

Santiviago et al., Supplementary Figure 1: NimbleGen tiling array data for T7 RNA polymerase transcripts from a pool of 1031 Kanamycin resistant specific deletion mutants.

The panels show median signal intensities of three oligos representing immediate adjacent regions on the same strand (running median of 3 probes). Peaks indicate the presence of transcript, and therefore the location of a successful deletion mutation slightly upstream in the opposite strand.

Each panel spans data for 10,000 bases of the Typhimurium LT2 genome with approximately 400 oligonucleotide probes in each strand. Red plots the top (positive) strand and blue plots the bottom (negative) strand. Corresponding Typhimurium 14028 gene numbers are given at the top of each panel with red indicating genes with a sense strand orientation, and blue indicating genes with an anti-sense strand orientation. The beginning and end of genes are marked with a triangle. Note that the genome locations are for LT2 as the very similar 14028 genome sequence has not been fully annotated as yet.



















































































































































































































































