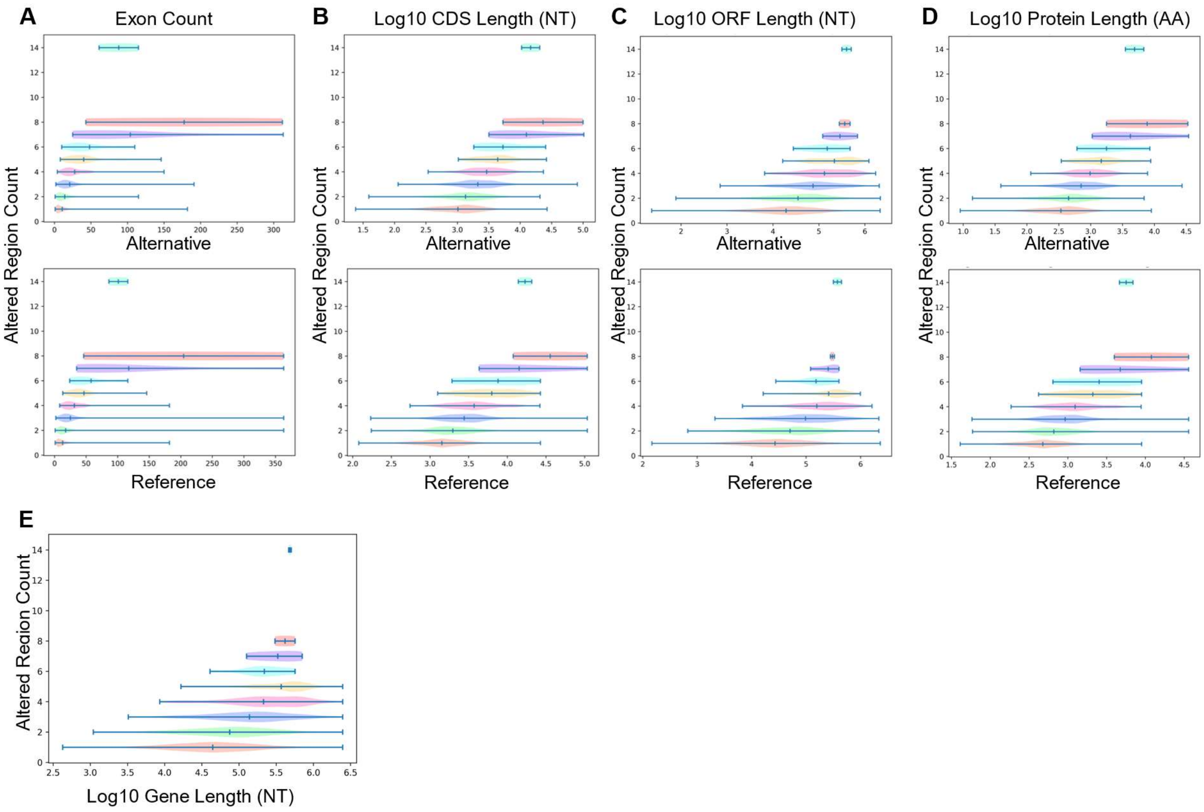

Supplementary Figure S4: Distribution of altered region in the GENCODE annotated human proteome.

Distribution of the number of altered regions per reference-alternative isoform pairs across the whole GENCODE annotated human proteome against (A) exon count in reference and alternative isoform, (B) CDS region length in reference and alternative isoform, (C) ORF region length in reference and alternative isoform, (D) protein sequence length in reference and alternative isoform, and (E) gene length for the reference-alternative pair. The length is measured in nucleotide (NT) or amino acid (AA).