



Figure 1- figure supplement 3. Transcriptional impact of  $\Delta hp1$ . (A) Volcano plot showing the log<sub>2</sub> fold-change for  $\Delta hp1$  compared to the wild-type (WT) grown in PDB culture. The adjusted p-value ( $-\log_{10}$ ) is shown in the y-axis to indicate statistical significance. Individual genes are shown as colored points, with genes in the core (blue) and those in LS (yellow) regions. Genes were considered differentially expressed if they were log<sub>2</sub> fold-change  $< -1$  or  $> 1$ , shown as vertical dashed lines, and an adjusted p-value  $< 0.01$ , shown as a horizontal dashed line. These cut-offs resulted in 1522 genes more highly expressed in  $\Delta hp1$ , and 587 more highly expressed in wild-type. (B) Bar plot showing the average and range of log<sub>2</sub> fold-change values for genes (n=1522) expressed significantly higher in  $\Delta hp1$  compared to wild-type from (A). The genes were grouped based on core (blue) versus LS (yellow) location. These groups were statistically significantly different based on Mann-Whitney U-test, p-value  $< 2.2e-16$ .