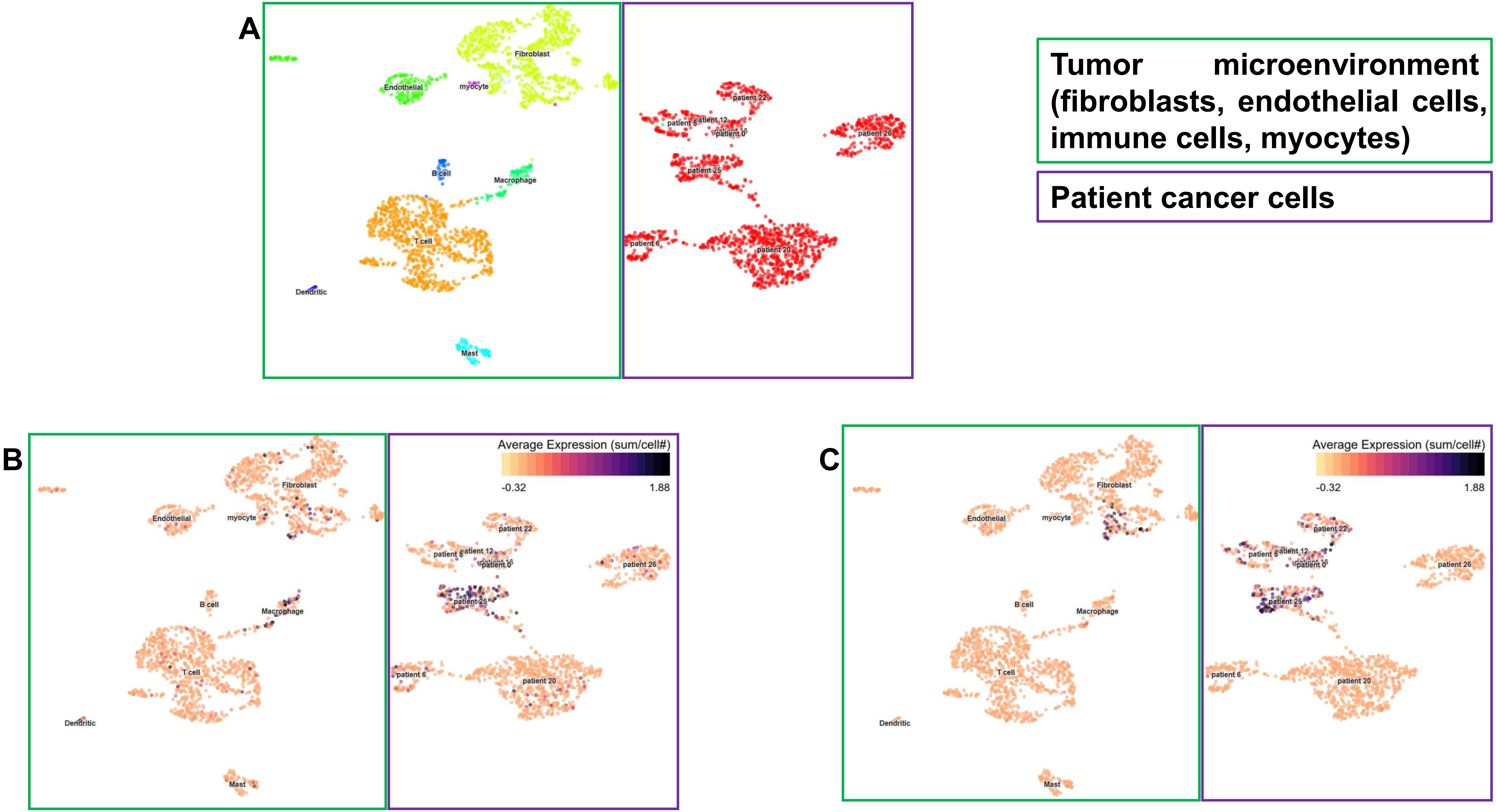
Supplementary Figure 1

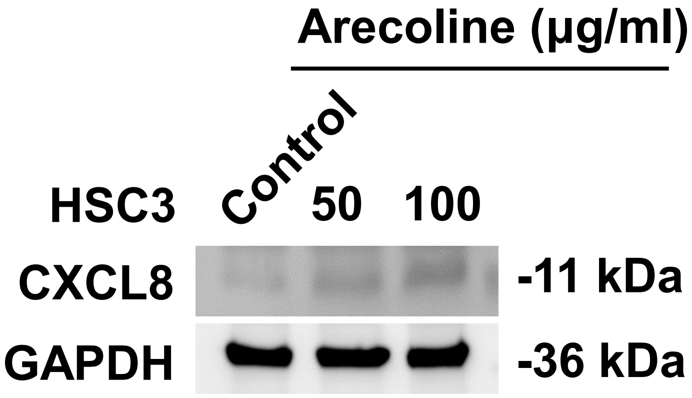


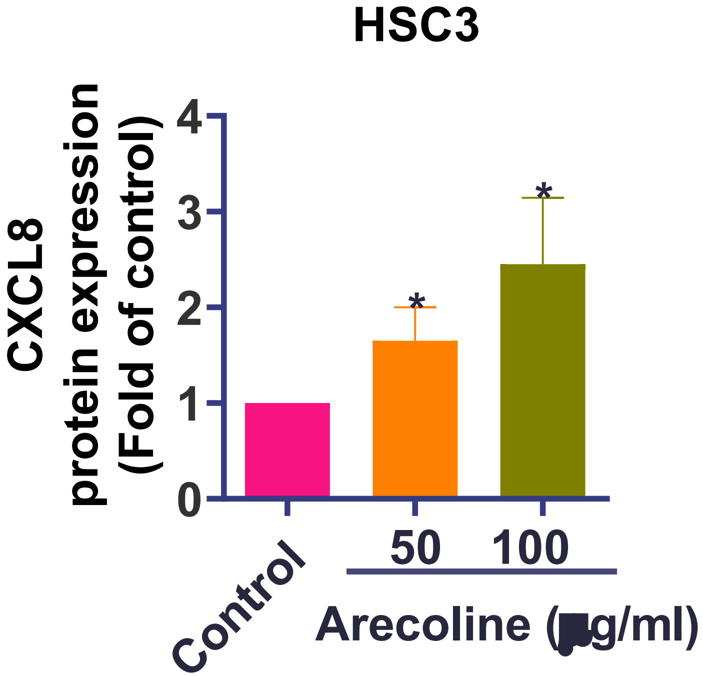
Tumor microenvironment (fibroblasts, endothelial cells, immune cells, myocytes)

Patient cancer cells

Supplementary Figure 1. Single-cell transcriptomic analysis of CXCL8 and MMP1 expression in head and neck cancer tissue. (A) Cell-type distribution and annotation of cancer cells, stromal cells, and immune cells from head and neck squamous cell carcinoma (HNSCC) patient tumors, visualized using UMAP plots via the UCSC Cell Browser platform (GSE103322). (B) CXCL8 gene expression levels in different cell populations within the tumor microenvironment.(C) MMP1 gene expression levels in corresponding cell types. Data were retrieved and visualized from public single-cell RNA-seq dataset (GSE103322) using the UCSC Cell Browser platform.

Supplementary Figure 2





Supplementary Figure 2. Arecoline induces CXCL8 protein expression in oral cancer cells. Western blot analysis of CXCL8 protein levels in HSC3 cells treated with increasing concentrations of arecoline (0, 50, and 100 µg/mL) for 24 hours. GAPDH was used as a loading control (n=4). Results are expressed as the mean ± SD of four independent experiments. $p < 0.05$ was considered statistically significant.