Fig.S1. The entire dataset of H-NS and Hha binding signals

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Fig.S1-30

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Fig. S1. The entire dataset of H-NS and Hha binding signals

The arrangement of genes (thick arrows) on the *E. coli* chromosome is shown at the top of the figure, and the distributions of the H-NS and Hha binding signals are shown below the gene arrangement. Red arrows correspond to genes that were up-regulated in both *hns/stpA* and *hha/ydgT* mutant cells, while green arrows show genes that were up-regulated in only *hns/stpA* mutant cells. H-NS binding signals in wild-type (W3110) and *hha/ydgT* mutant cells, as well as Hha binding signals in W3110 pQEHha and W3110 *hns*::Km *stpA*::Cm pQE80Hha cells, are shown as the relative ratios of the signal intensities from the ChIP and Sup fractions in each experiment. Each experiment was performed in duplicate, and the distributions of binding signals are represented by two columns, one for each experiment (e.g., wild-1 and wild-2). The H-NS binding regions in wild-type (W3110) and *hha/ydgT* mutant cells, and the Hha binding regions in W3110 pQEHha cells (see Materials and Methods) are shown as thick lines with the gene arrangement. The blue line shows the H-NS binding regions in wild-type cells (W3110); the purple line shows the H-NS binding regions in *hha/ydgT* mutant cells; the gray line shows the Hha binding regions in W3110 pQEHha cells; and the black line shows the H-NS binding regions that were determined by visual inspection. The class of each H-NS binding region determined by visual inspection is indicated under the black line by int (intergenic), single (coding [single])” or multiple (coding [multiple]).