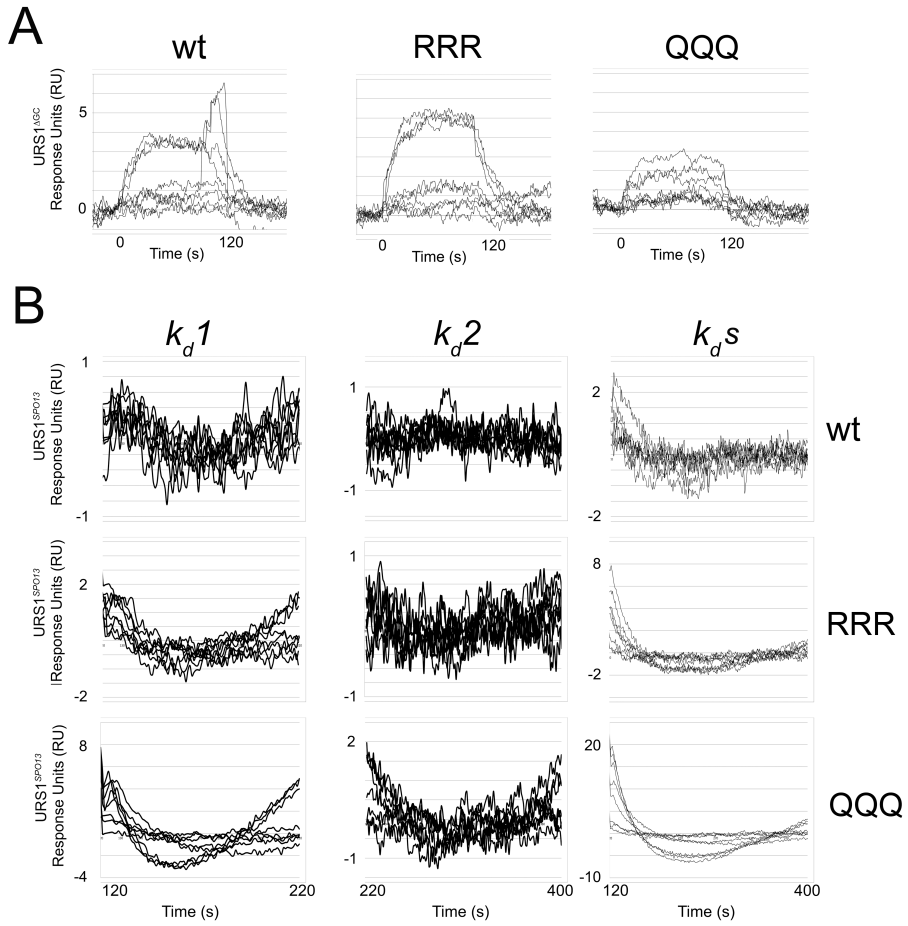

FIG S2 Mimicking lysine acetylation in cluster three reduces Ume6p binding to URS1^{SPO13} in vitro. (A) Biacore analysis was performed (see Materials and Methods) with the Ume6p peptides indicated injected over a bound mutant URS1 probe (URS1$^{\Delta GC}$) sequences lacking the consensus Ume6p binding site. Under identical conditions, Ume6p-URS1^{SPO13} interactions generated an RU value of >250 (see Fig. 2B). The sensorgrams with URS1$^{\Delta GC}$ exhibited an interaction value of ~5 RU indicating that stable protein/DNA complexes did not form. (B) The root mean square differences between the computer generated optimal two- (k_d1, k_d2) or single- (k_dS) dissociation curves and the raw data acquired in Fig. 2B. For the separate dissociation constants, k_d1 included the first 100s of buffer wash, while k_d2 calculated dissociation for the next 180s. Note the increase in

residual values observed in the single k_dS model for Ume6p and Ume6p^{K3R} relative to those observed when the dissociation is separated suggesting the two-component curve better fits the data. The elevated differences for Ume6p^{K3Q} compared to wild type reflect the overall instability of this complex.