Xu_Table S2. Analysis of E2F binding sites using ENCODE arrays

Cell type	Factor	Array ID	L1*	G2**	Factor	Array ID	L1	G2	Factor	Array ID	L1	G2	Merged Union***
Helas3	E2F1 A	92137	151		E2F4 A	98230	237		E2F6 A	92006	256		
	E2F1 B	X	X	77	E2F4 B	98229	166	177	E2F6 B	90938	191	183	270
	E2F1 C	92102	133		E2F4 C	98234	257		E2F6 C	92136	204		
Gm00690	E2F1 A	99020	223		E2F4 A	82778	184		E2F6 A	99096	77		
	E2F1 B	82781	194	110	E2F4 B	82771	190	128	E2F6 B	82738	110	47	187
	E2F1 C	82881	99		E2F4 C	79098	136		E2F6 C	88926	23		
Ntera2	E2F1 A	86900	22		E2F4 A	85985	29		E2F6 A	85200	325		
	E2F1 B	86783	13	6	E2F4 B	81737	14	21	E2F6 B	86912	349	226	232
	E2F1 C	86901	32		E2F4 C	88779	72		E2F6 C	77734	0		

*** L1 indicates the number of peaks called using the highest stringency criteria (see Bieda et al. 2006)**
**** G2 indicates the number of peaks that were the same in at least two of the three arrays, allowing 100 nts between the sites.**
***** Merged Union refers to merging the sets of E2F1, E2F4, and E2F6 sites for a given cell type (allowing 100 nt between the site)**