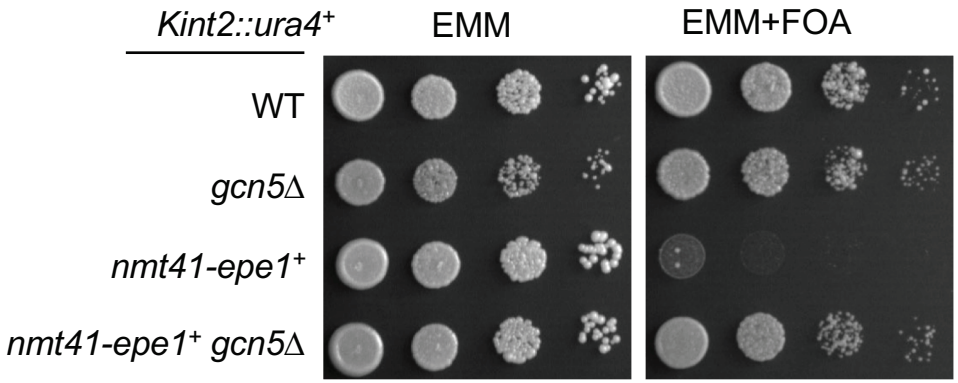
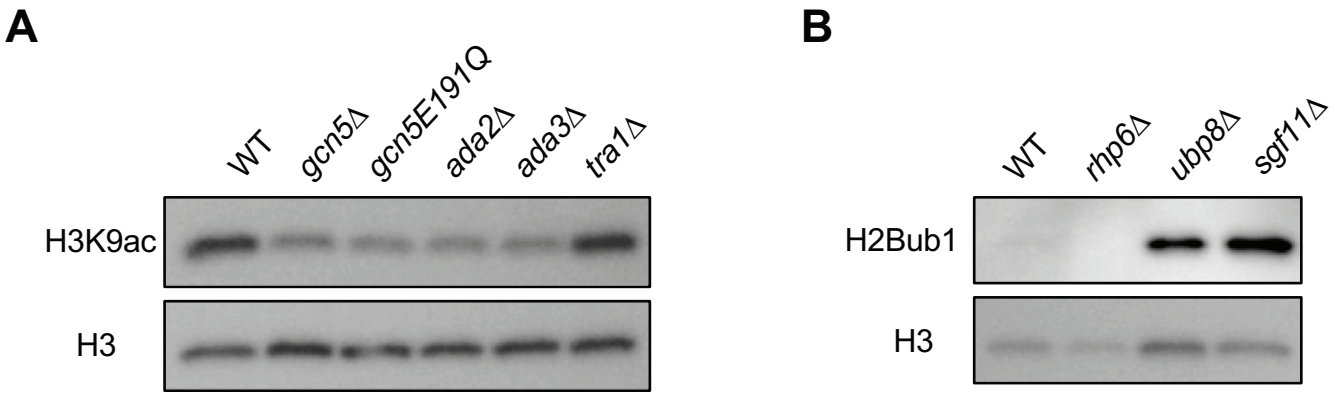
| | Gene deletion | Rescue score |
|---|---|---|
| HAT | *gcn5*Δ | 2 |
| | *ada2*Δ | 0 |
| | *ada3*Δ | 2 |
| | *sgf29*Δ | 0 |
| | *tra1*Δ | 2 |
| DUB | *ubp8*Δ | 0 |
| | *sgf73*Δ | 0 |
| | *sgf11*Δ | 0 |
| | *sus1*Δ | Not in Library |
| SPT | *ada1*Δ | Not in Library |
| | *spt8*Δ | 0 |
| | *spt3*Δ | 0 |
| | *spt7*Δ | Not in Library |
| | *spt20*Δ | Not in Library |
| TAF | *taf5*Δ | Essential Gene |
| | *taf6*Δ | Essential Gene |
| | *taf9*Δ | Essential Gene |
| | *taf10*Δ | Essential Gene |
| | *taf12*Δ | Essential Gene |

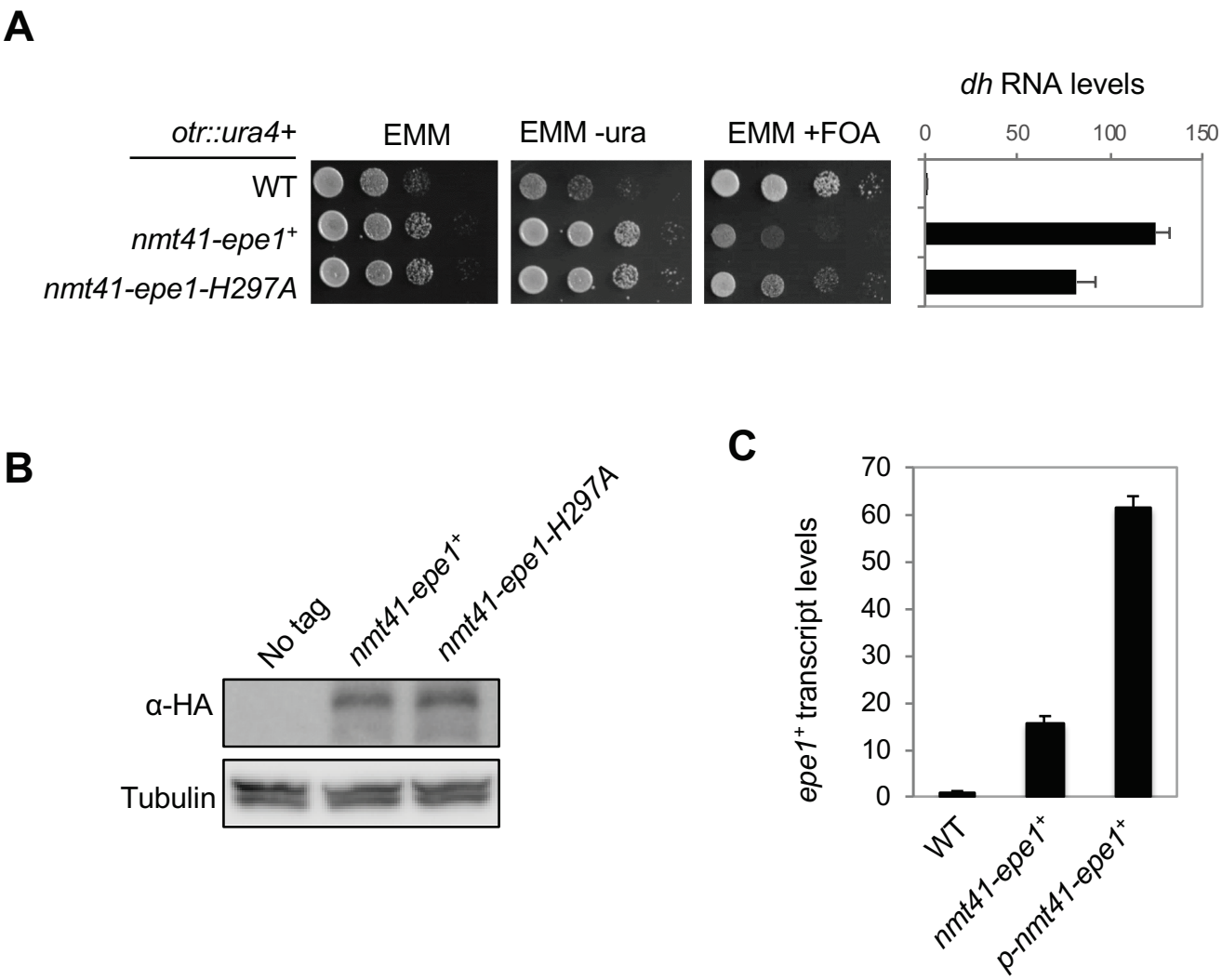
Supplementary Figure 1. Summary of SAGA subunits as suppressors of Epe1 overexpression from the screen with deletion library. Colony size were assigned scores between 0 and 3, with 0 indicates no growth and 3 indicates full growth.



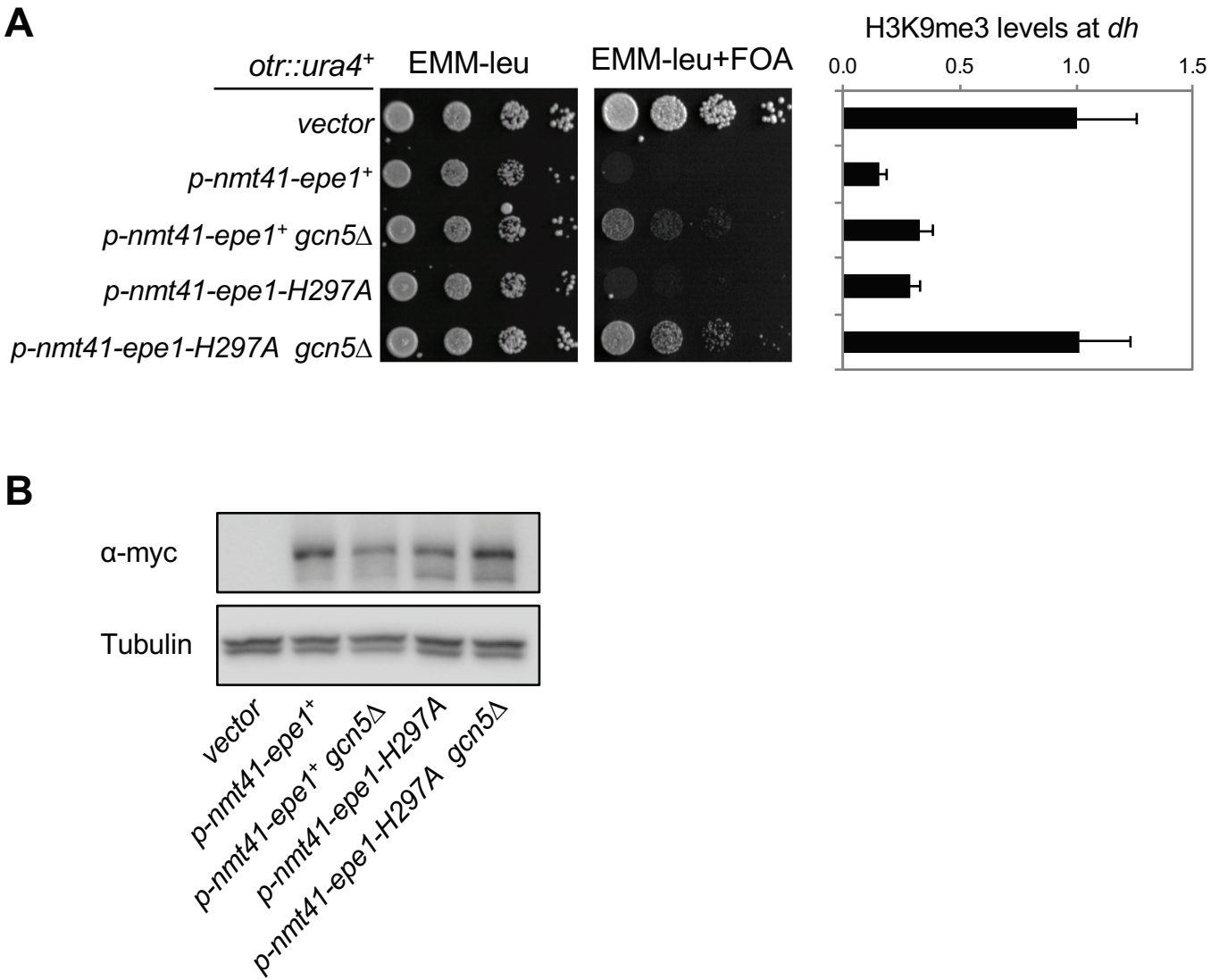

Supplementary Figure 2. *gcn5*Δ also rescues silencing defects at the mating-type region caused by Epe1 overexpression. Ten-fold serial dilution analyses of indicated yeast strains were grown on indicated media to measure the expression of the *Kint2::ura4*$^{+}$ reporter gene.



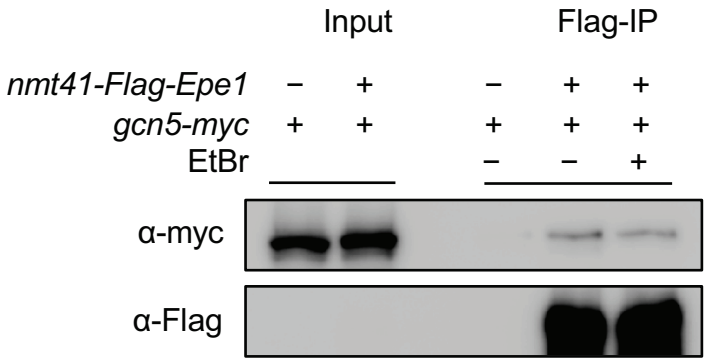

Supplementary Figure 3. Western blot analyses of H3K9ac (A) and H2Bub1 (B) levels of indicated yeast strains. H3 serves as a loading control.



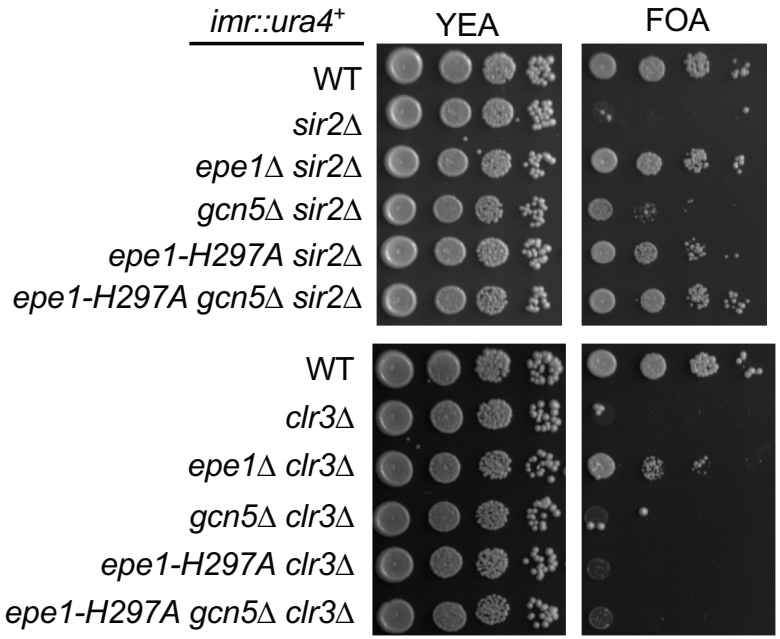

Supplementary Figure 4. Analysis of the Epe1-H297A mutant. (A) Left, ten-fold serial dilution analyses of indicated yeast strains were grown on indicated media to measure the expression of the *otr::ura4*$^{+}$ reporter gene. Right, qRT-PCR analysis of *dh* transcript levels, normalized to *act1*$^{+}$. (B) Western blot analyses to measure the levels of HA tagged Epe1 and Tubulin in indicated yeast strains. (C) qRT-PCR analysis of *epe1*$^{+}$ transcript levels, normalized to *act1*$^{+}$.



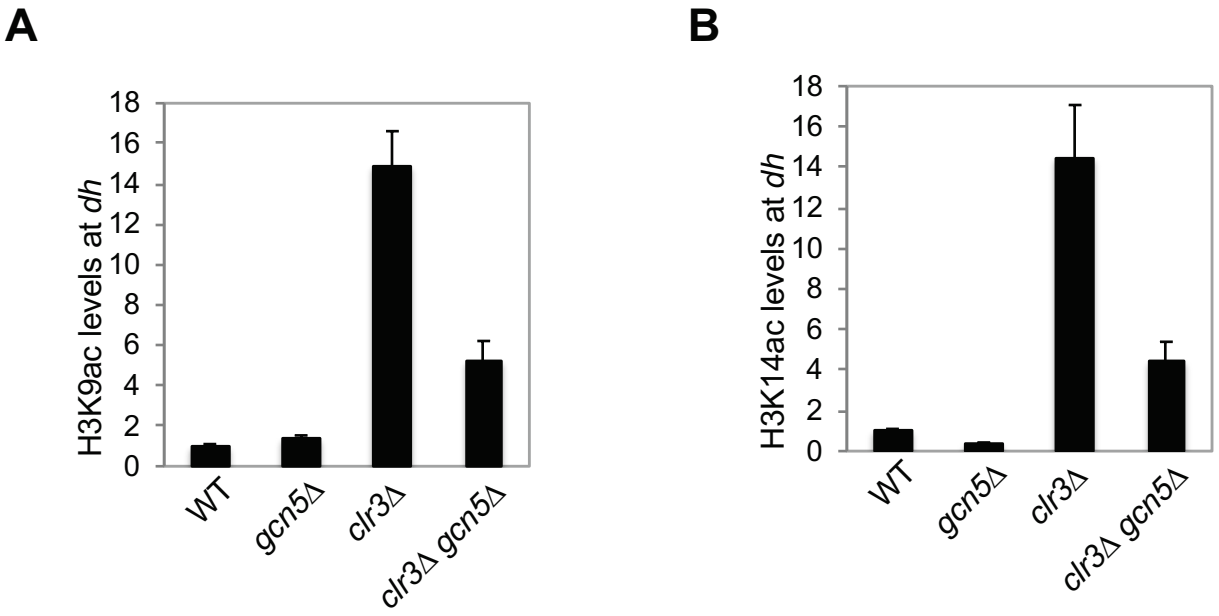

Supplementary Figure 5. *gcn5*Δ rescues silencing defects associated with overexpression of wild type Epe1 or an Epe1 demethylase mutant. Epe1 and Epe1-H297A are overexpressed from plasmids and under the control of the *nmt41* promoter. (A) Left, ten-fold serial dilution analyses of indicated yeast strains were grown on indicated media to measure the expression of the *otr::ura4*$^+$ reporter gene. Right, ChIP analyses of H3K9me3 levels at *dh*, normalized to *act1*$^+$. (B) Western blot analyses to measure the levels of myc-tagged Epe1 and Tubulin in indicated yeast strains.



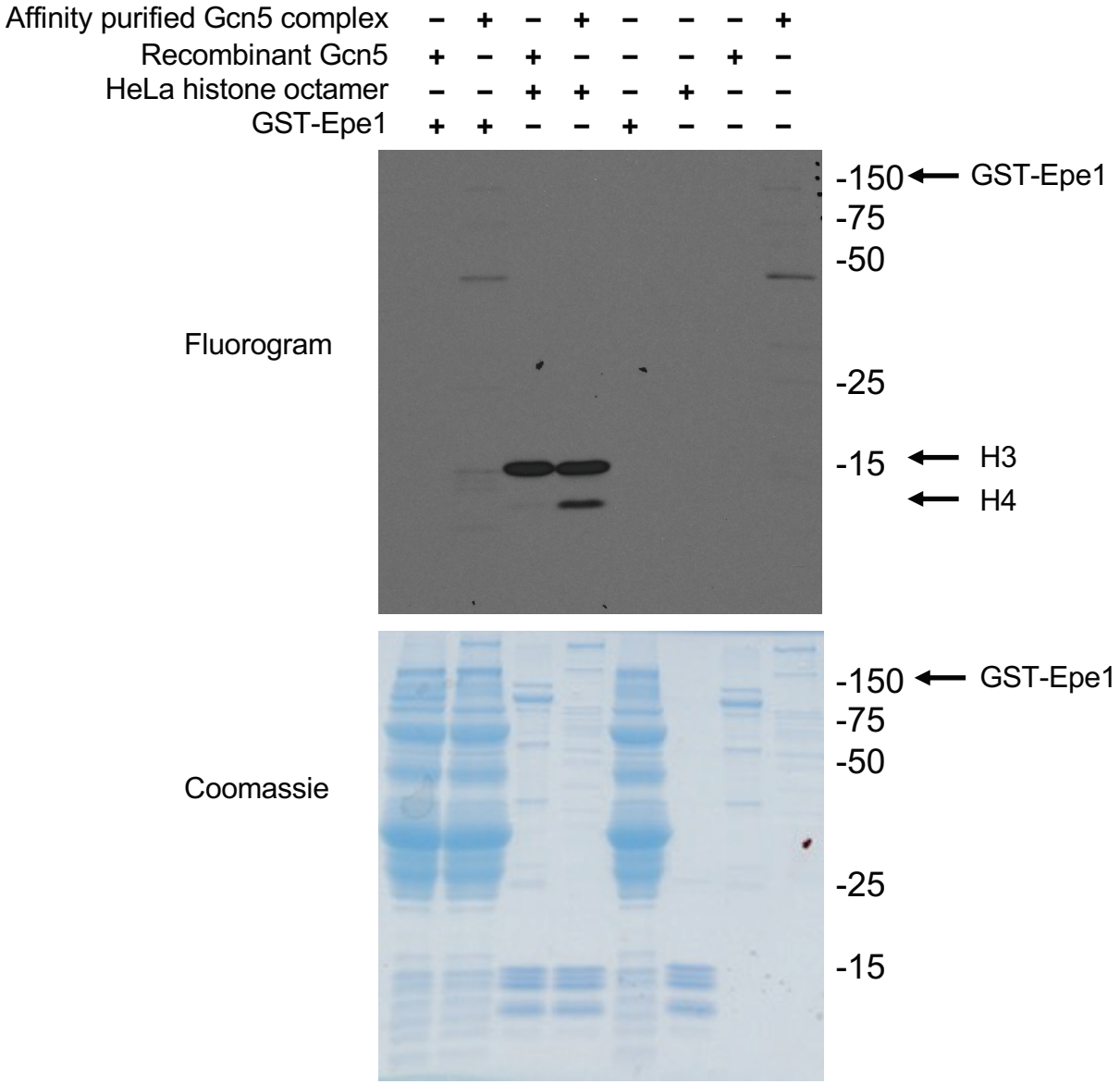

Supplementary Figure 6. The interaction between Epe1 and Gcn5 is not bridged by DNA. Co-immunoprecipitation analyses of Epe1 and Gcn5 either with or without treatment of the lysate with Ethidium Bromide (EtBr) to disrupt protein-DNA interactions.



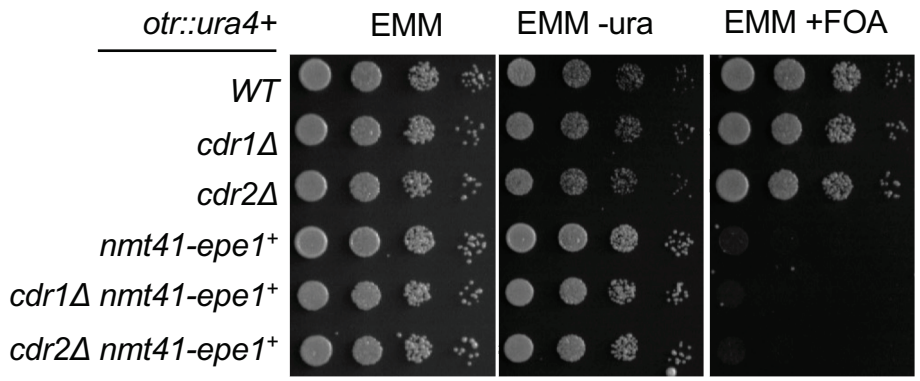

Supplementary Figure 7. Ten-fold serial dilution analyses of indicated yeast strains were grown on indicated media to measure the expression of the *imr::ura4*$^{+}$ reporter gene.



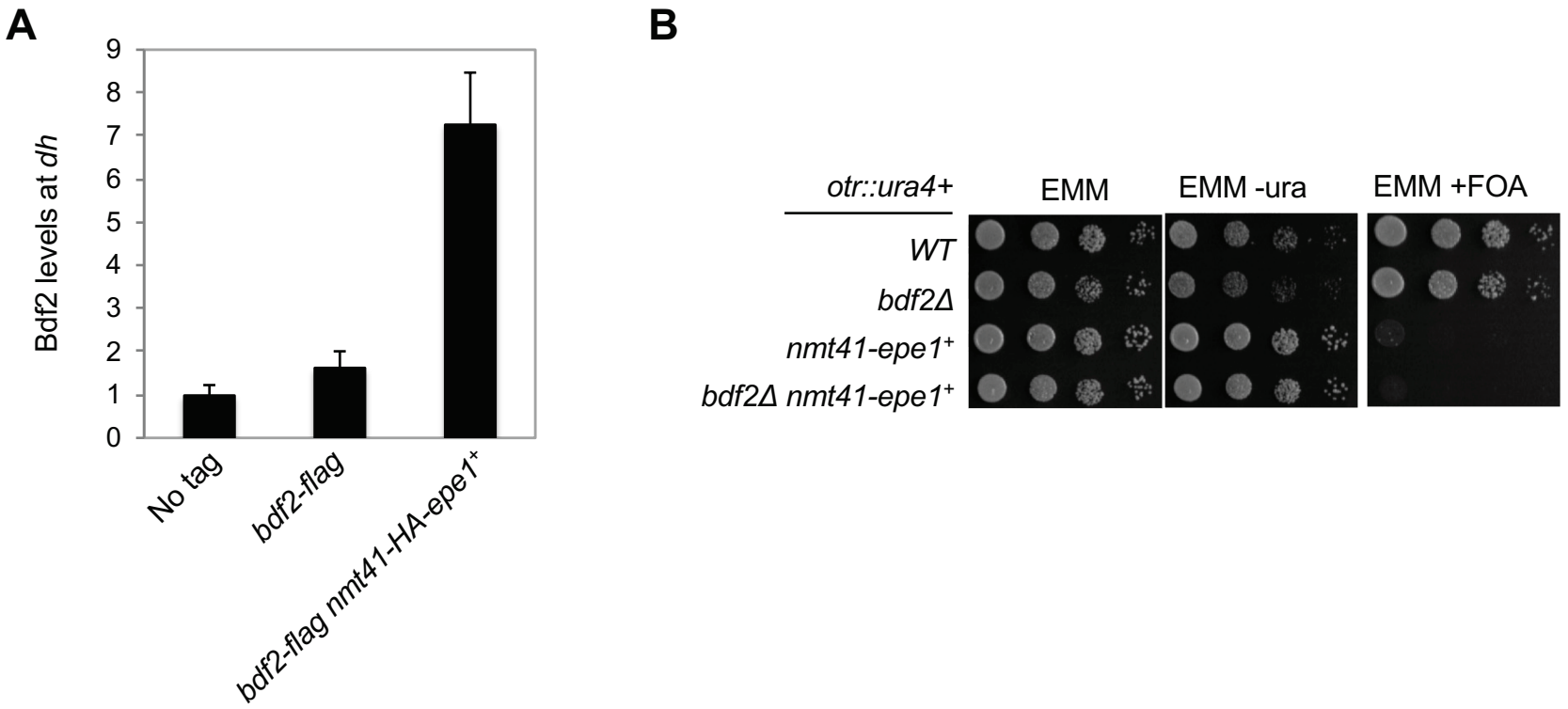

Supplementary Figure 8. ChIP analyses of H3K9ac and H3K14ac levels at pericentric *dh* repeat shown as ChIP/Input, normalized to WT.




Supplementary Figure 9. In vitro histone acetyltransferase assay using purified Gcn5 complex or recombinant Gcn5, with either recombinant GST-Epe1 or HeLa histones as substrates. Top, Fluorogram to measure the incorporation of $^{3}H$ labelled acetyl-CoA. Bottom, Coomassie stain to show proteins.




Supplementary Figure 10. Ten-fold serial dilution analyses of indicated yeast strains were grown on indicated media to measure the expression of the *otr::ura4*$^{+}$ reporter gene.




Supplementary Figure 11. Bdf2 and the effects of Epe1 overexpression on heterochromatin. (A) ChIP analyses of Bdf2 levels at pericentric *dh* repeats, normalized to *act1*$^+$. (B) Ten-fold serial dilution analyses of indicated yeast strains were grown on indicated media to measure the expression of the *otr::ura4*$^+$ reporter gene.