Supplementary Figure Legends

Figure S1: Response to NVP-BGJ398. A. Cell viability data for NVP-BGJ398 was obtained for 541 cancer cell lines in two high-throughput screens consisting of n=435 and n=424 cell lines respectively, with a total of 342 cell lines profiled in both screens. The scatter plots show the distribution of cell lines for screen 1 and screen 2 with respect to Amax and inflection point values derived from the proliferation assays. Cut-off for sensitivity is indicated with dotted lines (Amax≤-40 and inflection point≤1uM). Cell lines confirmed as NVP-BGJ398-sensitive in manual proliferation assays (see panel B) are indicated in red. **B.** Cell lines with Amax≤-40 and inflection point≤1uM in the high-throughput cell viability screens (n=35) were tested in manual cell proliferation assays along with 24 additional cell lines for which no high-throughput cell viability was available. IC50s were determined using Excelfit and shown in the graph bars. The cut-off for NVP-BGJ398 sensitivity (IC50<500 uM) is indicated with the dotted line.

Figure S2: FGFR pathway modulation by NVP-BGJ398. The indicated cancer cell lines were treated with NVP-BGJ398 or DMSO as a control and the impact on FGFR downstream signaling was determined by analyzing FRS2 tyrosine phosphorylation, Akt and Erk1/2 activation by Western blot. α-actinin, β-tubulin, total Akt, total Erk1/2 or total FRS2 Western blots show equal loading.

Figure S3: NVP-BGJ398 – predictive features. A. Heat map for the top five features in the predictive model is shown for the cell lines sensitive to NVP-BGJ398 (dark purple for discrete features, continuous Z scores for GeneSet expression signatures). **B.** Heat map for the GeneSet expression signatures ("Development FGF-family signaling" and "Inhibition of Hedgehog signaling in medulloblastoma stem cells") in the cell lines with FGFR genetic alterations for which NVP-BGJ398 pharmacological data was available (n=37). NVP-BGJ398 response is indicated in dark green for the sensitive cell lines and light green for the insensitive cell lines. Continuous Z scores for GeneSet expression signatures is used.

Figure S4: A. Relative *FGFR2-c3* mRNA expression in cell lines. *FGFR2-c3* isoform transcript expression was measured by RT-Q/PCR and expressed relative to β-actin, which was used as an internal control.*****cell lines with *FGFR2* gene amplification. **B. *FGFR2* DNA copy number in tumors.** A total of 169 genomic DNA samples originating from gastric and esophageal tumors were subjected to Q-PCR analysis for *FGFR2* locus copy number determination. Absolute copy number values are shown.

Figure S5: A. *FGF19* DNA copy number in CCLE cell lines. Upper panel: Boxplot showing *FGF19* DNA copy number, expressed as log2ratio for the 541 cell lines clustered according to cancer type. Abbreviations are as in Figure 4. Lower panel: Scatter plot showing the correlation between *FGF19* copy number and transcript expression of *FGF19*, *FGFR4* and *β-Klotho* (KLB) in CCLE lines. Cell lines are colored according to response to NVP-BGJ398: green: sensitive; red: insensitive. **B**. ***FGFR3* DNA copy number versus transcript expression in bladder cancer cell lines.** Scatter plot showing the distribution of bladder cancer cell lines with respect to *FGFR3* DNA copy number and transcript expression. Cell lines are marked according to their response to NVP-BGJ398 as in A.