



S4 Fig. Tumor mutational burden of STS in this study (n=34, somatic mutation only) and other cancer types in the TCGA dataset. X-axis represents cancer types, and Y-axis represents the number of mutations (log10 scale). The numbers above the plot indicate the sample size of the dataset. Maftools was used for this analysis in R. STS, soft tissue sarcoma; TCGA, The Cancer Genome Atlas; TMB, tumor mutation burden.