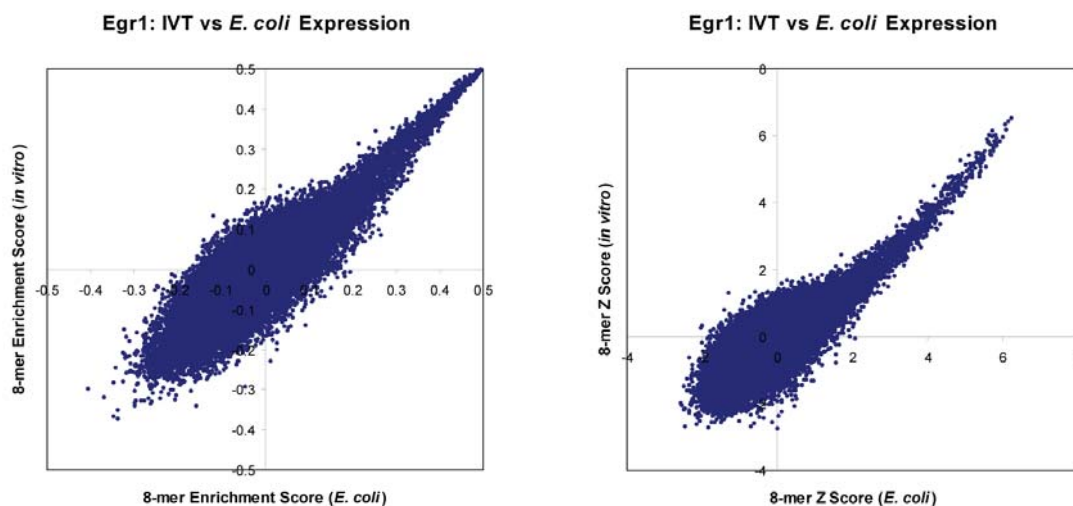


(A)

Protein	Motif <i>E. coli</i> purification	Motif <i>in vitro</i> purification	8-mer E-score Pearson (R)	8-mer E-score Spearman (R')
Arid3a			0.85	0.80
E2F2			0.92	0.85
E2F3			0.94	0.88
Egr1			0.89	0.82
Sfpi1			0.91	0.89
Tcf1			0.85	0.80

(B)



**Figure S3: *E. coli* *in vivo* versus *in vitro* protein expression.** We expressed six proteins both in *E. coli* (*in vivo*) and *in vitro* (see **Methods**) and performed PBM experiments to determine the data reproducibility for different methods of protein production. Proteins expressed *in vivo* were purified by GST affinity chromatography (see **Methods**). Each individual protein sample was applied to two PBMs of independent sequence designs, and we compared the motifs and 8-mer scores after combining the data from both arrays. (A) Both methods of protein expression produced essentially identical motifs by the Seed-and-Wobble algorithm and highly correlated Enrichment scores (E-scores) across all 8-mers. (B) Correlation of 8-mer E-scores (left) and Z-scores (right) for the C<sub>2</sub>H<sub>2</sub> zinc finger protein, Egr1.