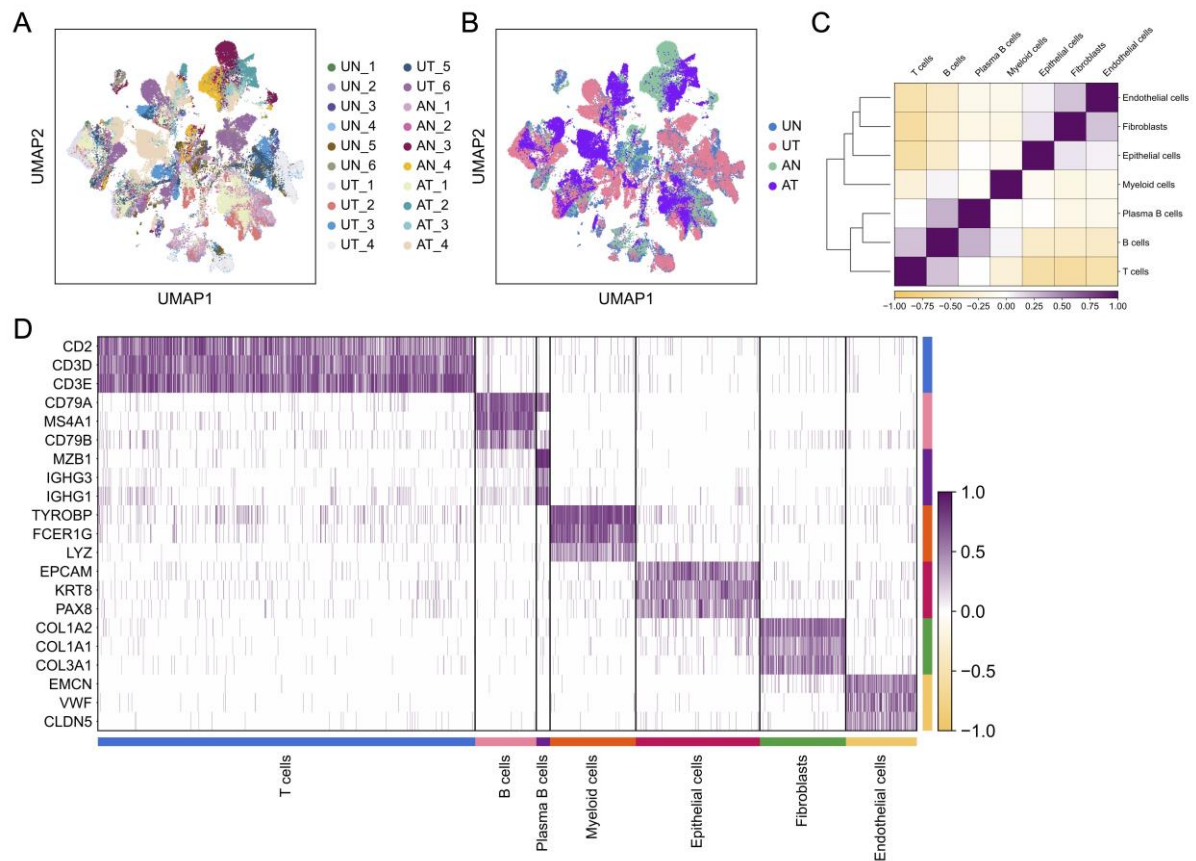
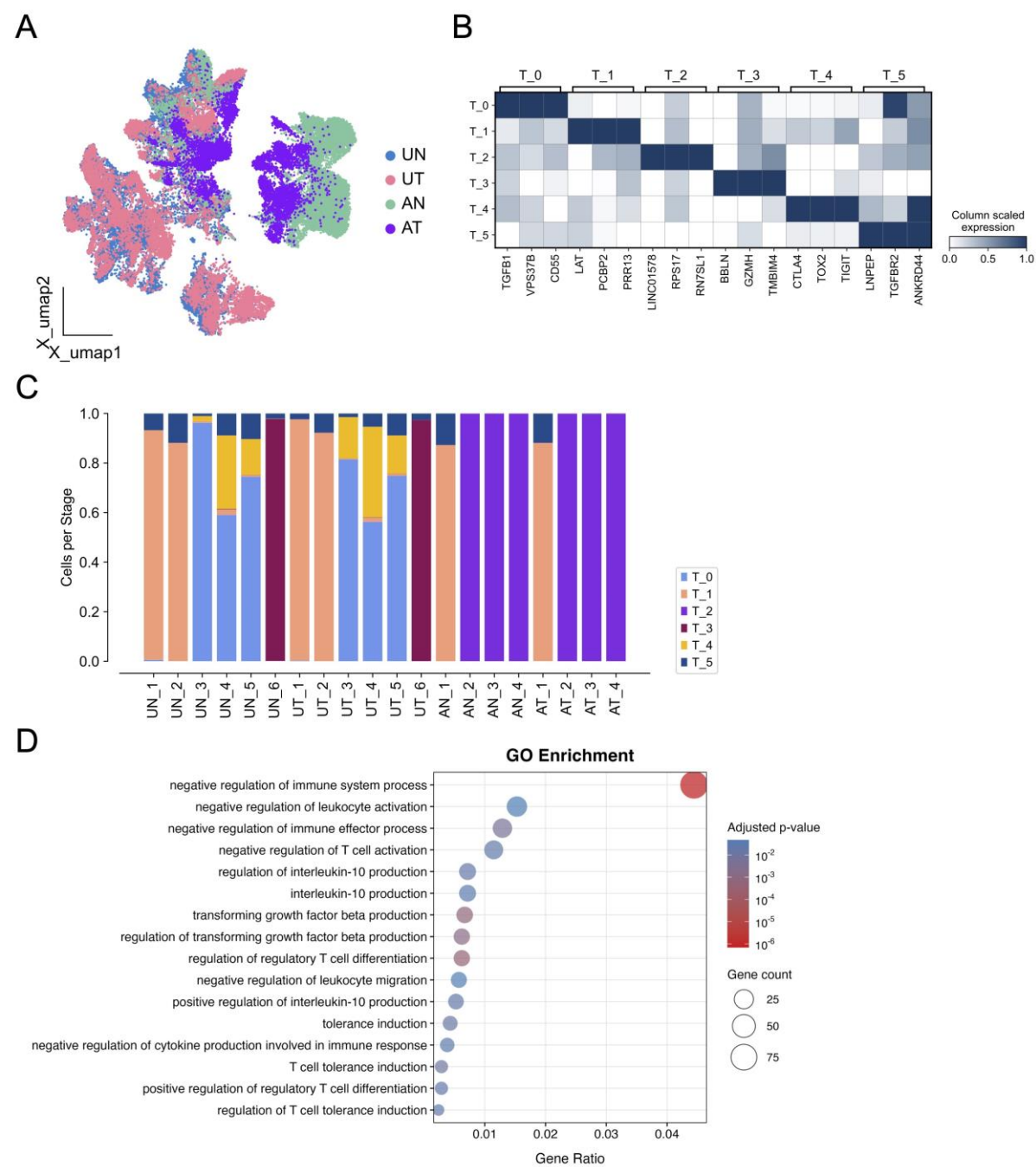


Supplementary Figure 1. Validation of cell type identification and sample integration.

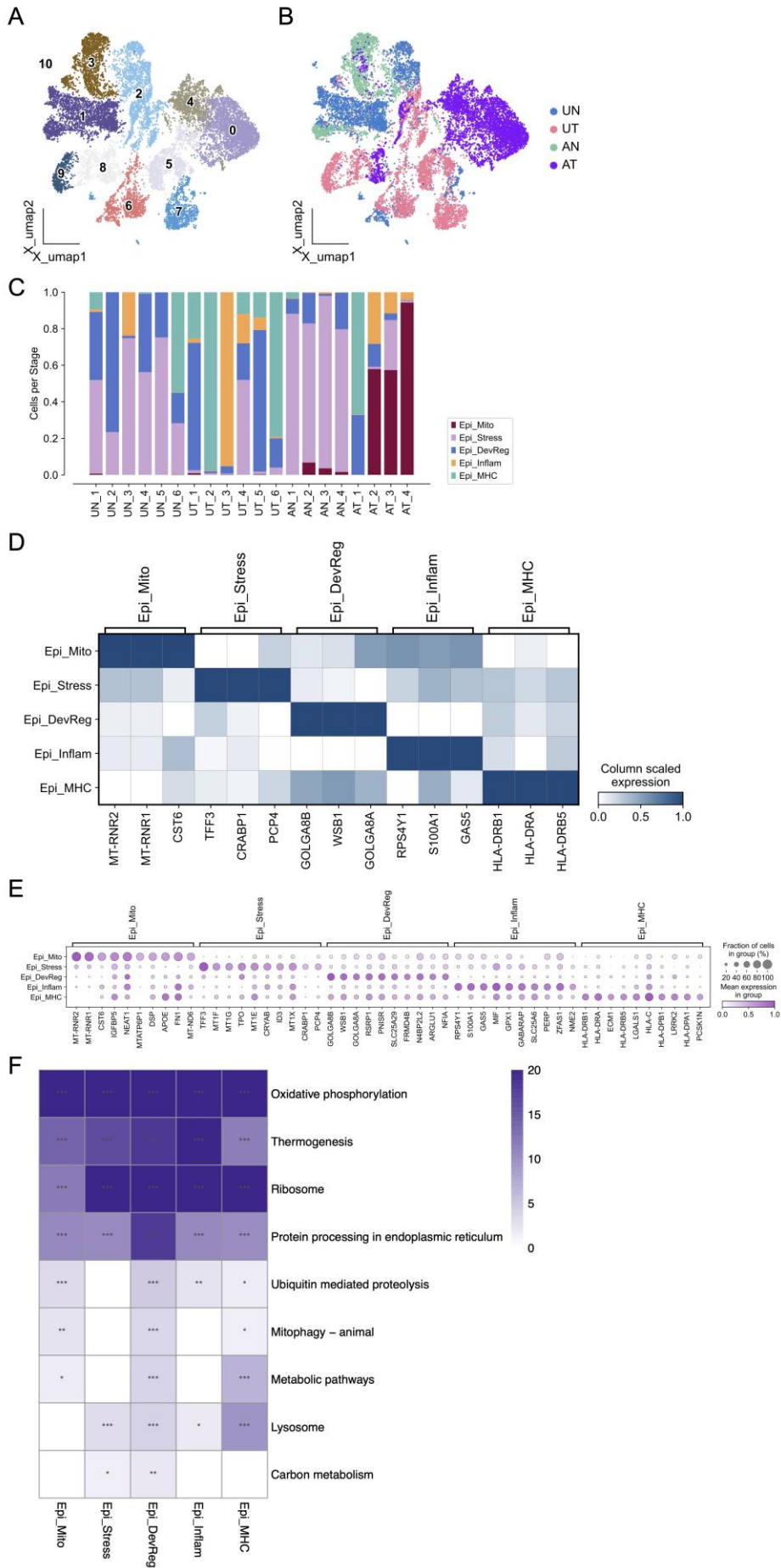
(A-B) UMAP plots showing cell distribution across individual samples and conditions. (C) Correlation heatmap of major cell types. (D) Heatmap of representative markers across all cells confirming cell type classification.



Supplementary Figure 2. Validation and functional annotation of T cell subsets. (A) UMAP projection showing T cell distribution across UN, UT, AN, and AT samples. (B) Heatmap of marker gene expression across T cell subsets. (C) Distribution of T cell subsets in individual samples. (D) GO enrichment analysis showing immunoregulatory processes including negative regulation of T cell activation, tolerance induction, and cytokine modulation.



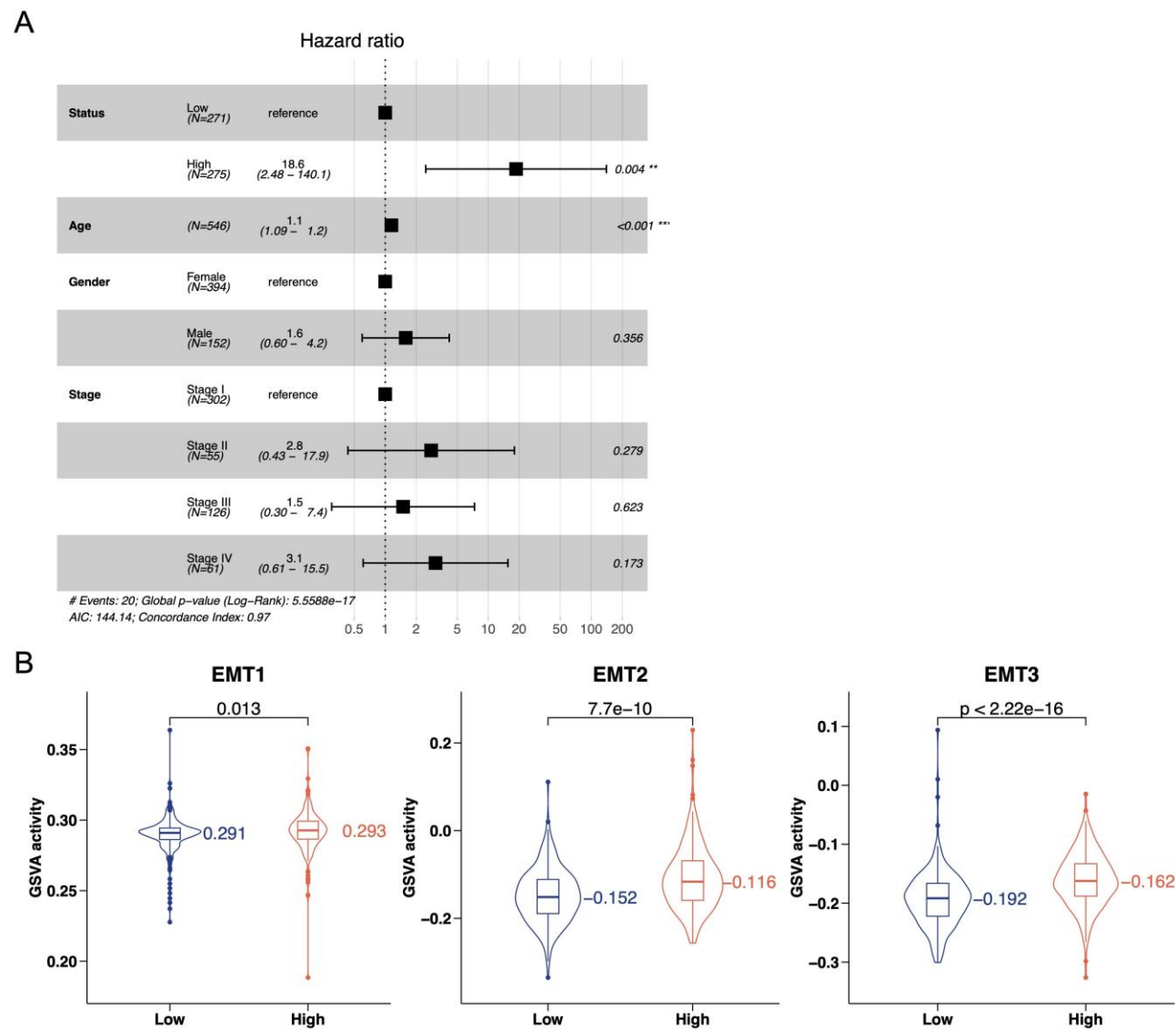
Supplementary Figure 3. Related analyses of epithelial subsets. (A-B) UMAP plots of epithelial clusters and their distribution across clinical groups. (C) Proportional distribution of subsets across individual samples. (D-E) Heatmap and dot plot showing marker expression across subsets. (F) KEGG enrichment highlighting functional specialization of epithelial subsets.



Supplementary Figure 4. Validation of TAM subtypes across thyroid cancer samples.

(A) Cross-sample integration confirming reproducibility of TAM subtype identification.

(B) Heatmap showing subset-specific marker expression across patients.



Supplementary Figure 5. EMT-related transcriptional reprogramming in thyroid cancer. (A-B) Boxplots showing increased expression of EMT regulators (*TGFB1*, *PHTF2*, *SNAI1*, *SLUG*, *TWIST1/2*, *ZEB1/2*) in high-signature tumors. (C) ESTIMATE score and tumor purity comparison between low- and high-signature groups.

