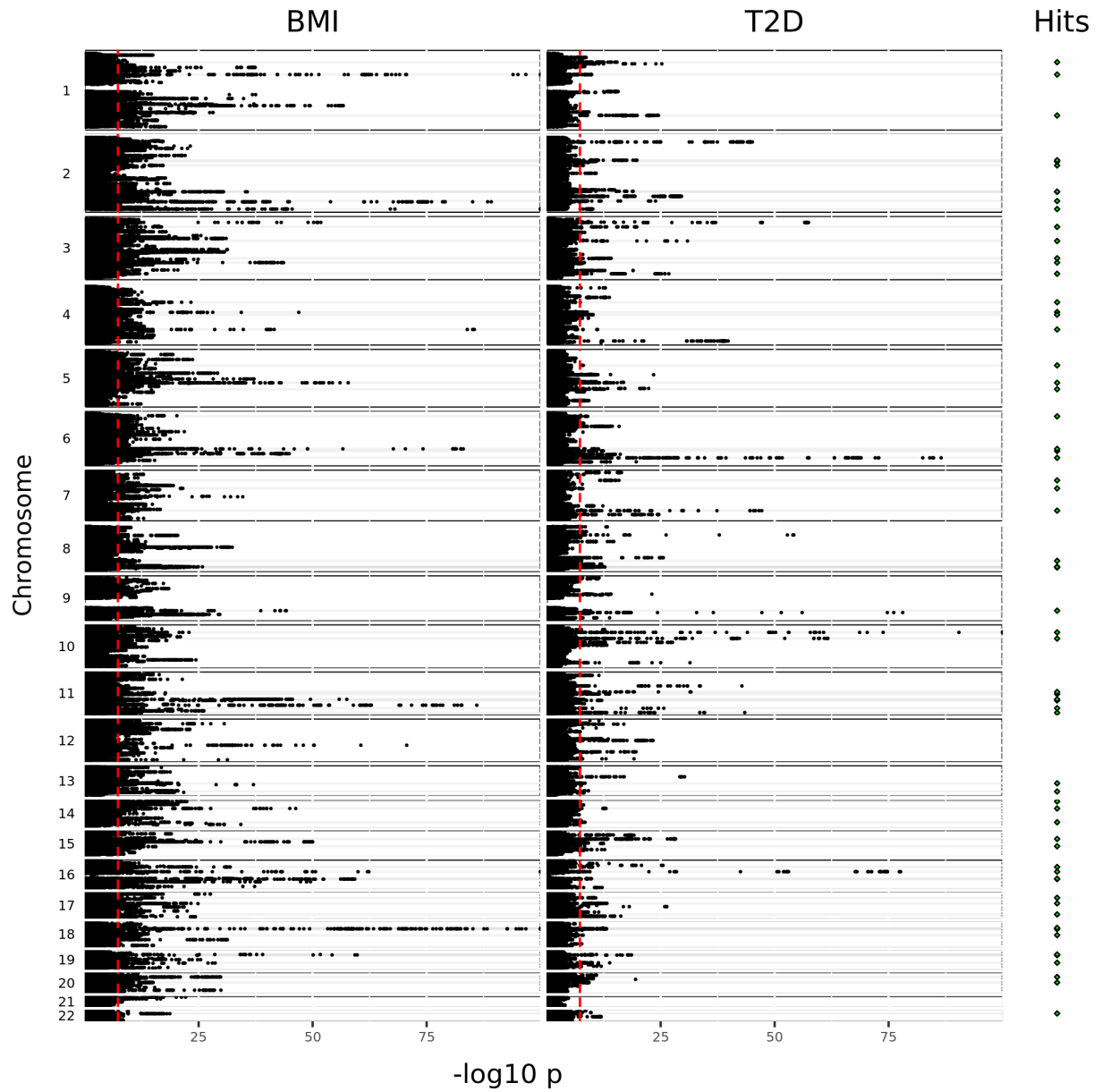
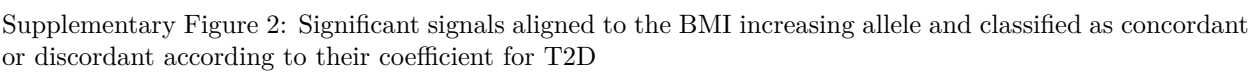
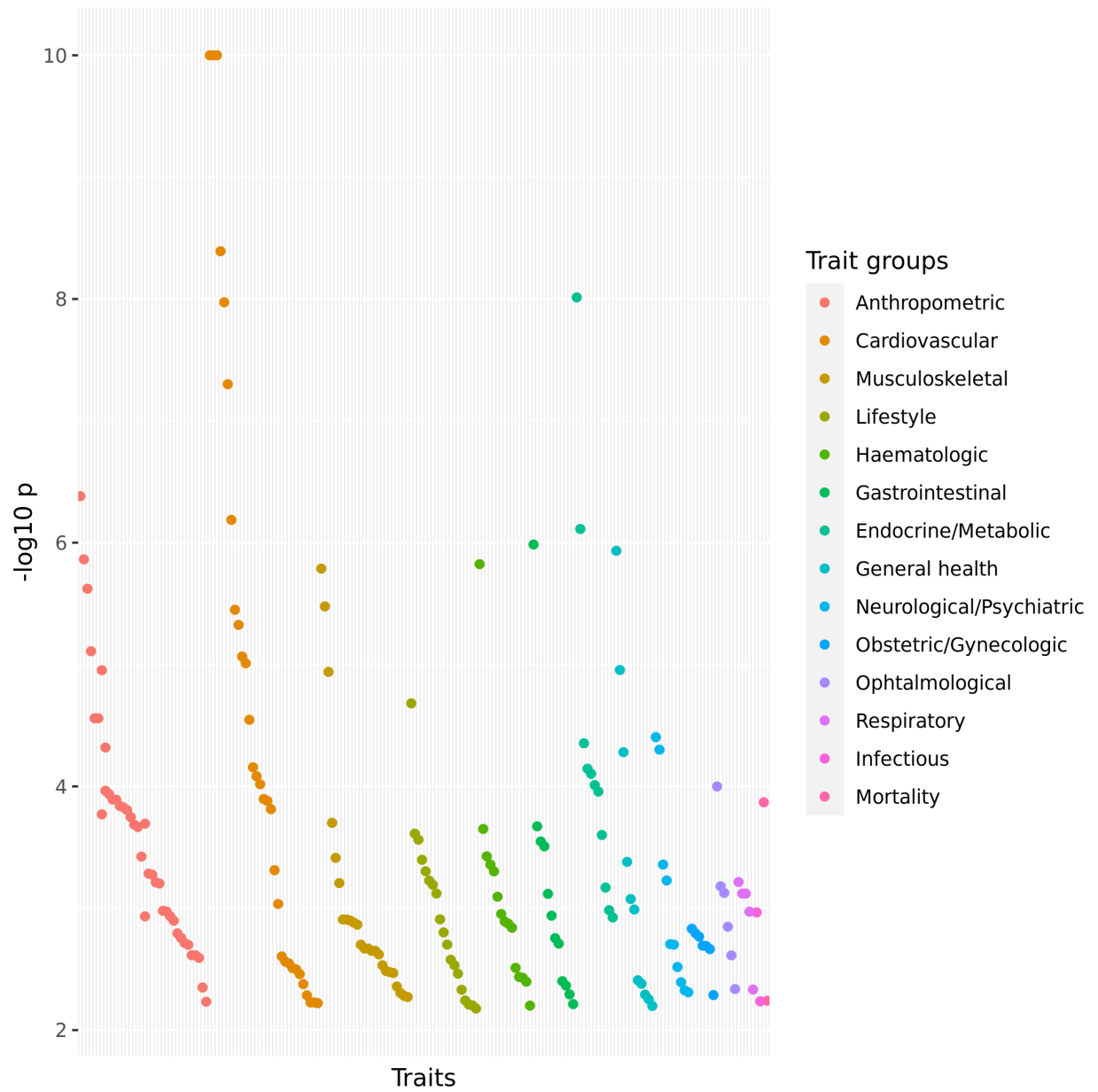


Supplementary Figures

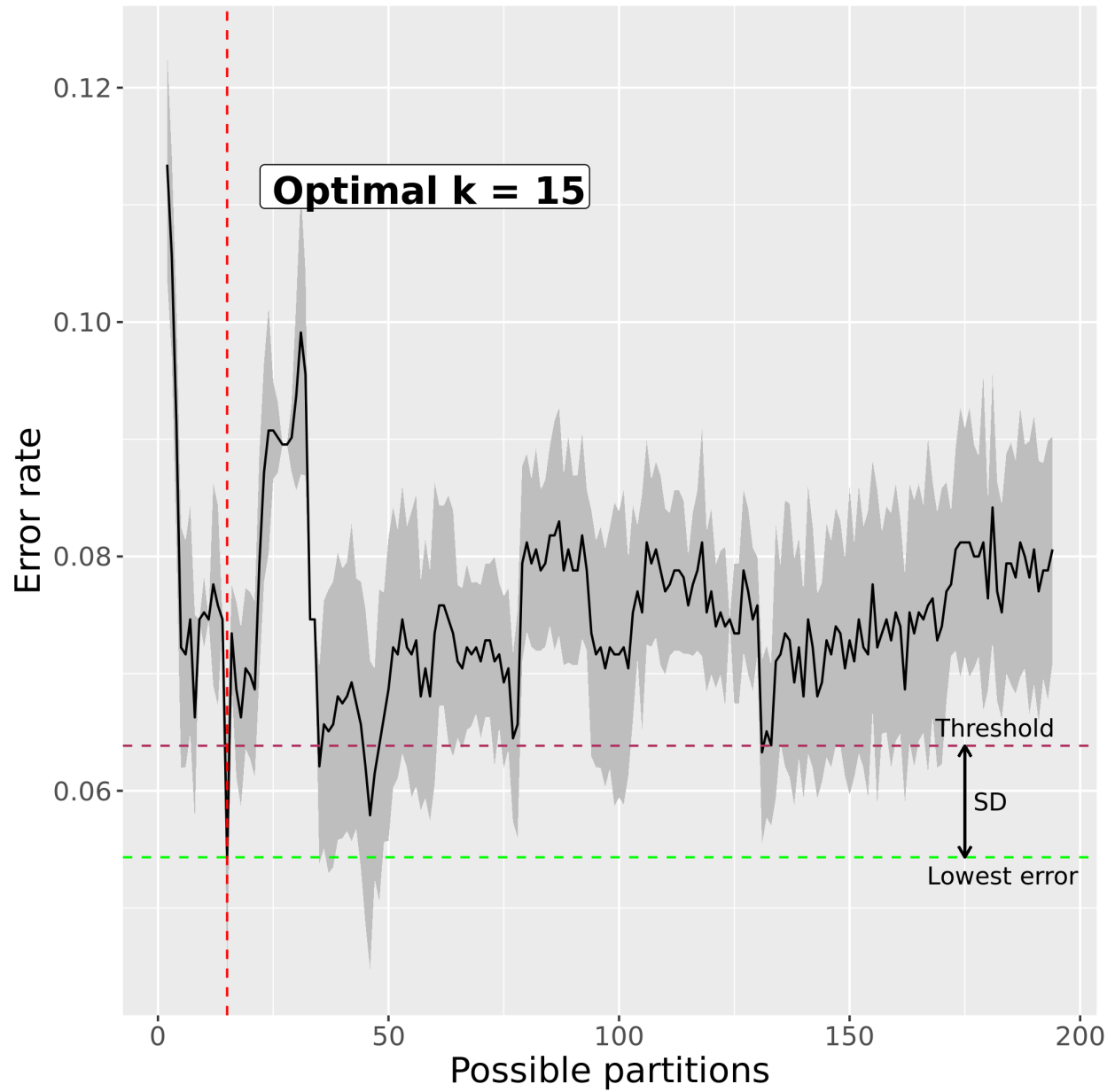


Supplementary Figure 1: Cross-referencing BMI and T2D GWAS and extracting significant independent signals for both conditions

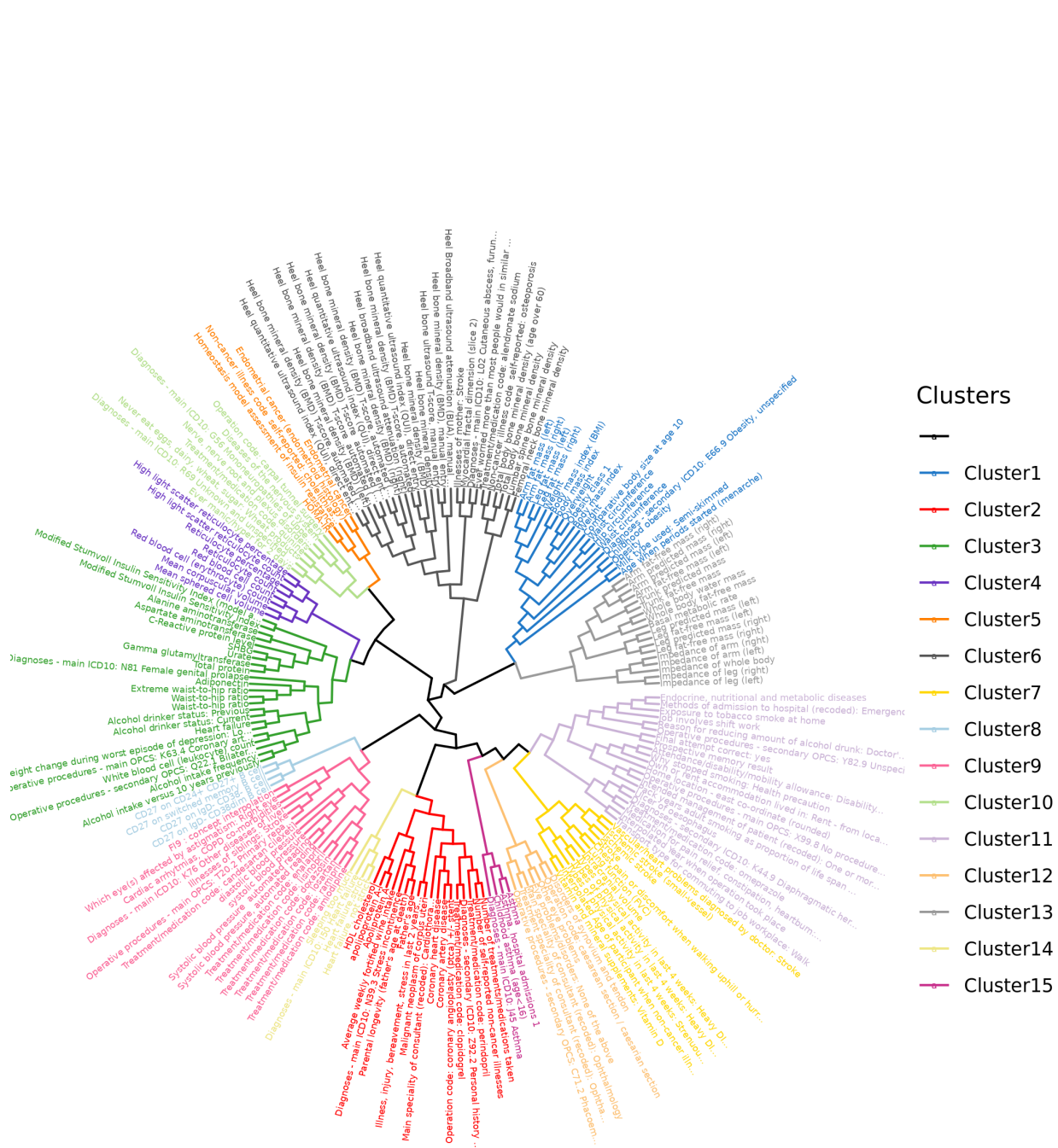




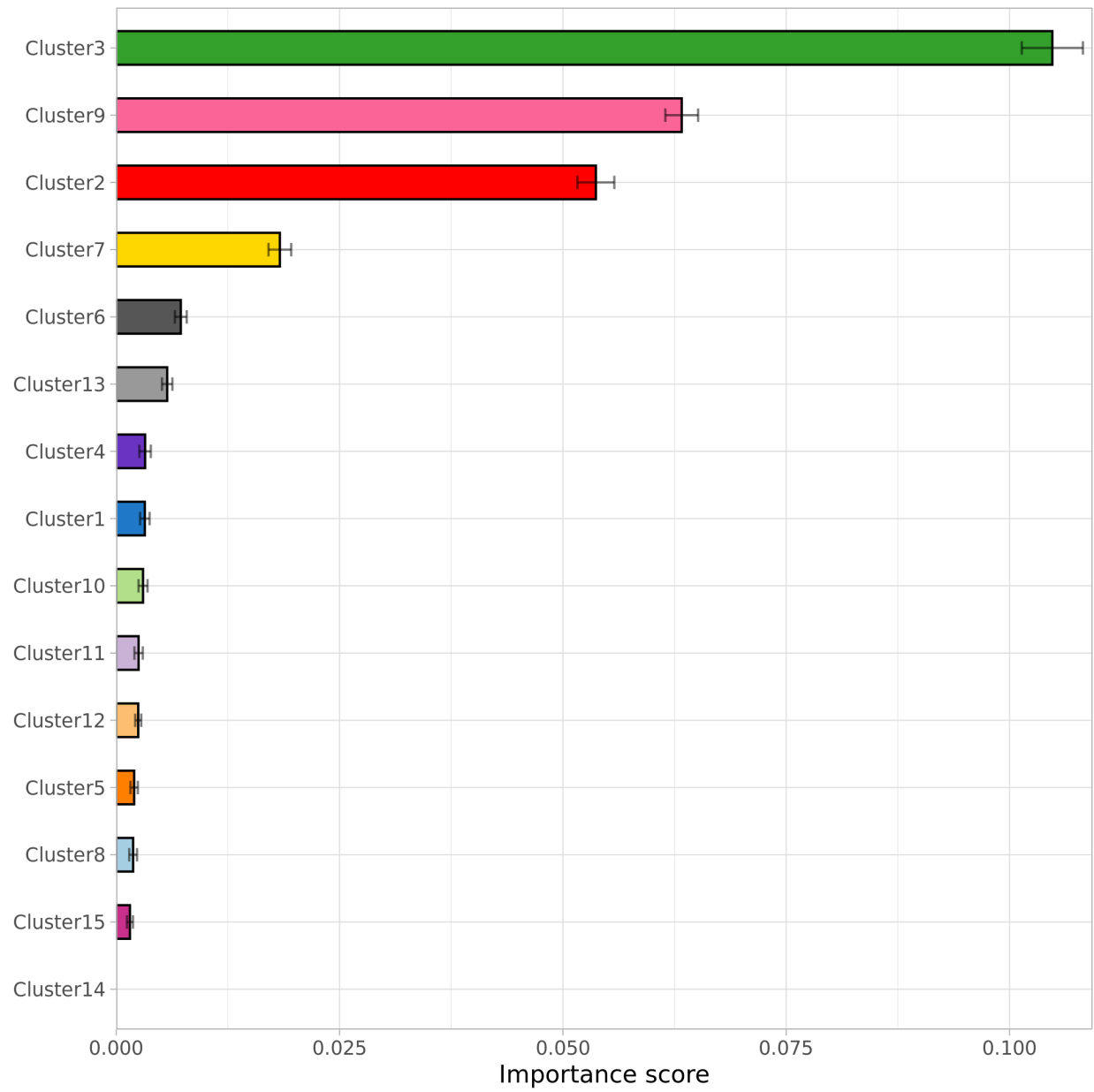
Supplementary Figure 3: P-values for the difference between concordant and discordant SNPs in traits that reached statistical significance after univariate filtering, spanning across multiple categories



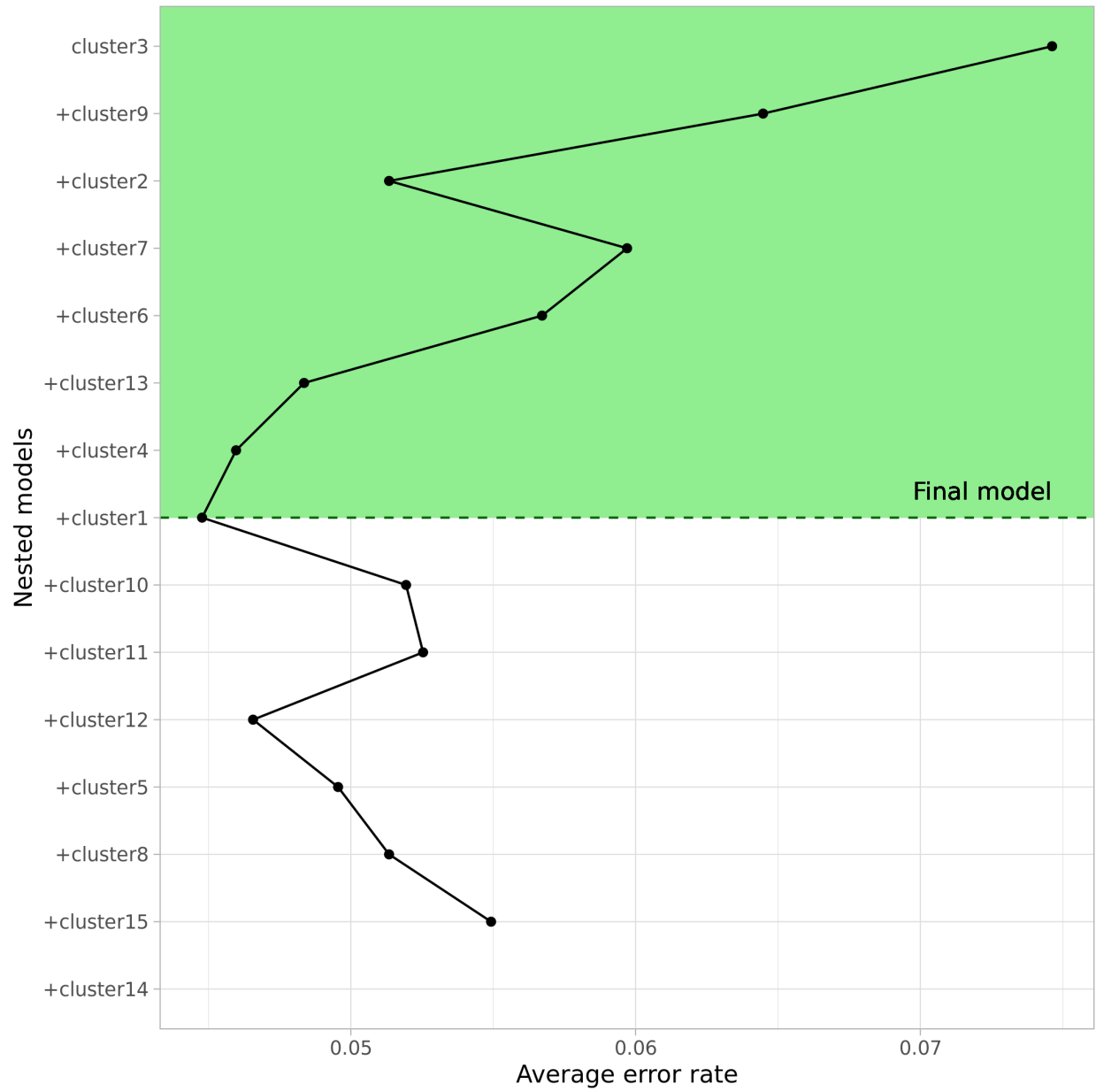
Supplementary Figure 4: Optimal partition of the SNP-trait matrix built with 67 concordant and discordant SNPs and 195 traits. The lowest error rate occurred occurred at a partition of 15 clusters



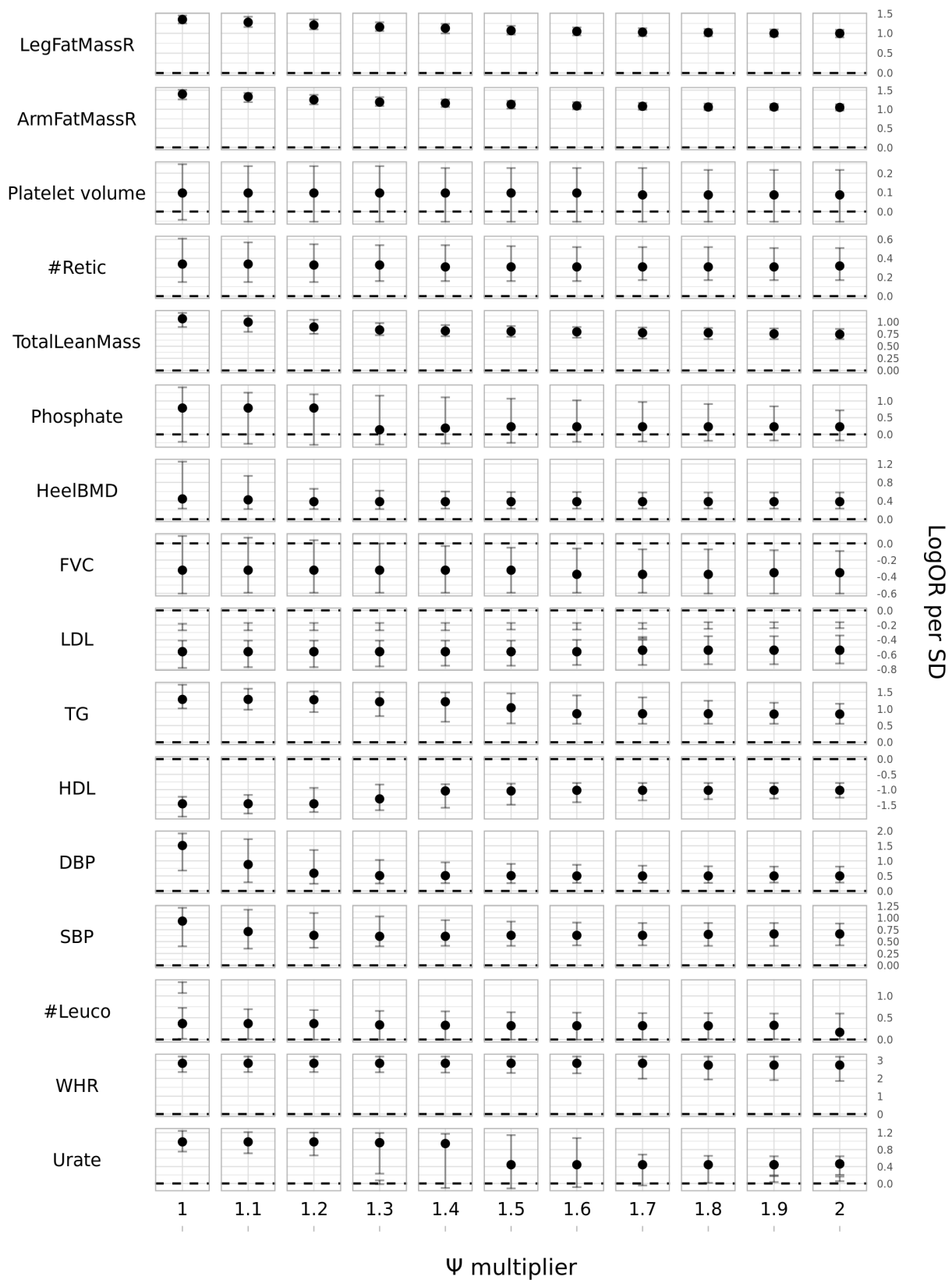
Supplementary Figure 5: Dendrogram of 195 traits of the SNP-trait matrix partitioned into the optimal 15 clusters



Supplementary Figure 6: Random forest importance scores of clusters in the optimal partition



Supplementary Figure 7: Nested random forest models in order of importance scores. The lowest error rate occurred in the model with the first 8 clusters.



Supplementary Figure 8: Sensitivity analysis of the causal estimates using multiple values of ψ in the contamination mixture method, which modifies the likelihood function that determines the configuration of valid and invalid instruments. Multiple disjoint confidence intervals were observed across all ψ in LDL.