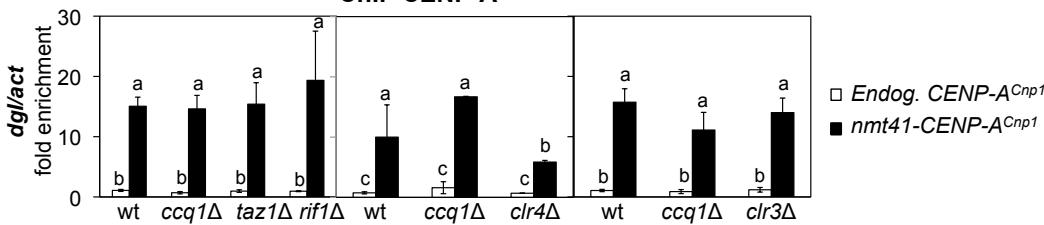


**Figure S5**

**A**

*Cen-otr-dg*

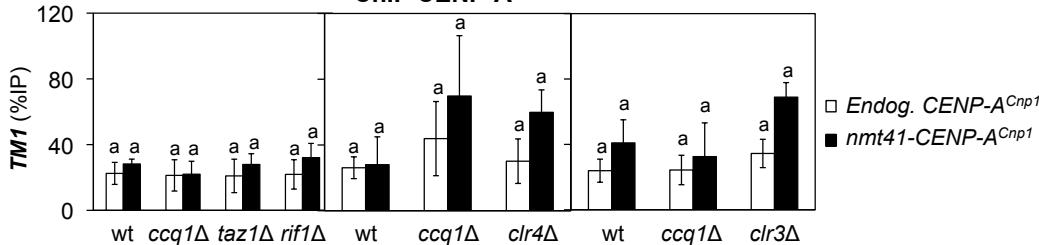
ChIP CENP-A<sup>Cnp1</sup>



**B**

*Cen-cnt1*

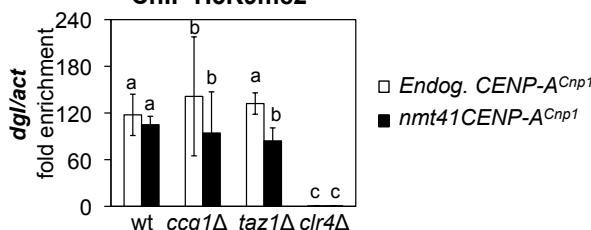
ChIP CENP-A<sup>Cnp1</sup>



**C**

*Cen-otr-dg*

ChIP H3K9me2



**Figure S5. Enrichment of CENP-A<sup>Cnp1</sup>, CENP-C<sup>Cnp3</sup> and H3K9me2 at centromeres in wild-type and mutant cells carrying the Ch16 *ura4+*-Tel minichromosome derivatives.**

ChIP-qPCR of CENP-A<sup>Cnp1</sup> levels on centromeric otr *dgl* repeats (**A**) and at TM1 in the central region of centromere 1 (**B**) in wild-type (wt) and mutant cells (*ccq1Δ*, *taz1Δ*, *rif1Δ*, *clr4Δ* and *clr3Δ*) carrying the Ch16-72 (*ura4+*-Tel) minichromosome and expressing endogenous (Endog. CENP-A<sup>Cnp1</sup>) or additional (*nmt41*-CENP-A<sup>Cnp1</sup>) CENP-A<sup>Cnp1</sup> levels. (**C**) ChIP-qPCR of H3K9me2 levels on centromeric otr *dgl* repeats in wild-type (wt) and mutant cells (*ccq1Δ*, *taz1Δ*, and *clr4Δ*) with the same configuration. Enrichment on *dgl* was normalized the signal obtained for the gene encoding actin (*act1+*). Enrichment at TM1 is reported as the percentage of immunoprecipitated chromatin (%IP). Error bars indicate S.D. from 3 biological replicates. Mean values marked with different letter (a, b or c) indicate results significantly different from each other, as established by One Way ANOVA and Holm-Sidak test for multiple comparison ( $P<0.01$  in (A) and (B) or  $P<0.05$  in (C)).