

# Supplementary figures of “Integrating eQTL data with GWAS summary statistics in pathway-based analysis”

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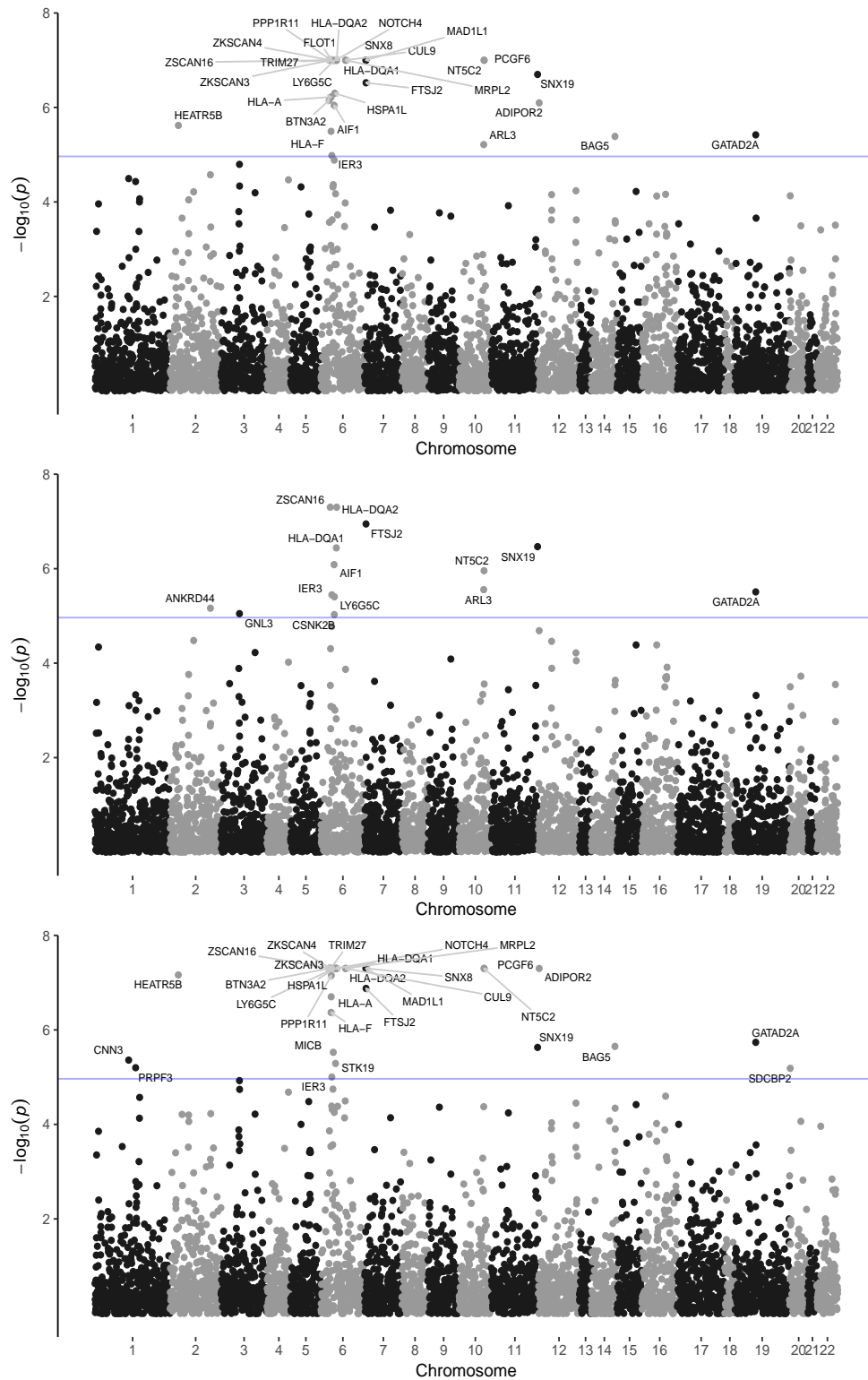


Figure 1: The Manhattan plots of aSPU (top), TWAS (middle), and SSU (bottom) applied to the SCZ1 data with the YFS-based weights. The p-values were truncated at  $5 \times 10^{-8}$ .

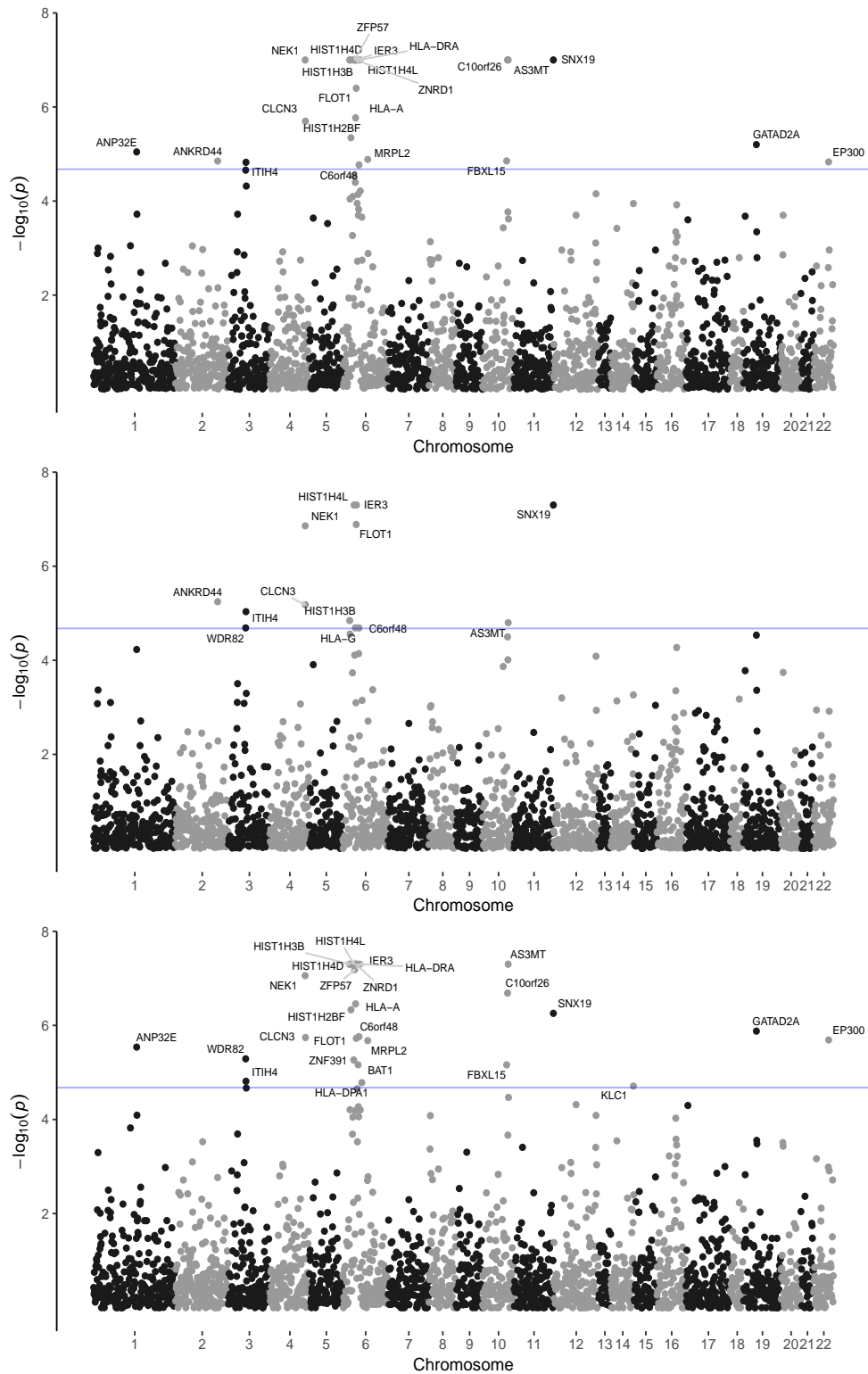


Figure 2: The Manhattan plots of aSPU (top), TWAS (middle), and SSU (bottom) applied to the SCZ1 data with the NTR-based weights. The p-values were truncated at  $5 \times 10^{-8}$ .

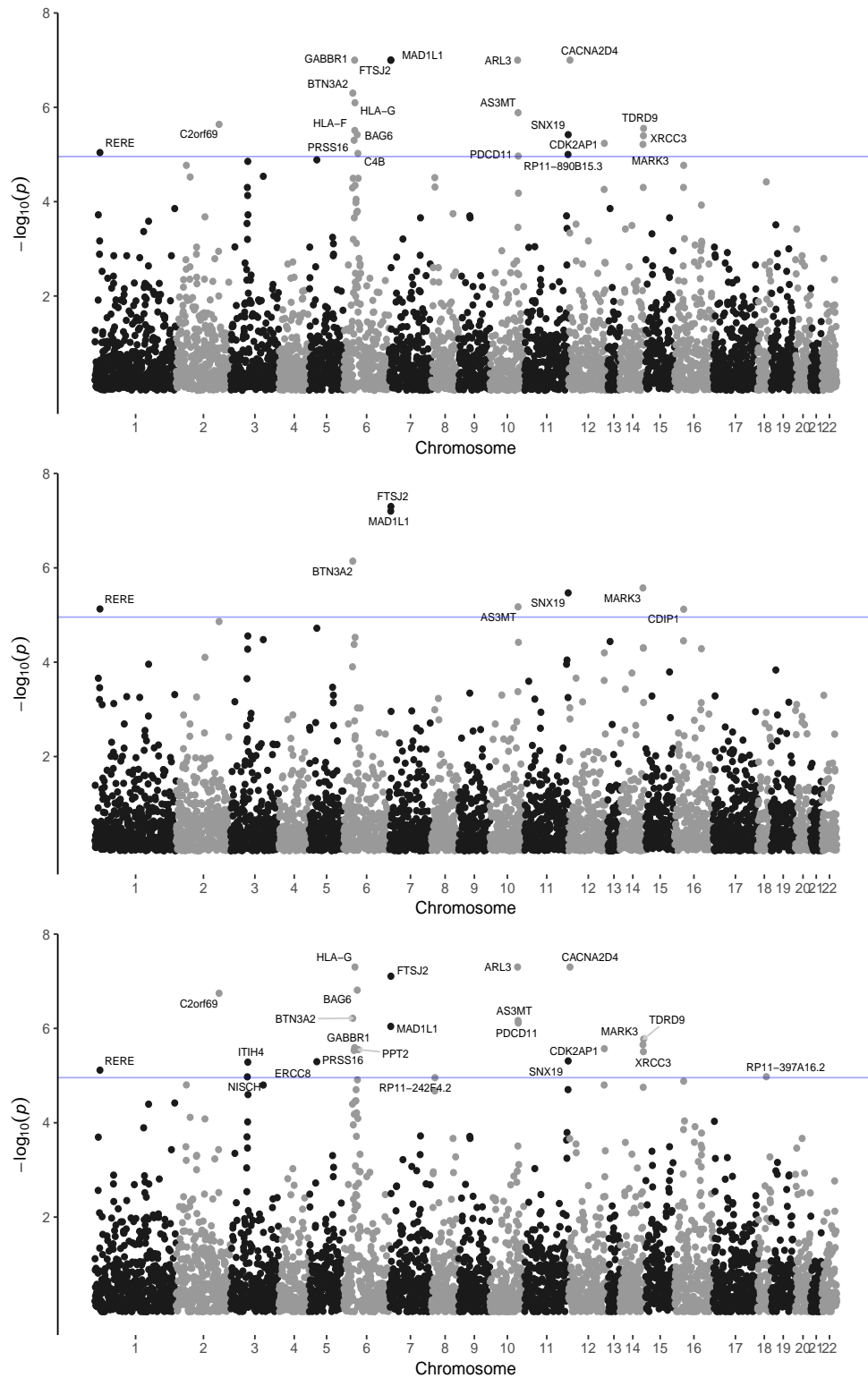


Figure 3: The Manhattan plots of aSPU (top), TWAS (middle), and SSU (bottom) applied to the SCZ1 data with the METSIM-based weights. The p-values were truncated at  $5 \times 10^{-8}$ .

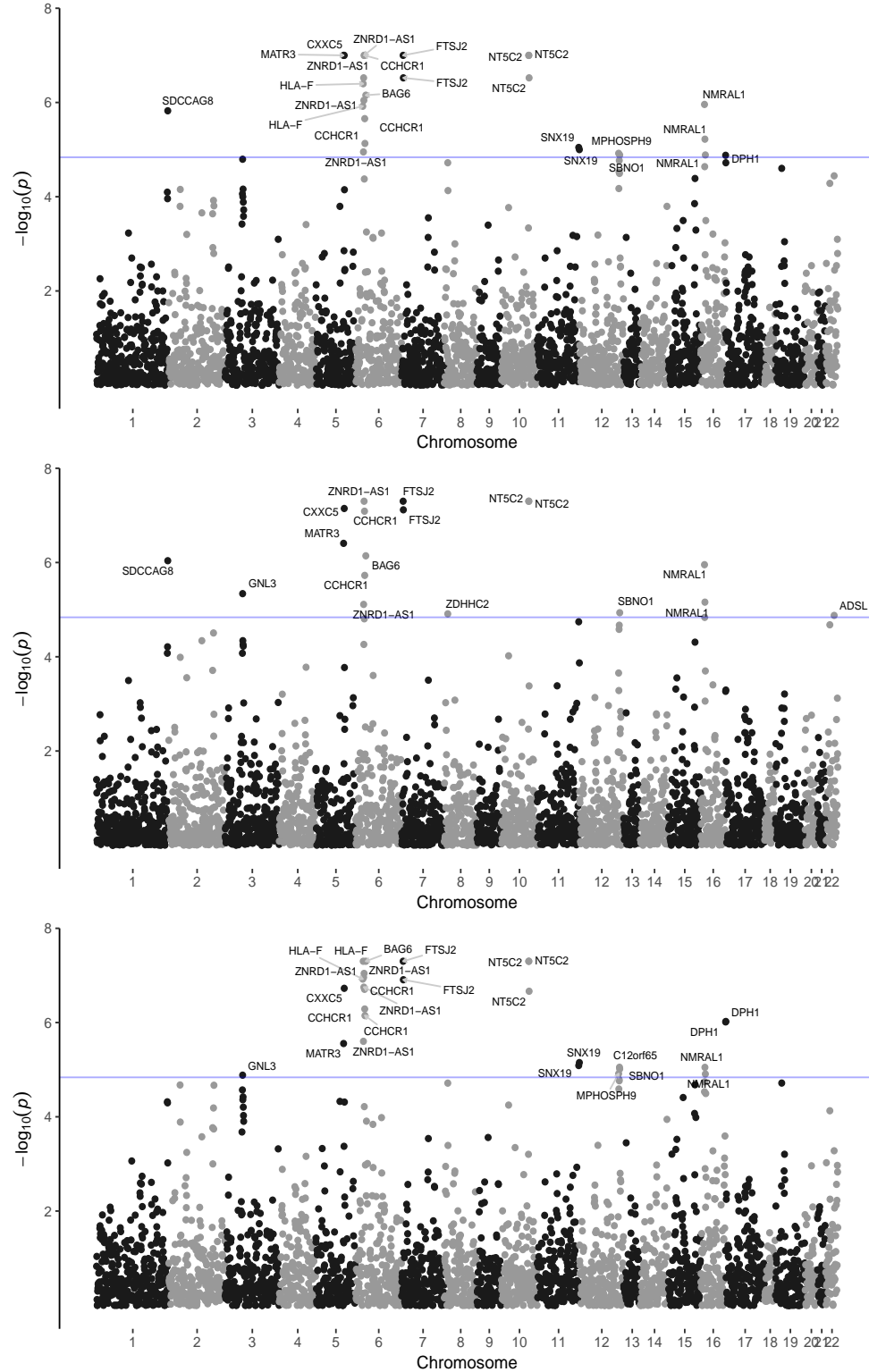


Figure 4: The Manhattan plots of aSPU (top), TWAS (middle), and SSU (bottom) applied to the SCZ1 data with the CMC-introns-based weights. The p-values were truncated at  $5 \times 10^{-8}$ .

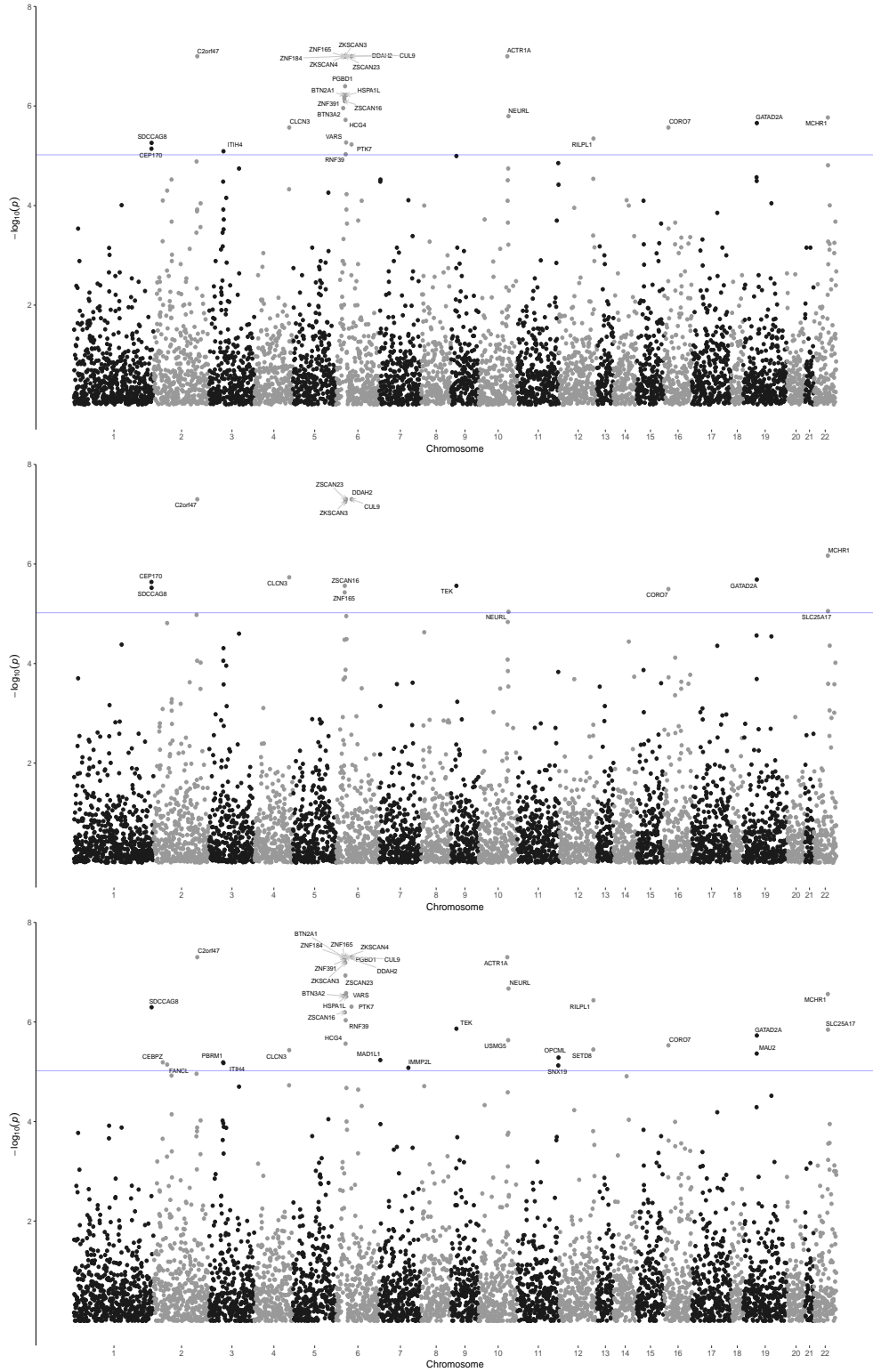
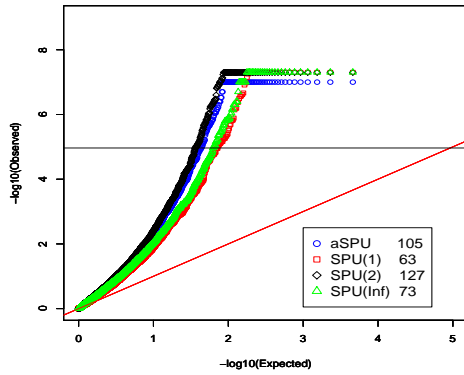
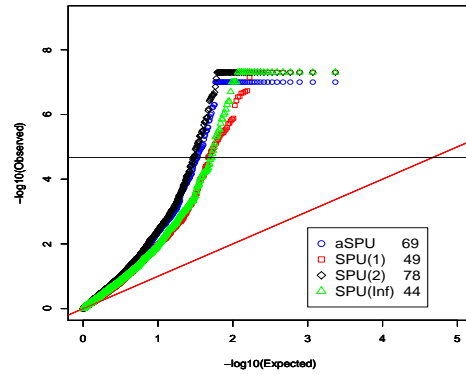


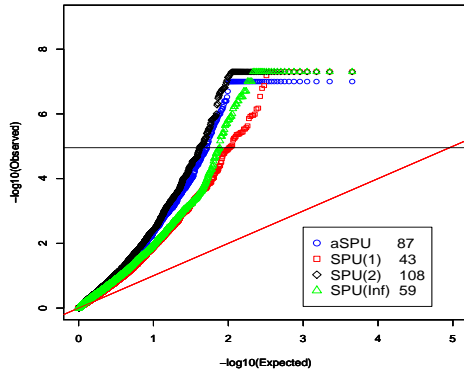
Figure 5: The Manhattan plots of aSPU (top), TWAS (middle), and SSU (bottom) applied to the SCZ1 data with the CMC-based weights. The p-values were truncated at  $5 \times 10^{-8}$ .



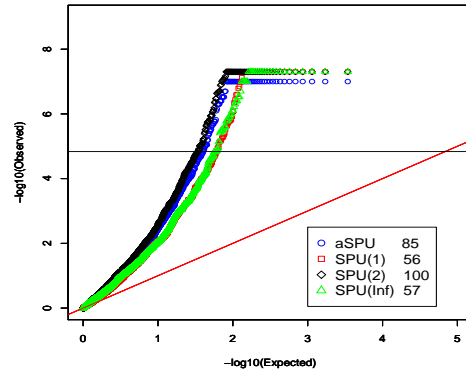
(a) SCZ2 data with the YFS-based weights



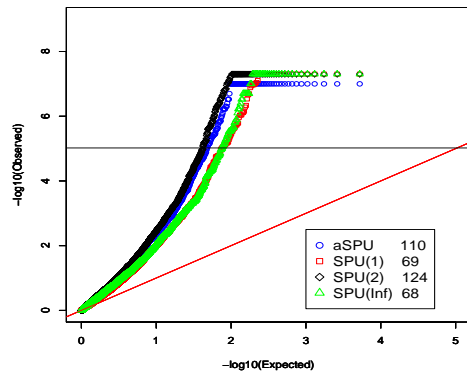
(b) SCZ2 data with the NTR-based weights



(c) SCZ2 data with the METSIM-based weights



(d) SCZ2 data with the CMC-introns-based weights



(e) SCZ2 data with the CMC-based weights

Figure 6: The Q-Q plots for the SCZ2 data. The p-values of aSPU and SPU( $\infty$ ) were truncated at  $1 \times 10^{-7}$ , while those of the other two were truncated at  $5 \times 10^{-8}$ .

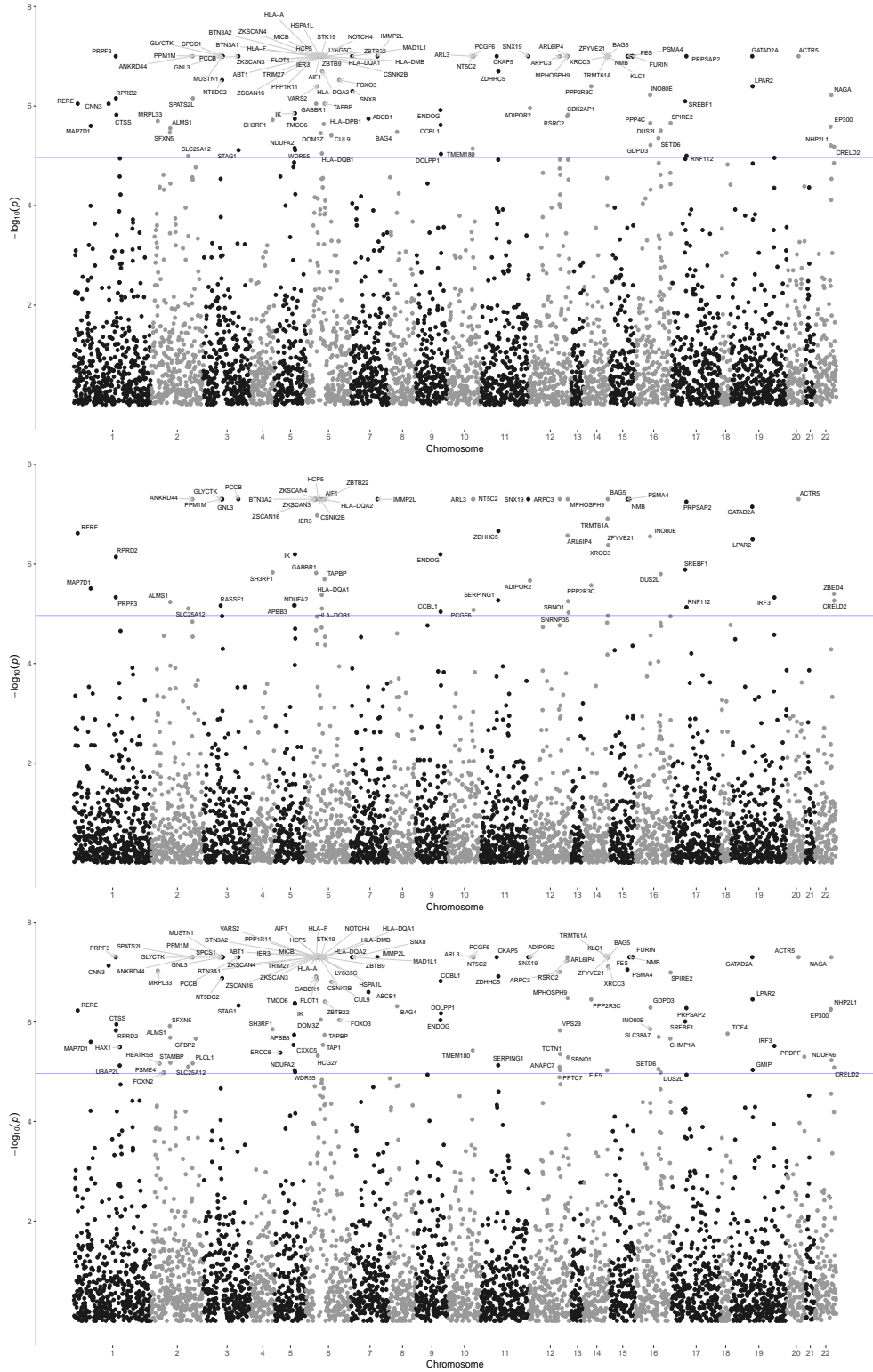


Figure 7: The Manhattan plots of aSPU (top), TWAS (middle), and SSU (bottom) applied to the SCZ2 data with the YFS-based weights. The p-values were truncated at  $5 \times 10^{-8}$ .



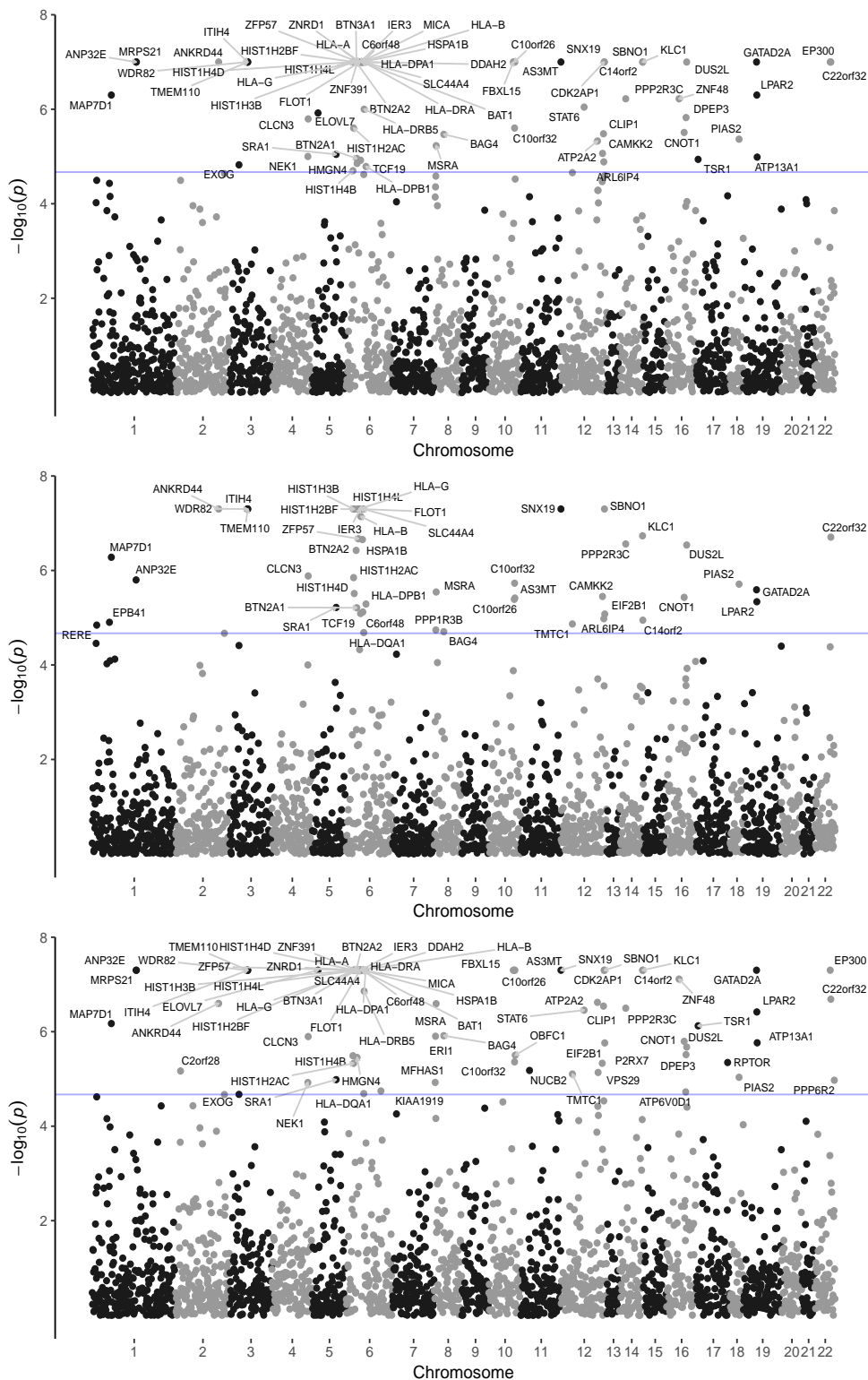


Figure 8: The Manhattan plots of aSPU (top), TWAS (middle), and SSU (bottom) applied to the SCZ2 data with the NTR-based weights. The p-values were truncated at  $5 \times 10^{-8}$ .

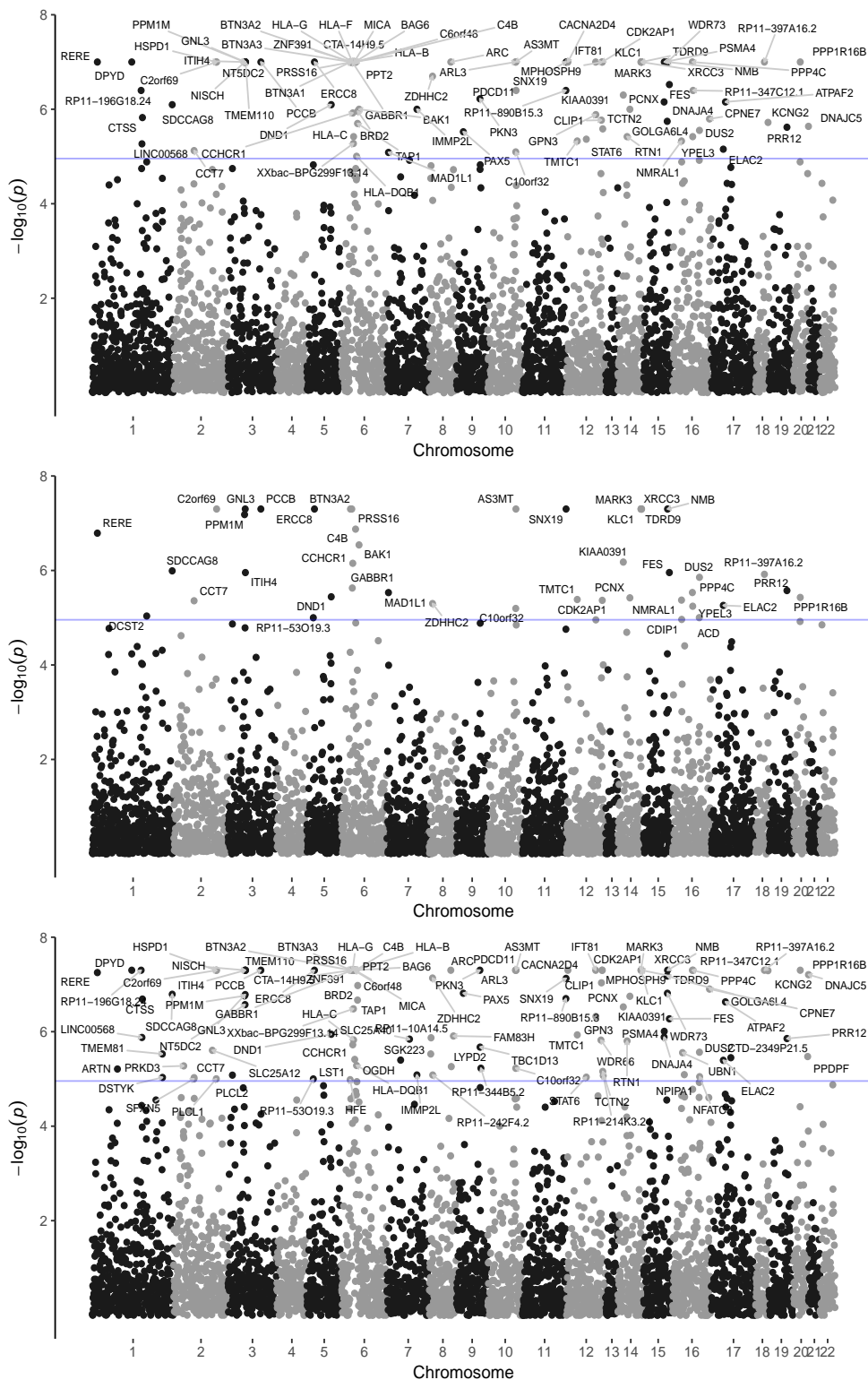


Figure 9: The Manhattan plots of aSPU (top), TWAS (middle), and SSU (bottom) applied to the SCZ2 data with the METSIM-based weights. The p-values were truncated at  $5 \times 10^{-8}$ .

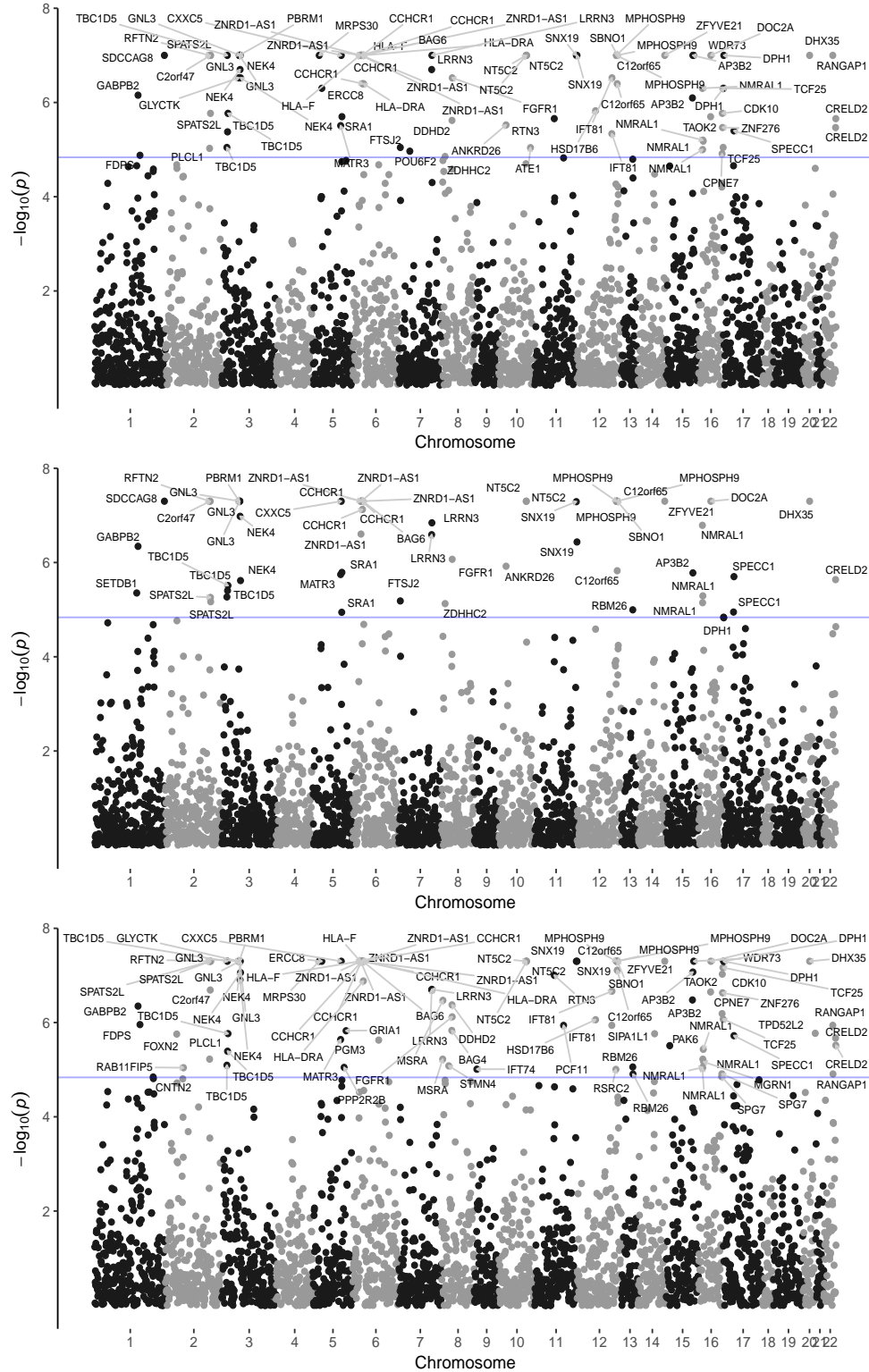


Figure 10: The Manhattan plots of aSPU (top), TWAS (middle), and SSU (bottom) applied to the SCZ2 data with the CMC-introns-based weights. The p-values were truncated at  $5 \times 10^{-8}$ .

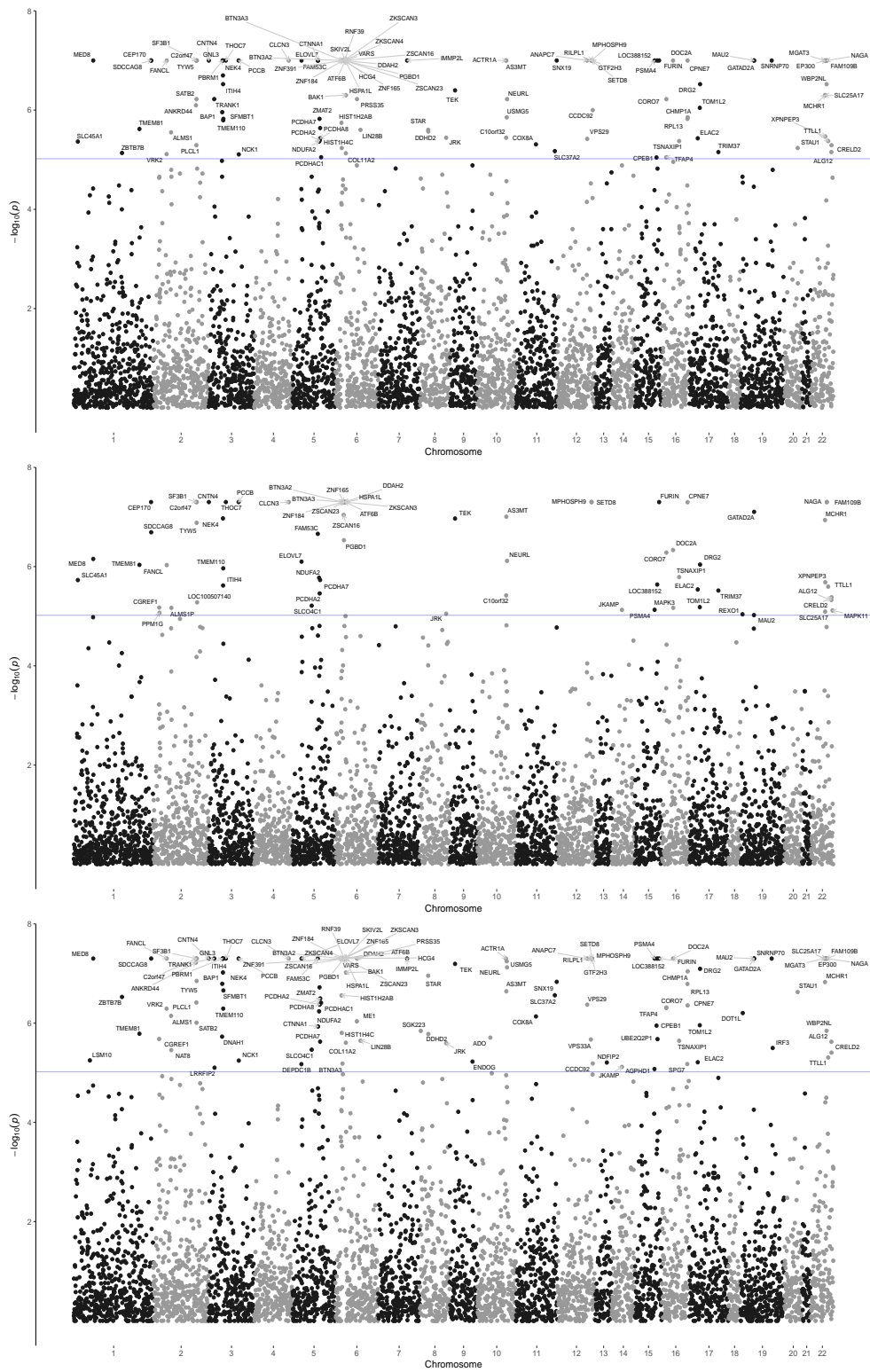


Figure 11: The Manhattan plots of aSPU (top), TWAS (middle), and SSU (bottom) applied to the SCZ2 data with the CMC-based weights. The p-values were truncated at  $5 \times 10^{-8}$ .

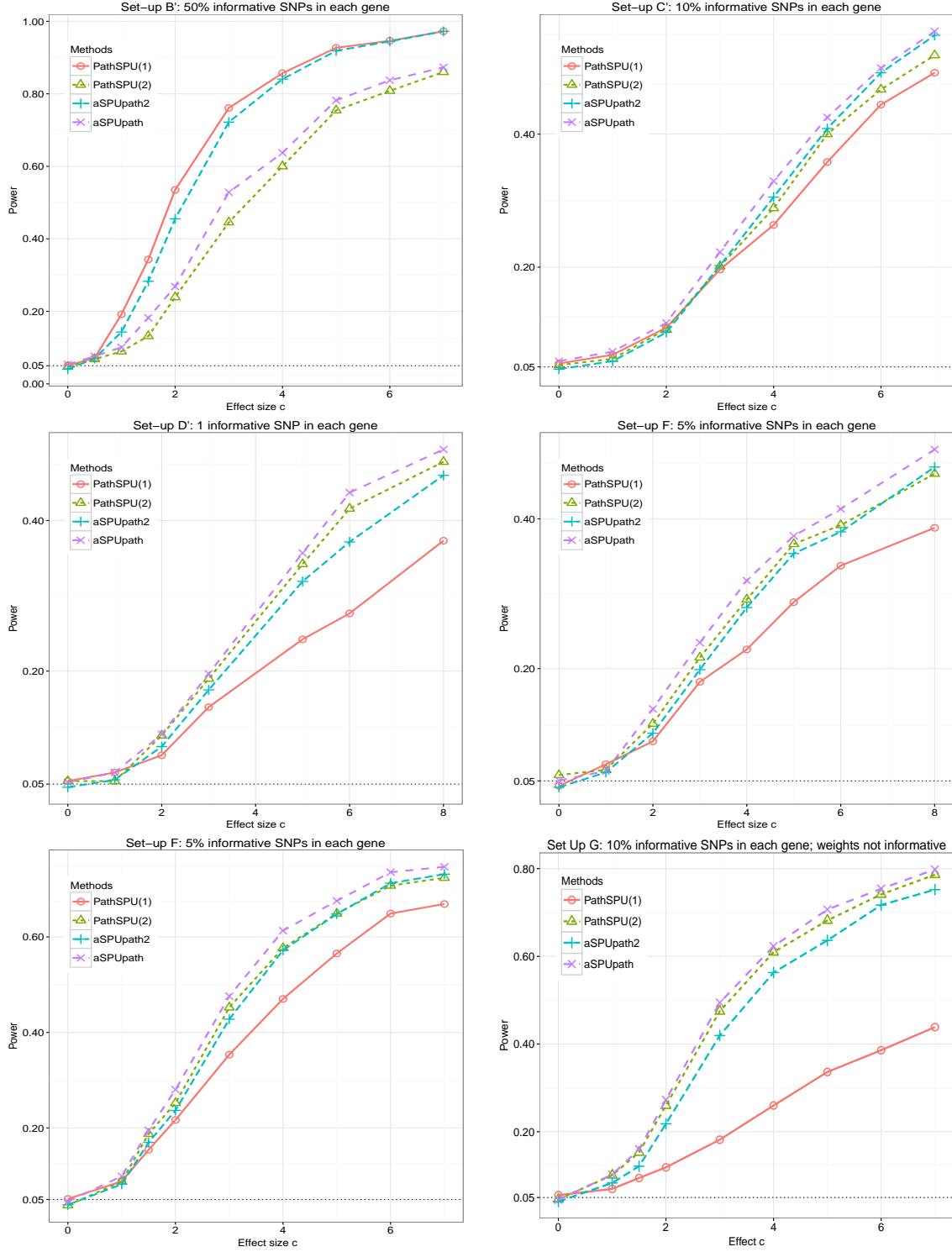


Figure 12: Empirical power under different set-ups. Set-ups B'–D' were similar to set-ups B–D except  $\mu_j = \text{sign}(W_j)c_j$  for informative SNPs with random  $c_j \sim U(0, c)$ , a uniform distribution between 0 and  $c$ . Set-up F' was similar to set-ups B'–D' except there were 5% informative SNPs in each gene. Set-up F was similar to set-ups B–D except there were 5% informative SNPs in each gene. Set-up G was similar to set-up C except  $\mu_j = c$  for informative SNPs (i.e. the weights  $W_j$ 's were not informative).