

1 **Supplementary figure legend**

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

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

23 **Fig. S2. Examples of the H-NS binding signals categorized as “intergenic,” “coding 24 (single)” and “coding (multiple)”**

25 Representative examples of the H-NS binding signals categorized as “intergenic” (A

26 and B), “coding (single)” (C and D) and “coding (multiple)” (E and F). Arrows indicate
27 the H-NS binding peaks (determined by visual inspection) in the “intergenic” and
28 “coding (single)” H-NS binding regions.

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30 **Fig. S3. The H-NS and Hha binding signals in and around the genes up-regulated**
31 **in both *hha/ydgT* and *hns/stpA* mutant cells**

32 H-NS and Hha binding profiles in and around all genes up-regulated in both *hha/ydgT*
33 mutant and *hns/stpA* mutant cells are shown. The localizations of H-NS binding signals
34 were classified as “intergenic” (A), “coding (single)” (B), coding (multiple)” (C), and
35 both “coding” and “intergenic” (D). “Intergenic” and “coding” H-NS binding regions
36 are shown by red and green boxes, respectively. H-NS and Hha binding signals are
37 shown as in Fig. S1, except that results of only one experiment for each strain are
38 shown.

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