

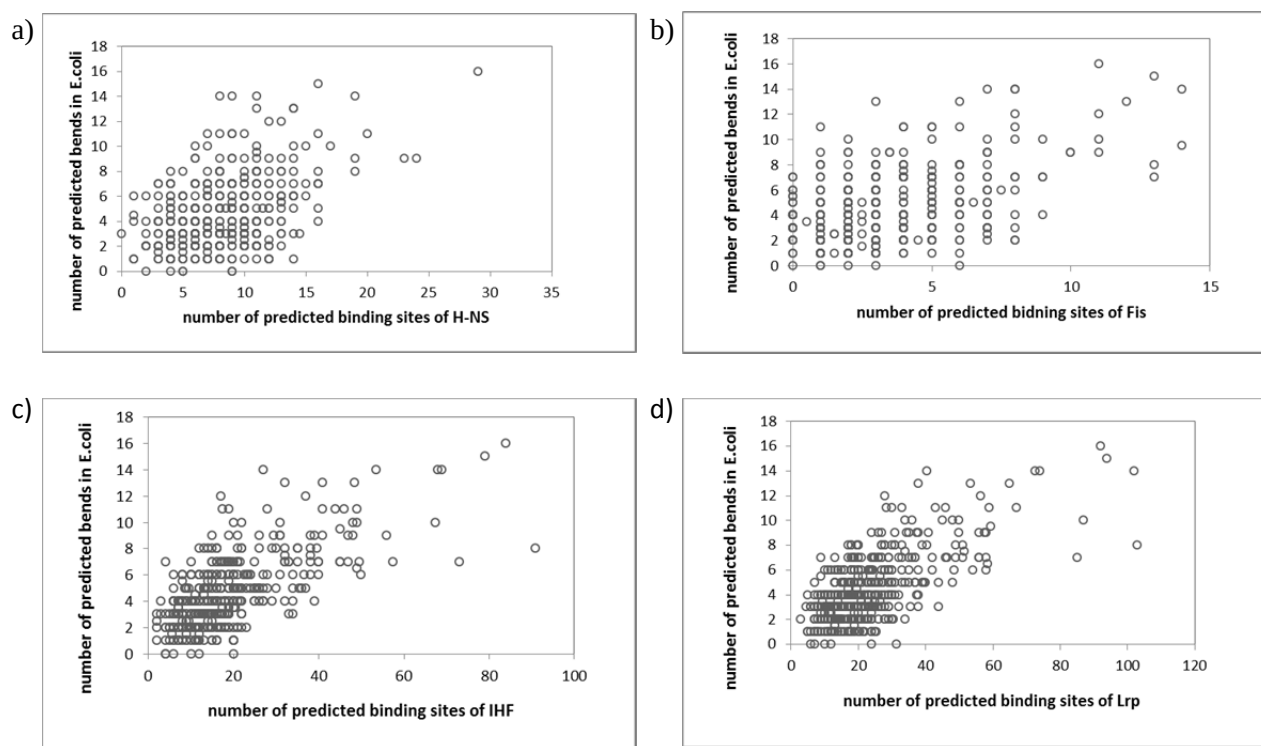


Figure S1 Correlation between the number of predicted DNA bends and the number of predicted binding sites in *E. coli* K12 for a) H-NS, b) Fis, c) IHF and d) Lrp with the alternative parameter set.

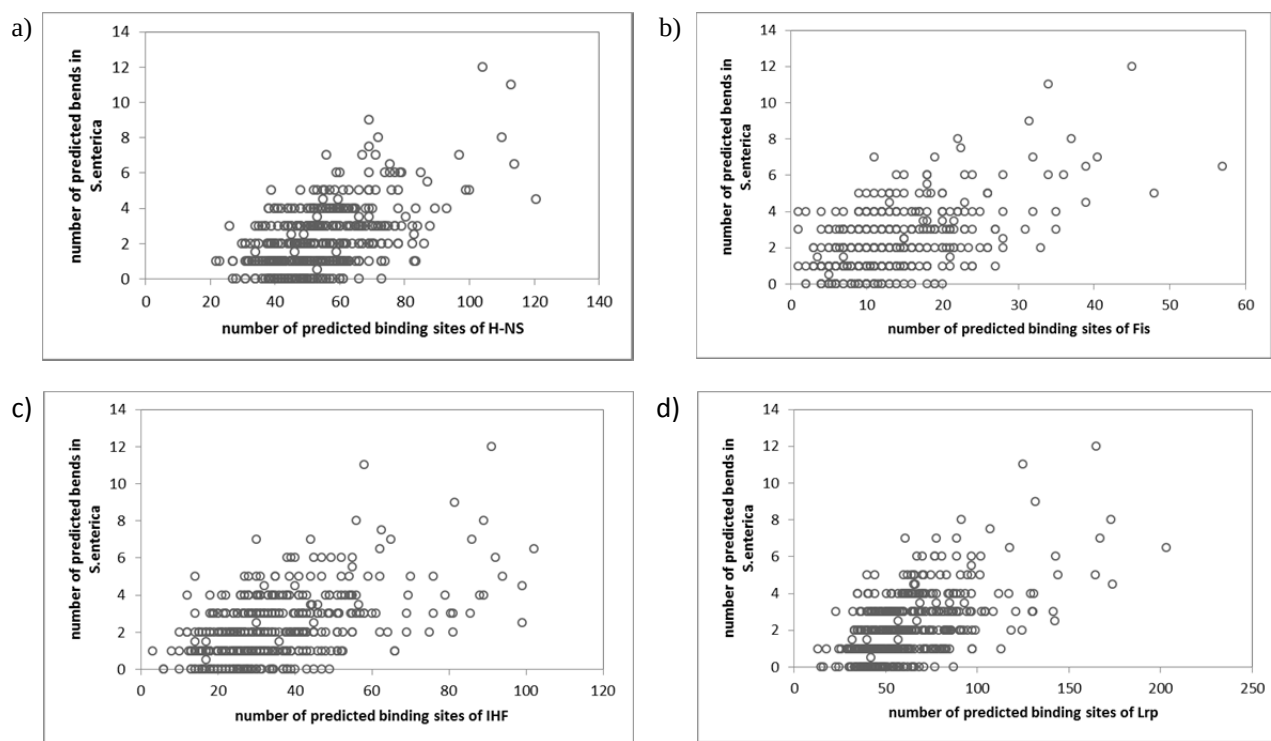


Figure S2 Correlation between the number of predicted DNA bends and the number of predicted binding sites in *S. enterica* LT2 for a) H-NS, b) Fis, c) IHF and d) Lrp with the preferred parameter set.

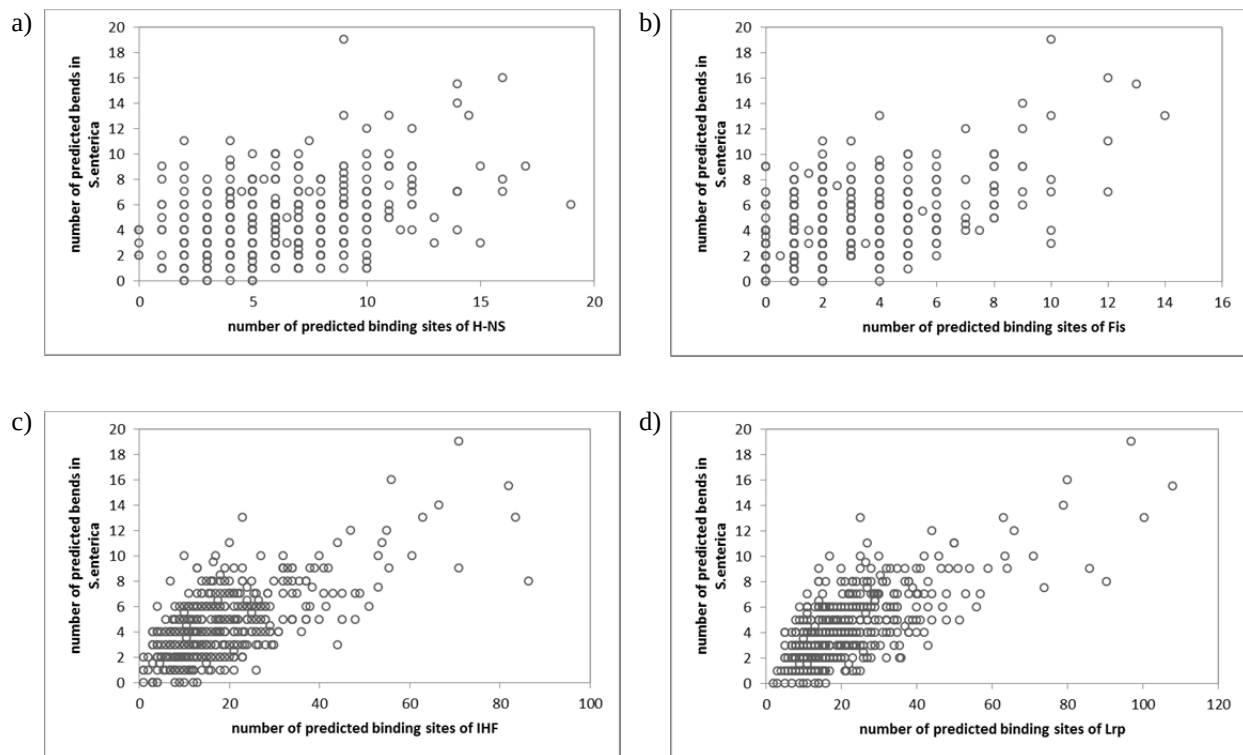


Figure S3 Correlation between the number of predicted DNA bends and the number of predicted binding sites in *S. enterica* LT2 for a) H-NS, b) Fis, c) IHF and d) Lrp with the alternative parameter set.