**(A)**

Protein	Primary Motif DNA Binding Domain	Primary Motif Full Length	Secondary Motif DNA Binding Domain	Secondary Motif Full Length	8-mer E-score Pearson (R)	8-mer E-score Spearman (R')
Max					0.81	0.72
Bhlhb2					0.88	0.80
Gata3					0.94	0.90
Rfx3					0.72	0.67
Sox7					0.94	0.93

Figure S2: Comparison of PBM data for DNA binding domain versus full-length protein.
We created two constructs for five transcription factors: one encompassing just the DNA binding domain, and one spanning the entire protein. Each protein was applied to two PBMs of independent sequence designs, and we compared the motifs and 8-mer scores after combining the data from these arrays. **(A)** Primary and secondary motifs from Seed-and-Wobble, and correlations of 8-mer enrichment scores (E-scores) for DNA binding domain and full-length proteins. Both constructs produced essentially identical motifs by the Seed-and-Wobble algorithm and highly correlated E-scores across all 8-mers. **(B) (next page)** Scatter plots of 8-mer E-scores for the two constructs (DNA binding domain versus full-length) of these five proteins.
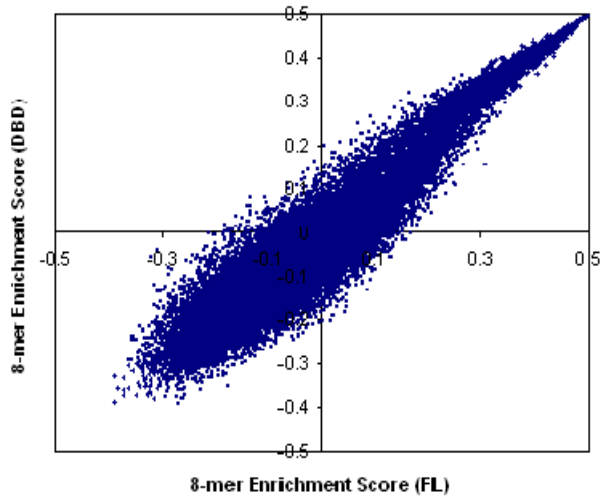
(B)
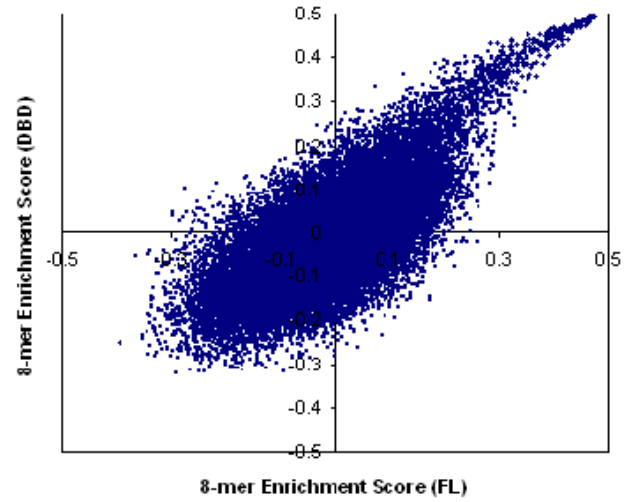
Max: DNA Binding Domain vs. Full Length
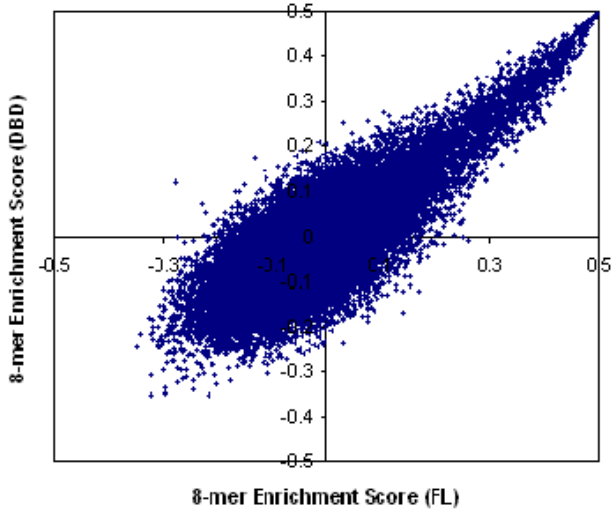
Bhlhb2: DNA Binding Domain vs. Full Length
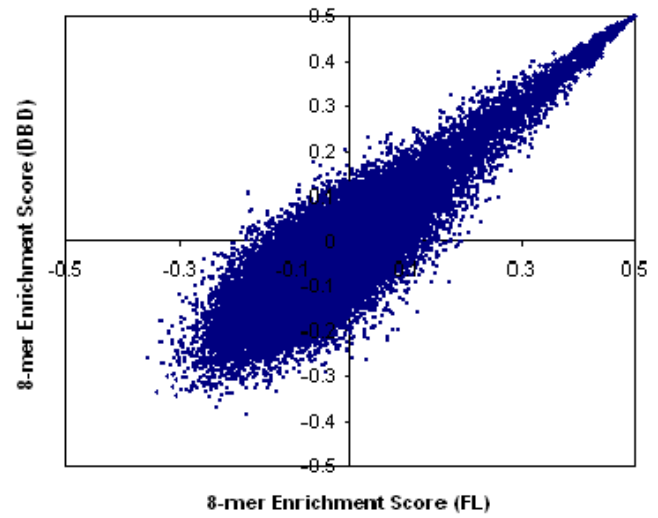
Gata3: DNA Binding Domain vs. Full Length

Rfx3: DNA Binding Domain vs. Full Length

Sox7: DNA Binding Domain vs. Full Length