

Supplement 3: Chromosomal sites of C/EBP α -dependent AR recruitment in LNCaP cells.

CHROMOSOME	PEAK_START	PEAK_END	PEAK_SCORE	PEAK_FDR
chr14	52601046	52601205	1.17	0.00E+00
chr2	1.06E+08	1.06E+08	1.04	2.83E-02
chr12	1.22E+08	1.22E+08	0.99	0.00E+00
chr12	44497748	44498402	0.96	0.00E+00
chr10	1.15E+08	1.15E+08	0.95	0.00E+00
chr4	71491589	71491943	0.92	1.72E-03
chr18	12536855	12537508	0.92	2.90E-03
chr8	38150762	38151115	0.9	3.99E-04
chr4	48351835	48352195	0.9	3.10E-03
chr4	75392767	75393121	0.87	4.21E-03
chr2	63521540	63521989	0.85	3.10E-03
chr11	5177756	5178012	0.84	1.46E-02
chr14	19284356	19284711	0.83	4.02E-03
chr3	98641259	98641713	0.82	4.21E-03
chr2	1.57E+08	1.57E+08	0.82	4.21E-03
chr17	64652066	64652422	0.82	4.78E-03
chr12	8959815	8960174	0.82	5.62E-03
chr11	1.02E+08	1.02E+08	0.81	5.62E-03
chr3	1.32E+08	1.32E+08	0.79	5.96E-03
chr3	1.43E+08	1.43E+08	0.79	2.38E-02
chr3	1.5E+08	1.5E+08	0.79	2.38E-02
chr4	1.15E+08	1.15E+08	0.78	1.17E-02
chr11	59917285	59917534	0.78	2.19E-02
chr6	1.22E+08	1.22E+08	0.78	2.70E-02
chr17	53852984	53853345	0.77	4.02E-03
chr10	63699722	63700482	0.76	1.17E-03
chr9	21219764	21220118	0.76	8.45E-03
chr8	81574333	81574990	0.76	8.45E-03
chr6	49941427	49941682	0.75	2.87E-02
chr21	37714424	37714981	0.74	8.14E-03
chr1	2.42E+08	2.42E+08	0.73	4.18E-03
chr9	13243342	13243796	0.73	1.17E-02
chr1	1.12E+08	1.12E+08	0.73	1.17E-02
chr1	1.15E+08	1.15E+08	0.73	1.17E-02
chr11	58033004	58033560	0.73	1.37E-02
chr8	94783170	94783419	0.73	2.87E-02
chr10	1.16E+08	1.16E+08	0.73	3.36E-02
chr14	98997272	98997829	0.72	1.37E-02
chr5	95091498	95092057	0.72	1.48E-02
chr6	1.28E+08	1.28E+08	0.72	3.28E-02
chr8	53786189	53786644	0.71	1.48E-02
chr3	88193695	88194155	0.71	1.48E-02
chr2	2.02E+08	2.02E+08	0.71	1.48E-02
chr12	4627032	4627382	0.71	1.99E-02
chr10	27023400	27023756	0.71	2.14E-02
chr19	9189663	9189921	0.71	2.19E-02

chr1	93029799	93030552	0.7	5.13E-03
chr1	2.15E+08	2.15E+08	0.7	1.48E-02
chr11	59238745	59239199	0.7	1.99E-02
chr6	1.13E+08	1.13E+08	0.7	2.14E-02
chr6	1.47E+08	1.47E+08	0.7	2.14E-02
chrX	1.03E+08	1.03E+08	0.7	2.48E-02
chr11	1.02E+08	1.02E+08	0.7	4.44E-02
chr18	12442365	12442721	0.69	2.48E-02
chr12	1.15E+08	1.15E+08	0.68	3.63E-03
chr16	33867894	33868450	0.68	8.14E-03
chr21	30666452	30667001	0.68	1.99E-02
chr21	30775357	30775806	0.68	1.99E-02
chr8	1.21E+08	1.21E+08	0.68	2.14E-02
chr9	1.25E+08	1.25E+08	0.68	2.14E-02
chr3	1.44E+08	1.44E+08	0.68	2.14E-02
chr12	91338665	91339118	0.68	2.48E-02
chr3	69253657	69253906	0.68	3.86E-02
chr2	1.72E+08	1.72E+08	0.68	3.86E-02
chr20	10144576	10145128	0.67	2.82E-03
chr1	1.58E+08	1.58E+08	0.67	2.14E-02
chr1	2.35E+08	2.35E+08	0.67	2.14E-02
chr11	85688035	85688498	0.67	2.48E-02
chr6	1.19E+08	1.19E+08	0.67	2.84E-02
chr5	1.48E+08	1.48E+08	0.67	2.84E-02
chr13	27645719	27646175	0.67	3.35E-02
chr3	88268251	88268610	0.66	2.84E-02
chr3	1.1E+08	1.1E+08	0.66	2.84E-02
chr3	1.47E+08	1.47E+08	0.66	2.84E-02
chr4	77121509	77122158	0.66	3.57E-02
chr4	1.29E+08	1.29E+08	0.66	3.57E-02
chr4	1.66E+08	1.66E+08	0.66	3.57E-02
chr1	1.96E+08	1.96E+08	0.65	1.08E-02
chr1	92313157	92313606	0.65	2.84E-02
chr1	1.58E+08	1.58E+08	0.65	2.84E-02
chr1	1.76E+08	1.76E+08	0.65	2.84E-02
chr12	8956115	8956473	0.65	3.35E-02
chr15	97613278	97614137	0.65	3.35E-02
chr8	41918701	41918956	0.65	5.00E-02
chr1	1.85E+08	1.85E+08	0.65	5.00E-02
chr17	26185761	26186211	0.64	1.99E-02
chr17	26647626	26648187	0.64	1.99E-02
chr17	64649860	64650323	0.64	1.99E-02
chr13	51933217	51933871	0.64	2.32E-02
chrX	1.01E+08	1.01E+08	0.64	2.32E-02
chr7	88264917	88265476	0.64	2.84E-02
chr7	1.56E+08	1.56E+08	0.64	2.84E-02
chr10	1.04E+08	1.04E+08	0.64	3.35E-02
chr5	69624826	69625179	0.64	3.57E-02
chr6	1.19E+08	1.19E+08	0.64	3.57E-02
chr6	1.39E+08	1.39E+08	0.64	3.57E-02

chr4	68511303	68511752	0.64	4.54E-02
chr4	1.11E+08	1.11E+08	0.64	4.54E-02
chr4	1.57E+08	1.57E+08	0.64	4.54E-02
chrX	16597366	16597815	0.64	4.65E-02
chr13	49362869	49363225	0.64	4.65E-02
chr2	18634759	18635519	0.63	1.92E-02
chr2	33668969	33669727	0.63	1.92E-02
chr2	33512319	33512671	0.63	3.57E-02
chr3	79721301	79721760	0.63	3.57E-02
chr2	80394015	80394664	0.63	3.57E-02
chr3	99732541	99733092	0.63	3.57E-02
chr3	1.09E+08	1.09E+08	0.63	3.57E-02
chr3	1.59E+08	1.59E+08	0.63	3.57E-02
chr2	1.92E+08	1.92E+08	0.63	3.57E-02
chr18	7743870	7744430	0.63	4.65E-02
chr8	58036974	58038334	0.62	0.00E+00
chr10	1.04E+08	1.04E+08	0.62	5.01E-03
chr8	173196	173747	0.62	3.57E-02
chr1	45695608	45695957	0.62	3.57E-02
chr9	74053456	74054115	0.62	3.57E-02
chr7	99646563	99647012	0.62	3.57E-02
chr1	1.73E+08	1.73E+08	0.62	3.57E-02
chr11	46522205	46522763	0.62	4.65E-02
chr15	91243248	91243805	0.62	4.65E-02
chr4	86038556	86039508	0.61	6.58E-03
chr16	18722733	18723291	0.61	2.48E-02
chr19	19995836	19996185	0.61	2.48E-02
chr19	22155973	22156327	0.61	2.48E-02
chr16	66312068	66312517	0.61	2.48E-02
chr22	29687623	29687879	0.61	4.44E-02
chr6	50893571	50894027	0.61	4.54E-02
chr6	96569389	96569838	0.61	4.54E-02
chr14	20566596	20567054	0.61	4.65E-02
chr9	21789934	21790389	0.6	4.54E-02
chr8	27946639	27947199	0.6	4.54E-02
chr3	52276544	52277198	0.6	4.54E-02
chr9	74055056	74055512	0.6	4.54E-02
chr9	1.02E+08	1.02E+08	0.6	4.54E-02
chr3	1.34E+08	1.34E+08	0.6	4.54E-02
chr2	1.83E+08	1.83E+08	0.6	4.54E-02
chr1	1.85E+08	1.85E+08	0.59	1.14E-02
chr7	1.48E+08	1.48E+08	0.59	2.27E-02
chr22	31182623	31183080	0.59	2.48E-02
chr10	1.21E+08	1.21E+08	0.59	3.02E-02
chr17	11440572	11441029	0.59	3.35E-02
chr20	11844595	11845157	0.59	3.35E-02
chr20	56682807	56683259	0.59	3.35E-02
chr17	63966722	63967377	0.59	3.35E-02
chr1	1.13E+08	1.13E+08	0.59	4.54E-02
chr1	1.72E+08	1.72E+08	0.59	4.54E-02

chr1	2.38E+08	2.38E+08	0.59	4.54E-02
chr14	19281926	19282884	0.58	3.02E-02
chr6	1.28E+08	1.28E+08	0.58	3.36E-02
chr4	23503338	23504091	0.58	4.53E-02
chr2	1.79E+08	1.79E+08	0.57	3.36E-02
chr1	2.08E+08	2.08E+08	0.57	3.36E-02
chr12	14857833	14858790	0.57	4.08E-02
chr14	90997365	90998024	0.56	4.08E-02
chr16	24456308	24456862	0.56	4.65E-02
chr19	57924697	57925155	0.56	4.65E-02
chr16	78195205	78195565	0.56	4.65E-02
chr18	23021127	23022276	0.55	1.78E-02
chr2	1.52E+08	1.52E+08	0.55	4.53E-02
chr7	24900069	24901118	0.54	4.53E-02
chr7	92697171	92698024	0.54	4.53E-02
chr3	18456458	18457613	0.52	2.70E-02
chr3	62837744	62838702	0.52	2.70E-02
chr7	1.12E+08	1.12E+08	0.51	0.00E+00
chr2	70376428	70377577	0.49	1.86E-02
chr1	1.51E+08	1.51E+08	0.46	8.77E-03
chr20	32159090	32160344	0.44	2.07E-02
chr17	31441341	31442197	0.43	3.69E-02
chr19	57996201	57997262	0.43	3.69E-02

LNCaP cells were nucleofected with either C/EBP α or the corresponding empty vector for 48 h; then the cells were treated for 2 h with either R1881 (1nM) or vehicle and the samples were subjected to ChIP-chip analysis using anti-AR antibody as described under Methods. The Table lists chromatin sites at which AR recruitment was dependent on the presence of C/EBP α . Only peaks with FDR<0.05 are included in this Table.