

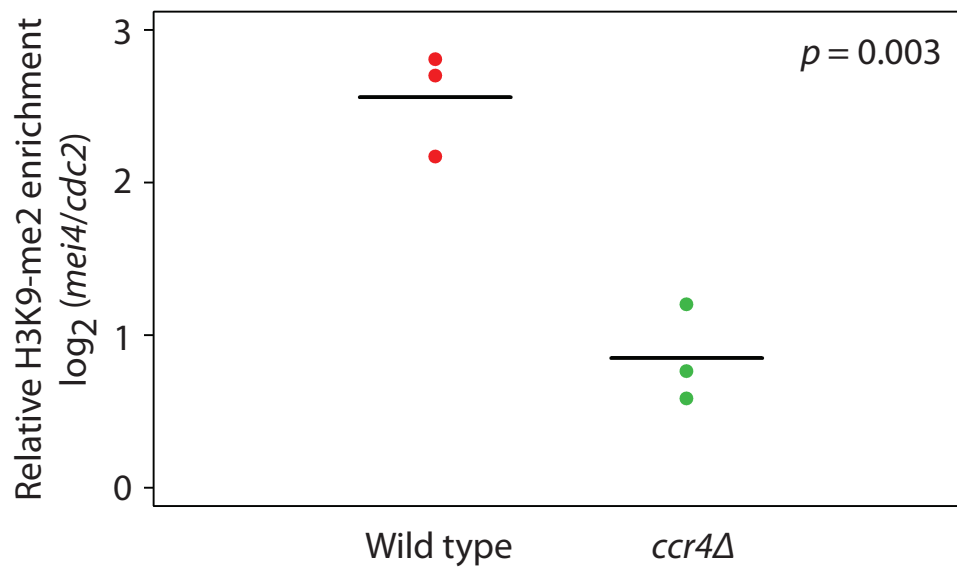


Figure S1. Effect of *ccr4* mutation on H3K9-me2 enrichment analysed by CHIP-qPCR.

The y axis shows the normalized enrichment in H3K9-me2 of the *mei4* locus relative to *cdc2* quantified using qPCR for wild type cells (left) and *ccr4Δ* mutants (right). Data are shown for three independent biological replicates (single dots, $n=3$) and the average is represented by horizontal line. The significance of the difference between both strains was calculated using Student's t-test.