

Figure S2. RNA-sequencing analysis of SpiD3-treated OSU-CLL cells.

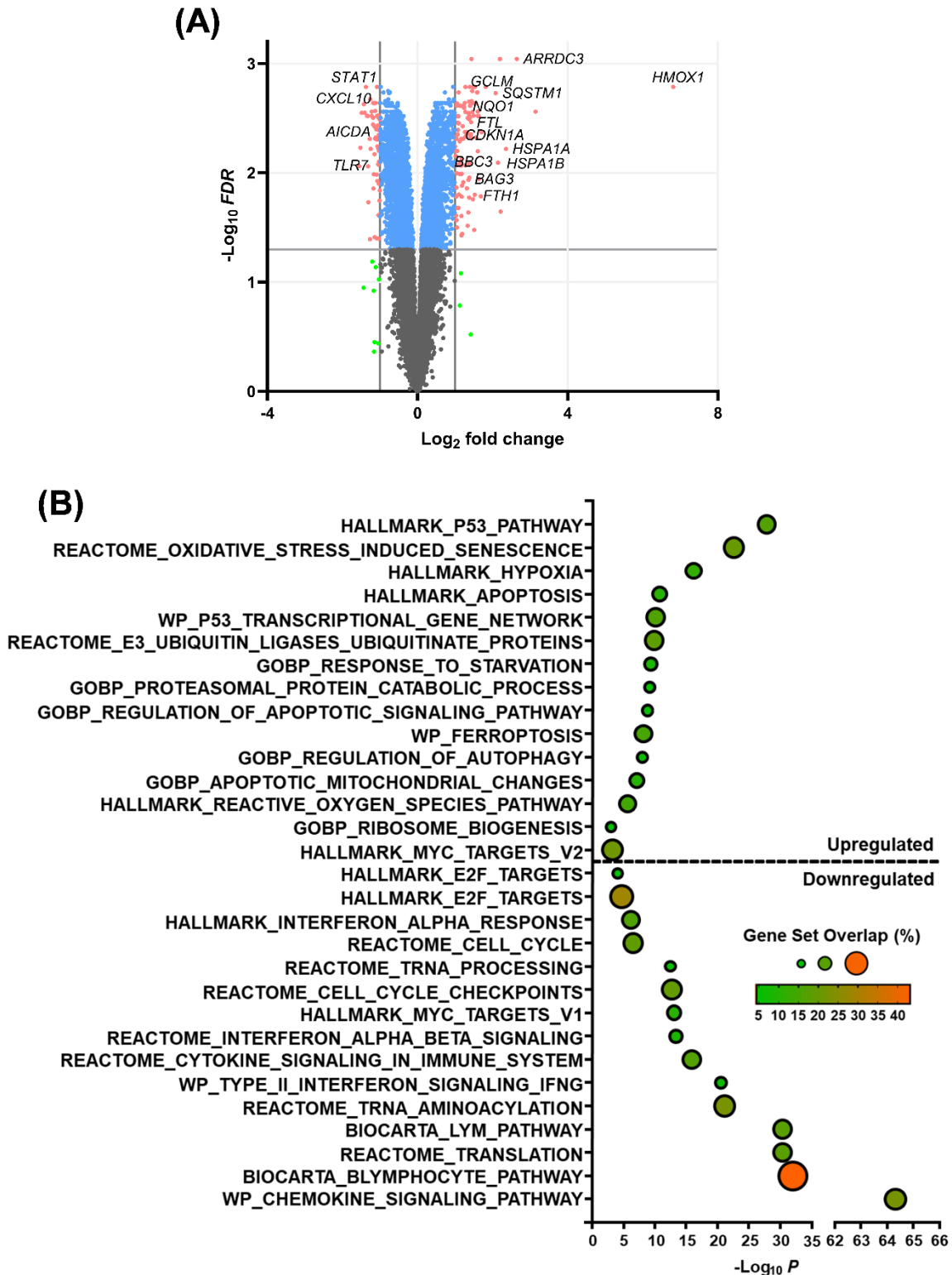


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(A) Volcano plot of differentially expressed genes (DEGs) in SpiD3-treated OSU-CLL cells (1 μ M, 4 h) with select disease-relevant genes labeled. Only genes that meet both the statistical significance ($FDR < 0.05$) and fold-change ($|\text{Log}_2 \text{FC}| > 1$) were used for downstream analysis (red). Genes that meet only statistical significance (blue), only fold-change (green), or neither threshold (grey) are shown for comparison. **(B)** Gene set enrichment analysis using the top 500 DEGs ($P < 0.05$) following treatment with 1 μ M SpiD3 (4 h, $n = 3$ independent RNA-seq experiments).