Supplementary figure legends

**Figure 1.** Genome wide view of transcriptional activity and H-NS and RNA polymerase binding sites. Transcriptional activity signals in wild type and *hns* inactivated cells and the binding signals of β, σ^D^ and H-NS are shown along the genome, together with the density of A-tract sequences (number of A-tracts in 100 bp window with 50 bp steps). The green, blue, red and gray boxes indicate essential protein, horizontally acquired protein, other non-essential protein and RNA coding genes, respectively. H-NS bound loci in Supplementary Table 1 are indicated below the H-NS signal. Purple and yellow lines under the gene map indicate fimbria and phage related genes, respectively. W3110 specific IS insertion sites are indicated by triangle, and W3110 specific phage deletion site is overlaid with grey box.

**Figure 2.** Derepression of divergent *mal* operons in the *hns* inactivated cell.

Transcriptional activity signals in wild type (W3110) and *hns* inactivated (Δ*hns*) cells and H-NS binding signals (H-NS), in a region covering the *malEFG* and *malK-lamB-malM* operons, are shown.
Figure 3. Correlation of RNA polymerase binding signals in wild type and \textit{hns}
inactivated cells. Scatter plots of signal intensities for $\beta$ (A) and $\sigma^D$ (B) subunits for
each 25-mer probe on the chip are shown.

Figure 4. Venn diagram representing overlaps among H-NS bound genes and
horizontally acquired genes.
Oshima et al., Fig. S1
Transcripts (W3110)

(+) malG → malF → malE → malK → lamB → malM

(-)

Transcripts (∆hns)

(+) malG → malF → malE → malK → lamB → malM

(-)

H-NS
Oshima et al., Fig. S3

A

\[ \Delta \text{hns } \beta \text{ subunit} \]

W3110 \( \beta \) subunit

B

\[ \Delta \text{hns } \sigma^D \text{ subunit} \]

W3110 \( \sigma^D \) subunit
Oshima et al., Fig. S4