

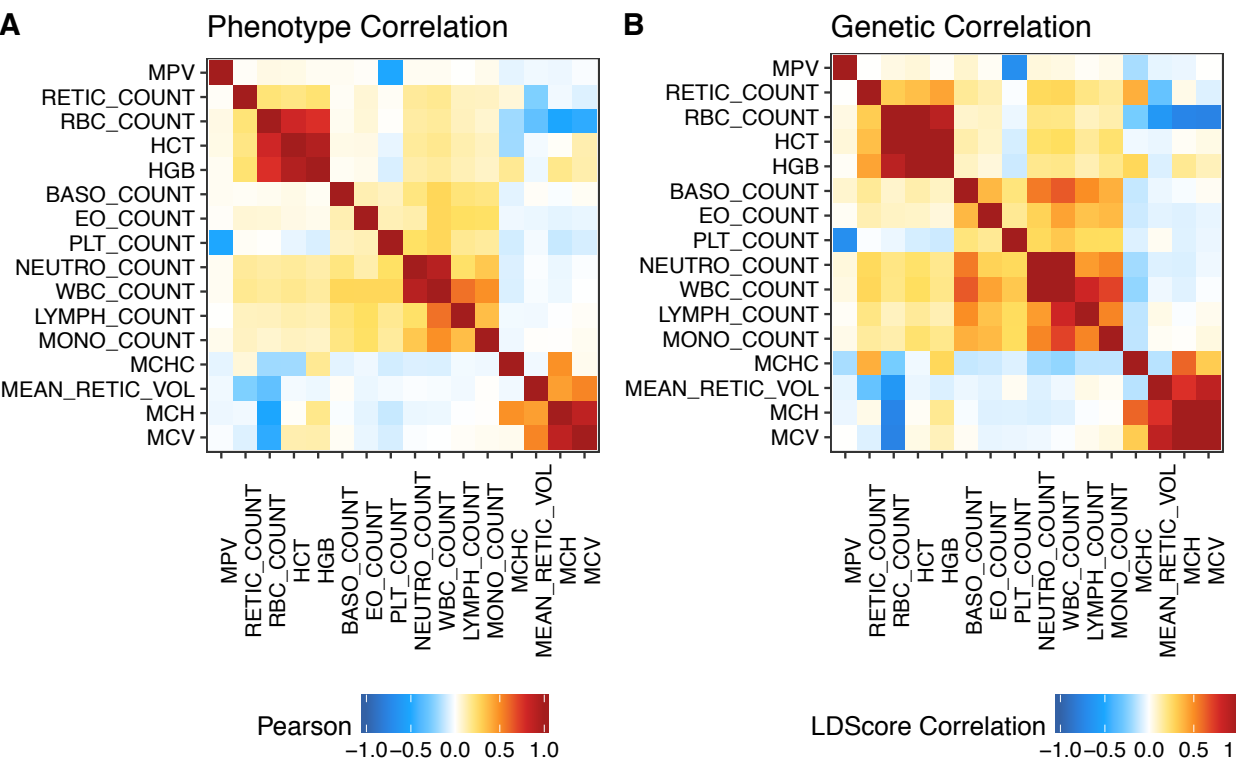
Interrogation of human hematopoietic traits at single-cell and single-variant resolution

(Caleb, Erik, Jacob), Will?, Hilary, Joel, (Martin, Jason, Vijay)

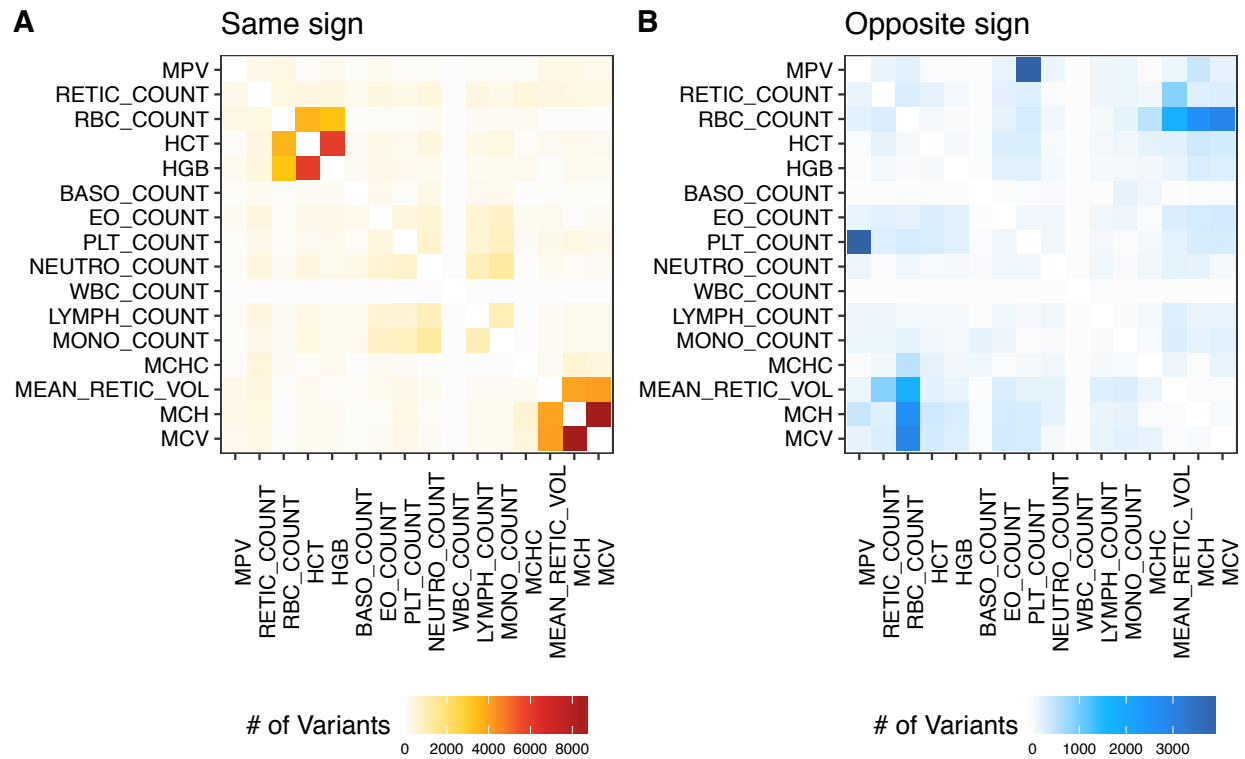
Supplemental Information

Overview of UK Biobank data

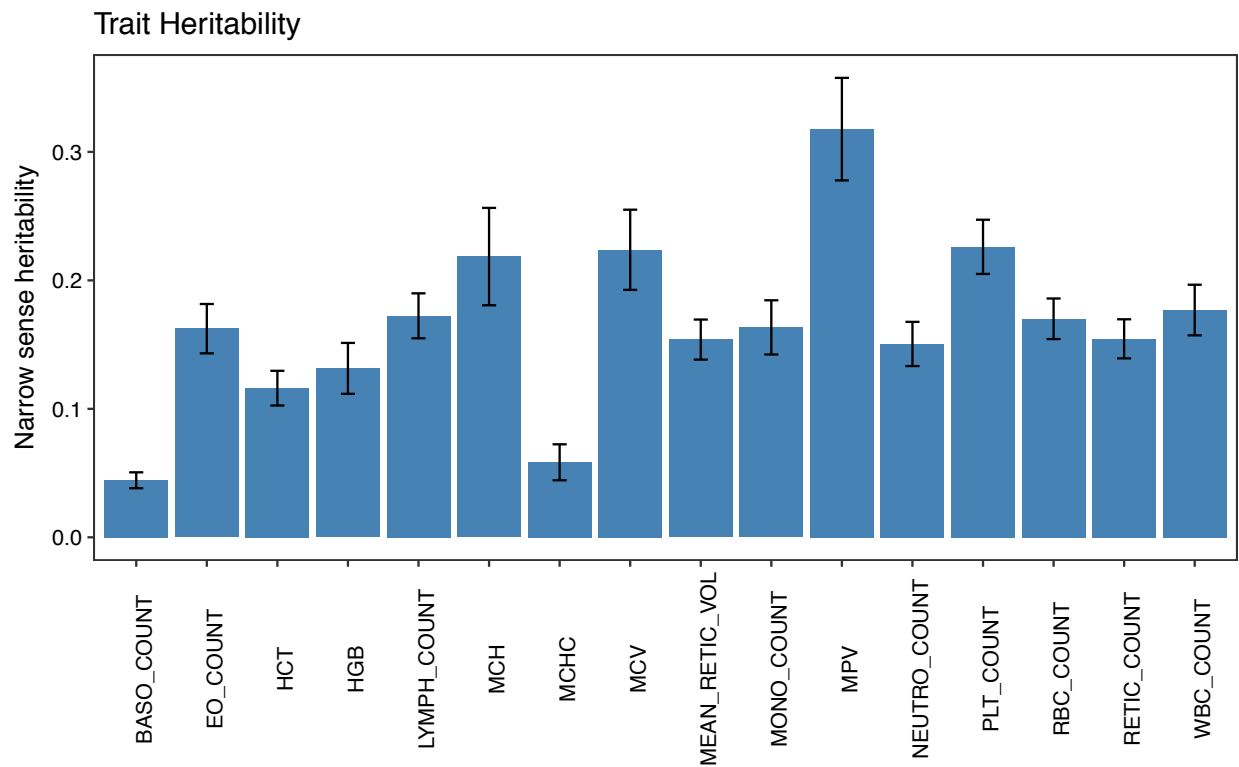
(A) a



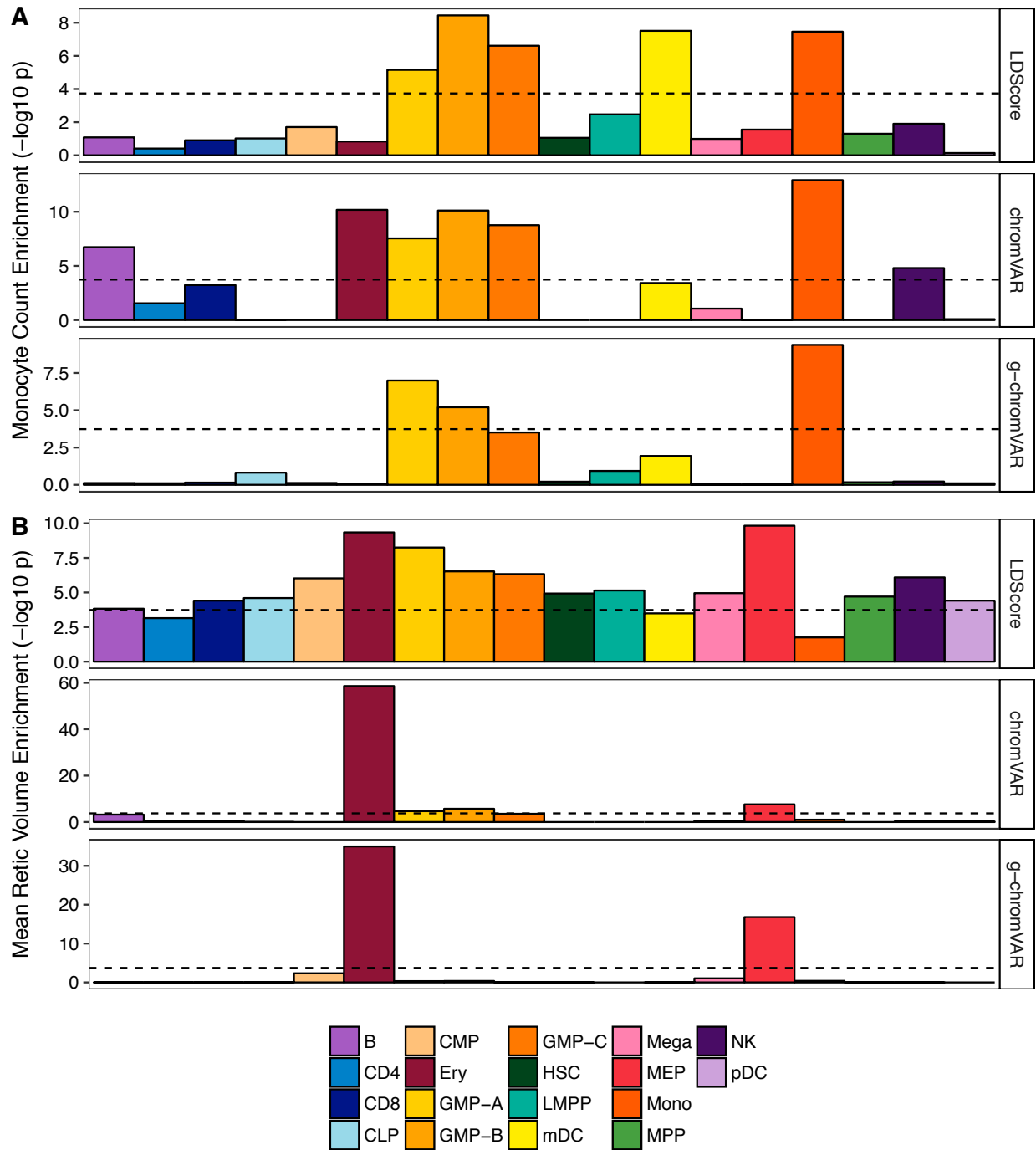
Supplemental Figure 1: Phenotypic and genetic correlations across the 16 traits examined.



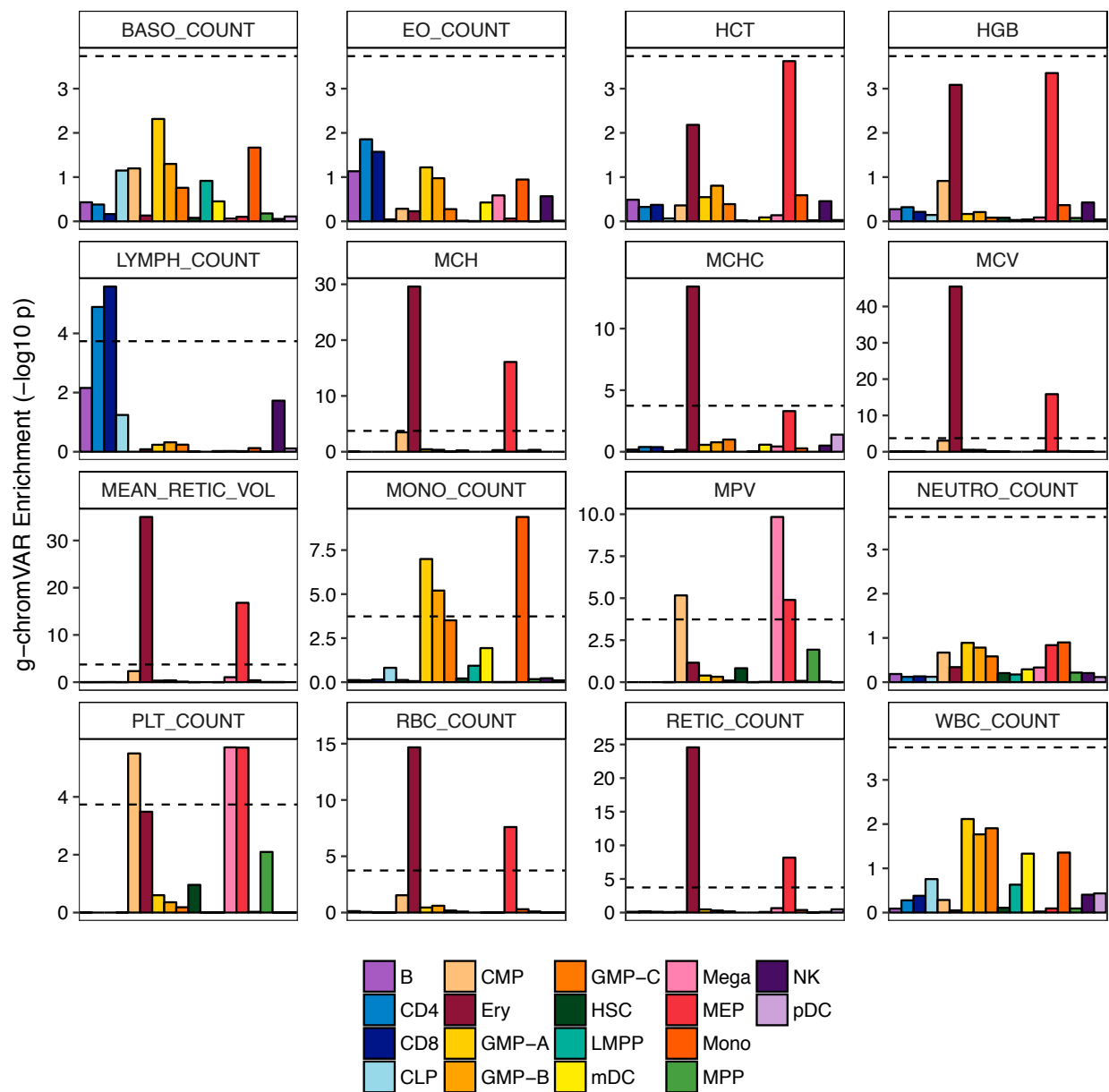
Supplemental Figure 2: Numbers of pleiotropic variants



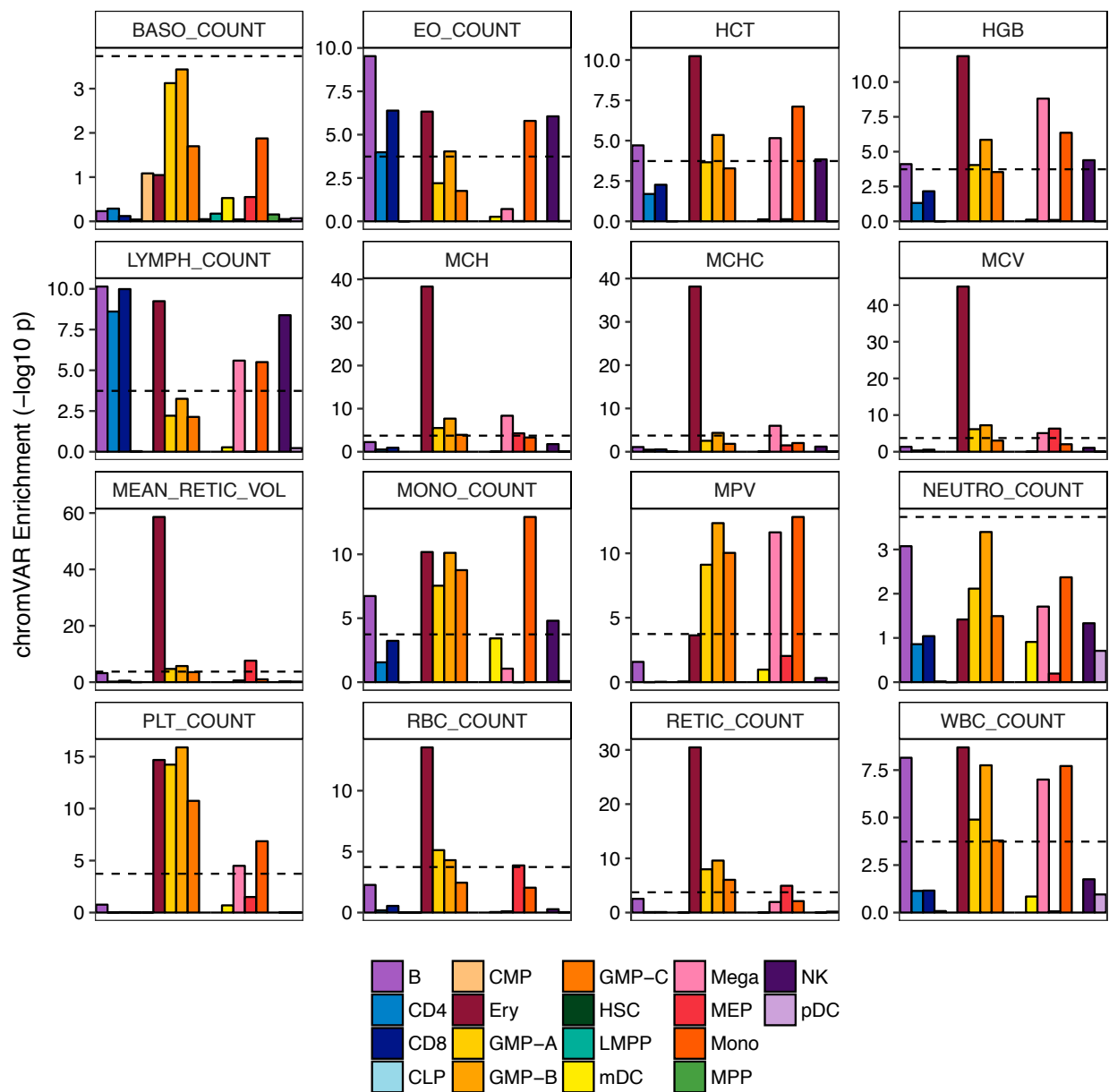
Supplemental Figure 3: Heritability estimates from LD Score Regression across 16 hematopoietic traits. The estimates of the narrow-sense SNP heritabilities are plotted with their corresponding standard errors.



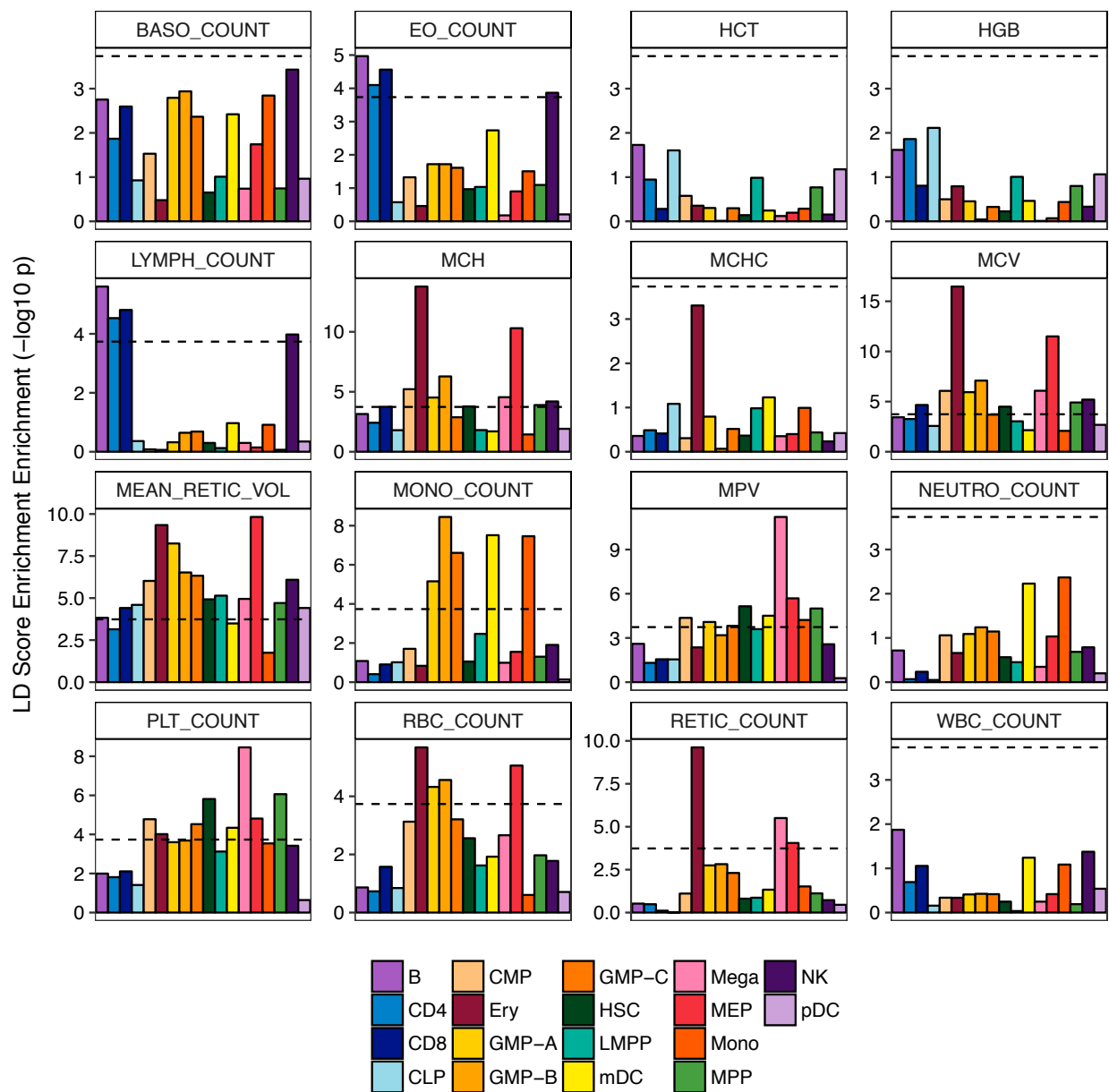
Supplemental Figure 4: Hematopoietic cell type enrichments for Mean Retic Volume and Monocyte count using various methods.



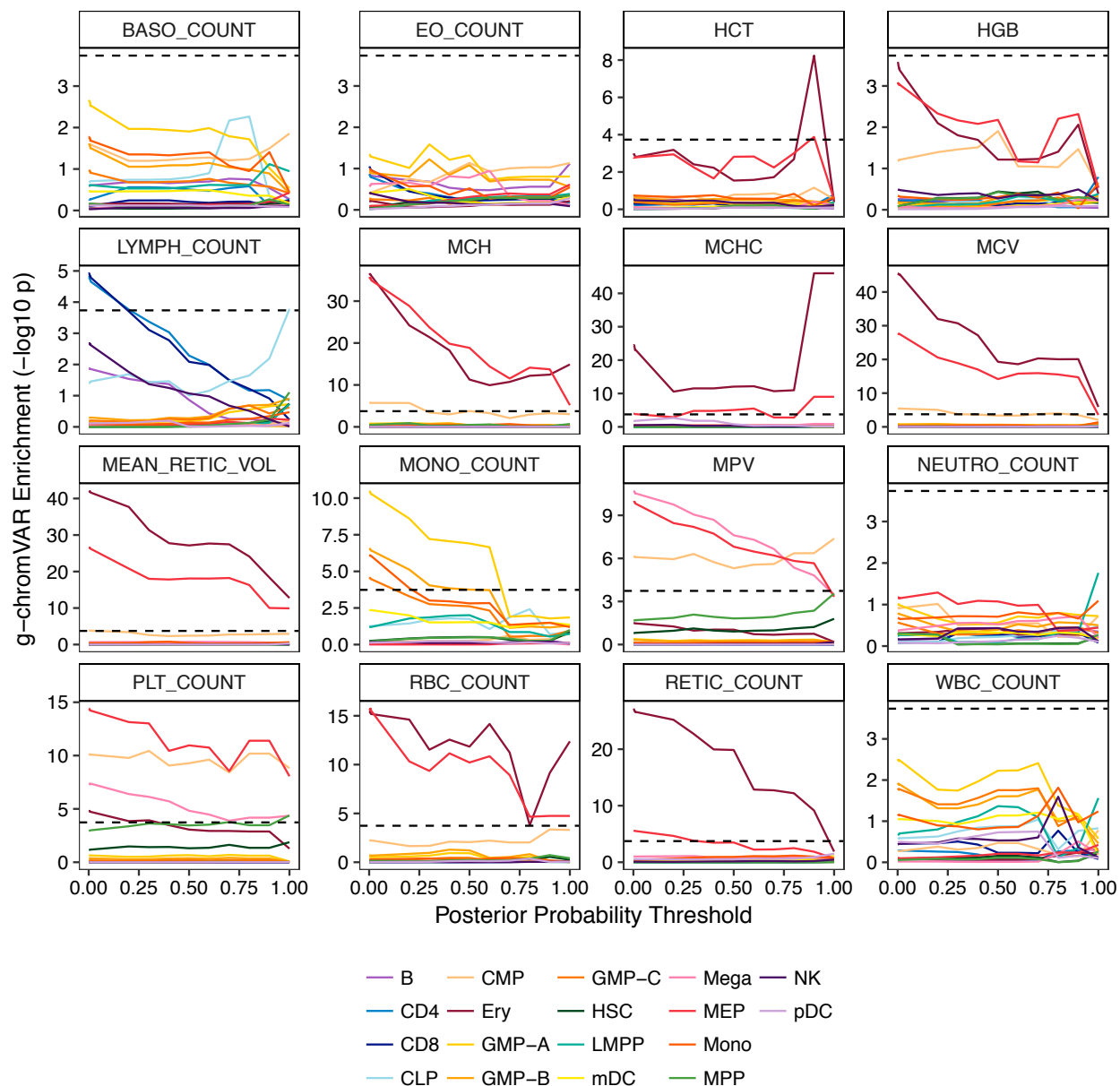
Supplemental Figure 5: All enrichments from g-chromVAR. The horizontal line shows a Bonferonni multiple testing adjusted threshold for statistical significance of enrichment.



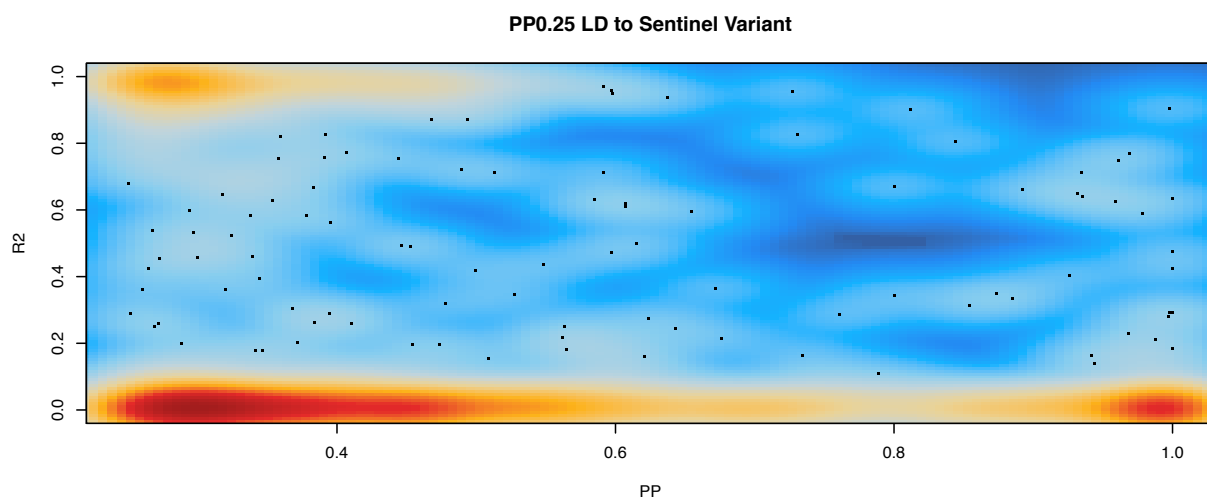
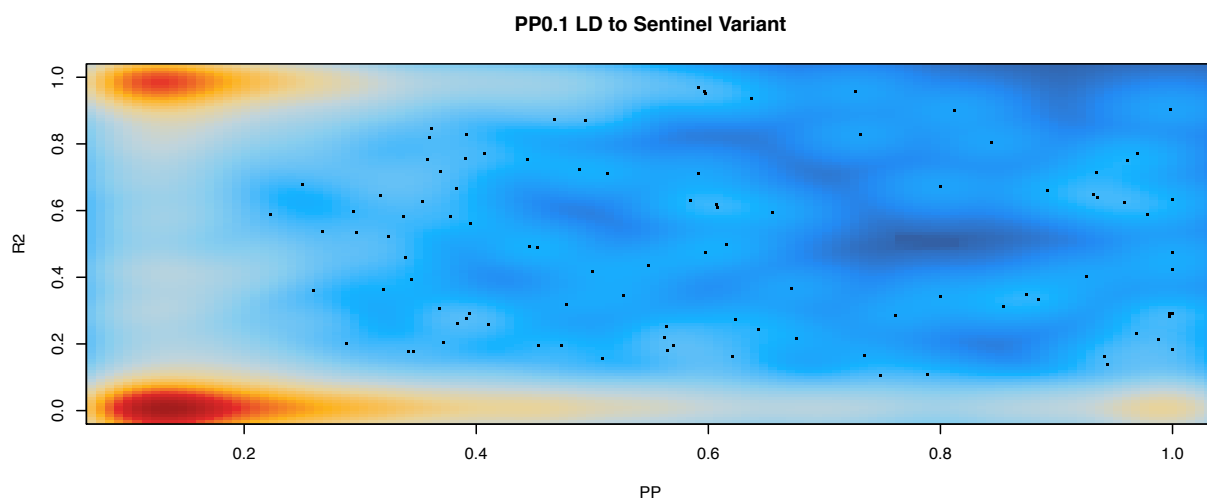
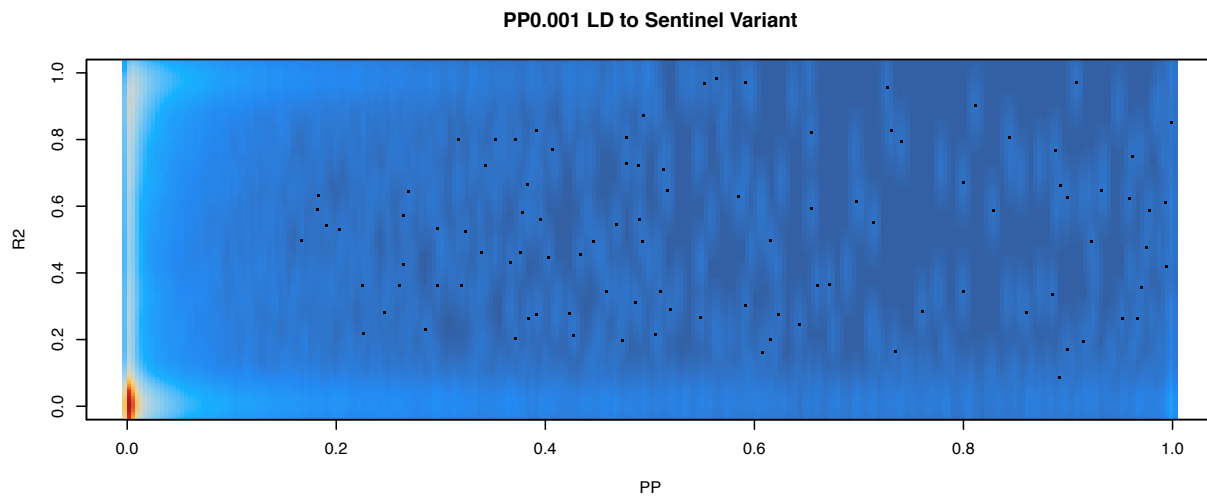
Supplemental Figure 6: All enrichments from chromVAR. The horizontal line shows a Bonferroni multiple testing adjusted threshold for statistical significance of enrichment.



Supplemental Figure 7: All enrichments from LD Score. The horizontal line shows a Bonferonni multiple testing adjusted threshold for statistical significance of enrichment.



Supplemental Figure 8: 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 9: Sample embedding of figure in document.

(B)