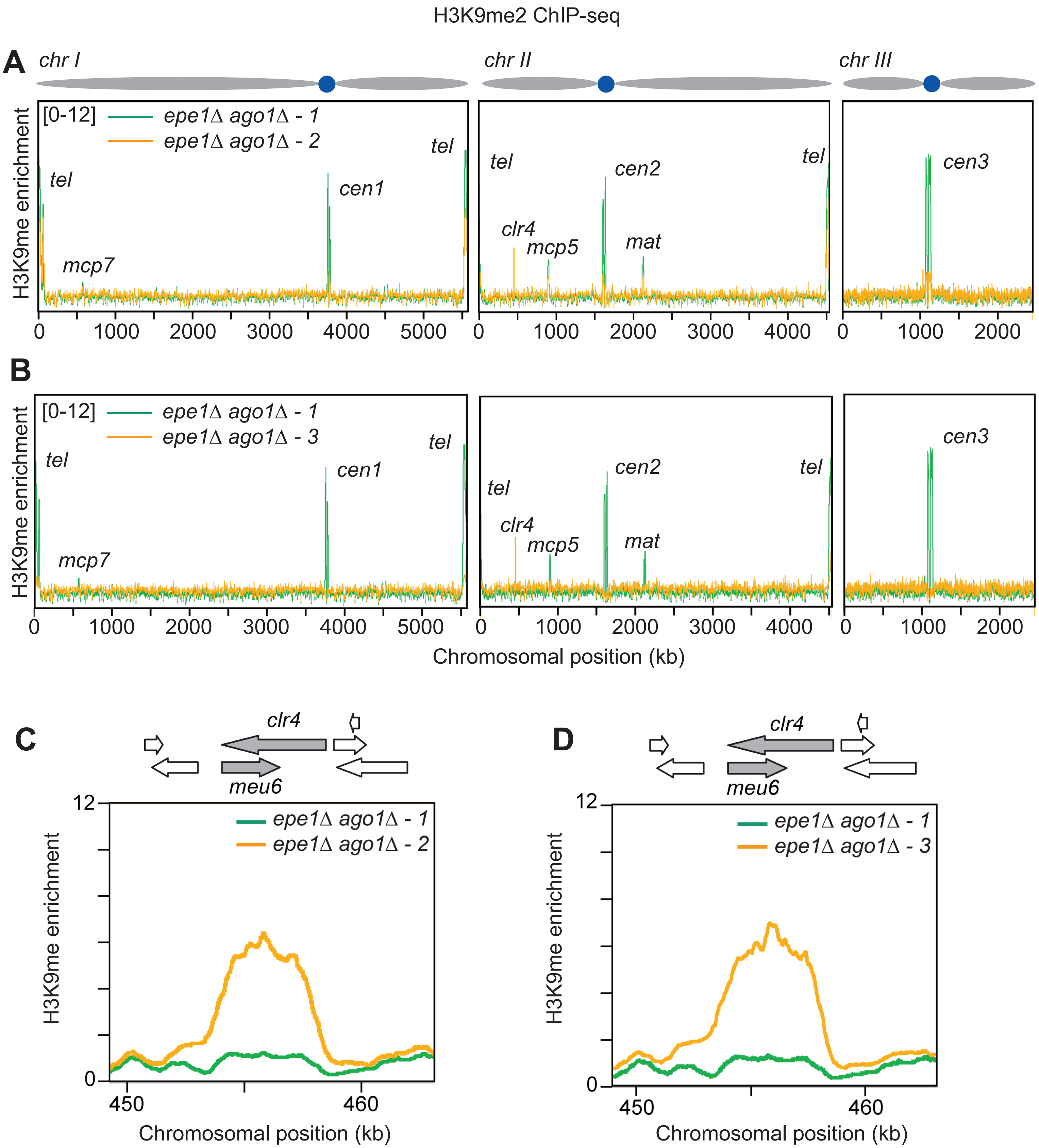
**Supplemental Figure S10.**



**Supplemental Figure S10. *epe1*Δ *ago1*Δ strains can adaptively silence the *clr4*$^+$ locus. A-B)** Whole genome H3K9me2 enrichment plots for two independent *epe1*Δ *ago1*Δ strains that accumulated H3K9me2 over the *clr4*$^+$ locus, *epe1*Δ *ago1*Δ*-2* (**A**) and *epe1*Δ *ago1*Δ*-3* (**B**) (in orange), compared to a isolate with normal distribution of H3K9me2 across the genome, *epe1*Δ *ago1*Δ*-1* (in green). **C-D)** Genome browser image of the enrichment of H3K9me2 over *clr4*$^+$ locus in *epe1*Δ *ago1*Δ*-2* (**C**) and *epe1*Δ *ago1*Δ*-3* (**D**).