

## Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Differentially expressed genes between lag phase and log phase in WT strain at pH 7.0. Differentially expressed genes were identified using glmTreat (t-test relative to a threshold) function of the *edgeR* package in R using log2 fold change (logFC) value significantly above 1.5 at an false discover rate (FDR) cut-off of 5%. (Related Figure 6)

File Name: Supplementary Data 2

Description: Differentially expressed genes between pH 7.0 and pH 5.0 in WT strain (SCV96). Differentially expressed genes were identified using glmTreat (t-test relative to a threshold) function of the *edgeR* package in R using log2 fold change (logFC) value significantly above 1.5 at an false discover rate (FDR) cut-off of 5%. (Related Figure 6).

File Name: Supplementary Data 3

Description: Differentially expressed genes between pH 7.0 and pH 5.0 in  $\Delta hupA\Delta hupB$  (SCV27). Differentially expressed genes were identified using glmTreat (t-test relative to a threshold) function of the *edgeR* package in R using log2 fold change (logFC) value significantly above 1.5 at an false discover rate (FDR) cut-off of 5%. (Related Figure 6).

File Name: Supplementary Data 4

Description: Differentially expressed genes between pH 7.0 and pH 5.0 in *hupAE34K* (SCV56). Differentially expressed genes were identified using glmTreat (t-test relative to a threshold) function of the *edgeR* package in R using log2 fold change (logFC) value significantly above 1.5 at an false discover rate (FDR) cut-off of 5%. (Related Figure 6).

File Name: Supplementary Data 5

Description: Differentially expressed genes between pH 7.0 and pH 5.0 in *hupAE34K* $\Delta hupB$  (SCV85). Differentially expressed genes were identified using glmTreat (t-test relative to a threshold) function of the *edgeR* package in R using log2 fold change (logFC) value significantly above 1.5 at an false discover rate (FDR) cut-off of 5%. (Related Figure 6).

File Name: Supplementary Movie 1

Description: Soft X-ray tomography volumetric 3-dimensional (3D) reconstructions show *E. coli* nucleoid region at Lag, exponential and stationary growth phase. Low bio-organic content was segmented at specific LAC value (see Methods) to highlight architecture of nucleoid macrodomains.

File Name: Supplementary Movie 2

Description: A morph between the HU $\alpha$ -HU $\alpha$  interface from the crystal structure of HU $\alpha$ -DNA at the pH 4.5 with interface seen in the crystal structure at the pH 5.5 (top panel) or crystal structure of HU $\alpha^{E34K}$ -DNA (bottom panel) shows decoupling of dimers at pH 5.5 and E34K mutation