



**Supplementary Figure S14: Analysis of internal protein altered regions across proteins in the WTC-11 long-read predicted proteome.**

(A) Frequencies of the categories of the splicing mechanism underlying alternative internal sequence changes. All sequence regions involve a reference-alternative isoform pair. (B) Frequencies of the categories of linked (compound) splicing events. (C) Frequencies of different splicing mechanisms, with hatches representing the proportion of altered regions for which the flanking, split-junction codons encode different AA residues, termed “ragged codons”.