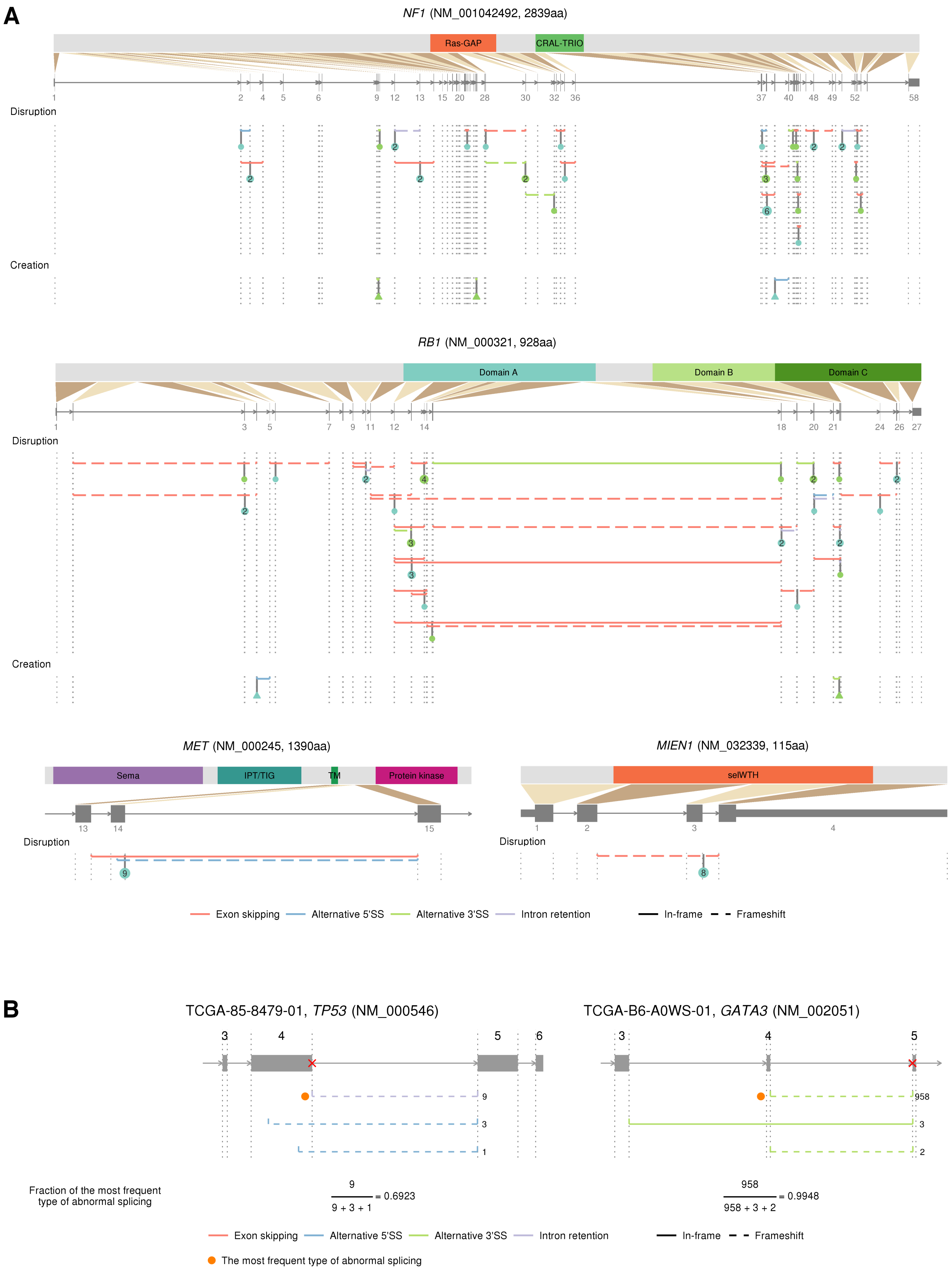

Supplementary Figure 7: Genes frequently affected by SAVs in human cancers.

(A) Distribution of SAVs and their resultant splicing outcomes for *NF1* (upper), *RB1* (middle), *MET* (lower left), and *MIEN1* (lower right). SS-disrupting SAVs are aggregated according to the authentic SSs. The number in circles represents the number of SAVs for each SS. **(B)** Schematics depicting methods to quantify the fraction of the most frequent relative to total associated splicing outcomes for each SS-level SAV hotspot. The number at each line represents the count of supporting reads.