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 1,997 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.
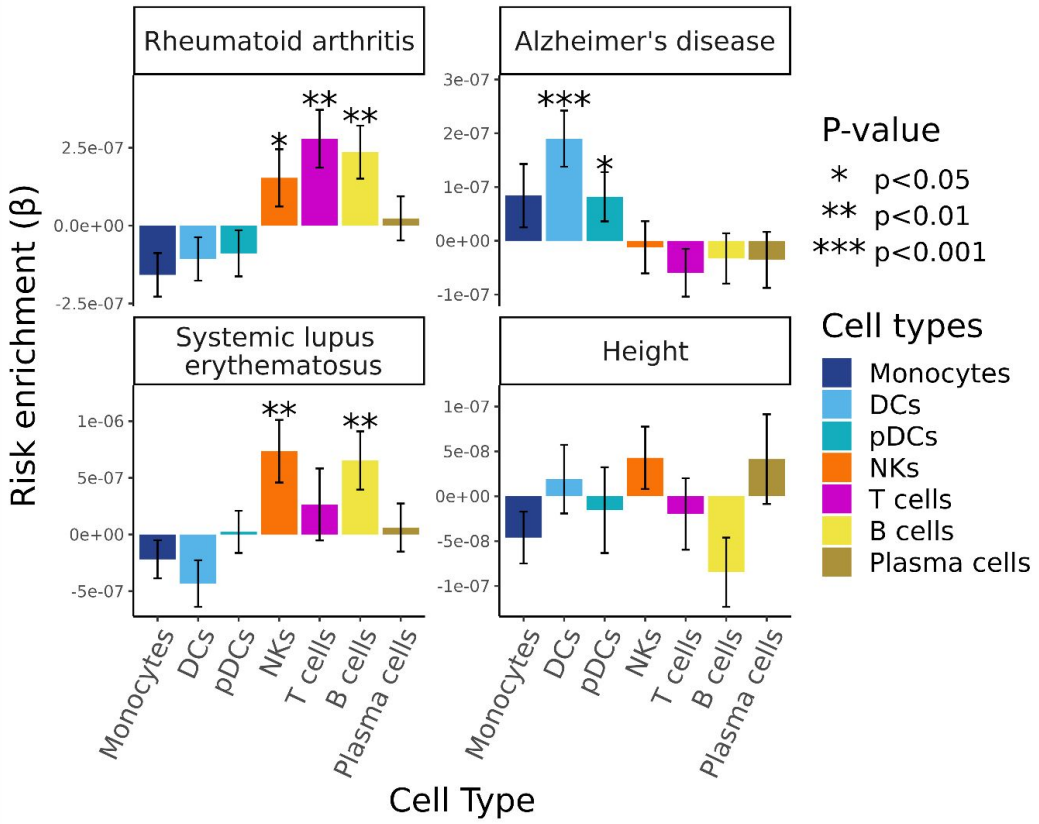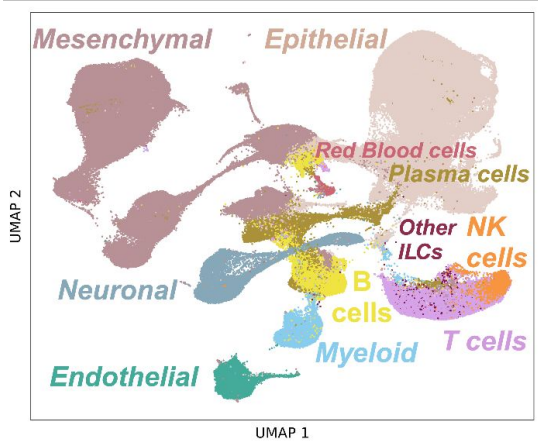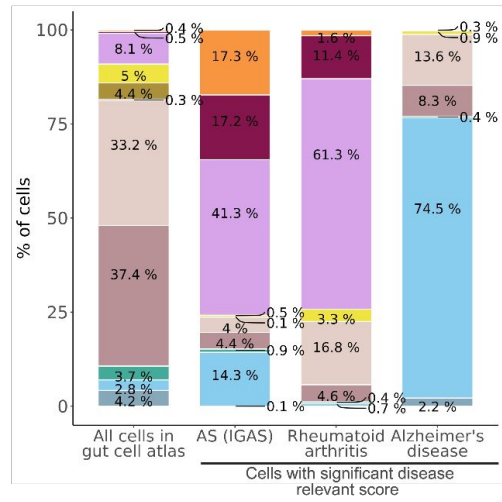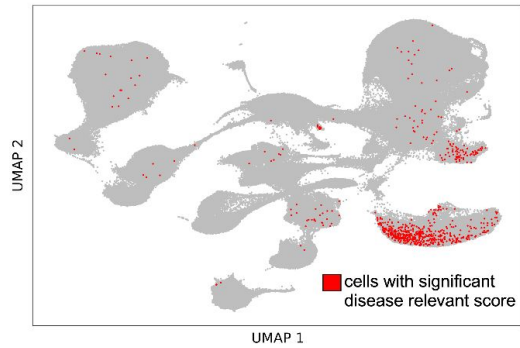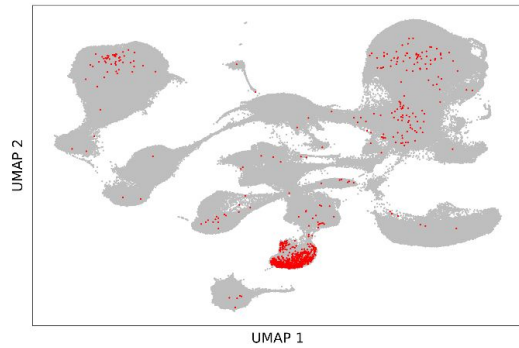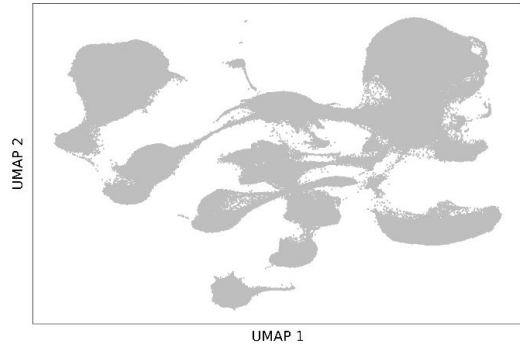
Figure S1

Figure S2