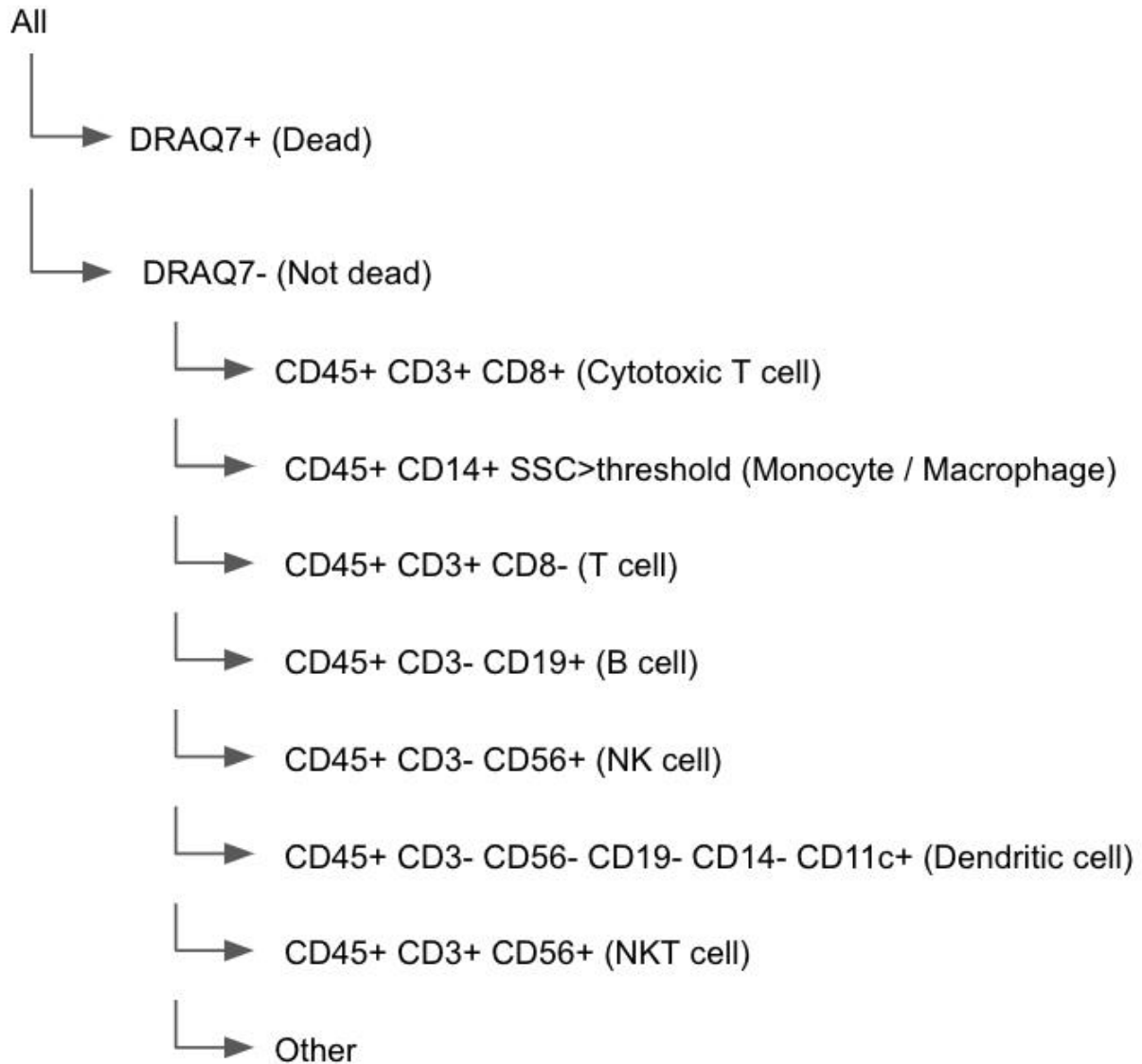
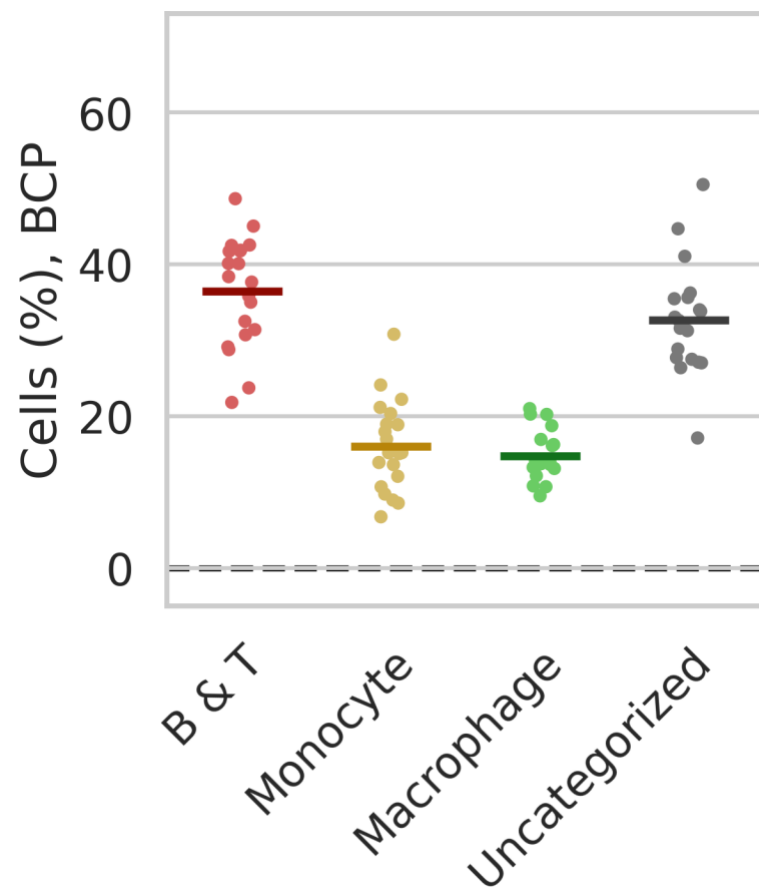


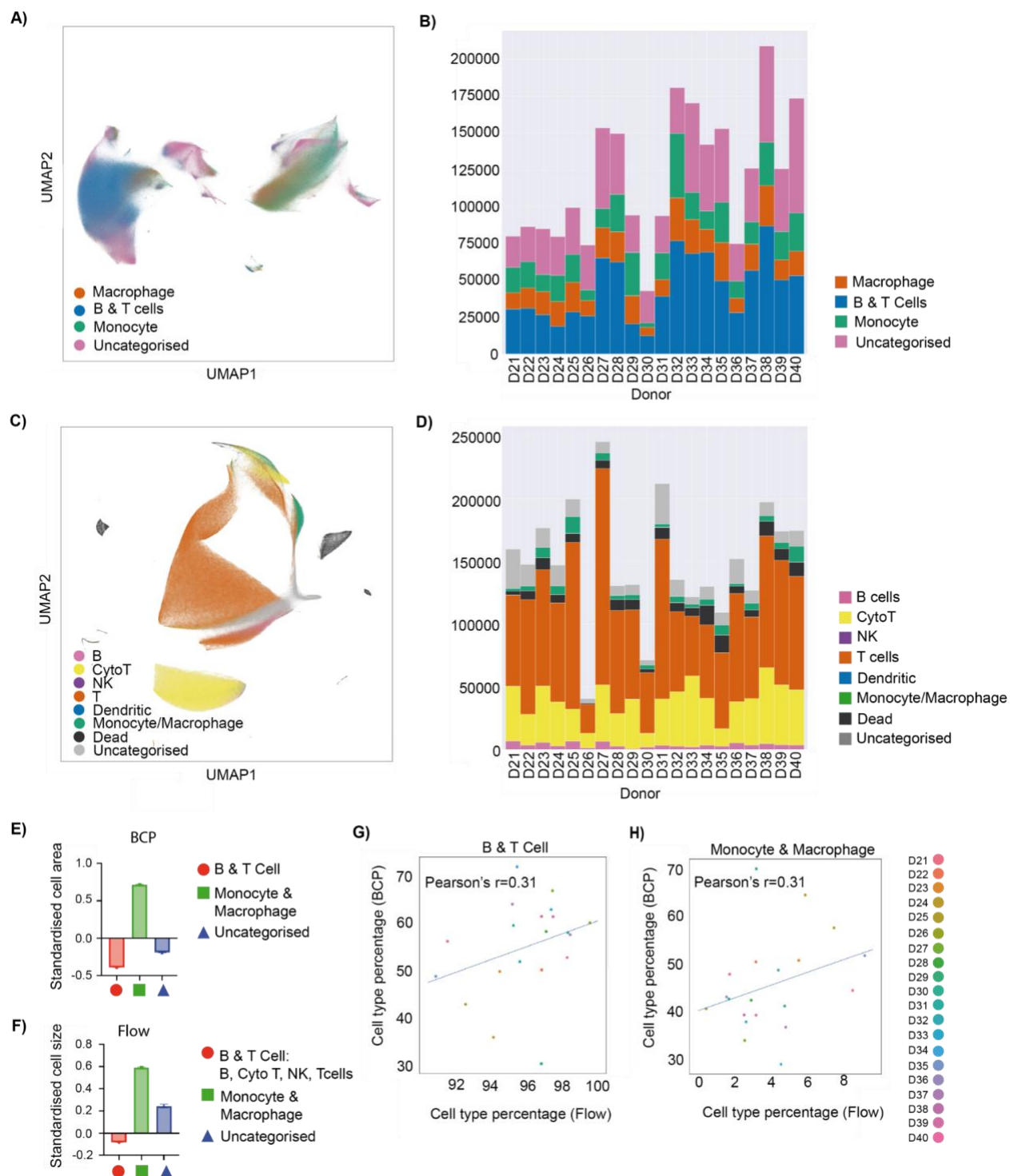
Supplementary Figures



Supplementary Figure 1. Gating strategy of flow cytometry cell typing.

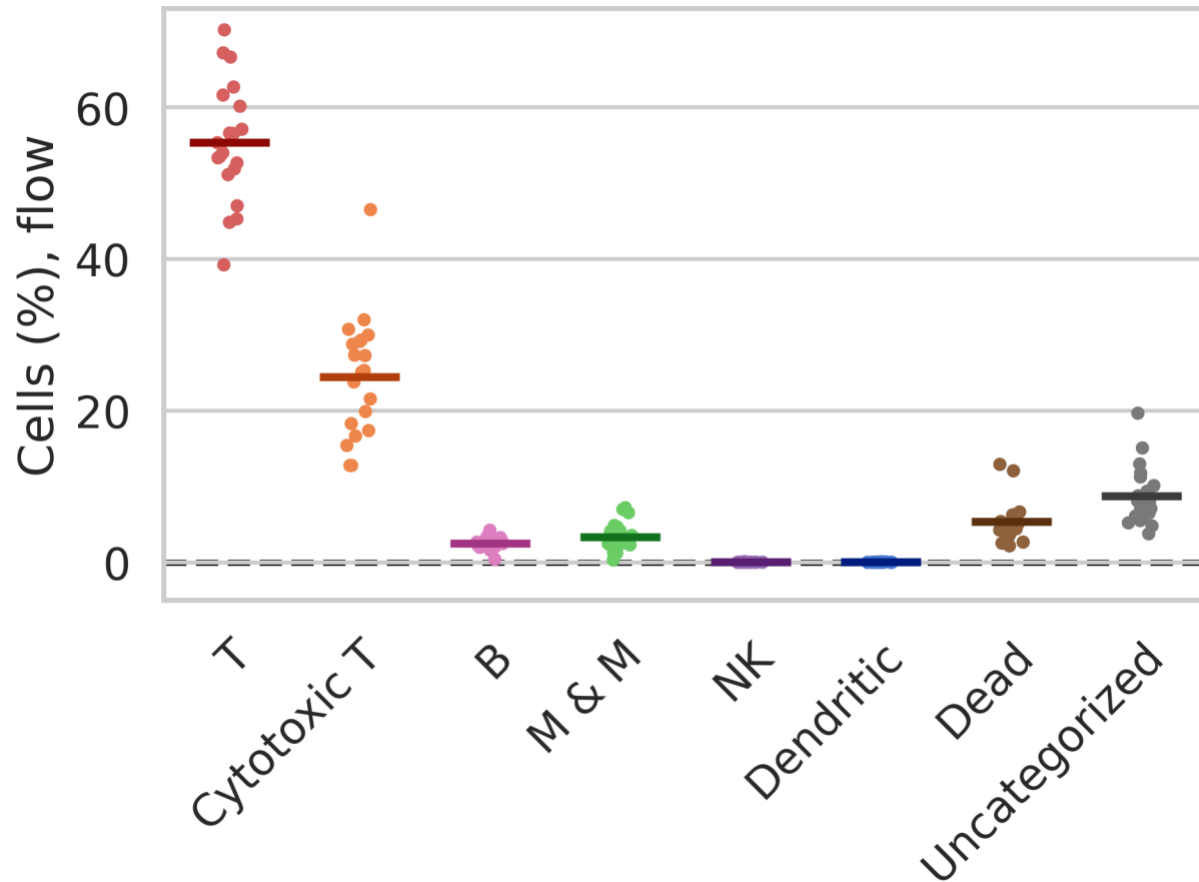


Supplementary Figure 2. Donor-specific proportions of cells by type assigned by the supervised learning procedure in the BCP data based expert annotation. Means indicated with lines.



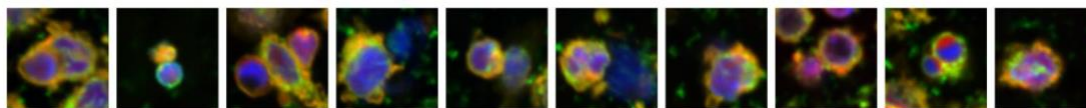
Supplementary Figure 3. Comparison of BCP and flow cytometry data for 20 healthy blood donors. A) UMAP representation of the BCP data. B) Frequency of cells by type in the BCP data (cell count on Y-axis). C) UMAP representation of the flow cytometry data. D) Frequency of cells by type in the flow cytometry data (cell count on Y-axis). E-F) Standardised cell areas derived from BCP (E) and flow cytometry (F), respectively. Barplots show a mean with a 95%

confidence interval. G) B and T cell, and H) macrophage and monocyte frequencies (%) detected in BCP (Y-axis) and flow cytometry (X-axis), with respect to the total number of B, T, macrophage and monocyte cells.

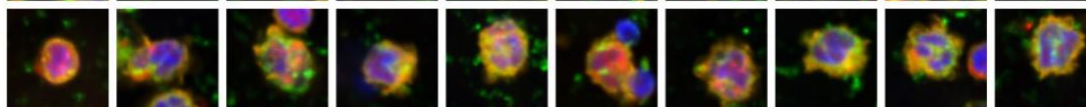


Supplementary Figure 4. Donor-specific proportions of cells by type assigned by the gating procedure (Suppl. Fig. 1) in flow cytometry data. Means indicated with lines. M & M, monocytes and macrophages.

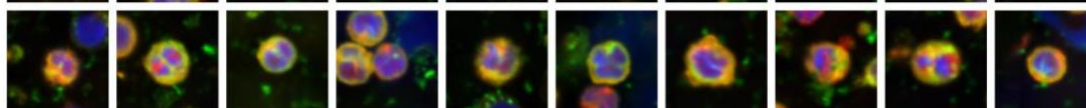
C3



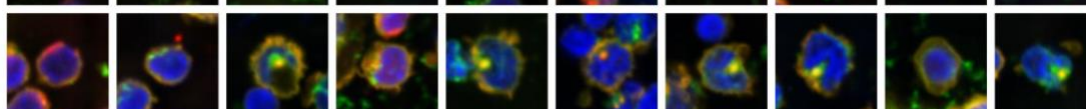
C4



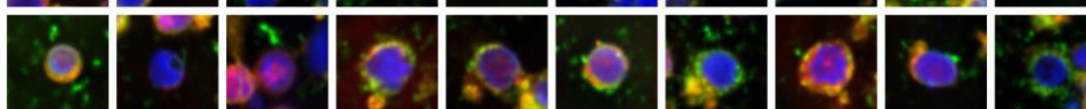
C5



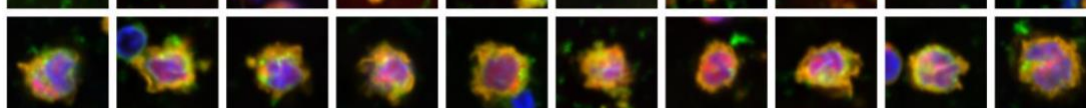
C6



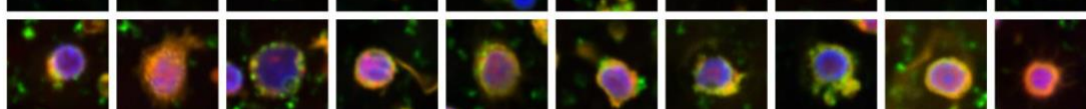
C8



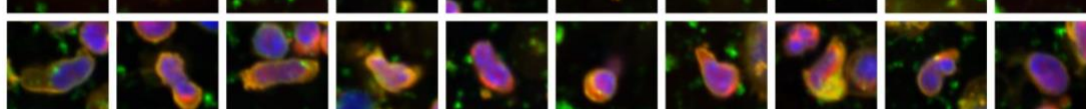
C9



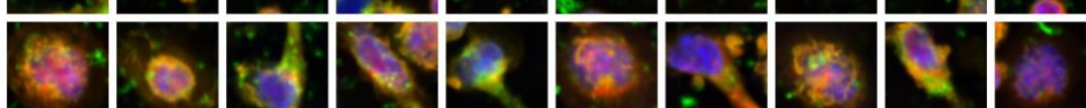
C10



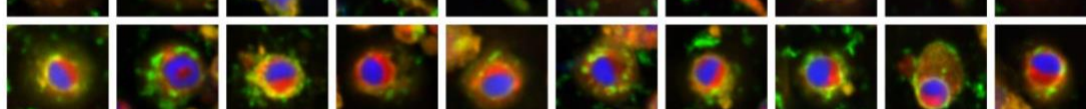
C11



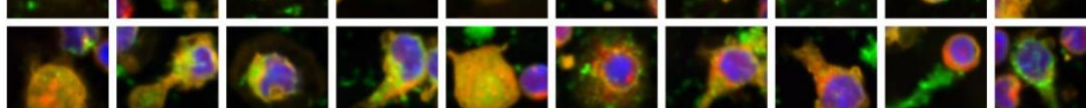
C12



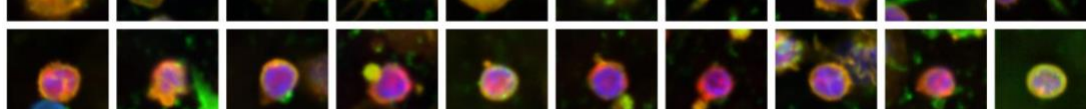
C13



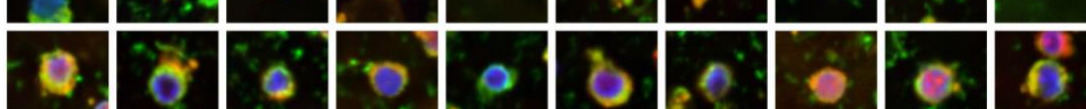
C14



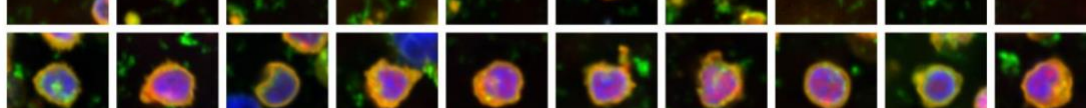
C15



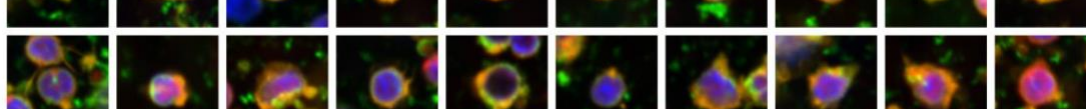
C16



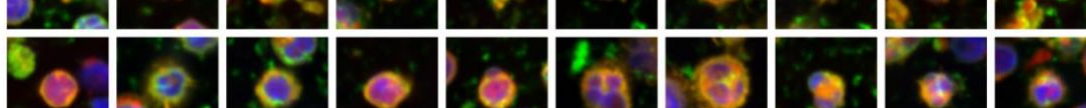
C17



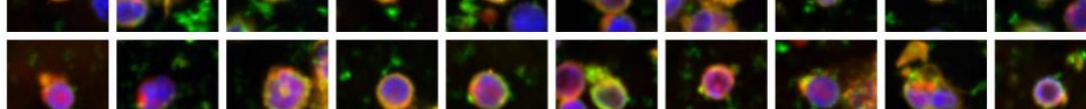
C18



C19

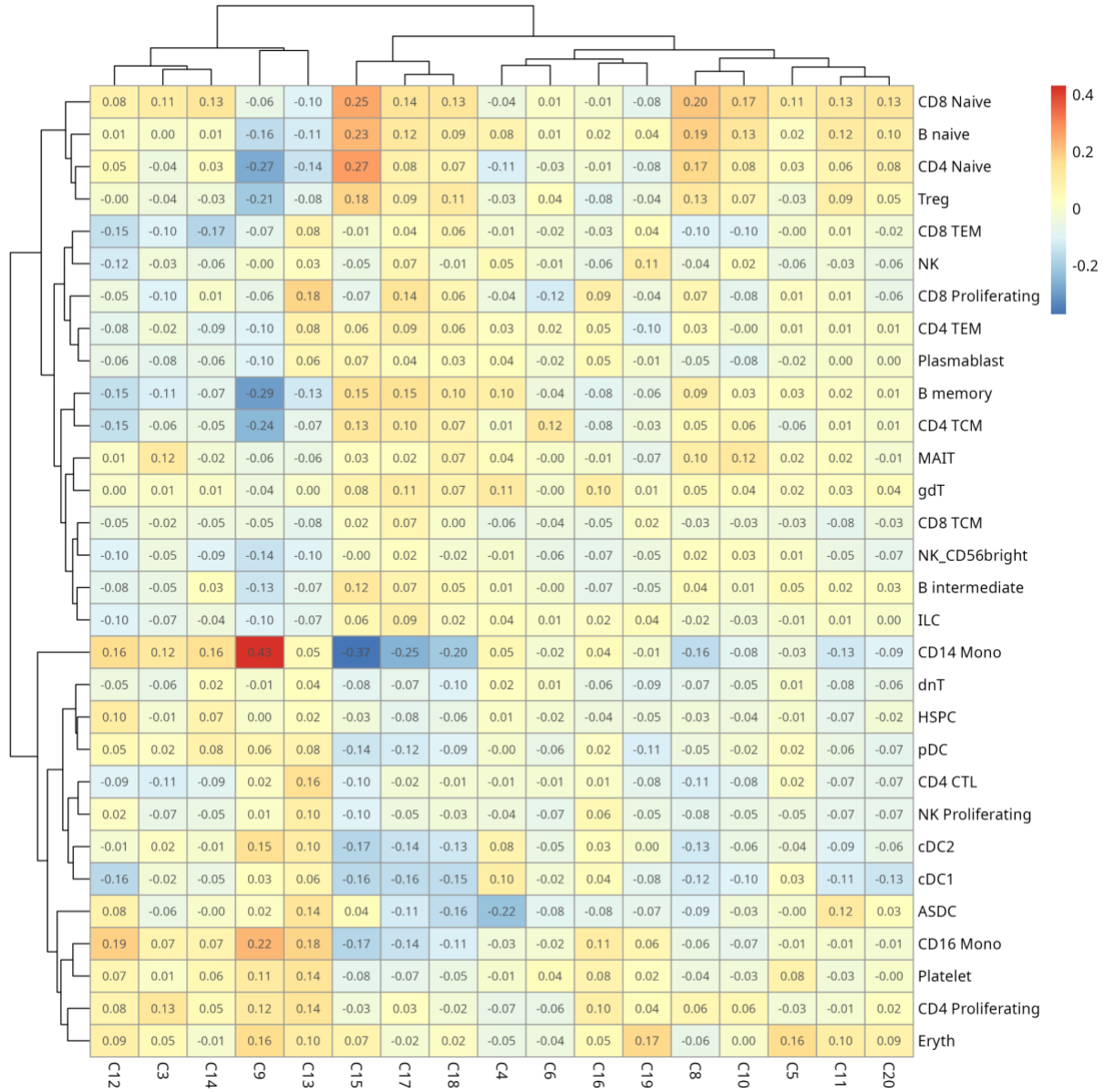


C20

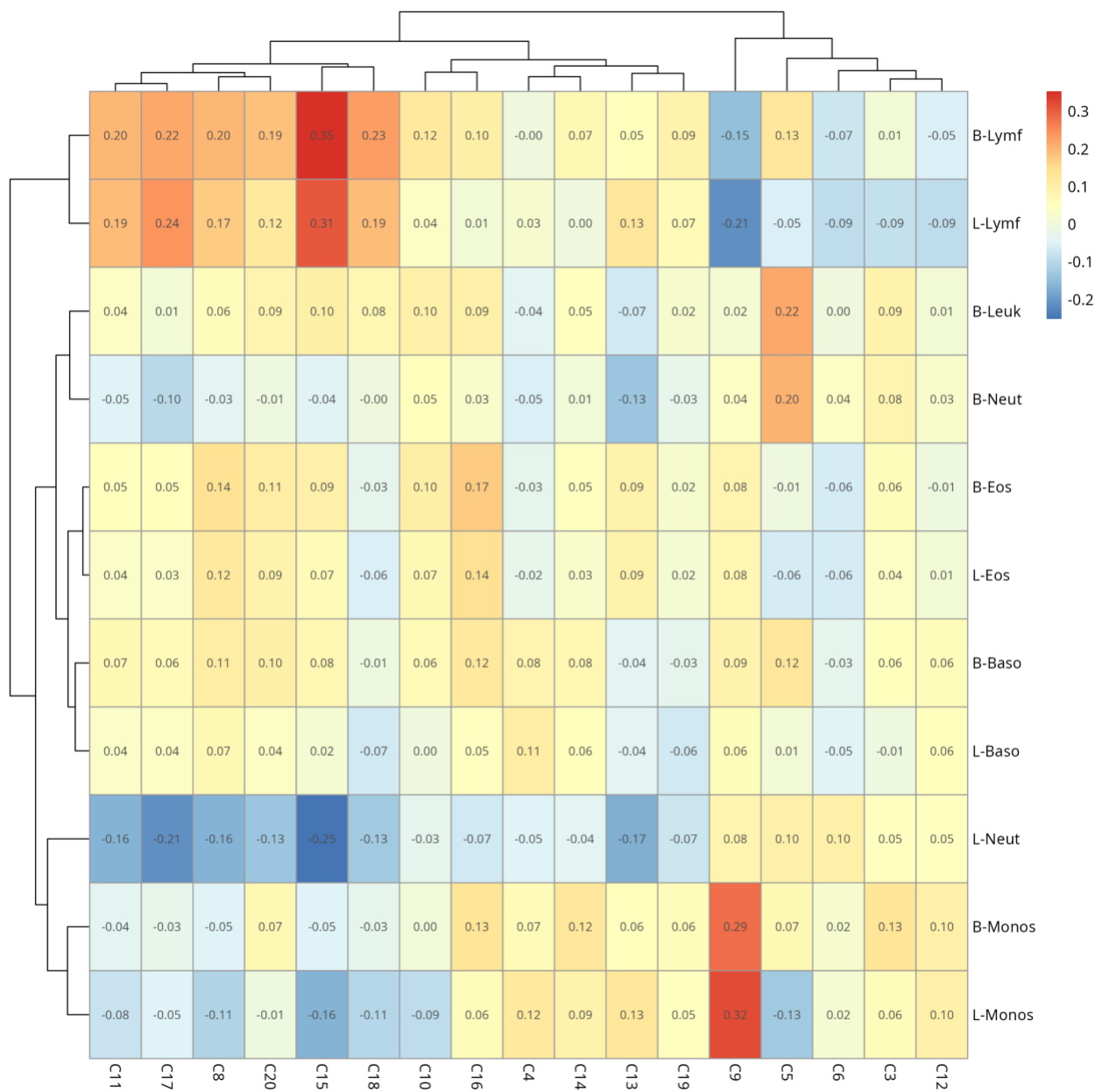


Supplementary Figure 5. Examples of cell images from each cluster C3-C20 except cluster C7 which was not used in analyses. Created with BioRender.com.

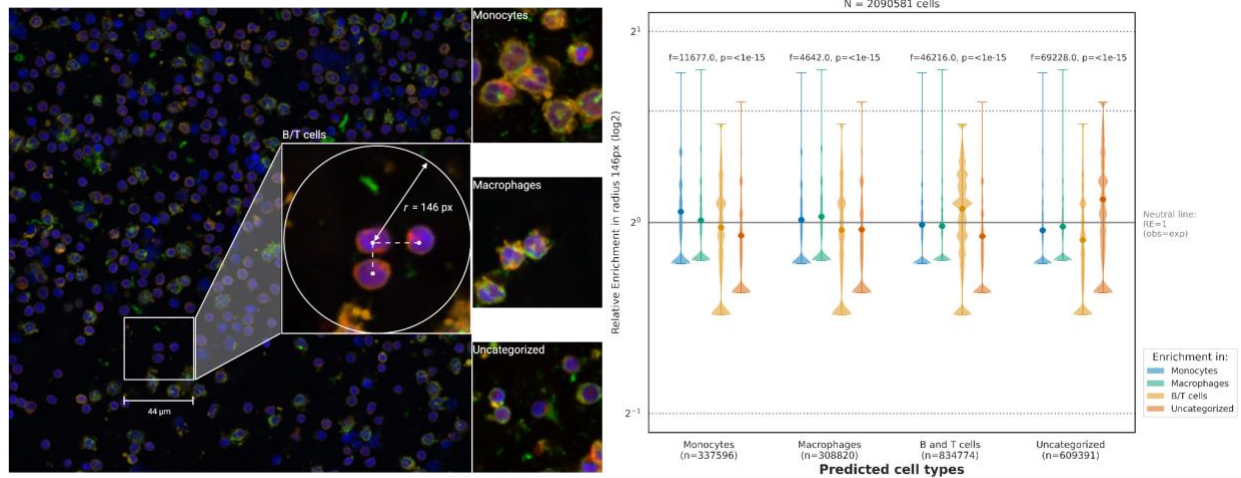
A)



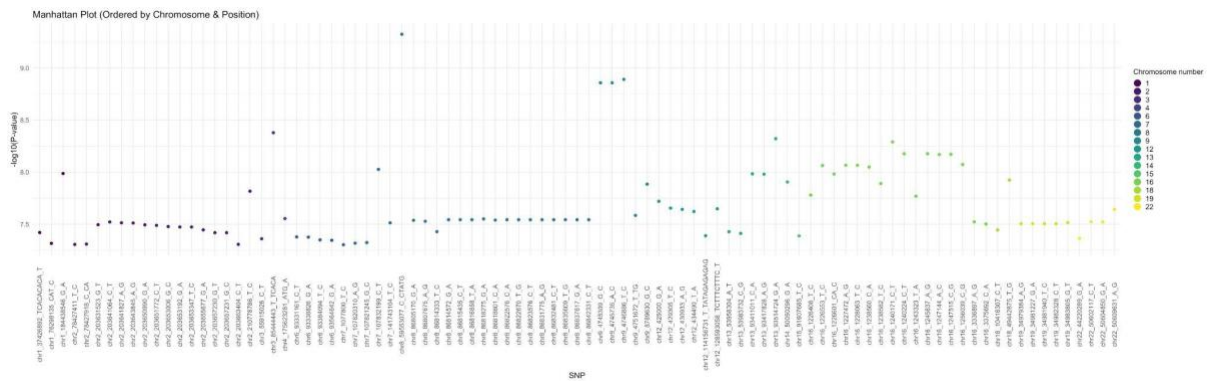
B)



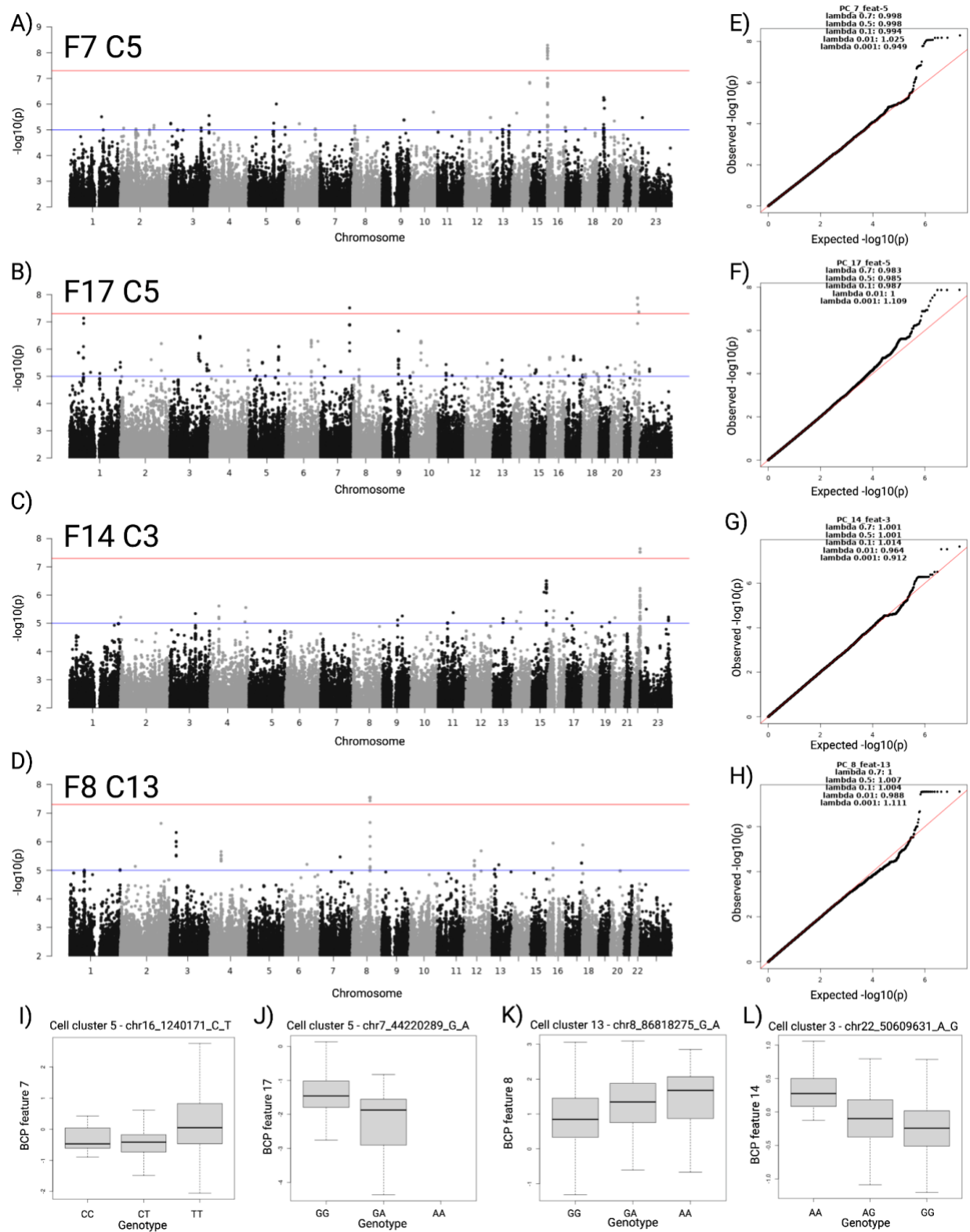
Supplementary Figure 6. A) The correlations between snRNA-seq cell type percentages and BCP clusters, B) the correlations between complete blood count values and BCP clusters.



Supplementary Figure 7. Examples of cell-cell interactions and relative enrichment in monocytes, macrophages, B/T cells, and uncategorized cells. One-way ANOVA F-statistics and p-values suggest significant differences between enrichment in each cell type in monocytes, macrophages, B/T cells, and uncategorized cells. Created with BioRender.com.



Supplementary Figure 8. All significant 93 genotype-phenotype associations visualized by their genomic position (X-axis) and $-\log_{10}(p)$ -value (Methods, GWAS QC).



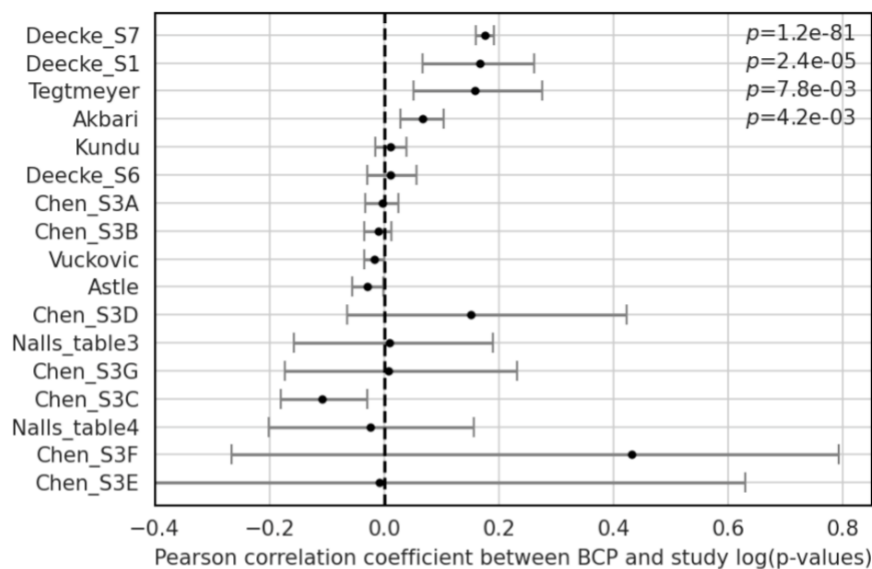
Supplementary Figure 9. GWAS results for the top four associating regions between principal components of BCP features and germline variants. A-D) Manhattan plots, E-H) quantile-

quantile plots for p-values, and I-L) genotype-phenotype effect plots, where on the x-axis 0 stands for homozygous reference, 1 for heterozygous and 2 for homozygous alternate. Created with BioRender.com.

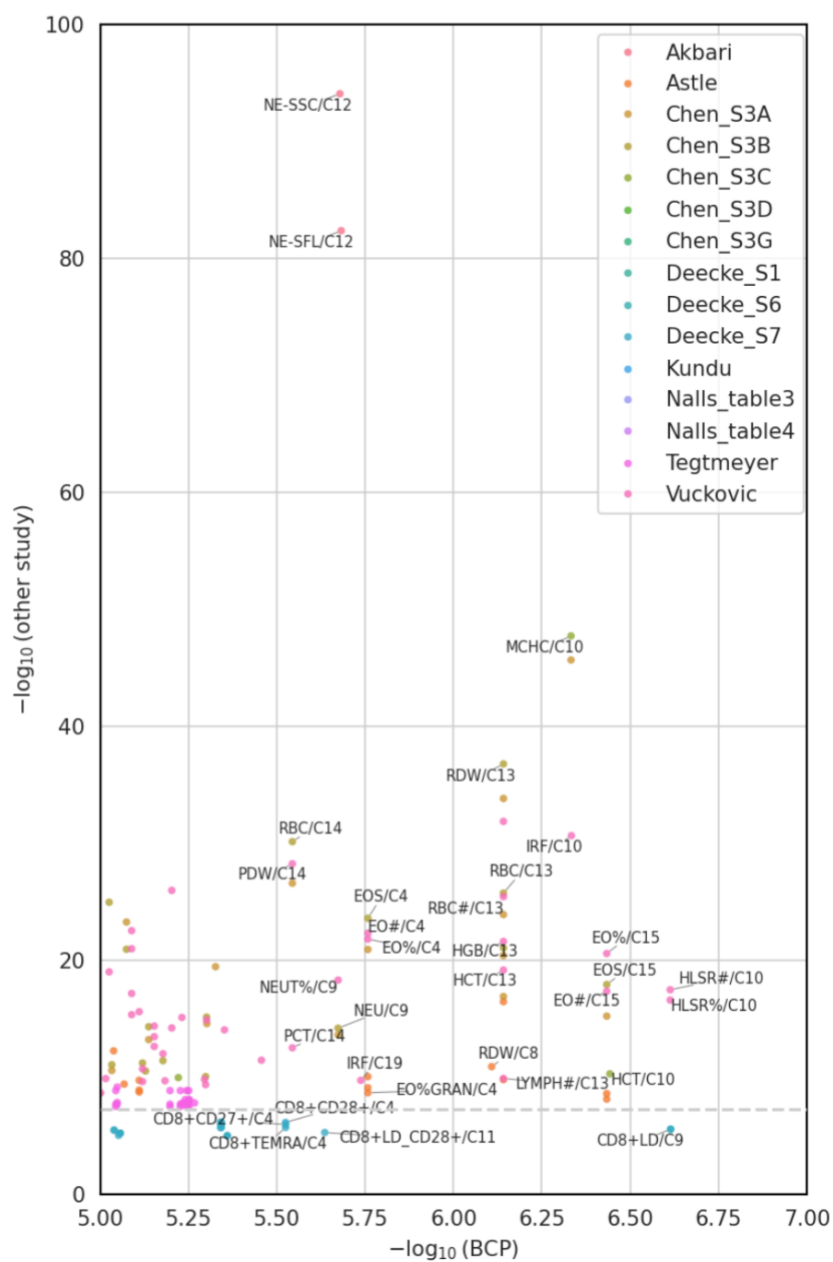


Supplementary Figure 10. Principal component loadings for selected four PCs and top ten shared BCP features.

A)



B)



Supplementary Figure 11. Comparison between variant association results obtained in our study and eight previous studies. A) Pearson correlations and 95% confidence intervals for $\log(p)$ values of variant associations reported in both studies. B) a scatterplot with $-\log_{10}(p)$ values for BCP GWAS (X-axis) and the other GWAS (Y-axis). Labels indicate the trait reported in the other GWAS and the cell cluster (C3-20) reported in the BCP GWAS for selected variants. Colors indicate the other study, and the result table when applicable. Created with BioRender.com.