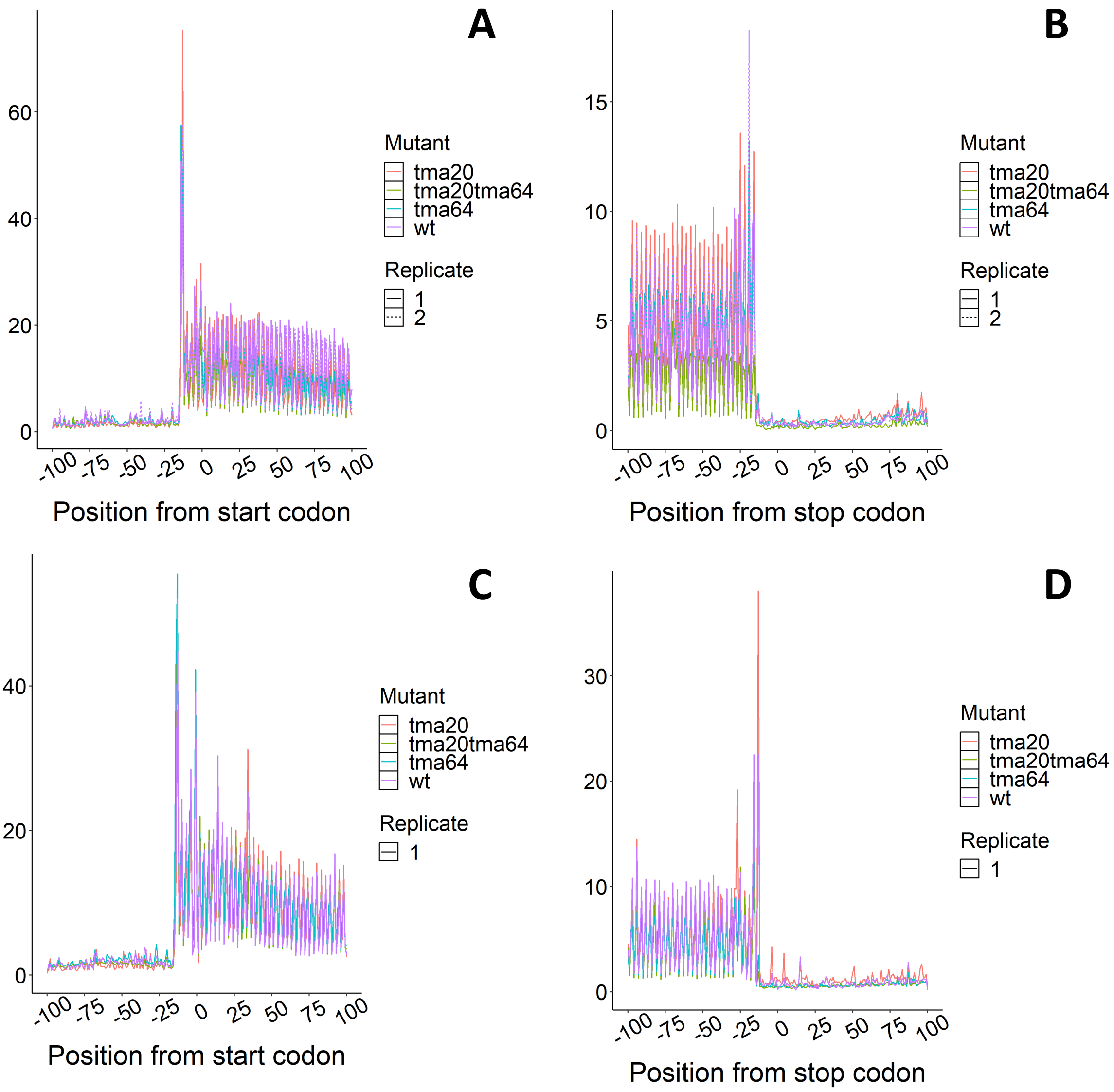

Fig. S1. Metagene profiles demonstrating aggregated coverage with 5’ ends of Ribo-Seq footprints in windows centered at start-codon (A, C) and stop-codon (B, D). Panels A and B: Ribo-Seq data of yeast strains maintained in YPD medium, panels C and D: Ribo-Seq data of yeast strains maintained in SD medium. X axis: relative location; Y axis: the coverage aggregated for all genes; for each gene, the values were normalized to the (total gene coverage / gene length).