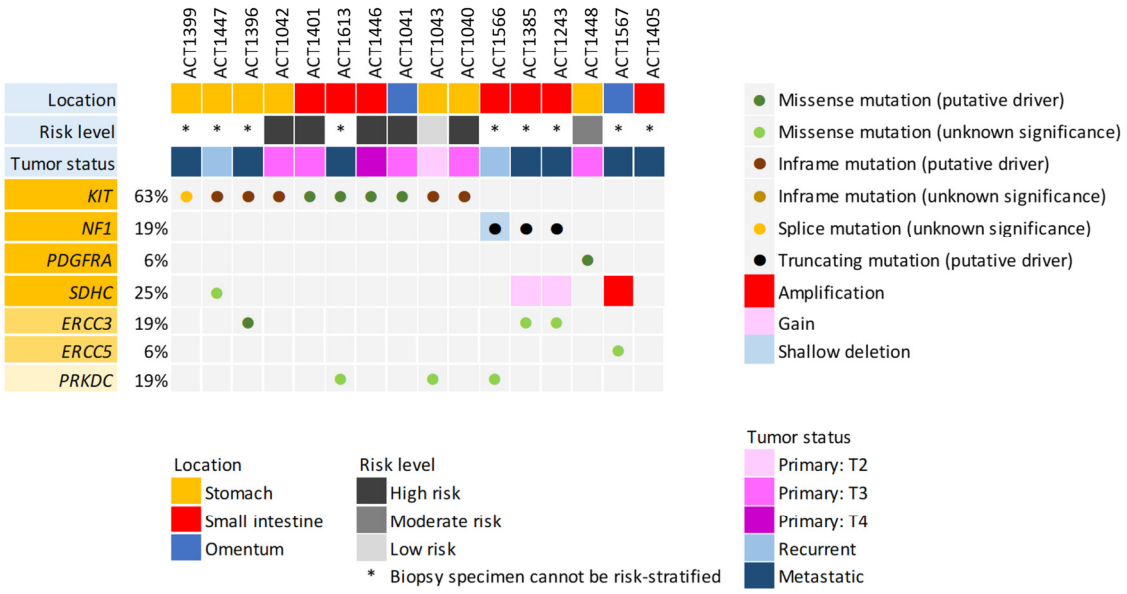

Figure S1. Mutational landscape of GISTs in nucleotide excision repair (NER) and non-homologous end-joining (NHEJ) pathways: In the targeted NGS panel, two genes in the NER pathway (ERCC3: p.K11E (*n* = 2) and p.S764L (*n* = 1); *ERCC5*: p.R71H (*n* = 1)) and one gene in the NHJE pathway (*PRKDC:* p.M3845I, p.P2456A, and p.G1030V in 1 each), all with missense mutations, are aberrated in 4 and 3 cases, respectively. Columns represent individual tumors and rows represent individual aberrated genes. DNA damage repair genes are collated based on the prevalence of SNVs/indels, following the primary GIST-driving mutations (*KIT, PDGFRA, NF1, SDHC*) and the baseline clinicopathologic characteristics, including tumor locations, NCCN risk levels, and status of tumor specimens. Asterisks indicate biopsy samples not amenable to precise risk-stratification by histology.