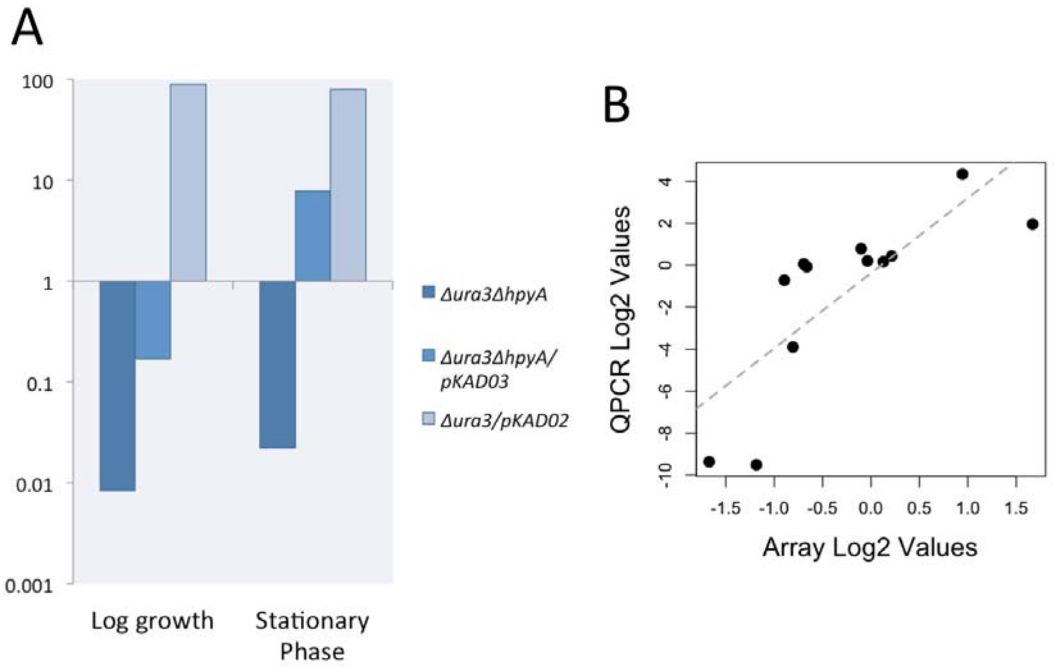

Supplementary Figure S2: qPCR verification of strains and array data. A) Using primers for *VNG0134G*, histone mutant gene expression dosage was verified *via* RT-qPCR. ΔΔCt was calculated for each strain relevant to the parent control and the reference locus *VNG1756G*. Shown here are the knock-out (Δ*ura3*Δ*hpyA*), the histone mutant rescue strain (Δ*ura3*Δ*hpyA*/*pKAD03*), and the overexpression strain (Δ*ura3/pKAD02)* ratios. B) Knock-out array data was verified using RT-qPCR of array mRNA samples. The following loci were tested in both logarithmic and stationary phase samples: *VNG1123G*, *VNG1317H*, *VNG1641H*, *VNG1815G*, *VNG5019G*, and *VNG5192H*. Pearson correlation between the two datasets = 0.79. The equation of the line of best fit: y = 3.5763x - 0.3758. Detailed methods are described in the Supplementary Text. Primers used are listed in Supplementary Table S5.