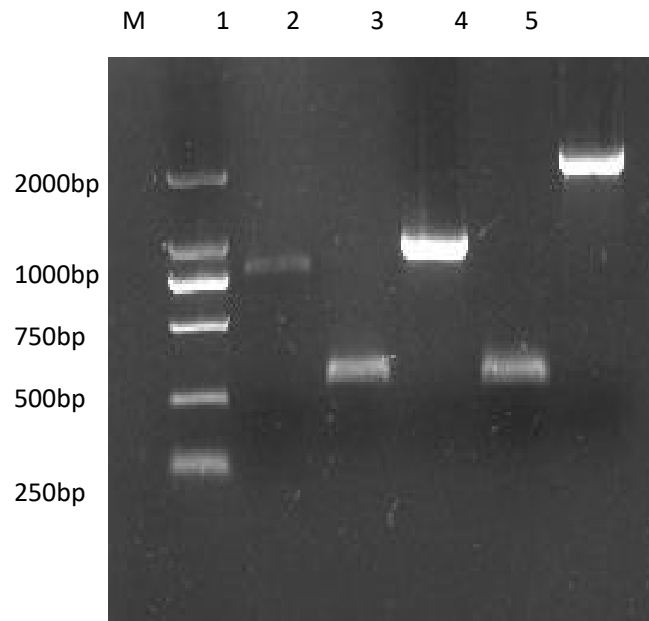
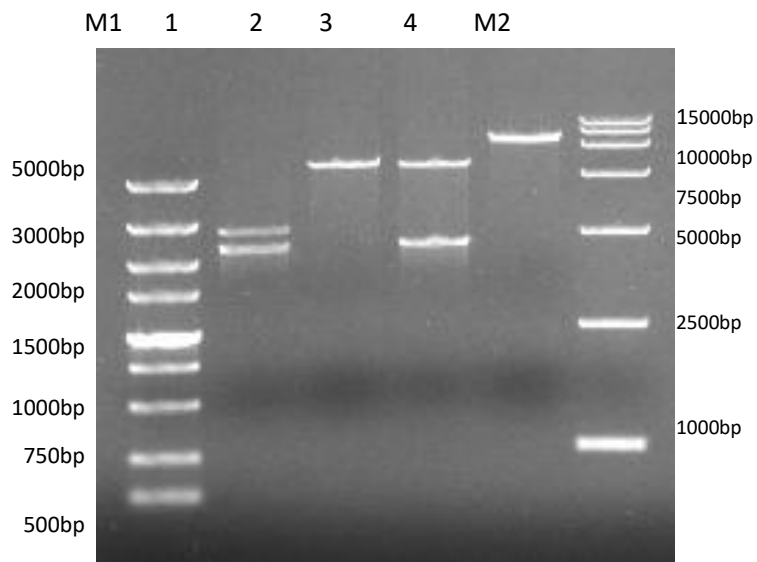


Fig. S1 Construction of PaXC expression box



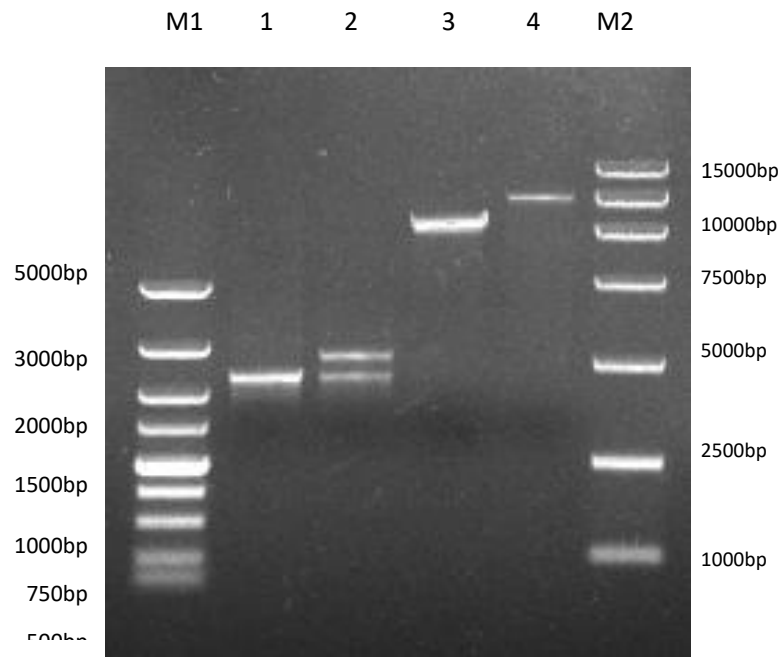
Lane M: 2000 DNA Marker; lane 1: 850 bp *PGK* sequence; lane 2: 254 bp α -factor sequence; lane 3: 984 bp *xynB* gene sequence; lane 4: 260 bp *CYC1* sequence; lane 5: 2365 bp PaXC sequence.

Fig. S2 Construction of plasmid pYES2-PaXC



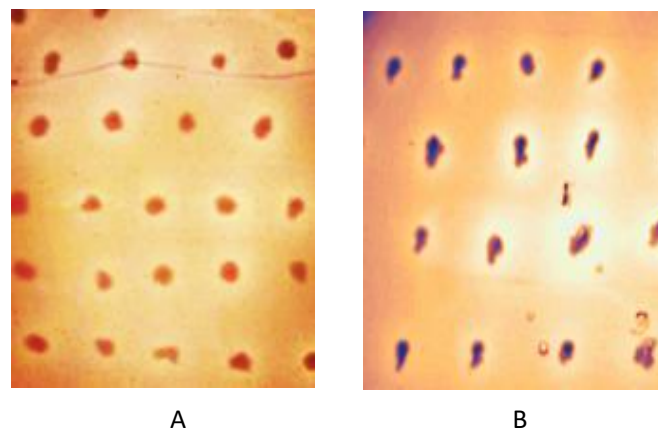
Lane M1: 5000 DNA Marker; lane 1: PMD19-T-PaXC double-enzyme digestion; lane 2: pYES2 double-enzyme digestion; lane 3: pYES2-PaXC double-enzyme digestion; lane 4: pYES2-PaXC single-enzyme digestion; lane M2: 15000 DNA Marker.

Fig. S3 Construction of plasmid pYES2-P α XC-rDNA



Lane M1: 15000 DNA Marker; lane 1: rDNA sequence amplification; lane 2: pMD19-T-rDNA single-enzyme digestion; lane 3: pYES2-P α XC single-enzyme digestion; lane 3: pYES2-P α XC-rDNA single-enzyme digestion; lane M2: 15000 DNA Marker.

Fig. S4 Screening of *S. cerevisiae* strains



(A) Recombinant *S. cerevisiae* strain pYES2-P α XC. (B) Recombinant *S. cerevisiae* strain

pYES2-PaXC-rDNA.

Fig. S5 Detection of *xynB* copy number in *S. Cerevisiae* INVSc1-pYES2-PaXC-rDNA transformants by ddPCR.

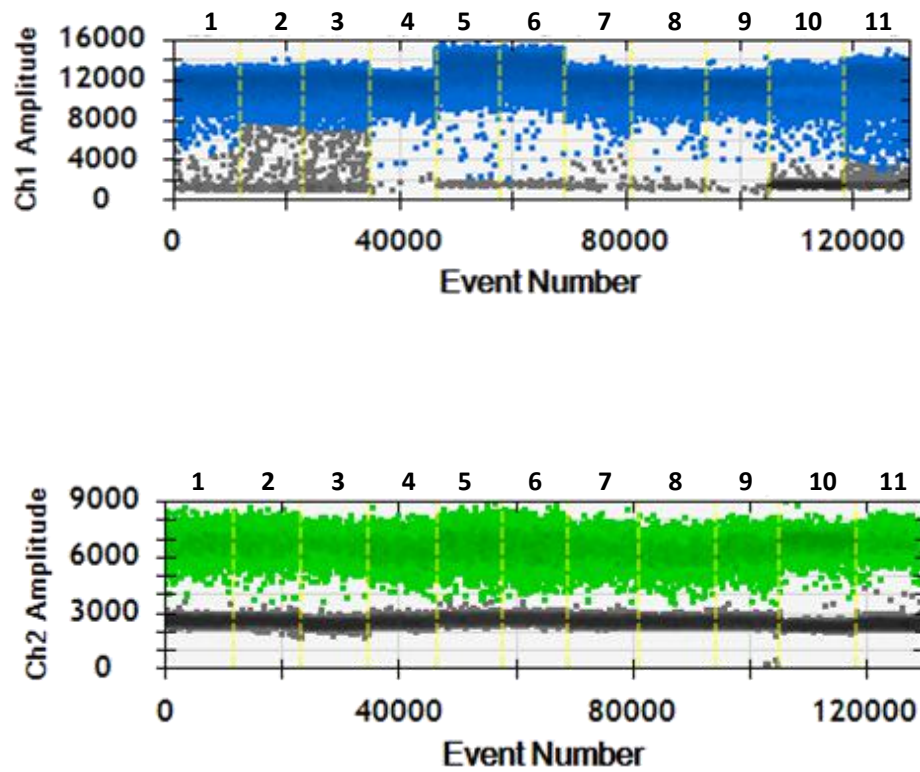
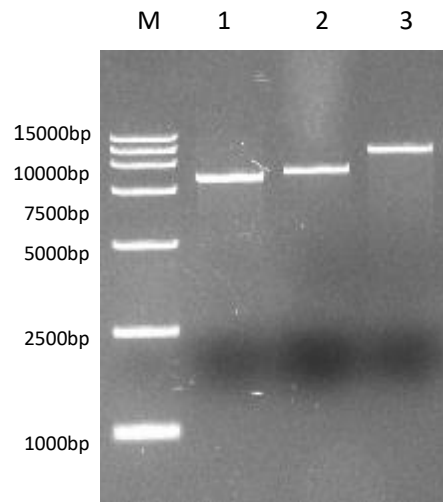


Fig. S6 Construction of plasmid pYES6-PGK-HAC1



Lane M: 15000 DNA Marker; lane 1: pYES6 double-enzyme digestion; lane 2: pYES-*PGK* double-enzyme digestion; lane 3: pYES6-*PGK-HAC1* single-enzyme digestion.

Fig. S7 Screening of *S. cerevisiae* *HAC1* overexpression strains

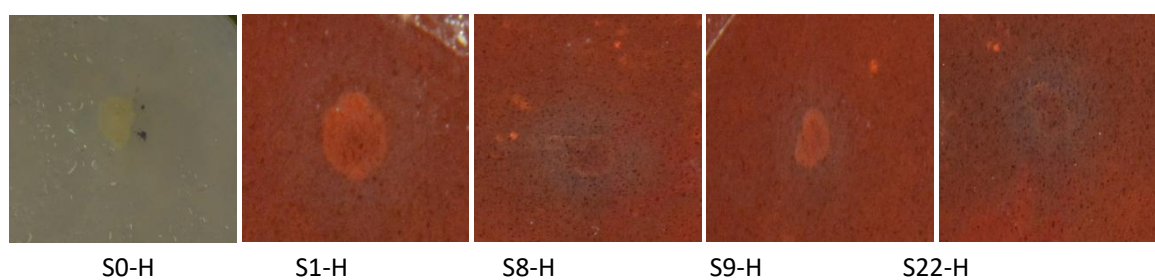


Fig. S8 Comparative analysis of protein folding-associated genes in strains S0 and S0-H at 24 h (A), 48 h (B), and 72 h (C) post-inoculation.

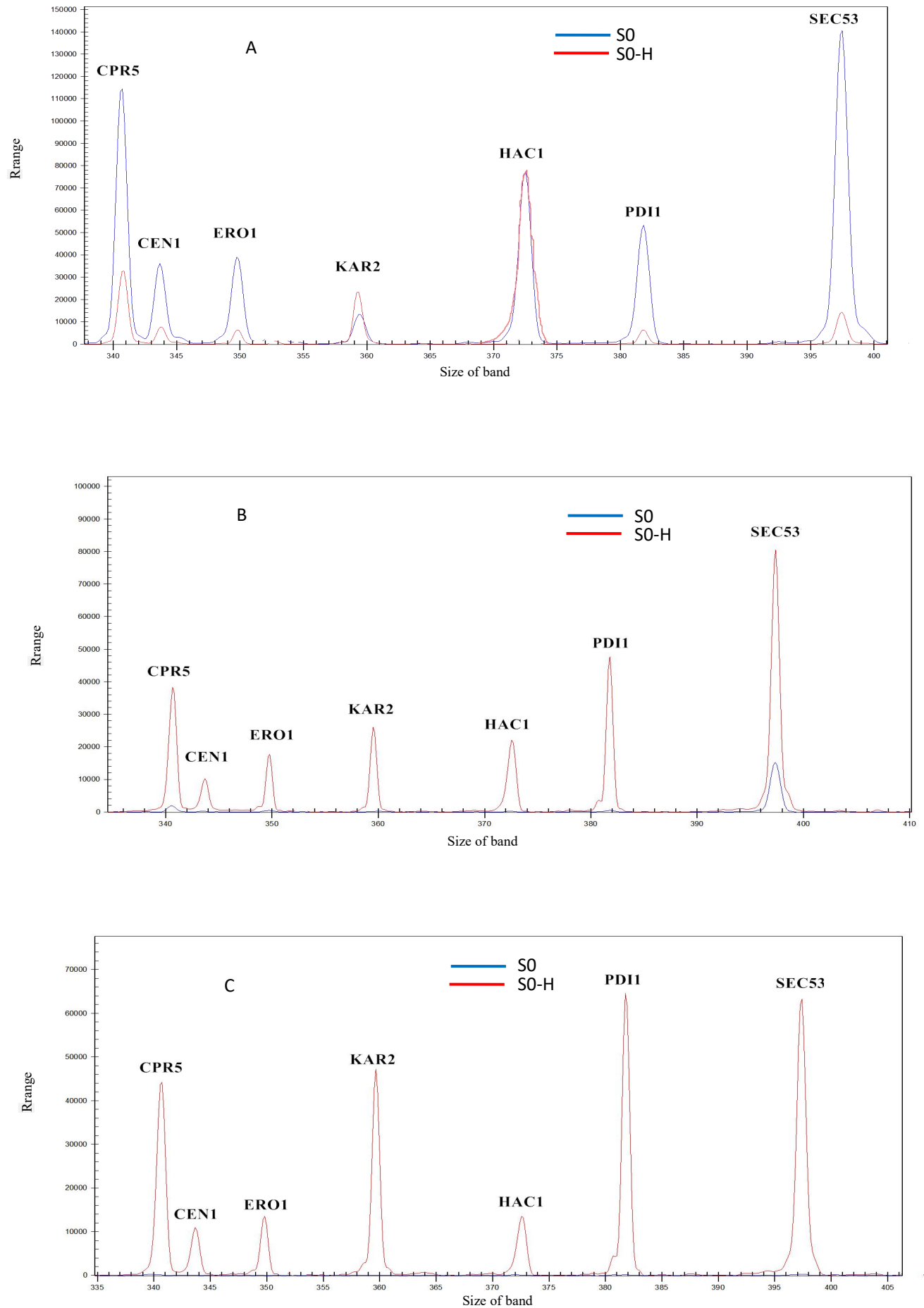


Fig. S9 Comparative analysis of protein folding-associated genes in strains S8 and S8-H at 24 h (A), 48 h (B), and 72 h (C) post-inoculation.

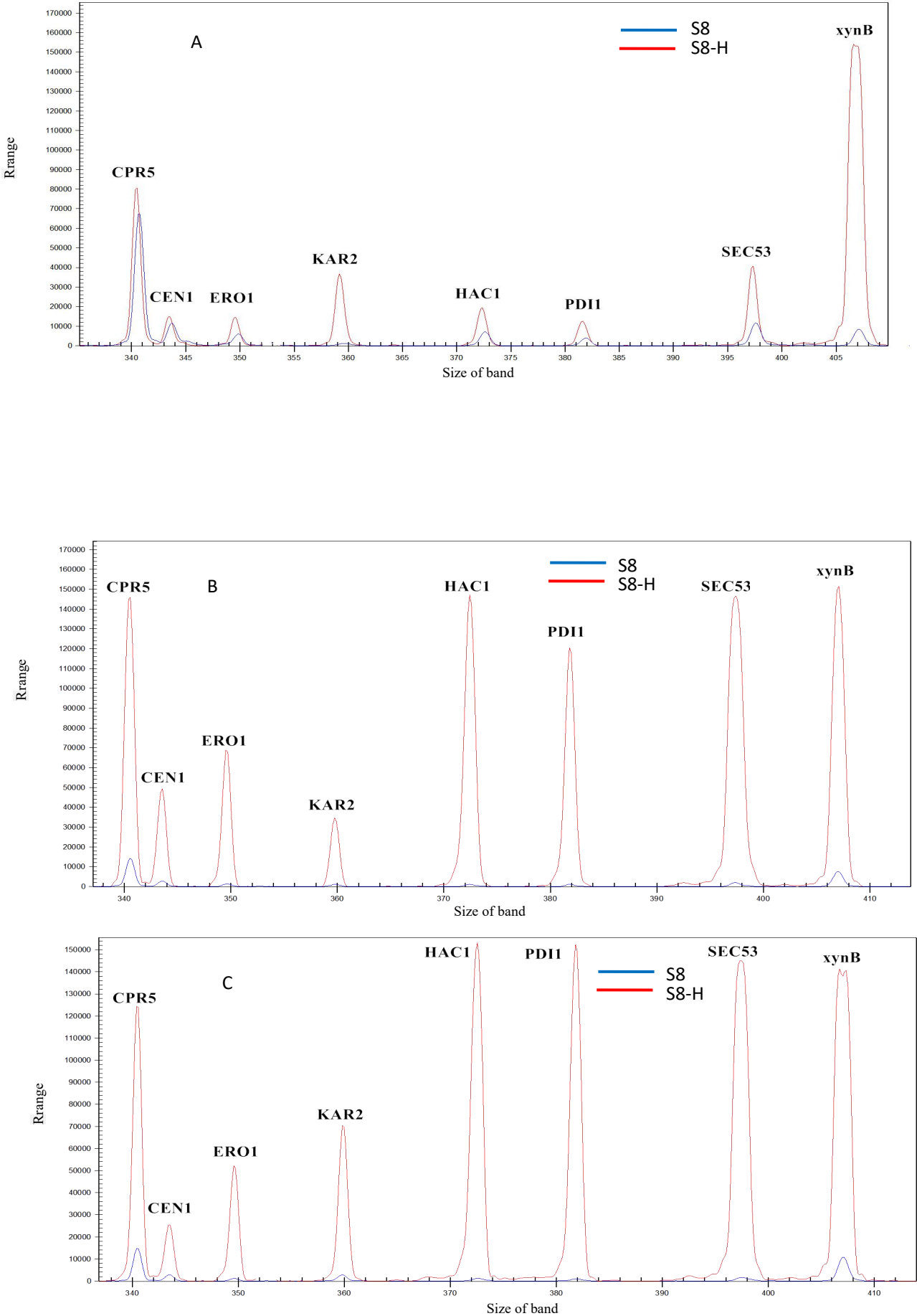


Fig. S10 Sequential changes in protein folding-associated genes in strain S0-H.

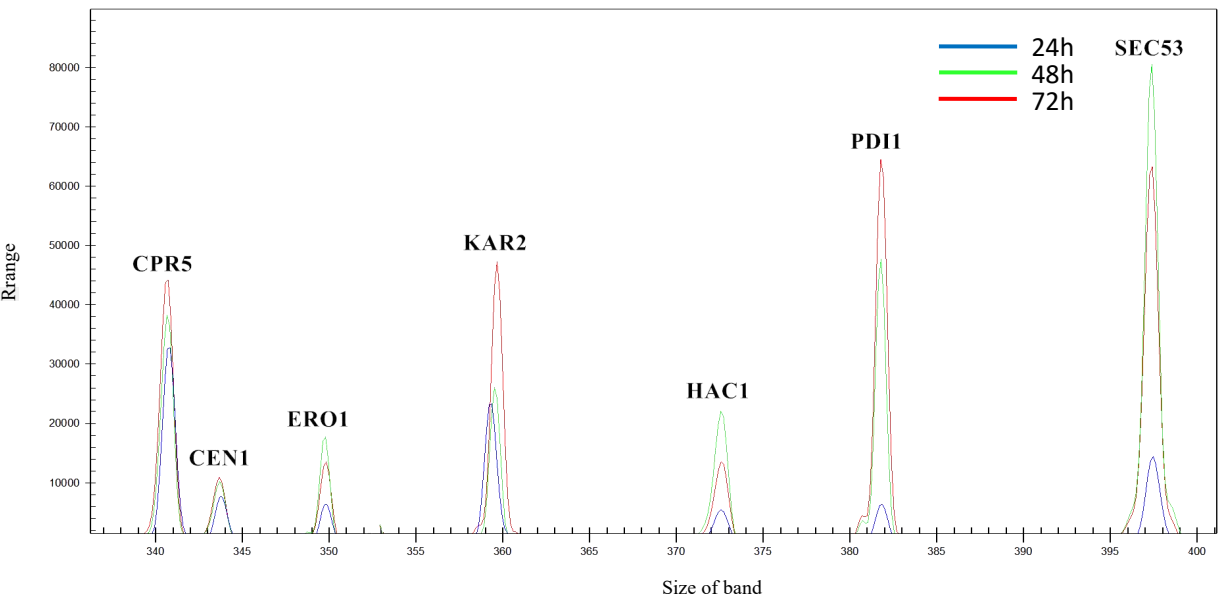


Fig. S11 Sequential changes in protein folding-associated genes in strain S1-H.

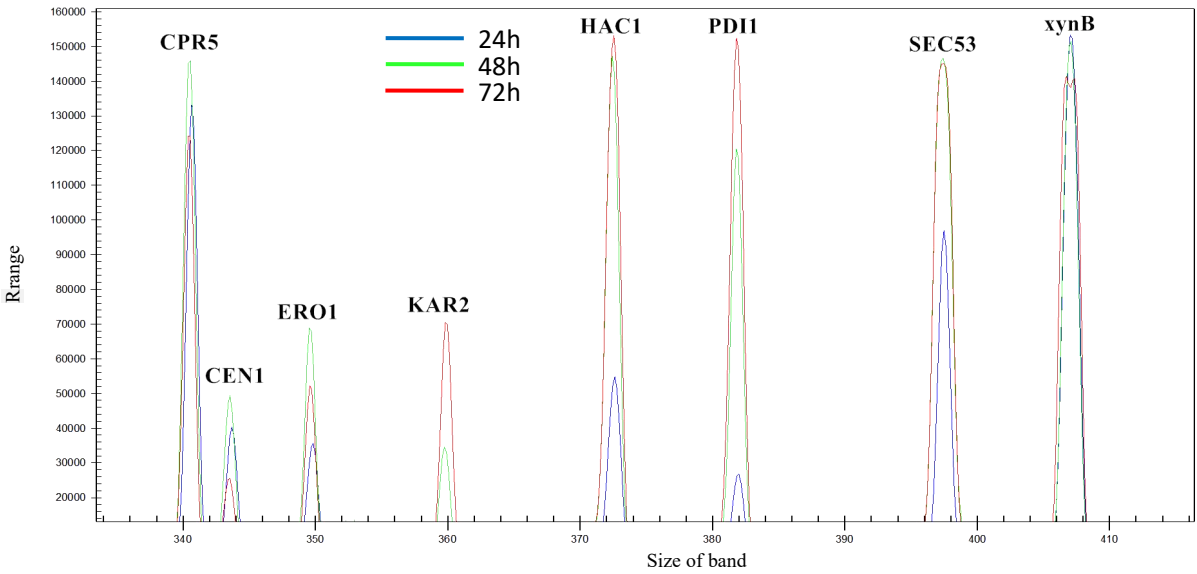


Fig. S12 Sequential changes in protein folding-associated genes in strain S8-H.

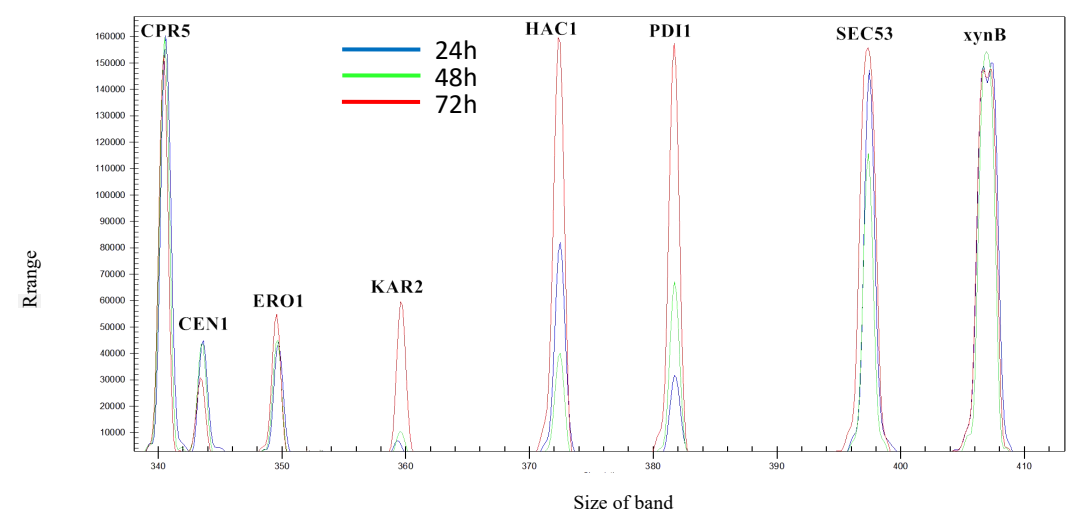


Fig. S13 Comparative analysis of protein folding-associated genes in strains S22 and S22-H.

