Data S4

DNA shape features improve transcription factor binding site predictions *in vivo*

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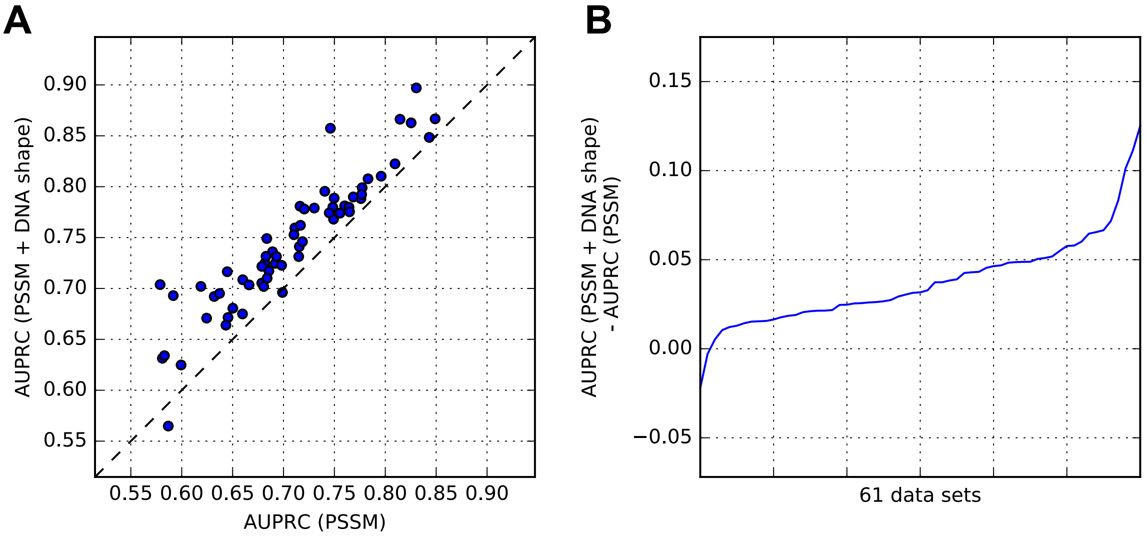
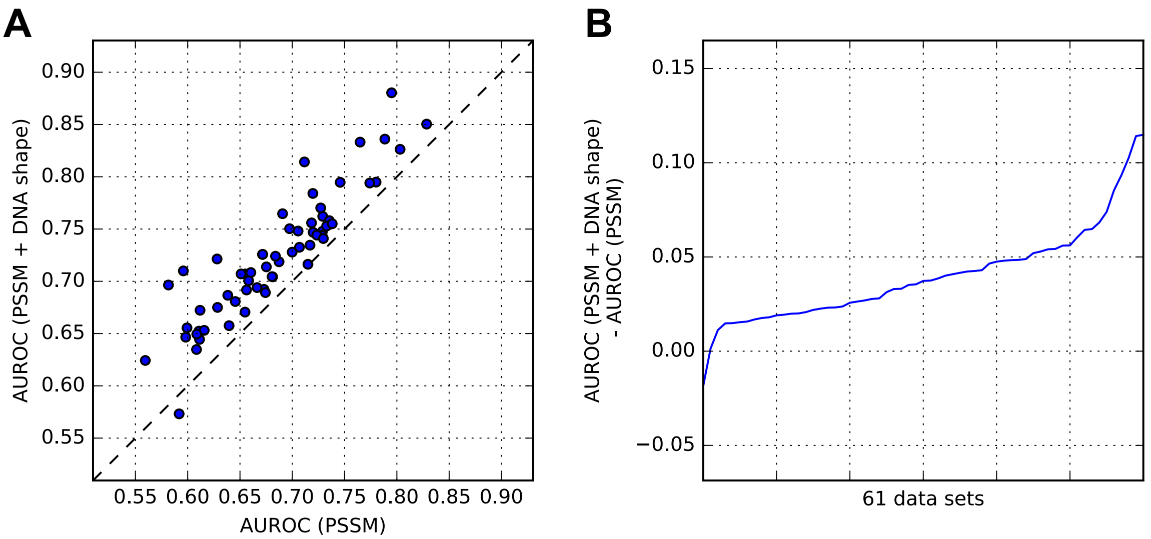


Related to Figure 2. Impact of DNA shape on predicting TFBSs when considering recurrent ChIP-seq regions for each TF. ***A.*** *Comparison of the AUPRC obtained for the recurrent ENCODE human ChIP-seq peak regions associated with 61 TFs when using either the PSSM scores (x-axis) or the PSSM + DNA shape classifiers (y-axis). The dashed line represents equal AUPRC values obtained with the two methods.* ***B.*** *Improvement in predictive power obtained when considering DNA shape features (y-axis) as the difference between AUPRC values obtained with the PSSM + DNA shape classifiers and PSSM scores. The higher the difference, the stronger the improvement when DNA shape information is incorporated. Note that the data sets (x-axis) were ranked by increasing difference values.*



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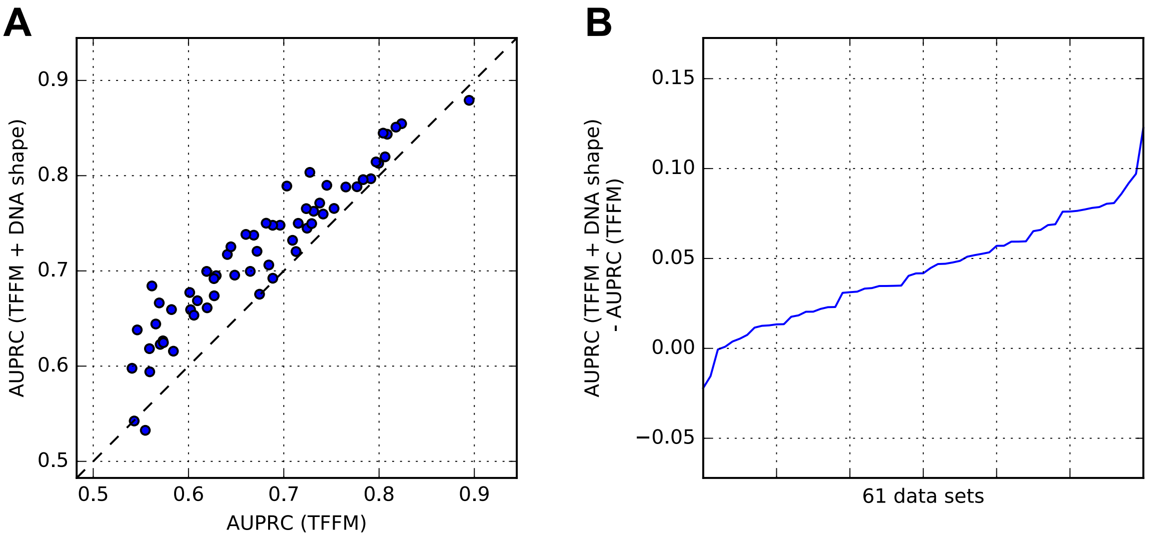

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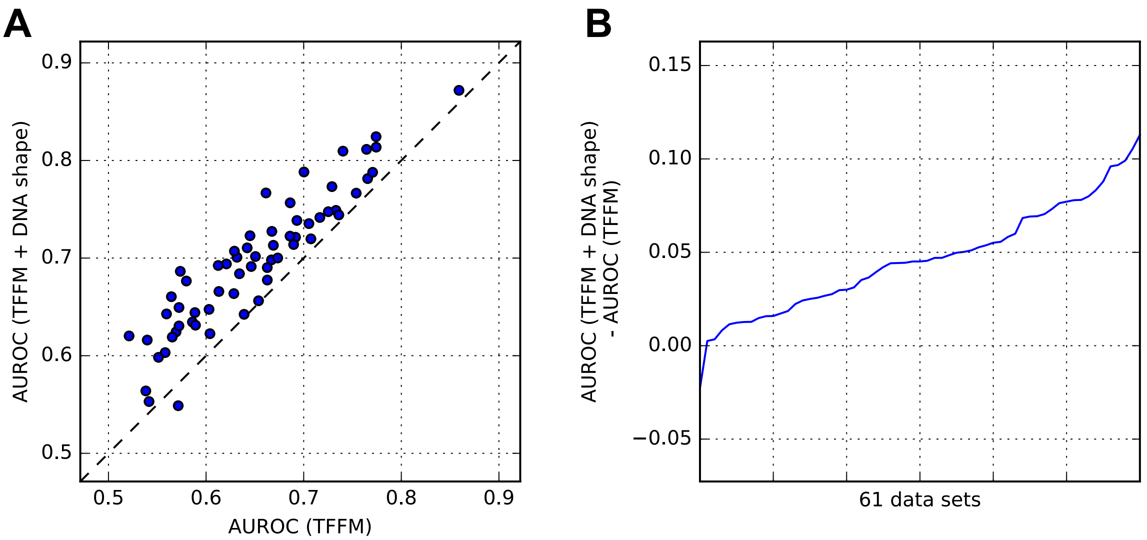

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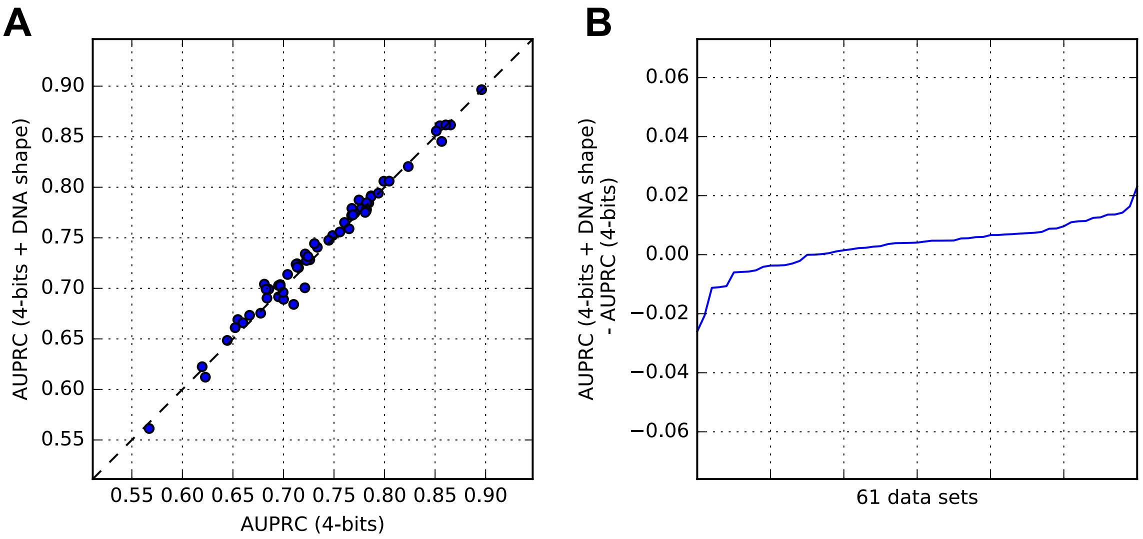

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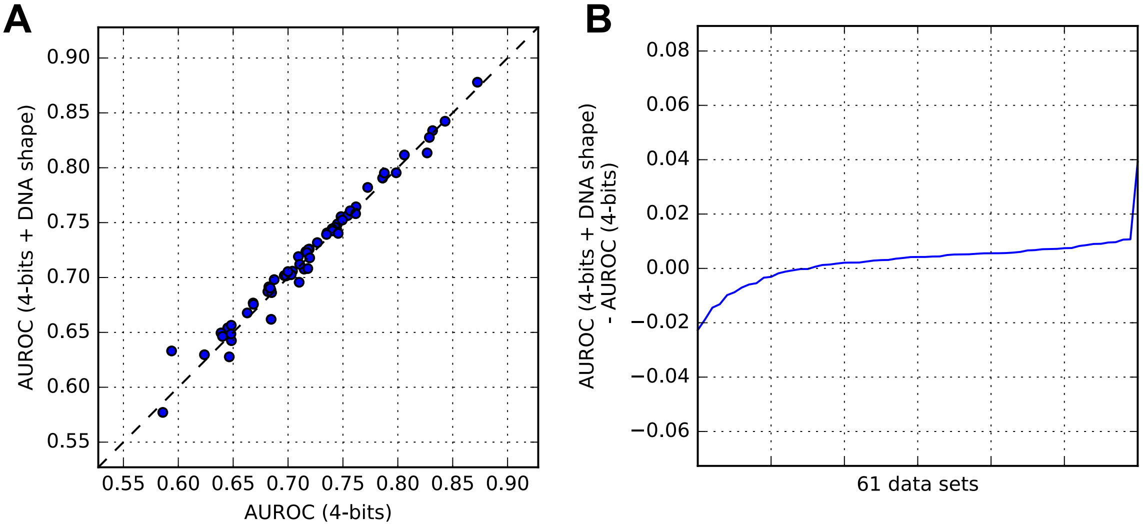

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