



Supplementary Figure 4: The exon-intron architecture affected by SS-disrupting SAVs based on their splicing outcomes.

(A) Lengths of exons affected by SAVs, and their 5' and 3' introns were compared among the five splicing groups. **(B)** MaxEnt scores (before substitution) at authentic splicing donor (left) and acceptor (right) sites according to splicing outcomes. **(C)** H-bond scores (before substitution) at authentic splicing donor sites according to splicing outcomes. **(D-F)** Matrices of the significance of differences in GC content **(D)**, length **(E)** of exons affected by SAVs and their 5' and 3' introns, and splicing strength (based on MaxEnt or H-bond scores) of affected SSs **(F)** among the splicing groups. The significant differences were quantified by the negative logarithm of the P-value of one-sided Wilcoxon rank-sum tests whose alternative hypotheses are that either the splicing pattern 1 is less (blue) or greater (red) than splicing pattern 2. The smaller P-value between the two alternative hypotheses is shown.