

Figure S3. Proteomic analysis of SpiD3-treated CLL cells using TMT-labeling.

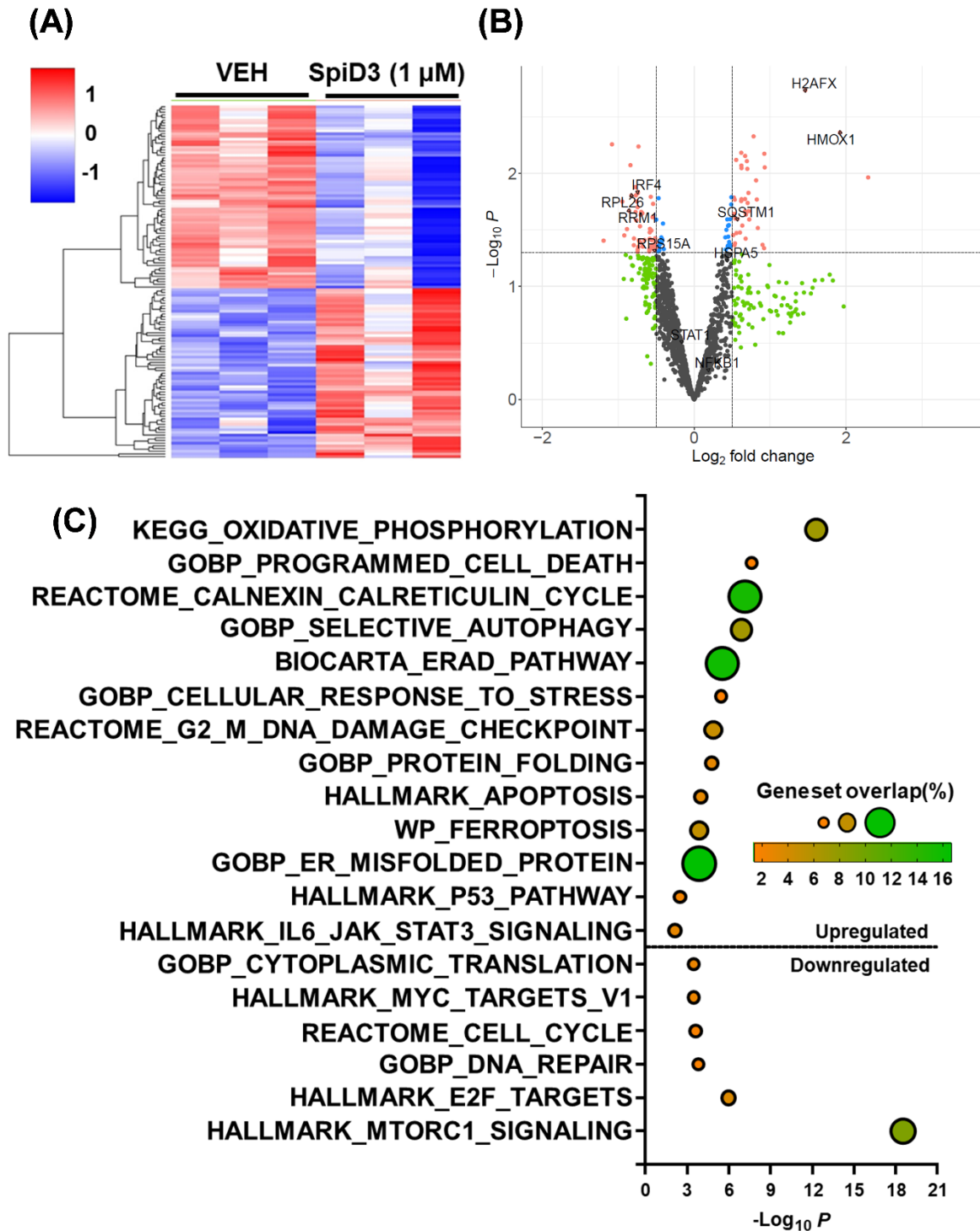


Figure S3. Proteomic analysis of SpiD3-treated CLL cells using TMT-labeling.

(A) Hierarchical clustering of differentially expressed proteins ($n = 131$, $P < 0.05$) in OSU-CLL cells treated with DMSO vehicle (VEH) or SpiD3 ($1 \mu\text{M}$) for 24 h ($n = 3$ independent experiments).

(B) Volcano plot of differentially expressed proteins in SpiD3-treated OSU-CLL cells with select disease-relevant proteins labeled. Only proteins that meet both the statistical significance ($P < 0.05$) 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. **(C)** Gene set enrichment analysis of the differentially expressed proteins following SpiD3 treatment.