

Figure S6. Heat maps to illustrate Tup1 occupancy vs. RNA expression in *tup1(S649F)* vs. wild-type a strains.

Shown is the Tup1 occupancy vs. RNA expression data for clusters of Tup1 peaks in **a** strains, analyzed in the same manner as the  strains in Fig 7B. Each square within the 3 x 3 heat maps represents a unique combination of Tup1 occupancy and RNA expression of the downstream gene, where “Up” and “Down” indicate increased or decreased occupancy/expression in *tup1(S649F)*  vs. wild-type , respectively, and “NC” (No Change) indicates less than 1.5-fold alteration in levels. The color scale at the right indicates the percentage of genes in each category. Genes were separated by cluster from Fig 7A and were only included if they were located downstream of a Tup1 peak and had a valid expression level from RNA-Seq (993 total). Peaks were counted twice if present between divergent genes. Some genes were counted more than once, due to two or three Tup1 peaks within the intergenic region upstream of the gene (53 total).