



Supplementary Figure S1 (A) Splice graph representation of LSV involving novel exon skipping event within *Fubp3* from mouse cerebellum (top) and adrenal gland (bottom) with reads detected from RNA-Seq data displayed above each junction. Junctions quantified directly within the LSV are colored. **(B)** Primer table that suggests possible forward (left) and reverse (right) primers. Additional information for each primer can be displayed by clicking the "i". **(C)** UCSC Genome Browser snapshot with custom tracks produced by MAJIQ-SPEL as labeled. Pfam domains show this alternative exon overlaps with the first annotated KH domain, suggesting skipping could affect RNA binding of *Fubp3*. **(D)** Isoform table that displays PSI (ψ) quantifications (left) and possible isoforms (right). Nucleotide sizes correspond to products produced using the selected primers from (B). Red stop sign indicates premature termination codon (PTC) introduction upon exon skipping that may induce nonsense mediated decay (NMD). **(E)** RT-PCR validation of predicted product sizes and quantification using the primers selected in (B) on total RNA from mouse cerebellum (left) and adrenal gland (right). Average inclusion of the cassette exon by RT-PCR with standard deviation is given. Asterisks corresponds to a background band that does not run true to size.