Data S7

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

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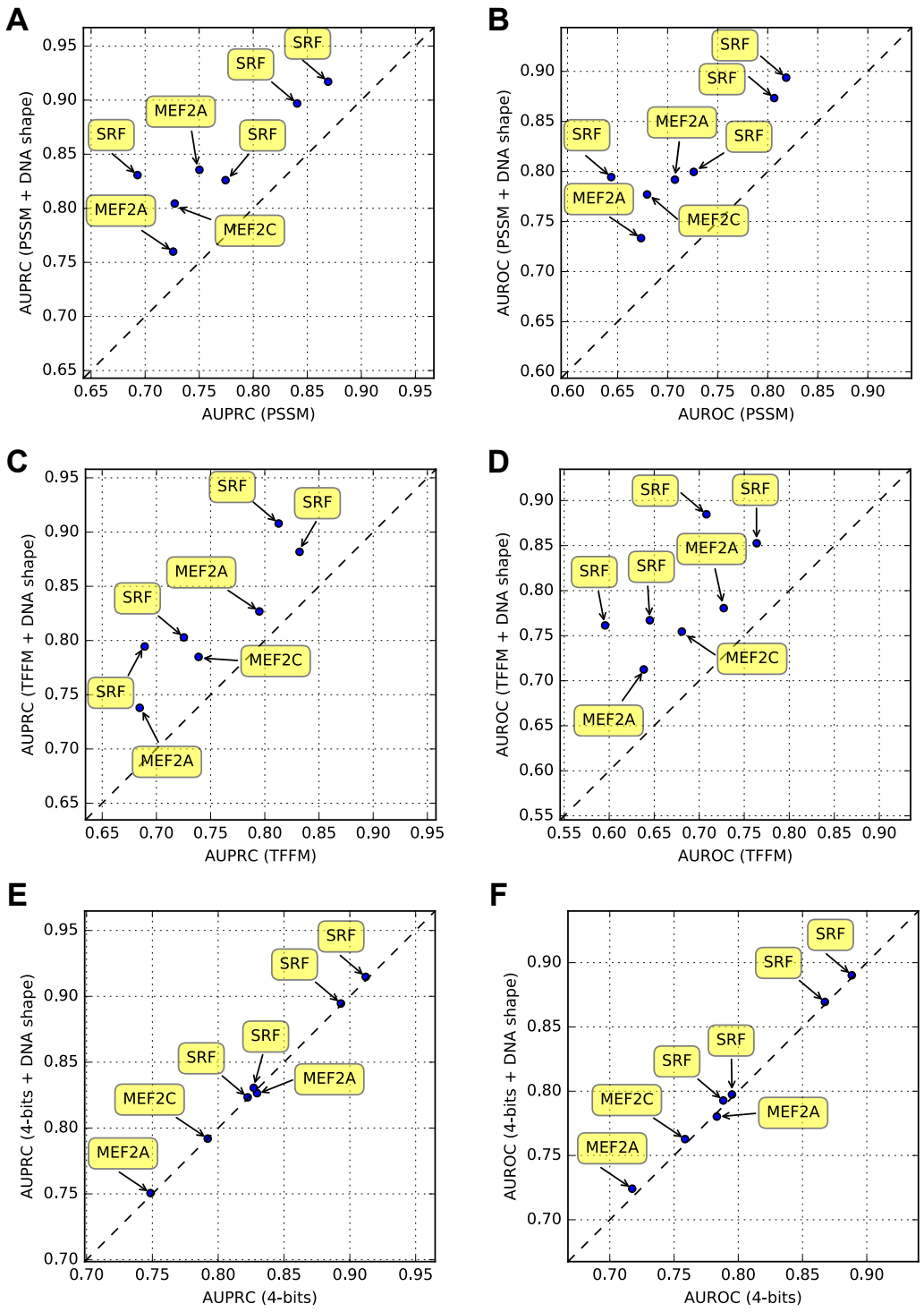
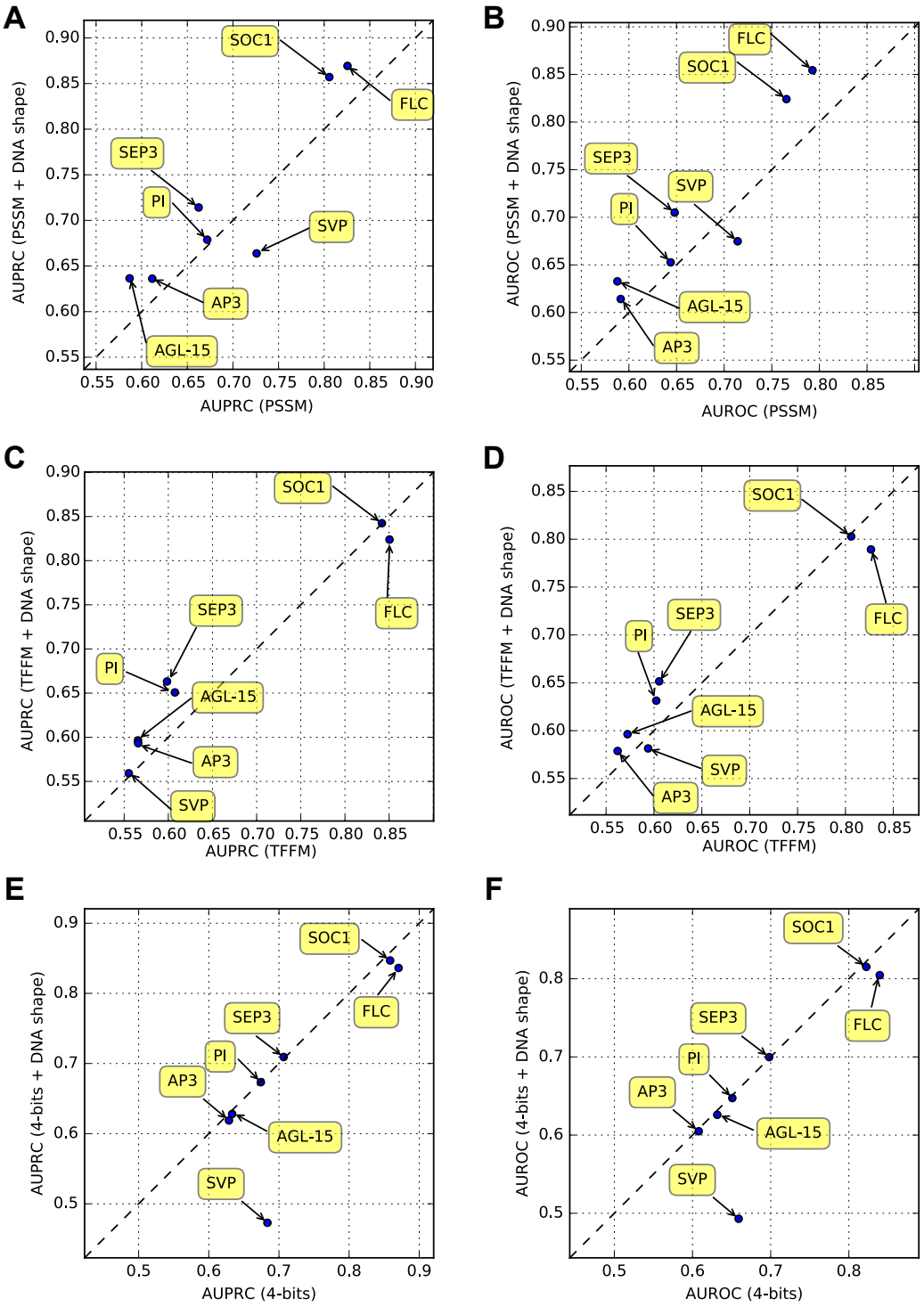
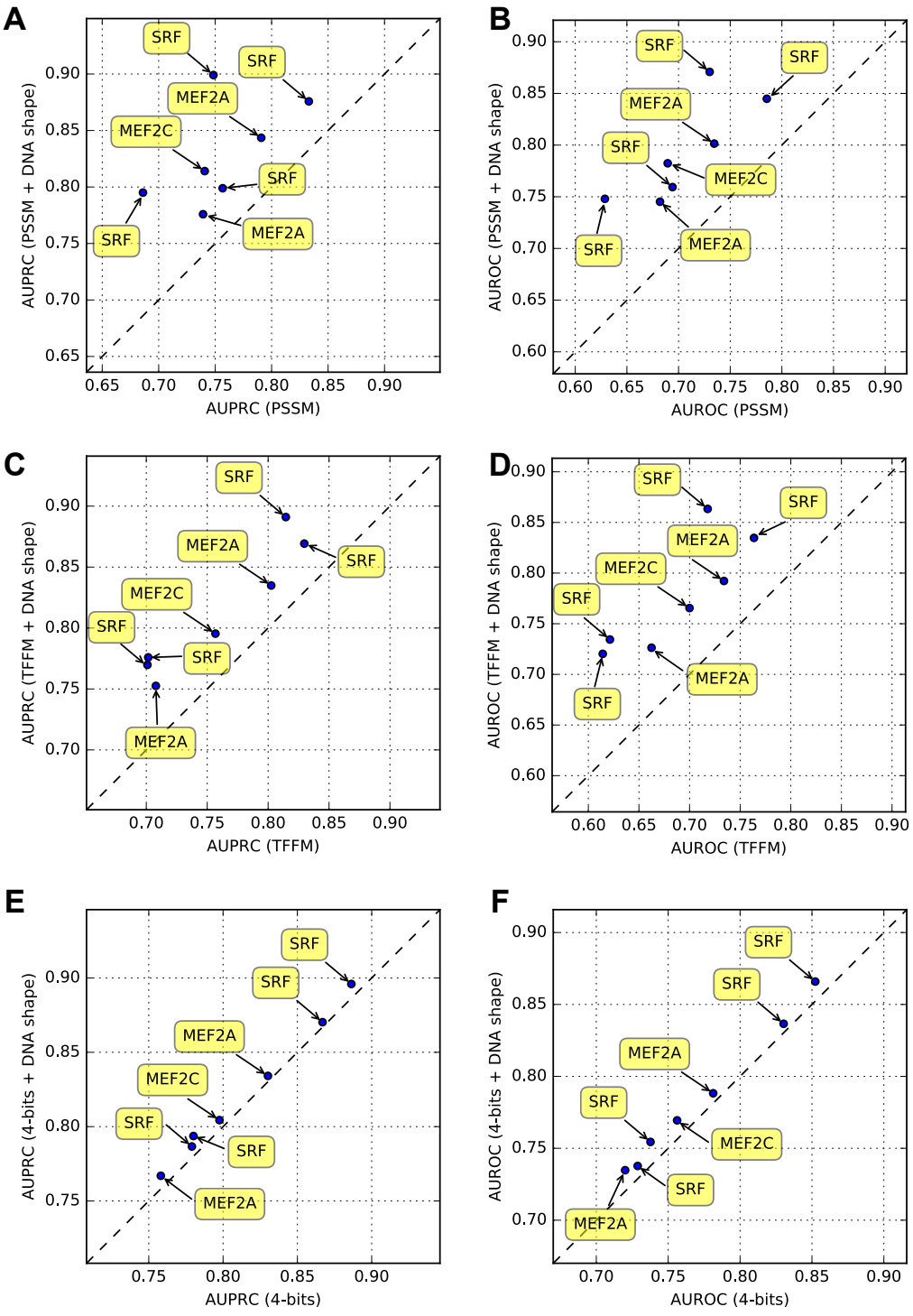


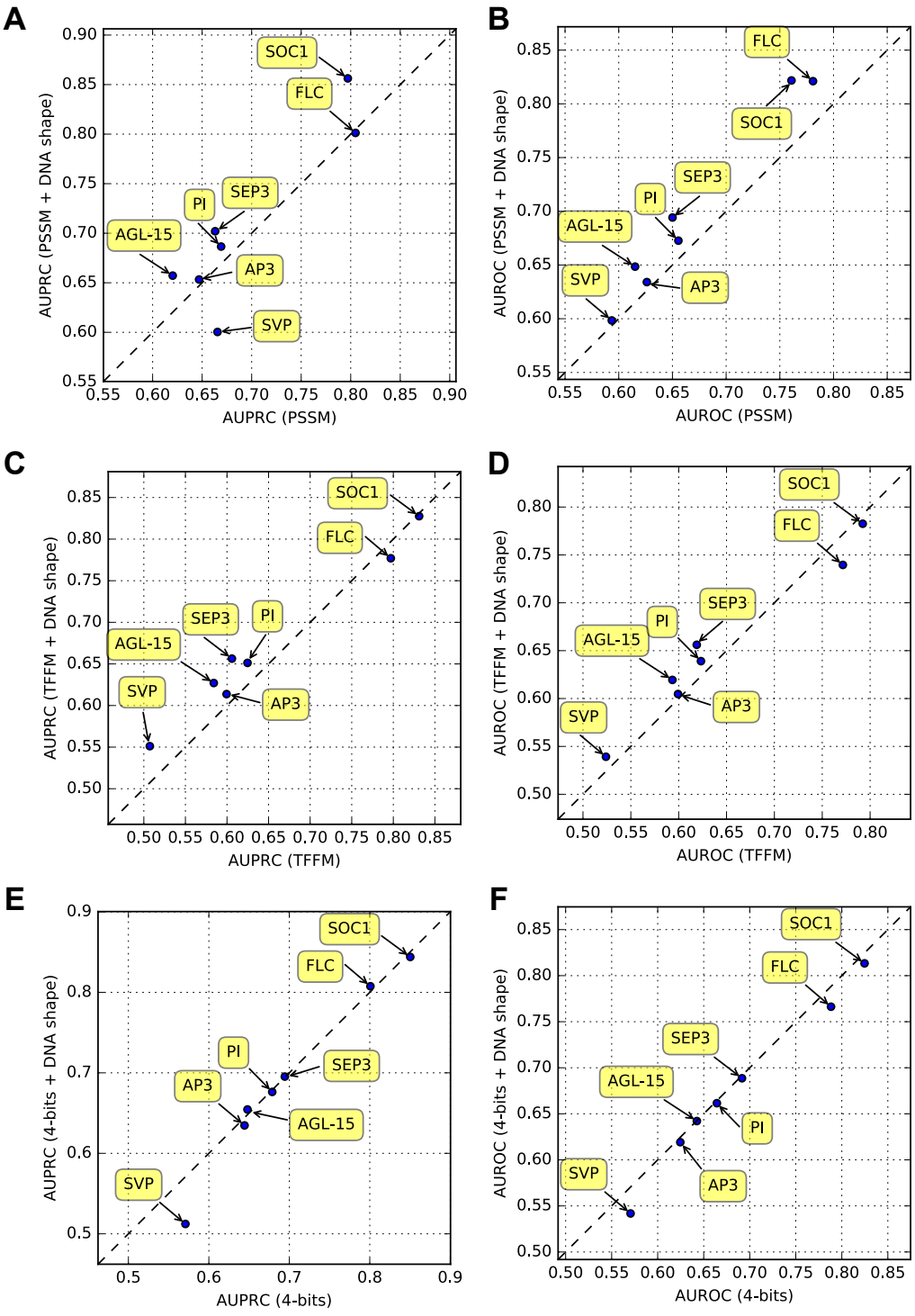
*Related to Figure 2. Comparison of the AUPRC (**A**, **C**, and **E**) or AUROC (**B**, **D**, and **F**) obtained for the 7 human ENCODE MADS TF ChIP-seq data sets when using the PSSM scores (x-axis; **A**-**B**), the TFFM scores (x-axis; **C**-**D**), or the 4-bits classifier (x-axis; **E**-**F**; see (Zhou* et al.*, 2015) for the 4-bits encoding) versus the PSSM + DNA shape (y-axis; **A**-**B**), TFFM + DNA shape (y-axis; **C**-**D**), or 4-bits + DNA shape (y-axis; **E**-**F**) classifiers.*



*Related to Figure 2. Comparison of the AUPRC (**A**, **C**, and **E**) or AUROC (**B**, **D**, and **F**) obtained for the 7 plant MADS TF ChIP-seq data sets when using the PSSM scores (x-axis; **A**-**B**), the TFFM scores (x-axis; **C**-**D**), or the 4-bits classifier (x-axis; **E**-**F**; see (Zhou* et al., *2015) for the 4-bits encoding) versus the PSSM + DNA shape (y-axis; **A**-**B**), TFFM + DNA shape (y-axis; **C**-**D**), or 4-bits + DNA shape (y-axis; **E**-**F**) classifiers.*



*Related to Figure 2. Impact of DNA shape on predicting human MADS-box TFBSs with background sequences matching the dinucleotide composition of ChIP-seq regions. Comparison of the AUPRC (**A**, **C**, and **E**) or AUROC (**B**, **D**, and **F**) obtained for the 7 human ENCODE MADS TF ChIP-seq data sets when using the PSSM scores (x-axis; **A**-**B**), the TFFM scores (x-axis; **C**-**D**), or the 4-bits classifier (x-axis; **E**-**F**; see (Zhou* et al.*, 2015) for the 4-bits encoding) versus the PSSM + DNA shape (y-axis; **A**-**B**), TFFM + DNA shape (y-axis; **C**-**D**), or 4-bits + DNA shape (y-axis; **E**-**F**) classifiers.*



*Related to Figure 2. Impact of DNA shape on predicting plant MADS-box TFBSs with background sequences matching the dinucleotide composition of ChIP-seq regions.Comparison of the AUPRC (**A**, **C**, and **E**) or AUROC (**B**, **D**, and **F**) obtained for the 7 plant MADS TF ChIP-seq data sets when using the PSSM scores (x-axis; **A**-**B**), the TFFM scores (x-axis; **C**-**D**), or the 4-bits classifier (x-axis; **E**-**F**; see (Zhou* et al., *2015) for the 4-bits encoding) versus the PSSM + DNA shape (y-axis; **A**-**B**), TFFM + DNA shape (y-axis; **C**-**D**), or 4-bits + DNA shape (y-axis; **E**-**F**) classifiers.*