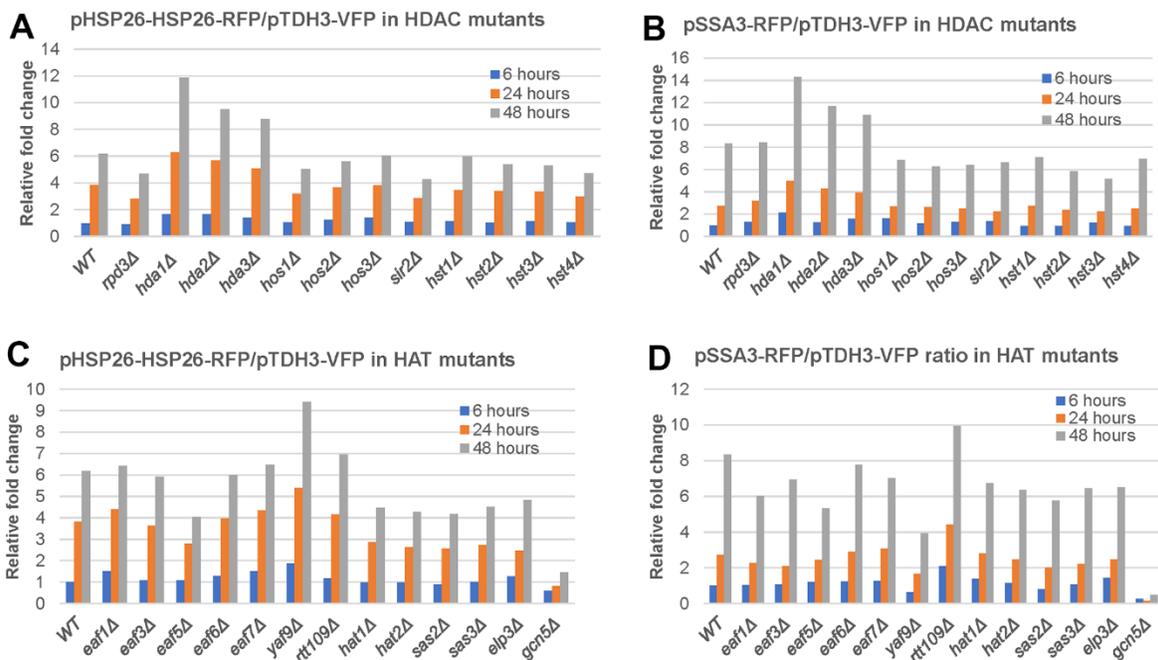
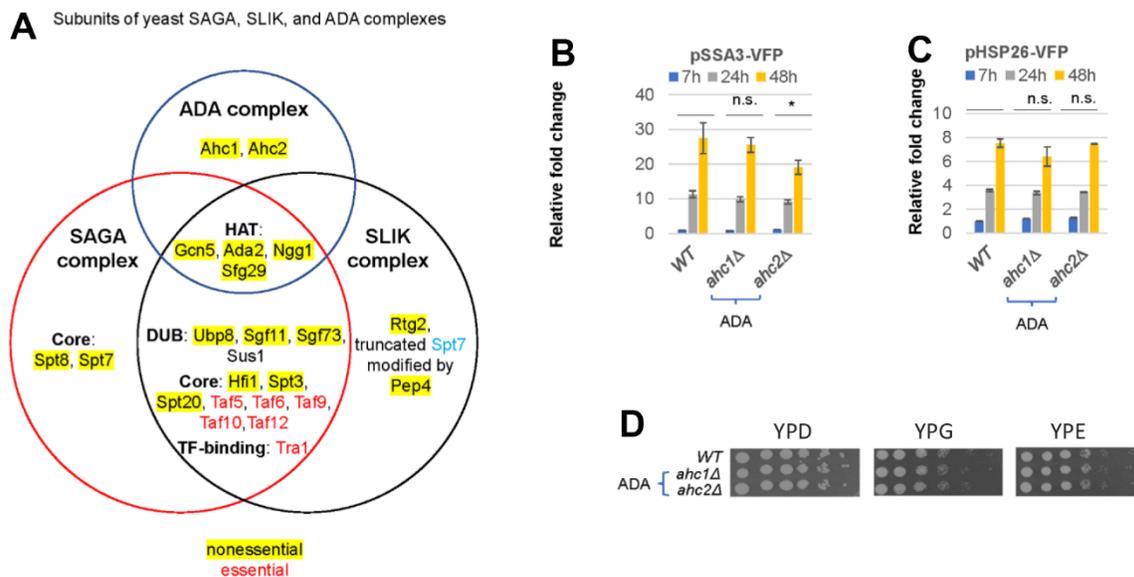


**SUPPLEMENTARY FIGURES**

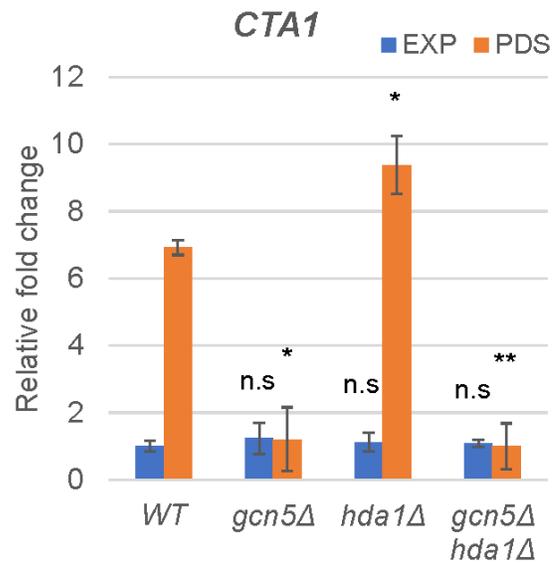
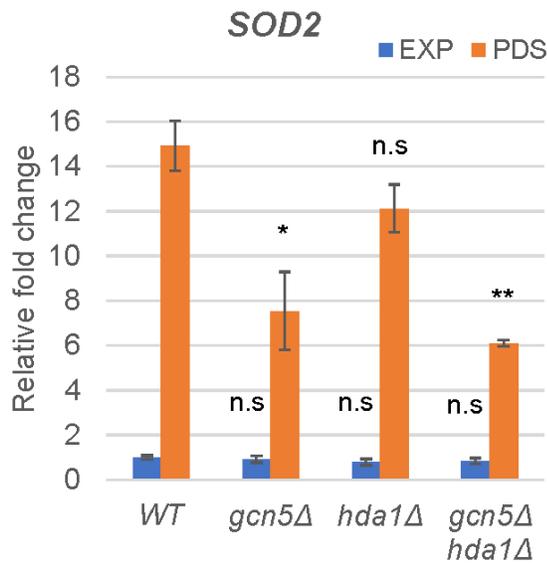


**Supplementary Figure 1.** Relative pSSA3-RFP and pHSP26-HSP26-RFP levels in HDAC (A, B) and HAT (C, D) mutants. The mean RFP fluorescence from 20,000 cells was normalised to that of the pTDH3-VFP at each time point to correct for cell growth differences.



**Supplementary Figure 2.** (A) Schematic illustration of the SAGA/SLIK/ADA complexes; (B, C) Relative levels of pSSA3-VFP (B) and pHSP26-VFP (C) in the ADA-specific mutants; (D) Spotting assays of cell growth on YPD (2% glucose), YPG (3% glycerol) and YPE (1% Ethanol). Error bars represent standard deviation calculated from biological triplicates. HAT, histone acetyltransferase module; DUB, deubiquitinase module; Core, Core module; SLIK, SAGA-like complex. The significance of difference between WT and mutants over all time points was revealed by two-factor ANOVA analysis (\*\*\*:  $p < 0.001$ , \*\*:  $0.001 < p < 0.01$ , \*:  $0.01 < p < 0.05$  and n.s.:  $p > 0.05$ ).





**Supplementary Figure 5. Relative levels of *SOD2* and *CTA1* transcripts.** The raw read counts of either gene were normalised to that of *ACT1* in the corresponding samples, followed by normalisation to the expression level in *WT* at EXP to calculate relative fold change for comparison among different strains. Error bars represent standard deviation calculated from biological triplicates. Student's t-test was performed to reveal the significance of differences (\*\*\*: p-value < 0.001, \*\*: p-value < 0.01, \*: p-value < 0.05, and n.s.: p-value > 0.05). Abbreviation: EXP, exponential phase; PDS, post-diauxic shift phase.