Interrogation of human hematopoietic traits at single-cell and single-variant resolution

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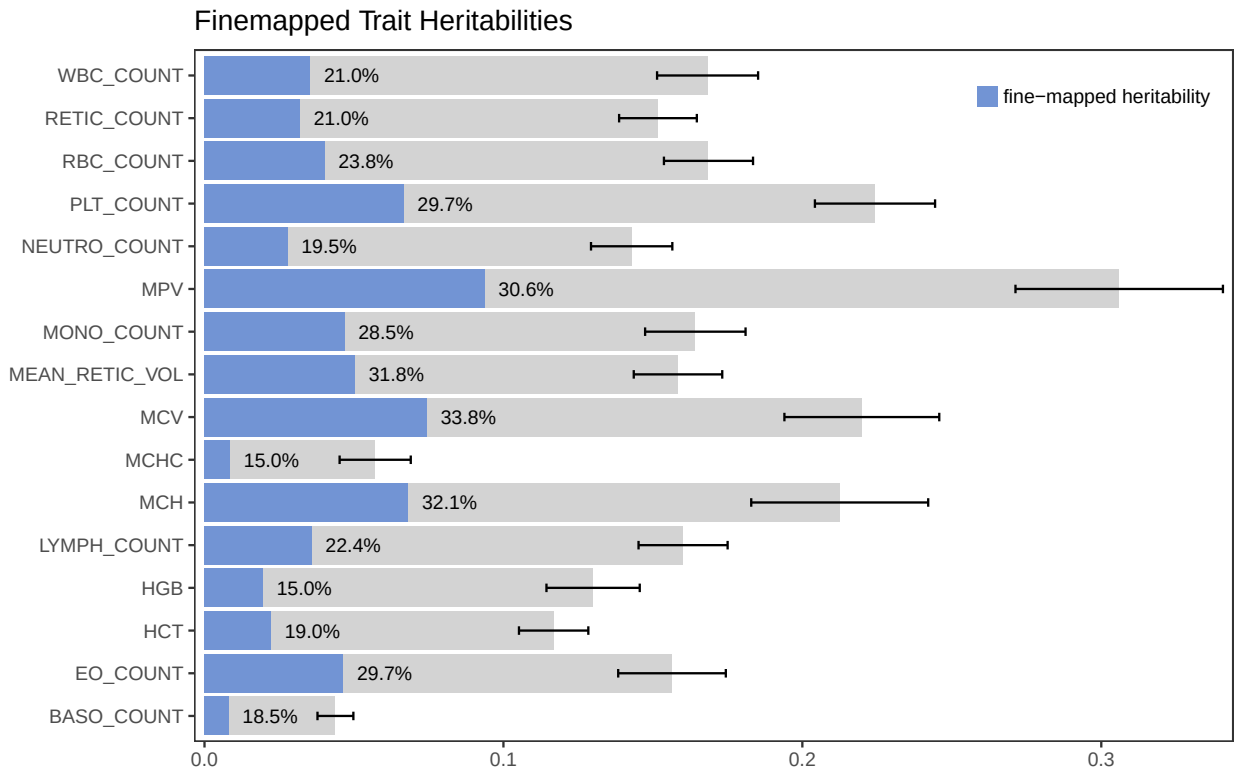
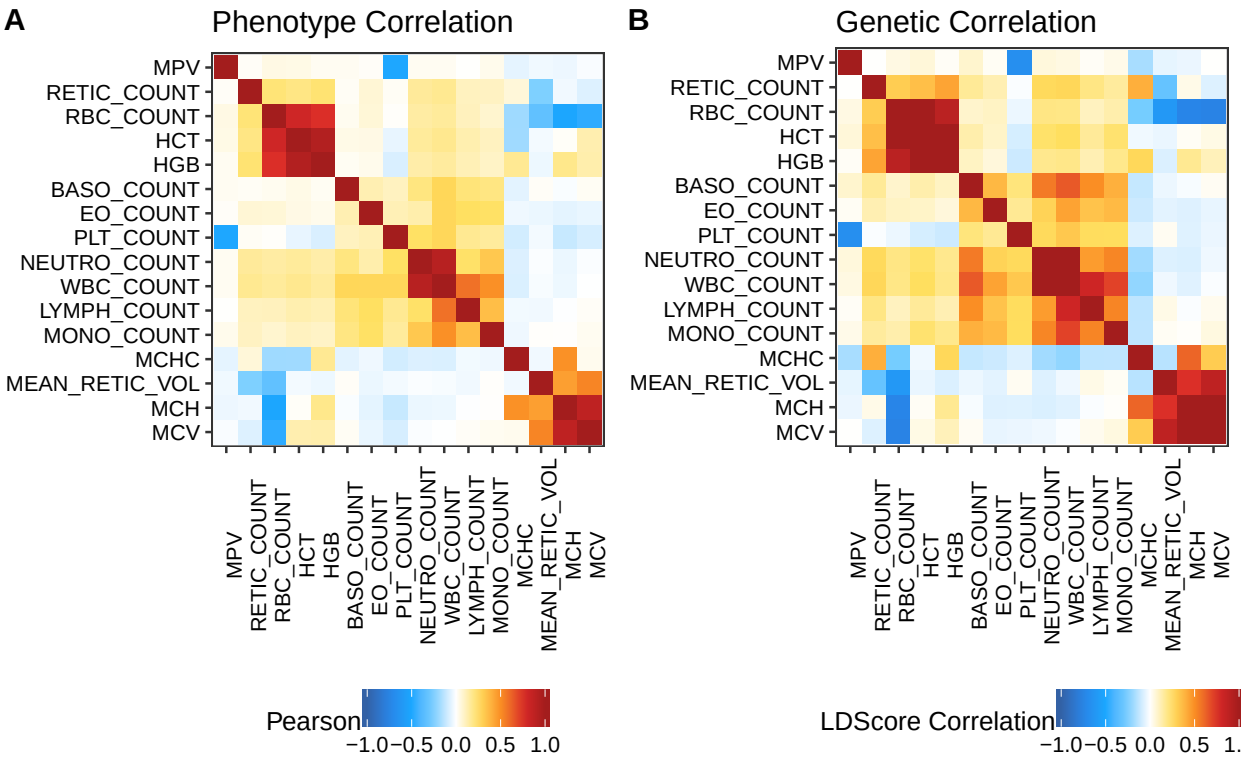
Supplemental Information

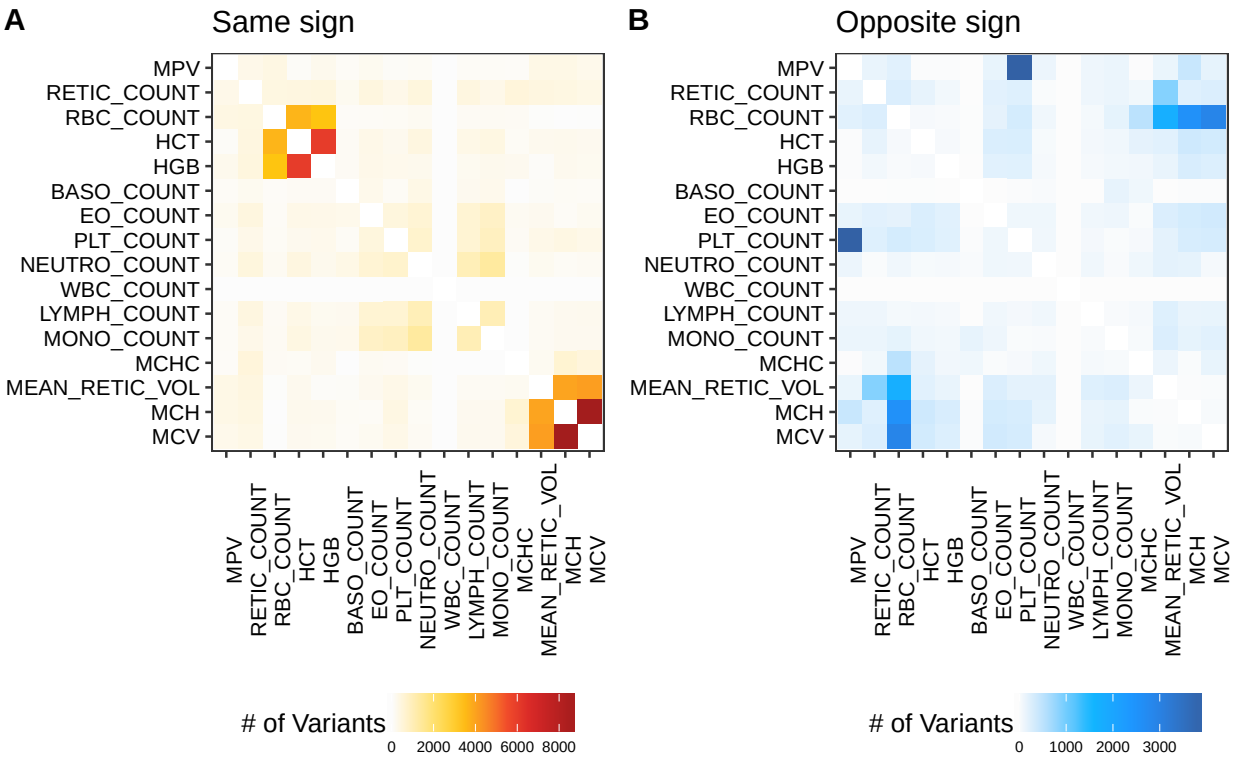
Overview of UK Biobank data



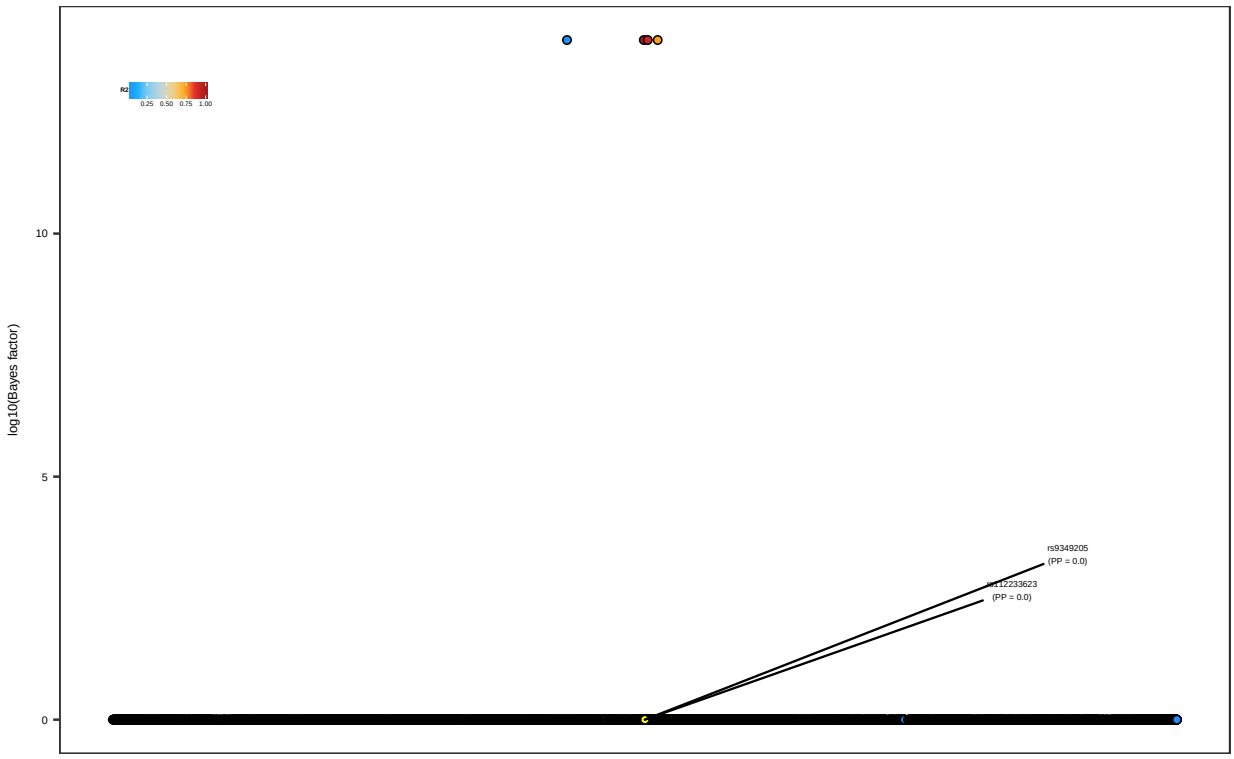
Supplemental Figure 1: Heritability estimates from LD Score Regression across 16 hematopoetic traits. The estimates of the narrow-sense SNP heritabilities are plotted in gray with their corresponding standard erors. Heritability estimates for all variants with fine-mapped posterior probability ¿ 0.001 are plotted in blue for each trait, and the proportions of total narrow-sense heritability captured by these fine-mapped variants (blue bar / gray bar) are indicated by the numbered labels.



Supplemental Figure 2: Phenotypic and genetic correlations across the 16 traits examined.

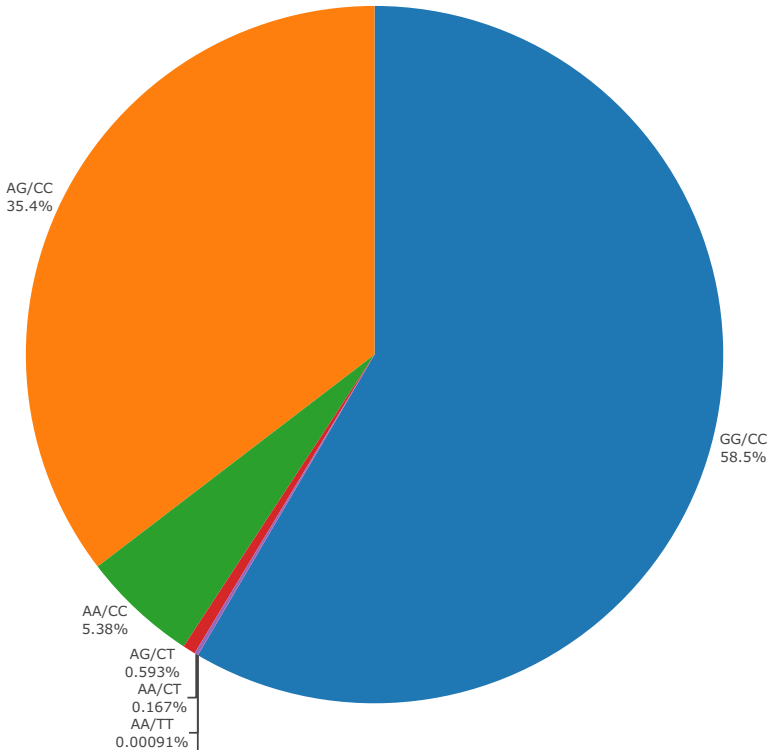


Supplemental Figure 3: Numbers of pleiotropic variants

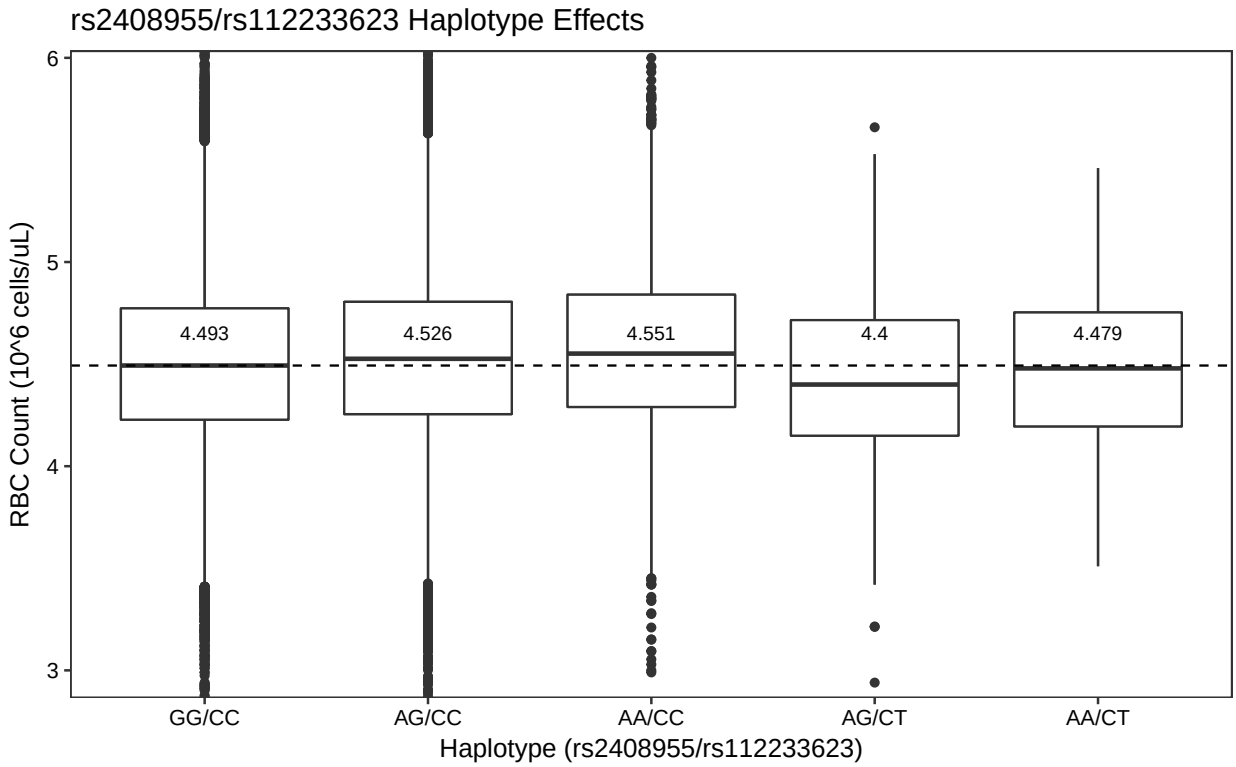


Supplemental Figure 4: Fine-mapped log10(Bayes factor) values for CCND3 variants, with LD estimated from a reference panel of 3,677 individuals from the UK10K cohort.

(A)



Supplemental Figure 5: Haplotypes frequencies of the CCND3 variants rs2408955 and rs112233623 in the UKBB Population. Haplotype labels are formatted as rs2408955/rs112233623.

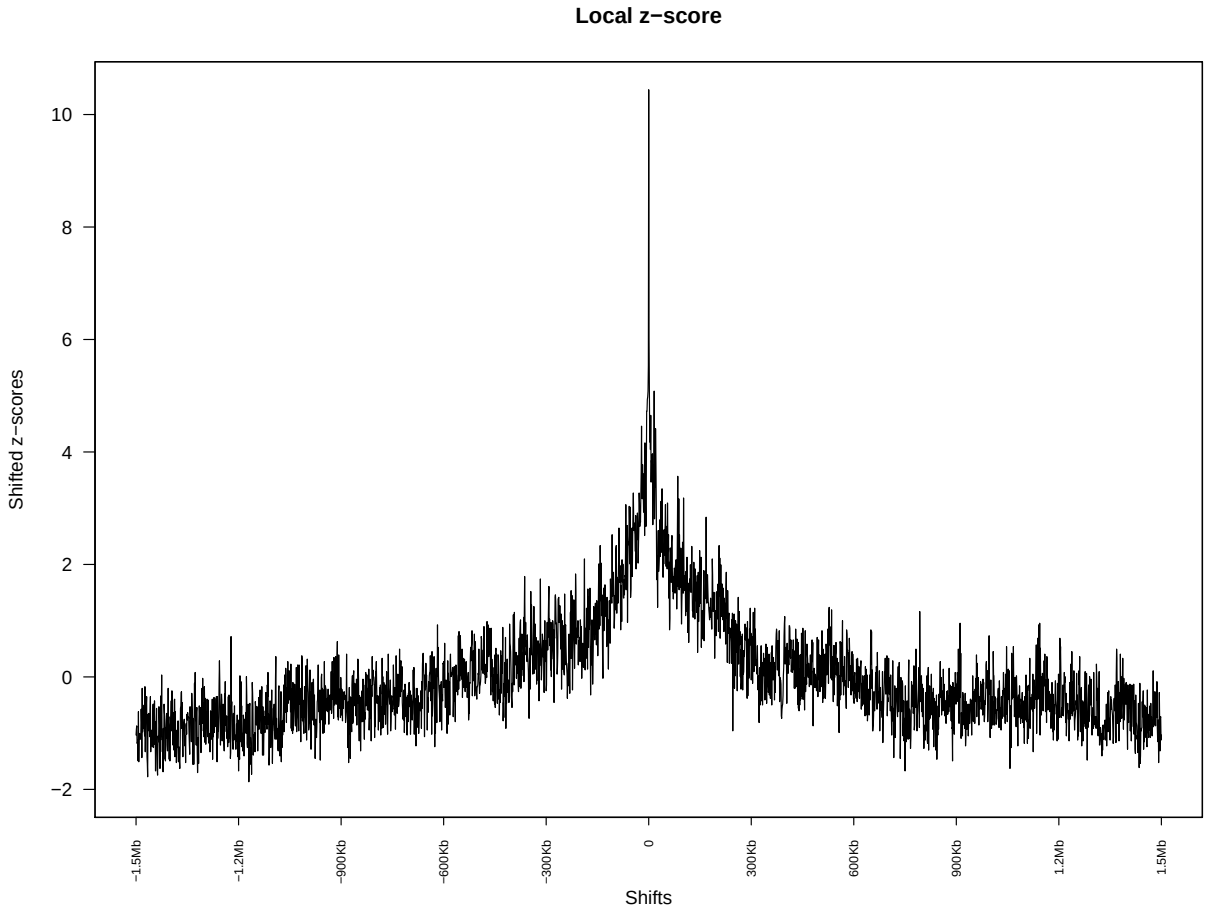


Supplemental Figure 6: Moderating effects of CCND3 haplotypes on red blood cell count.

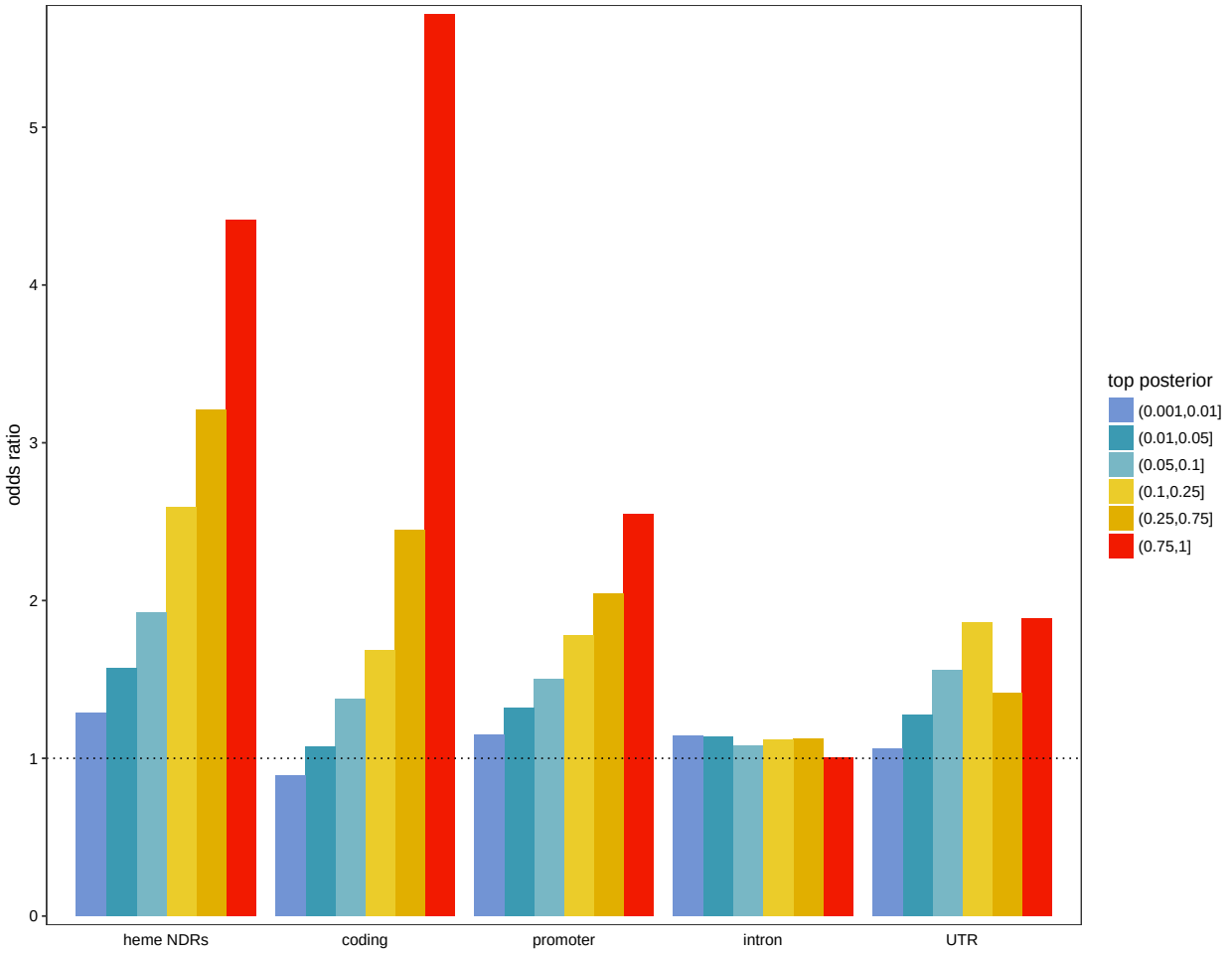
(B)

(C)

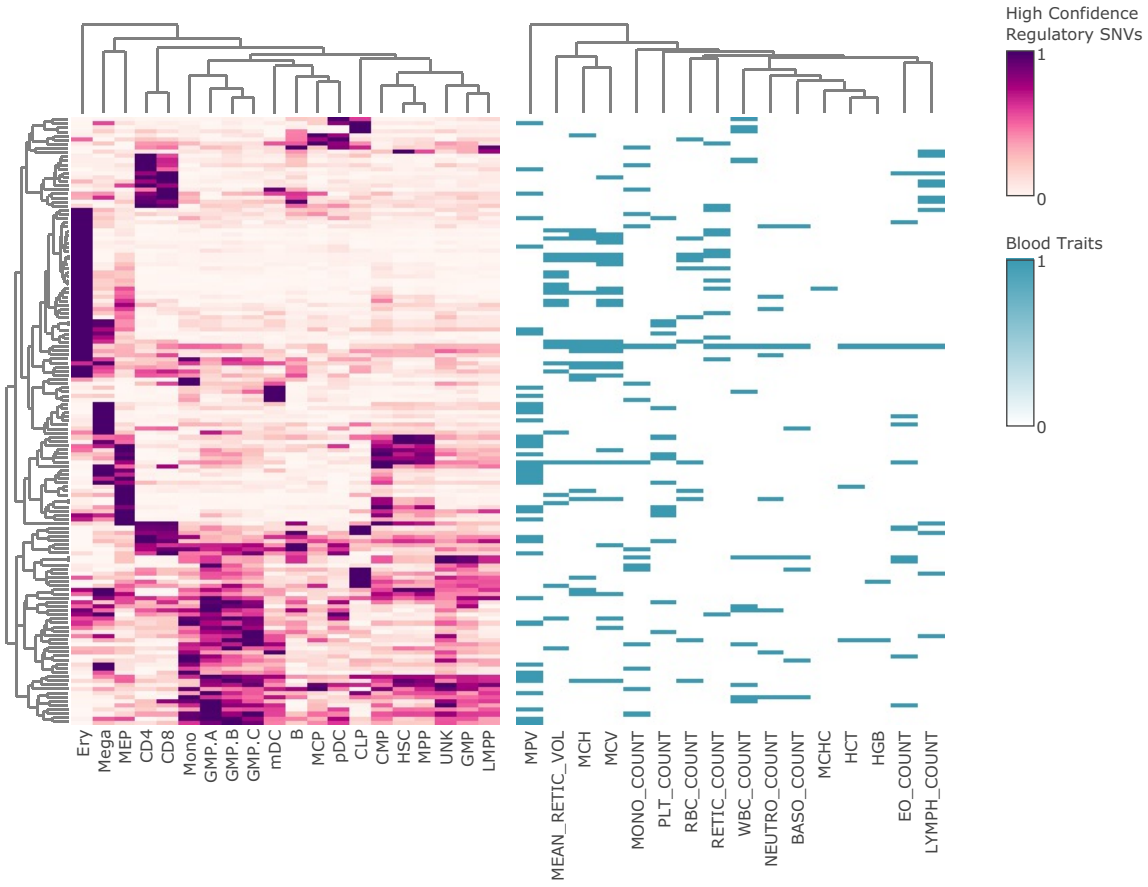
(D)



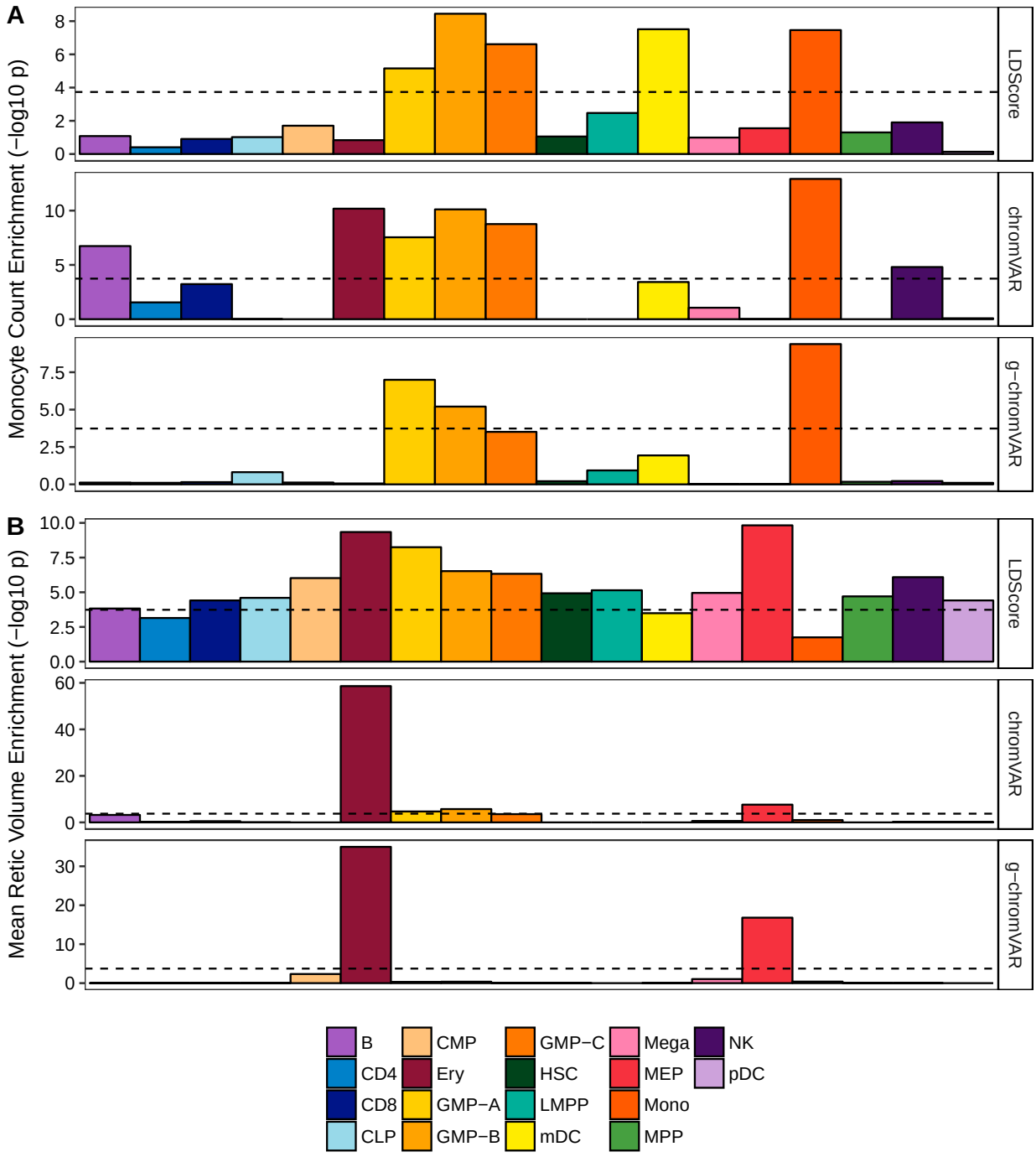
Supplemental Figure 7: Local z-scores for enrichment of hematopoietic nucleosome-depleted regions in the set of fine-mapped variants with posterior probability > 0.10.



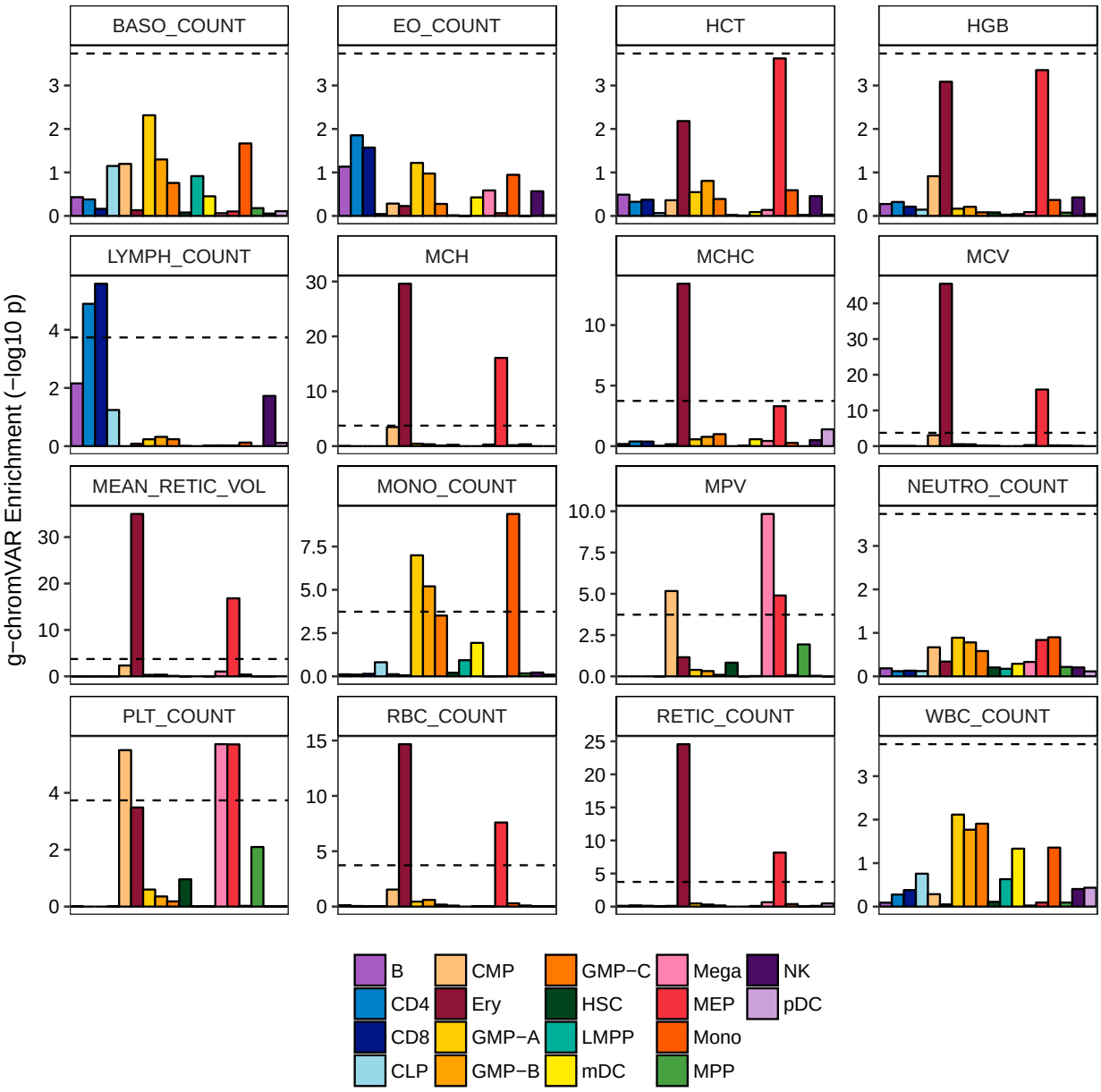
Supplemental Figure 8: Local annotation enrichments for fine-mapped variants, excluding all fine-map variants with $R^2 > 0.80$ to the sentinel variant of any region.



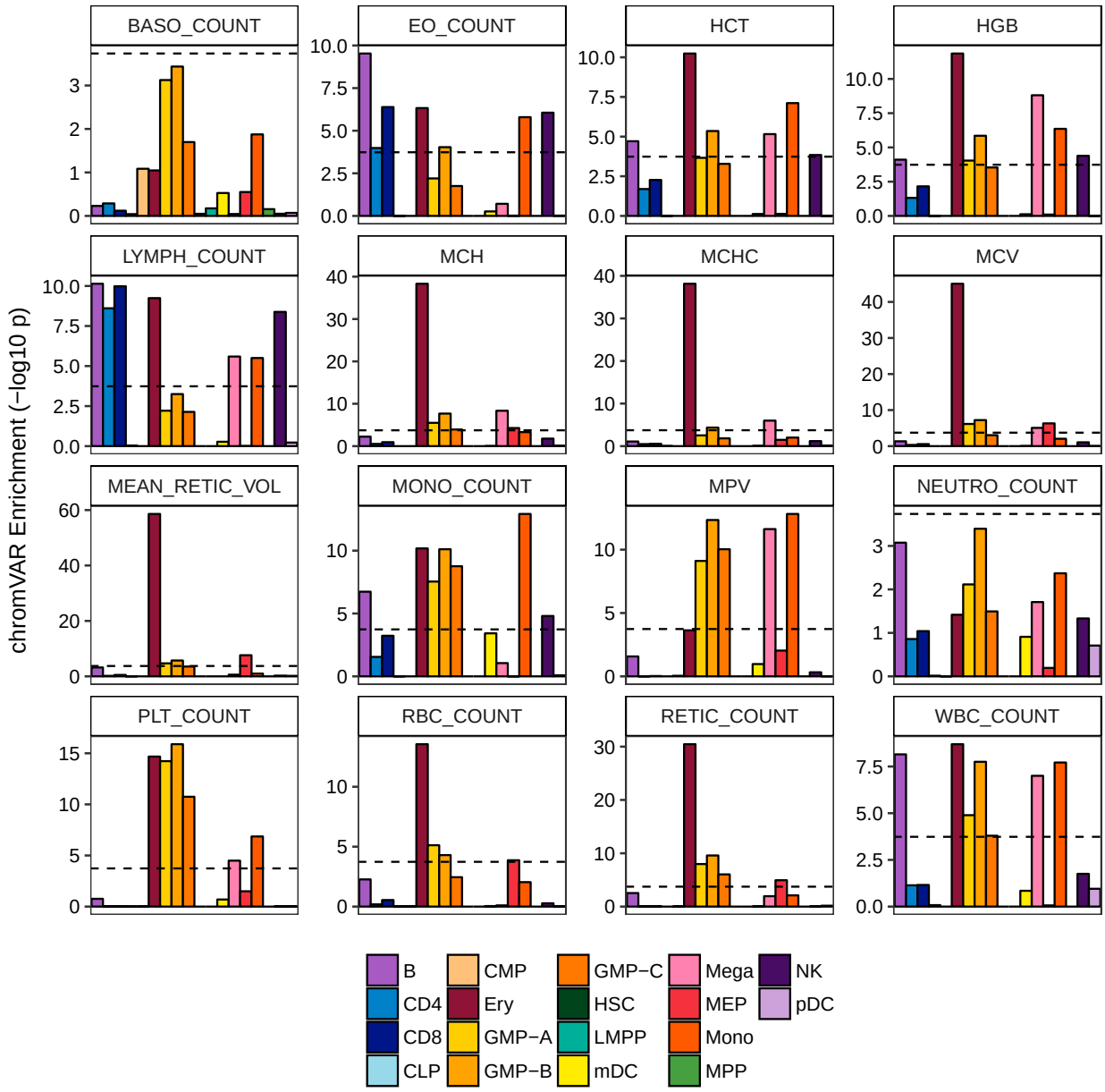
Supplemental Figure 9: Side-by-side heatmaps showing overlap of hematopoietic nucleosome-depleted regions by cell type with fine-mapped variants ($PP > 0.50$) by trait. The two heatmaps share a common y-axis of specific variants.



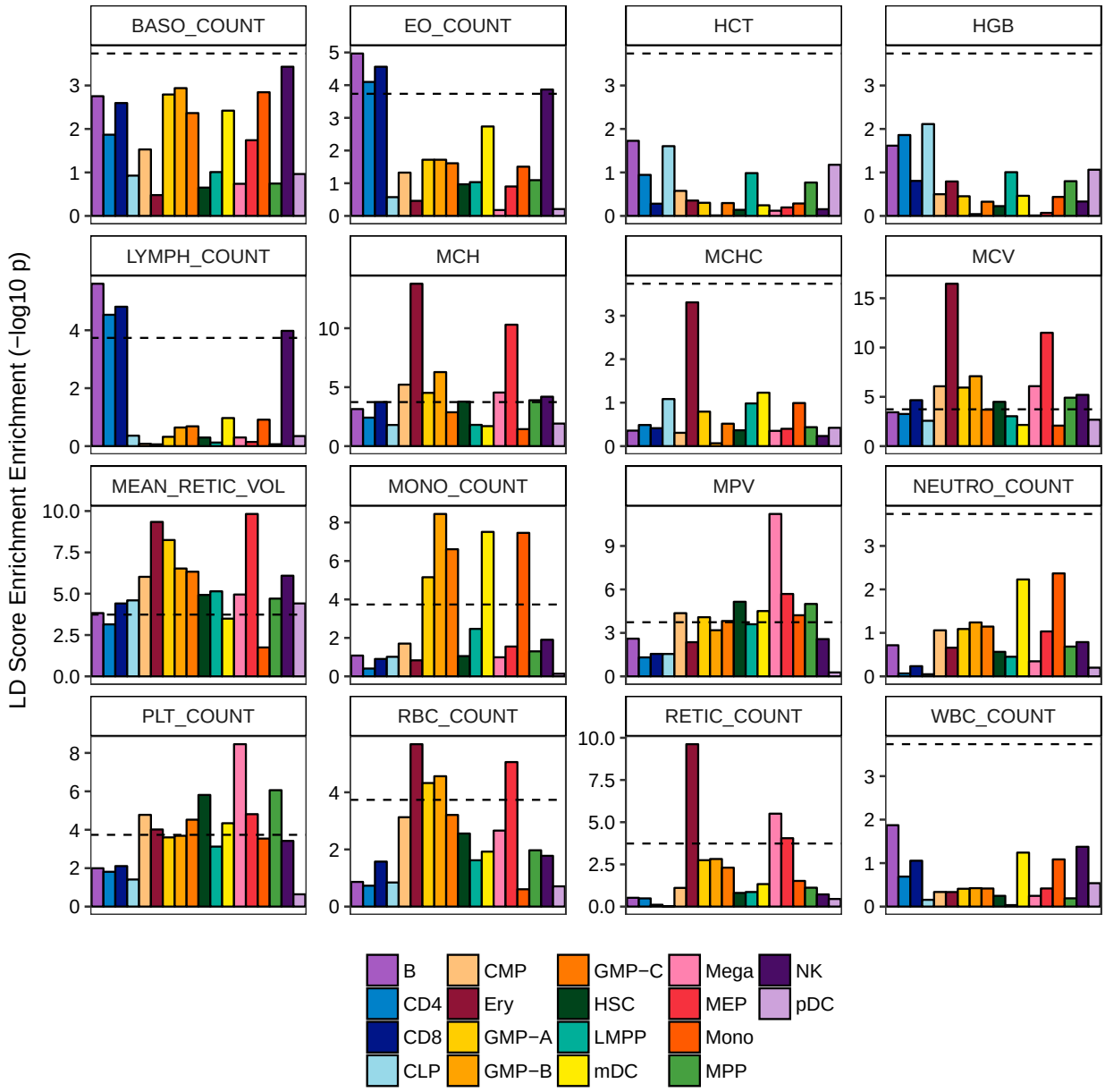
Supplemental Figure 10: Hematopoetic cell type enrichments for Mean Retic Volume and Monocyte count using various methods.



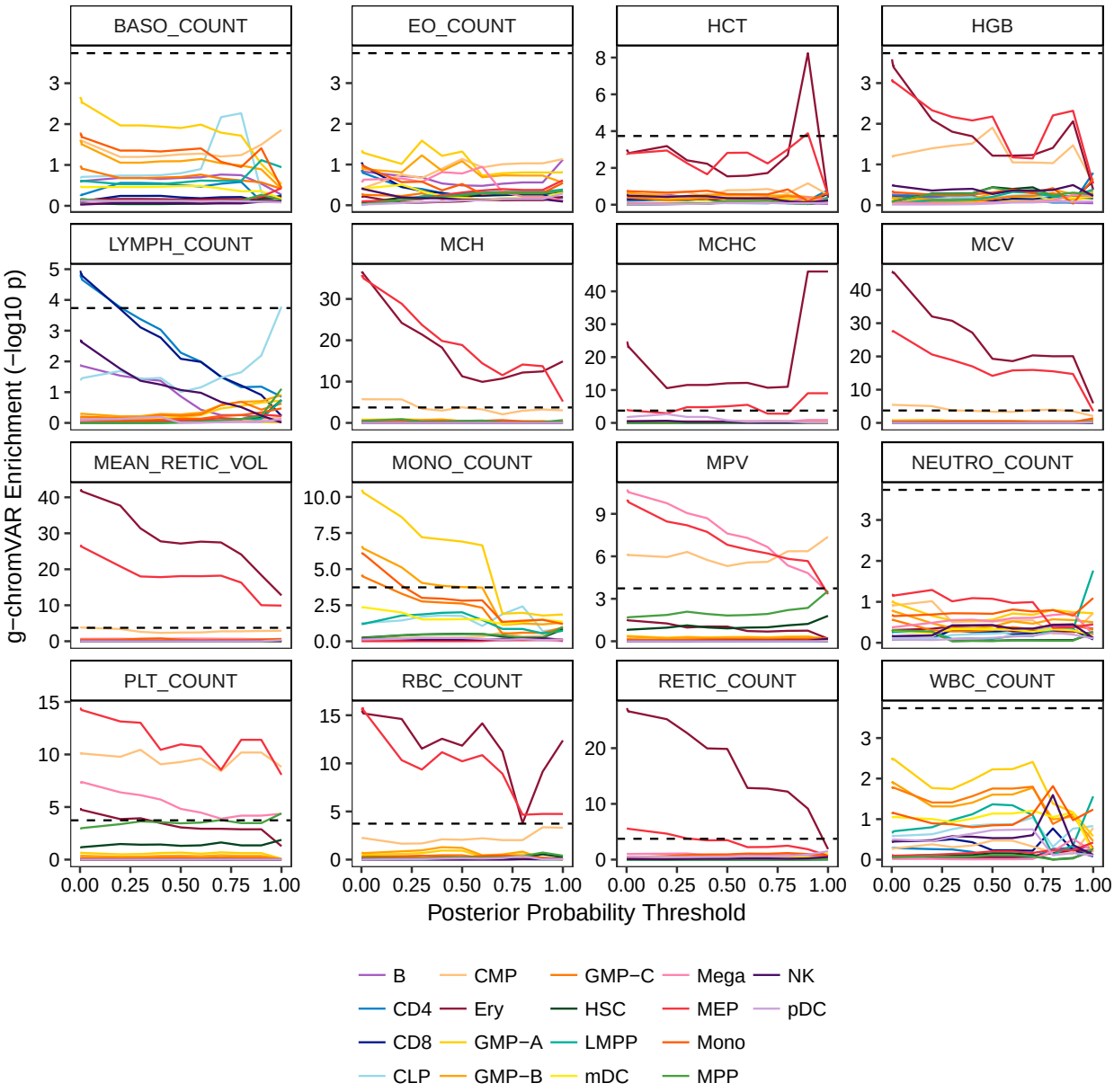
Supplemental Figure 11: All enrichments from g-chromVAR. The horizontal line shows a Bonferonni multiple testing adjusted threshold for statistical significance of enrichment.



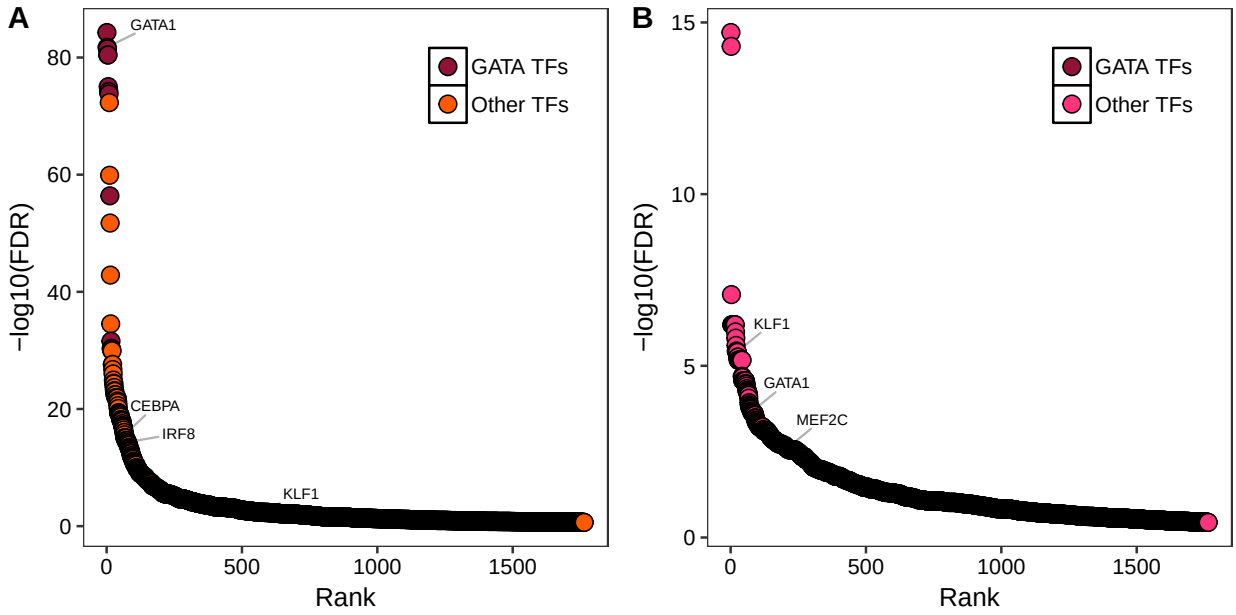
Supplemental Figure 12: All enrichments from chromVAR. The horizontal line shows a Bonferonni multiple testing adjusted threshold for statistical significance of enrichment.



Supplemental Figure 13: All enrichments from LD Score. The horizontal line shows a Bonferonni multiple testing adjusted threshold for statistical significance of enrichment.



Supplemental Figure 14: Cell type - trait enrichments for g-chromVAR across different finemap variants posterior probability cutoffs. The horizontal line shows a Bonferonni multiple testing adjusted threshold for statistical significance of enrichment.



Supplemental Figure 15: Two subpopulations of CMP and MEP cells were obtained by k-means clustering on ATAC principal components or g-ChromVAR enrichments, respectively. Rank-order plots showing transcription factor binding sites ranked by difference in chromVAR enrichment between the two clusters of (A) CMP and (B) MEP populations

(E)