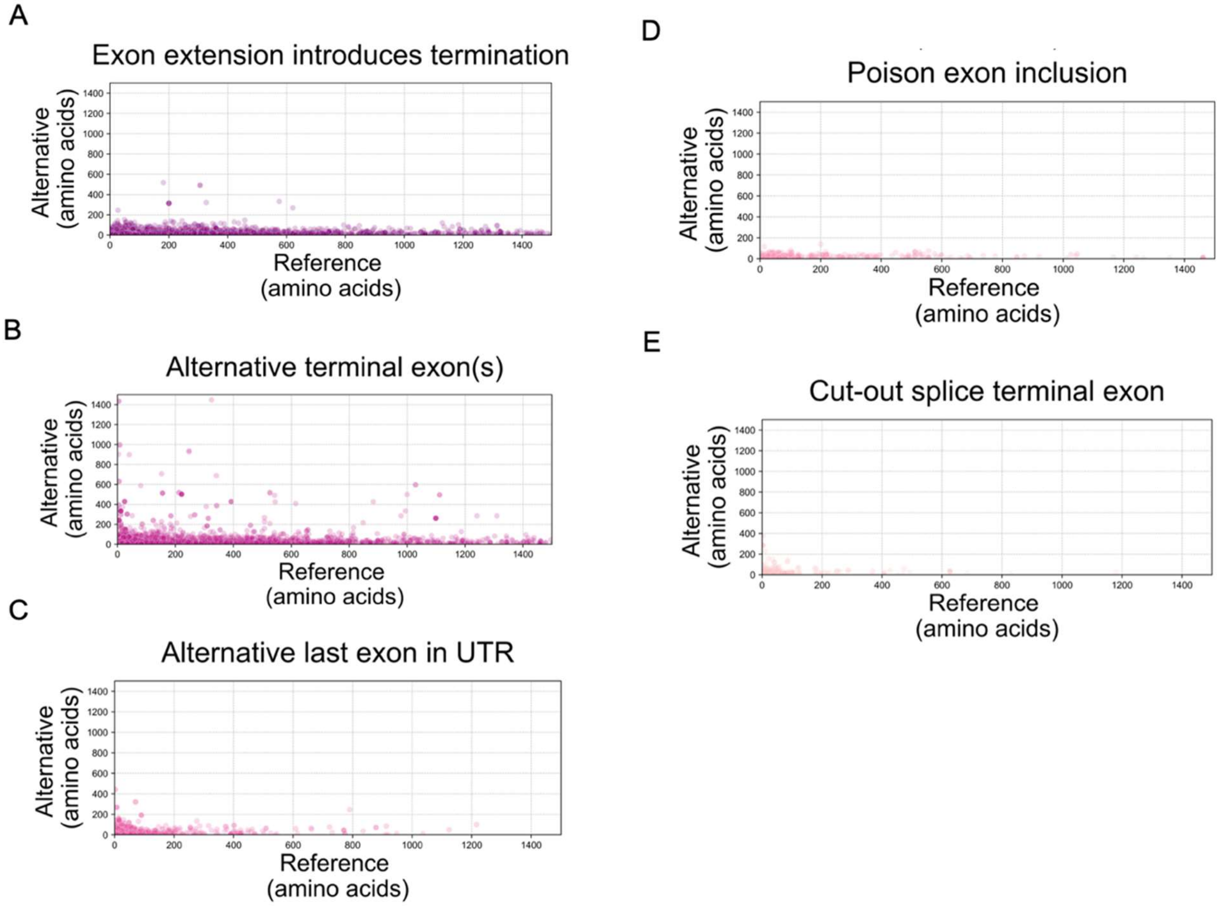

Supplementary Figure S6: Distribution of the normalized altered region lengths for the splice-driven patterns in the GENCODE annotated human proteome.

(D) Distribution of the normalized altered region lengths for (A) Exon extension introduces termination (EXIT), (B) Alternative terminal exon(s) (ATE), (C) Alternative last exon in the untranslated region (ALE in UTR), (D) Poison exon inclusion, and (E) Cut-out splice terminal exon (COSTE).