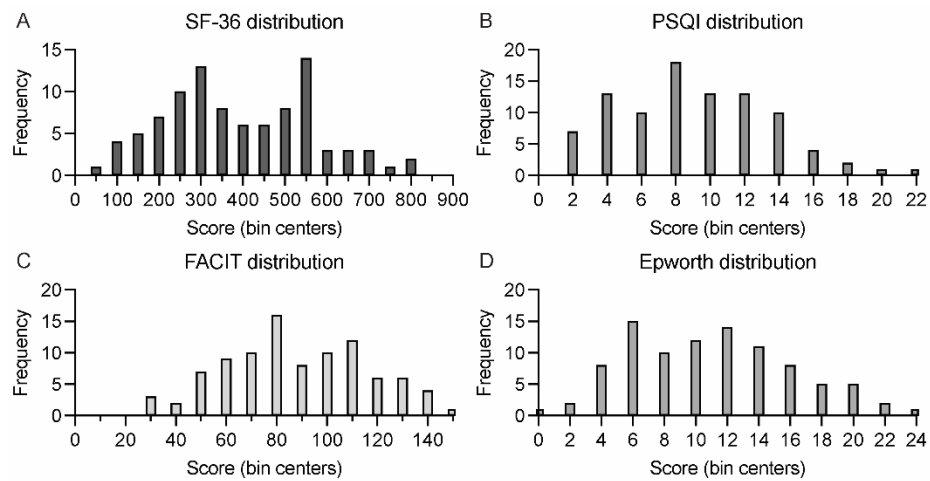
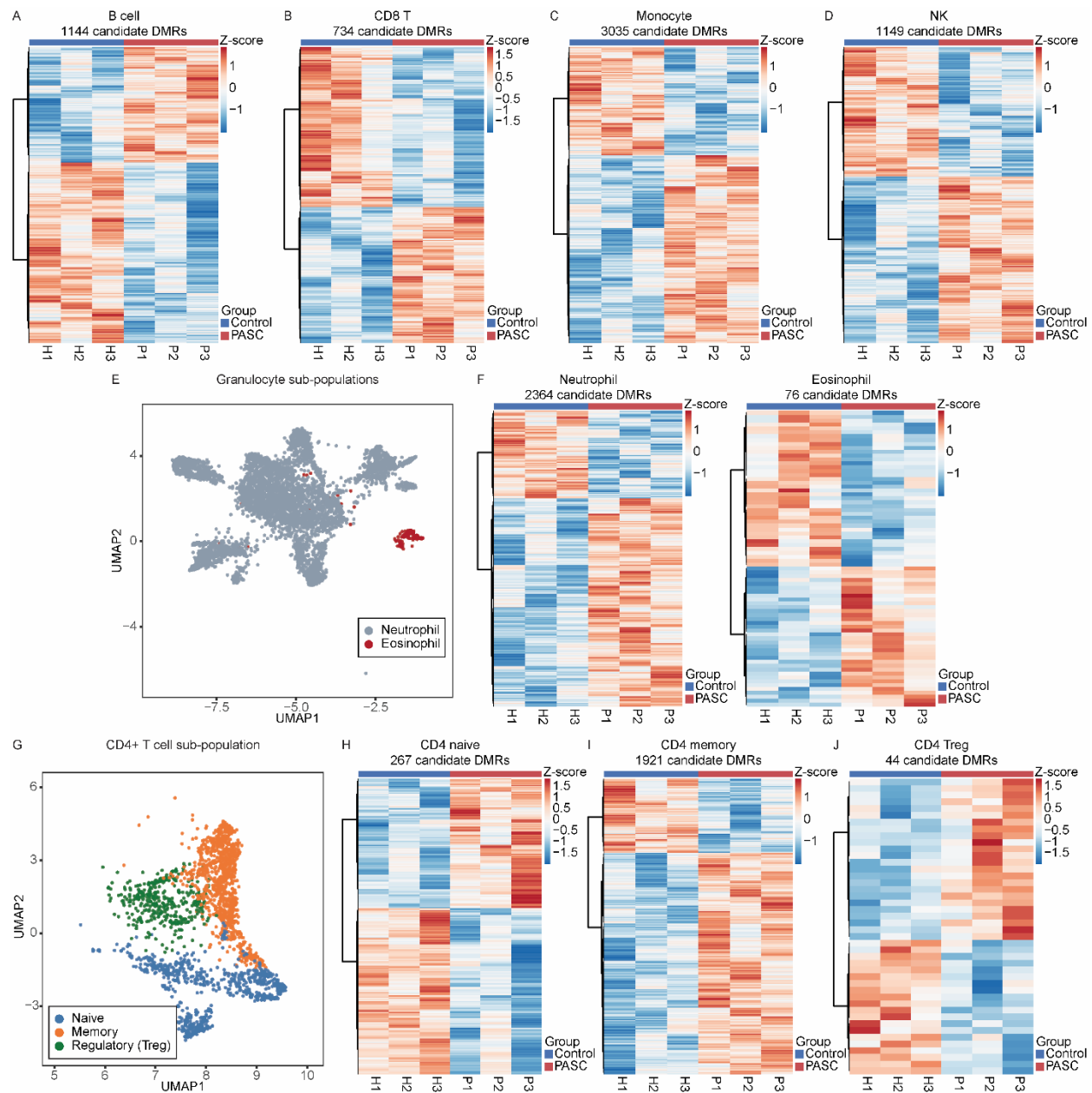
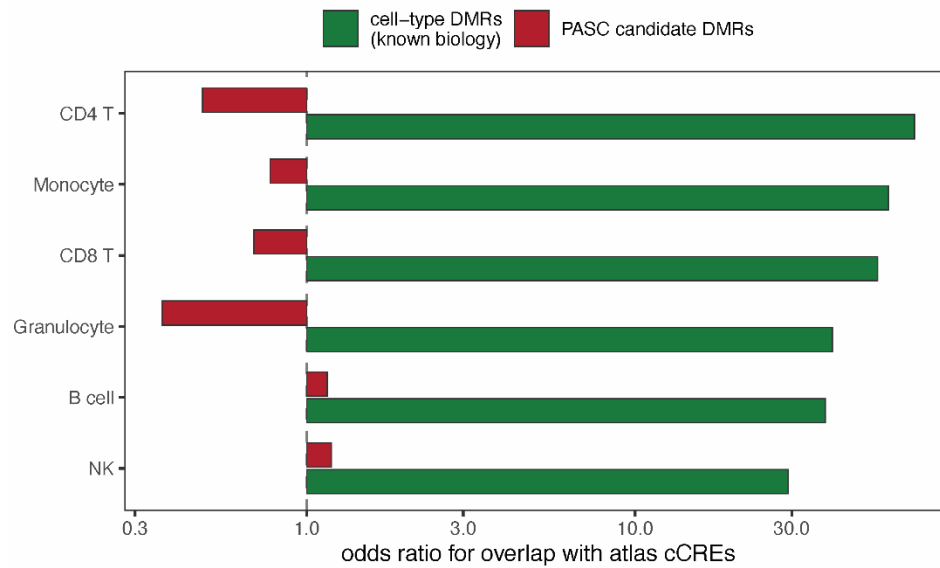




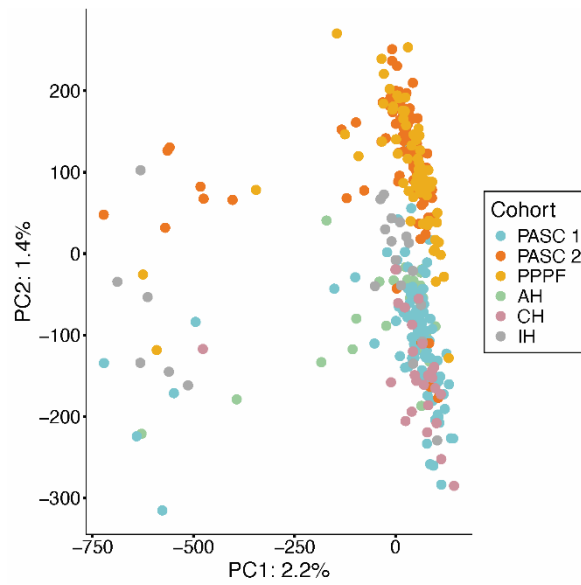
Supplementary Figure 1: Distribution of questionnaire values in the population included in this study, indicating a diverse disease and symptomatic burden.



Supplementary Figure 2: Heatmaps of the identified single-cell level DMRs within **A:** B cells, **B:** CD8+ T cells, **C:** monocytes, and **D:** NK cells. **E:** UMAP plot zoomed in on the granulocyte cluster identified sub-populations. **F:** Heatmaps of the identified single-cell level DMRs within granulocyte sub-populations. **G:** UMAP plot zoomed in on the CD4+ T cell cluster identified sub-populations. **H-J:** Heatmaps of the identified single-cell level DMRs within CD4+ T cell sub-populations. For heatmaps, columns represent individual samples and tiles are redder when relatively hypermethylated and bluer when relatively hypomethylated compared to healthy controls. DMRs plotted in the heatmap were called at the single-cell level using R package limma which places a linear model on the data, using a nominal p-value threshold of 0.05 and >10% difference between PASC vs Control cells.



Supplementary Figure 3: Bar plot shows the odds ratio enrichment of sc-DNA_m cell-type DMRs in relation to cell-type specific cis-regulatory elements (cCREs) (green) and PASC-specific candidate DMRs in relation to cCREs (red), previously identified in a deposited gene atlas (GSE306525). Significance of the overlap of single-cell cell-type DMRs and PASC-associated DMRs with known cCREs was tested by Fisher's exact test, drawing 10,000 random region sets from the same background matched on width, using a p-value < 0.05 to determine significance.



Supplementary Figure 4: Principal component analysis (PCA) of all samples used in the bulk sequencing study.