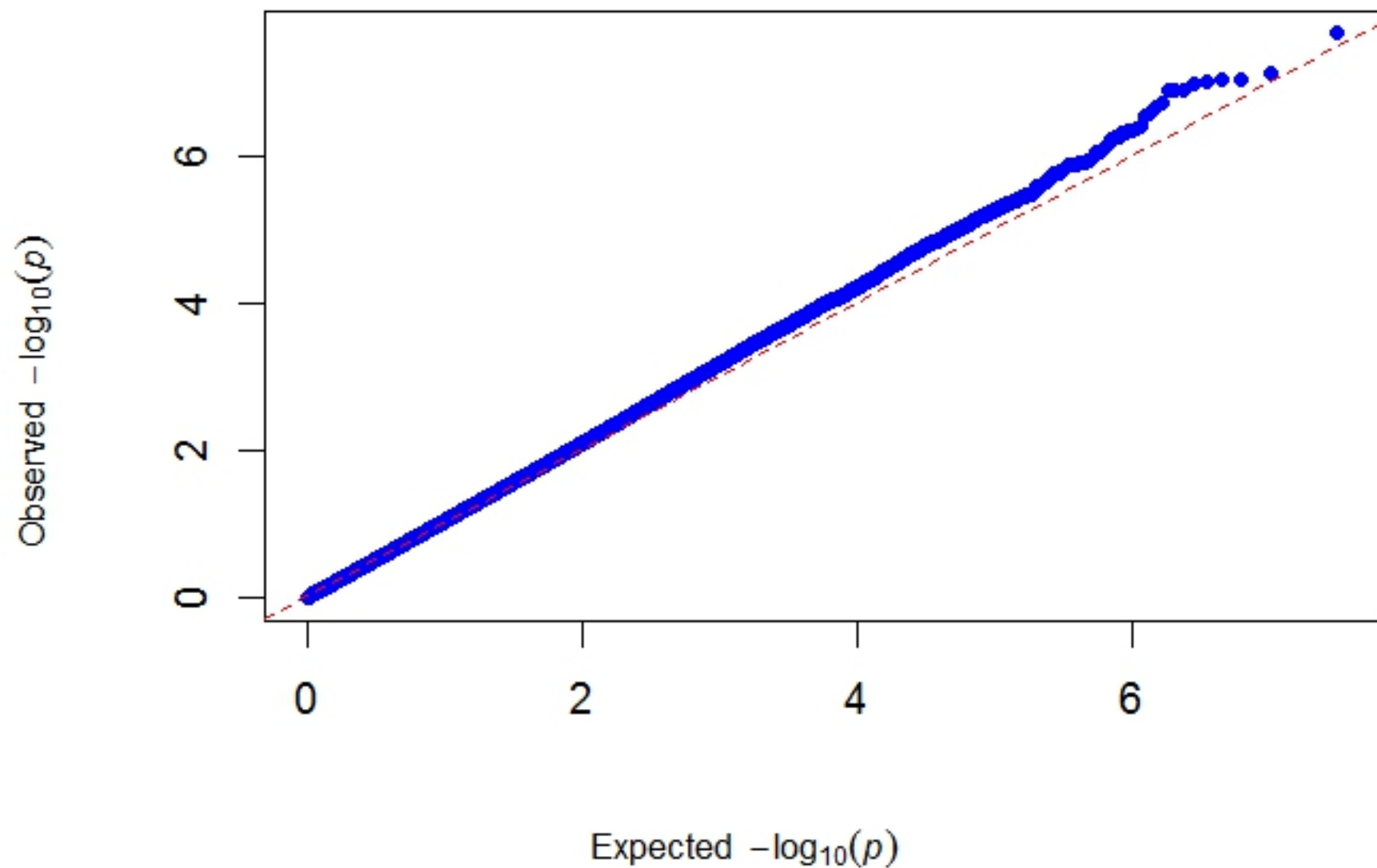
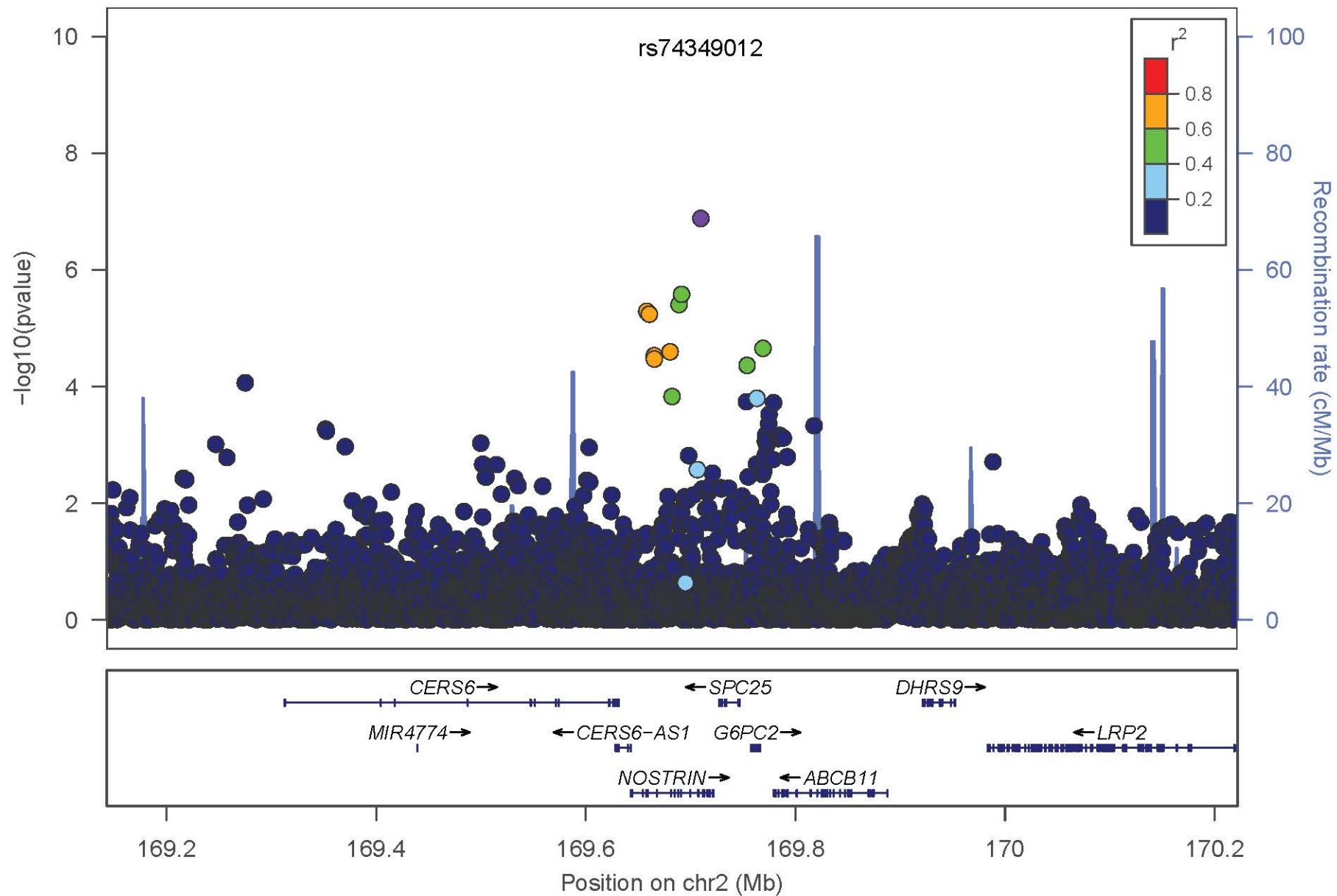
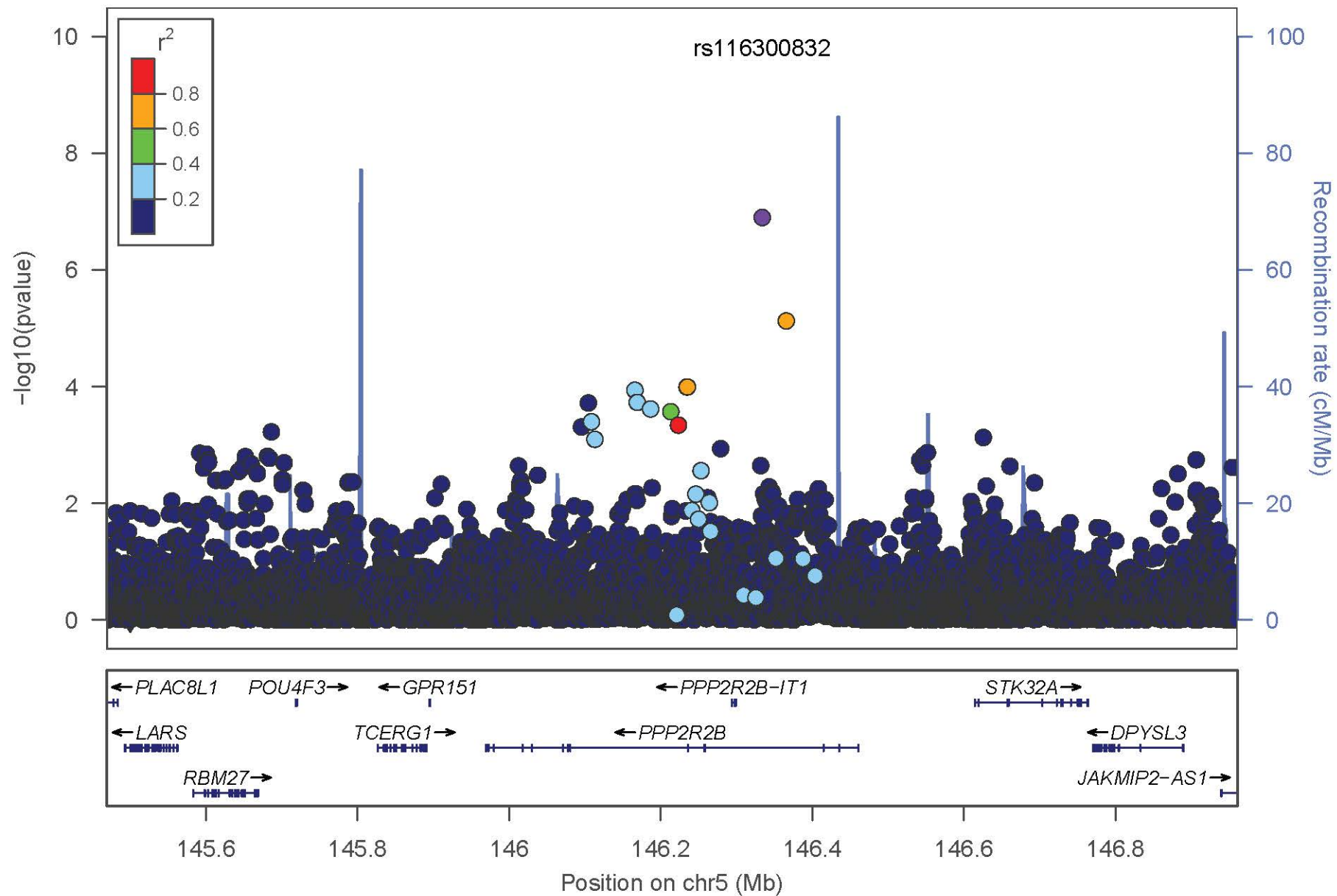
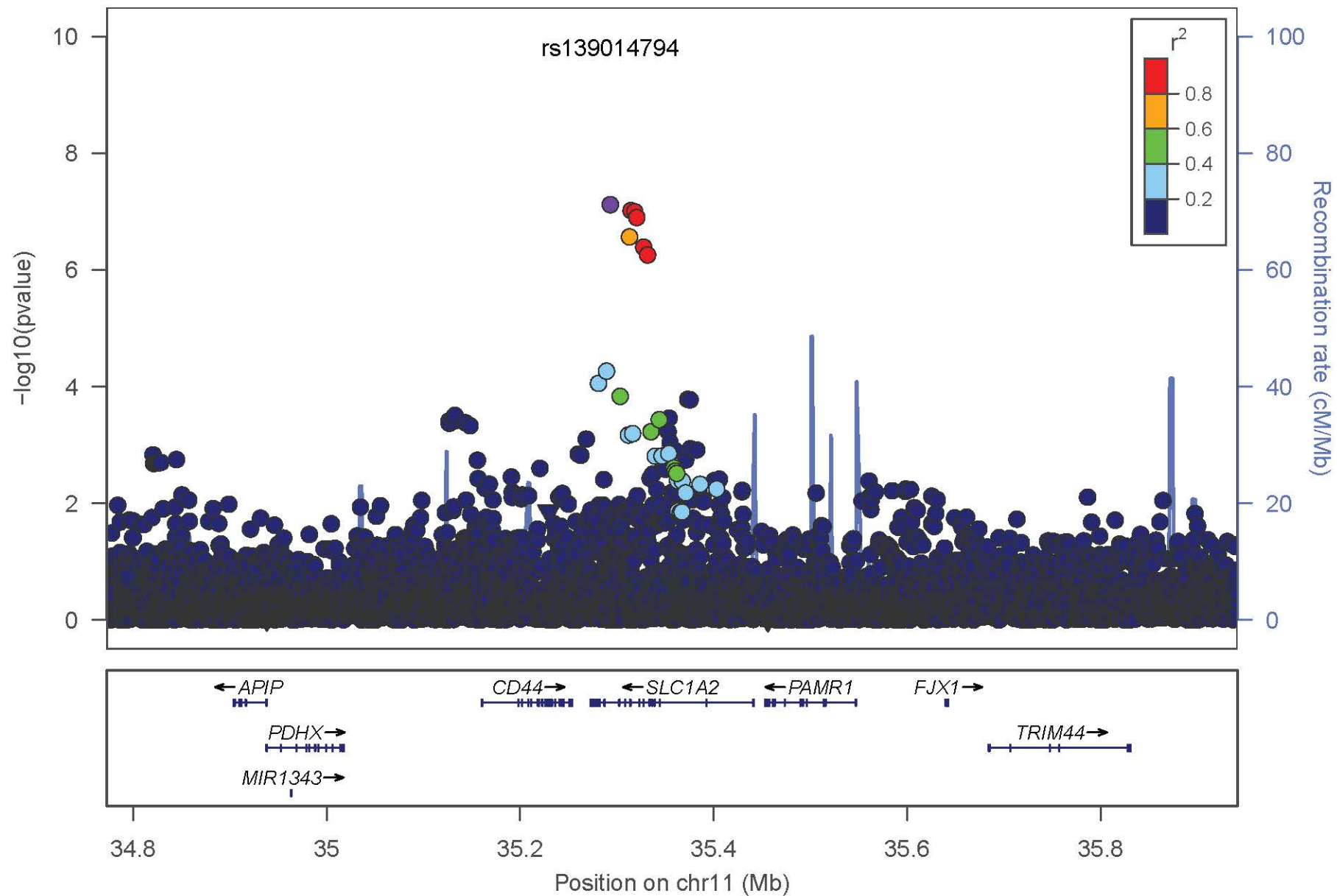


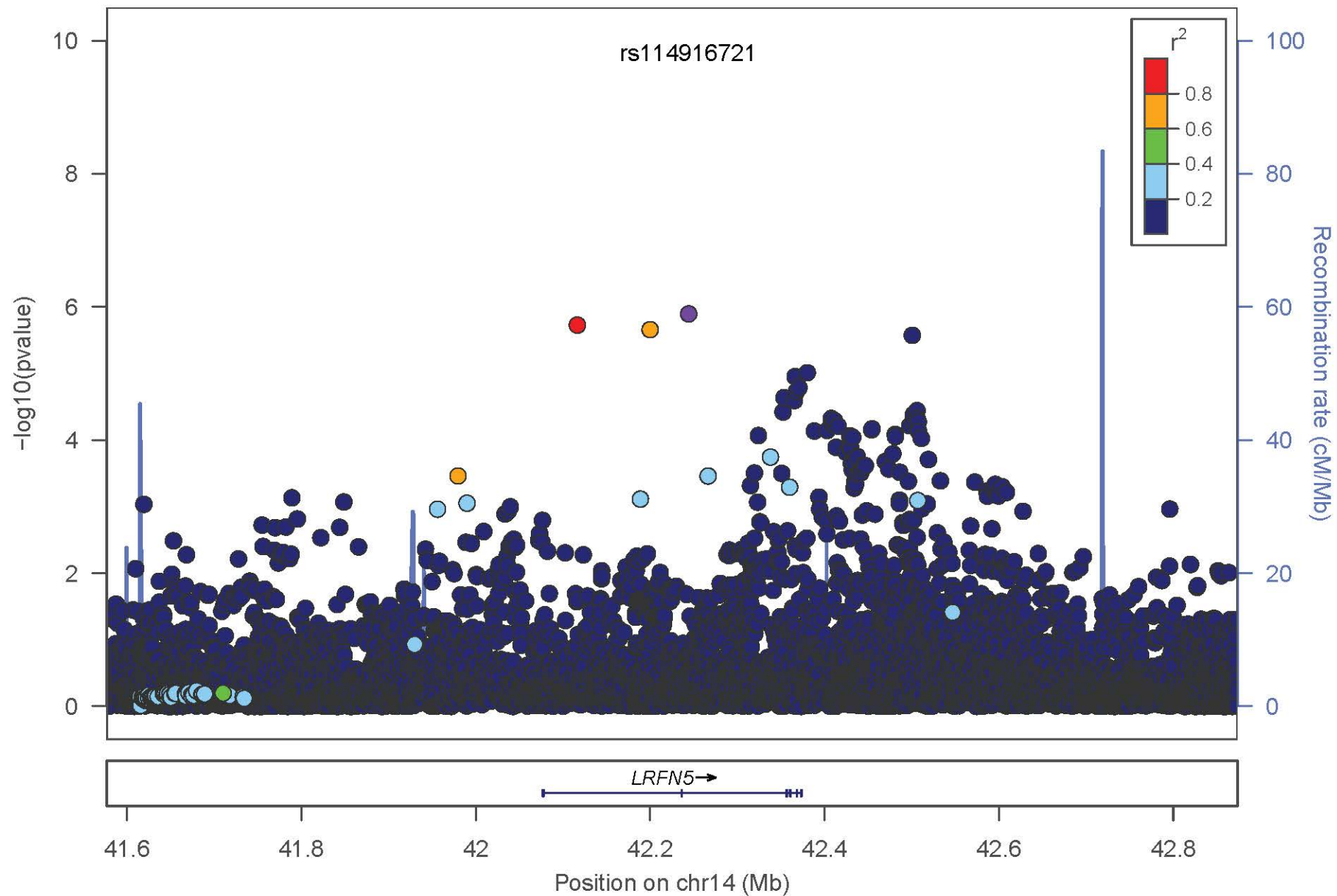
Quantile-quantile plot of p values

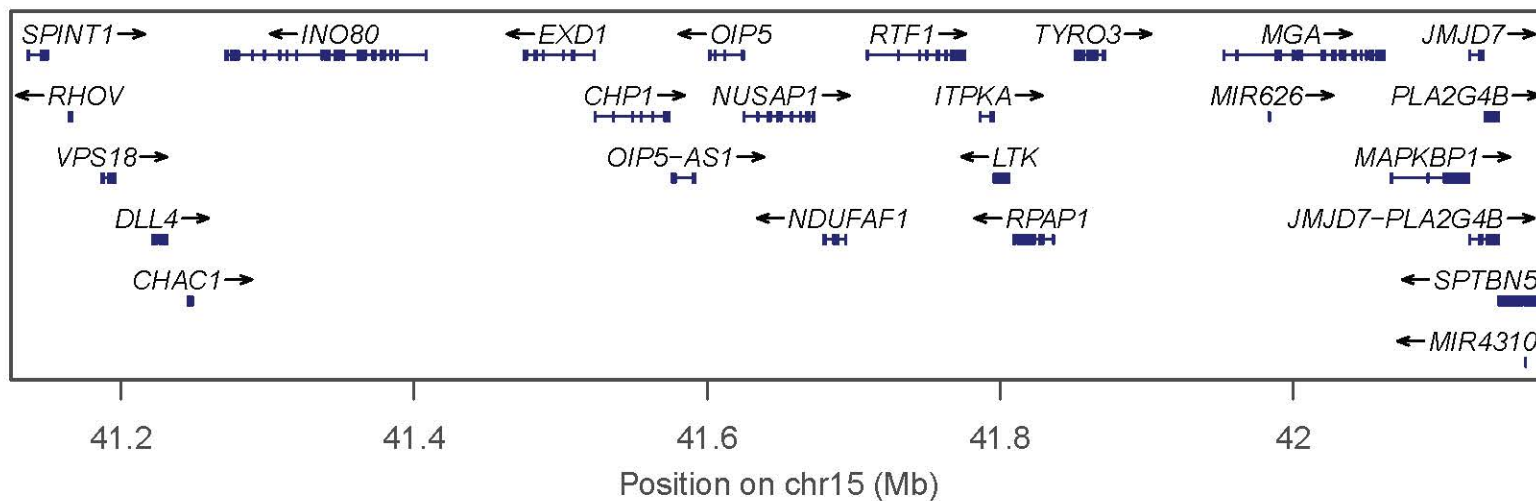
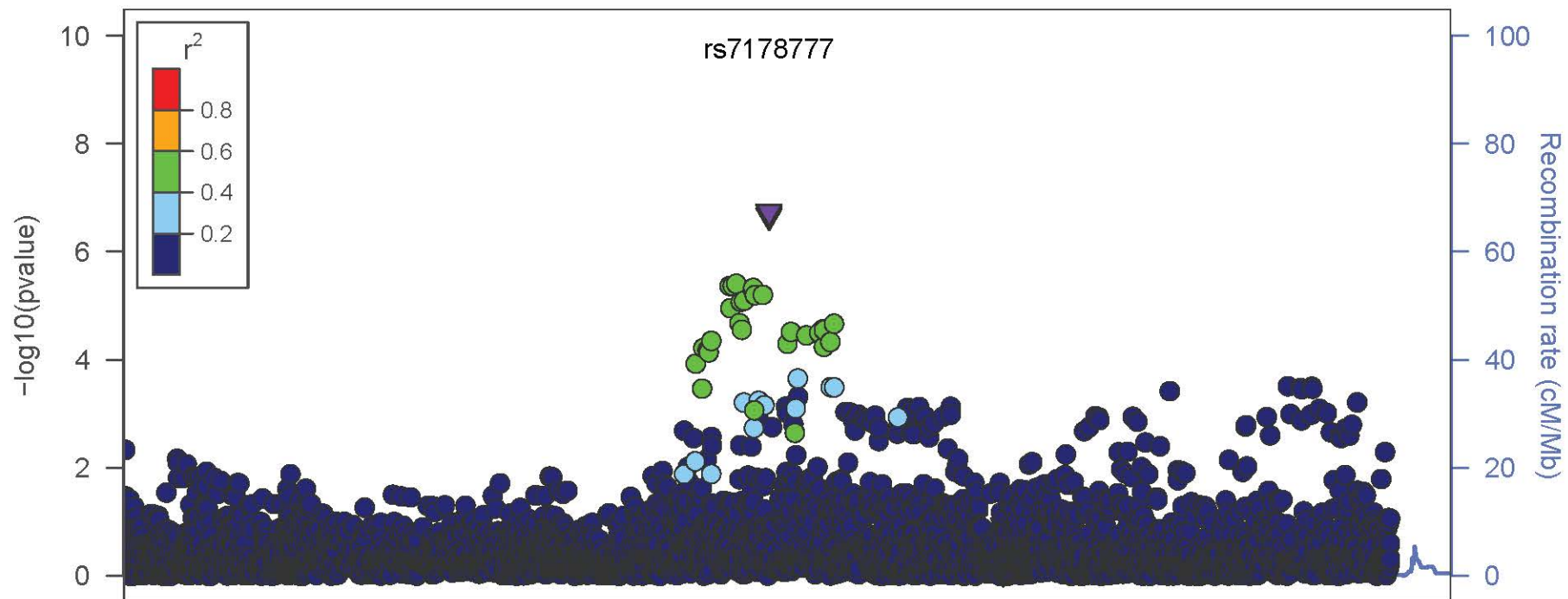












Legends:

Figure S1: Quantile-quantile of p -values for BMI genome-wide association results. The x-axis represents expected p -values and the y-axis represents observed p -values, $\lambda = 1.01$.

Figure S2: *NOSTRIN* regional plot. The x-axis represents positions (Mb) and the y-axis represents $-\log_{10}(p\text{-values})$. The recombination rates and r^2 scores were calculated from AFR samples in the 1000 Genomes Project (phase1, V3).

Figure S3: *PPP2R2B* regional plot. The x-axis represents positions (Mb) and the y-axis represents $-\log_{10}(p\text{-values})$. The recombination rates and r^2 scores were calculated from AFR samples in the 1000 Genomes Project (phase1, V3).

Figure S4: *SLC1A2* regional plot. The x-axis represents positions (Mb) and the y-axis represents $-\log_{10}(p\text{-values})$. The recombination rates and r^2 scores were calculated from AFR samples in the 1000 Genomes Project (phase1, V3).

Figure S5: *LRFN5* regional plot. The x-axis represents positions (Mb) and the y-axis represents $-\log_{10}(p\text{-values})$. The recombination rates and r^2 scores were calculated from AFR samples in the 1000 Genomes Project (phase1, V3).

Figure S6: *NUSAP1* regional plot. The x-axis represents positions (Mb) and the y-axis represents $-\log_{10}(p\text{-values})$. The recombination rates and r^2 scores were calculated from AFR samples in the 1000 Genomes Project (phase1, V3).