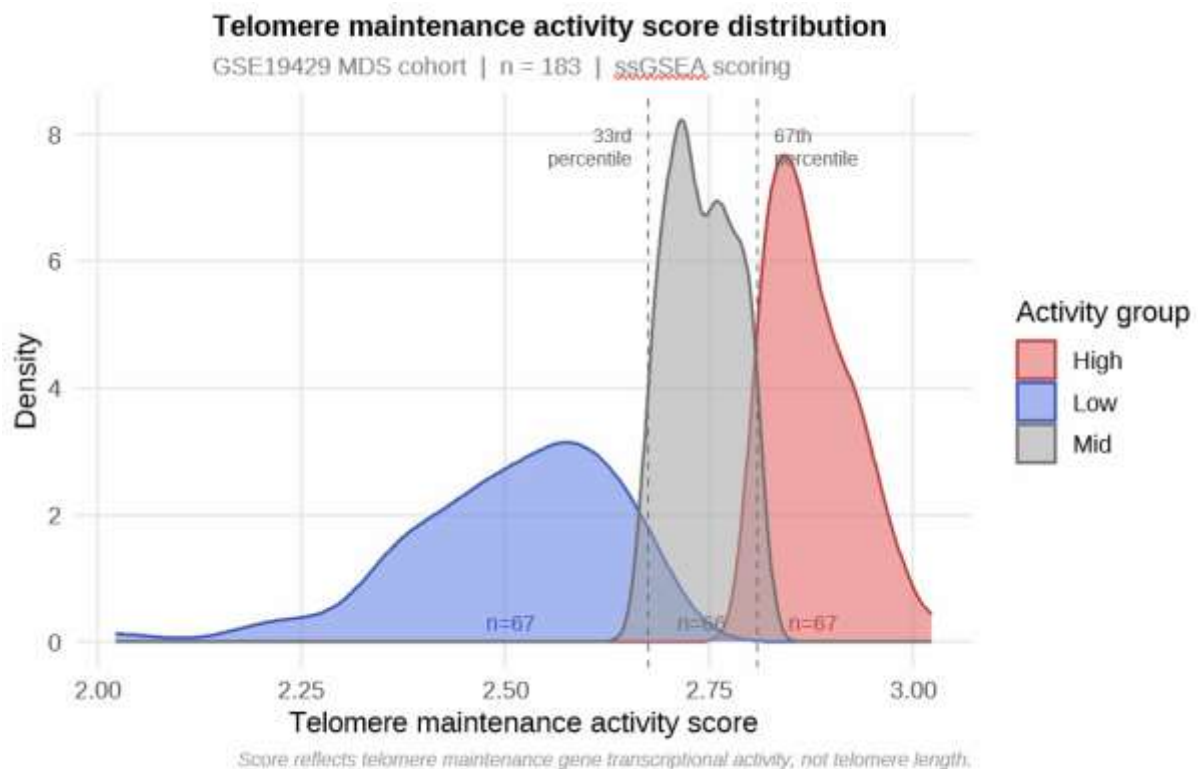
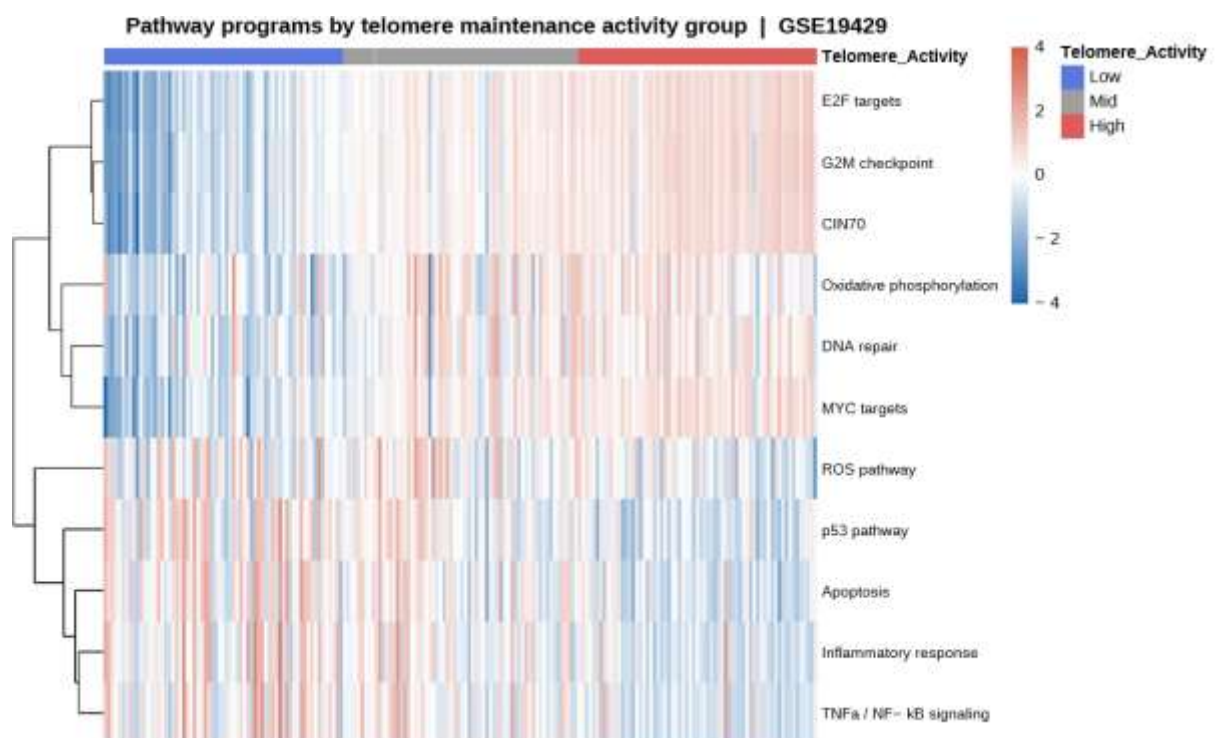




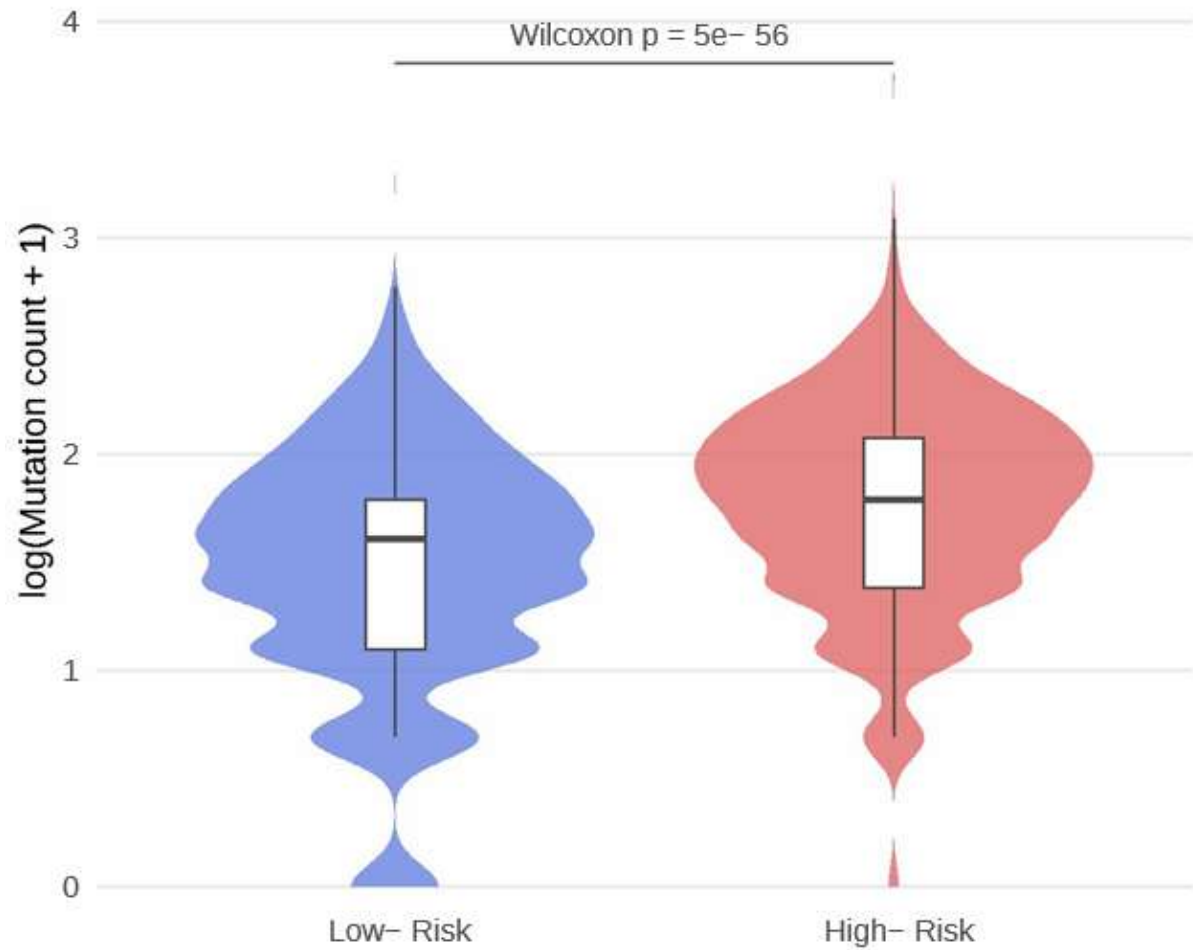
Supplementary Figure S1: Telomere maintenance activity score distribution. Density plot across 183 MDS patients (GSE19429). Low = blue, Mid = grey, High = red. Dashed lines: 33rd and 67th percentile cut points. n=67, 66, 67.



Supplementary Figure S2: Pathway programs by the telomere maintenance activity group. Heatmap of ssGSEA pathway scores across 183 MDS samples ordered by score. 11 Hallmark pathways and CIN70. Row-scaled. The annotation bar indicates the tertile group.

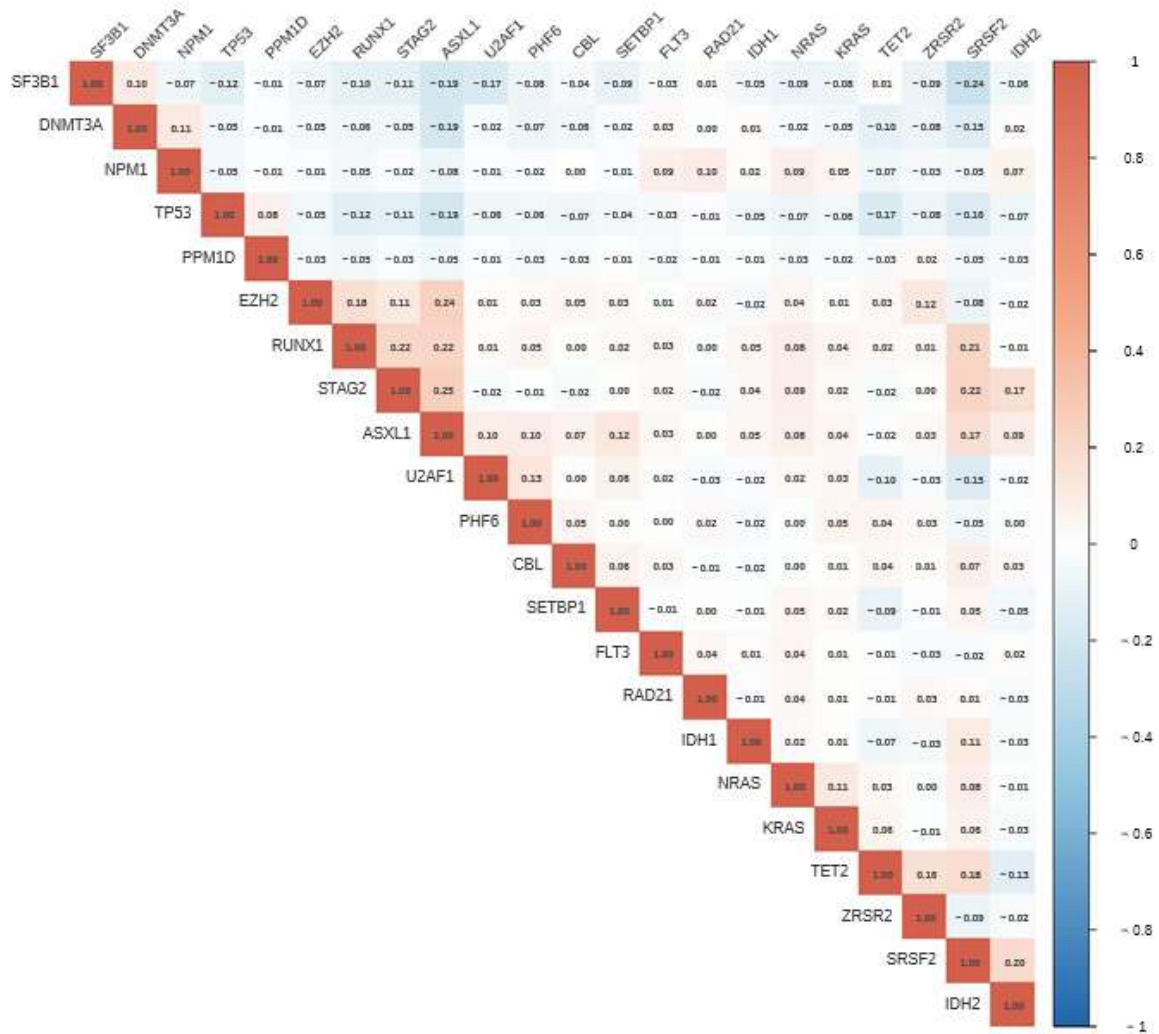
Total mutation burden by clinical risk group

IWG 2022 MDS cohort | n = 3,323



Supplementary Figure S3: Total mutation burden by clinical risk group. Violin plot (n=3,323). log-transformed mutation counts. Wilcoxon p -value annotated.

Driver mutation co-occurrence (phi correlation) | IWG 2022 MDS | n = 3,323



Supplementary Figure S4: Driver mutation co-occurrence matrix. Pearson phi correlations across 22 driver genes (IWG 2022, n=3,323). Hierarchical clustering order. Spliceosome gene clustering consistent with published MDS mutation landscapes.