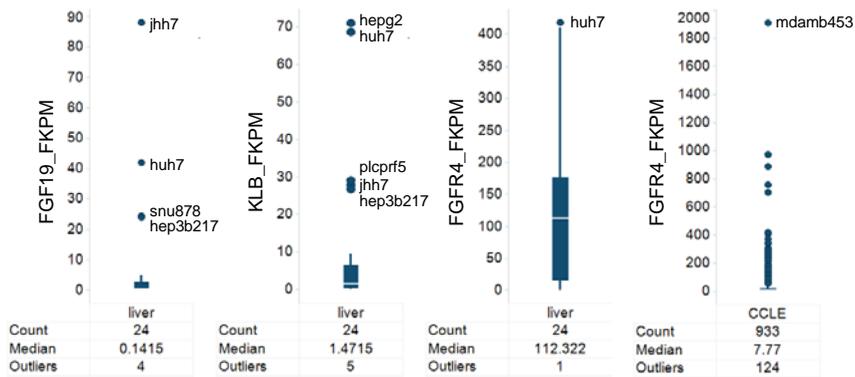
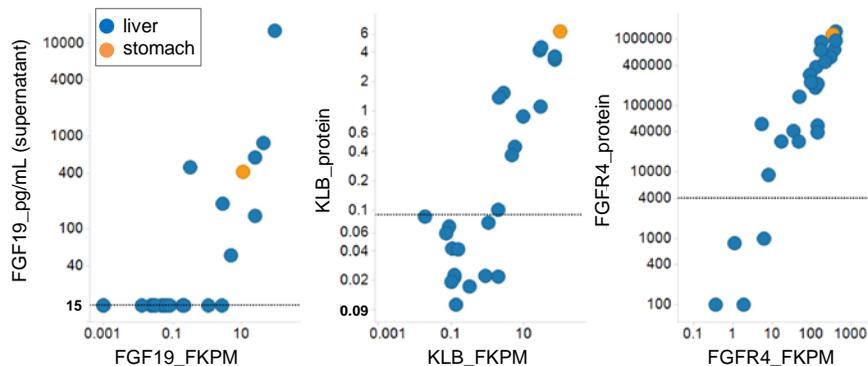
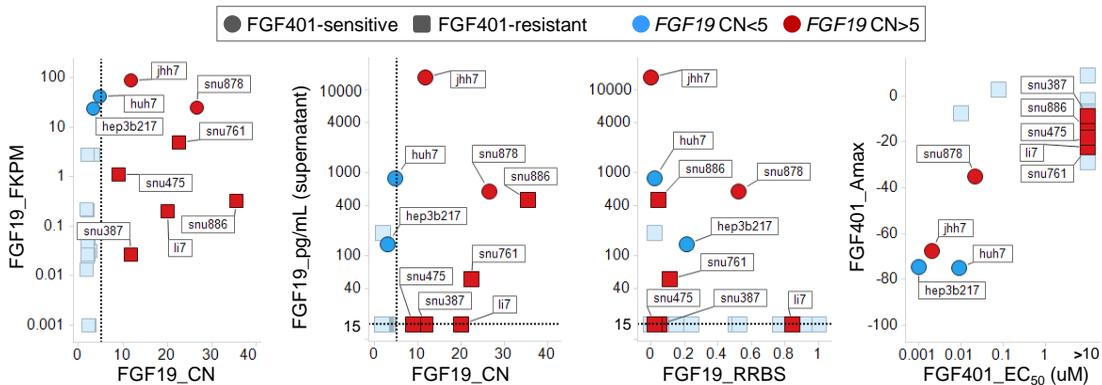
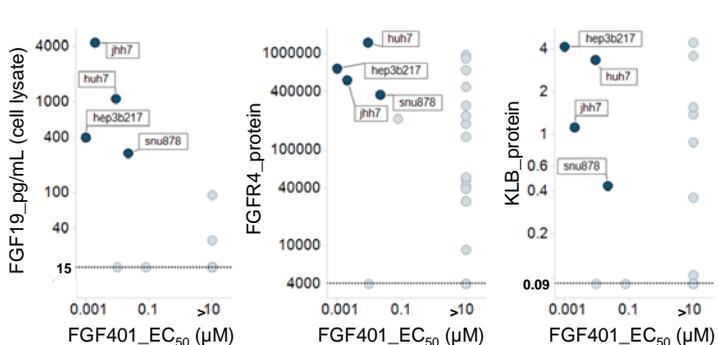


Supplementary Figure S1. FGF401 activity in cancer cell lines. A. Box-plots showing FGF19, KLB and FGFR4 expression measured by RNAseq in 24 HCC cell lines, or FGFR4 expression (RNAseq) in 933 cancer cell lines covering multiple lineages. B. Scatter plots showing the correlation between mRNA levels (RNAseq) and protein levels for FGF19, KLB and FGFR4 in 24 HCC cell lines and FU97 gastric cancer cell line. The dotted lines indicate the LOD for FGF19 and LOQ for KLB and FGFR4. C. Scatter plots showing the distribution of HCC cell lines according to FGF19 CN vs. FGF19 transcript (RNAseq) or vs. protein levels in the supernatant; FGF19 RRBS vs. protein; response to FGF401. The vertical dotted line indicates CN=5, the horizontal dotted line indicates the LOD of the FGF19 ELISA assay. The cell lines with FGF19 CN>5, as well as the FGF401 sensitive cell lines are highlighted in the four plots. RRBS: reduced representation bisulfite sequencing. D. Scatter-plots of 26 HCC cell lines showing their distribution according to FGF401 activity (EC_{50}) and FGF19, KLB and FGFR4 protein expression. The four HCC cell lines sensitive to FGF401 are highlighted in the three plots. E. Differential gene expression analysis of Hep3B2.1-7, JHH7 and HUH7 cells treated with 0.5 μ M of FGF401 or DMSO for 18 h. The volcano plot highlights some of the most significantly upregulated and downregulated genes across the three cell lines. FC: fold-change of FGF401-treated cells vs. DMSO-treated cells.

A**B****C****D****E**