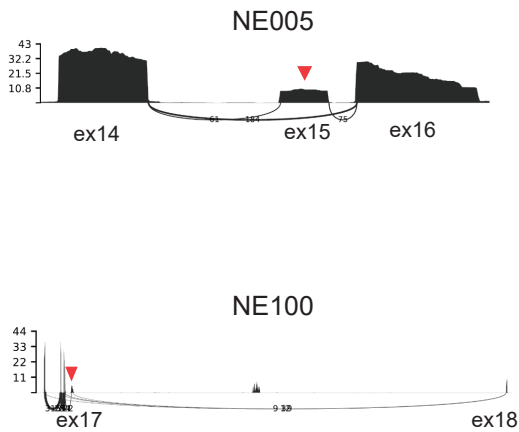


Supplementary Figure S17. Exon skipping in the *RB1* gene.

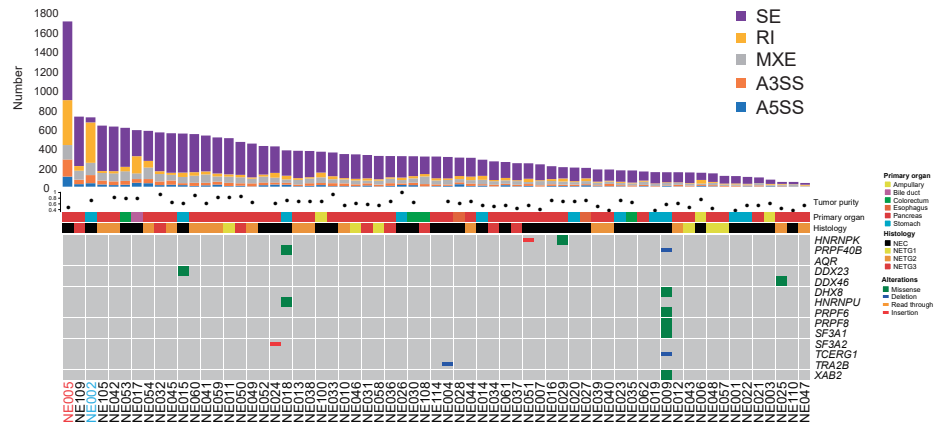
A

Sample	Pathology	SE location	Exon number	DNA-seq	Mutation
NE005	Pancreatic NEC	chr13:48380052 - 48380084	exon 15	WGS	No
NE100	Ampullary NEC	chr13:48381246 - 48381443	exon 17	WES (FFPE)	splice site (Exon 17)

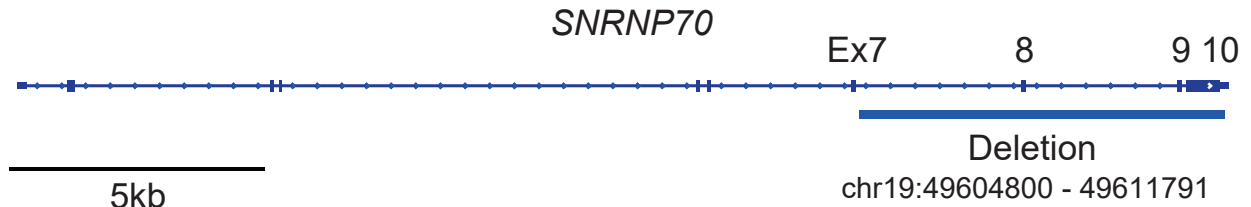
B



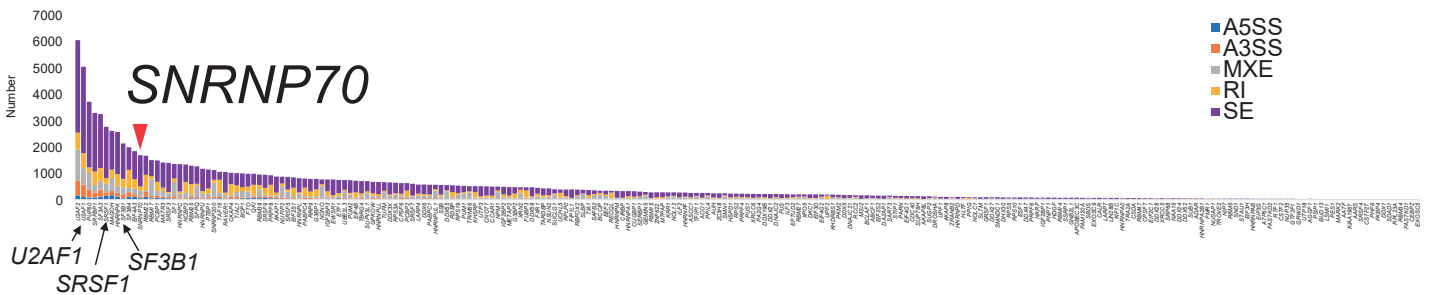
C



D



E



A, Exon skipping in *RB1* was identified in two samples, splice site mutations being found in one cases (NE100). NE005 had no splice mutation by WGS and targeted gene sequencing. **B**, Sashimi plots of the skipped exon locus in each sample. Red arrowheads indicate the skipped exons. ex, Exon. **C**, The upper panel shows the number of alternative splicing sites in each sample identified by rMATS (7). NE005 (written in red letters) had by far the most alternative splicing of all the patients. Of note, in a gastric NEC with the Merkel cell polyomavirus (MCPyV) (NE002, written in blue letters), most alternative splicing featured RI. Alterations of spliceosome genes mapped on KEGG (Kyoto Encyclopedia of Genes and Genomes) pathway were found as shown in the lower panel. SE, skipped exons; RI, retained intron; MXE, mutual exclusive exons; A3SS, alternative 3' -end splice sites; A5SS, alternative 5' -end splice sites. **D**, A large deletion around 7kb including exons 8, 9, and 10 in *SNRNP70* was detected by WGS in NE005. **E**, The number of total alternative splicing sites in HepG2 cells by knockdown/RNA-seq analysis of 237 RNA-binding protein genes from the ENCODE paper (8). Among the 237 genes, *SNRNP70* took the 10th place in terms of amount of total alternative splicing. Red arrowhead indicates *SNRNP70*.