Data S6

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

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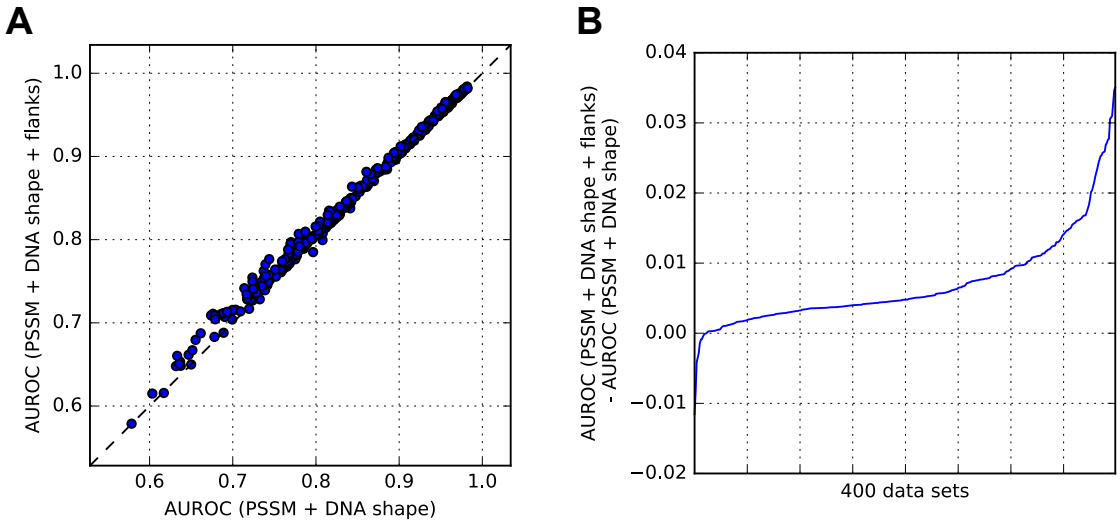
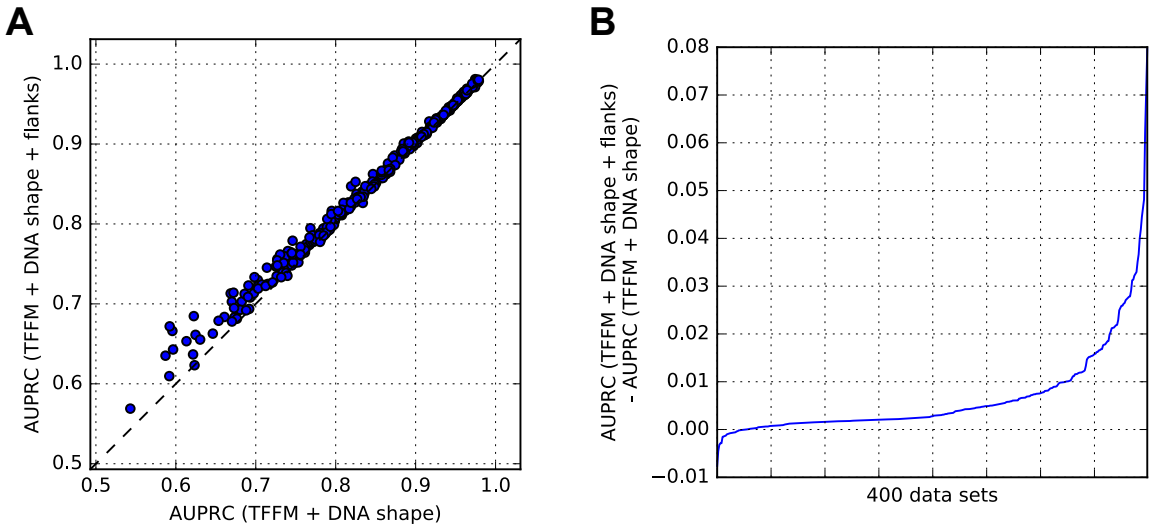
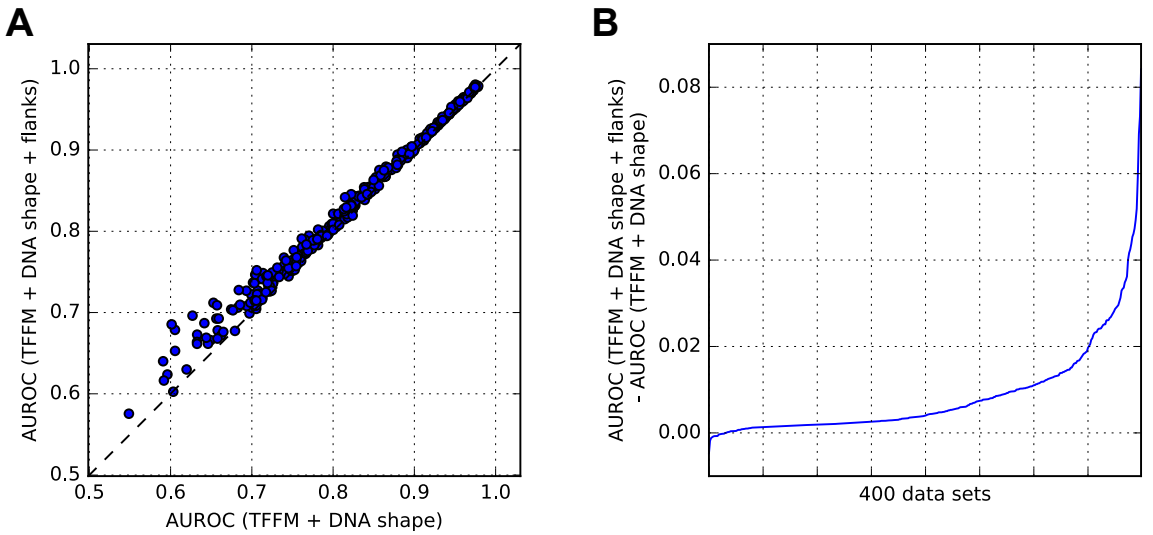


Related to Figure 4. Assessment of the predictive power of DNA shape features at TFBS flanking regions. ***A.*** *Comparison of the AUROC obtained for the 400 human ENCODE ChIP-seq data sets when using the classifiers combining PSSM scores and DNA shape features at the core TFBSs (x-axis) and the classifiers combining PSSM scores and DNA shape features at both the core TFBSs and the surrounding 15 bp on each side (y-axis). The dashed line represents equal AUROC values for the two methods.* ***B.*** *AUROC value differences (y-axis) between the flank-augmented classifiers and the PSSM + DNA shape classifiers. Data sets (x-axis) are ranked by increasing difference values.*



Related to Figure 4. Assessment of the predictive power of DNA shape features at TFBS flanking regions. ***A.*** *Comparison of the AUPRC obtained for the 400 human ENCODE ChIP-seq data sets when using the classifiers combining TFFM scores and DNA shape features at the core TFBSs (x-axis) and the classifiers combining TFFM scores and DNA shape features at both the core TFBSs and the surrounding 15 bp on each side (y-axis). The dashed line represents equal AUPRC values for the two methods.* ***B.*** *AUPRC value differences (y-axis) between the flank-augmented classifiers and the TFFM + DNA shape classifiers. Data sets (x-axis) are ranked by increasing difference values.*



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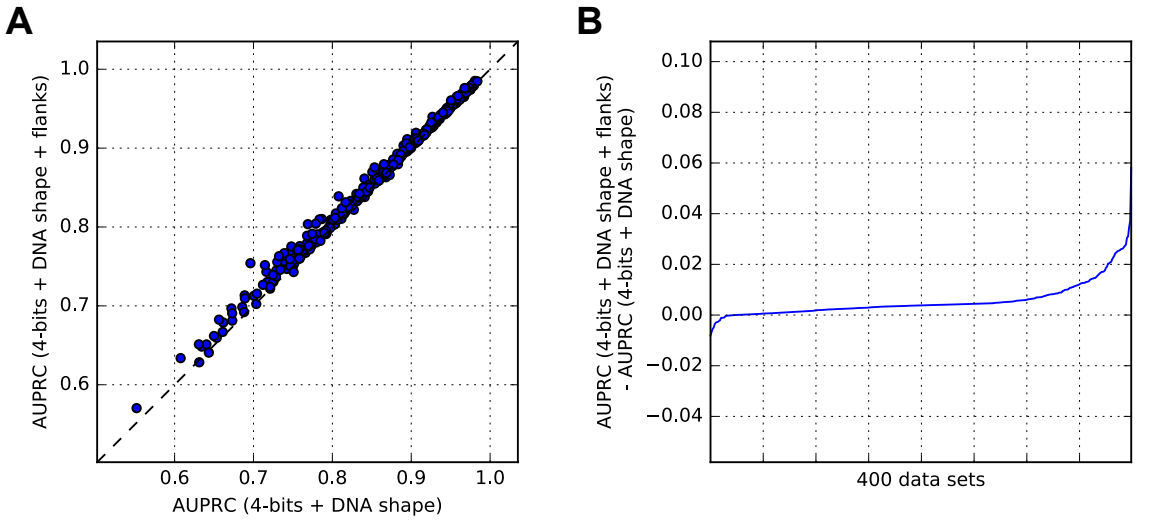

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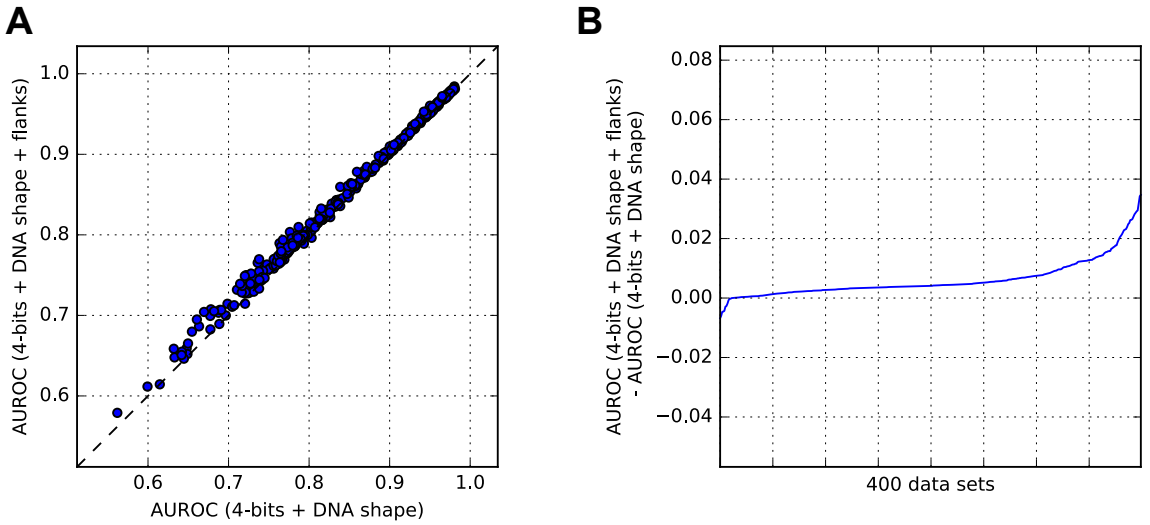

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