## Supplementary Data

**Supplementary Data 1. ChIP-seq data, enrichment and quality control metrics.** ChIP-seq quality control metrics including number of aligned reads, percent duplicate reads, MACS peaks called. Including metadata for sample identification, antibody and gender.

**Supplementary Data 2. Quantitative trait loci results.** Results from Limix QTL analysis for each feature tested for PU.1, C/EBPβ, CTCF, H3K4me3 and H3K27me3 in neutrophils and the statistical test results for each sentinel SNP.

**Supplementary Data 3. Proximal and distal quantitative trait loci results for sentinel PU.1 SNPs.** Classification of proximal and distal PU.1 tfQTLs reaching the significance threshold (FDR<0.05).

**Supplementary Data 4. PU1 tfQTLs that overlap autoimmune diseases and UK Biobank myeloid traits.** Summary results from colocalisation analysis for PU.1 tfQTL with selected disease and full blood count traits.

**Supplementary Data 5. Annotation of PU1 tfQTLs.** PU.1 tfQTL were annotated for significant allele-specific effect (RASQUAL analysis), neutrophil gene expression QTL, baited genes through PCHi-C interaction data and whether QTL summary statistics colocalise with any of the GWAS traits tested.