



Figure S2: Measurement of steady-state mRNA levels by RNA-seq is unable to detect a genome-wide shutdown of transcription after HS. DESeq2 analysis of RNA-seq reads between 30min HS-treated and NHS cells displayed as an MA plot. Significantly changed genes were defined using an FDR of 0.001. Activated genes are labeled in magenta and repressed genes in blue. The number of genes in each class is shown in the plot. fc = fold-change.