Figure S1. Transcription start sites (TSS) identified in S. Typhimurium genome. Venn diagram showing TSS identified at 0 h and 2 h post-infection (p.i.) (a). Bar chart showing % TSS at 0 h (green) and 2 h p.i. (blue). classified as Inter_S, Intra_S, Inter_A, or Intra_A (b).

Figure S2. Gene set enrichment analysis performed using the fgsea package. Positive (normalized) enrichment scores indicate upregulation of bacterial genes in trial library pathway. Negative (normalized) enrichment scores indicate downregulation of bacterial genes in trial library pathway. Operon pathway annotation was determined against KEGG database.

Table S1. General RNA-Seq statistics and alignment report

Table S2. Statistics of TSS in Salmonella Typhimurium 14028S genome

Table S3. Differential expression of operons