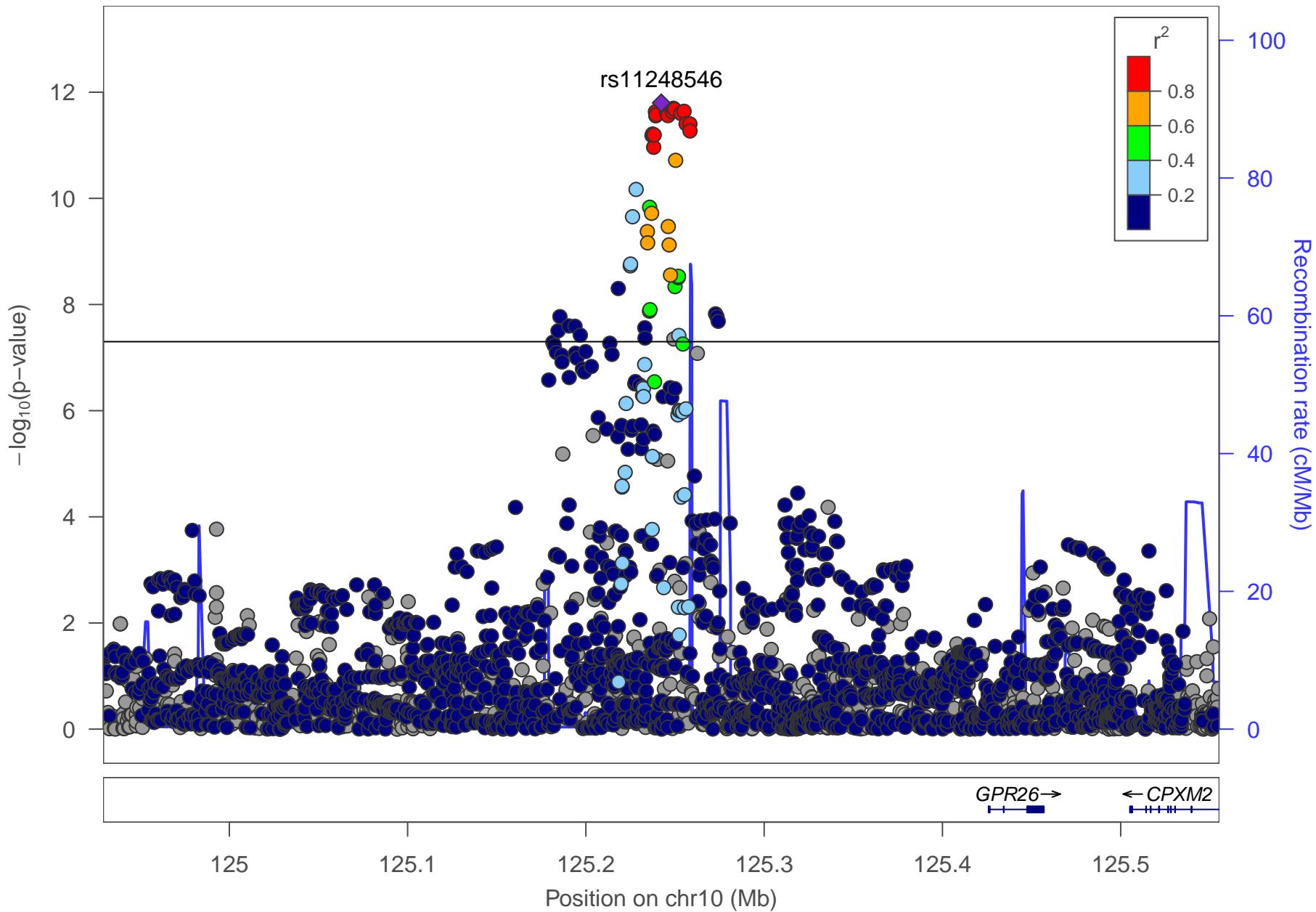


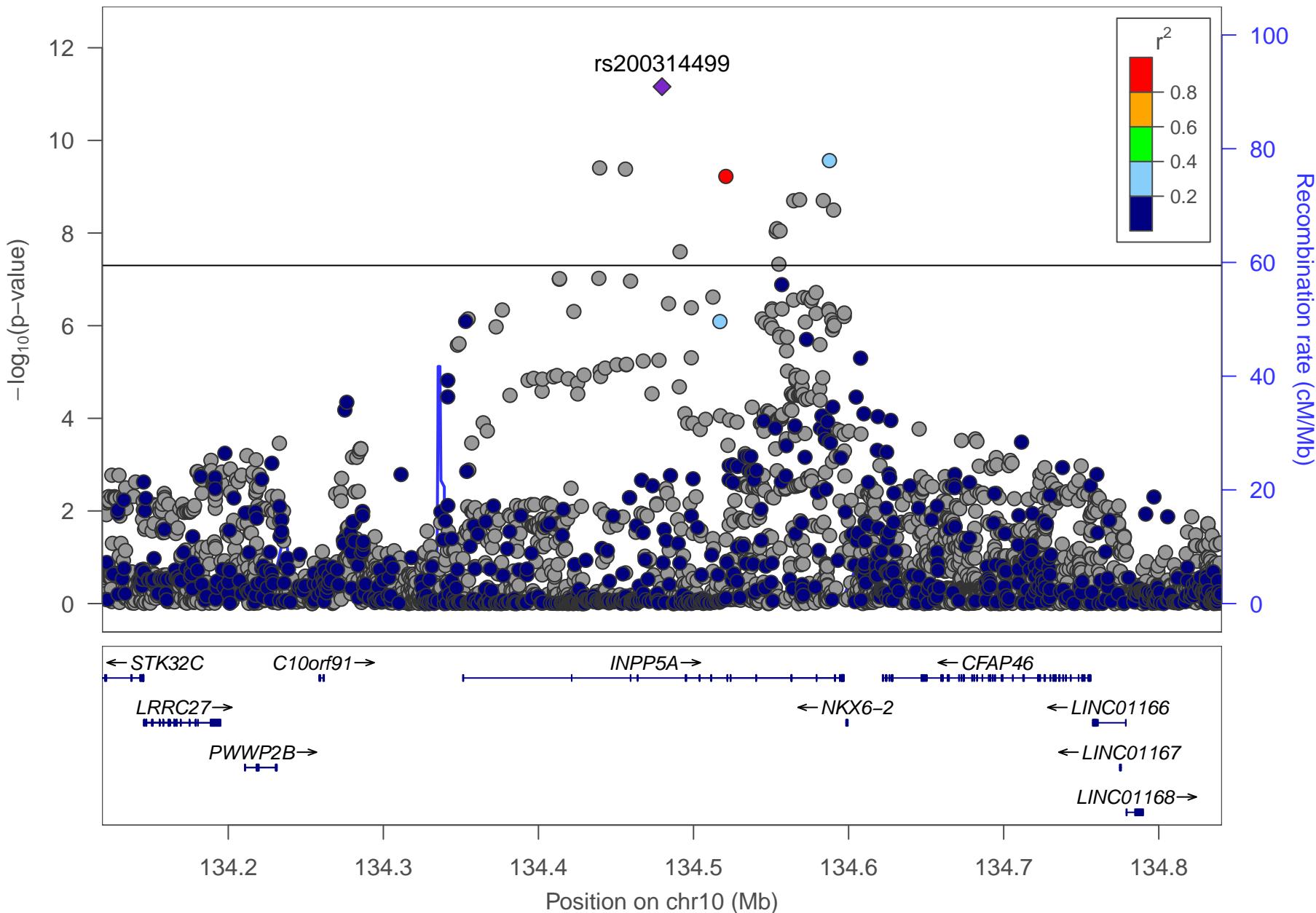


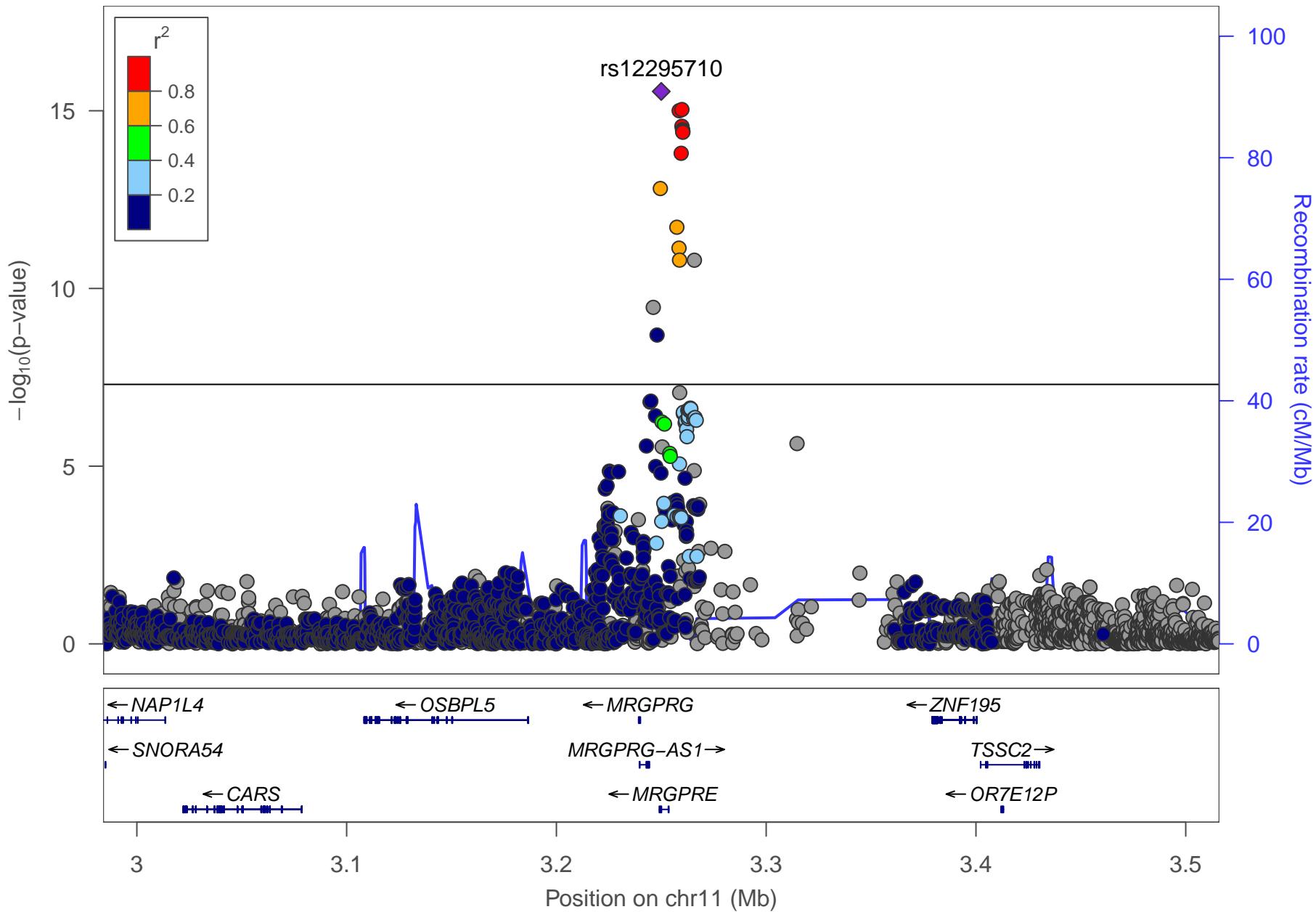


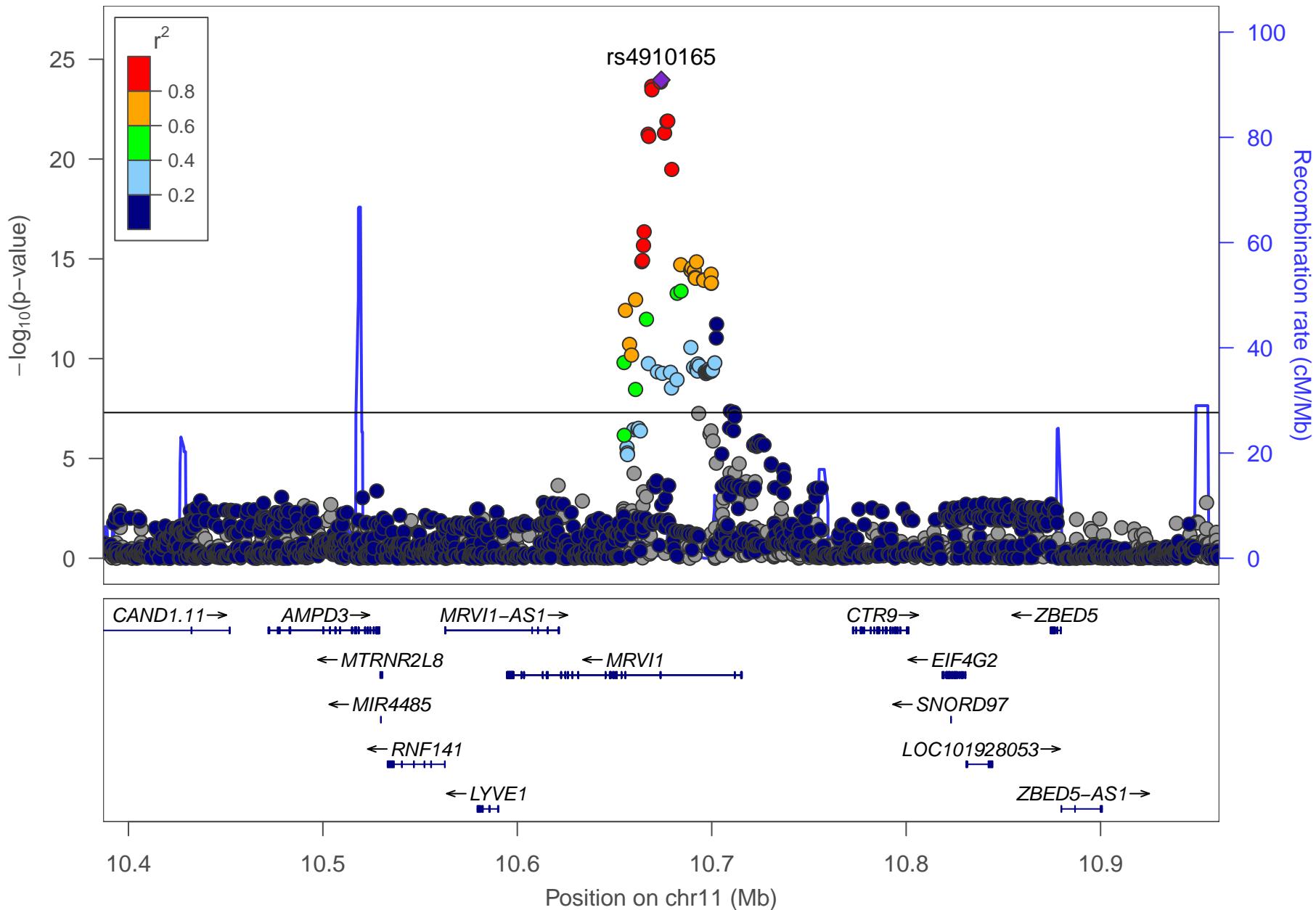


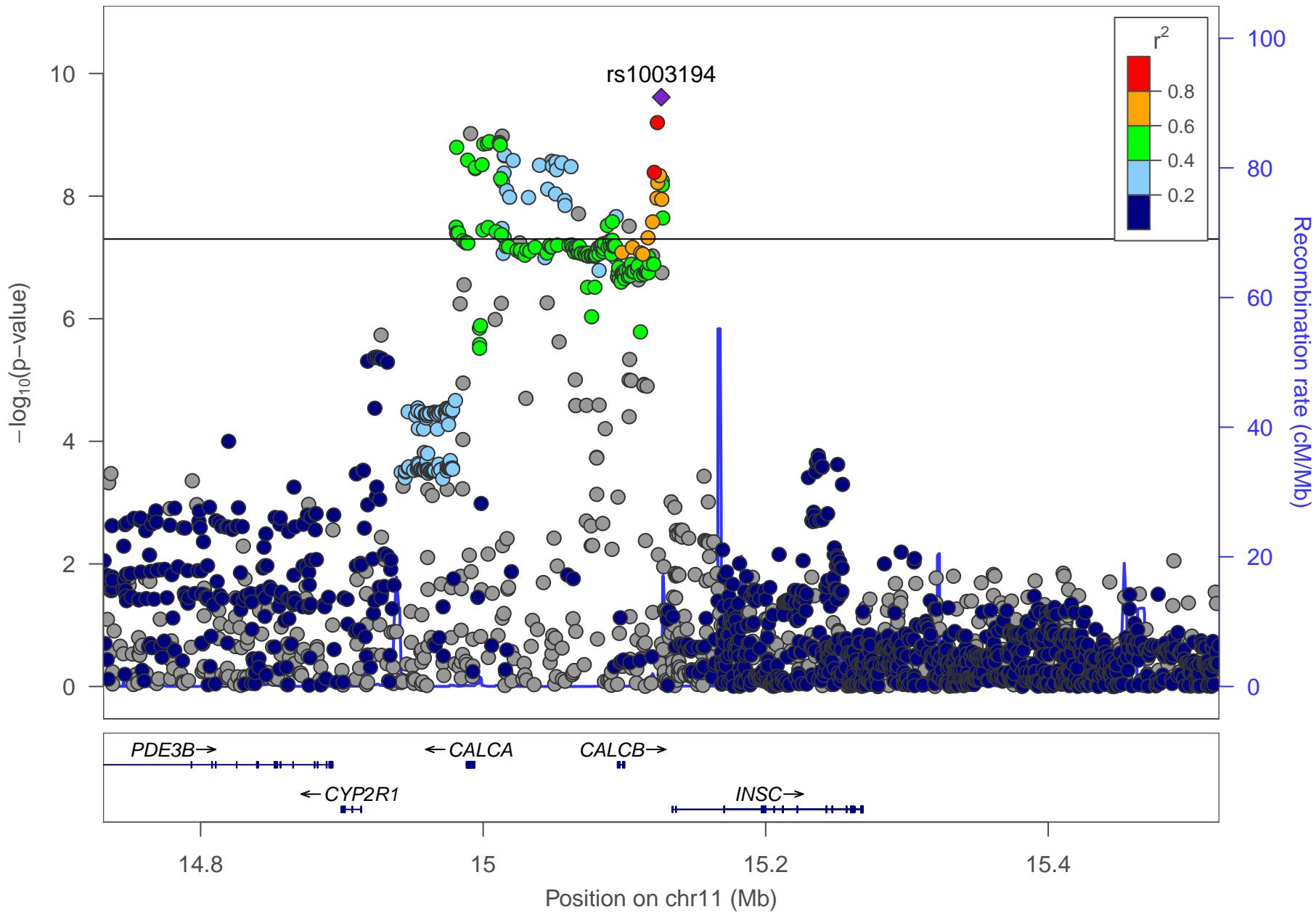


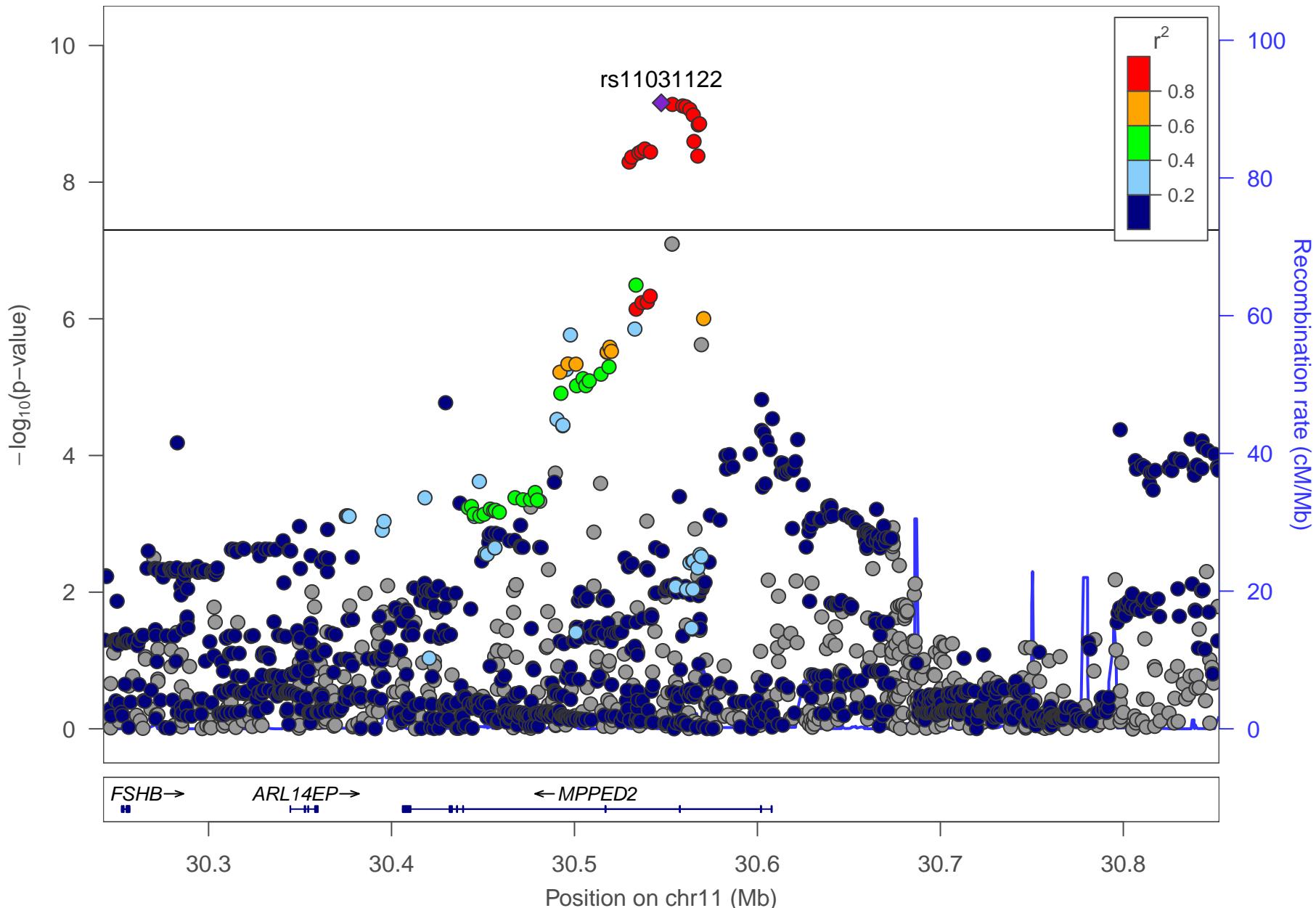


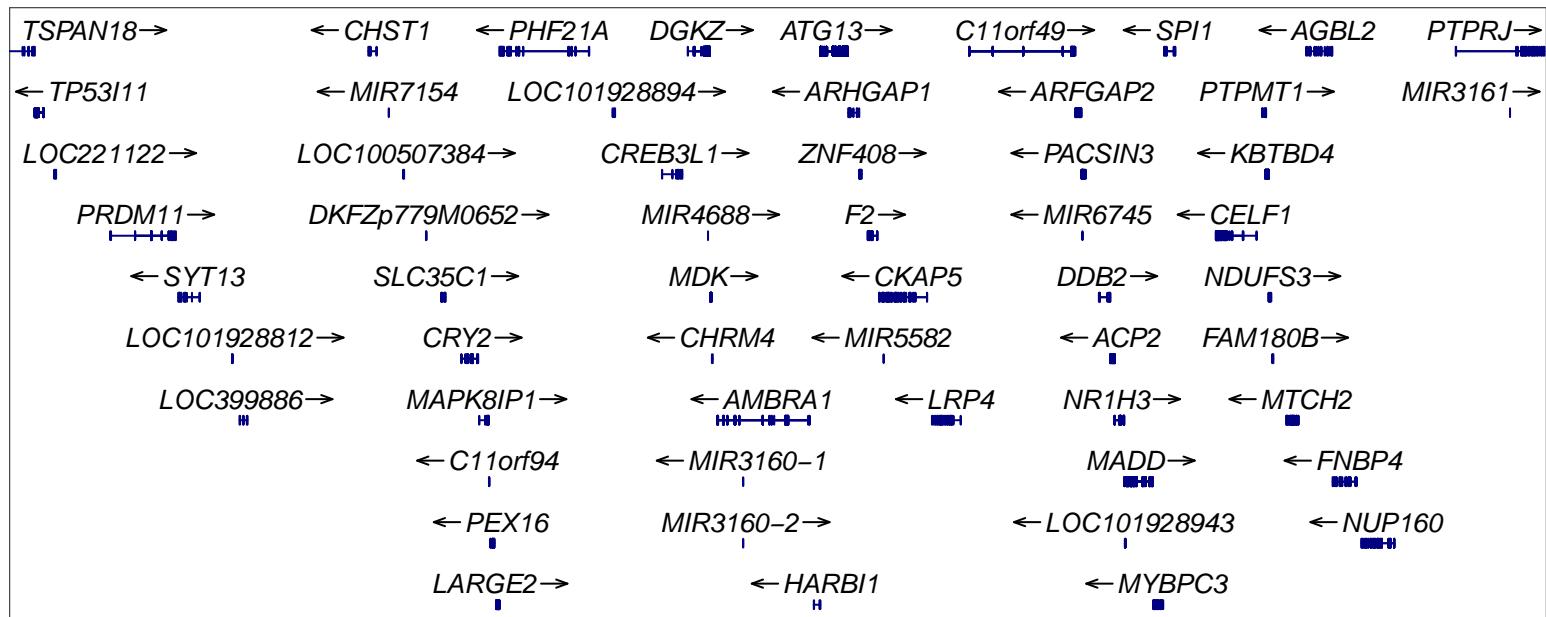
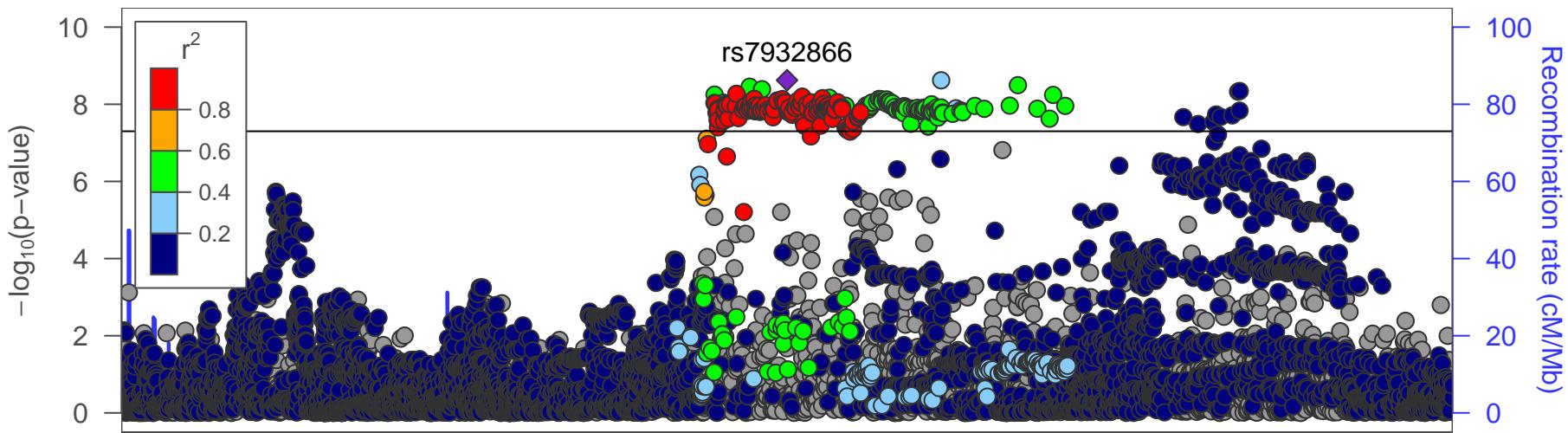












45 45.5 46 46.5 47 47.5 48

Position on chr11 (Mb)

7 genes
omitted

