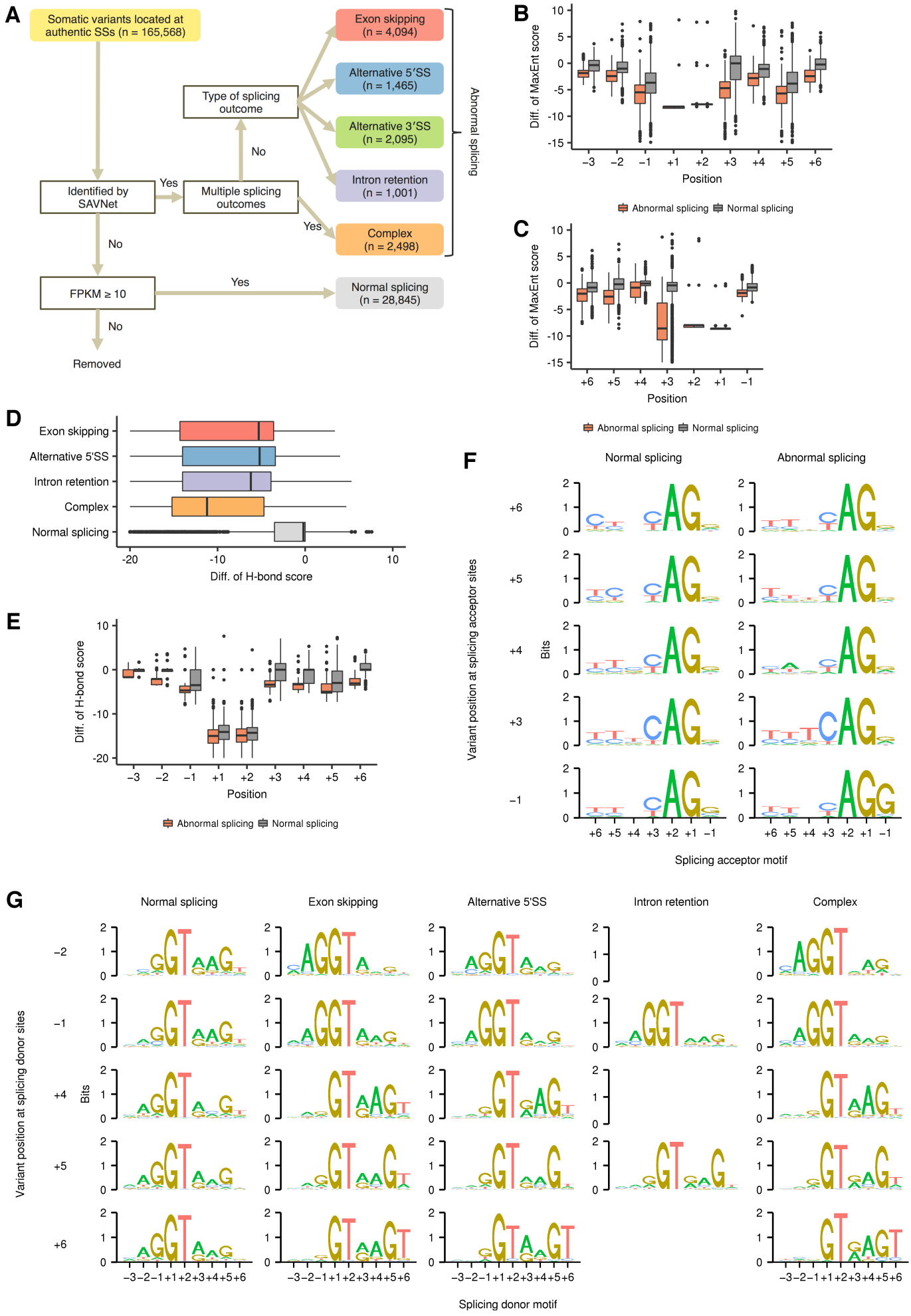
A
Somatic variants located at authentic SSs (n = 165,568)
Identified by SAVNet
Yes
Multiple splicing outcomes
No
Type of splicing outcome
Exon skipping (n = 4,094)
Alternative 5′SS (n = 1,465)
Alternative 3′SS (n = 2,095)
Intron retention (n = 1,001)
Yes
Complex (n = 2,498)
Abnormal splicing
No
FPKM ≥ 10
Yes
Normal splicing (n = 28,845)
No
Removed
B
Diff. of MaxEnt score
Position
Abnormal splicing
Normal splicing
C
Diff. of MaxEnt score
Position
Abnormal splicing
Normal splicing
D
Exon skipping
Alternative 5'SS
Intron retention
Complex
Normal splicing
Diff. of H-bond score
E
Diff. of H-bond score
Position
Abnormal splicing
Normal splicing
F
Normal splicing
Abnormal splicing
Variant position at splicing acceptor sites
Bits
Splicing acceptor motif
G
Normal splicing
Exon skipping
Alternative 5'SS
Intron retention
Complex
Variant position at splicing donor sites
Bits
Splicing donor motif

Supplementary Figure 3: Genomic features of SSs affected by SS-disrupting SAVs based on their splicing outcomes.

(A) Schematics depicting the classification methods for somatic variants affecting authentic SSs by their splicing outcomes**. (B, C)** Changes in MaxEnt scores by somatic variants were compared between normal and abnormal splicing groups according to the substituted position of donor **(B)** or acceptor **(C)** sites. “Normal splicing” represents samples lacking the relevant splicing alterations in the presence of somatic variants. **(D)** Change in H-bond scores triggered by somatic variants at authentic splicing donor sites according to splicing outcomes. **(E)** Changes in H-bond scores by somatic variants were compared between normal and abnormal splicing groups according to the substituted position of donor sites. **(F)** Sequence motifs of splicing acceptor sites at which somatic SNVs lead to normal (left) or abnormal splicing (right; identified by SAVNet) according to the variant position. **(G)** Sequence motifs of splicing donor sites at which somatic SNVs lead to normal splicing, exon skipping, alternative 5′SS, intron retention, or complex abnormalities. Categories whose number of SAVs is less than 25 are not displayed.