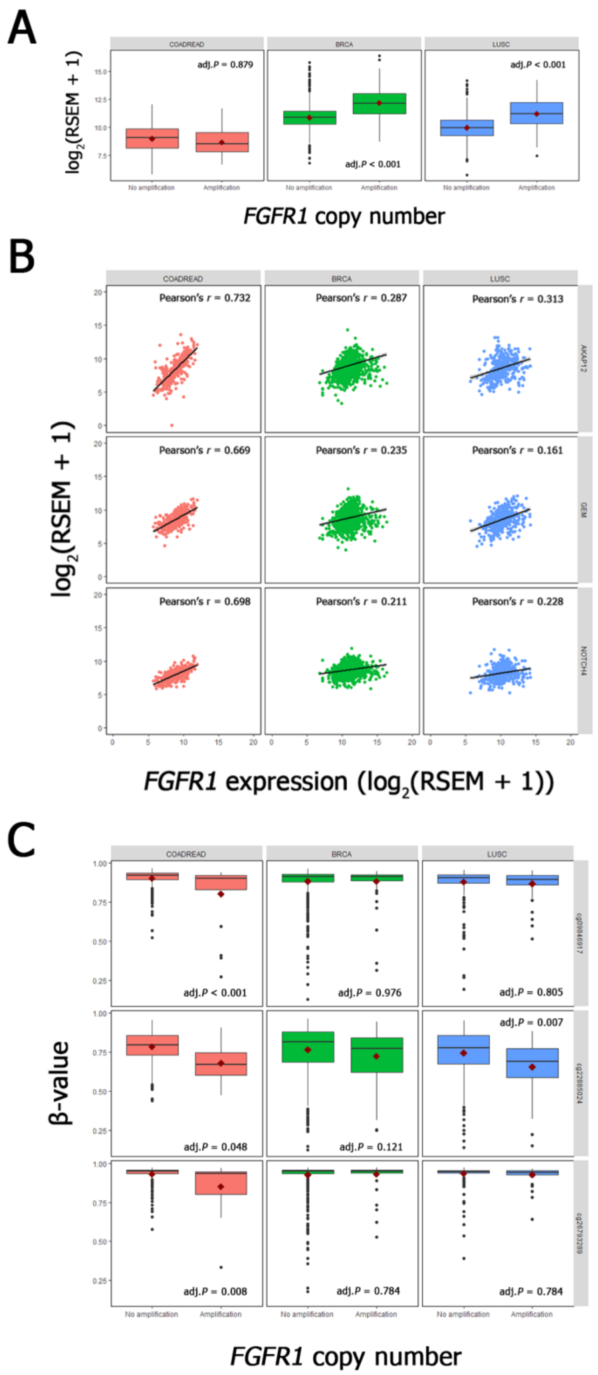

S5 Fig. Genome-wide methylation and transcriptome analysis in The Cancer Genome Atlas (TCGA) colon and rectum adenocarcinoma (COADREAD), breast invasive carcinoma (BRCA), and lung squamous cell carcinoma (LUSC) dataset. (A) Fibroblast growth factor receptor 1 (*FGFR1*) mRNA expression according to *FGFR1* copy number status. (B) mRNA expression of *AKAP12*, *GEM*, and *NOTCH4* according to *FGFR1* mRNA expression. (C) Methylation levels of differentially methylated CpGs according to *FGFR1* copy number status.