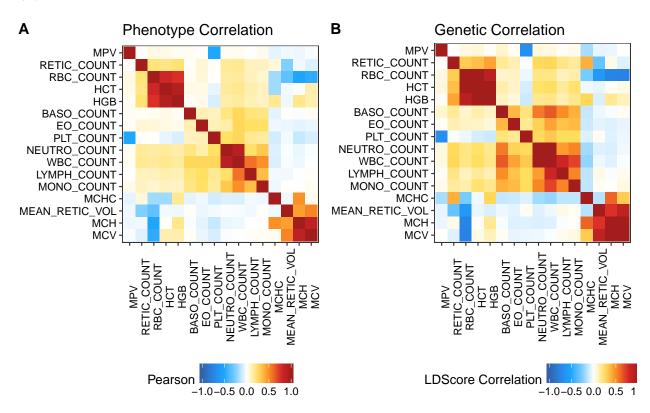
## Interrogation of human hematopoietic traits at single-cell and single-variant resolution

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

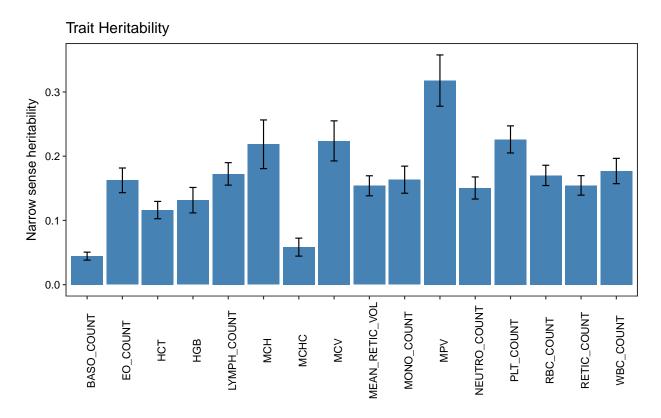
Supplemental Information

## Overview of UK Biobank data

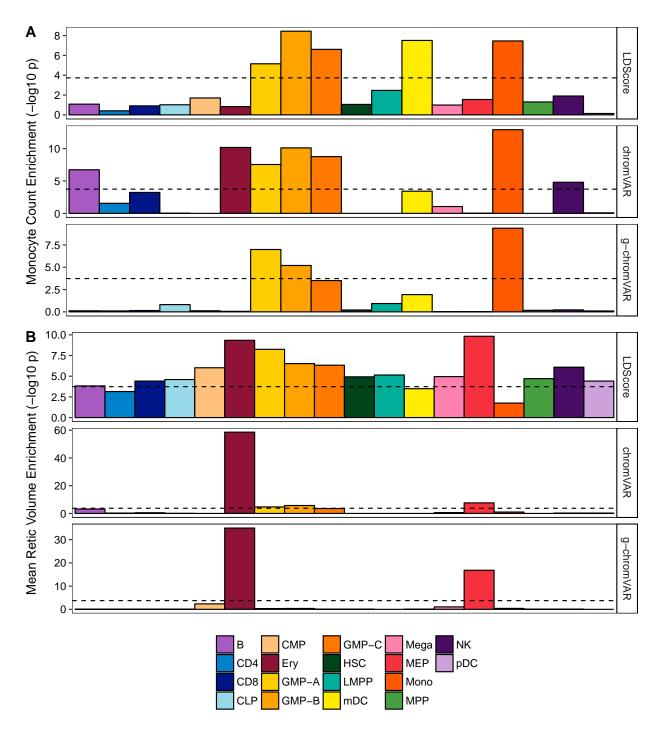
(A) a



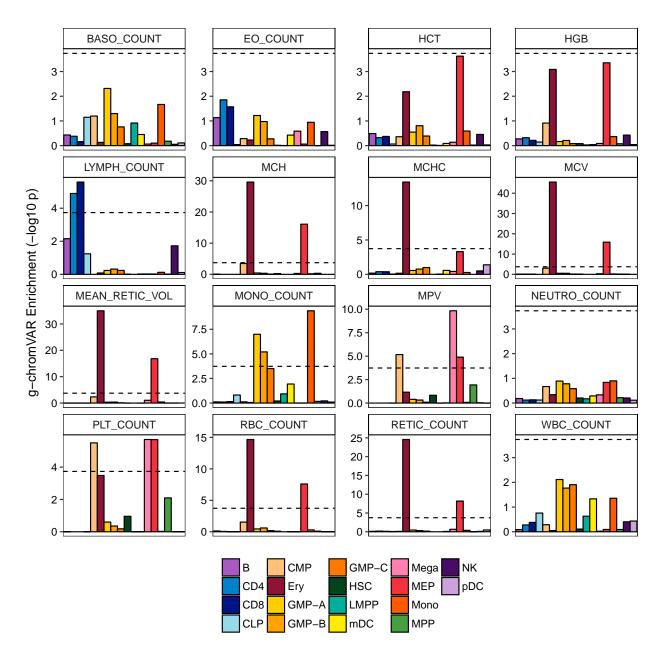
Supplemental Figure 1: Phenotypic and genetic correlations across the 16 traits examined.



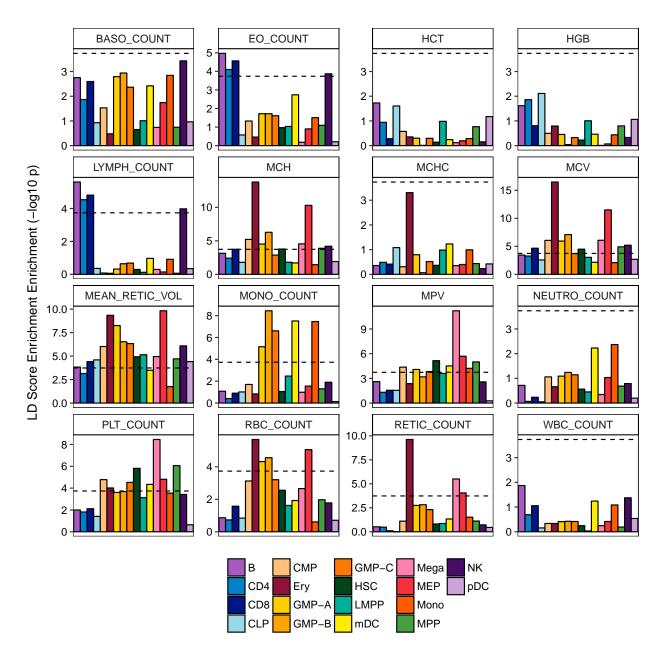
Supplemental Figure 2: Heritiability estimates from LD Score Regression across 16 hematopoetic traits. The estimates of the narrow-sense SNP heritabilities are plotted with their corresponding standard erors.



Supplemental Figure 3: Hematopoetic cell type enrichments for Mean Retic Volume and Monocyte count using various methods.

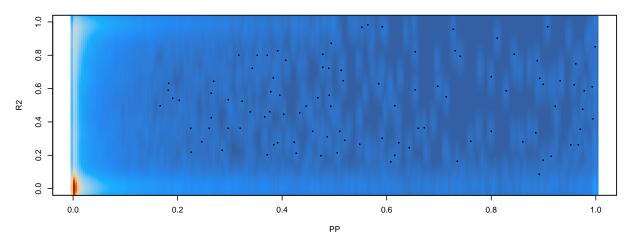


Supplemental Figure 4: All enrichments from g-chromVAR. The horizontal line shows a Bonferonni multiple testing adjusted threshold for statistical significance of enrichment.

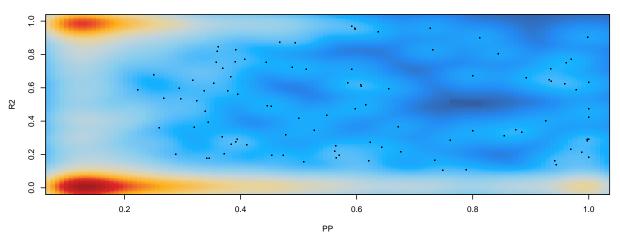


Supplemental Figure 5: All enrichments from LD Score. The horizontal line shows a Bonferonni multiple testing adjusted threshold for statistical significance of enrichment.

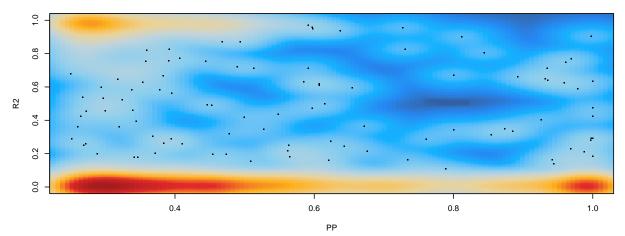
## PP0.001 LD to Sentinel Variant



## **PP0.1 LD to Sentinel Variant**



PP0.25 LD to Sentinel Variant



Supplemental Figure 6: Sample embedding of figure in document.

(B)