



### Figure S1. 11q13 genes are frequently co-amplified in SCC

**a.** Frequency of amplification of *MYC*, *PIK3CA*, *EGFR*, and 11q13 genes across all 32 TCGA PanCancer Atlas Studies tumors (n = 10950).

**b.** Fraction of HNSCC tumors that have indicated gene amplified when 11q13 gene is amplified (n = 519).

**c.** Fraction of HNSCC (n = 30) and ESCC (n = 24) CCLE cell lines with 11q13 amplification.

**d.** Frequency of amplification of genes in 11q13 region in hepatocellular carcinoma (HCC, n = 378).

**e.** Correlation between gene expression and copy number in ESCC (TCGA, n = 161). R2 value represents Spearman coefficient, p values calculated with Holm correction.

**f.** Correlation between gene expression and copy number in LSCC (TCGA, n = 500). R2 value represents Spearman coefficient, p values calculated with Holm correction.

**g.** Gene expression of 11q13 genes relative to *ACTB* expression in FaDu cells. D. Upper and lower whiskers represent the largest and smallest observed values within 1.5 times the interquartile range from the ends of the box. \*\*\*p < 0.001.