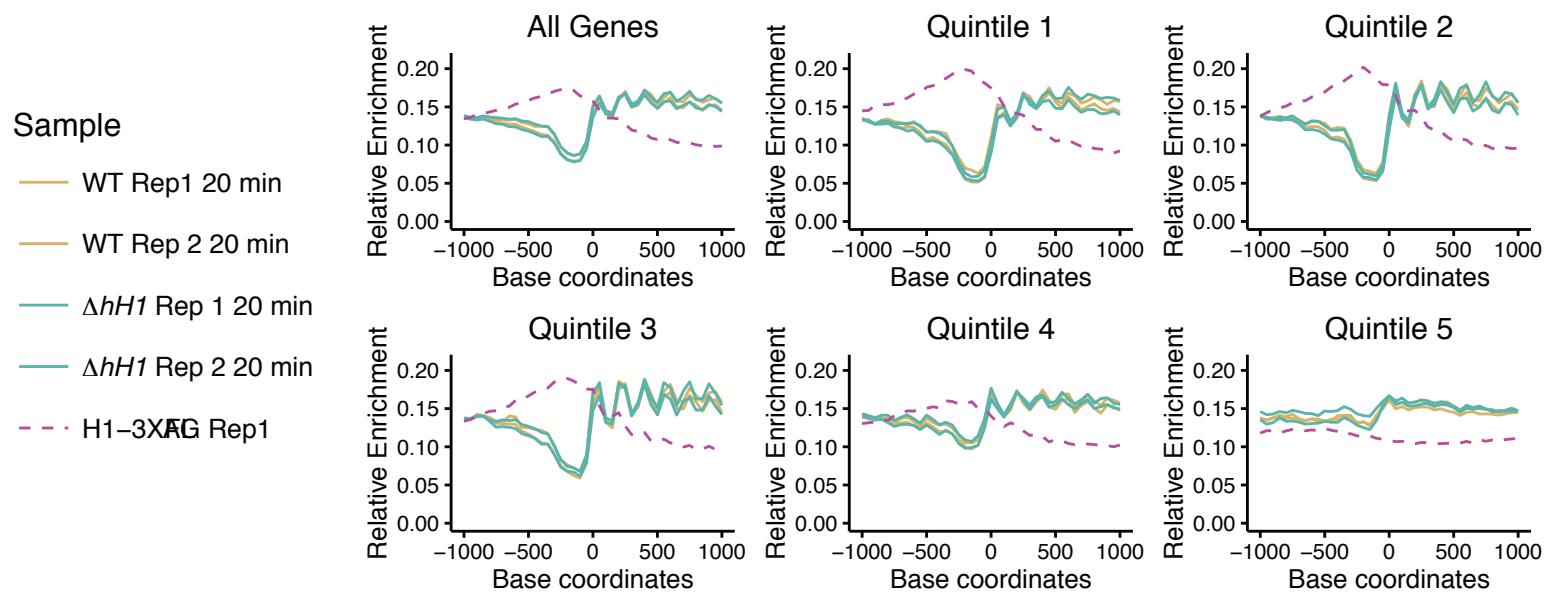


A



B

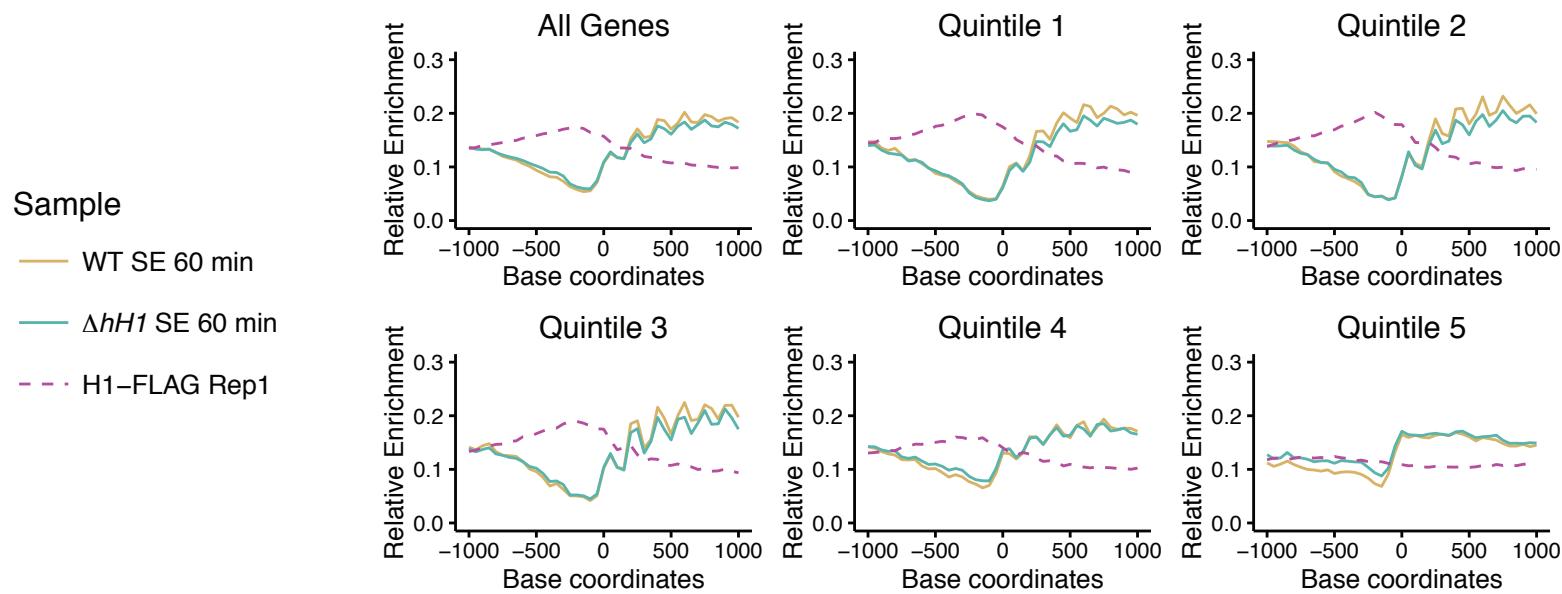


Figure S1 Metaplots depict the average sequencing depth on the + strand across all *N. crassa* genes or for gene expression groups. For expression group analysis, all *N. crassa* genes were ranked by expression level and split into quintile groups, ranging from highest expression (Quintile 1) to lowest expression (Quintile 5). (A) Data from paired-end MNase-seq from a 20 minute MNase digest. Plots show data from two biological replicates each for wildtype and $\Delta hH1$. (B) Data from single-end MNase-seq from a 60 minute MNase digest. For all plots, the coverage of + strand reads from an H1-3XFLAG ChIP-seq experiment is shown as a dashed line.