



**Figure S2** Comparison of RNA Pol II occupancy across ChIP-seq datasets. Matrix shows Pearson correlation coefficients for pair-wise comparisons of genome-wide RNA Pol II occupancy measured by ChIP-seq in wild-type (labeled wt),  $\Delta hog1$ , and  $\Delta sko1 \Delta hot1$  (labeled  $\Delta TF$ ) strains in the presence and absence of osmotic shock by 0.4 M KCl for five minutes. (ORFs with no alignable reads were excluded from the analysis.)