**Figure S1** Correlation between the number of predicted DNA bends and the number of predicted binding sites in *E. coli* K12 for a) H-NS, b) Fis, c) IHF and d) Lrp with the alternative parameter set.

**Figure S2** Correlation between the number of predicted DNA bends and the number of predicted binding sites in *S. enterica* LT2 for a) H-NS, b) Fis, c) IHF and d) Lrp with the preferred parameter set.
Figure S3 Correlation between the number of predicted DNA bends and the number of predicted binding sites in *S. enterica* LT2 for a) H-NS, b) Fis, c) IHF and d) Lrp with the alternative parameter set.