

Supplementary Figures:

Figure S1. Enrichment of 8-mers in GR, c-Jun and Hoxa2 ChIP-seq Peaks. (A) Enrichment of GR-like split 8-mers (N-NNN---NNN-N) and their occurrences in the GR ChIP-seq peaks. (B) Enrichment of AP-1-like 8-mers (NNNNNNNN) and their occurrences in the c-Jun ChIP-seq peaks. (C) Enrichment of 8-mers (NNNNNNNN) and their occurrences in the Hoxa2 ChIP-seq peaks.

Figure S2. Average intrinsic nucleosome occupancy score for canonical motifs. (A) Average INOS by Tillo's model [1-2] near (± 750 -bps) canonical GR motifs (G-ACA---TGT-C): GR ChIP-seq peaks contain 523 canonical motifs in pre-programmed DHS, 665 in re-programmed DHS, 205 without DHS, and unbound GR motifs. Fraction of peaks containing the canonical motif is shown in percent. (B) Average INOS by Tillo's model near (± 750 -bps) canonical AP-1 motifs (TGA^C/_GTCA): c-Jun ChIP-seq peaks contain 10,673 canonical motifs in pre-programmed DHS, 96 in re-programmed DHS, and 495 without DHS. The average INOS for 260,047 unbound AP-1 motifs is shown. 100,000 randomly selected sequences are shown. Fraction of peaks containing the canonical motif is shown as a percent (%). (C) Average intrinsic nucleosome occupancy probability by Segal's model [3] near (± 750 -bps) canonical GR motifs. (D) Average intrinsic nucleosome occupancy probability by Segal's model near (± 750 -bps) canonical AP-1 motifs. (E) Average INOS near (± 750 -bps) canonical GR motifs (G-ACA--TGT-C) with INOS from -2 to -1; 38 bound and 1,786 unbound GR motifs are shown.

Figure S3. (A) Average INOS near (± 750 -bps) the center of c-Jun ChIP-seq peaks with and without AP-1 motif (TGA^C/_GTCA). (B) Average INOS near (± 750 -bps) the center of GR ChIP-seq peaks with and without GR motifs (G-ACA---TGT-C). (C) The histogram shows the distribution of INOS for all c-Jun ChIP-seq peaks with (blue)/without (red) AP-1 motif. (D) The histogram shows the distribution of INOS for all c-Jun ChIP-seq peaks with (blue)/without (red) GR motif.

Figure S4. Chromatin accessibility of GR and AP-1 motifs in 3134 cell line. (A) Number of sequencing reads within 150-bps for c-Jun ChIP-seq data at each of the AP-1 8-mers motifs (ATGAGTCA) in the genome compared to DHS reads. Motifs are labeled depending on their presence at pre-, re- and unprogrammed DHS. Unbound AP-1 motifs are presented in grey. (B) Number of sequencing reads within 150-bps for GR ChIP-seq at each of the GR motifs in the

genome compared to DHS reads. Sequence reads for GR and c-Jun ChIP-seq are normalized. **(C)** Density of sequenced tags for GR, c-Jun ChIP-seq, and DNase-seq were counted in 3-Kb up and downstream of the bound GR motifs. **(D)** Density of sequenced tags for GR, c-Jun ChIP-seq and DNase-seq were counted in 3-Kb up and downstream of the bound AP-1 motifs (ATGAGTCA). The bin size used is 300-bps with 150-bps sliding window.

Figure S5. Clusters of GR and AP-1 motifs are better bound. **(A)** The occurrence of clustered GR canonical motifs (G-ACA---TGT-C) in the genome and percent bound by GR are presented in different genomic scales from 150-bps to 100-Kbps. The black line denotes percent of GR motifs that are bound in GR peaks. **(B)** The occurrence of clustered AP-1 canonical motifs (TGA^C/_GTCA) and percent bound by c-Jun are presented in different genomic scales from 150-bps to 20-Kbps.

Figure S6. Co-occurrence of AP-1 motifs (TGA^C/_GTCA) within a nucleosomal distance promotes GR binding. **(A)** The occurrence of pairs of canonical GR and AP-1 motifs with space less than 150-bps in the GR ChIP-seq peaks. **(B)** GR binds preferentially to the GR motifs with co-occurrence of AP-1 motifs and with higher INOS. The blue solid histogram shows all 1,448 pairs of GR and AP-1 motifs with space less than 150-bps in genome, and the red blank histogram shows the binding ratio in GR peaks (average is 15.3%, black dashed line). **(C-D)** Enrichment of split 8-mers (N-NNN---NNN-N) vs. all continuous 8-mers in the **(C)** c-Jun and **(D)** Hoxa2 ChIP-seq peaks. Red dots represent the canonical GR motif and 1-bp variants, and the mismatched base is labeled in red. Blue dots represent the 8-mers with AP-1 motif.

Figure S7. The 1-bp variants of canonical GR motif need more co-occurrence of canonical AP-1 motifs to facilitate GR binding. **(A)** The relative occurrence of the canonical GR motif and 1-bp variants in pre-, re- and un-programmed GR peaks. The relative occurrence of motifs is calculated as the number of motifs bound per 1000 GR peaks. The motifs are ordered by the enrichment in GR peaks. **(B)** Correlation of tag-density of GR peaks and enrichment of the canonical GR motif and the other 12 1-bp variants in pre-programmed GR peaks. **(C-E)** Correlation of tag-density of GR peaks and co-occurrence of AP-1 motifs in **(C)** pre-programmed, **(D)** re-programmed and **(E)** un-programmed GR peaks with the canonical and 1-bp variants of GR motif. For each dot, the horizontal axis of tag-density is the average tag-density of GR peaks with this motif, and the vertical axis indicates the percentage of GR motifs with AP-1

motifs within 150 bps. The 118 canonical motifs and 3 variants (occurrence < 50) with AP-1 motifs nearby in pre-programmed GR peaks are labeled in each panel. **(F)** Enrichment of all GR-like (NN-NNN---NNN-NN) and AP-1-like (NNNNNNNNNN) 10-mers in the GR ChIP-seq peaks. The enrichment of each 10-mer is calculated as the normalized ratio of occurrence in GR peaks (± 150 bps from the center of GR peaks) over occurrence in neighbors (± 750 to ± 150 from center of GR peaks). As expected, [G/A]G-ACA---TGT-C[C/T] and AG-ACA---CGT-C[C/T] are enriched, as high as nearly 40. A new pattern of AC-TAG---TGG-AC [gACtTAGggc] also shows a high enrichment.

Figure S8. Effect of A-FOS on GR binding to the canonical GR motif and 1-bp variants depends on the presence of an AP-1 motif within 150-bps. **(A-C)** Percent of GR motifs with (blue) /without (Red) an nearby AP-1 motif that loses GR binding after inhibition of c-Jun binding by expressing the dominant negative A-FOS) in **(A)** pre-programmed, **(B)** re-programmed and **(C)** un-programmed GR peaks.

References:

1. Tillo D, Hughes TR: **G+C content dominates intrinsic nucleosome occupancy.** *BMC Bioinformatics* 2009, **10**:442.
2. Tillo D, Kaplan N, Moore IK, Fondufe-Mittendorf Y, Gossett AJ, Field Y, Lieb JD, Widom J, Segal E, Hughes TR: **High nucleosome occupancy is encoded at human regulatory sequences.** *PLoS One*, **5**:e9129.
3. Kaplan N, Moore IK, Fondufe-Mittendorf Y, Gossett AJ, Tillo D, Field Y, LeProust EM, Hughes TR, Lieb JD, Widom J, Segal E: **The DNA-encoded nucleosome organization of a eukaryotic genome.** *Nature* 2009, **458**:362-366.

Figure S2. Nucleosome occupancy at regulatory sites

Tillo's Model

Segal's Model

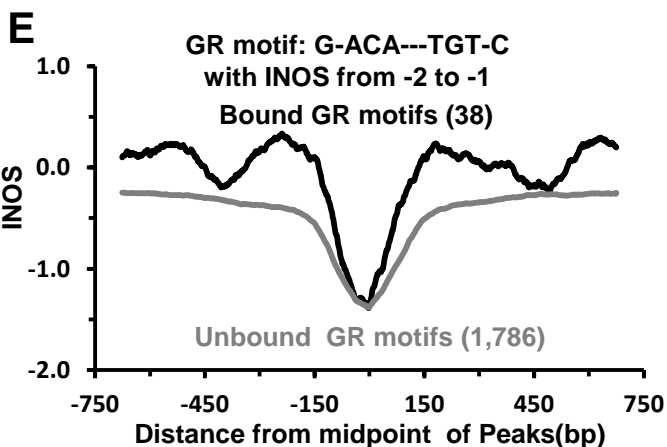
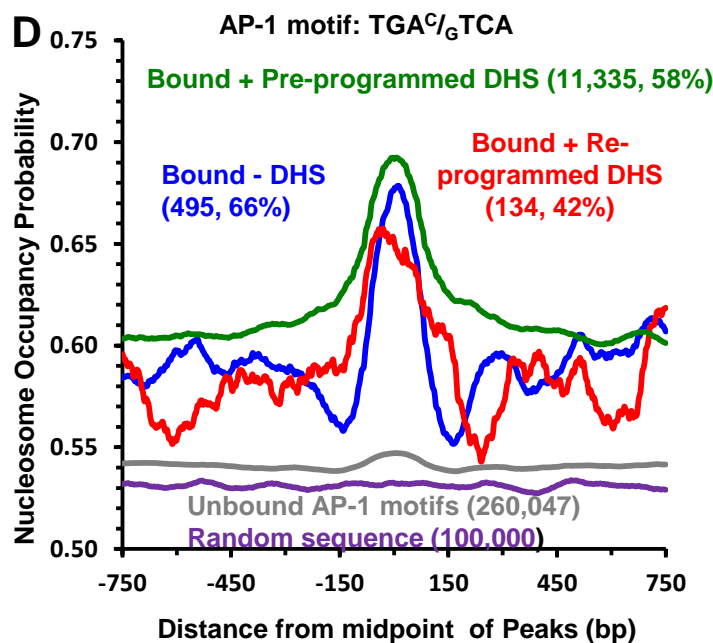
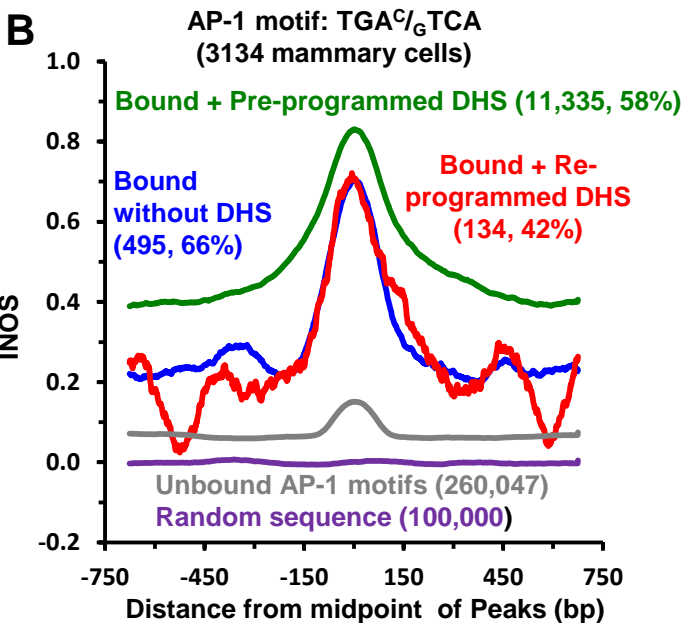
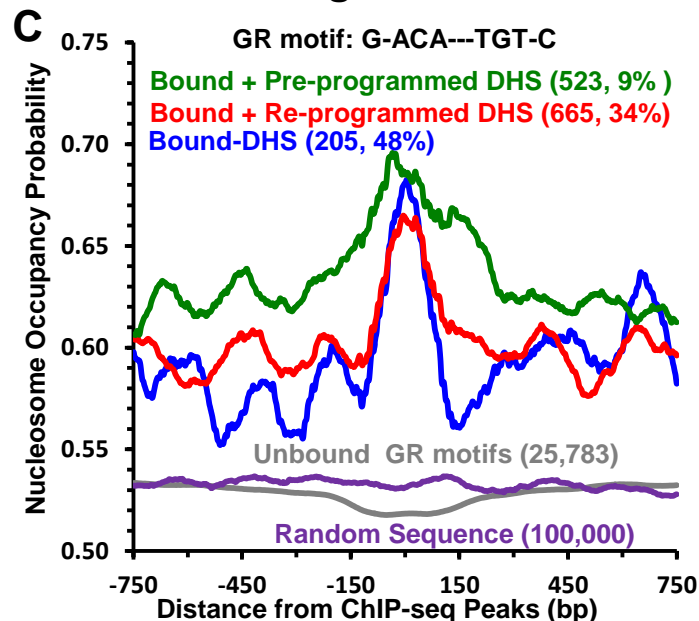
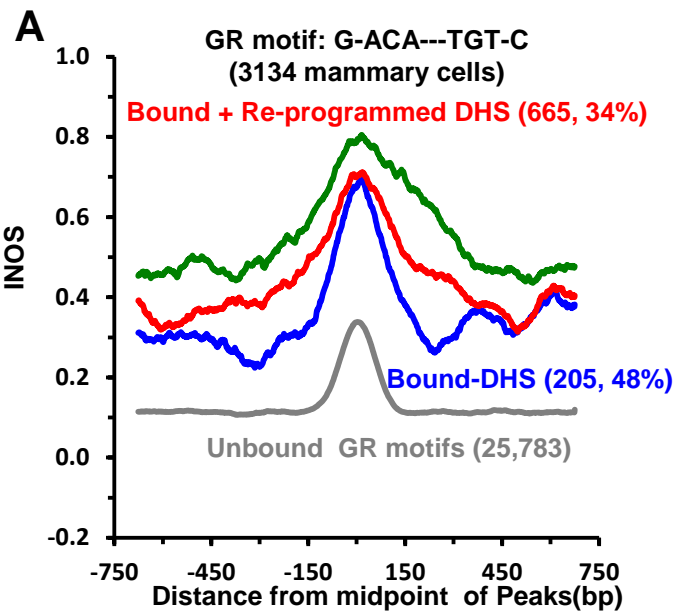


Figure S3. Nucleosome occupancy at regulatory sites

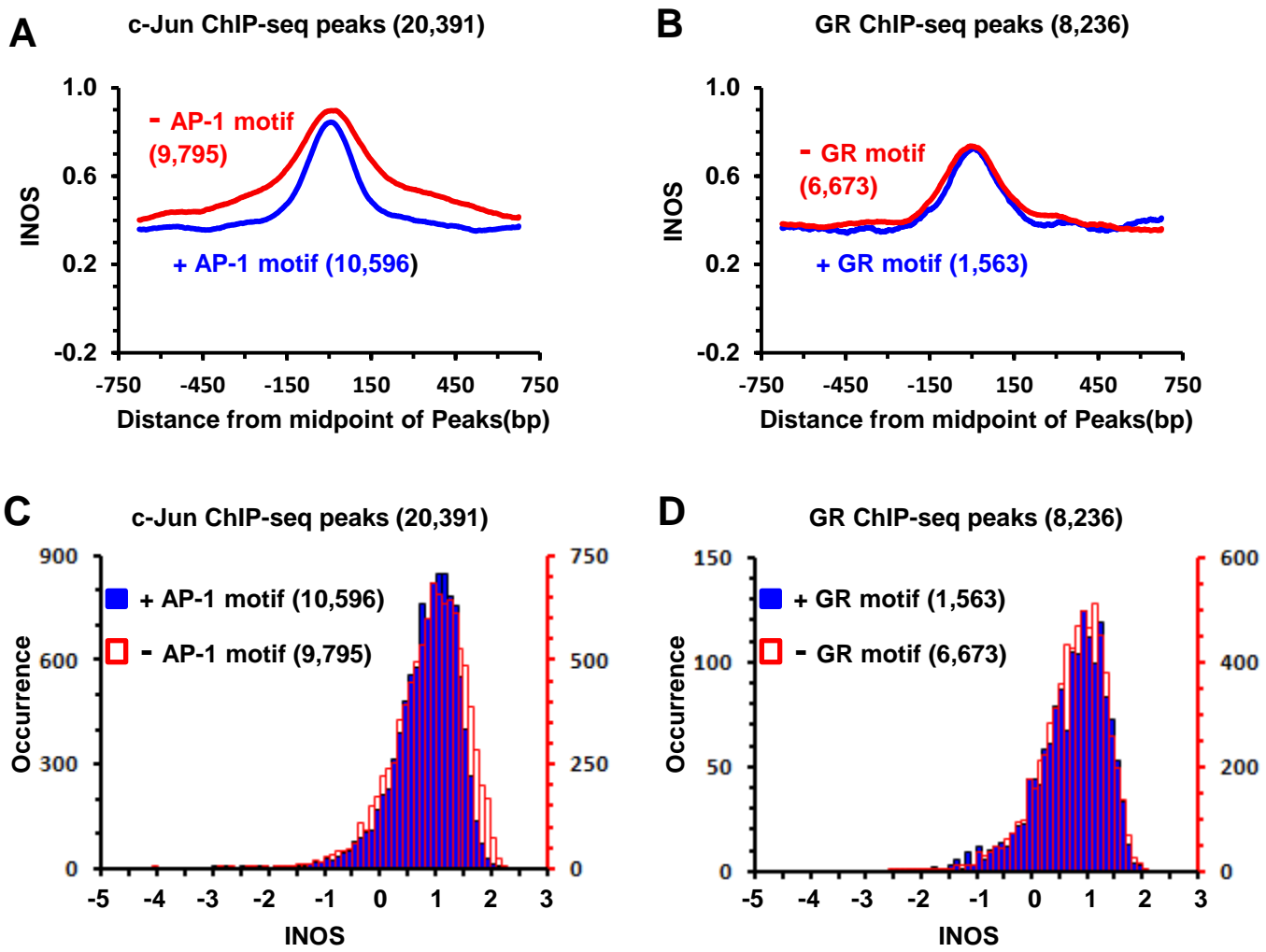


Figure S4. Chromatin accessibility of GR and AP-1 canonical motifs *in vivo*

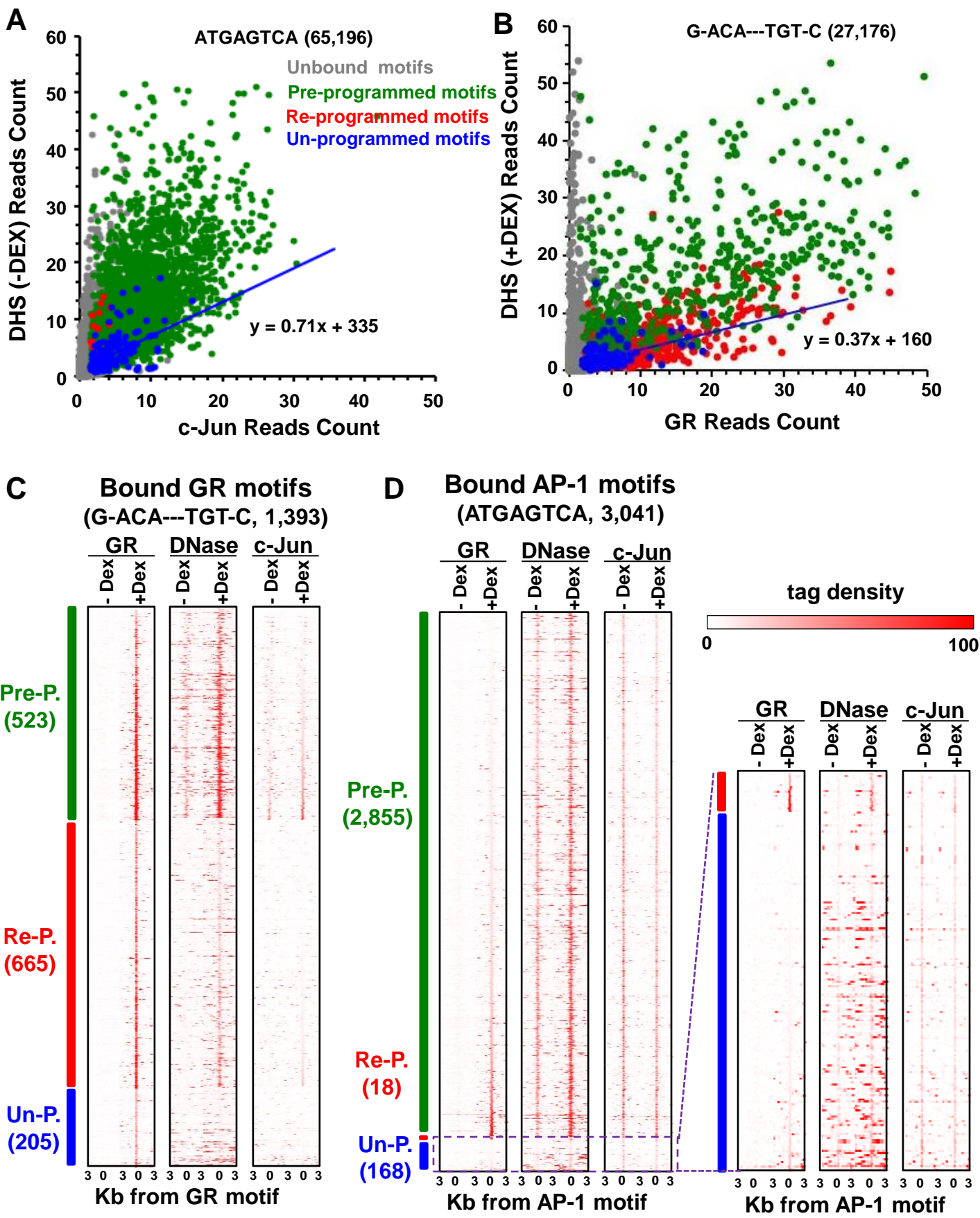


Figure S5. Clusters of GR and AP-1 motifs are better bound

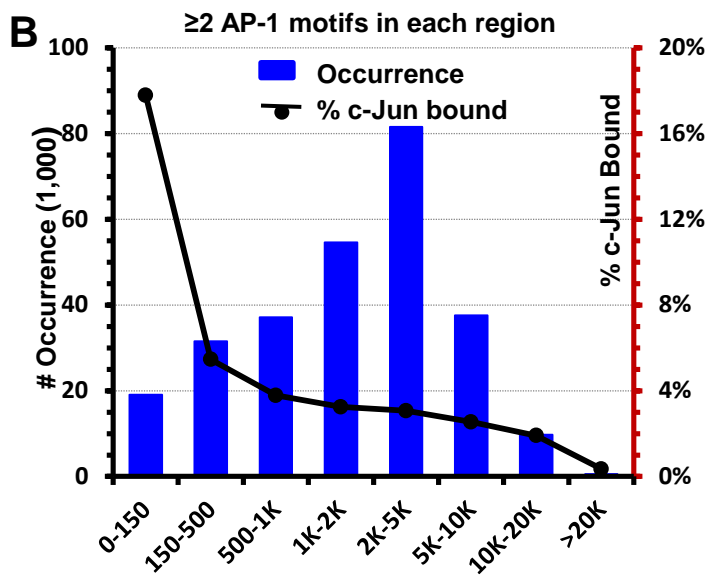
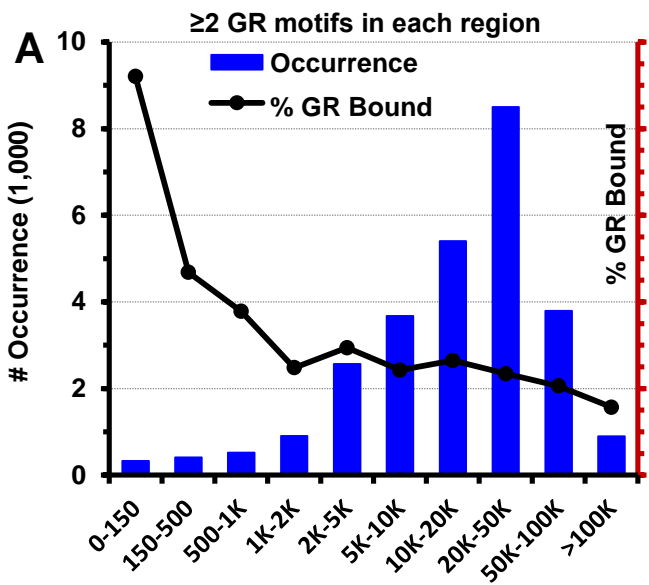


Figure S6. Co-occurrence of AP-1 motifs (TGA^C/_GTCA) within a nucleosome range promotes GR binding

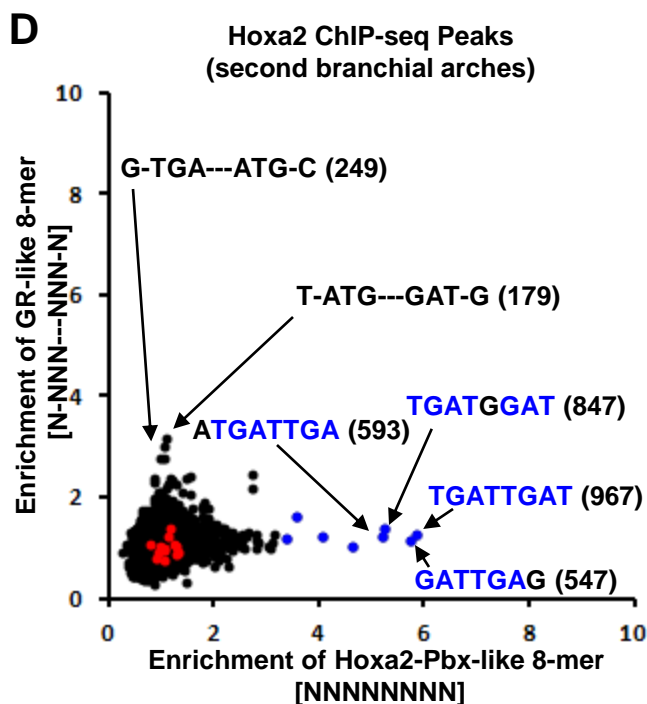
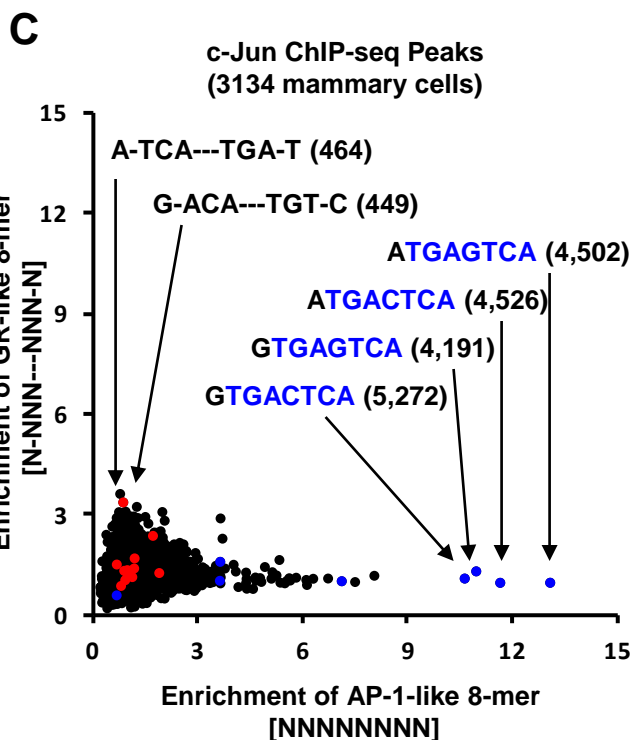
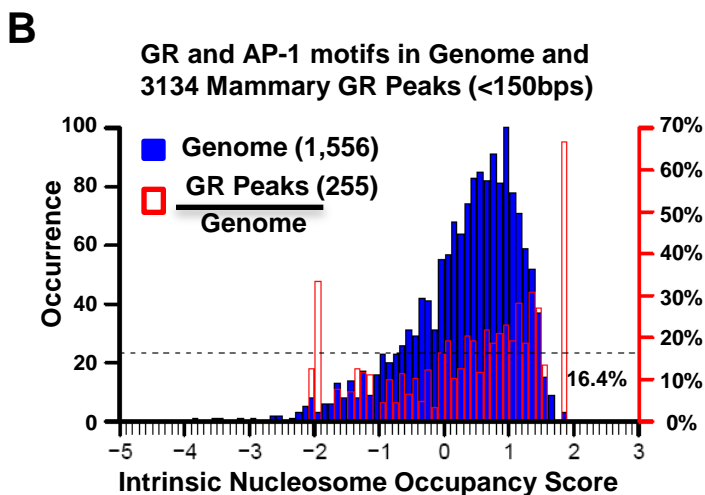
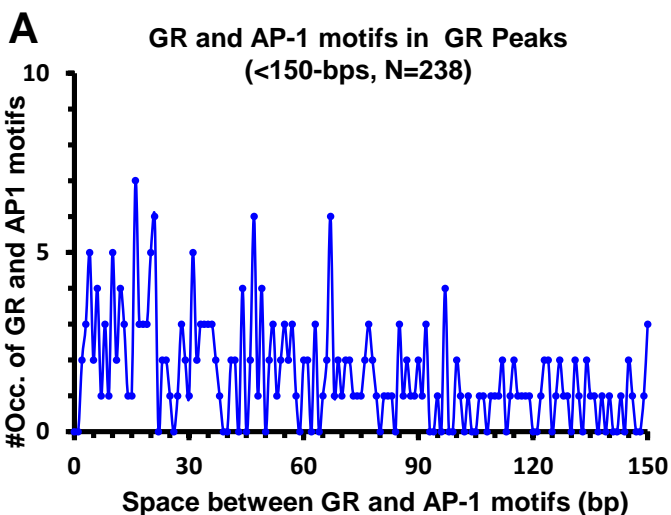


Figure S7. The 1-bp variants of GR motifs need more co-occurrence of AP-1 motifs to facilitate GR binding.

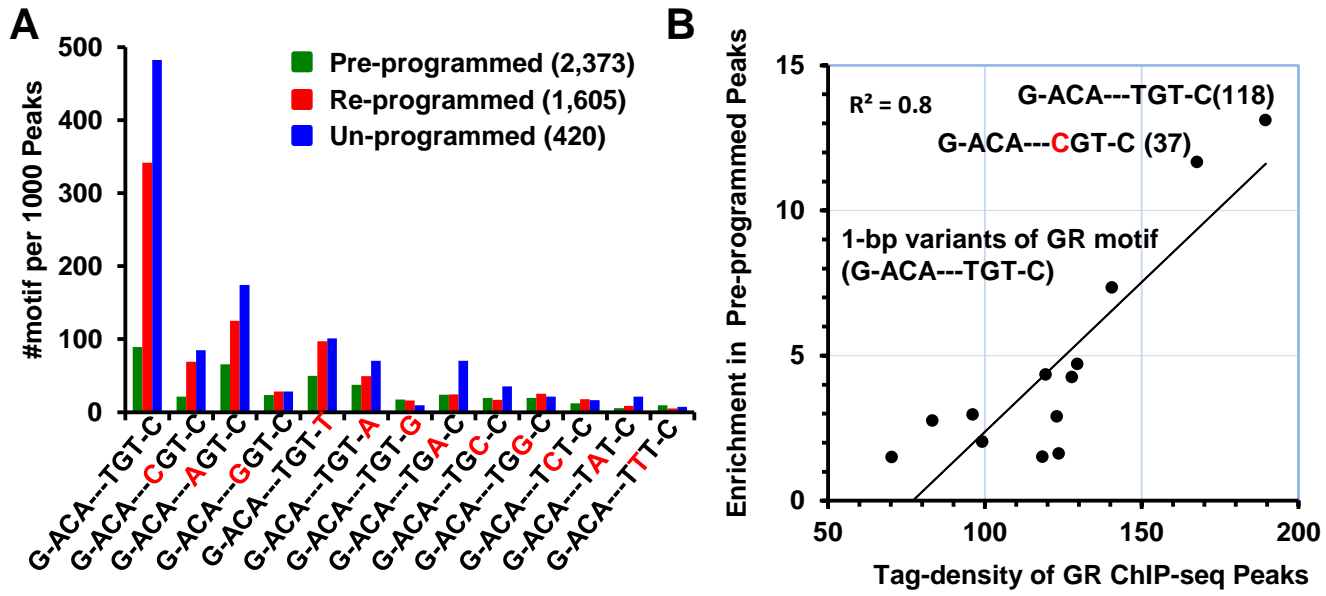
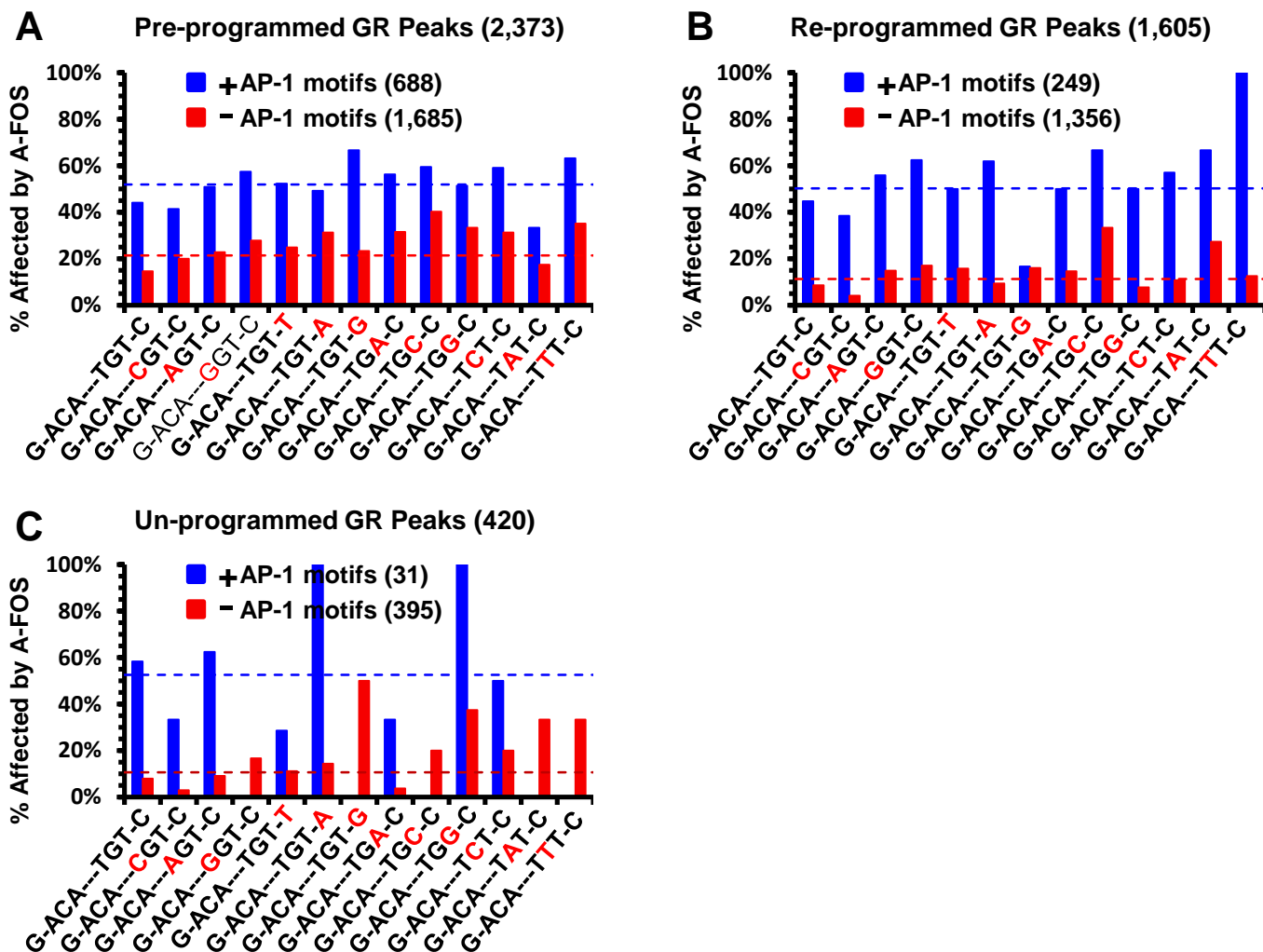


Figure S8. Effect of A-FOS on GR binding to the GR motif and 1-bp variants depends on the presence of an AP-1 motif within 150-bps.



Supplementary Table 1A. Modeling the c-Jun binding of consensus AP-1 motif (TGACTCA|ATGAGTCA) using generalized linear models (GLM)

Evaluated parameters	ATGAGTCA						TGAGTCA					
	PVE(%)		CV.err		AUC		PVE(%)		CV.err		AUC	
	+Motif			-Motif			+Motif			-Motif		
A1. Peak	10.4	0.05	0.76	9.9	0.05	0.75	10.3	0.04	0.76	7.4	0.04	0.72
A2. Background	5.6	0.05	0.69	5.6	0.05	0.69	6.5	0.04	0.70	6.5	0.04	0.70
A3. Relative peak	2.5	0.05	0.63	2.3	0.05	0.63	1.9	0.04	0.62	1.6	0.04	0.61
A. INOS (A1+A2+A3)	11.3	0.05	0.77	10.9	0.05	0.76	11.5	0.04	0.77	8.2	0.04	0.73
B. Overlap with CGIs	0.8	0.05	0.53	0.8	0.05	0.53	0.9	0.04	0.53	0.9	0.04	0.53
C. Cluster of AP-1 motifs	0.8	0.05	0.53	-	-	-	5.5	0.04	0.66	-	-	-
D. Co-occurrence of GR motifs	0.1	0.05	0.51	0.1	0.05	0.51	0.2	0.04	0.51	0.2	0.04	0.51
E. Chromatin Accessibility (DHS)	55.1	0.05	0.94	55.1	0.05	0.94	56.5	0.04	0.93	56.5	0.04	0.93
A+B	11.4	0.05	0.77	11.1	0.05	0.77	12.3	0.04	0.78	8.3	0.04	0.73
A+B+C	12.2	0.05	0.78	11.9	0.05	0.77	13.9	0.04	0.79	13.5	0.04	0.78
A+B+C+D	12.3	0.05	0.78	12.0	0.05	0.77	14.0	0.04	0.79	13.6	0.04	0.78
A+B+C+D+E	56.1	0.04	0.96	56.1	0.04	0.96	59.6	0.03	0.96	59.5	0.03	0.96

PVE: Percent of variance explained (%) = 1-(deviance/null.deviance)

Supplementary Table 1B. Modeling the GR binding of consensus GR motifs (G-ACA---TGT-C) in different cell lines using generalized linear models (GLM)

Evaluated Parameters	3134 (1,393/8,236)						AtT-20 (390/3,104)					
	PVE(%)		CV.err		AUC		PVE(%)		CV.err		AUC	
	+Motif			-Motif			+Motif			-Motif		
A1. Peak	2.9	0.05	0.63	2.7	0.05	0.63	2.2	0.02	0.63	2.1	0.02	0.63
A2. Background	3	0.05	0.64	3	0.05	0.64	1.6	0.02	0.62	1.6	0.02	0.62
A3. Relative peak	0.2	0.05	0.53	0.2	0.05	0.53	0.4	0.02	0.56	0.4	0.02	0.56
A. INOS (A1+A2+A3)	3.9	0.05	0.66	3.9	0.05	0.66	2.6	0.02	0.65	2.6	0.02	0.65
B. Overlap with CpG islands (CGIs)	0.1	0.05	0.51	0.1	0.05	0.51	0.2	0.02	0.52	0.2	0.02	0.52
C. Cluster of GR motifs	0.6	0.05	0.51	-	-	-	0.1	0.02	0.50	-	-	-
D1. Co-occurrence with canonical AP-1 motifs	2.6	0.05	0.57	2.6	0.05	0.57	0.1	0.02	0.51	0.1	0.02	0.51
D2. Co-occurrence with ≥2 canonical AP-1 motif	0.3	0.05	0.51	0.3	0.05	0.51	0	0.02	0.50	0	0.02	0.50
D3. Co-occurrence with 1-bp variants of AP-1 motif	0.4	0.05	0.55	0.4	0.05	0.55	0	0.02	0.50	0	0.02	0.50
D4. Co-occurrence with E-BOX motifs	0.2	0.05	0.50	0.2	0.05	0.50	1.1	0.02	0.55	1.1	0.02	0.55
E. Chromatin Accessibility (DHS)	39.3	0.04	0.82	39.3	0.04	0.82	-	-	-	-	-	-
F. c-Jun Occupancy (in c-Jun Peaks)	18.6	0.04	0.64	18.6	0.04	0.64	-	-	-	-	-	-
A+B	3.9	0.05	0.66	3.9	0.05	0.66	2.6	0.02	0.65	2.6	0.02	0.65
A+B+C	4.2	0.05	0.67	4.2	0.05	0.67	2.7	0.02	0.65	2.7	0.02	0.65
A+B+C+D1	6.7	0.05	0.70	6.7	0.05	0.70	2.7	0.02	0.65	2.7	0.02	0.65
A+B+C+D1+D2+D3+D4	7.0	0.05	0.71	7.0	0.05	0.71	3.5	0.02	0.67	3.5	0.02	0.67
A+B+C+D1+D2+D3+D4+E	42.4	0.03	0.88	42.4	0.03	0.88	-	-	-	-	-	-
A+B+C+D1+D2+D3+D4+E+F	43.8	0.03	0.88	43.8	0.03	0.88	-	-	-	-	-	-

Supplementary Table 1C. Modeling the Hoxa2 binding to of consensus Pbx motif (TGATTGAT) using GLM

Evaluated parameters	TGATTGAT (638/59,802)		
	PVE (%)	CV.err	AUC
A1. Peak	0.5	0.01	0.57
A2. Background	0.1	0.01	0.50
A3. Relative peak	0.6	0.01	0.57
A. INOS (A1+A2+A3)	0.6	0.01	0.57
B. Overlap with CGIs	0.0	0.01	0.51
C. Cluster of Pbx motifs	0.1	0.01	0.51
D. Co-occurrence of GR-like motif (G-TGA---ATG-C)	0.1	0.01	0.51
A+B	0.6	0.01	0.57
A+B+C	0.7	0.01	0.58
A+B+C+D	0.8	0.01	0.58

Supplementary Table 2A. Comparison of modeling the c-Jun binding to canonical AP-1 motif with 2 selected 1-bp variants using generalized linear models (GLM)

Evaluated parameters	TGCGTCA (11,926/271,973)			TGCGTCA (318/23,163)			GGACTCA (452/183,687)		
	PVE(%)	CV.err	AUC	PVE(%)	CV.err	AUC	PVE(%)	CV.err	AUC
	A1. Peak	10.3	0.04	0.76	6.0	0.01	0.72	3.5	0.01
A2. Background	6.5	0.04	0.70	4.5	0.01	0.69	1.3	0.01	0.62
A3. Relative peak	1.9	0.04	0.62	0.6	0.01	0.58	1.0	0.01	0.61
A. INOS (A1+A2+A3)	11.5	0.04	0.77	7.1	0.01	0.74	3.5	0.01	0.69
B. Overlap with CGIs	0.9	0.04	0.53	6.8	0.01	0.68	1.2	0.01	0.56
C. Cluster of AP-1 motifs	5.5	0.04	0.66	0.1	0.01	0.50	0.1	0.01	0.50
D. Co-occurrence of GR motifs	0.2	0.04	0.51	0.1	0.01	0.50	0.1	0.01	0.50
E. Chromatin Accessibility (DHS)	56.5	0.04	0.93	44.7	0.01	0.95	41.4	0.01	0.95
A+B	12.3	0.04	0.78	9.8	0.01	0.77	4.0	0.01	0.70
A+B+C	13.9	0.04	0.79	10.0	0.01	0.77	4.0	0.01	0.70
A+B+C+D	14.0	0.04	0.79	10.0	0.01	0.77	4.0	0.01	0.70
A+B+C+D+E	59.6	0.04	0.96	45.1	0.01	0.95	42.7	0.01	0.95

Supplementary Table 2B. Comparison of modeling the c-Jun binding to canonical AP-1 motif (8-mer) with 3 selected control 8-mers using generalized linear models (GLM)

Evaluated parameters	ATGAGTCA (3,041/65,689)			TAATATCA (33/74,570)			TGCATCAA (47/47,424)			AGACCTGC (97/49,012)		
	PVE(%)	CV.err	AUC	PVE(%)	CV.err	AUC	PVE(%)	CV.err	AUC	PVE(%)	CV.err	AUC
	A1. Peak	10.4	0.05	0.76	7.4	0.01	0.82	5.5	0.01	0.75	3.5	0.01
A2. Background	5.6	0.05	0.69	2.6	0.01	0.70	4.1	0.01	0.72	1.9	0.01	0.65
A3. Relative peak	2.5	0.05	0.63	2.8	0.01	0.71	1.0	0.01	0.60	0.5	0.01	0.57
A. INOS (A1+A2+A3)	11.3	0.05	0.77	7.6	0.01	0.83	6.6	0.01	0.77	3.8	0.01	0.71
B. Overlap with CGIs	0.8	0.05	0.53	0.2	0.01	0.51	0.4	0.01	0.52	0.7	0.01	0.55
C. Cluster of AP-1 motifs	0.8	0.05	0.53	0.0	0.01	0.50	0.1	0.01	0.51	0.0	0.01	0.50
D. Co-occurrence of GR motifs	0.1	0.05	0.51	0.1	0.01	0.51	0.2	0.01	0.51	0.5	0.01	0.52
E. Chromatin Accessibility (DHS)	55.1	0.05	0.94	40.3	0.04	0.88	44.0	0.01	0.94	42.9	0.01	0.97
A+B	11.4	0.05	0.77	8.1	0.01	0.84	7.5	0.01	0.78	4.0	0.01	0.72
A+B+C	12.2	0.05	0.78	8.1	0.01	0.84	7.6	0.01	0.79	4.0	0.01	0.72
A+B+C+D	12.3	0.05	0.78	8.2	0.01	0.84	7.8	0.01	0.79	4.5	0.01	0.72
A+B+C+D+E	56.1	0.04	0.96	43.3	0.01	0.94	47.5	0.01	0.96	44.5	0.01	0.98

Supplementary Table 2C. Comparison of modeling the GR binding to canonical GR motif with 1-bp variants using generalized linear models (GLM)

Evaluated parameters	G-ACA---TGT-C (1,393/27,176)			G-ACA---CGT-C (277/7,267)			G-ACA---TCT-C (109/61,528)		
	PVE(%)	CV.err	AUC	PVE(%)	CV.err	AUC	PVE(%)	CV.err	AUC
	A1. Peak	2.9	0.05	0.63	1.2	0.04	0.59	1.5	0.01
A2. Background	3	0.05	0.64	1.2	0.04	0.59	0.4	0.01	0.59
A3. Relative peak	0.2	0.05	0.53	0.1	0.04	0.52	0.7	0.01	0.59
A. INOS (A1+A2+A3)	3.9	0.05	0.66	1.7	0.04	0.60	1.5	0.01	0.65
B. Overlap with CGIs	0.1	0.05	0.51	0.1	0.04	0.51	0.2	0.01	0.51
C. Cluster of GR motifs	0.6	0.05	0.51	0.1	0.04	0.51	0.1	0.01	0.50
D. Co-occurrence of AP-1 motifs	2.6	0.05	0.57	1.7	0.04	0.57	2.7	0.01	0.63
E. Chromatin Accessibility (DHS)	39.3	0.04	0.82	28.5	0.04	0.81	35.4	0.01	0.90
A+B	3.9	0.05	0.66	2.2	0.04	0.62	1.9	0.01	0.66
A+B+C	4.2	0.05	0.67	2.2	0.04	0.62	1.9	0.01	0.66
A+B+C+D	6.7	0.05	0.70	3.8	0.04	0.65	4.6	0.01	0.72
A+B+C+D+E	42.4	0.03	0.88	34.9	0.04	0.84	39.8	0.01	0.91

Supplementary Table 3A. Distribution of Intrinsic Nucleosome Occupancy Scores (INOS) of c-Jun motifs (TGACTCA) on the whole mouse genome

Relative Peaks	Average of PNPS in Background (-750...-150 AND +150...+750)						Total
	[-2,-1)	[-1,0)	[0,0.5)	[0.5,0.8)	[0.8,1.2)	[1.2,2)	
[2,3)	558(3.4%)	440(9.5%)	NA	NA	NA	NA	998(6.1%)
[1.2,2)	2,484(1.6%)	12,209(5.8%)	2,198(11.9%)	89(18%)	3(66.7%)	NA	16,983(6%)
[0.8,1.2)	1,846(0.5%)	16,923(3.7%)	10,427(9%)	2,184(14.4%)	378(23.3%)	5(60%)	31,763(6.2%)
[0.5,0.8)	1,374(0.3%)	15,197(2.6%)	13,839(6.5%)	5,766(10%)	2,596(16.9%)	125(27.2%)	38,897(6%)
[0,0.5)	2,001(0.1%)	23,465(1.6%)	24,128(4.6%)	13,010(7.4%)	10,464(10.7%)	1,661(14.4%)	74,729(5.1%)
[-1,0)	2,204(0%)	28,078(0.8%)	26,439(2.4%)	13,490(4.4%)	10,207(7.1%)	2,213(9.6%)	82,631(2.9%)
[-3,-1)	497(0%)	9,647(0.3%)	9,120(1.1%)	3,846(2.5%)	1,949(3.6%)	206(6.8%)	25,265(1.2%)
[-5,-3)	1(0%)	166(0.6%)	304(0.7%)	147(0.7%)	86(8.1%)	2(0%)	706(1.6%)
Total	10,965(0.7%)	106,125(2.3%)	86,455(4.6%)	38,532(6.7%)	25,683(9.6%)	4,212(11.9%)	271,972(4.4%)

Supplementary Table 3B. Distribution of Intrinsic Nucleosome Occupancy Scores (INOS) of GR-motifs (G-ACA---TGT-C) on the whole mouse genome

Relative Peaks	Average of PNPS in Background (-750...-150 AND +150...+750)						Total
	[-2,-1)	[-1,0)	[0,0.5)	[0.5,0.8)	[0.8,1.2)	[1.2,2)	
[2,3)	80(0%)	90(1.1%)	NA	NA	NA	NA	170(0.6%)
[1.2,2)	256(2%)	1,592(4.9%)	343(5.8%)	25(12%)	NA	NA	2,216(4.8%)
[0.8,1.2)	161(2.5%)	1,722(3.9%)	1,356(7.4%)	344(10.8%)	68(8.8%)	1(0%)	3,652(5.9%)
[0.5,0.8)	134(2.2%)	1,431(3.1%)	1,567(7.5%)	833(7.8%)	414(8.7%)	30(16.7%)	4,409(6.1%)
[0,0.5)	177(0.6%)	2,110(2.3%)	2,309(5%)	1,440(7.6%)	1,300(9.7%)	267(11.6%)	7,603(5.7%)
[-1,0)	143(0%)	2,235(1.4%)	2,356(4.2%)	1,270(5.7%)	965(8.6%)	260(8.1%)	7,229(4.3%)
[-3,-1)	25(0%)	672(1.2%)	679(3.2%)	299(4.3%)	149(10.1%)	21(14.3%)	1,845(3.3%)
[-5,-3)	NA	13(0%)	18(0%)	11(0%)	5(0%)	2(0%)	49(0%)
Total	976(1.3%)	9,865(2.8%)	8,628(5.5%)	4,222(7.1%)	2,901(9.2%)	581(10.3%)	27,173(5.1%)

Supplementary Table 4A. Gene Expression of Near GR ChIP-seq Peaks (<2K)

		Down-regulation (10% decrease)		No-Change		Up-regulation (10% Increase)		Total
		#	%	#	%	#	%	#
GR Peaks (1,347, 16.4%)	PRE	221	21.8%	566	55.7%	229	22.5%	1,016
	REP	60	21.1%	152	53.3%	73	25.6%	285
	UNP	11	23.9%	24	52.2%	11	23.9%	46
	Total	292	21.7%	742	55.1%	313	23.2%	1,347
GR Peaks with G-ACA---TGT-C (272, 3.3%)	PRE	14	12.0%	63	53.8%	40	34.2%	117
	REP	24	18.9%	73	57.5%	30	23.6%	127
	UNP	8	28.6%	16	57.1%	4	14.3%	28
	Total	46	16.9%	152	55.9%	74	27.2%	272
GR Peaks without G-ACA---TGT-C (1,075, 13.1%)	PRE	207	23.0%	503	56.0%	189	21.0%	899
	REP	36	22.8%	79	50.0%	43	27.2%	158
	UNP	3	16.7%	8	44.4%	7	38.9%	18
	Total	246	22.9%	590	54.9%	239	22.2%	1,075

Supplementary Table 4B. Gene Expression of Near GR ChIP-seq Peaks (<5K)

		Down-regulation (10% decrease)		No-Change		Up-regulation (10% Increase)		Total
		#	%	#	%	#	%	#
GR Peaks (2,254, 27.4%)	PRE	374	22.3%	929	55.4%	373	22.3%	1,676
	REP	120	24.4%	258	52.4%	114	23.2%	492
	UNP	14	16.3%	51	59.3%	21	24.4%	86
	Total	508	22.5%	1,238	54.9%	508	22.5%	2,254
GR Peaks with G-ACA---TGT-C (456, 5.5%)	PRE	28	14.5%	109	56.5%	56	29.0%	193
	REP	52	24.1%	122	56.5%	42	19.4%	216
	UNP	10	21.3%	28	59.6%	9	19.1%	47
	Total	90	19.7%	259	56.8%	107	23.5%	456
GR Peaks without G-ACA---TGT-C (1,798, 21.8%)	PRE	346	23.3%	820	55.3%	317	21.4%	1,483
	REP	68	24.6%	136	49.3%	72	26.1%	276
	UNP	4	10.3%	23	59.0%	12	30.8%	39
	Total	418	23.2%	979	54.4%	401	22.3%	1,798

Supplementary Table 4C. Gene Expression of Near GR ChIP-seq Peaks (<20K)

		Down-regulation (10% decrease)		No-Change		Up-regulation (10% Increase)		Total
		#	%	#	%	#	%	#
GR Peaks (4,226, 51.3%)	PRE	672	21.8%	1746	56.7%	662	21.5%	3,080
	REP	213	22.6%	522	55.3%	209	22.1%	944
	UNP	46	22.8%	119	58.9%	37	18.3%	202
	Total	931	22.0%	2,387	56.5%	908	21.5%	4,226
GR Peaks with G-ACA---TGT-C (835, 10.1%)	PRE	48	14.3%	196	58.5%	91	27.2%	335
	REP	94	23.7%	222	56.1%	80	20.2%	396
	UNP	23	22.1%	62	59.6%	19	18.3%	104
	Total	165	19.8%	480	57.5%	190	22.8%	835
GR Peaks without G-ACA---TGT-C (3,391, 41.2%)	PRE	624	22.7%	1,550	56.5%	571	20.8%	2,745
	REP	119	21.7%	300	54.7%	129	23.5%	548
	UNP	23	23.5%	57	58.2%	18	18.4%	98
	Total	766	22.6%	1907	56.2%	718	21.2%	3,391

Supplementary Table 5A. GR canonical motif (G-ACA---TGT-C) with/without co-occurrence of AP-1 canonical motif and 1-bp variants in the mouse genome and 3134 GR peaks (<150-bps)

	– AP-1 motif				+1 AP-1 motif				≥2 AP-1 motifs			
	#	GR peak	% bound	p-value	#	GR peak	% bound	p-value	#	GR peak	% bound	p-value
0 variants	10,201	364	3.6%	-	590	90	15.3%	NA	-	-	-	-
1 variant	9,329	437	4.7%	9.9E-05	544	79	14.5%	0.79	-	-	-	-
2 variants	4,274	217	5.1%	3.0E-05	369	71	19.2%	0.13	-	-	-	-
3 variants	1,343	82	6.1%	8.2E-06	-	-	-	-	-	-	-	-
≥4 variants	473	38	8.0%	1.2E-06	-	-	-	-	-	-	-	-
Total	25,620	1,138	4.4%	-	1,503	240	16.0%	< 2.2E-16	53	15	28.3%	8.52E-16

Supplementary Table 5B. 1-bp variant of GR canonical motif (G-ACA---AGT-C) with/without co-occurrence of AP-1 canonical motif and 1-bp variants in the mouse genome and 3134 GR peaks (<150-bps)

	– AP-1 motif				+1 AP-1 motif				≥2 AP-1 motifs			
	#	GR peak	% bound	p-value	#	GR peak	% bound	p-value	#	GR peak	% bound	p-value
0 variants	16,789	169	1.0%	-	953	47	4.9%	-	-	-	-	-
1 variant	15,660	225	1.4%	4.9E-04	924	61	6.6%	0.15	-	-	-	-
2 variants	7,492	130	1.7%	2.7E-06	652	47	7.2%	0.07	-	-	-	-
3 variants	2,367	50	2.1%	3.6E-06	-	-	-	-	-	-	-	-
≥4 variants	720	14	1.9%	2.5E-02	-	-	-	-	-	-	-	-
Total	43,028	588	1.4%	-	2,529	155	6.1%	< 2.2E-16	84	16	19.0%	< 2.2E-16

Supplementary Table 5C. GR canonical motif (G-ACA---TGT-C) with/without co-occurrence of AP-1 and E-Box canonical motif in the mouse genome and AtT-20 GR peaks (<150-bps)

	Genome	GR peak	%bound	p-value
– AP-1 motif	25,620	359	1.4%	-
+1 AP-1 motif	1,503	31	2.1%	0.05
≥2 AP-1 motifs	53	0	0.0%	0.78
– E-Box motif	25,373	327	1.3%	-
+1 E-Box motif	1,444	45	3.1%	1.5E-08
≥2 E-Box motifs	359	18	5.0%	4.6E-09
Total	27,176	1,393	5.1%	-