



**Figure 1 - Supplemental Figure 7: Comparison of alternative splicing events identified using the gencode transcriptome or the gencode + *de novo* transcriptome.** (A) Schematic describing the steps taken to analyze alternative splicing using either the publicly available gencode.gtf or our gencode + *de novo*.gtf. Venn diagrams show unique and common genes when mapping RNA-sequencing libraries using the publicly available gencode gtf file and the *de novo* transcriptome file using nanopore sequencing for alternative splicing events including: (B) alternative acceptor, (C) alternative donor, (D) alternative last exon, (E) cassette, (F) coordinated cassette, (F) intron retention and (H) mutually exclusive.