

Figure S1. Transcriptome analysis of OSCC. GO enrichment analysis for the biological process of upregulated (A) or down-regulated (B) genes in OSCC was performed with g:Profiler. Data was extracted and analyzed from NCBI GEO profile database (GEO accession: GSE70665). Determination of DEGs was based on fold-change ≥ 2 and $P < 0.05$. OSCC, oral squamous cell carcinoma.

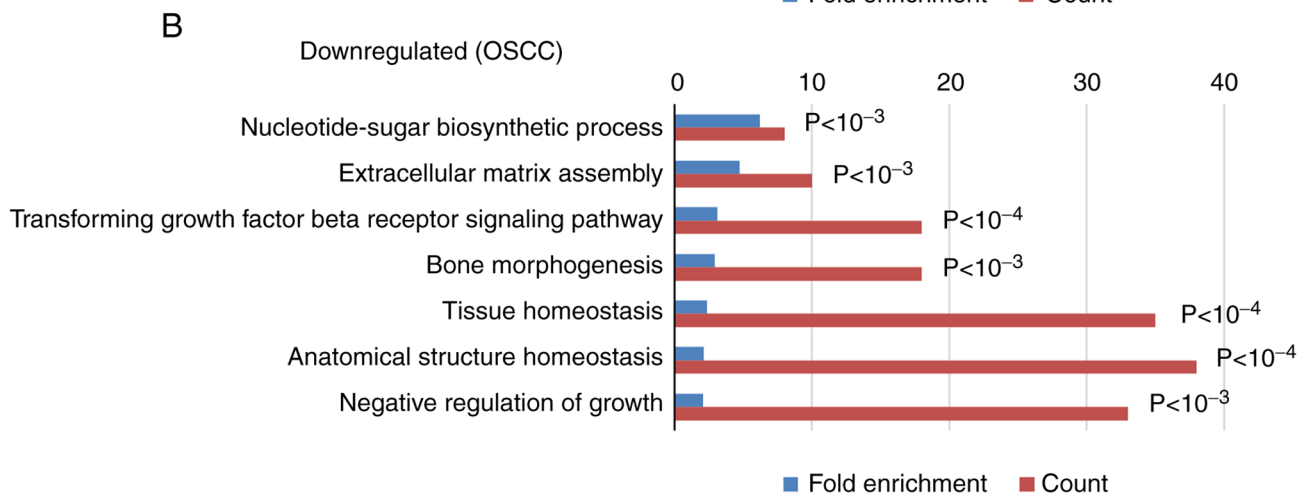
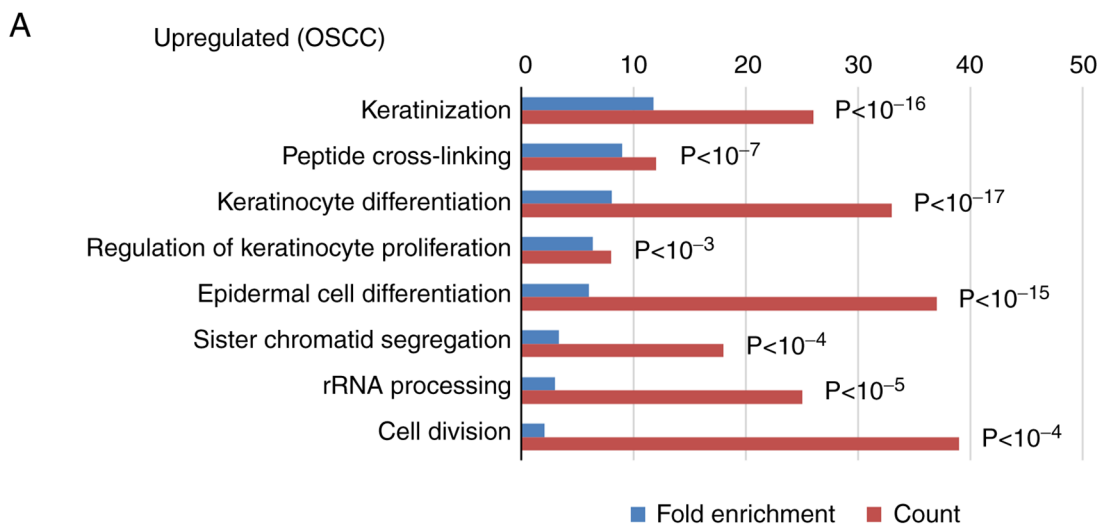


Figure S2. FoxO1 does not affect acute inflammatory response in OSCC. (A) Immunoblot analysis of indicated phosphorylated proteins in control and FoxO1-deficient cells upon TNF α treatment. Total proteins were used as loading controls. (B) mRNA levels of indicated genes in control and FoxO1-deficient cells, with or without TNF α treatment. **P<0.01, ***P<0.001. n.s., not significant. FoxO1, forkhead transcriptional factor O1; phospho, phosphorylated; ns, not significant; CCL20, chemokine (C-C motif) ligand 20.

