The impact of cohesin mutations: Insights into a hidden regulator of alternative splicing in leukemia

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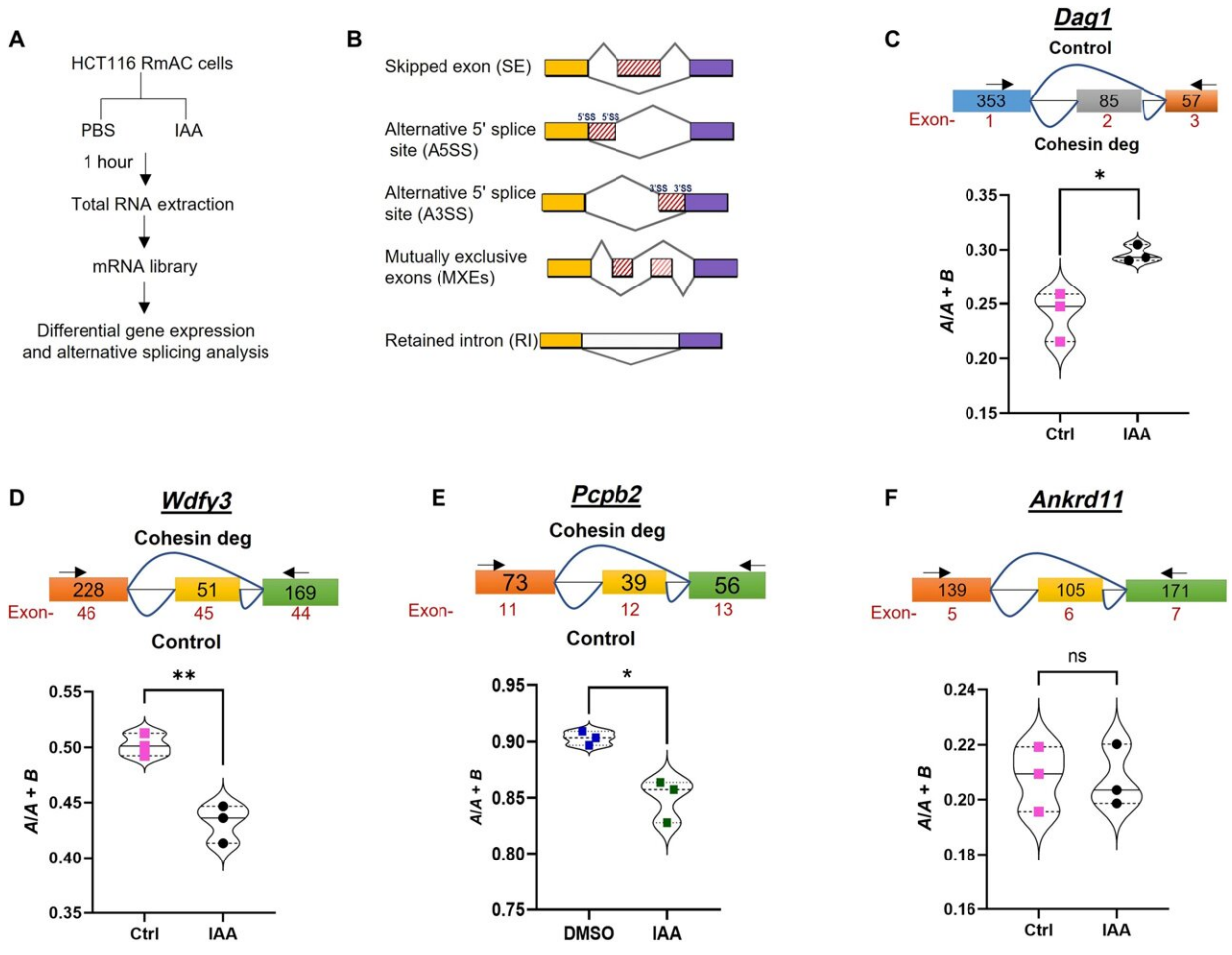

Cohesin regulates alternative splicing. (A) Flowchart showing the experimental protocol, as detailed in Materials and Methods. (B) Schematic showing five different classes of alternative splicing events. (C to F) Top: Schematic representations of genes Dag1 (C), Wdfy3 (D), Pcbp2 (E), and Ankrd11 (F)

focusing on alternatively spliced exons. Colored boxes represent exons, and the horizontal black lines represent the introns; the numbers below the colored boxes refer to the exon number, and numbers inside the boxes represent the length of the exons. The arrowheads depict the approximate reverse transcription polymerase chain reaction (RT-PCR) primer location, and curved lines depict the splicing pattern. (C to E) Bottom: The RT-PCR products derived from total RNA isolated from the cells treated with control or indole-3 acetic acid (IAA) were analyzed on agarose gels as shown in Supplementary Figures. The gels were used to quantify the included (A) and excluded (B) exon transcripts. The violin plots represent the ratios of A/A + B (ratios of included exon transcript/total transcript) used to measure alternative splicing events and represent the data of three independent biological replicates with standard mean deviation. Variables of significance: *P