

Supplemental Figure and Table Legends

Supplemental Figure S1. Expression of *FGFR1-4*, *FGF1-23*, *KIT*, *ETV1*, *PRKCQ*, *ANO1*, *EGFR*, *ERBB2-4*, *MET*, *IGF1R*, *HGF*, *EGF* and *NRG1* in multiple primary tumor types and cancer cell lines. **A**, gene expression in multiple primary tumor types. Normalized gene expression was calculated as the Z-score. Each dot represents an individual primary tumor sample. More than 30,000 primary tumor tissue samples were sorted by the expression level of the gene and plotted. Ninety primary GIST tumor tissue samples are indicated by blue arrows. **B**, gene expression in cell lines of multiple lineages. Normalized gene expression was calculated as the Z-score. Each dot represents an individual cell line. More than 1,000 cell lines were sorted by the expression level of the gene and plotted. Four GIST cell lines are indicated by blue arrows.

Supplemental Table 1. Annotation of primary tumor tissues.

Supplemental Table 2. Annotation of cell lines.

Supplemental Table 3. Differentially expressed genes (DEGs) identified from RNA-Seq by DeSeq between control and imatinib-treated GIST cell lines. GIST-T1 and GIST882 cells were treated with imatinib (1 μ M) for 4 hours.

Supplemental Table 4. Gene expression levels in GIST cell lines. GIST-T1 and GIST882 cells were treated with imatinib (1 μ M) for 4 or 72 hours, and imatinib for 72 hours and then BGJ398 for 4 hours prior to the end of the treatment. Gene expression was quantified by FPKM. FPKM, Fragments Per Kilobase of transcript per Million fragments mapped.