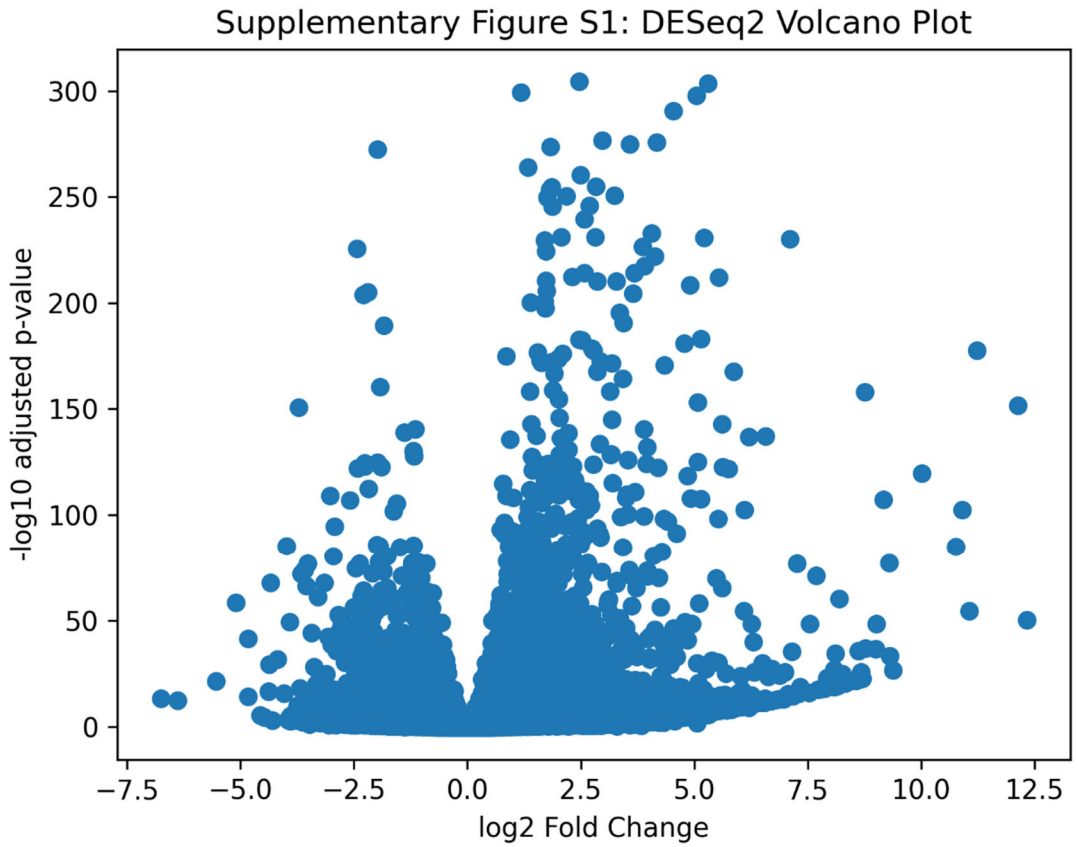


Supplementary Figure S1. DESeq2-based differential expression analysis of stimulated versus control dendritic cells. Volcano plot showing genome-wide differential gene expression between stimulated and control human dendritic cells based on DESeq2 analysis of raw count data. The x-axis represents $\log_2$ fold change (stimulated vs control), and the y-axis represents $-\log_{10}$ adjusted p-value (FDR). Each point corresponds to a single gene. Genes meeting the predefined significance thresholds ($|\log_2 \text{fold change}| \geq 1$ and adjusted p-value (FDR) < 0.05) are considered differentially expressed. The distribution of points illustrates widespread transcriptional remodeling following stimulation, with both upregulated and downregulated genes observed across the transcriptome.