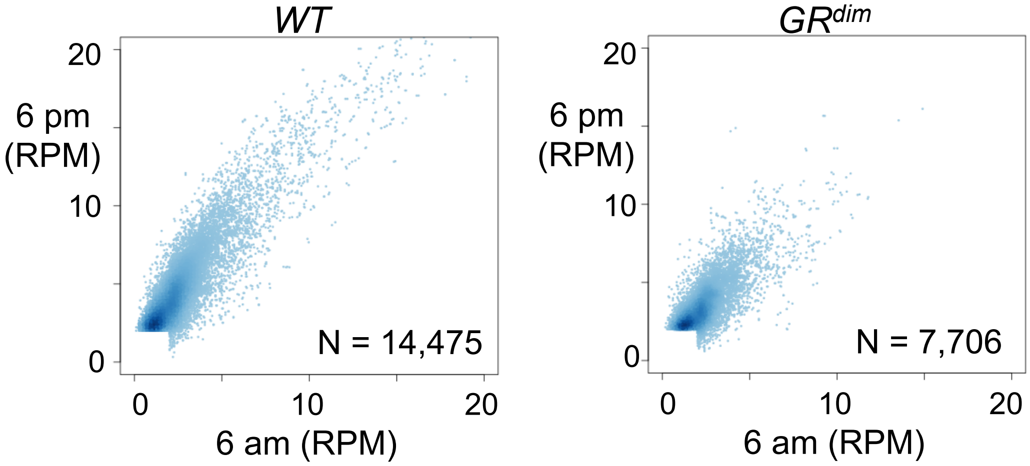
Supplemental Material

Genomic Redistribution of GR Monomers and Dimers Mediates Transcriptional Response to Exogenous Glucocorticoid In Vivo

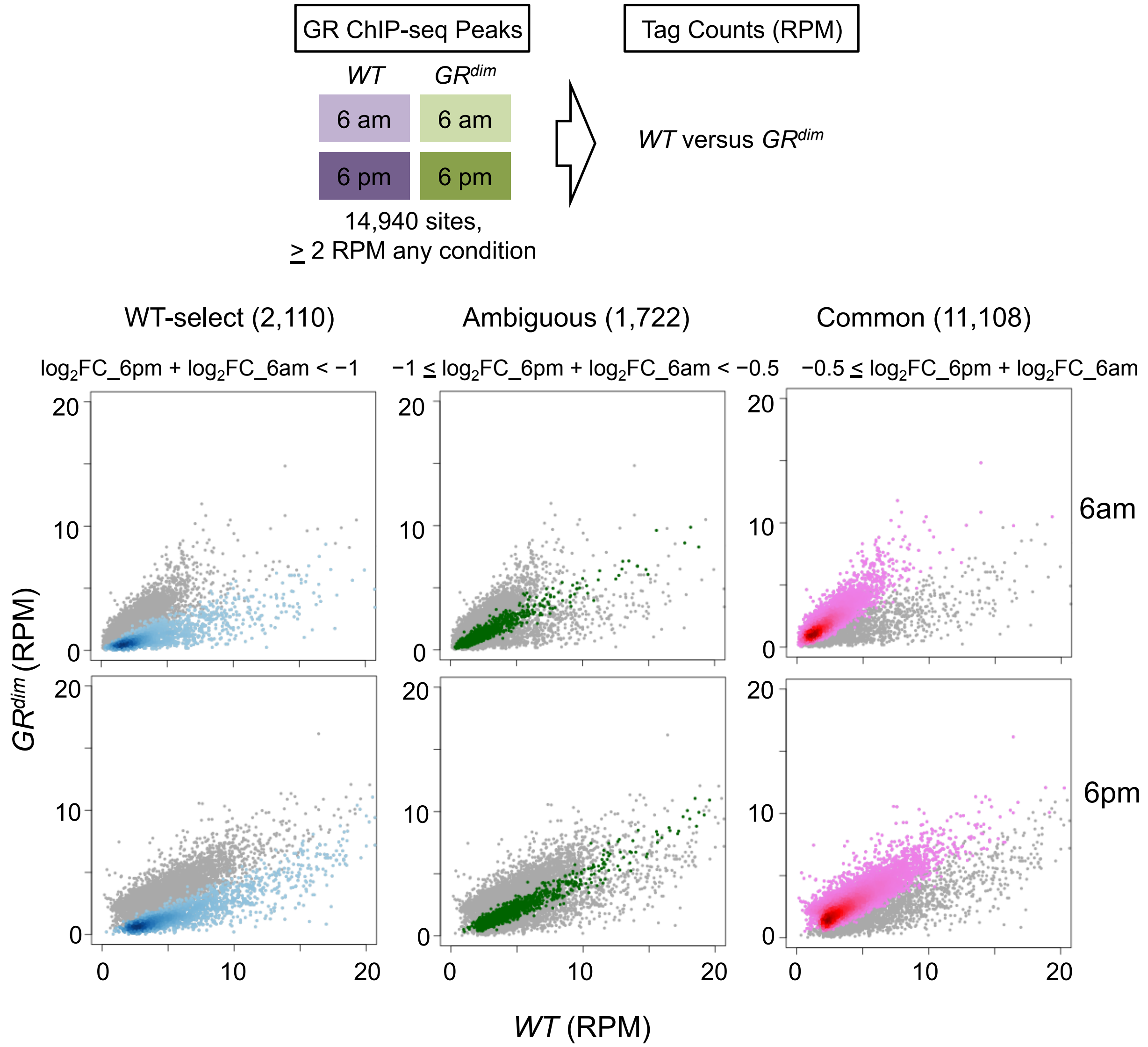
Lim et al. (2015)

This document contains the following information:

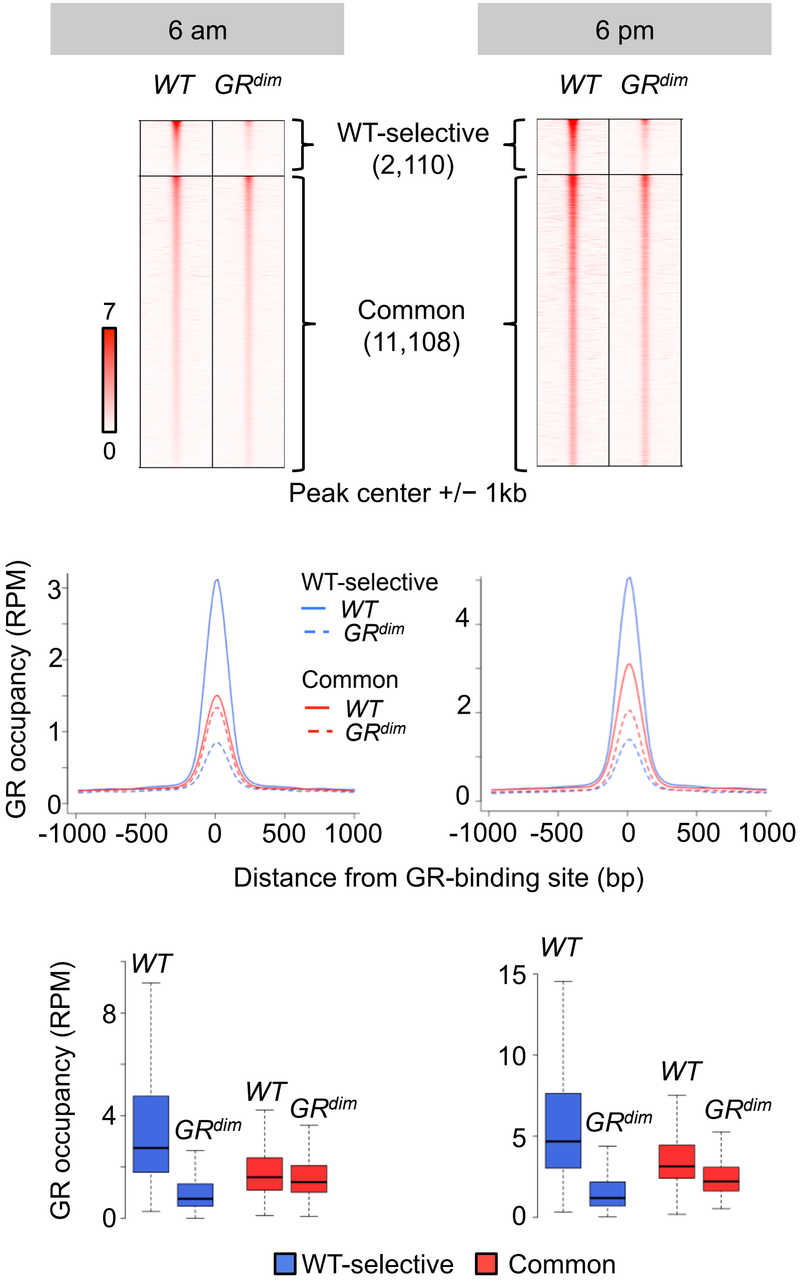
SUPPLEMENTAL FIGURES



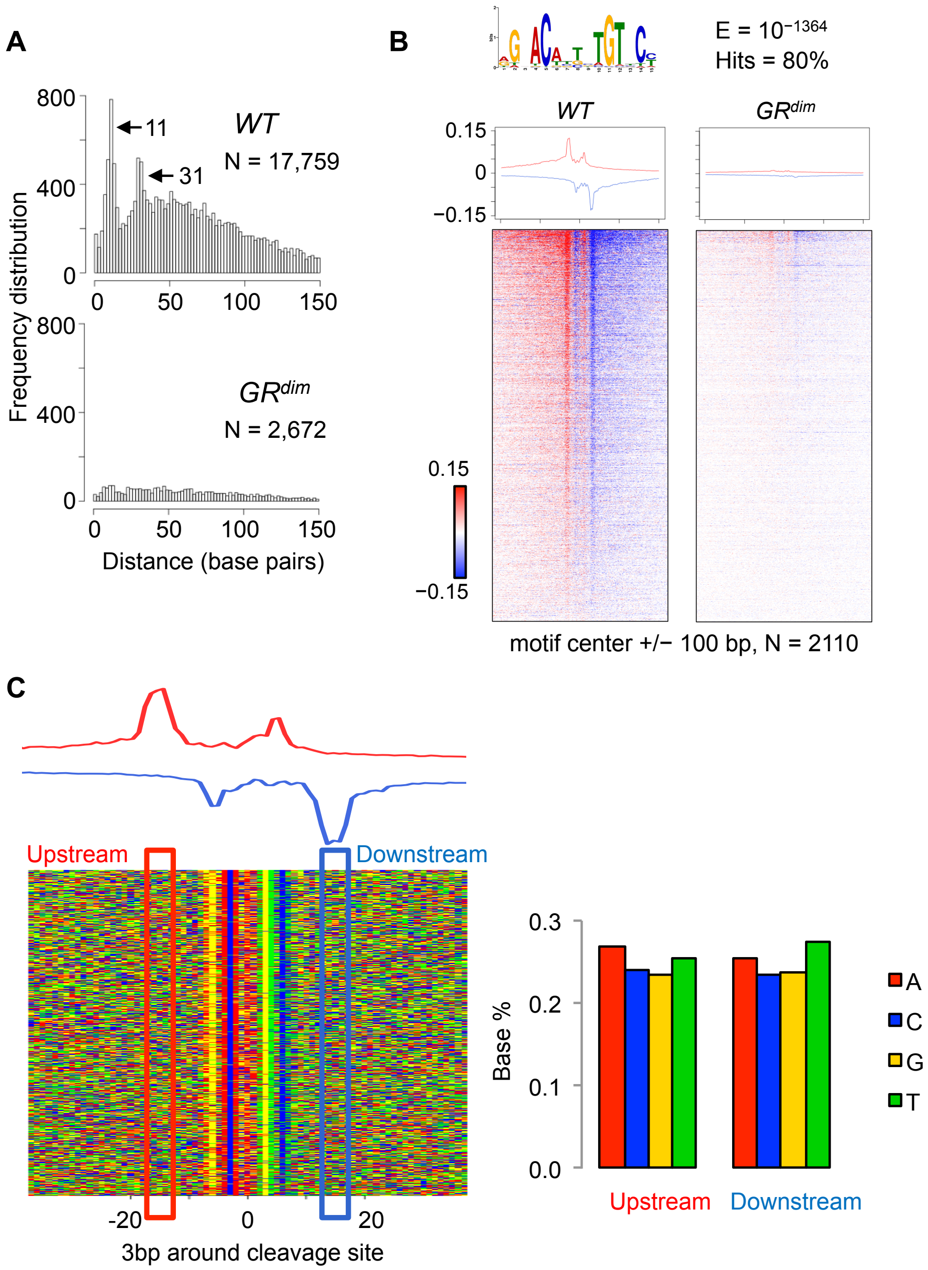
Supplemental Figure 1. Comparison of GR ChIP-seq peaks at 6 am and 6 pm in *WT* and *GR*^{dim} mice, related to Figure 1. Scatter plots comparing sequence tags from GR ChIP-seq peaks at 6 am and 6 pm with at least 2 reads per million (RPM) in livers isolated from *WT* (left) and *GR*^{dim} (right) mice.



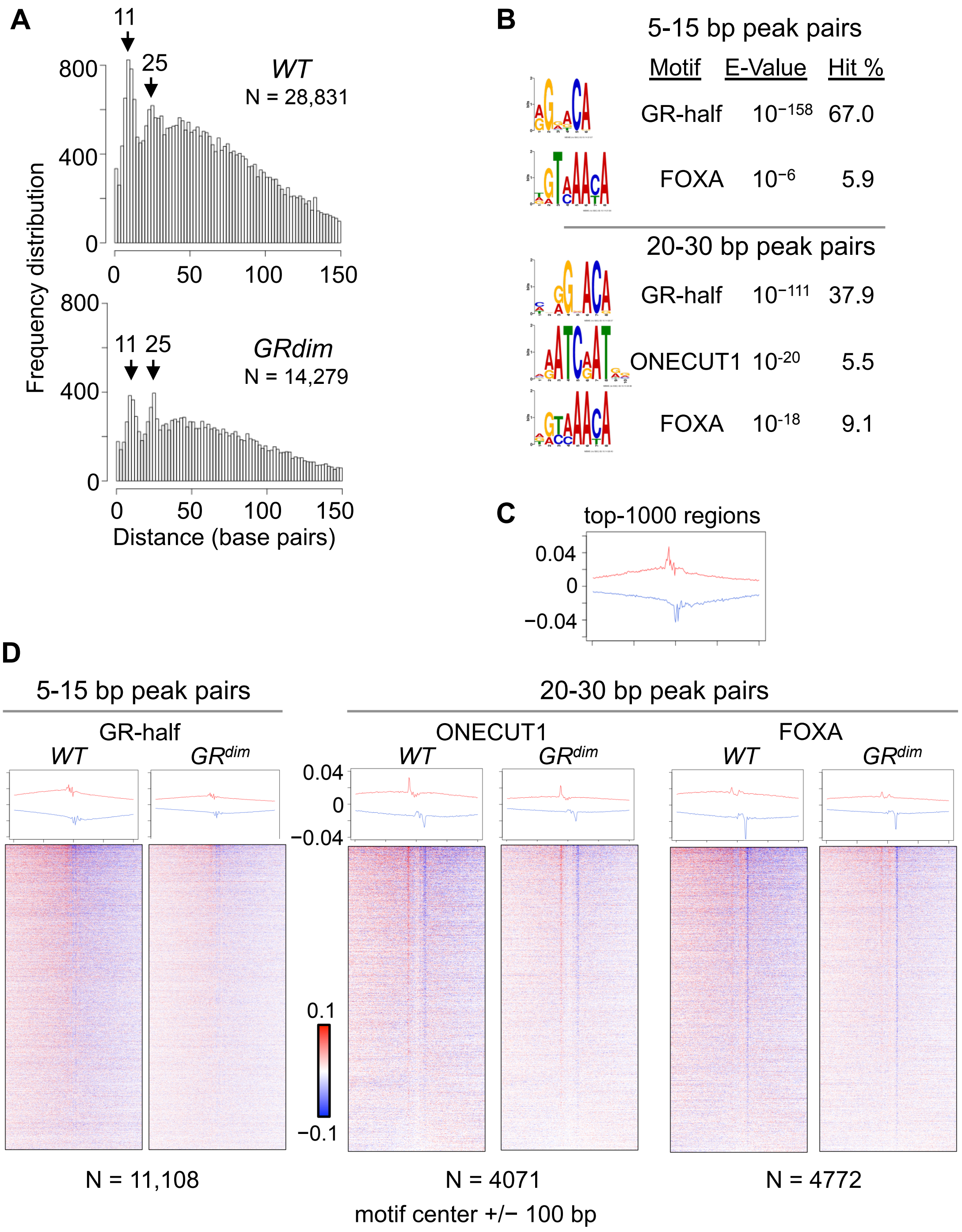
Supplemental Figure 2. Classification of GR-binding sites in *WT* and *GR^{dim}* mice, related to Figure 1. Peak calling was performed separately for each condition and peaks with at least 2 RPM in any condition were pooled to yield 14,940 peaks. Peaks were classified into three groups based on peak-height changes for GR between *WT* and *GR^{diim}* mice. WT-selective (blue), common (red), and ambiguous (green) sites are indicated on the scatter plots for the 6 am and 6 pm cistromes.



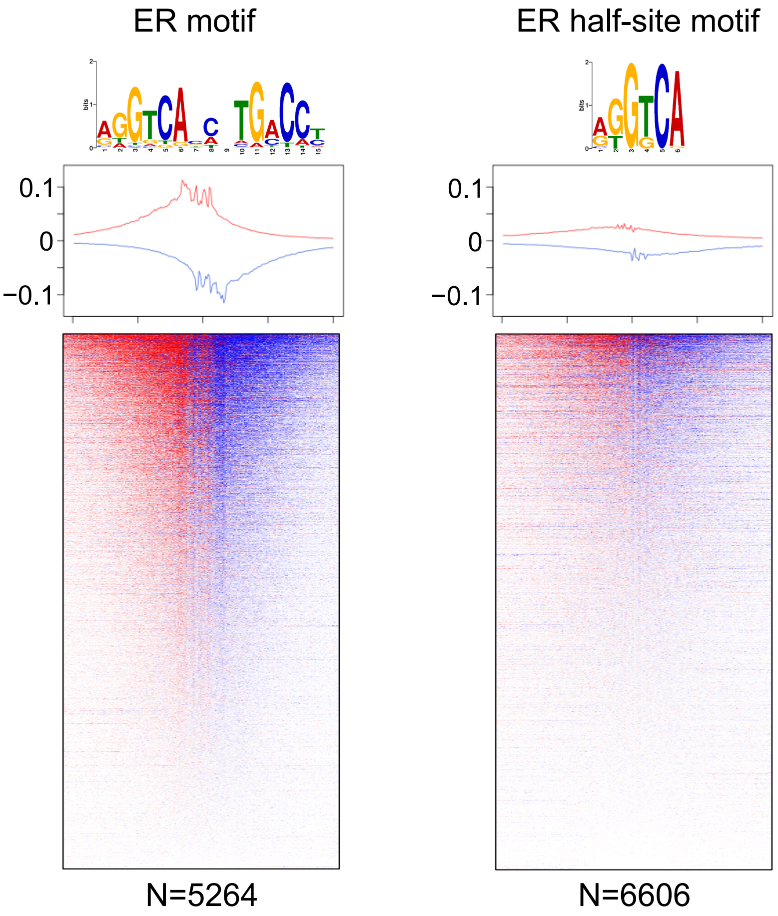
Supplemental Figure 3. Comparison WT-selective and common GR-binding sites in *WT* and *GR*^{dim} mice, related to Figure 1. Density heat maps (top), average profiles (middle) and box plots (bottom) for GR-binding sites at 6 am (left) and 6 pm (right).



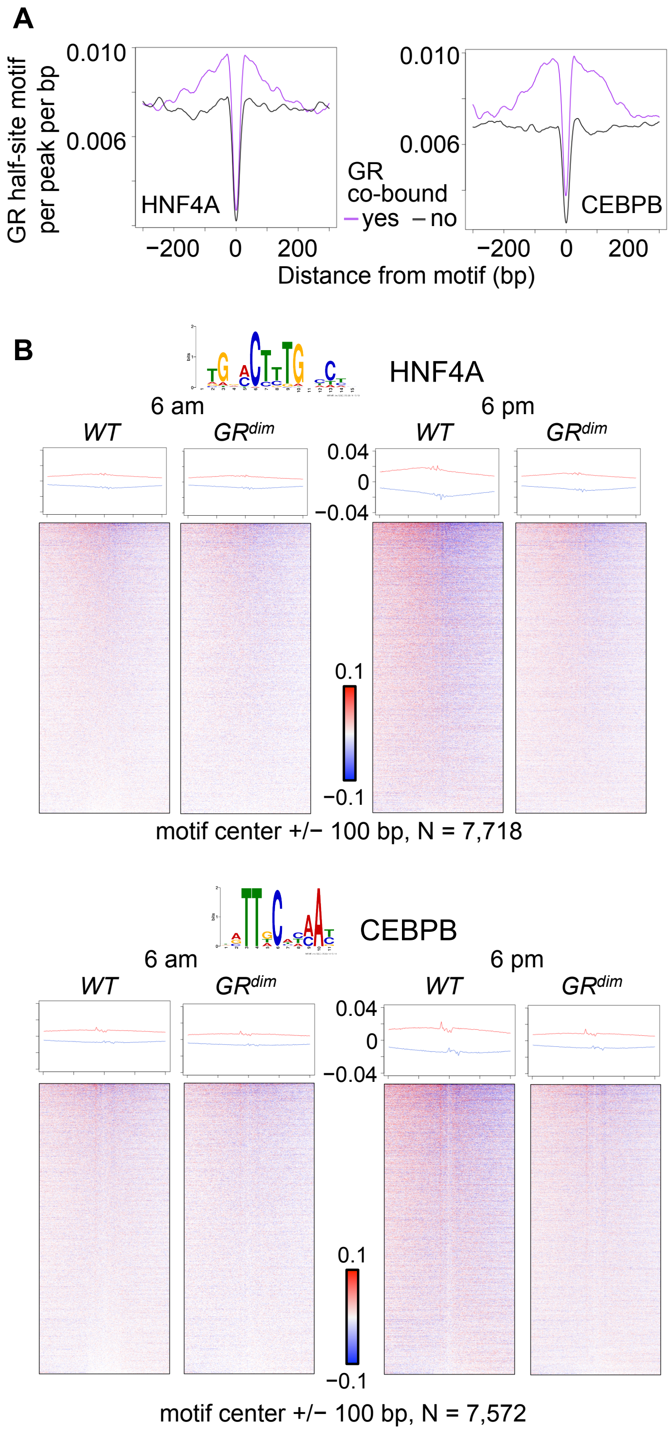
Supplemental Figure 4. GR ChIP-exo at WT-selective sites in liver isolated at 6 pm, related to Figure 1. (A) Distance distribution for opposite-stranded peaks with at least 0.2 RPM from *WT* and *GR^{dim}* mice. Prominent peak distances and the total number of peak pairs are indicated. (B) MEME top-ranked de novo sequence from GR ChIP-exo with a hit count of at least 5% is shown at the top. Average profiles (middle) and density heat maps (bottom) of the raw sequence tags are shown for both mouse models. Red and blue indicate the 5’ ends of the forward- and reverse-stranded tags, respectively. (C) Examination of sequence bias at the external lambda exonuclease cleavage sites for WT-selective sites. Left, color chart corresponds to the GR ChIP-exo density heat maps from B, with the average profile aligned. Right, histogram shows read counts in a 3-bp interval encompassing cleavage sites.



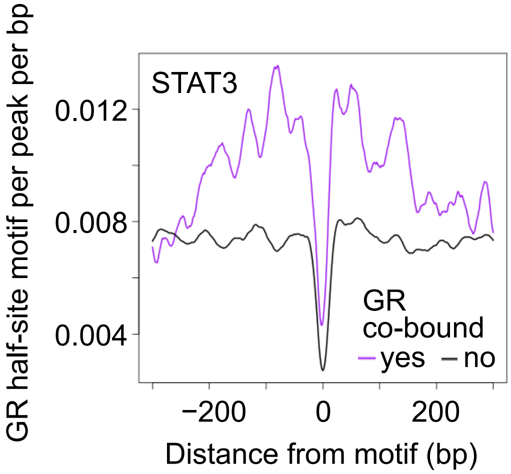
Supplemental Figure 5. GR ChIP-exo at common GR-binding sites at 6 pm, related to Figures 2 and 3. (A) The distance distribution for opposite-stranded peaks with at least 0.2 RPM from GR ChIP-exo in liver isolated at 6 pm is shown for sites commonly bound in *WT* and *GR*^{dim} mice, with the number of peak pairs and prominent peak distances indicated. (B) MEME de novo sequences from 6 pm common site peak pairs separated by 5-15 bp or 20-3- bp and with a hit count of at least 5%. (C) Average GR ChIP-exo profile for the top-1000 common sites ranked by peak pair reads. (D) GR ChIP-exo at 6 pm common sites, with average profiles and density heat maps for the half-site, ONECUT1 and FOXA motifs shown for both mouse models. Red and blue indicate the 5' ends of the forward- and reverse-stranded tags, respectively.



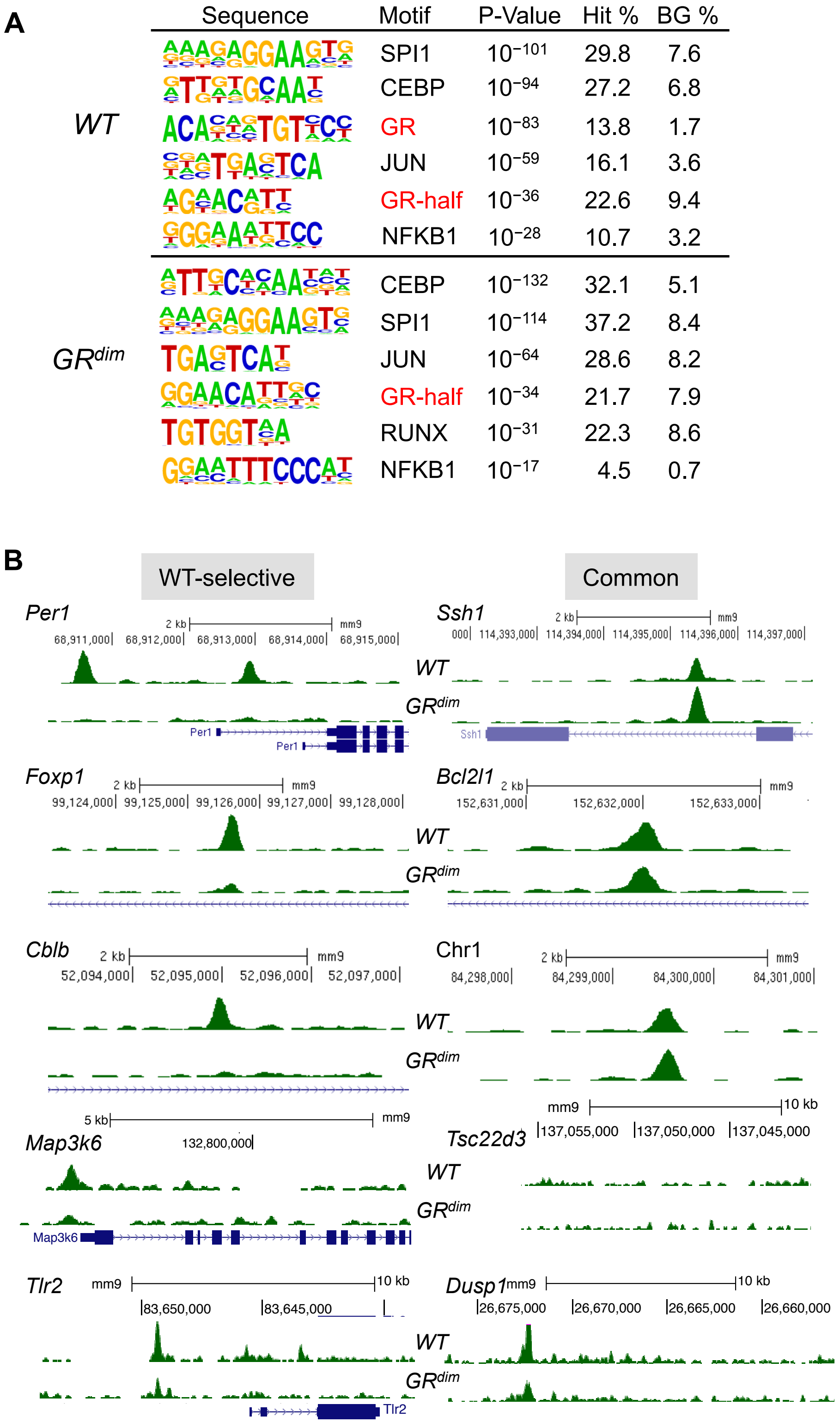
Supplemental Figure 6. Estrogen receptor 1 (ESR1) ChIP-exo, related to Figure 2. Average profiles and density heat maps of the raw sequence tags are shown for ESR1 ChIP-exo in MCF-7 cells. Red and blue indicate the 5’ ends of the forward- and reverse-stranded tags, respectively. Raw data were obtained from (Serandour et al. 2013). ER full and half-site motif calls were taken from (Gertz et al. 2013; Joseph et al. 2010).



Supplemental Figure 7. GR ChIP-exo at HNF4A- and CEBPB-binding sites, related to Figure 3. (A) Distribution of the GR half-site motif relative to neighboring motifs at common sites co-bound by HNF4A (top) or CEBPB (bottom). Results for HNF4A and CEBPB liver sites without GR are shown for comparison. (B) GR ChIP-exo peak pairs flanking the HNF4A (top) or CEBPB (bottom) motifs at the co-bound sites from A. Average profiles and density heat maps of the raw sequence tags are shown for both mouse models at 6 am and 6 pm. Red and blue indicate the 5’ ends of the forward- and reverse-stranded tags, respectively.

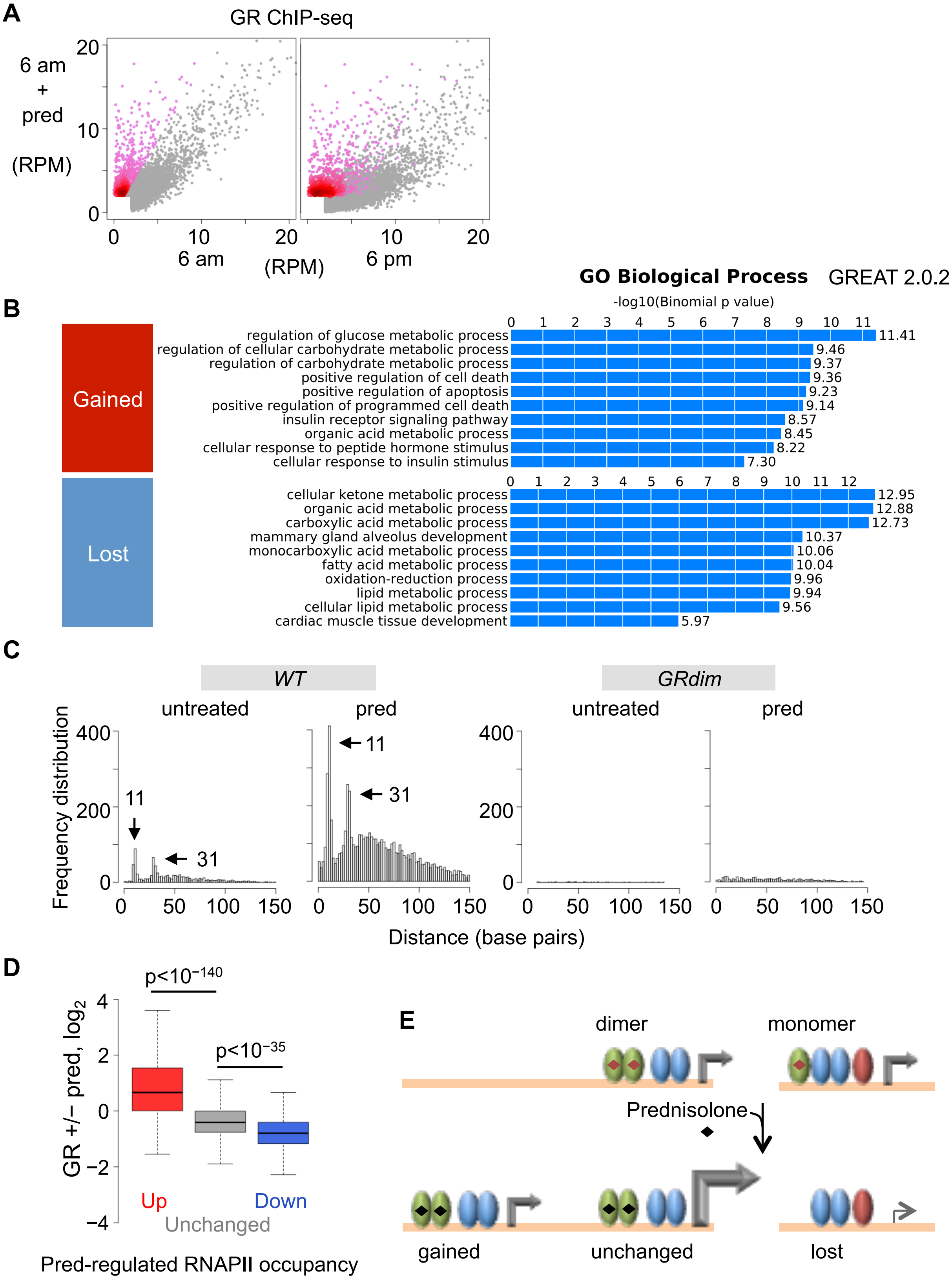


Supplemental Figure 8. GR half-site motif at STAT3-binding sites, related to Figure 3. Distribution of the GR half-site motif relative to the STAT motif at AtT-20 sites thought to have GR tethered to STAT3. Results for STAT3 sites without GR are shown for comparison. The analysis was performed with previously published datasets (Langlais et al. 2012).



	Sequence	Motif	P-Value	Hit %	BG %
WT	AAAGAGGAAGTG	SPI1	10^{-101}	29.8	7.6
	GTTGTGCAAT	CEBP	10^{-94}	27.2	6.8
	ACACAGTGTCCC	GR	10^{-83}	13.8	1.7
	CGATGAGTCA	JUN	10^{-59}	16.1	3.6
	AGAACATT	GR-half	10^{-36}	22.6	9.4
	GGGAAATTCC	NFKB1	10^{-28}	10.7	3.2
GR^{dim}	ATTGCACAATAT	CEBP	10^{-132}	32.1	5.1
	AAAGAGGAAGTG	SPI1	10^{-114}	37.2	8.4
	TGAGTCAT	JUN	10^{-64}	28.6	8.2
	GGAACATTGC	GR-half	10^{-34}	21.7	7.9
	TGTGGTAA	RUNX	10^{-31}	22.3	8.6
	GGAATTTCCCAT	NFKB1	10^{-17}	4.5	0.7

Supplemental Figure 9. GR ChIP-seq in primary macrophages from *WT* and *GR*^{diim} mice, related to Figure 5. (A) HOMER de novo motif analyses of the GR cistromes. Top-ranked motifs are shown. (B) Examples of WT-selective and common GR-binding sites from *WT* and *GR*^{diim} mice. ChIP-seq tracks are RPM normalized and presented with the same y-axis scale (0 - 5).


A
GR ChIP-seq
6 am
+
pred
(RPM)
20
10
0
0
10
20
6 am
(RPM)
10
20
6 pm
B
GO Biological Process
GREAT 2.0.2
-log10(Binomial p value)
Gained
regulation of glucose metabolic process 11.41
regulation of cellular carbohydrate metabolic process 9.46
regulation of carbohydrate metabolic process 9.37
positive regulation of cell death 9.36
positive regulation of apoptosis 9.23
positive regulation of programmed cell death 9.14
insulin receptor signaling pathway 8.57
organic acid metabolic process 8.45
cellular response to peptide hormone stimulus 8.22
cellular response to insulin stimulus 7.30
Lost
cellular ketone metabolic process 12.95
organic acid metabolic process 12.88
carboxylic acid metabolic process 12.73
mammary gland alveolus development 10.37
monocarboxylic acid metabolic process 10.06
fatty acid metabolic process 10.04
oxidation-reduction process 9.96
lipid metabolic process 9.94
cellular lipid metabolic process 9.56
cardiac muscle tissue development 5.97
C
WT
GRdim
untreated
pred
untreated
pred
Frequency distribution
400
200
0
11
31
11
31
0
50
100
150
Distance (base pairs)
D
GR +/− pred, log₂
4
2
0
−2
−4
p<10⁻¹⁴⁰
p<10⁻³⁵
Up
Unchanged
Down
Pred-regulated RNAPII occupancy
E
dimer
monomer
Prednisolone
gained
unchanged
lost

Supplemental Figure 10. GR regulation by prednisolone, related to Figure 6. (A) Scatter plot of sequence tags from 6839 GR ChIP-seq peaks in *WT* liver isolated at 6 am comparing prednisolone treatment for 24 h with untreated control (left panel). The 889 sites displaying gained binding in response to treatment are highlighted in red. Right panel shows the comparison of the pred-treated peaks with the untreated 6 pm peaks. The same sites from the left panel are highlighted, revealing that most of the gained sites are weakly bound at 6 pm, and suggesting that prednisolone does not transform the 6 am cistrome into a reflection of that from 6 pm. (B) Ten top-ranked gene ontology categories for gained and lost sites after prednisolone treatment. (C) Distance distributions for opposite-stranded peaks with at least 0.2 RPM from GR ChIP-exo in liver isolated at 6 am with or without prednisolone treatment from *WT* and GR^{dim} mice. Prominent peak distances are indicated. (D) Box plot comparing the fold-change for GR occupancy at sites with pred-regulated RNAPII binding in *WT* mice. (E) Prednisoline redistributes GR from monomeric to dimeric sites at regulated genes in liver. GR dimers and monomers (green) activate transcription when bound by endogenous corticosterone (red diamond). Prednisolone treatment increases gene transcription near dimer sites with unchanged and gained occupancy for GR and co-localized TFs such as CEBPB, concomitant with monomer evacuation of sites near repressed genes.

SUPPLEMENTAL METHODS

ChIP-seq data processing

Liver ChIP-seq reads for GR, C/EBPβ, and RNAPII were aligned to build mm9 of the mouse genome using Bowtie with options '-k 1 -m 1 --best -strata' (Langmead et al. 2009). Down-sampling analysis was performed to control for sequencing depth variability and to avoid read saturation in highly enriched regions. Specifically, after randomly selecting 15 million reads from each ChIP-seq run, redundant reads were removed, and peak calling was performed using Homer (Heinz et al. 2010) with matched inputs for each sample. Peaks located in the ENCODE blacklist regions were discarded (ENCODE Project Consortium et al. 2012). Data from biological replicates were gathered for all conditions, and reproducibility was confirmed using Spearman's rank correlation coefficient. Replicates were subsequently averaged to control for ultradian rhythm and stress response differences at the time of animal sacrifice by pooling down-sampled reads into a single data set for each condition, followed by final peak calling. Peaks were re-sized to 200 bp, and those meeting a threshold of 2 RPM were chosen for further study. De novo motif analysis was performed with Homer using random background unless specified differently. GR ChIP-seq reads from primary macrophages were down-sampled to 20 million reads and processed similarly.

For the classification of GR-binding sites, peaks at both 6 am and 6 pm from *WT* and GR^{dim} mice were pooled together to construct a master set of binding sites. Overlapping peaks were merged and resized to 200 bp if the distance between peak centers was < 100 bp. For each master peak, GR occupancy was measured as RPM-normalized tag counts. Log_2-fold change (log_2FC) for GR occupancy in GR^{dim} versus *WT* mice at each site was linearly combined for the 6 am and 6 pm conditions, where GR occupancy was median-normalized for each time point and minimum value 1 was added for variance stabilization at weak peaks when calculating the log_2FC. GR peaks were classified into three distinct groups according to the following criteria: 'WT-selective' if the sum of log_2FC from 6pm and 6am was below -1; 'common' if it is ≥ -0.5; 'ambiguous' for the remaining sites not meeting these thresholds. For GR ChIP-seq in primary macrophages, a binding site was considered WT-selective if occupancy decreased more than 2-fold in GR^{dim} versus *WT* mice. For the identification of prednisolone-regulated GR-binding sites, peaks from biological replicates were pooled and merged for untreated and prednisolone-treated liver samples from *WT* mice. Gained and lost peaks were defined by 2-fold change of median-normalized GR occupancy. Gene ontology analysis was performed using GREAT (McLean et al. 2010).

The integrative analyses with lineage TFs were performed with previously published ChIP-seq data. Liver TFs: HNF4A (E-TABM-722) (Schmidt et al. 2010), ONECUT1 (E-MTAB-438) (Laudadio et al. 2012) and FOXA proteins (E-MTAB-805) (Li et al. 2012). Macrophage TFs: SPI1 (Ostuni et al. 2013), CEBP proteins (Heinz et al. 2010), JUN and NFKB1 (Uhlenhaut et al. 2013). Wilcoxon rank-sum test was used when comparing ChIP-seq signals between any two groups of regions. For differential analysis of RNAPII occupancy in liver, GR peaks were pooled from 6 am untreated and prednisolone-treated samples isolated from *WT* mice, and merged if the distance between two peak centers was < 100 bp. The number of raw sequence tags for each biological replicate was determined for the 1 kb window around binding sites, and sites whose RNAPII signal was < 1 RPKM for both replicates were discarded as inactive. GR sites with an FDR < 0.05 from an exact test using 'edgeR' (Robinson et al. 2010) were considered prednisolone-regulated.

ChIP-exo data processing

ChIP-exo can determine the potential boundaries of chromatin-bound TFs in high resolution when pairs of opposite-stranded peaks tightly flank binding positions with a fixed distance. However, the correct peak-to-peak distance is not known in advance and the pairing between opposite-stranded ChIP-exo peaks cannot be performed unambiguously. Several approaches have been used previously, but they work best when the binding configuration is homogeneous. For unbiased interrogation of the ChIP-exo data, we used a strand cross-correlation technique, a popular method to estimate a fragment length for ChIP-seq data. However, here we applied it to ChIP-exo peaks not individual reads. The basic assumption is that when we consider all the possible distances between opposite-stranded ChIP-exo peaks, then the real peak-to-peak distance corresponding to prevalent and strong configurations would stand out of the total distribution of distances. Furthermore, a motif responsible for the binding would be enriched within peak-pairs having the given distance.

First, ChIP-exo reads were aligned to the mouse genome, build mm9, as described for ChIP-seq. To define a preliminary set of ChIP-exo peaks on the forward and reverse strands, initial peak calling was performed separately for each biological replicate by examining the 5‘ ends of reads using GeneTrack (Albert et al. 2008) with options, '-s 3 -e 10'. Peak calling was also performed after pooling replicates for each condition. Reproducible and strong peaks were selected from pooled replicates if they overlapped peaks from each replicate by at least by 5 bp (out of 10 bp), and met a 0.2 RPM cut-off. Any peaks located within the ENCODE blacklist regions were discarded. These ChIP-exo peaks were used to investigate detailed GR-binding configurations in the WT-selective and common sites. Strand cross-correlation analysis was performed using ChIP-exo peaks for each group of GR site and specific and abundant distances between peak pairs were estimated by local maxima in the histogram using 'pastecs' package in R (http://cran.r-project.org/web/packages/pastecs). To identify enriched DNA sequences at peak pairs, we selected the top-1000 with a specific spacing +/− 5 bp and performed de novo motif analysis within the 50 bp (WT-selective) or 30 bp (common) regions surrounding the peak-pair centers using MEME (Bailey and Elkan 1994). The occurrence of motifs within corresponding groups of GR-binding sites was determined by FIMO (Grant et al. 2011). For the visualization analyses, only the 5' ends of sequence reads were considered when anchoring on a single motif instance with the lowest p-value per ChIP-seq peak after motif scanning. The GR-half motif was treated differently because of its high abundance and simplicity. After initial scanning, we selected the single motif instance with the strongest ChIP-exo signal per ChIP-seq peak. Lastly, when checking GR-half motif density around lineage TF motifs, any GR half motif instances that met the p-value criteria were considered if the major consensus g/aGnACA was not altered, and weighted moving average with a window size of 20 bp was applied to smoothen the profile.

For the analysis of ER ChIP-exo in MCF-7 cell, we used previously published data (E-MTAB-1827) (Serandour et al. 2013). Fastq files for five replicates were downloaded and aligned to human genome, build hg19. ChIP-exo peak calling and quality control were performed as described above, and reproducible peaks, which were called in at least three replicates out of five, were selected for further analysis. Because there are no available ChIP-seq data for an ER dimerization mutant, we used previously published ER full motif and half motif sites as putative dimmeric and monomeric binding sites (Joseph et al. 2010). ChIP-exo visualization anchoring on ER full and half motifs was performed as described for GR.

Microarray analysis

The association study between GR-binding sites and prednisolone-regulated gene expression used previously published microarray data [GSE21048] (Frijters et al. 2010). Gene expression data were GCRMA normalized. Data from male mice were selected to remain consistent with the ChIP-seq strategy. Differential gene expression analysis was performed using 'limma' package in R (Smyth 2004), and genes with an FDR < 0.05 were defined as prednisolone-regulated.

Oligos for Subcloning Candidate Enhancers Interrogated by Luciferase Assays

Map3k6-XhoI-EcoRV	cgctcgaggatatcCTCTGAGGAAAGCGCTTGTC
Map3k6-HindIII-EcoRV	cgaagcttgatatcCACAGGTCACAGAAGAGTCC
Tlr2-XhoI-EcoRV	cgctcgaggatatcGTCTATAAATTGCACAGAGG
Tlr2-HindIII-EcoRV	cgaagcttgatatcTGTACTAGAAGAGCCAATCC
Dusp1_Fw	CGctcgagGCTATGAGCAGCATTCCAGG
Dusp1_Rv	CGaagcttATCAGCTCAGGGAAGACAGC
Dusp1_mut_Fw	caaTTCCCTTTCCCAACACAG
Dusp1_mut_Rv	aaccTTCAGCGCTAGAAGAGAC
Tsc22d3_Fw	CGctcgagCCTAGTCTGATTCCCACAGG
Tsc22d3_Rv	CGaagcttGGCTTAGGTGGAAGTGTTGG
Tsc22d3_Mut_Fw	gaaTGCTCTGGACTGCTGCCG
Tsc22d3_Mut_Rv	agaaTTCTCCTGAGCAGATGCAAACATTC

Luciferase Reporter Regions, primer targets, putative GR motif

Dusp1
GCTATGAGCAGCATTCCAGGATGAAGGCAAGTTCAAGGTCAGAGGAAGAGGAGATTTGAG
CTTCGAACAGAAGTTGTGGTATGGCCCTGGCTTTGAGCTCACTTCCTGTTTTGTGGGGGCC
TGAGTGGGTCTCTTCTAGCGCTGAACATTCTGTTCCCTTTCCCAACACAGAACGTCCAGCT
CCAGCCTGCTGATCAGTGCTCATCTAGTGGGAAAGTGGACCCAGCTGTACCCCAAGATGT
CAGTTCACCCTAAGATGCCTTGGGGATTTCACCAAGTGTTTAGAGAAGTAGAGGCTGCCCT
GAGTCACAGGCCCTGTGAGTTCATTGCCTGTCAGAACTGAGAGGGGCAGCAGGAGGAAG
AAGTGGATTGCGGCACTGCGAAGTAGAAGCTGGGCTTAGAGTCAGAGCTGTCTTCCCTGA
GCTGAT

Tsc22d3
CCTAGTCTGATTCCCACAGGAGGCCTTTGGAGTGTTCTTTGAGATTGCCTTGTCTCTGGCC
TGGCCCCTCTGGCCAGGGACAGTGATTCACCCAACTCAGAATGTTTGCATCTGCTCAGGA
GAACACTGTGTGCTCTGGACTGCTGCCGGAGCCCAAGGGAAAAGGGAAGTGCGCAGGAC
CAACAGGCCAAGAGAAAATCTGGGAGGGGTTCTGCTGTGGCAGCAGCTCCAACACTTCCA
CCTAAGCC

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SUPPLEMENTAL RESULTS FOR DE NOVO MOTIF ANALYSES

Homer de novo motif analysis of GR peaks (N=14,475) in liver from *WT* mice, related to Figure 1.

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1		1e-1814	-4.178e+03	49.91%	16.84%	47.5bp (64.4bp)	MA0114.1_HNF4A/Jaspar More Information | Similar Motifs Found	motif file (matrix)
2		1e-1173	-2.703e+03	21.63%	4.46%	48.8bp (67.0bp)	MA0102.2_CEBPA/Jaspar More Information | Similar Motifs Found	motif file (matrix)
3		1e-831	-1.914e+03	34.45%	14.02%	51.6bp (66.1bp)	FOXA1(Forkhead)/LNCAP-FOXA1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
4		1e-651	-1.499e+03	13.78%	3.15%	50.4bp (64.7bp)	HNF6(Homeobox)/Liver-Hnf6-ChIP-Seq(ERP000394) More Information | Similar Motifs Found	motif file (matrix)
5		1e-582	-1.340e+03	12.39%	2.83%	32.9bp (62.4bp)	GRE/RAW264.7-GRE-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
6		1e-536	-1.235e+03	9.37%	1.73%	54.9bp (65.8bp)	Hnf1(Homeobox)/Liver-Foxa2-Chip-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
7		1e-443	-1.021e+03	39.15%	22.44%	54.5bp (66.0bp)	NF1-halfsite(CTF)/LNCaP-NF1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
8		1e-428	-9.859e+02	56.15%	37.94%	51.5bp (65.1bp)	AR-halfsite(NR)/LNCaP-AR-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
9		1e-269	-6.217e+02	47.93%	33.76%	55.0bp (64.5bp)	MA0161.1_NFIC/Jaspar More Information | Similar Motifs Found	motif file (matrix)
10		1e-225	-5.182e+02	8.57%	3.02%	49.2bp (59.6bp)	STAT1(Stat)/HelaS3-STAT1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
11		1e-173	-3.994e+02	14.33%	7.48%	54.2bp (64.6bp)	Reverb(NR/DR2)/BLRP(RAW)-Reverba-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
12		1e-148	-3.418e+02	2.02%	0.27%	53.4bp (66.3bp)	PB0002.1_Arid5a_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
13		1e-128	-2.957e+02	9.08%	4.40%	58.4bp (67.3bp)	MA0161.1_NFIC/Jaspar More Information | Similar Motifs Found	motif file (matrix)
14		1e-86	-2.001e+02	4.82%	2.07%	50.0bp (63.3bp)	EWS:ERG-fusion(ETS)/CADO_ES1-EWS:ERG-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
15		1e-78	-1.815e+02	11.85%	7.42%	56.6bp (58.0bp)	POL003.1_GC-box/Jaspar More Information | Similar Motifs Found	motif file (matrix)
16		1e-78	-1.811e+02	6.09%	3.05%	51.7bp (67.1bp)	AARE(HLH)/mES-cMyc-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
17		1e-78	-1.801e+02	2.22%	0.63%	49.5bp (57.8bp)	Foxo1(Forkhead)/RAW-Foxo1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
18		1e-74	-1.719e+02	6.98%	3.75%	51.9bp (63.8bp)	EBF1(EBF)/Near-E2A-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
19		1e-66	-1.524e+02	8.78%	5.29%	56.0bp (62.1bp)	Gata4(Zf)/Heart-Gata4-ChIP-Seq(GSE35151)/Homer More Information | Similar Motifs Found	motif file (matrix)
20		1e-49	-1.144e+02	4.51%	2.39%	55.7bp (65.0bp)	USF1(HLH)/GM12878-Usf1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)

Homer de novo motif analysis for GR peaks (N=7,706) in liver from *GR*^{dim} mice, related to Figure 1.

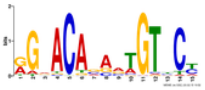
Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1		1e-1080	-2.488e+03	54.15%	18.31%	47.9bp (65.5bp)	MA0114.1_HNF4A/Jaspar More Information | Similar Motifs Found	motif file (matrix)
2		1e-794	-1.829e+03	25.14%	4.79%	49.0bp (64.0bp)	MF0006.1_bZIP_cEBP-like_subclass/Jaspar More Information | Similar Motifs Found	motif file (matrix)
3		1e-423	-9.749e+02	14.75%	2.98%	48.2bp (64.5bp)	HNF6(Homeobox)/Liver-Hnf6-ChIP-Seq(ERP000394) More Information | Similar Motifs Found	motif file (matrix)
4		1e-415	-9.578e+02	38.90%	17.75%	52.3bp (67.3bp)	FOXP1(Forkhead)/H9-FOXP1-ChIP-Seq(GSE31006)/Homer More Information | Similar Motifs Found	motif file (matrix)
5		1e-368	-8.484e+02	63.25%	40.01%	50.8bp (65.0bp)	AR-halfsite(NR)/LNCaP-AR-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
6		1e-223	-5.144e+02	49.83%	32.24%	55.8bp (67.6bp)	NF1-halfsite(CTF)/LNCaP-NF1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
7		1e-200	-4.608e+02	20.88%	9.41%	49.2bp (61.2bp)	Reverb(NR/DR2)/BLRP(RAW)-Reverba-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
8		1e-146	-3.381e+02	7.40%	2.03%	56.6bp (62.2bp)	Hnf1(Homeobox)/Liver-Foxa2-Chip-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
9		1e-143	-3.315e+02	24.23%	13.38%	51.9bp (63.3bp)	RARg(NR)/ES-RARg-ChIP-Seq(GSE30538)/Homer More Information | Similar Motifs Found	motif file (matrix)
10		1e-123	-2.838e+02	24.62%	14.38%	53.7bp (63.8bp)	MF0004.1_Nuclear_Receptor_class/Jaspar More Information | Similar Motifs Found	motif file (matrix)
11		1e-119	-2.748e+02	16.86%	8.56%	52.4bp (63.0bp)	NF1(CTF)/LNCAP-NF1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
12		1e-104	-2.410e+02	28.78%	18.56%	56.9bp (62.3bp)	GATA3(Zf)/iTreg-Gata3-ChIP-Seq(GSE20898)/Homer More Information | Similar Motifs Found	motif file (matrix)
13		1e-101	-2.343e+02	7.44%	2.66%	47.7bp (62.4bp)	STAT4(Stat)/CD4-Stat4-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
14		1e-84	-1.937e+02	39.36%	28.98%	52.6bp (63.6bp)	p53(p53)/p53-ChIP-Chip/Homer More Information | Similar Motifs Found	motif file (matrix)
15		1e-82	-1.904e+02	2.80%	0.53%	38.4bp (37.6bp)	PRDM1/BMI1(Zf)/Hela-PRDM1-ChIP-Seq(GSE31477)/Homer More Information | Similar Motifs Found	motif file (matrix)
16		1e-47	-1.100e+02	10.13%	5.85%	54.1bp (66.3bp)	PB0104.1_Zscan4_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
17		1e-39	-9.024e+01	2.67%	0.91%	57.2bp (67.7bp)	MA0161.1_NFIC/Jaspar More Information | Similar Motifs Found	motif file (matrix)
18		1e-27	-6.351e+01	1.53%	0.46%	52.3bp (65.2bp)	ATF3(bZIP)/K562-ATF3-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
19		1e-25	-5.893e+01	0.30%	0.01%	50.9bp (46.1bp)	NFY(CCAAT)/Promoter/Homer More Information | Similar Motifs Found	motif file (matrix)
20		1e-15	-3.607e+01	0.14%	0.00%	65.6bp (0.0bp)	PB0002.1_Arid5a_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)

MEME de novo motif analysis of the top-1000 ChIP-exo peak pairs at WT-selective GR sites in mouse liver, related to Figure 1.

6am ChIP-exo peak-pairs

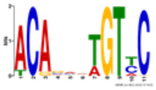
#1

- 2.3e-1258
- 743 sites



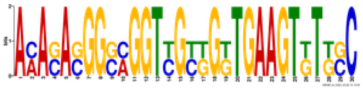
#2

- 3.3e-019
- 82 sites



#3

- 1.5e+002
- 4 sites



#4

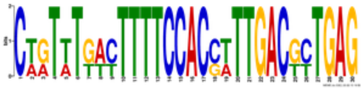
- 3.7e+003
- 4 sites

#5

- 4.5e+002
- 34 sites

#6

- 4.4e+003
- 3 sites



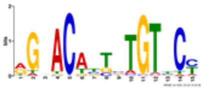
#7

- 6.9e+003
- 4 sites

6pm ChIP-exo peak-pairs

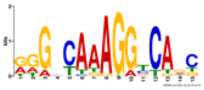
#1

- 3.6e-1364
- 796 sites



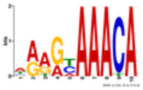
#2

- 3.9e-003
- 46 sites



#3

- 2.1e-004
- 57 sites

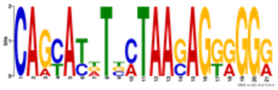


#4

- 4.1e-001
- 10 sites

#5

- 1.0e+001
- 6 sites



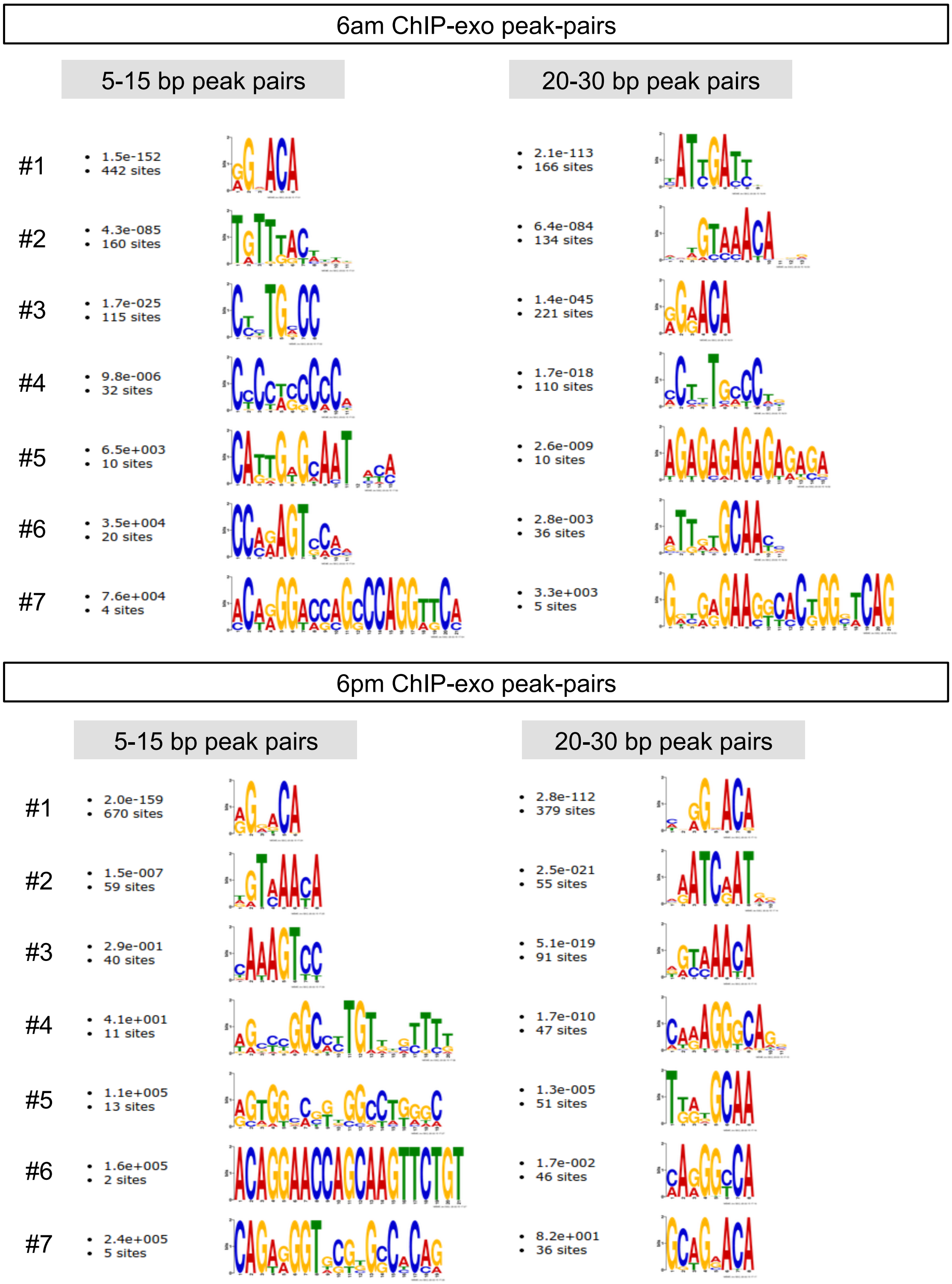
#6

- 9.2e+001
- 7 sites

#7

- 2.1e+002
- 3 sites

MEME de novo motif analysis of the top-1000 ChIP-exo peak pairs at common GR sites in mouse liver, related to Figures 2 and 3.



Homer de novo motif analysis for GR peaks (N=2,110) at dimeric sites in mouse liver, related to Figure 4.

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1		1e-1311	-3.020e+03	69.95%	5.55%	28.1bp (61.9bp)	GRE/RAW264.7-GRE-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
2		1e-146	-3.366e+02	18.44%	3.77%	50.8bp (66.2bp)	MF0006.1_bZIP_cEBP-like_subclass/Jaspar More Information | Similar Motifs Found	motif file (matrix)
3		1e-123	-2.854e+02	29.19%	10.45%	49.6bp (62.7bp)	MA0114.1_HNF4A/Jaspar More Information | Similar Motifs Found	motif file (matrix)
4		1e-98	-2.271e+02	14.27%	3.29%	54.6bp (63.0bp)	HNF6(Homeobox)/Liver-Hnf6-ChIP-Seq(ERP000394) More Information | Similar Motifs Found	motif file (matrix)
5		1e-97	-2.248e+02	36.07%	16.97%	54.0bp (66.4bp)	Foxo1(Forkhead)/RAW-Foxo1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
6		1e-81	-1.880e+02	41.04%	22.32%	55.7bp (64.5bp)	NF1-halfsite(CTF)/LNCaP-NF1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
7		1e-70	-1.632e+02	6.49%	0.87%	38.7bp (59.8bp)	PR(NR)/T47D-PR-ChIP-Seq(GSE31130)/Homer More Information | Similar Motifs Found	motif file (matrix)
8		1e-67	-1.559e+02	12.42%	3.50%	49.9bp (64.9bp)	STAT1(Stat)/HelaS3-STAT1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
9		1e-39	-9.013e+01	3.32%	0.40%	60.3bp (56.2bp)	Hnf1(Homeobox)/Liver-Foxa2-Chip-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
10		1e-35	-8.279e+01	15.69%	7.49%	51.1bp (64.0bp)	MF0004.1_Nuclear_Receptor_class/Jaspar More Information | Similar Motifs Found	motif file (matrix)
11		1e-20	-4.611e+01	0.47%	0.00%	58.6bp (0.0bp)	POL009.1_DCE_S_II/Jaspar More Information | Similar Motifs Found	motif file (matrix)
12		1e-19	-4.524e+01	4.22%	1.34%	55.1bp (60.1bp)	RARg(NR)/ES-RARg-ChIP-Seq(GSE30538)/Homer More Information | Similar Motifs Found	motif file (matrix)
13		1e-18	-4.177e+01	8.77%	4.34%	54.2bp (59.1bp)	Gata2(Zf)/K562-GATA2-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
14		1e-17	-4.071e+01	0.43%	0.00%	31.8bp (0.0bp)	MA0009.1_T/Jaspar More Information | Similar Motifs Found	motif file (matrix)
15		1e-16	-3.891e+01	7.06%	3.28%	55.7bp (61.7bp)	POL004.1_CCAAT-box/Jaspar More Information | Similar Motifs Found	motif file (matrix)
16		1e-16	-3.728e+01	1.85%	0.34%	51.5bp (58.3bp)	Tlx?/NPC-H3K4me1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
17		1e-15	-3.542e+01	0.38%	0.00%	50.5bp (4.4bp)	PB0154.1_Osr1_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
18		1e-15	-3.542e+01	0.38%	0.00%	58.6bp (0.0bp)	MA0148.1_FOXA1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
19		1e-14	-3.451e+01	0.43%	0.01%	22.7bp (14.6bp)	PU.1(ETS)/ThioMac-PU.1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
20		1e-14	-3.407e+01	0.52%	0.01%	52.6bp (31.5bp)	PB0145.1_Mafb_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)

Homer de novo motif analysis for GR peaks (N=11,108) at monomeric sites in mouse liver, related to Figure 4.

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1		1e-1590	-3.663e+03	53.17%	17.35%	47.0bp (63.9bp)	MA0114.1_HNF4A/Jaspar More Information | Similar Motifs Found	motif file (matrix)
2		1e-940	-2.165e+03	22.43%	4.61%	48.2bp (65.8bp)	MA0102.2_CEBPA/Jaspar More Information | Similar Motifs Found	motif file (matrix)
3		1e-646	-1.489e+03	32.34%	12.49%	50.5bp (64.5bp)	HNF6(Homeobox)/Liver-Hnf6-ChIP-Seq(ERP000394) More Information | Similar Motifs Found	motif file (matrix)
4		1e-601	-1.386e+03	31.64%	12.55%	50.9bp (65.7bp)	FOXA1(Forkhead)/LNCAP-FOXA1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
5		1e-475	-1.094e+03	66.00%	43.98%	51.3bp (64.5bp)	AR-halfsite(NR)/LNCaP-AR-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
6		1e-370	-8.543e+02	57.85%	38.48%	55.6bp (67.1bp)	MA0161.1_NFIC/Jaspar More Information | Similar Motifs Found	motif file (matrix)
7		1e-284	-6.544e+02	5.16%	0.72%	54.2bp (63.9bp)	Hnf1(Homeobox)/Liver-Foxa2-Chip-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
8		1e-269	-6.214e+02	7.62%	1.74%	49.2bp (64.8bp)	CEBP:AP1/ThioMac-CEBPb-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
9		1e-161	-3.715e+02	14.15%	6.81%	52.5bp (64.4bp)	MA0141.1_Esrrb/Jaspar More Information | Similar Motifs Found	motif file (matrix)
10		1e-107	-2.469e+02	6.03%	2.28%	47.3bp (61.3bp)	Stat3(Stat)/mES-Stat3-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
11		1e-86	-1.994e+02	23.62%	16.32%	57.3bp (63.7bp)	GATA3(Zf)/iTreg-Gata3-ChIP-Seq(GSE20898)/Homer More Information | Similar Motifs Found	motif file (matrix)
12		1e-85	-1.969e+02	26.31%	18.70%	54.8bp (66.3bp)	PB0153.1_Nr2f2_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
13		1e-77	-1.781e+02	14.71%	9.19%	55.5bp (57.8bp)	POL003.1_GC-box/Jaspar More Information | Similar Motifs Found	motif file (matrix)
14		1e-72	-1.669e+02	26.52%	19.46%	55.9bp (64.9bp)	MA0081.1_SPIB/Jaspar More Information | Similar Motifs Found	motif file (matrix)
15		1e-69	-1.598e+02	9.23%	5.14%	54.5bp (66.3bp)	USF1(HLH)/GM12878-Usf1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
16		1e-63	-1.465e+02	2.02%	0.51%	42.0bp (35.5bp)	PRDM1/BMI1(Zf)/Hela-PRDM1-ChIP-Seq(GSE31477)/Homer More Information | Similar Motifs Found	motif file (matrix)
17		1e-50	-1.165e+02	0.28%	0.00%	51.9bp (24.4bp)	NF1(CTF)/LNCAP-NF1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
18		1e-49	-1.130e+02	1.67%	0.45%	49.8bp (64.6bp)	Tlx?/NPC-H3K4me1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
19		1e-35	-8.103e+01	7.29%	4.61%	52.5bp (63.8bp)	Nr5a2(NR)/mES-Nr5a2-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
20		1e-34	-8.016e+01	0.21%	0.00%	42.3bp (27.3bp)	AR-halfsite(NR)/LNCaP-AR-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)

Homer de novo motif analysis for dimeric GR sites in mouse liver using the monomeric sites as background, related to Figure 4.

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1		1e-1338	-3.082e+03	52.80%	1.73%	26.0bp (59.5bp)	GRE(NR/IR3)/A549-GR-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
2		1e-44	-1.025e+02	38.72%	24.81%	50.3bp (58.4bp)	Ets1-distal(ETS)/CD4+-PolII-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
3		1e-39	-9.118e+01	11.61%	4.50%	47.3bp (62.5bp)	PB0115.1_Ehf_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
4		1e-28	-6.472e+01	1.09%	0.03%	43.8bp (33.1bp)	PH0083.1_Irx3_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
5		1e-22	-5.272e+01	0.71%	0.01%	48.8bp (4.4bp)	PB0152.1_Nkx3-1_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
6		1e-22	-5.272e+01	0.71%	0.02%	39.8bp (0.0bp)	PB0068.1_Sox1_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
7		1e-19	-4.408e+01	0.62%	0.01%	33.4bp (0.0bp)	MA0041.1_Foxd3/Jaspar More Information | Similar Motifs Found	motif file (matrix)
8		1e-17	-3.987e+01	0.57%	0.01%	47.4bp (42.7bp)	MA0100.1_Myb/Jaspar More Information | Similar Motifs Found	motif file (matrix)
9		1e-17	-3.987e+01	0.57%	0.02%	54.5bp (11.4bp)	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
10		1e-15	-3.574e+01	0.52%	0.02%	56.2bp (41.9bp)	PB0146.1_Mafk_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
11		1e-15	-3.574e+01	0.52%	0.01%	50.8bp (4.4bp)	SPDEF(ETS)/VCaP-SPDEF-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
12		1e-15	-3.574e+01	0.52%	0.02%	40.1bp (0.0bp)	PB0192.1_Tcfap2e_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
13		1e-15	-3.574e+01	0.52%	0.01%	47.4bp (32.6bp)	PB0111.1_Bhlhb2_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
14		1e-15	-3.574e+01	0.52%	0.02%	45.4bp (11.0bp)	MA0104.2_Mycn/Jaspar More Information | Similar Motifs Found	motif file (matrix)
15		1e-15	-3.574e+01	0.52%	0.02%	52.4bp (0.0bp)	Cdx2(Homeobox)/mES-Cdx2-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
16		1e-15	-3.525e+01	0.62%	0.02%	50.7bp (2.0bp)	PB0128.1_Gcm1_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
17		1e-15	-3.525e+01	20.85%	14.37%	53.3bp (58.6bp)	STAT5(Stat)/mCD4+-Stat5a|b-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
18		1e-13	-3.207e+01	0.81%	0.06%	62.2bp (61.2bp)	SD0003.1_at_AC_acceptor/Jaspar More Information | Similar Motifs Found	motif file (matrix)
19		1e-13	-3.173e+01	0.57%	0.02%	54.5bp (24.2bp)	BORIS(Zf)/K562-CTCFL-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
20		1e-13	-3.173e+01	0.57%	0.02%	59.1bp (38.0bp)	CHR/Cell-Cycle-Exp/Homer More Information | Similar Motifs Found	motif file (matrix)

Homer de novo motif analysis for monomeric GR sites in mouse liver using the dimeric sites as background, related to Figure 4.

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1		1e-205	-4.732e+02	41.60%	28.05%	49.0bp (55.2bp)	MA0114.1_HNF4A/Jaspar More Information | Similar Motifs Found	motif file (matrix)
2		1e-174	-4.007e+02	2.07%	0.18%	42.4bp (74.4bp)	PRDM1/BMI1(Zf)/Hela-PRDM1-ChIP-Seq(GSE31477)/Homer More Information | Similar Motifs Found	motif file (matrix)
3		1e-114	-2.634e+02	30.37%	21.15%	52.9bp (56.9bp)	PB0030.1_Hnf4a_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
4		1e-102	-2.353e+02	1.27%	0.11%	47.5bp (2.6bp)	MA0036.1_GATA2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
5		1e-88	-2.032e+02	0.91%	0.09%	48.9bp (11.1bp)	MA0156.1_FEV/Jaspar More Information | Similar Motifs Found	motif file (matrix)
6		1e-87	-2.021e+02	8.08%	3.92%	53.7bp (57.1bp)	E2A-nearPU.1(HLH)/Bcell-PU.1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
7		1e-86	-2.000e+02	1.80%	0.34%	54.2bp (40.7bp)	MA0158.1_HOXA5/Jaspar More Information | Similar Motifs Found	motif file (matrix)
8		1e-85	-1.973e+02	0.89%	0.06%	55.3bp (51.1bp)	SD0003.1_at_AC_acceptor/Jaspar More Information | Similar Motifs Found	motif file (matrix)
9		1e-82	-1.907e+02	2.68%	0.73%	58.4bp (59.0bp)	MA0133.1_BRCA1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
10		1e-79	-1.829e+02	0.85%	0.05%	56.0bp (0.0bp)	Tlx?/NPC-H3K4me1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
11		1e-78	-1.801e+02	1.95%	0.40%	55.9bp (29.8bp)	MA0124.1_NKX3-1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
12		1e-78	-1.800e+02	0.84%	0.10%	60.8bp (14.3bp)	SD0002.1_at_AC_acceptor/Jaspar More Information | Similar Motifs Found	motif file (matrix)
13		1e-77	-1.780e+02	1.06%	0.14%	52.1bp (54.2bp)	PB0014.1_Esrra_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
14		1e-75	-1.731e+02	1.53%	0.26%	48.4bp (22.6bp)	MF0004.1_Nuclear_Receptor_class/Jaspar More Information | Similar Motifs Found	motif file (matrix)
15		1e-74	-1.714e+02	1.66%	0.33%	54.5bp (64.7bp)	PB0153.1_Nr2f2_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
16		1e-73	-1.685e+02	1.03%	0.14%	52.1bp (12.7bp)	HNF4a(NR/DR1)/HepG2-HNF4a-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
17		1e-69	-1.600e+02	1.17%	0.18%	56.5bp (60.8bp)	PB0164.1_Smad3_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
18		1e-67	-1.548e+02	0.76%	0.09%	51.2bp (33.7bp)	PB0032.1_IRC900814_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
19		1e-63	-1.452e+02	17.88%	12.34%	53.4bp (58.7bp)	MA0019.1_Ddit3::Cebpa/Jaspar More Information | Similar Motifs Found	motif file (matrix)
20		1e-61	-1.408e+02	0.92%	0.13%	56.4bp (28.7bp)	MA0031.1_FOXD1/Jaspar More Information | Similar Motifs Found	motif file (matrix)

Homer de novo motif analysis for GR peaks in primary macrophages isolated from *WT* mice, related to Figure 5.

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1		1e-101	-2.332e+02	29.83%	7.64%	52.5bp (68.8bp)	PB0058.1_Sfpi1_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
2		1e-94	-2.172e+02	27.23%	6.77%	49.0bp (72.5bp)	MA0102.2_CEBPA/Jaspar More Information | Similar Motifs Found	motif file (matrix)
3		1e-83	-1.918e+02	13.75%	1.69%	39.6bp (87.3bp)	GRE/RAW264.7-GRE-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
4		1e-59	-1.371e+02	16.08%	3.60%	50.6bp (78.2bp)	HIF1b(HLH)/O785-HIF1b-ChIP-Seq(GSE34871)/Homer More Information | Similar Motifs Found	motif file (matrix)
5		1e-36	-8.465e+01	22.58%	9.43%	49.5bp (69.4bp)	AR-halfsite(NR)/LNCaP-AR-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
6		1e-28	-6.546e+01	10.69%	3.16%	55.4bp (65.0bp)	MA0107.1_RELA/Jaspar More Information | Similar Motifs Found	motif file (matrix)
7		1e-15	-3.585e+01	8.36%	3.16%	54.4bp (119.1bp)	PB0130.1_Gm397_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
8		1e-13	-3.055e+01	4.65%	1.31%	47.2bp (76.2bp)	Atf1(bZIP)/K562-ATF1-ChIP-Seq(GSE31477)/Homer More Information | Similar Motifs Found	motif file (matrix)
9		1e-13	-2.994e+01	9.67%	4.36%	55.6bp (95.7bp)	POL009.1_DCE_S_II/Jaspar More Information | Similar Motifs Found	motif file (matrix)
10		1e-12	-2.861e+01	13.94%	7.52%	54.3bp (85.8bp)	MA0089.1_NFE2L1::MafG/Jaspar More Information | Similar Motifs Found	motif file (matrix)
11 *		1e-11	-2.760e+01	2.97%	0.62%	62.5bp (56.9bp)	PU.1-IRF/Bcell-PU.1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
12 *		1e-9	-2.198e+01	11.99%	6.74%	54.0bp (85.3bp)	PB0032.1_IRC900814_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
13 *		1e-8	-2.009e+01	10.59%	5.89%	51.8bp (113.9bp)	MA0032.1_FOXC1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
14 *		1e-8	-1.987e+01	1.49%	0.21%	52.0bp (57.6bp)	AR-halfsite(NR)/LNCaP-AR-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
15 *		1e-8	-1.875e+01	8.92%	4.79%	54.6bp (114.0bp)	PRDM1/BMI1(Zf)/Hela-PRDM1-ChIP-Seq(GSE31477)/Homer More Information | Similar Motifs Found	motif file (matrix)
16 *		1e-7	-1.720e+01	4.55%	1.89%	52.4bp (76.3bp)	AARE(HLH)/mES-cMyc-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
17 *		1e-7	-1.695e+01	9.57%	5.47%	54.6bp (103.5bp)	PH0082.1_Irx2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
18 *		1e-6	-1.406e+01	0.65%	0.05%	54.1bp (42.6bp)	PB0132.1_Hbp1_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
19 *		1e-5	-1.217e+01	2.32%	0.82%	55.7bp (70.0bp)	PB0099.1_Zfp691_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
20 *		1e-4	-1.007e+01	0.28%	0.01%	37.1bp (32.6bp)	PB0091.1_Zbtb3_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)

*Possible false positive

Homer de novo motif analysis for GR peaks in primary macrophages isolated from GR^{dim} mice, related to Figure 5.

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1		1e-132	-3.046e+02	32.12%	5.05%	48.7bp (70.7bp)	MA0102.2_CEBPA/Jaspar More Information | Similar Motifs Found	motif file (matrix)
2		1e-114	-2.635e+02	37.23%	8.42%	47.7bp (67.4bp)	PB0058.1_Sfpi1_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
3		1e-64	-1.485e+02	28.59%	8.24%	50.2bp (71.1bp)	AP-1(bZIP)/ThioMac-PU.1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
4		1e-34	-7.872e+01	21.65%	7.88%	48.2bp (72.4bp)	AR-halfsite(NR)/LNCaP-AR-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
5		1e-31	-7.348e+01	22.26%	8.61%	53.4bp (85.7bp)	RUNX2(Runt)/PCa-RUNX2-ChIP-Seq(GSE33889)/Homer More Information | Similar Motifs Found	motif file (matrix)
6		1e-24	-5.624e+01	16.79%	6.35%	49.1bp (77.7bp)	AARE(HLH)/mES-cMyc-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
7		1e-17	-3.969e+01	4.50%	0.73%	50.3bp (58.2bp)	MA0107.1_RELA/Jaspar More Information | Similar Motifs Found	motif file (matrix)
8		1e-15	-3.525e+01	15.21%	7.01%	56.2bp (94.2bp)	MA0442.1_SOX10/Jaspar More Information | Similar Motifs Found	motif file (matrix)
9		1e-12	-2.818e+01	1.09%	0.03%	37.9bp (42.2bp)	MA0078.1_Sox17/Jaspar More Information | Similar Motifs Found	motif file (matrix)
10 *		1e-9	-2.249e+01	0.85%	0.02%	38.8bp (52.2bp)	CEBP:AP1/ThioMac-CEBPb-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
11 *		1e-9	-2.095e+01	23.24%	15.17%	54.0bp (91.8bp)	MA0442.1_SOX10/Jaspar More Information | Similar Motifs Found	motif file (matrix)
12 *		1e-8	-2.009e+01	3.04%	0.70%	41.7bp (97.9bp)	PB0130.1_Gm397_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
13 *		1e-7	-1.826e+01	0.49%	0.00%	60.6bp (16.9bp)	HEB?/mES-Nanog-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
14 *		1e-7	-1.631e+01	15.94%	10.00%	58.3bp (69.4bp)	PB0139.1_Irf5_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
15 *		1e-6	-1.551e+01	0.49%	0.01%	39.9bp (25.2bp)	MafA(bZIP)/Islet-MafA-ChIP-Seq(GSE30298)/Homer More Information | Similar Motifs Found	motif file (matrix)
16 *		1e-6	-1.511e+01	6.57%	3.08%	50.6bp (114.5bp)	PH0083.1_Irx3_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
17 *		1e-5	-1.230e+01	0.61%	0.03%	58.3bp (32.4bp)	MA0018.2_CREB1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
18 *		1e-4	-9.623e+00	0.49%	0.03%	55.6bp (64.9bp)	PB0104.1_Zscan4_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
19 *		1e-3	-8.349e+00	0.36%	0.02%	23.7bp (53.9bp)	FOXA1:AR/LNCAP-AR-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
20 *		1e-2	-6.869e+00	0.24%	0.01%	50.4bp (29.9bp)	PB0089.1_Tcfe2a_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)

*Possible false positive

HOMER de novo motif analysis for WT-selective GR sites in primary mouse macrophages, related to Figure 5.

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1		1e-90	-2.084e+02	22.02%	2.05%	36.5bp (77.5bp)	GRE/RAW264.7-GRE-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
2		1e-31	-7.167e+01	25.21%	8.87%	52.1bp (69.5bp)	PB0058.1_Sfpi1_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
3		1e-19	-4.491e+01	9.24%	2.02%	48.8bp (68.2bp)	CEBP(bZIP)/CEBPb-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
4		1e-19	-4.408e+01	11.26%	3.01%	50.6bp (72.1bp)	AP-1(bZIP)/ThioMac-PU.1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
5		1e-18	-4.281e+01	21.51%	9.27%	49.9bp (73.1bp)	PB0194.1_Zbtb12_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
6		1e-16	-3.722e+01	23.19%	11.15%	56.4bp (75.8bp)	MF0002.1_bZIP_CREB/G-box-like_subclass/Jaspar More Information | Similar Motifs Found	motif file (matrix)
7		1e-12	-2.889e+01	4.54%	0.75%	57.1bp (114.1bp)	MA0033.1_FOXL1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
8 *		1e-11	-2.688e+01	3.03%	0.32%	45.3bp (73.1bp)	AARE(HLH)/mES-cMyc-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
9 *		1e-10	-2.450e+01	3.87%	0.65%	46.3bp (79.2bp)	PB0146.1_Mafk_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
10 *		1e-9	-2.116e+01	23.03%	13.72%	52.5bp (98.3bp)	PB0044.1_Mtf1_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
11 *		1e-7	-1.650e+01	0.67%	0.01%	63.1bp (11.4bp)	MA0081.1_SPIB/Jaspar More Information | Similar Motifs Found	motif file (matrix)
12 *		1e-7	-1.630e+01	4.71%	1.44%	51.6bp (77.0bp)	PBX1(Homeobox)/MCF7-PBX1-ChIP-Seq(GSE28007)/Homer More Information | Similar Motifs Found	motif file (matrix)
13 *		1e-6	-1.601e+01	1.85%	0.22%	58.4bp (55.8bp)	PB0203.1_Zfp691_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
14 *		1e-6	-1.479e+01	1.18%	0.07%	41.9bp (37.8bp)	ZNF711(Zf)/SH-SY5Y-ZNF711-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
15 *		1e-5	-1.336e+01	10.92%	5.88%	60.0bp (80.9bp)	PB0208.1_Zscan4_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
16 *		1e-5	-1.239e+01	2.86%	0.75%	58.2bp (79.4bp)	MA0090.1_TEAD1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
17 *		1e-5	-1.163e+01	2.18%	0.48%	51.7bp (128.9bp)	PRDM1/BMI1(Zf)/Hela-PRDM1-ChIP-Seq(GSE31477)/Homer More Information | Similar Motifs Found	motif file (matrix)
18 *		1e-4	-1.091e+01	6.05%	2.79%	55.2bp (89.4bp)	RUNX2(Runt)/PCa-RUNX2-ChIP-Seq(GSE33889)/Homer More Information | Similar Motifs Found	motif file (matrix)
19 *		1e-4	-1.075e+01	6.89%	3.40%	49.7bp (91.4bp)	MA0095.1_YY1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
20 *		1e-3	-8.735e+00	0.34%	0.00%	29.1bp (0.0bp)	PB0055.1_Rfx4_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)

*Possible false positive

HOMER de novo motif analysis for common GR sites in primary mouse macrophages, related to Figure 5.

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1		1e-164	-3.779e+02	33.70%	6.06%	47.3bp (73.3bp)	MA0102.2_CEBPA/Jaspar More Information | Similar Motifs Found	motif file (matrix)
2		1e-142	-3.283e+02	31.57%	6.12%	50.0bp (68.7bp)	PB0058.1_Sfpi1_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
3		1e-85	-1.958e+02	26.74%	7.17%	49.8bp (75.9bp)	HIF1b(HLH)/O785-HIF1b-ChIP-Seq(GSE34871)/Homer More Information | Similar Motifs Found	motif file (matrix)
4		1e-41	-9.628e+01	49.86%	29.95%	50.0bp (73.6bp)	AR-halfsite(NR)/LNCaP-AR-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
5		1e-27	-6.319e+01	20.15%	9.16%	52.4bp (78.5bp)	RUNX2(Runt)/PCa-RUNX2-ChIP-Seq(GSE33889)/Homer More Information | Similar Motifs Found	motif file (matrix)
6		1e-26	-6.059e+01	18.29%	8.06%	55.0bp (77.8bp)	MA0089.1_NFE2L1::MafG/Jaspar More Information | Similar Motifs Found	motif file (matrix)
7		1e-23	-5.515e+01	8.45%	2.37%	53.5bp (62.2bp)	NFkB-p65(RHD)/GM12787-p65-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
8		1e-17	-4.124e+01	5.76%	1.50%	56.6bp (133.0bp)	PB0026.1_Gm397_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
9		1e-16	-3.895e+01	10.40%	4.25%	49.4bp (80.3bp)	ETS:RUNX/Jurkat-RUNX1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
10		1e-16	-3.762e+01	4.92%	1.22%	56.8bp (64.9bp)	PB0058.1_Sfpi1_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
11		1e-14	-3.282e+01	2.60%	0.38%	52.8bp (59.8bp)	c-Jun-CRE(bZIP)/K562-cJun-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
12 *		1e-11	-2.649e+01	3.81%	1.03%	54.6bp (124.1bp)	PH0082.1_Irx2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
13 *		1e-10	-2.500e+01	8.08%	3.66%	60.7bp (88.3bp)	MA0442.1_SOX10/Jaspar More Information | Similar Motifs Found	motif file (matrix)
14 *		1e-10	-2.454e+01	10.58%	5.44%	52.2bp (86.8bp)	Esrrb(NR)/mES-Esrrb-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
15 *		1e-8	-2.068e+01	0.93%	0.06%	51.5bp (130.1bp)	MA0157.1_FOXO3/Jaspar More Information | Similar Motifs Found	motif file (matrix)
16 *		1e-8	-1.995e+01	4.55%	1.73%	55.8bp (77.4bp)	ERE(NR/IR3)/MCF7-ERa-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
17 *		1e-8	-1.860e+01	0.46%	0.01%	33.0bp (32.3bp)	PH0098.1_Lhx8/Jaspar More Information | Similar Motifs Found	motif file (matrix)
18 *		1e-5	-1.157e+01	0.74%	0.09%	56.6bp (57.4bp)	HIF2a(HLH)/O785-HIF2a-ChIP-Seq(GSE34871)/Homer More Information | Similar Motifs Found	motif file (matrix)
19 *		1e-1	-3.459e+00	0.09%	0.00%	61.6bp (12.8bp)	Gfi1b(Zf)/HPC7-Gfi1b-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)

*Possible false positive

Homer de novo motif analysis for WT-selective GR sites in primary mouse macrophages using the common sites as background, related to Figure 5.

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1		1e-125	-2.896e+02	14.12%	0.25%	32.1bp (28.3bp)	GRE/RAW264.7-GRE-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
2		1e-27	-6.231e+01	3.70%	0.08%	47.6bp (0.0bp)	NF1-halfsite(CTF)/LNCaP-NF1-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
3		1e-23	-5.493e+01	3.36%	0.16%	49.7bp (4.1bp)	PB0203.1_Zfp691_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
4		1e-22	-5.290e+01	4.54%	0.36%	54.9bp (59.1bp)	PB0148.1_Mtf1_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
5		1e-20	-4.775e+01	3.03%	0.06%	47.3bp (0.0bp)	PB0203.1_Zfp691_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
6		1e-20	-4.775e+01	3.03%	0.17%	51.6bp (16.3bp)	CHR/Cell-Cycle-Exp/Homer More Information | Similar Motifs Found	motif file (matrix)
7		1e-20	-4.775e+01	3.03%	0.10%	43.6bp (0.0bp)	MA0099.2_AP1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
8		1e-19	-4.424e+01	2.86%	0.17%	57.7bp (42.3bp)	MA0039.2_Klf4/Jaspar More Information | Similar Motifs Found	motif file (matrix)
9		1e-18	-4.157e+01	3.36%	0.26%	52.7bp (23.8bp)	PB0124.1_Gabpa_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
10		1e-18	-4.157e+01	3.36%	0.20%	49.6bp (26.2bp)	PB0109.1_Bbx_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
11		1e-17	-4.079e+01	2.69%	0.08%	47.9bp (0.0bp)	PB0091.1_Zbtb3_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
12		1e-17	-4.079e+01	2.69%	0.09%	51.9bp (0.0bp)	PB0154.1_Osr1_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
13		1e-17	-4.079e+01	2.69%	0.16%	49.1bp (29.3bp)	PB0130.1_Gm397_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
14		1e-17	-4.079e+01	2.69%	0.14%	48.3bp (46.6bp)	PB0122.1_Foxk1_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
15		1e-17	-3.916e+01	3.70%	0.37%	57.2bp (54.1bp)	PH0084.1_Irx3_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
16		1e-16	-3.865e+01	3.19%	0.26%	46.0bp (41.2bp)	PH0148.1_Pou3f3/Jaspar More Information | Similar Motifs Found	motif file (matrix)
17		1e-16	-3.740e+01	2.52%	0.18%	46.2bp (61.1bp)	PB0090.1_Zbtb12_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
18		1e-16	-3.740e+01	2.52%	0.17%	52.2bp (41.8bp)	POL013.1_MED-1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
19		1e-15	-3.578e+01	3.03%	0.22%	50.4bp (34.0bp)	PB0208.1_Zscan4_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
20		1e-15	-3.572e+01	3.87%	0.45%	55.0bp (33.2bp)	PH0095.1_Lhx5/Jaspar More Information | Similar Motifs Found	motif file (matrix)

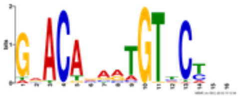
Homer de novo motif analysis for common GR sites in primary mouse macrophages using the WT-selective sites as background, related to Figure 5.

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1		1e-55	-1.269e+02	29.90%	12.04%	49.0bp (43.4bp)	CEBP(bZIP)/CEBPb-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
2		1e-47	-1.100e+02	5.39%	0.42%	51.4bp (27.6bp)	Tbet(T-box)/CD8-Tbet-ChIP-Seq(GSE33802)/Homer More Information | Similar Motifs Found	motif file (matrix)
3		1e-46	-1.072e+02	5.29%	0.47%	46.6bp (24.8bp)	PB0150.1_Mybl1_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
4		1e-39	-9.165e+01	3.81%	0.21%	46.0bp (0.0bp)	CEBP:AP1/ThioMac-CEBPb-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
5		1e-37	-8.538e+01	3.62%	0.32%	56.7bp (9.1bp)	MA0081.1_SPIB/Jaspar More Information | Similar Motifs Found	motif file (matrix)
6		1e-37	-8.538e+01	3.62%	0.33%	52.7bp (51.7bp)	MA0080.1_SPI1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
7		1e-33	-7.757e+01	4.27%	0.36%	47.6bp (4.9bp)	PB0183.1_Sry_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
8		1e-32	-7.407e+01	4.83%	0.55%	49.1bp (36.6bp)	POL004.1_CCAAT-box/Jaspar More Information | Similar Motifs Found	motif file (matrix)
9		1e-31	-7.245e+01	4.09%	0.49%	52.3bp (7.6bp)	PB0046.1_Mybl1_1/Jaspar More Information | Similar Motifs Found	motif file (matrix)
10		1e-30	-7.020e+01	3.16%	0.33%	47.9bp (48.8bp)	MA0150.1_NFE2L2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
11		1e-30	-6.993e+01	3.99%	0.50%	51.5bp (16.8bp)	c-Jun-CRE(bZIP)/K562-cJun-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
12		1e-28	-6.593e+01	6.50%	1.35%	53.8bp (61.0bp)	MA0056.1_MZF1_1-4/Jaspar More Information | Similar Motifs Found	motif file (matrix)
13		1e-27	-6.250e+01	3.71%	0.45%	52.9bp (77.3bp)	PH0082.1_Irx2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
14		1e-26	-6.144e+01	2.88%	0.25%	56.1bp (15.8bp)	MA0122.1_Nkx3-2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
15		1e-26	-6.144e+01	2.88%	0.22%	52.1bp (0.0bp)	Usf2(HLH)/C2C12-Usf2-ChIP-Seq(GSE36030)/Homer More Information | Similar Motifs Found	motif file (matrix)
16		1e-25	-5.858e+01	2.79%	0.29%	46.1bp (0.0bp)	MA0089.1_NFE2L1::MafG/Jaspar More Information | Similar Motifs Found	motif file (matrix)
17		1e-24	-5.685e+01	4.64%	0.83%	53.0bp (23.7bp)	RUNX-AML(Runt)/CD4+-PolII-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
18		1e-24	-5.531e+01	3.44%	0.50%	56.1bp (34.2bp)	PB0200.1_Zfp187_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)
19		1e-23	-5.422e+01	3.99%	0.65%	57.2bp (39.8bp)	Srebp1a(HLH)/HepG2-Srebp1a-ChIP-Seq/Homer More Information | Similar Motifs Found	motif file (matrix)
20		1e-23	-5.326e+01	9.94%	3.37%	59.0bp (63.1bp)	PB0133.1_Hic1_2/Jaspar More Information | Similar Motifs Found	motif file (matrix)

MEME de novo motif analysis for GR sites regulated by prednisolone, related to Figure 6.

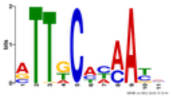
Gained GR sites in response to prednisolone

#1
- 4.1e-1017
- 645 sites



#2
- 8.2e-254
- 26 sites

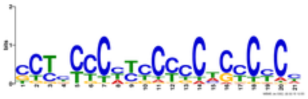
#3
- 4.2e-066
- 328 sites



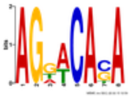
#4
- 1.8e-033
- 16 sites

#5
- 2.8e-016
- 7 sites

#6
- 1.7e-015
- 72 sites

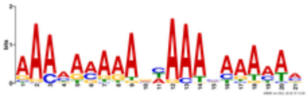


#7
- 3.2e-004
- 142 sites

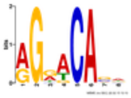


Lost GR sites in response to prednisolone

#1
- 2.8e-039
- 55 sites



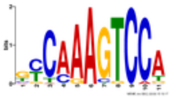
#2
- 2.3e-035
- 573 sites



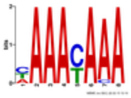
#3
- 2.8e-013
- 11 sites

#4
- 4.0e-011
- 71 sites

#5
- 2.5e-005
- 44 sites



#6
- 1.6e+002
- 55 sites



#7
- 1.3e+003
- 9 sites