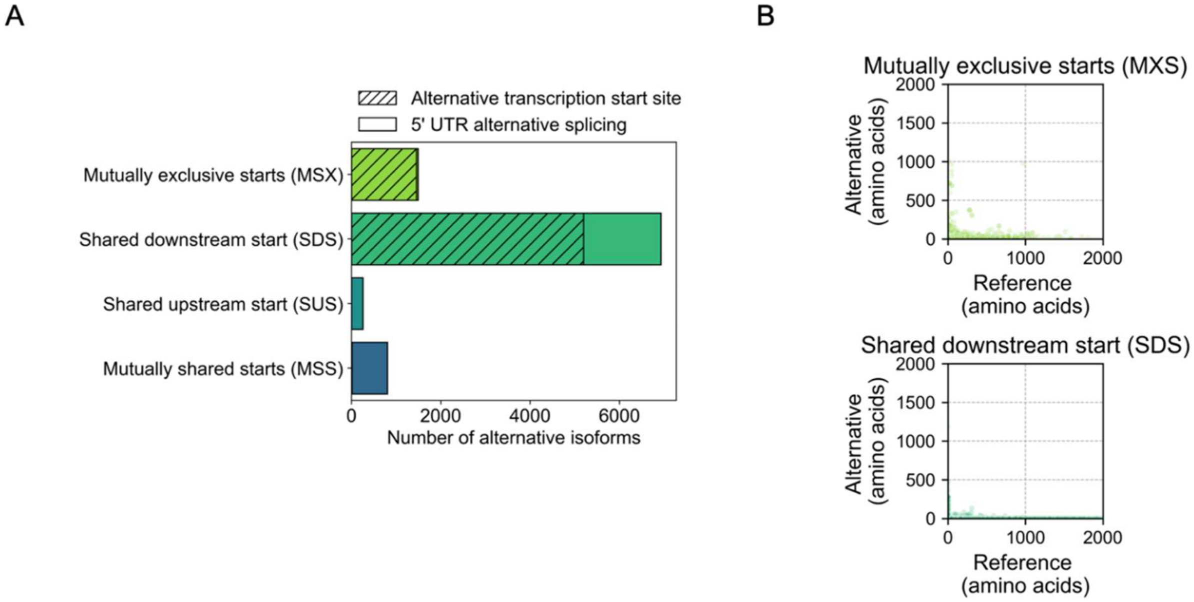

Supplementary Figure S13: Analysis of mechanisms underlying variable N-terminal proteins across the WTC-11 long-read predicted proteome.

(A) Distribution of the types of alternative N-terminal regions, classified based on presence and/or usage of the ATG start codon. Proportion of alternative N-terminal regions associated with alternative transcription start sites, as opposed to 5' UTR alternative splicing are marked using hatches. (B) Changes in N-terminal length for mutually exclusive starts (MXS) and shared downstream start (SDS) between reference and alternative isoforms.