Data S5

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

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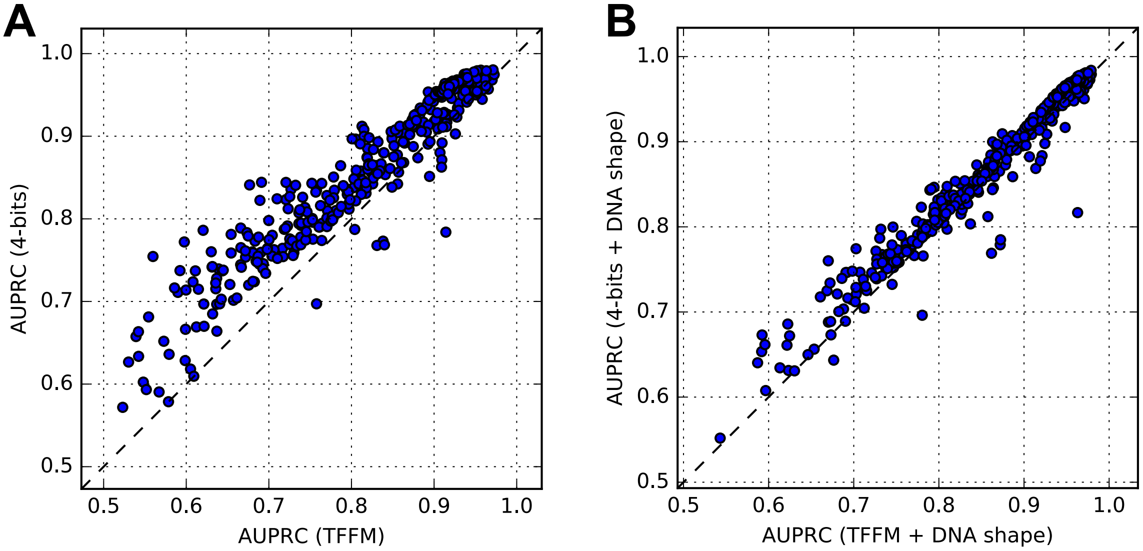
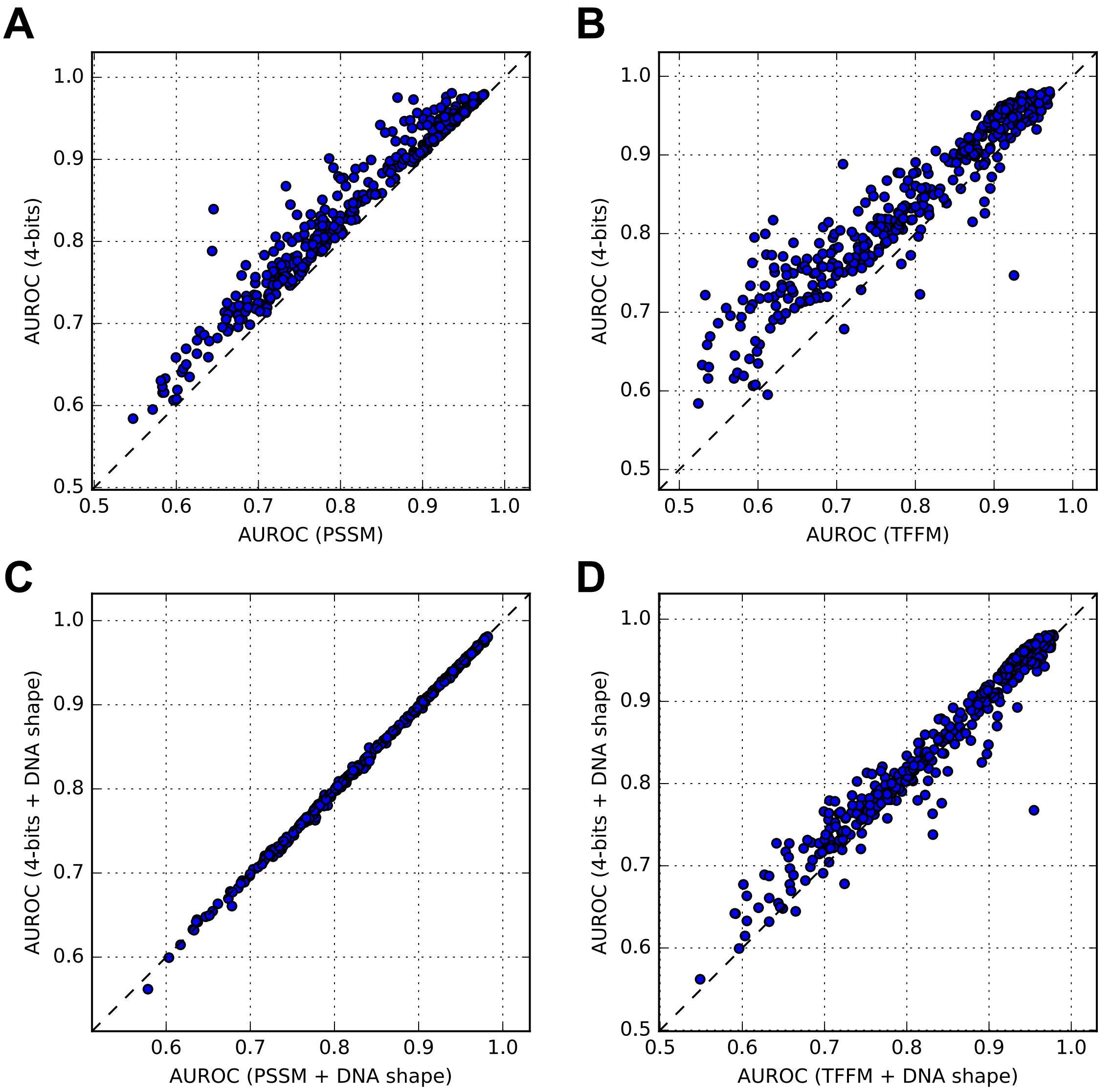
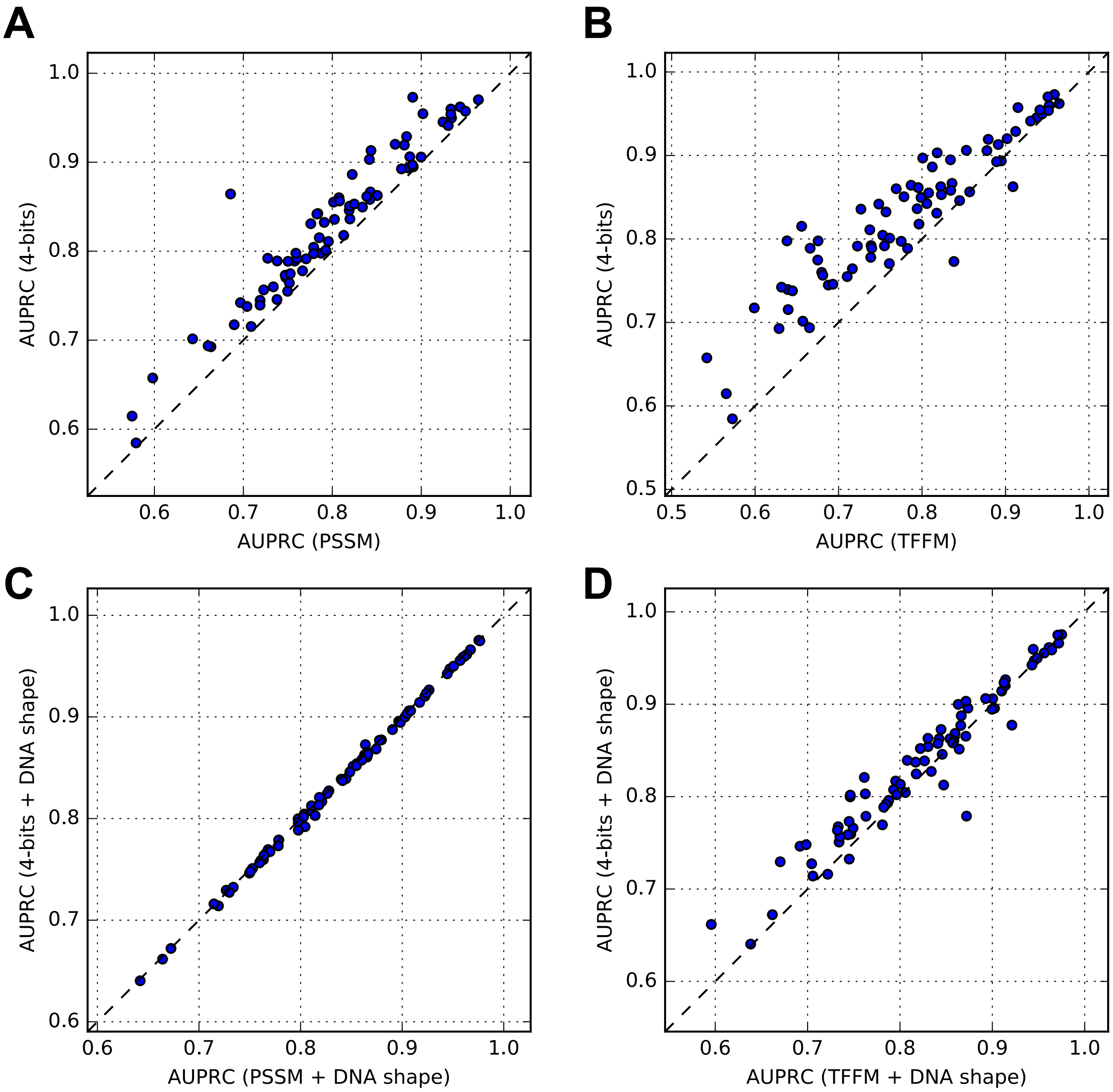


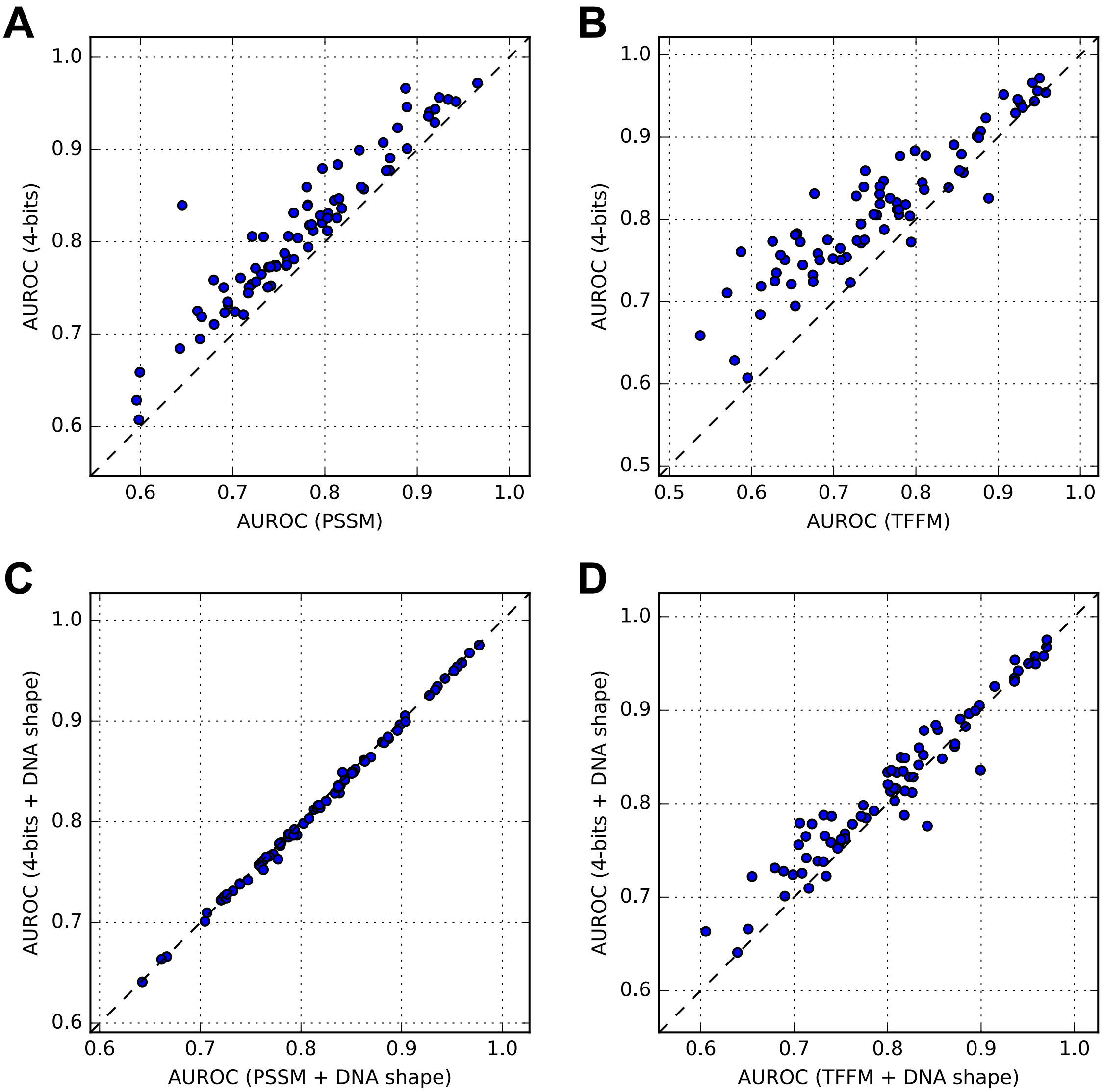
Related to Figure 3. Assessment of the predictive power of the TFFM and 4-bits approaches (see (Zhou et al.*, 2015) for the 4-bits encoding)to predict TFBSs in ChIP-seq regions. Comparison of the AUPRC obtained for the 400 human ENCODE ChIP-seq data sets when **A.** TFFM scores (x-axis) and 4-bits classifiers (y-axis) and **B.** TFFM + DNA shape (x-axis) and 4-bits + DNA shape (y-axis) classifiers are considered.*



Related to Figure 3. Assessment of the predictive power of the PSSM, TFFM, and 4-bits approaches (see (Zhou et al.*, 2015) for the 4-bits encoding)to predict TFBSs in ChIP-seq regions. Comparison of the AUROC obtained for the 400 human ENCODE ChIP-seq data sets when* ***A.*** *PSSM scores (x-axis) and 4-bits classifiers (y-axis),* ***B.*** *TFFM scores (x-axis) and 4-bits classifiers (y-axis),* ***C.*** *PSSM + DNA shape (x-axis) and 4-bits + DNA shape (y-axis) classifiers, and* ***D.*** *TFFM + DNA shape (x-axis) and 4-bits + DNA shape (y-axis) classifiers are considered.*



Related to Figure 3. Assessment of the predictive power of the PSSM, TFFM, and 4-bits approaches (see (Zhou et al.*, 2015) for the 4-bits encoding)to predict TFBSs in ChIP-seq regions. Comparison of the median AUPRC over all human ENCODE ChIP-seq data sets associated with each TF (one point per TF) when* ***A.*** *PSSM scores (x-axis) and 4-bits classifiers (y-axis),* ***B.*** *TFFM scores (x-axis) and 4-bits classifiers (y-axis),* ***C.*** *PSSM + DNA shape (x-axis) and 4-bits + DNA shape (y-axis) classifiers, and* ***D.*** *TFFM + DNA shape (x-axis) and 4-bits + DNA shape (y-axis) classifiers are considered.*



Related to Figure 3. Assessment of the predictive power of the PSSM, TFFM, and 4-bits approaches (see (Zhou et al., *2015) for the 4-bits encoding)to predict TFBSs in ChIP-seq regions. Comparison of the median AUPRC over all human ENCODE ChIP-seq data sets associated with each TF (one point per TF) when* ***A.*** *PSSM scores (x-axis) and 4-bits classifiers (y-axis),* ***B.*** *TFFM scores (x-axis) and 4-bits classifiers (y-axis),* ***C.*** *PSSM + DNA shape (x-axis) and 4-bits + DNA shape (y-axis) classifiers, and* ***D.*** *TFFM + DNA shape (x-axis) and 4-bits + DNA shape (y-axis) classifiers are considered.*