Description of Additional Supplementary Files

Supplementary Data 1: Clinical characteristics in this study.
Supplementary Data 2: Quality control of the WES, WGS and RNA-seq in this study.
Supplementary Data 3: The annotation of somatic coding mutations (SNVs and indels) in GISTs.
Supplementary Data 4: The results of MutSig2CV in GISTs.
Supplementary Data 5: Clinicopathologic classification and Y*LPM1* status in GISTs.
Supplementary Data 6: Methylated CpG sites within the *YLPM1* promoter region in GISTs.
Supplementary Data 7: Decomposition of de novo CNV signatures to reference signatures in GISTs.
Supplementary Data 8: Analysis of chromosome arm level CNVs and their correlation with risk.
Supplementary Data 9: The results of focal CNVs and the genes selected for correlation analysis between copy number alterations (CN) and gene expression (GE).
Supplementary Data 10: Breakpoint information of structural variations (SVs) and a statistical compilation of genes impacted by SVs.
Supplementary Data 11: The characteristics of chromothripsis in GIST WGS Cohort.
Supplementary Data 12: Gene set enrichment analysis in each molecular subtype using GSEA with Hallmark gene sets obtained from MSigDB.
Supplementary Data 13: The list of primer sequences used in this study.
Supplementary Data 14: The characteristics of gene fusions in GISTs.