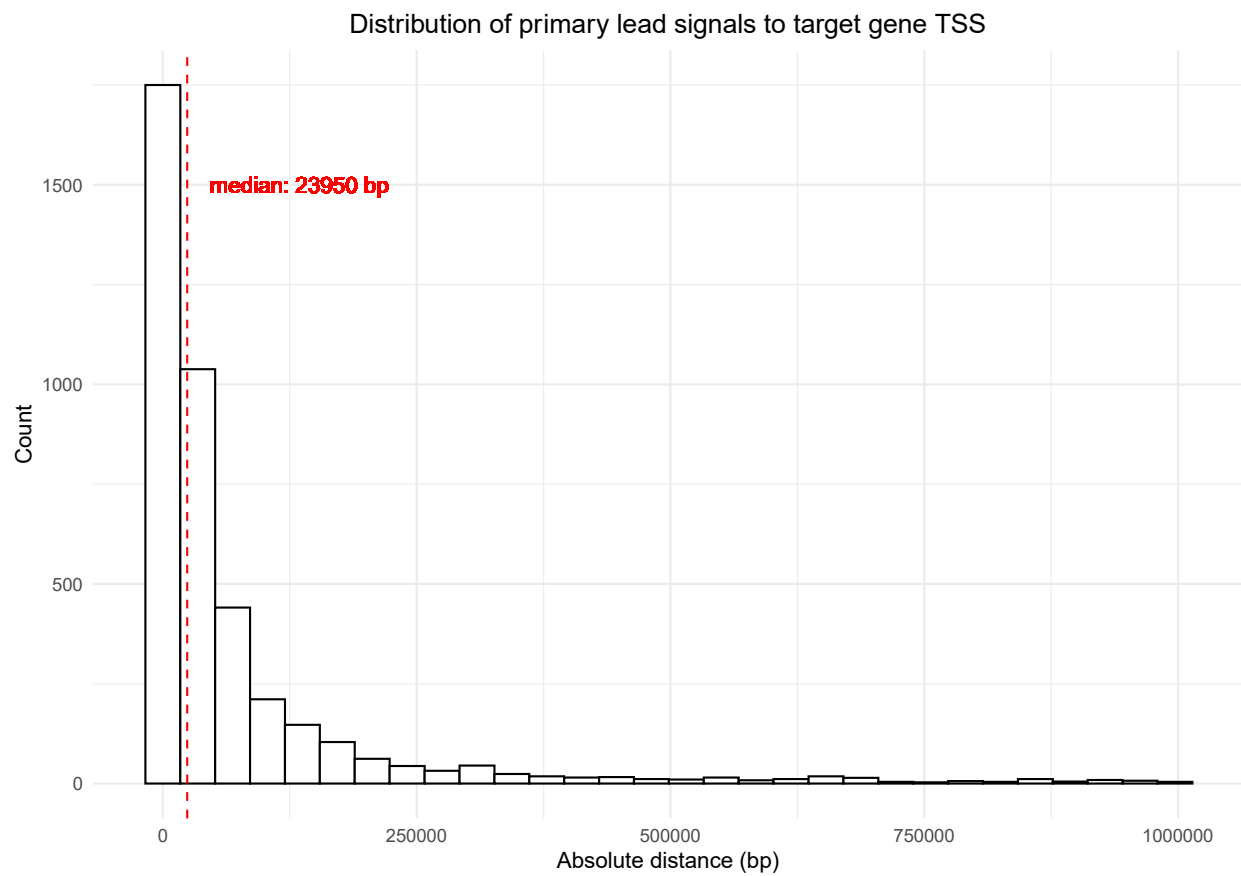


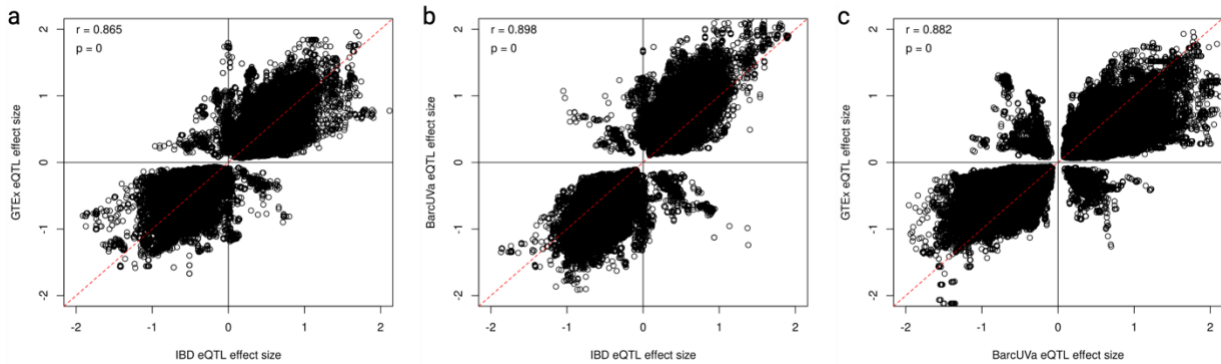
Supplementary Figures



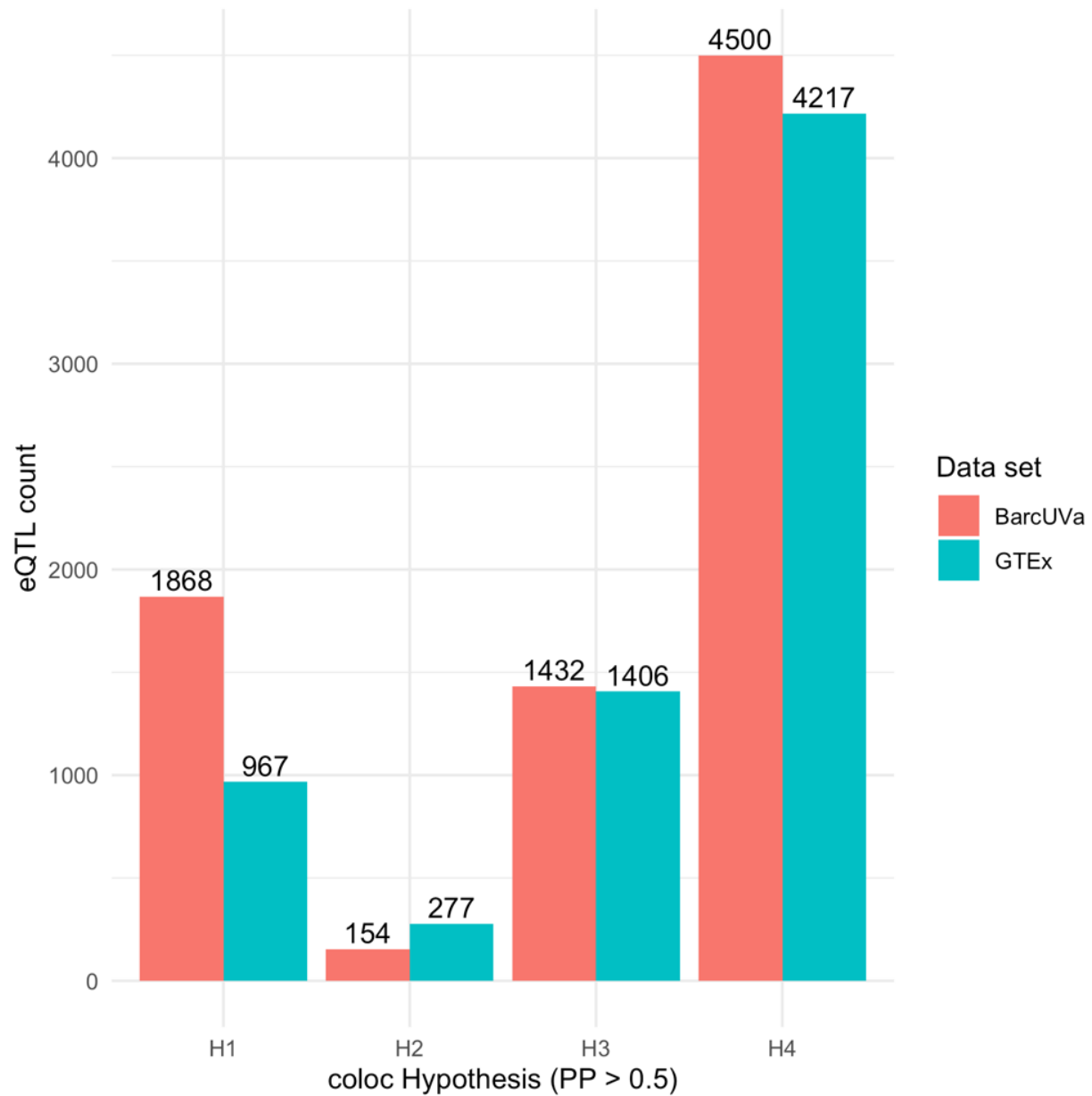
Supplementary Figure 1 Primary lead eQTL signals are proximal to target gene transcription start site (TSS). Source data are provided as a Source Data file.



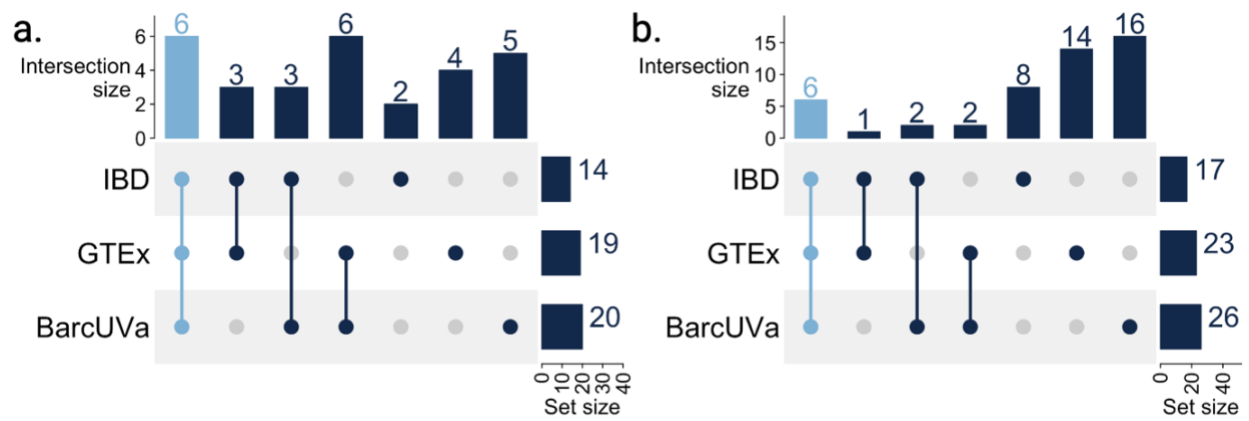
Supplementary Figure 2 Distribution of distance from lead eVariant to target gene TSS by signal rank. Boxplots were defined using a center median. Lower and upper hinges represent the 25th and 75th percentiles. Whiskers represent 1.5x the interquartile range. Source data are provided as a Source Data file.



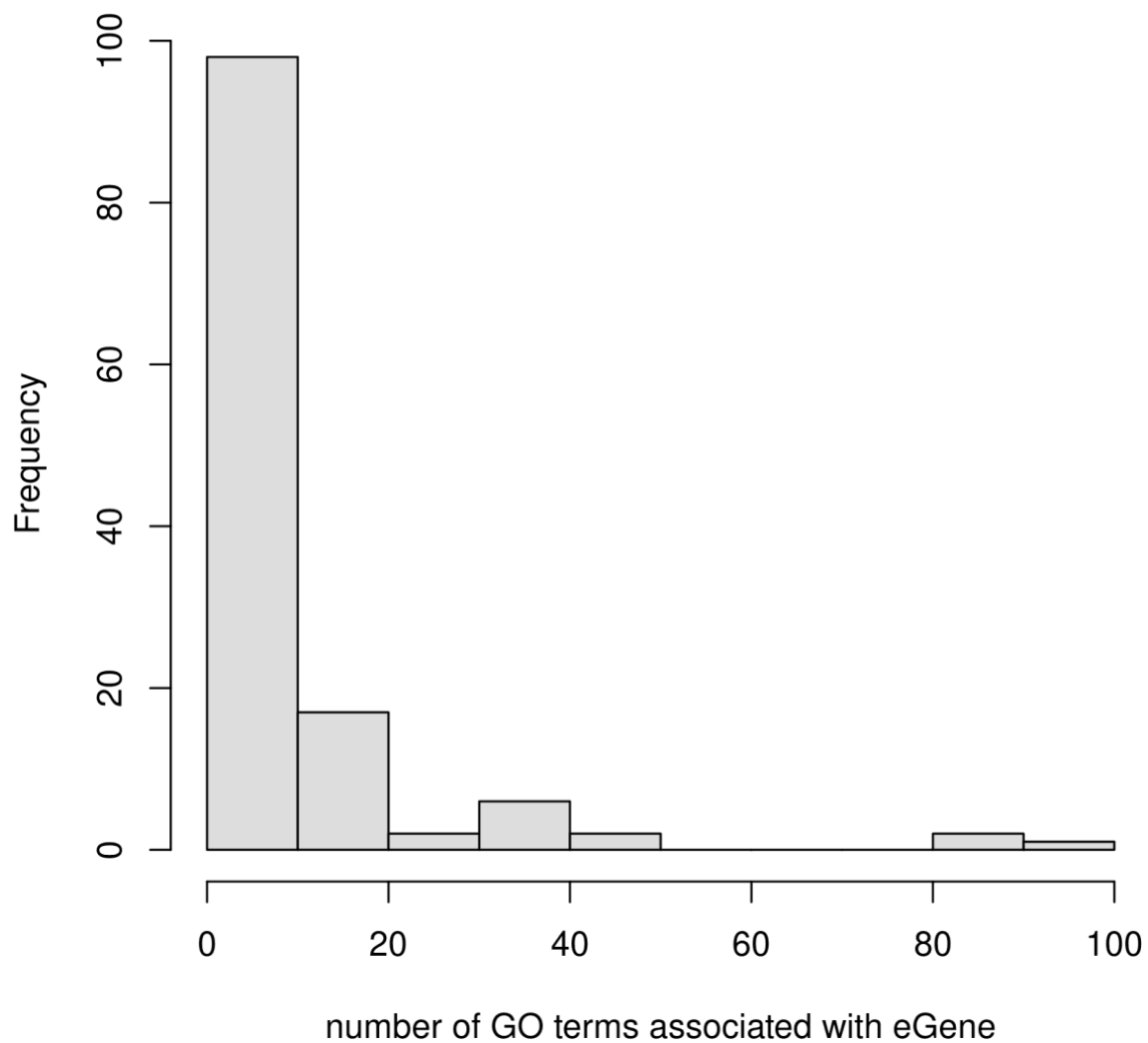
Supplementary Figure 3 Effect Size Correlation between all significant shared eVariant-eGene pairs. Pearson's correlation coefficient and p-values using a two-sided test for effect size estimates are shown. Red dashed line represents the (0,1) intercept. Source data are provided as a Source Data file.



Supplementary Figure 4 Bar plot of GTEx eQTL-BarcUVa eQTL colocalization results by coloc hypothesis (PP > 0.5): H1, significant signal detected in reference data set only (self); H2, significant signal detected in comparison data set only; H3, significant signal detected in both data sets but different causal variants; H4, significant signal detected in both data sets, same causal variant. Source data are provided as a Source Data file.

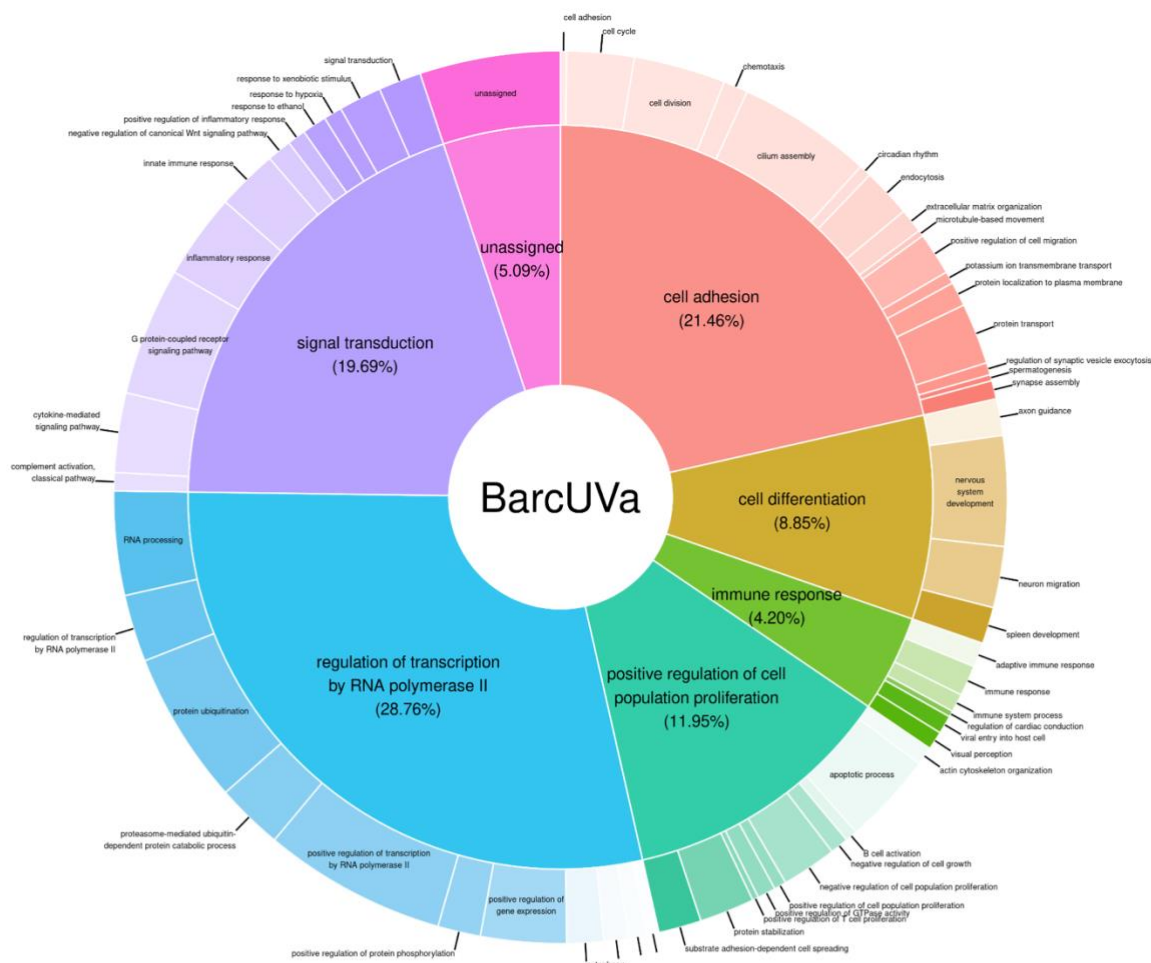


Supplementary Figure 5 Sharing of colocalization results for newly reported IBD GWAS loci. *a.* UpSet plot showing overlap of newly reported colocalizing GWAS loci across studies. *b.* UpSet plot showing overlap of eGenes that colocalize with newly reported IBD GWAS loci across studies. Source data are provided as a Source Data file.

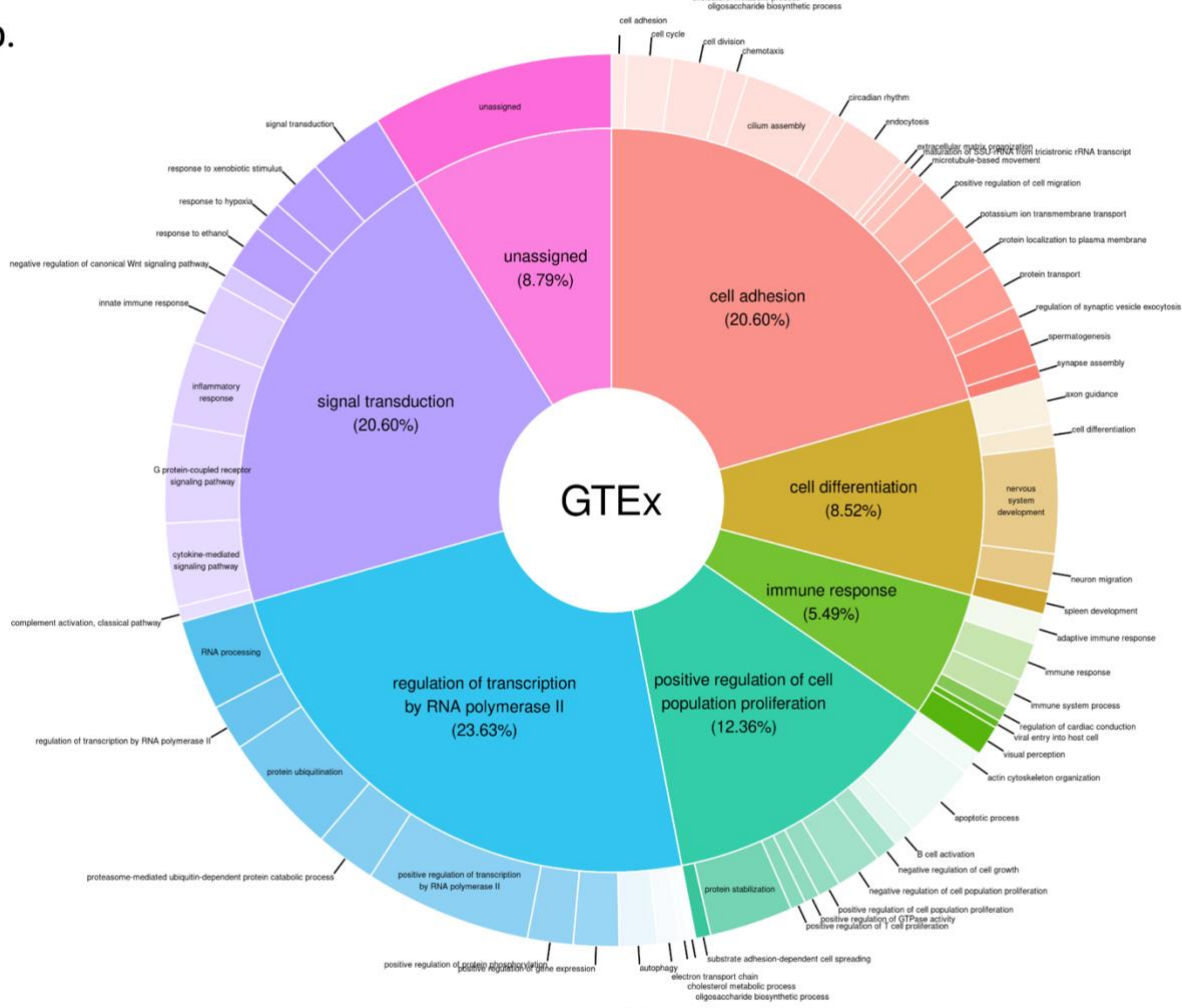


Supplementary Figure 6 Histogram of the number of GO terms associated with colocizing eGenes. Source data are provided as a Source Data file.

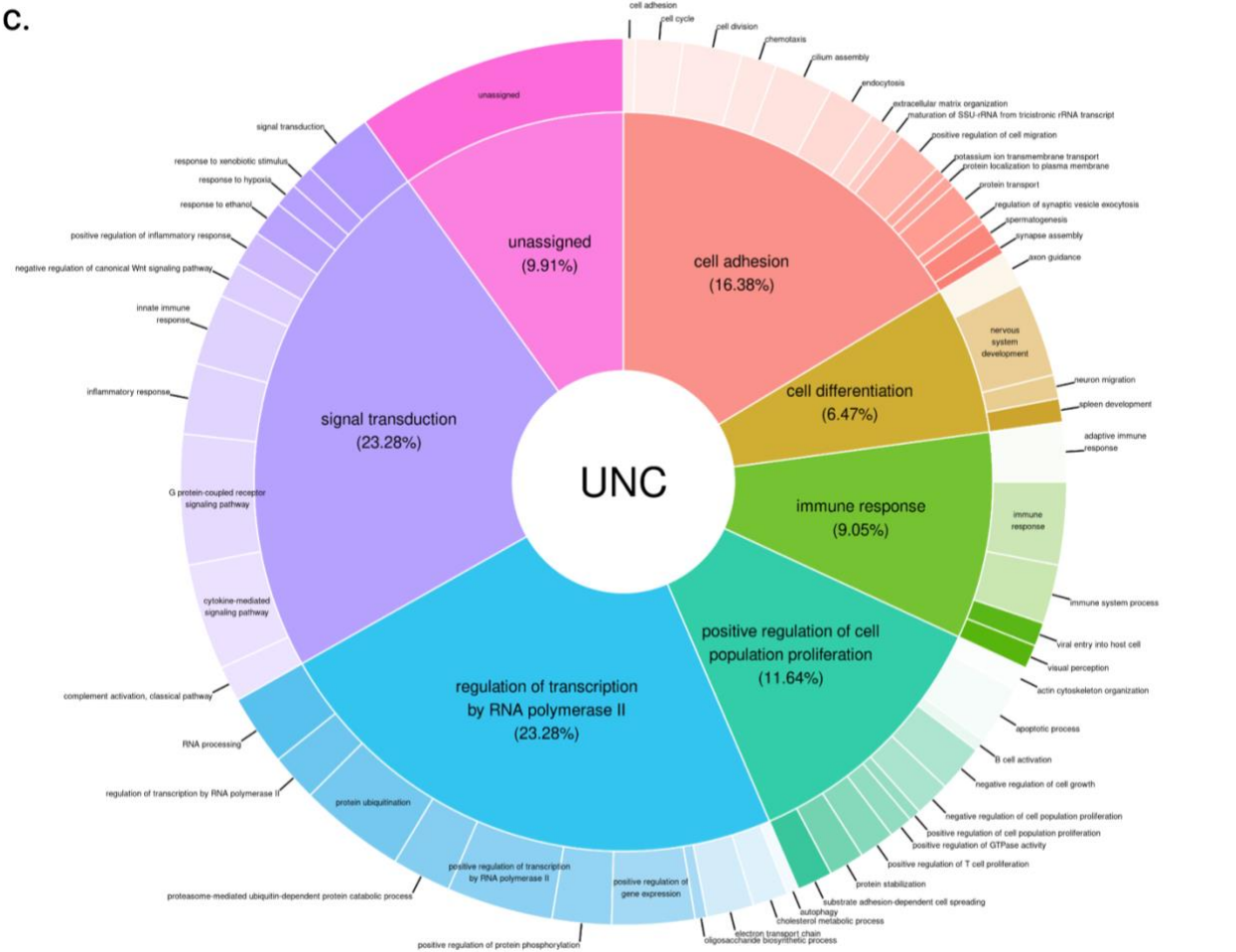
a.



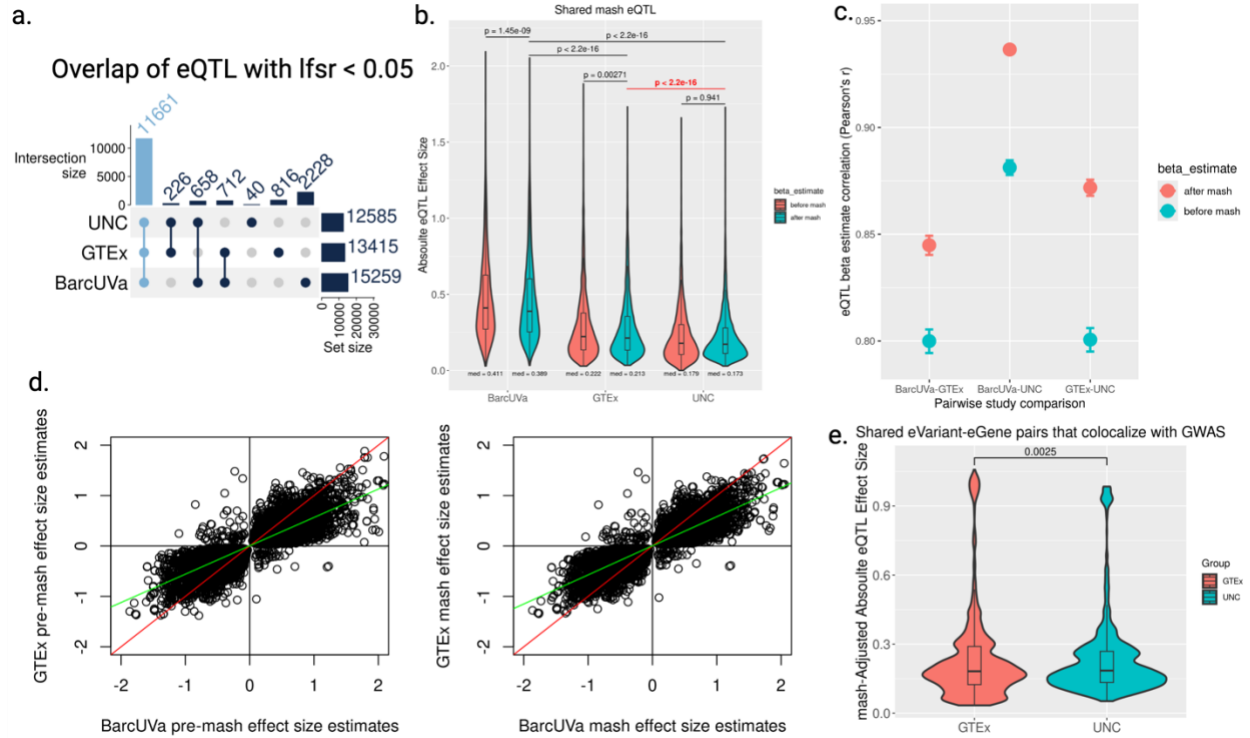
b.



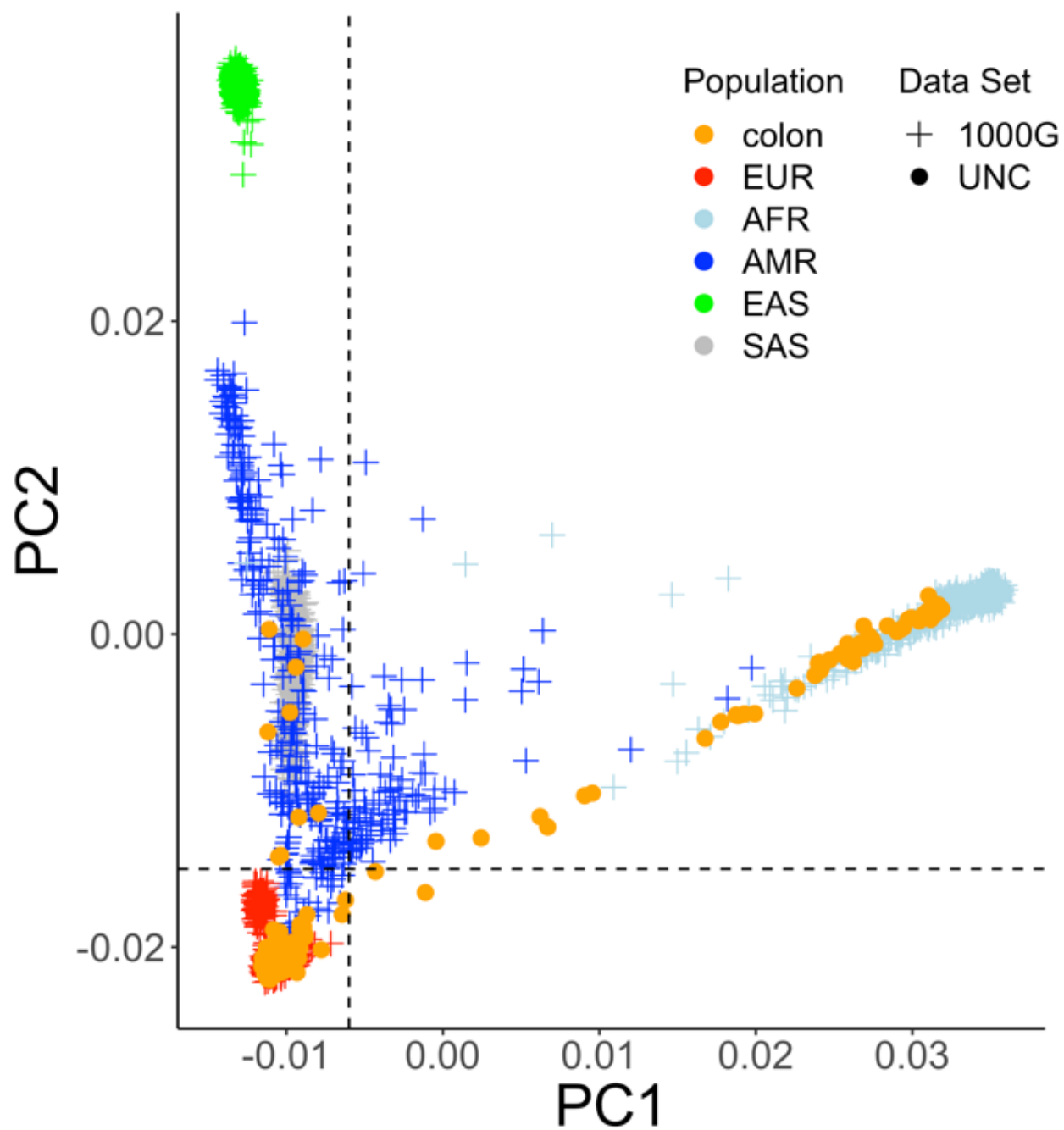
C.



Supplementary Figure 7 Pie-Donut charts representing clustered GO terms associated with colocalizing eGenes. Inner pie slices show the proportion of colocalizing eGenes that map to primary clusters. Outer slices represent proportion of colocalizing eGenes that map to secondary sub-clusters. Source data are provided as a Source Data file.

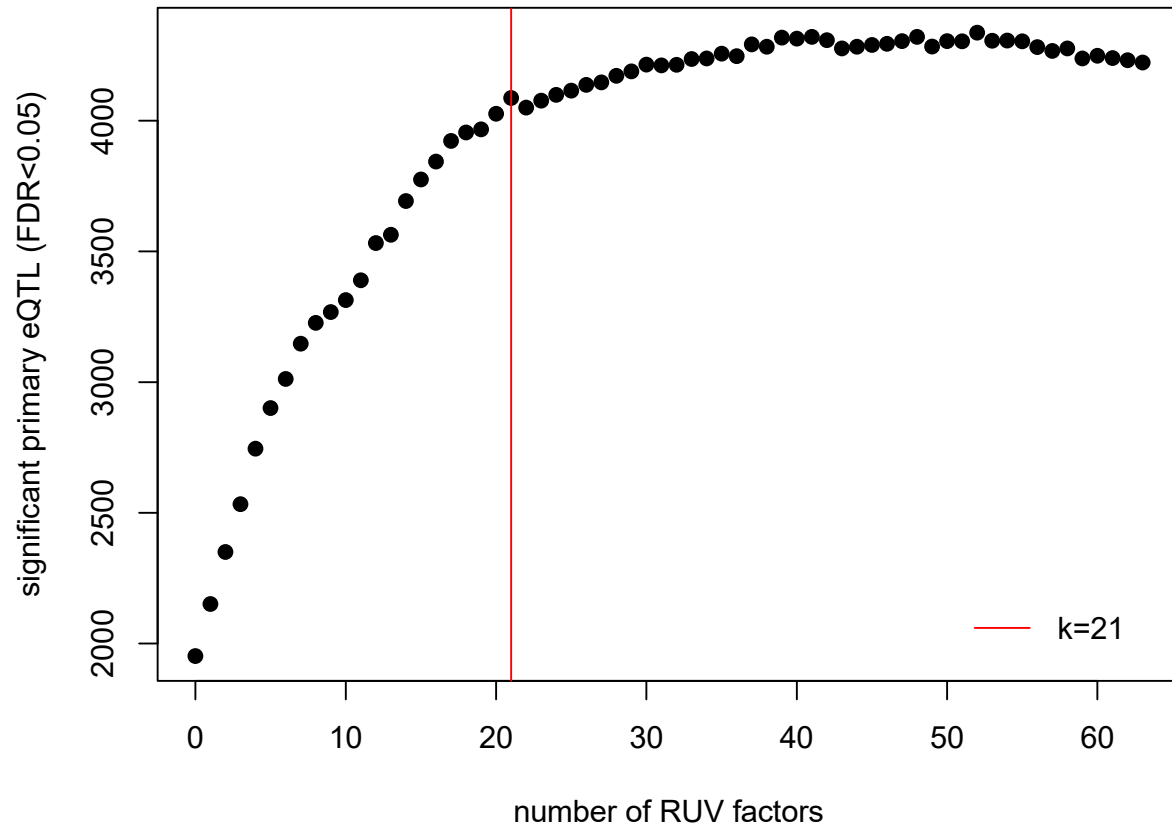


Supplementary Figure 8 Shared mash results. *a.* UpSet plot of overlap for eQTL with $lfsr < 0.05$. The 11,661 overlapping eQTL highlighted in Carolina blue were used to generate data in panels b-d. *b.* Violin plots of absolute eQTL effect size distributions for the 11,661 overlapping top eQTL before and after applying mash show UNC eQTL have significantly smaller adjusted effect sizes after mash. p -values calculated from the Mann-Whitney U statistic. Boxplots in panels b and e were defined using a center median. Lower and upper hinges represent the 25th and 75th percentiles. Whiskers represent 1.5x the interquartile range. *c.* Scatterplot of correlation estimates for pairwise eQTL study comparisons of effect size estimates before and after applying mash. Vertical bars represent the 95% confidence interval for each estimate. *d.* Effect size correlation for non-IBD eQTL before and after applying mash. The red line represents the (0,1) intercept. The green line represents the regression fit. *e.* Violin plots of absolute eQTL effect size distributions for the 6315 shared eVariant-eGene pairs that colocalize with GWAS loci. p -value calculated from the Mann-Whitney U statistic. Source data are provided as a Source Data file.



Supplementary Figure 9 IBD patients used in this study are of primarily inferred European genetic ancestry. UNC samples are denoted by orange circles. Source data are provided as a Source Data file.

cis-eQTL results: RUV Factor Testing



Supplementary Figure 10 Scatter plot of the number of significant primary lead eQTL mapped using IBD tissue using increasing number of RUV factors included in eQTL model. The red vertical line indicates the point of maximum curvature detected by kneedle and the final number of RUV factors included in the eQTL model. Source data are provided as a Source Data file.