

Supplementary Figure 1. Heritability enrichment results for control traits. (A) Bar graphs display the genetic risk enrichment coefficient (y-axis) and standard error for cell-type specific open chromatin accounting for control peaks and baseline annotations. Open chromatin data were taken from the Calderon et al. study. Risk enrichment was assessed using GWAS summary statistics for the positive control traits rheumatoid arthritis, Alzheimer's disease, systemic lupus erythematosus, and the negative control trait height. Bars marked with “*” indicate $P < 0.05$, “***” indicates $P < 0.01$, “****” indicates $P < 0.001$.

Supplementary Figure 2. Single-cell disease relevant score results for control traits. (A) Visualization of the Space-Time Gut Cell Atlas using Uniform Manifold Approximation and Projection (UMAP) on the top 20 principal components from 1997 variable genes from the single-cell RNA-seq expression matrix. Cells are colored based on the coarse cell type annotations from the Space-Time Gut Cell Atlas. (B) Barplots shows the cell type proportions within the whole Space-Time Gut Cell Atlas and within cells with significant disease relevant score (20% FDR) for AS (using IGAS GWAS), Alzheimer's disease (AD) and rheumatoid arthritis (RA). (C) Same UMAP visualization as in A, where cells with significant scDRS score (20% FDR) are colored in red and non-significant cells are colored in gray, for each control trait.

Figure S1

A

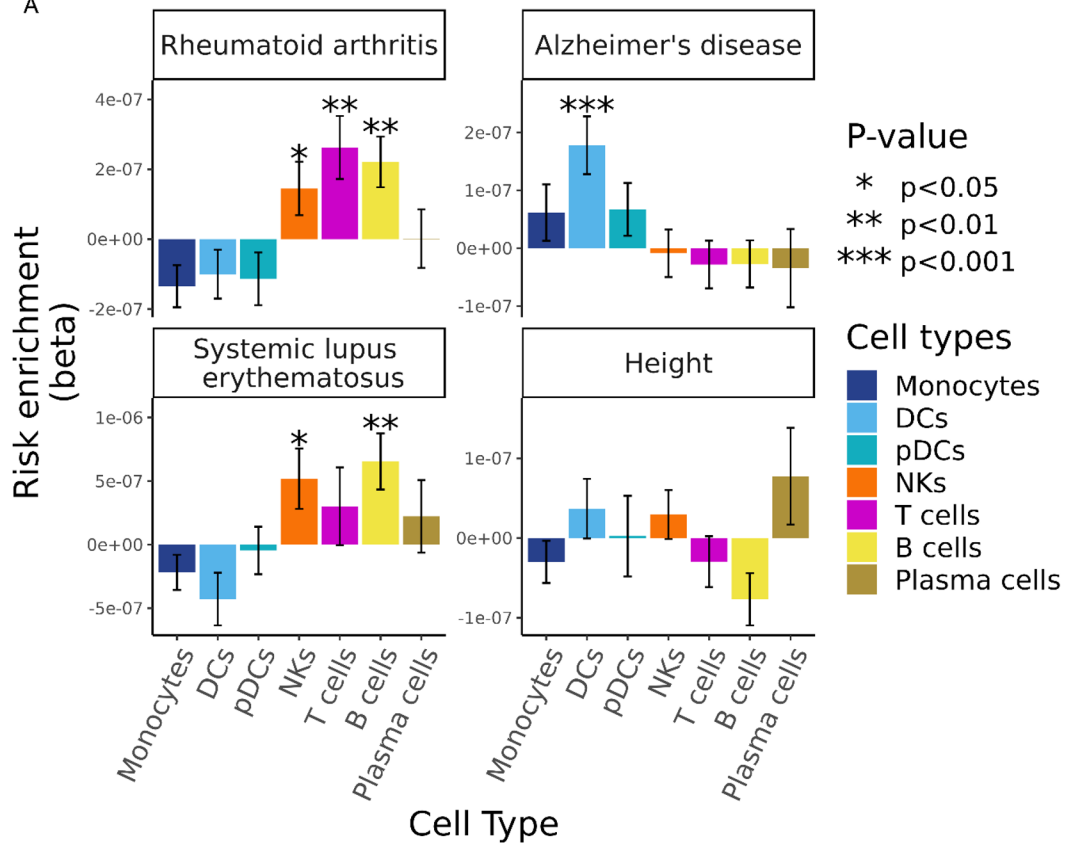
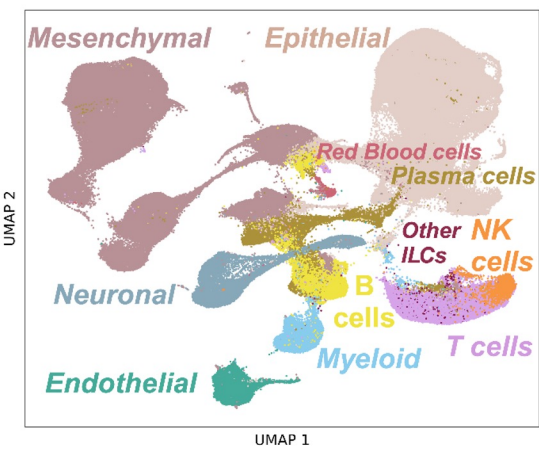
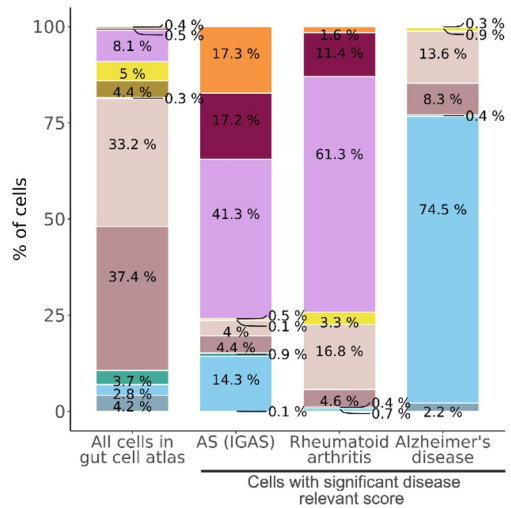


Figure S2

A

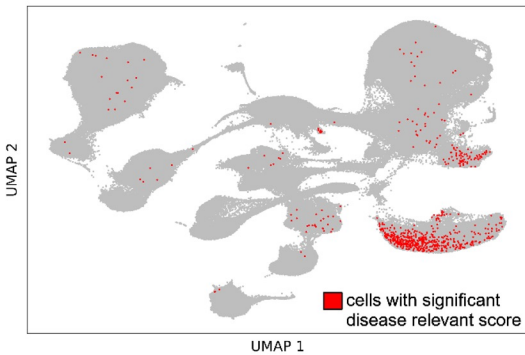


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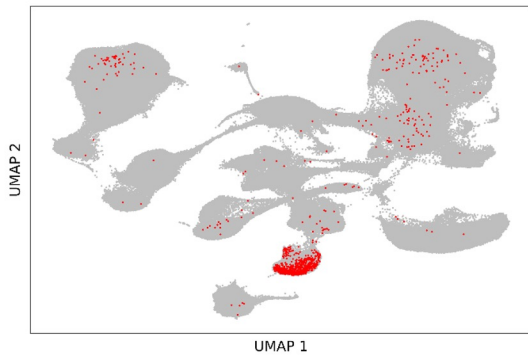


C

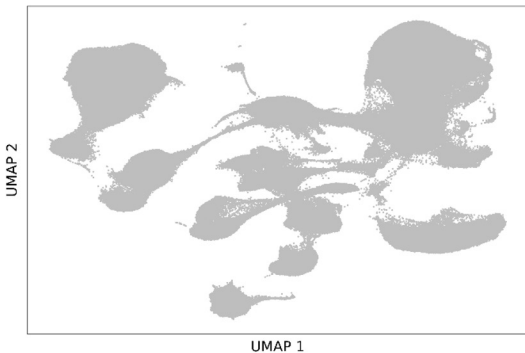
Rheumatoid arthritis



Alzheimer's disease



Systemic lupus erythematosus



Height

