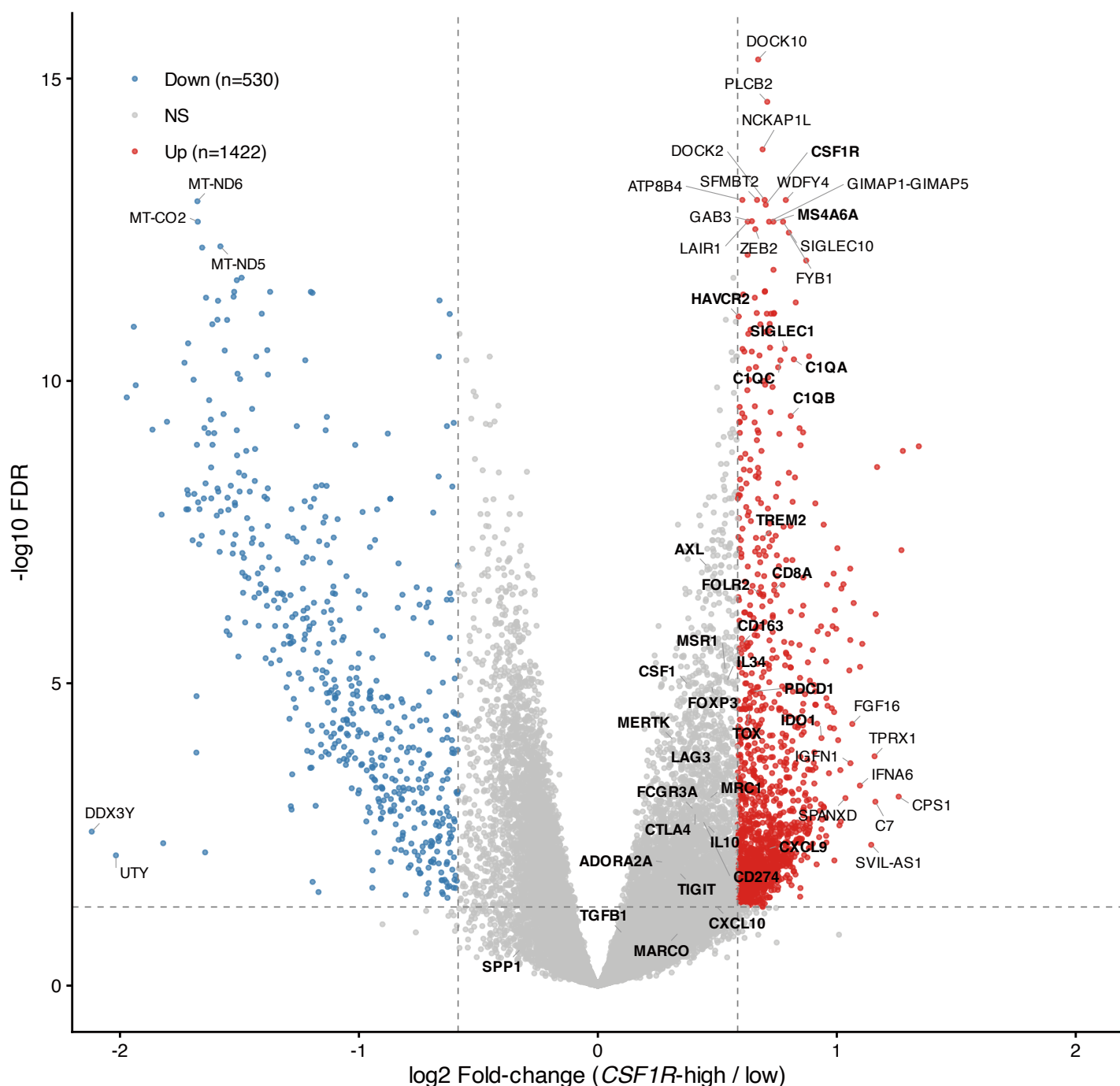


Supplementary Figure S2



Supplementary Figure S2. Genome-wide differential expression analysis according to *CSF1R* expression. Volcano plot showing differential expression between *CSF1R*-high and *CSF1R*-low tumors. Differential expression was assessed using limma on normalized count data. Genes with $\text{FDR} < 0.05$ and $|\log_2 \text{FC}| > 0.585$ were considered differentially expressed. Red points indicate upregulated genes in *CSF1R*-high tumors, blue points indicate downregulated genes, and gray points indicate non-significant genes. FDR, false discovery rate; FC, fold change.