Supplementary figure S1: DNA sequence of mreB region. The mreBCD region is located at ~3 min in the E. coli chromosome. Three α-dependent promoters contribute to mreB transcription (PmreAB, PmreCD, and PmreD) and are indicated as black boxes. Probable transcription initiation sites (-269, -106 and -42) are indicated in bold. Note that -106 initiation site is atypical and could in fact result from a post-transcriptional cleavage by an RNAse. Translation initiation codon of mreB is indicated. The region of mreB that anneals with DsrA is underlined with a waveline. The coding sequence of mreB is indicated in light grey, whereas the beginning of mreC coding sequence appears in dark grey. Stop codon of mreB and yhdc upstream gene (located nearby PmreDJ) are italicized.

Supplementary figure S2: Influence of DsrA on MreB concentration. Left panel: MreB quantifications were made by Western Blot as described in methods and Fig.1. Two plasmids allowing the expression of DsrA under the control of $P_{\text{nst}}$ (pNM1; $\pm$ 0.01% ampicillin) and constitutive $P_{\text{LacO}}$ (pZE12) promoters were used. Both plasmids resulted in a significant diminution of MreB levels. Right panel: an example of Western Blot using a cell extract in the presence (lane 2) or not (lane 1) of a plasmid that express DsrA (constitutive expression). As shown, anti-MreB antibody is specific.
Supplementary figure 53: DsrA-mediated riboregulation on mreB-lacZ translational and transcriptional reporter fusion. β-galactosidase activities were assayed in cell extracts of the indicated strains grown at 16°C (exponential phase). Drawing is a schematic representation of the mreB-lacZ reporter fusion. We observe that DsrA affects mreB expression and that DsrA expression from pNM13 (+0.001% L-arabinose) in a ΔdsrA background complements ΔdsrA phenotype, while the empty pNM12 vector does not. Note that the effect observed for ΔdsrA strain is slightly less than that seen for the protein level (Fig. 1). Nevertheless, fusion reflects mreB-lacZ RNA and MreB-lacZ protein stabilities, which is different from mreB mRNA and MreB protein stabilities.
Supplementary figure S4: The secondary structure model of mreB-DsrA complexes predicted using RNAfold server (http://rna.ibi.univie.ac.at/cgi-bin/RNAfold.cgi). The mreB AUG start codon is highlighted. Both WT and mutated mreB and DsrA pairings are shown.