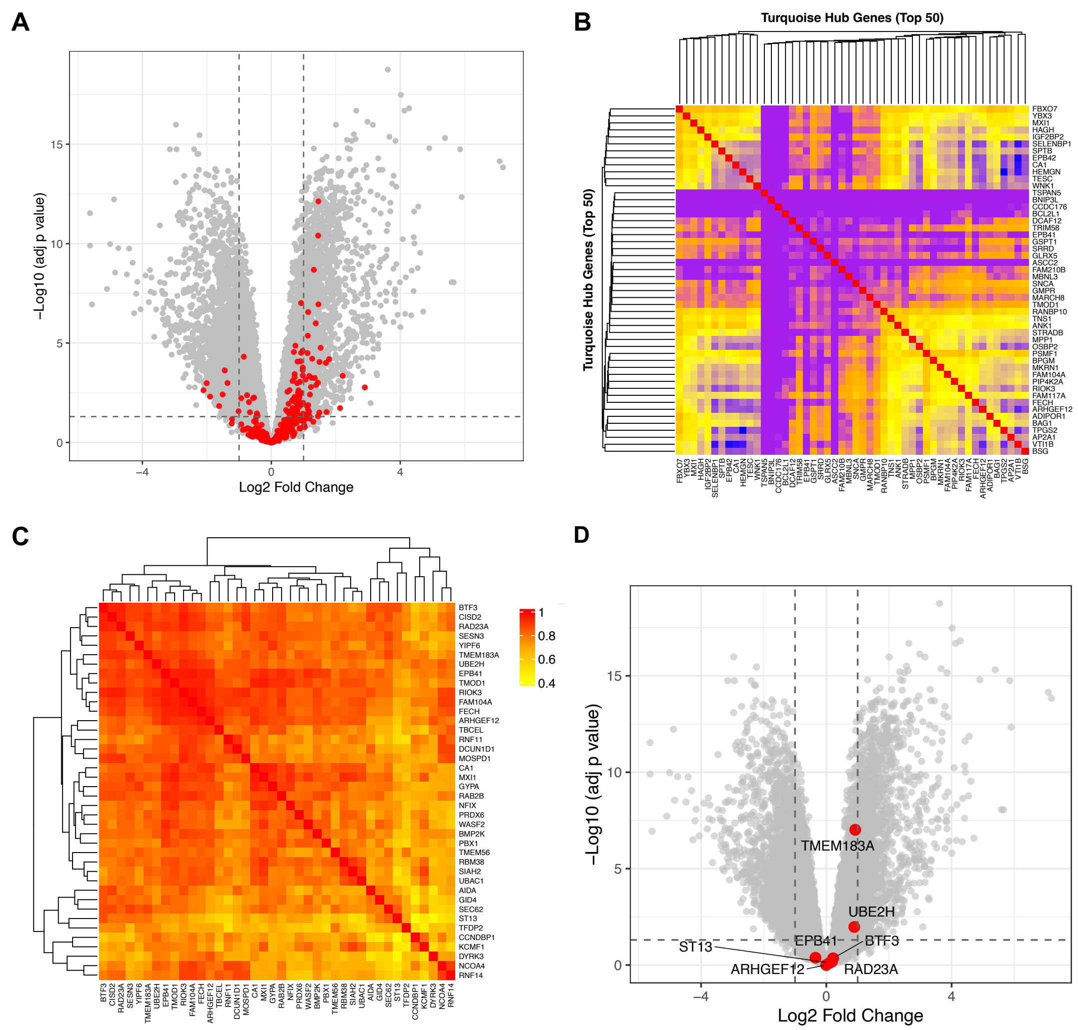
Supplementary Fig. 3



Characterization of turquoise module genes and miRNAs in the ARDS cohort

(A) Volcano plot highlighting hub genes belonging to the turquoise module. Differentially expressed genes between patients with ARDS and healthy controls are shown. Dashed lines indicate thresholds of $\log_2$ fold change = ±1 and $-\log_{10}$ adjusted p value = 0.05. Hub genes are highlighted in red.

(B) Topological overlap matrix heatmap of the top 50 hub genes in the turquoise module. Color intensity represents the strength of pairwise gene correlations, visualizing a highly interconnected co-expression structure within a module.

(C) Correlation heatmap of 40 predicted mRNAs in the ARDS cohort, showing strong co-expression clusters consistent with an internal network structure

(D) Volcano plot highlighting the miRNAs validated in the ARDS cohort. Differentially expressed miRNAs between patients with ARDS and healthy controls are shown, with dashed lines indicating thresholds of $\log_2$ fold change = ±0.3 and $-\log_{10}$ adjusted p value < 0.05. Validated miRNAs are highlighted in red.