



Supplementary Figure S12: Characterization of altered protein regions (Biosurfer p-blocks) across the WTC-11 long-read predicted proteome.

(A) Distribution of the number of alternative protein isoforms per gene. (B) The proteome-wide distribution of the number of affected protein regions observed per alternative isoform. (C) Distribution of the length of altered protein regions across the annotated proteome. These altered protein regions include cases of 1) deleted regions, 2) inserted regions, and 3) the region (in the reference isoform) in which one polypeptide subsegment is substituted for another. In other words, this distribution represents an aggregation of the distributions shown in panels D-F. (D-F) Distribution of altered region lengths for (D) deletions, (E) insertions, (F) substituted region in the reference isoform, and (G) substituted region in the alternative isoform. (H) Fraction of altered protein regions affected by insertions, deletions, and substitutions. (I) Comparison of the lengths of altered regions in the reference versus alternative isoforms for substitutions.