



**Figure 5 – figure supplement 2:** Gene expression changes in *rsc1Δ*, *rsc2Δ*, and *rsc30Δ* mutants. (A) Number of genes affected by *rsc* deletions. For each mutation, the number of genes up or downregulated two fold or more compared to WT. *rsc1Δ* (↑129↓45), *rsc2Δ* (↑160↓129), *rsc30Δ* (↑66↓168), *rsc1Δrsc30Δ* (↑162↓204), *rsc2Δrsc30Δ* (↑601↓589). (B) Gene Expression changes. Violin plots showing log2 fold change of RNA in mutants at all pol II genes (6145 genes) and at ribosomal protein genes (132 genes) compared to WT expression. Change in expression reflects an average of three biological replicates, Figure 5- Source Data 3. (C) Rsc mutation redundancy relationship. (D) Genome snapshots. Shown for select genes are low- (GSM1891202) and high- (GSM1891207) MNase-digested fragment coverage from Kubik et al, 2015, Rsc1 and Rsc2 ChIP seq log2 fold enrichments, Hmo1 ChIP Seq log2 fold enrichments (GSM1509041) from Knight et al, 2014, and RNAseq coverage (unstranded) from an average of three replicates of RNAseq for WT (YBC604), *rsc1Δ* (YBC774), *rsc2Δ* (YBC82), *rsc30Δ* (YBC695), *rsc1Δ rsc30Δ* (YBC839), and *rsc2Δ rsc30Δ* (YBC910).