



Supplementary Figure S1. Analysis of the TCGA HNSCC dataset. (A) NSD1 and PIP4K2B ($n = 521$), (B) NSD1 and MTOR ($n = 521$), (C) PIP4K2B and MTOR ($n = 521$) mRNA expression correlation in human tumor TCGA samples visualized by UALCAN database. (D, E) Kaplan–Meier analysis of overall (D) and progression-free (E) survival in TCGA RNA-seq HNSCC dataset ($n=500$), PIP4K2B mRNA expression automatically split by optimal cutoff value (low vs. high). (F) Analysis of PIP4K2B mRNA expression in HNSCC tissues and normal tissues, and (G) classification by tumor stages using the TCGA dataset, visualized by UALCAN database.

