

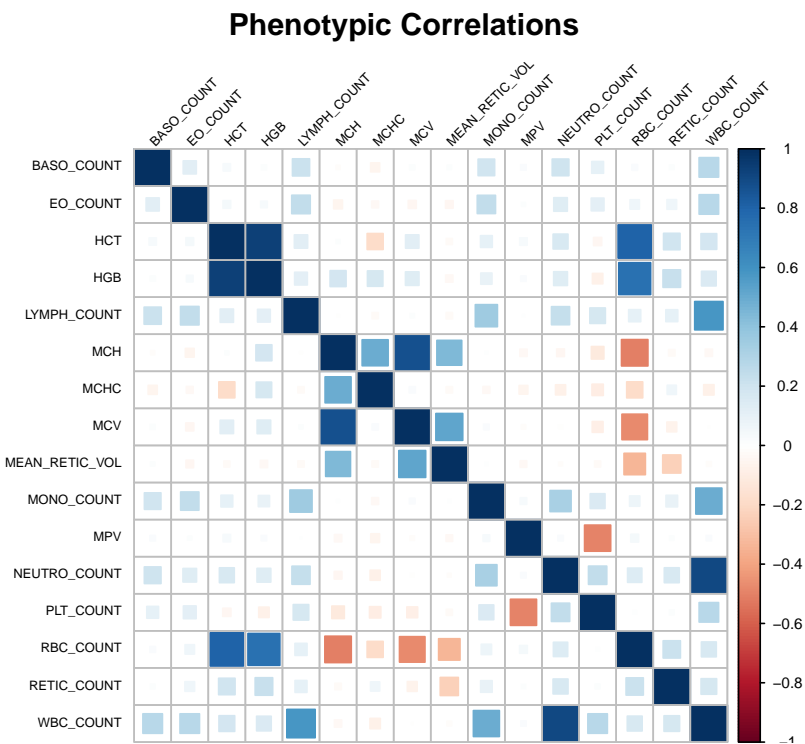
# Interrogation of human hematopoietic traits at single-cell and single-variant resolution

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Supplemental Information

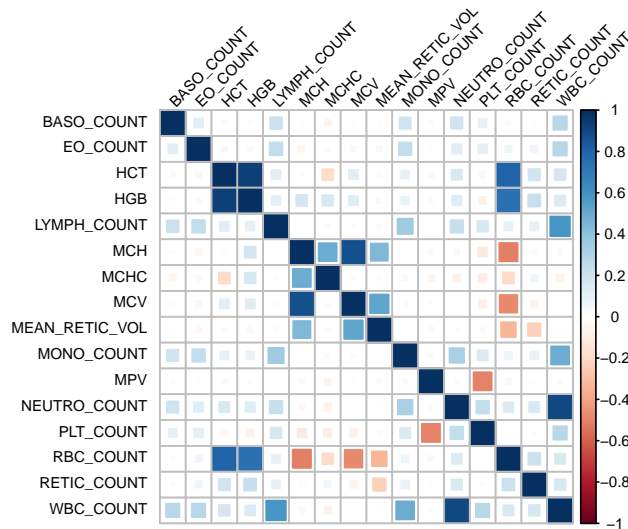
## Overview of UK Biobank data

(A) a



Supplemental Figure 1: Fold change enrichment of individually resolved peaks

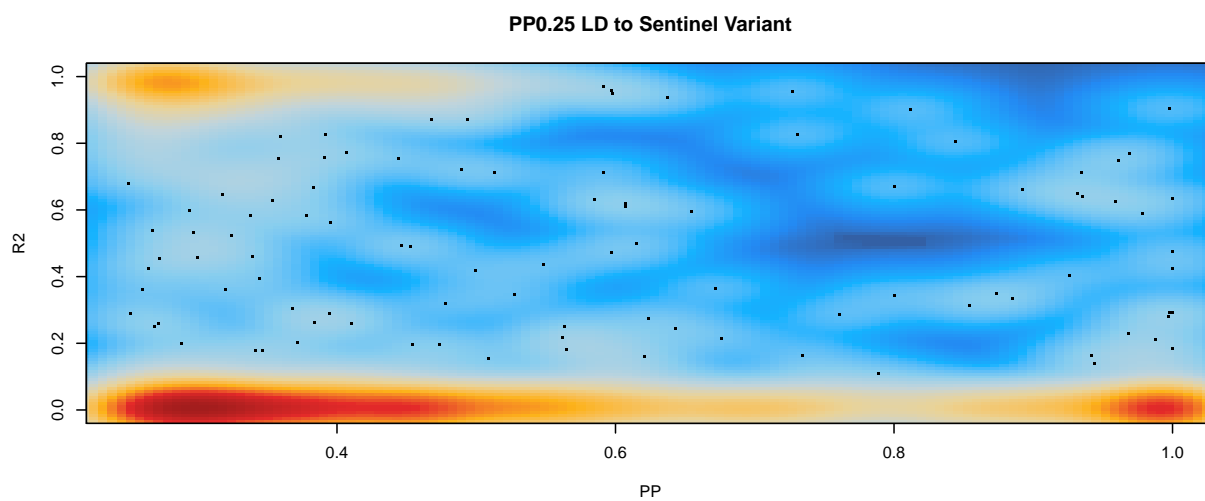
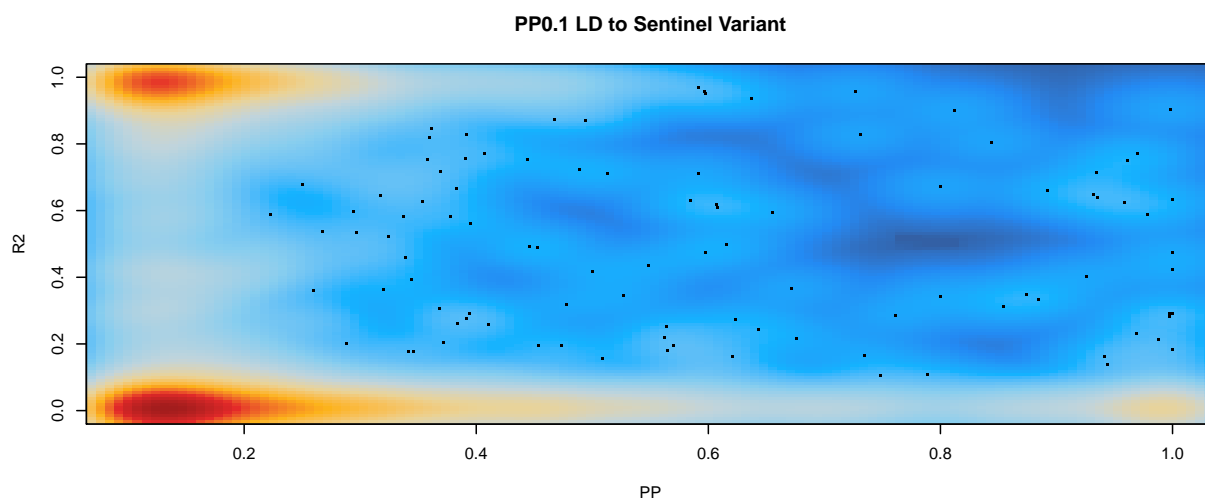
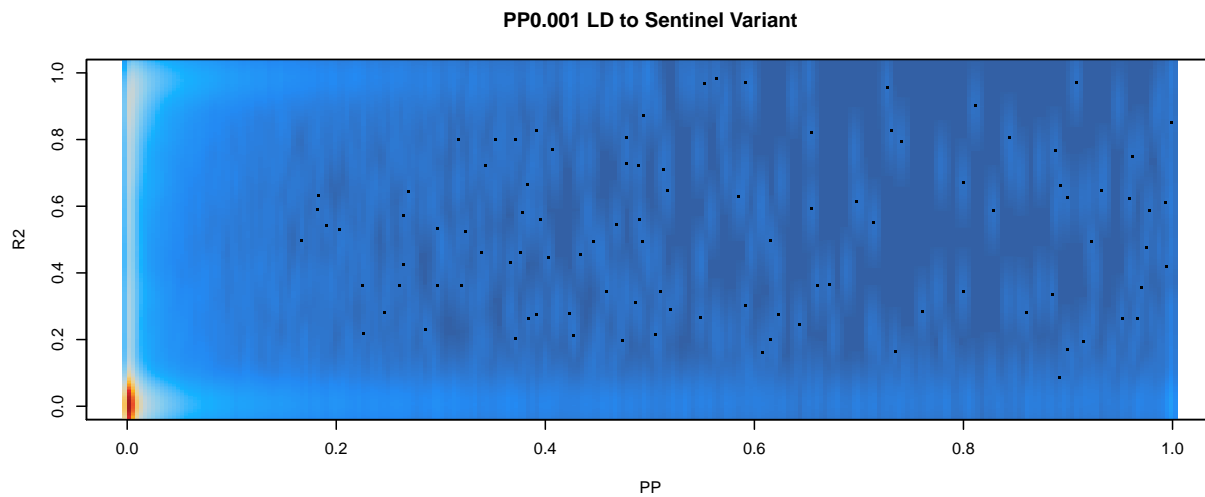
```
## Error in file(file, "rt"): cannot open the connection
## Error in gc.matrix[i, j]: incorrect number of dimensions
## Error in gc.matrix[i, j]: incorrect number of dimensions
## Error in corrplot(output, method = "square", order = "hclust", hclust.method = "complete",
: object 'output' not found
```



Supplemental Figure 2: Fold change enrichment of individually resolved peaks

```
## Error in corplot(output, method = "square", order = "hclust", tl.cex = 0.6, : object
'output' not found
## Error in eval(expr, envir, enclos): object 'output' not found
## Error in genotriangle[lower.tri(genotriangle, diag = FALSE)] <- 0: object 'genotriangle'
not found
## Error in melt(phenotriangle): could not find function "melt"
## Error in melt(genotriangle): could not find function "melt"
## Error in melt(phenocors): could not find function "melt"
## Error in paste(genomelt$Var1, genomelt$Var2): object 'genomelt' not found
## Error in paste(phenomelt$Var1, phenomelt$Var2): object 'phenomelt' not found
## Error in colnames(genomelt)[3] <- "GenoCor": object 'genomelt' not found
## Error in colnames(phenomelt)[3] <- "PhenoCor": object 'phenomelt' not found
## Error in merge(genomelt, phenomelt, by = "traitpairs"): object 'genomelt' not found
## Error in merged[, c("Var1.x", "Var2.x")] <- NULL: object 'merged' not found
## Error in eval(expr, envir, enclos): object 'merged' not found
## Error in is.data.frame(data): object 'merged' not found
## Error in attach(merged): object 'merged' not found
## Error in ggplot(merged, aes(x = GenoCor, y = PhenoCor, pairs = traitpairs)): object
'merged' not found
## Error: Column 'h2_obs' not found
## Error in FUN(X[[i]], ...): object 'h_obs' not found
```

Supplemental Figure 3: Fold change enrichment of individually resolved peaks



Supplemental Figure 4: Sample embedding of figure in document.

(B)

## Description of single-cell enrichment

```
print("part2")  
## [1] "part2"
```