



Figure 6– Supplement 1. *L. pneumophila* induced block in host protein synthesis can occur at the level of translation elongation and initiation. (A-B) Metagene profile plot around the translation start (A) or stop (B) site of all harringtonine treated conditions normalized to mitochondrial read counts of each condition. (C-F) Global weighted averages across transcripts were calculated for BMMs left uninfected (C) or infected with $\Delta flaA$ (D), $\Delta dotA \Delta flaA$ (E), or $\Delta 7 \Delta flaA$ (F) *L. pneumophila*. Weighted averages were generated by scaling each transcript's ribosome occupancy profile according to the average density from codon 250 to codon 349 and then averaging across the entire condition. Transcripts with very low density in the 250-349 codon region (or shorter than 349 codons) are excluded from averaging. If the weighted average is less than 1 this shows that this region has reduced ribosome footprints, while if the weighted average is greater than 1 this shows that there are more ribosome footprints in this region. Following a brief pulse of cells with harringtonine (red line) there is a change in the distribution of ribosomes from the 5' end of the mRNA to the 3' end of the mRNA (i.e., as the ribosomes continue to move 5' to 3'; C-F) as compared to untreated cells (blue line). This can be seen by an increase in the weighted average at the 3' end of mRNAs (C, E, F) but the lack of this change shows a block in translation elongation (D). We also expect an accumulation of ribosomes at the ATG following harringtonine treatment, which is also seen as a peak in the weighted average at the start site (C-F). Data are representative of two independent experiments (A-F).