



Figure S11. ChIP-seq of myc-DnaA in *M. smegmatis*. DNA sequencing coverage plots are shown for the 5 most significantly enriched regions as determined by MACS2 analysis (see methods) as visualized in Artemis (<https://www.sanger.ac.uk/science/tools/artemis>). The red represents sequencing depth from a myc-tagged strain and the blue line represents sequencing depth from an untagged strain used as a negative control. The fold-enrichment values from MACS2 are annotated onto each plot. Mtb homologs of *M. smegmatis* genes are shown below each panel.