Loss of mRNA surveillance pathways results in widespread protein aggregation

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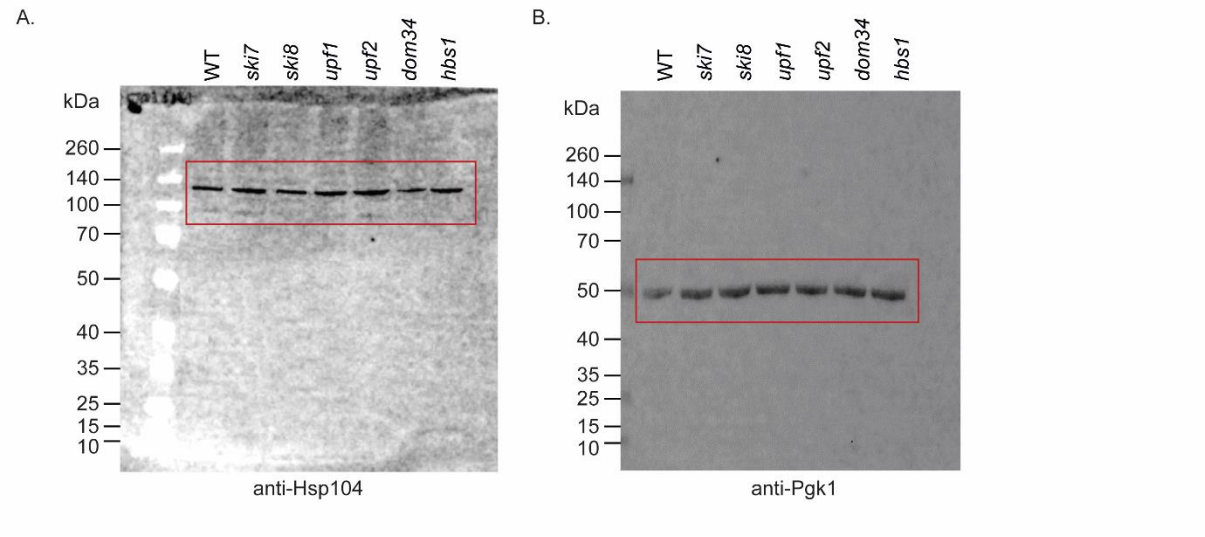
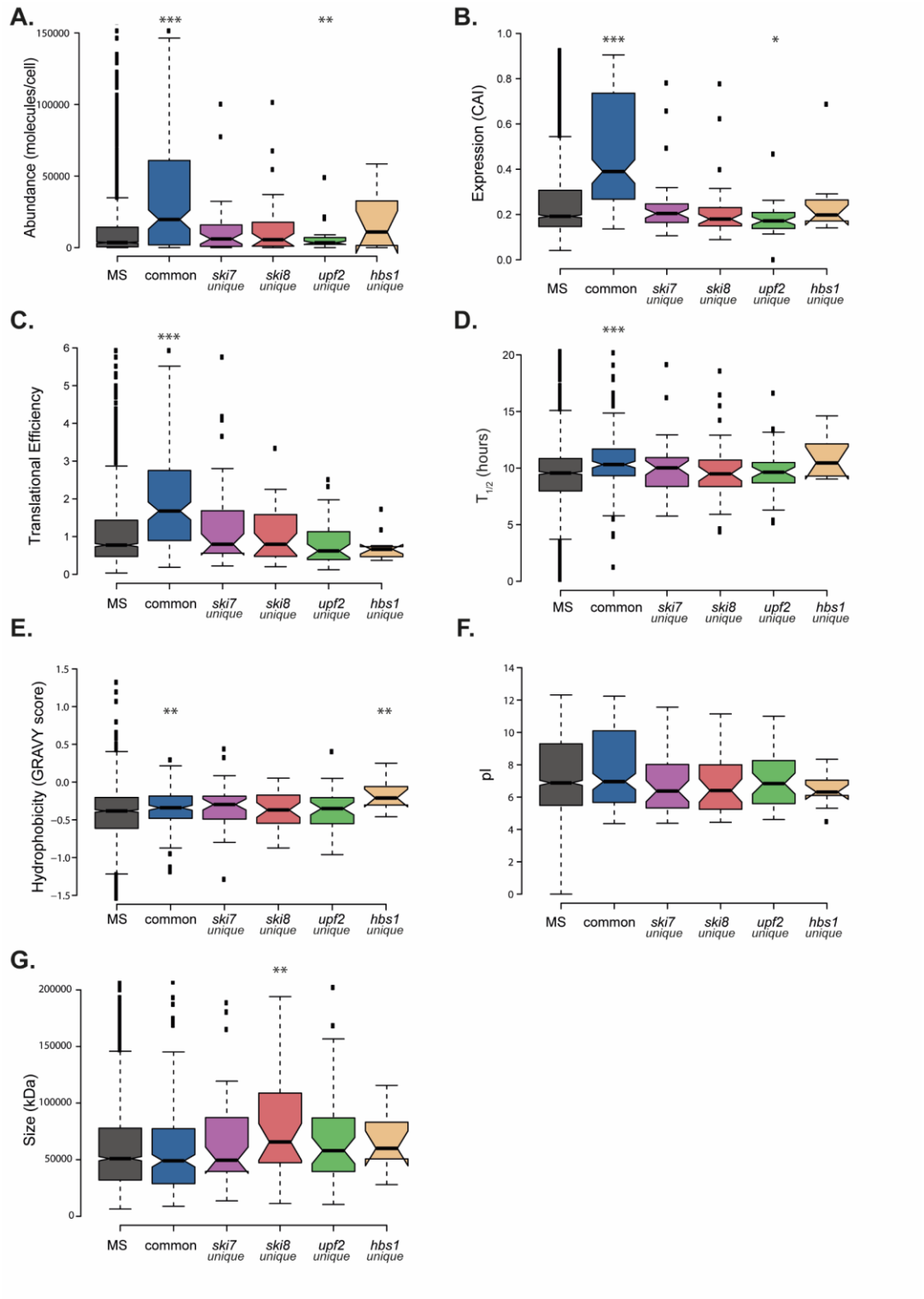


Supplementary Fig. 1. Western blot analysis of Hsp104 and PGK1 in mRNA surveillance mutants. The red boxes indicate the segments of the blots that were cropped and presented in Fig. 1C.



Supplementary Fig. 2. Analysis of physicochemical properties of aggregated proteins. Comparison of the proteins present in the Common-set (198 proteins) with proteins present in mRNA surveillance mutant unique sets (ski7, n=42; ski8, n=36; upf2, n=42; hbs1, n=11). Aggregated proteins were compared with a list of unaggregated proteins identified by mass-spectrometry referred to as the MS-set. **A.** The abundance of proteins (molecules/cell), **B.** The codon adaptation index (CAI), **C.** Translational efficiency, **D.** Protein stability (protein half-lives in hours), **E.** Grand average of hydrophobicity (GRAVY), **F.** Isoelectric points (pI) and **G.** protein sizes (kDa). Mann–Whiney U-tests were used to assess any statistical significances compared with the MS-set: *p < 0.05, **p < 0.01, *** p < 0.001.