

Supplementary figures

Analysis of LexA binding sites and transcriptomics in response to genotoxic stress in *Leptospira interrogans*

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Fig. S1

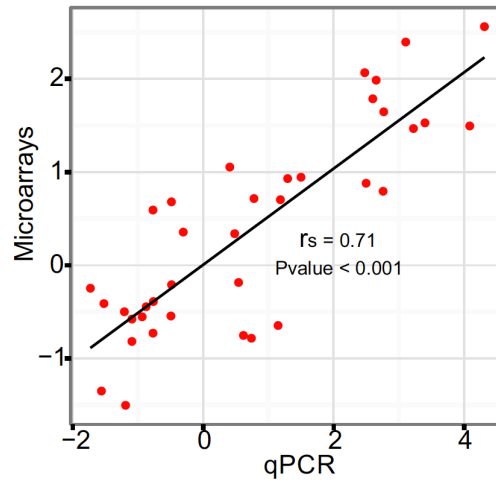


Figure S1. Correlation between gene expression data collected by DNA microarrays and RT-qPCR. Axes represent log2 fold change for both techniques, and both correlation coefficient (r_s) and P-value were computed by Spearman's method.

Fig. S2

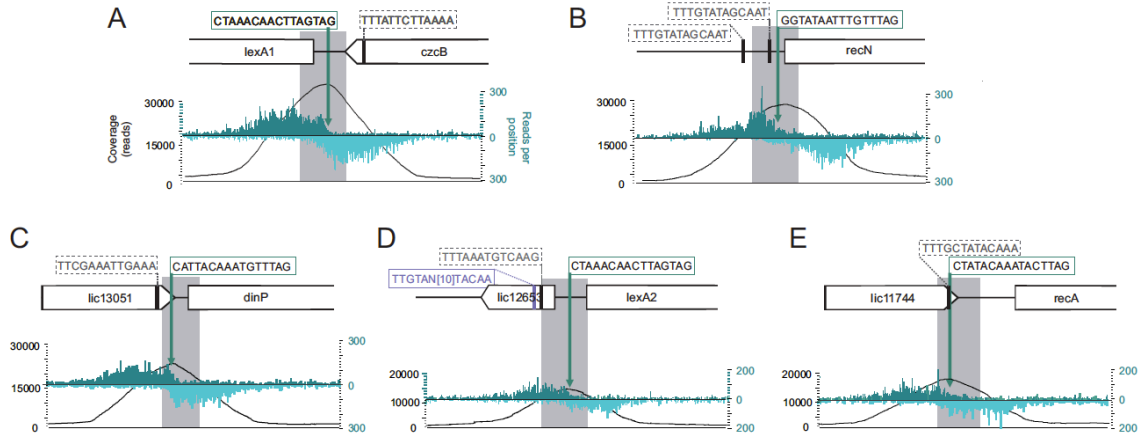


Figure S2. Localization of SOS boxes in relation to some sequences used for EMSA. The panels represent 1kb windows of the operator region of *lexA1* (A), *recN* (2), *dinP* (3), *lexA2* (D) and *recA* (E). For each one, a schematic genetic map is shown. The region used for EMSAs shown in Fig. 4B is shaded, while the LexA1 binding site identified by ChIP-seq is indicated by the green arrow, pointing to the ChIP-seq reads coverage map (black line). Reads per position are shown in dark green for the forward strand, and lighter green for the reverse strand. Black vertical rectangles indicate the location of the previously described SOS boxes (21), and for *lexA2*, the LexA2 box is indicated in purple.

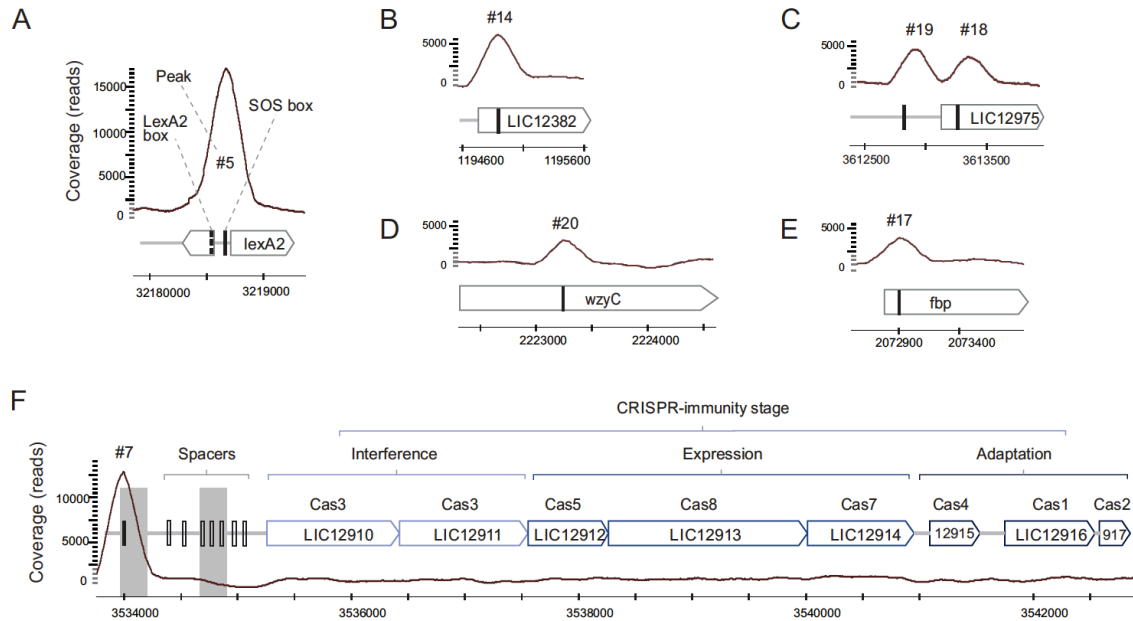


Figure S3. Association of LexA1 with selected regions in the leptospiral chromosome I. Regions around peaks #5 (*lexA2*, A), #14 (LIC12382, B), #18-19 (LIC12975, C), #20 (*wzyC*, D), #17 (*fbp*, E) and #7 (CRISPR-Cas, F): genomic features are indicated below the read coverage line, including black horizontal lines representing LexA1 boxes and arrows indicating genes. Coordinates are given in base pairs, below each panel. In (F), boxes represent spacers within the CRISPR region upstream a Cas gene cluster and shaded boxes, regions where ncRNA were detected by qPCR. The step in CRISPR/Cas immunity in which each gene is involved is also indicated.