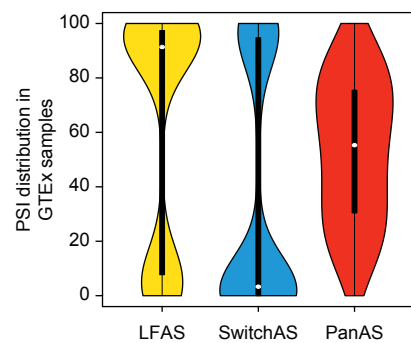
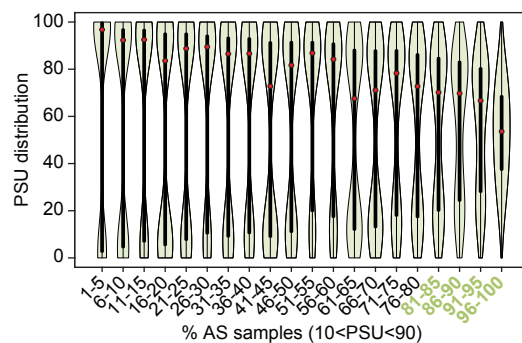
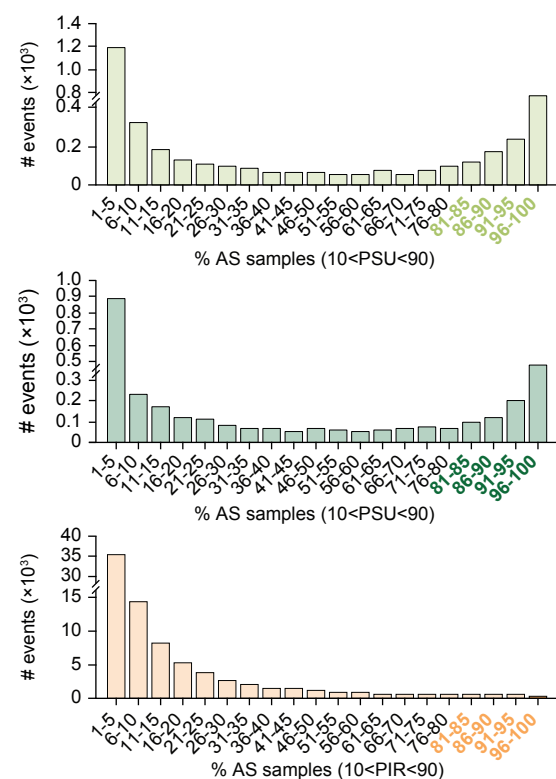
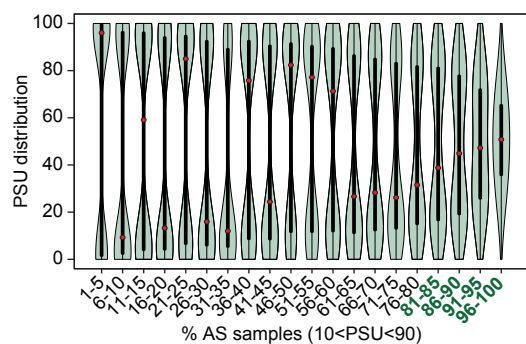
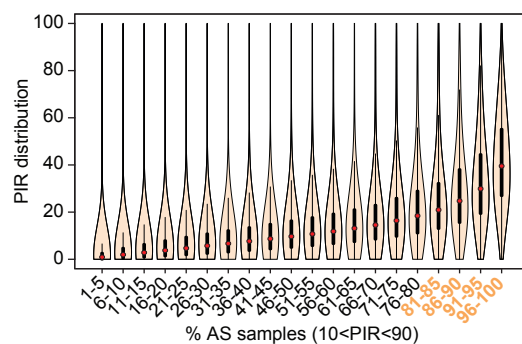
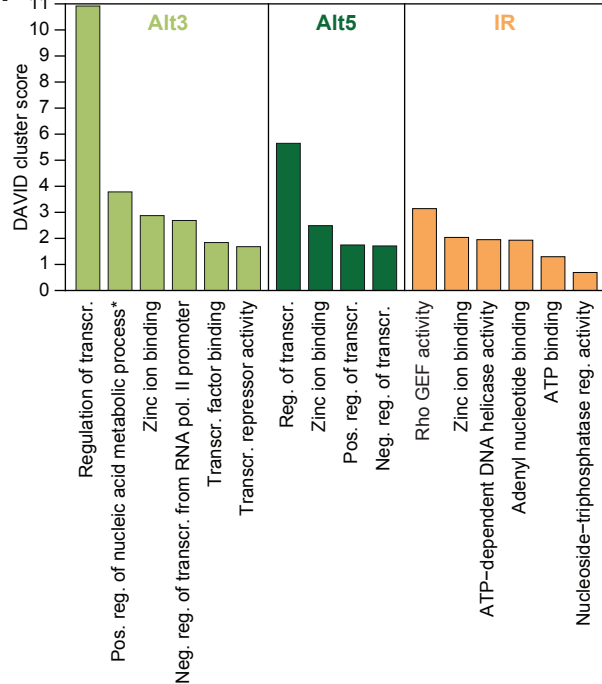
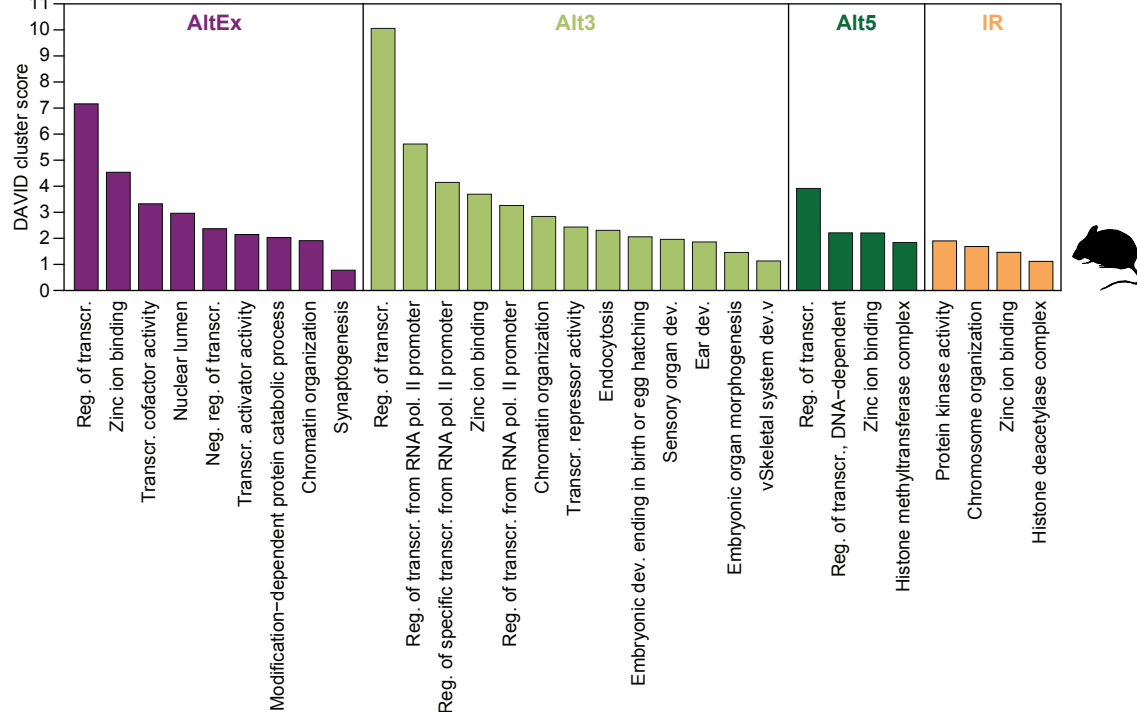
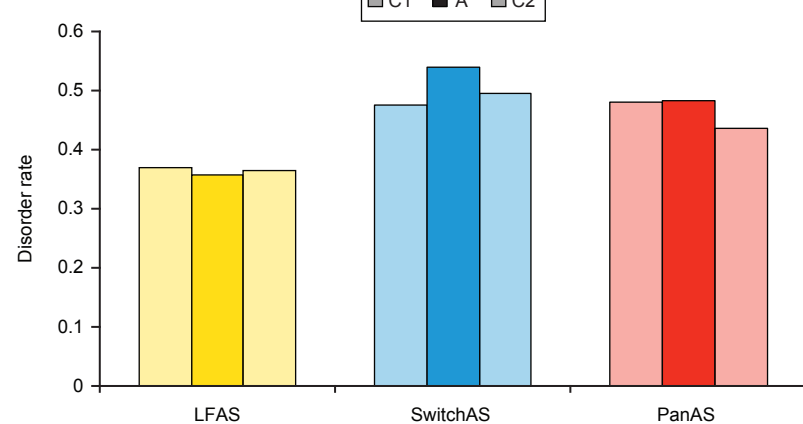
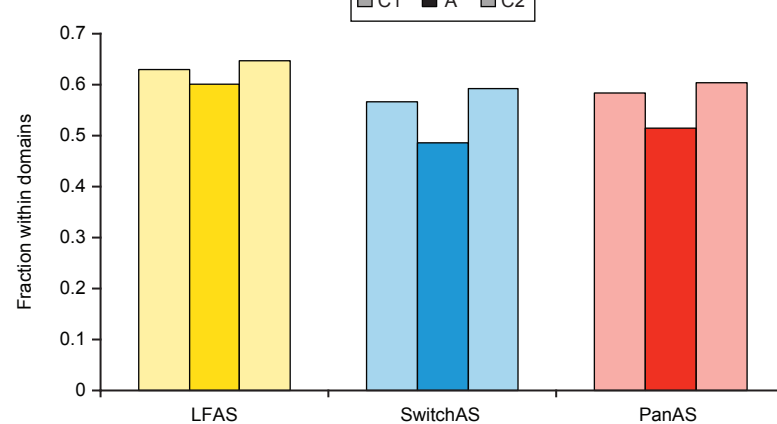


A**B****E****C****D****F****G****H****I**

Supplemental Figure S10 – Functional and proteomic features of PanAS events

A) Distribution of PSIs across 400 samples from 16 tissues from GTEx for low-frequency AS (LFAS, yellow), SwitchAS (blue) and PanAS (red) events. B-D) Distribution of PSIs for groups of Alt3 (B), Alt5 (C) and IR (D) that are alternatively spliced ($10\% < \text{PSI} < 90\%$) in an increasing fraction of samples. Red dots, median PSI of the bin. E) Total number of AS events in each of the bins in the violin plots of B-D. F) Enriched Gene Ontology categories using DAVID scores for human genes harboring Alt3, Alt5 and IR events that are alternatively spliced in $>80\%$ of the samples. (*) Complete GO term: Positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process. G) Enriched Gene Ontology categories using DAVID scores for mouse genes harboring AltEx, Alt3, Alt5 and IR events that are alternatively spliced in $>80\%$ of the samples. H) Mean disorder rate of residues encoded by alternative (A) and neighboring (C1, C2) exons for each regulatory category: LFAS (yellow), SwitchAS (blue) and PanAS (red). I) Fractions of residues from alternative (A) and neighboring (C1, C2) exons that overlap structured domains for each regulatory category: LFAS, SwitchAS and PanAS.