



**Supplemental Figure S6. Swi2 binding to *HO* URS2 by ChIP analysis.**

(A) Binding of Swi2-V5 to *HO* URS2 by ChIP analysis (green), compared with *HO* RNA expression levels (red) in mutant strains. Cells for ChIP and RNA originated from the same cultures that were split upon harvesting; these samples are identical to those used in Fig 11. Strain genotypes are indicated on the left. Error bars show the standard deviation of 3 biological replicates. The qPCR following ChIP was performed using primers that amplify *HO* sequence from -897 to -798. Swi2-V5 enrichment for each sample was normalized to that of the promoter of *CTS1*, and to the corresponding input sample and graphed relative to wild type enrichment. *HO* expression was normalized to *RPR1* and expressed relative to wild type.

(B) Comparison of binding of Swi2-V5 to *HO* URS1 (blue) vs. *HO* URS2 (green), using the same data presented in Figs 11 and S6A. Swi2-V5 enrichment for each sample was normalized to that of the promoter of *CTS1*, and to the corresponding input sample and graphed relative to wild type enrichment at URS1.