Xu_Figure S1

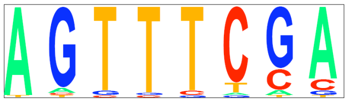
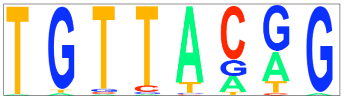
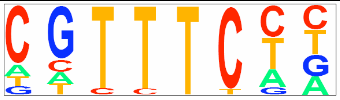
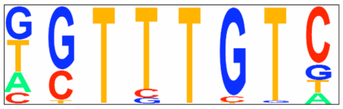
E2F	Cell line	Motif Logo	Thresholds (Core/PWM)	*p*-value
E2F1	HeLa		1.0/0.70	2.0 x10^{-3}
E2F4	HeLa		1.0/0.80	1.6 x10^{-4}
E2F6	HeLa		1.0/0.80	3.3 x10^{-6}
E2F1	GM00690		1.0/0.89	0
E2F4	GM00690		1.0/0.87	3.0 x10^{-3}
E2F6	Ntera2		1.0/0.85	1.1 x10^{-4}

Figure S1. Identification of an in vivo E2F family member binding motif. The ChIPsMotifs approach (Jin et al. 2007) was used to identify motifs that were present in the E2F1, E2F4, or E2F6 binding sites identified by ChIP-chip assay using ENCODE arrays (see Methods for details). An in vivo core consensus motif STTTS was identified for all E2F family members in the different cell lines. The threshold for the core consensus was determined to be 1.0 and for the threshold for a match to the PWM was 0.7 to 0.89 (with all matches having significant p-values less than 0.003).