SUPPLEMENTAL MATERIALS

Supplemental Figure 1.

a. 3% thioglycollate-elicited mouse peritoneal macrophages were infected with either Ad-GFP or Ad-FoxO1-CA at 100 M.O.I.; 48 hours posted infection, cells were exposed to 100ng/ml LPS for 30 minutes and subsequently lysed for immunoblotting assays with the indicated antibodies. Relative amount of phosphorylated versus total protein levels for P65 and JNK were quantitated by NIH-Image J; and the results are shown as bar graphs (M±SD) to the right. Letters above the bars show statistical groups (ANOVA, $p < 0.05$). *b.* RAW264.7 cells were infected with Ad-GFP, Ad-FoxO1-WT, or Ad-FoxO1-CA at 100 M.O.I.; 48 hours posted infection, cells were exposed to 100ng/ml LPS for 6 hours. mRNA expressions of various inflammatory genes were quantitated by ArrayPlate mRNA Assay (High Throughput Genomics, Inc. Tuscon, AZ). Notice that the LPS response of almost every genes were enhance by WT or CA-FoxO1.

Supplemental Figure 2.

a-b. Construction and validation of lentiviral short hairpin RNA against mouse FoxO1 (shFoxO1). Shown are schematic representation of short hairpin RNA (shRNA) lentiviral vector and the oligonucleotide sequences for constructing shFoxO1 lentivirus. SIN-LTR, self-inactivating long terminal repeat; Ψ, packaging signal; cPPT, central polypurine track; MCS, multiple cloning site; CMV, cytomegalovirus promoter; WRE, woodchuck hepatitis virus response element. *c.* Stable RAW264.7 macrophage cells were established by transduction of lentivirus encoding shFoxO1 and subsequent two rounds of sorting for

GFP-positive cells. Shown is endogenous FoxO1 mRNA in RAW264.7 macrophage cells stably expressing shFoxO1.

Supplemental Figure 3.

a. Bone marrow derived macrophages (BMDMs) derived from FoxO1 +/- or WT male mice were starved overnight in 0.1% BSA-containing medium, and treated with 100ng/ml LPS for 30 minutes. The cells were subsequently lysed for immunoblotting assays with the indicated antibodies. *b-c.* Relative amount of phosphorylated versus total protein levels for JNK (*b*) and P65 (*c*) were quantitated by NIH-Image J; and the results are shown as bar graphs (M±SD). Letters above the bars show statistical differences (ANOVA, $p < 0.05$).

Supplemental Figure 4.

Hepatocytes were isolated in the conventional manner from HFD liver. Kupffer cells were then separated from the non-Kupffer cell-containing fraction by purifying cells on CD11b antibody magnetic beads. In each fraction, TNFα *(a)*, IL-1β*(b)*, IL-6*(c)* and, Tlr4*(d)* mRNA expressions were quantitated by realtime PCR. It is evident that essentially all of the TNFα, IL-1β, IL-6 and, Tlr4 mRNA is expressed in the Kupffer cell (CD11b+) fraction, with none in hepatocytes and very little in the CD11b- non-hepatocyte cell fraction. *e*, mRNA expression of Tlr4 in adipocytes and SVF fractions from adipose tissue of 60% high fat diet (HFD) fed mice. Expression level in adipocytes is set to 1. Data are presented as the average ± SD. Letters above the bars show statistical groups (ANOVA, $p < 0.05$).

Supplemental Figure 5.

FoxO1 does not affect PPARγ-dependent repression of LPS-induced iNOS expression in RAW264.7 cells. *a*. RAW264.7 cells were co-transfected with FoxO1-WT or control vector together with an iNOS-luc reporter and pcDNA-PPARγ, and then exposed to 100ng/ml LPS, 1μM Rosiglitazone or both for 6 hours prior to luciferase assay. *b*. FoxO1-DBD-M was applied as an alternate of FoxO1-WT in *a*, and its effect on PPARγ transrepression was assayed. Data are presented as the average ± SD. Letters above the bars show statistical groups (ANOVA, $p < 0.05$).

Supplemental Figure 6.

Schematic outline of BLRP-BirA tagging system and ChIP-Seq workflow. We applied an *in vivo* biotin tagging methodology in which FoxO1 is tagged at the N-terminus with BLRP, a substrate for the *E. coli* biotin ligase, BirA. Introduction of these tagged proteins into cell lines that express BirA resulted in their efficient biotinylation, enabling subsequent purification with streptavidin matrices. We generated two genetic expression vectors for this purpose. In one, BirA cDNA was placed under transcriptional control of the beta-actin promoter into a neomycin-resistant plasmid. This plasmid was then used to generate stable cell lines in mouse RAW264.7 macrophages. In the other, BLRP-tagged FoxO1 under the control of the beta-actin promoter was inserted into a puromycin-resistant plasmid. As seen in the figure, this latter vector was designed to place the BLRP peptide at the amino terminus of FoxO1 and to include a polyglycine spacer and TEV cleavage site. Stable cell lines expressing both BirA and BLRP-tagged FoxO1 were selected in the presence of puromycin and neomycin, and clones that expressed the tagged protein at low or equivalent levels to the endogenous protein were selected.

Cells grown under the described experimental conditions of interest were subjected to formaldehyde cross-linking. Chromatin was prepared, sonicated into 200-300 bp fragments, and subjected to high affinity purification on a streptavidin affinity matrix. The matrix was subjected to TEV proteolysis to release the tagged protein and DNA adducts from the matrix, leaving behind any other biotinylated or non-specific bound proteins. Protein-DNA crosslinks were reversed by heating, and the resulting DNA was quantified and utilized to generate libraries for sequencing. Parall sequencing was performed using the Illumina Genome Analyzer, and short reads (24bp) were mapped to the mouse reference genome. Identical reads were combined, and peaks were defined using standard software packages with robust statistical cutoffs. Secondary analysis included computational motif discovery to identify enriched sequence elements in genomic binding sites.

Supplemental Figure 7.

Functional confirmation of BLRP-FoxO1 fusion protein. *a-b.* Transactivational activity of BLRP-FoxO1 was assayed by testing the ability to induce an artificial FoxO1 target promoter (3×IRS-Luc) and a native target gene (G6Pase) promoter in HIRC-B cells. *c.* The ability of BLRP-FoxO1 to transrepress PPARγ-mediated gene expression was assayed in HIRC-B cells. In comparison to WT control, BLRP-FoxO1 exhibited normal transactivational and transrepressional activities.

Supplemental Figure 8.

Specific and effective biotinylation of BLRP-FoxO1 by BirA. BLRP-FoxO1 and/or BirA were ectopically expressed in HEK293 or HIRC-B cells as shown. Proper expression of BLRP-FoxO1 was confirmed by anti-FoxO1 blotting. Biotinylation of BLRP-FoxO1, but not wild type FoxO1, was confirmed by streptavidin-HRP recognition. Since AKT-mediated phosphorylation is a major mechanism that regulates FoxO1 biological function, we further confirmed that the phosphorylation status of FoxO1 did not alter biotinylation. In HEK293 cells cultured in full serum medium (constitutively active AKT), the specific and potent AKT inhibitor (AKTi) did not alter BLRP-FoxO1 biotinylation. On the other hand, in serum-starved HIRC-B (inactive AKT), insulin, which induces robust AKT activation, also did not alter BLRP-FoxO1 biotinylation.

Supplemental Figure 9.

a. Double stable RAW264.7 cell lines that expressed both BirA and BLRP-FoxO1 were selected in the presence of puromycin and neomycin. Expression levels of BLRP-FoxO1 were assayed by anti-FoxO1 blotting, and clones that expressed the tagged protein at low or equivalent levels to the endogenous protein were selected. Clones 24 and 25 were used in the present study. *b.* Overnight-starved double stable RAW264.7 were formaldehyde-crosslinked, and chromatin was prepared and fragmented to 200-300 bp fragments by sonication and subjected to high affinity purification on Streptavidin Magnetic Beads. The beads with bound chromatin-transcriptional complex were subjected to AcTEV Protease digestion to release the tagged protein and DNA adducts from the matrix, leaving behind any other biotinylated or non-specific bound proteins. *c.* Protein-DNA crosslinks were reversed by heating and the resulting DNA was purified. Q-PCR was conducted to confirm a high enrichment of known FoxO1 target gene sequences (p27 gene) over background (AcTEV negative group). The non-related Gapdh promoter was included as a negative control.

Supplemental Figure 10.

Reconstitution of TLR4 signaling in HEK293 cells. An artificial Tlr4 signaling cascade was set up in HEK293 cells by co-expression of Tlr4, cDNA of which is driven by CMV promoter and therefore un-regulatable by FoxO1, together with CD14 and MD2. Responses of NFκB-luc were assayed in response to either PBS or LPS stimulation.

Supplemental Figure 11.

WT(*a* and *c*) or Tlr4KO(*b* and *d*) primary peritoneal macrophages were infected with either Ad-GFP or Ad-FoxO1-CA at 100 M.O.I.. 48 hours later, cells were exposed to LPS (100ng/ml), TNFα (20ng/ml), TPA(100ng/ml) or PBS for 6 hours. IL6 mRNA (*a* and *b*) and MCP1 mRNA (*c* and *d*) was quantitated. mRNA levels in PBS groups were set to 1. Data are presented as the average ± SD. Asterisks indicate statistical significant difference (ANOVA, $p < 0.05$).

Supplemental Figure 12.

a. RAW264.7 cells were starved overnight in 0.1% BSA DMEM(LG) medium and subsequently exposed to vehicle, 5μM AKTi, 300μM FFAs or FFAs+AKTi for 30 minutes; cells were then fixed, and the distribution of endogenous FoxO1 was detected by immunostaining with anti-FoxO1 antibody. DAPI DNA staining was performed to indicate nuclei. *b-c*. We first surveyed 6 individual fatty acids (laurate, Myristate, Oleate, Palmitate, α-linolenic acid and DHA) for their ability to activated AKT, and found that saturated fatty acids with a relatively shorter chain (laurate (C12:0) and Myristate (C14:0)) are more potent than those with a longer chain (Palmitate (C16:0) and Oleate(C18:0)); the unsaturated FA α-linolenic acid (C18:3) also activated AKT. We then performed dose-dependent activation of AKT by laurate, myristate and α-linolenic acid. For these experiments, RAW264.7 cells were starved overnight in 0.1%BSA DMEM (LG) medium and subsequently exposed to laurate, myristate or α-linolenate at indicated concentration for 30', and then assayed for AKT activation by immunoblotting.

Supplemental Figure 13.

3% thioglycollate-elicited mouse peritoneal macrophages were infected with Ad-FoxO1-WT at 100 M.O.I.; 48 hours later, cells were subjected to overnight starvation in 0.1% BSA DMEM(LG) medium and subsequent exposure to 100ng/ml LPS or LPS+5μM AKTi for 30 minutes. Cells were then fixed for immunostaining with HA probe (153) antibody and DAPI DNA staining. Ad-FoxO1-CA infected peritoneal macrophages were also treated with LPS and stained with HA probe antibody.

Supplemental Figure 14.

RAW264.7 cells were starved overnight in 0.1% BSA DMEM(LG) medium and subsequently treated with 100ng/ml LPS for 30 minutes. Cells were then fixed and immunostained with anti-FoxO1 antibody. DAPI staining was performed to indicate nuclei.

Supplemental Figure 15.

a, Cell extracts of elicited peritoneal macrophages (IP-Mac, lane 1 and 2) or RAW264.7 cells (lane 4 and 5) were immunoblotted with specific antibodies against either Akt1 or Akt2. Recombinant Akt2 proteins were loaded (lane 3 and 6) to control antibody specificity. β-tubulin was also blotted for loading control. Note both peritoneal macrophages and RAW264.7 cells express exclusively Akt1. *b,* RAW264.7 cells were infected with either Ad-GFP or Ad-FoxO1-CA at 100 M.O.I.. 48 hours later, cells were exposed to 100ng/ml LPS for 15 or 30 minutes and then lysed for immunoblotting with antibodies against phospho-Akt (Ser 473), total Akt or the loading control Hsp90.

Supplemental Figure 16.

a, RAW264.7 macrophages were serum-starved in 0.1% BSA (endotoxin free)-containing medium for 16 hours. The cells were then treated with 100ng/ml of insulin for 15 and 30 minutes. Phosphorylation of IR and IRS1 (assayed by anti–phospho-Tyr**,** PY20 antibody) and Akt (Ser437) were blotted. Blots for total proteins were also shown. These data indicate the presence of a functional insulin signaling system in these cells. *b-e,* Serum-starved RAW264.7 cells were pretreated with 100ng/ml insulin or BSA control for 16 hours, and then 6 hours of 100ng/ml LPS-induced mRNA expression of TNFα (*b*), IL-6 (*c*), MCP1 (*d*), and iNOS (*e*) was quantitated by qPCR. Data are presented as the average ± SD. Letters above the bars show statistical groups (ANOVA, $p < 0.05$).

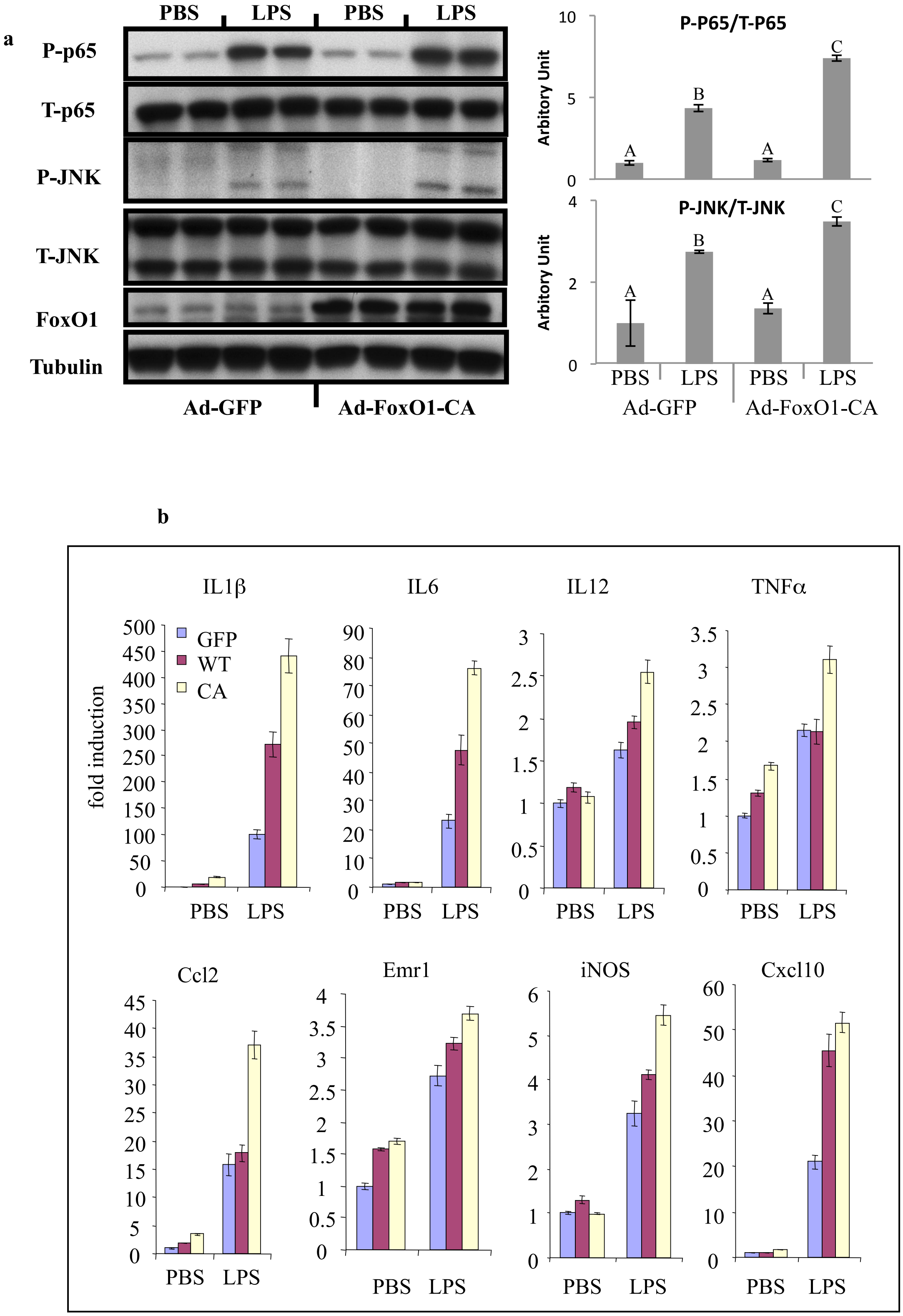
Supplemental Figure 17.

a, BMDMs were prepared from FoxO1+/- and WT mice. The cells were serum-starved and pretreated with or without 100ng/ml of insulin for 16 hours before stimulated with 100ng/ml LPS for 15 minutes. Phosphorylation of JNK and IKK were then assayed by specific antibodies. It's evident that pretreatment of BMDMs with insulin led to decreased IKK, and JNK activation by LPS in WT macrophages. Whereas, this effect was blurred in FoxO1+/- cells. *b-e,* BMDMs were similarly pre-treated with insulin and subjected to 6 hours of LPS stimulation at concentration of 100ng/ml. LPS-mediated mRNA expression of TNFα (*b*), IL6 (*c*), MCP1(*d*) and iNOS(*e*) was assayed by qPCR. Data are presented as the average ± SD. Letters above the bars show statistical groups (ANOVA, $p < 0.05$).

Supplemental Figure 18.

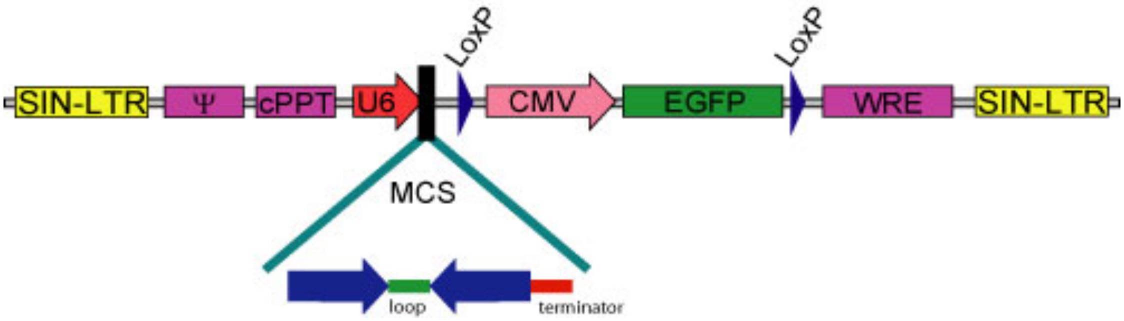
a-b, Epididymal fat pads from 60% HDF-fed (for 20 weeks from 6-weeks of age) and age-matched normal chow diet (NC)-fed mice were fixed and subjected to immunohistostaining for F4/80 (green) and FoxO1(red). Nuclear DNA was stained with 4′,6-diamidino-2-phenylindole (DAPI, blue). Notice that F4/80 positive cells are dramatically increased in HFD-fed mice. Importantly, in ATMs of lean mice, endogenous FoxO1 is predominantly located in nuclei, whereas, in ATMs of HFD/obese mice, endogenous FoxO1 is predominantly cytoplasmic. *c.* mRNA expression of Tlr4 in adipocytes from HFD- or NC-fed mice. Expression levels in NC adipocytes are set to 100. Data are presented as the average ± SD. Letters above the bars show statistical groups (ANOVA, $p < 0.05$).

Fan W, et al. Supplemental Fig. 1



Fan W, et al. Supplemental Fig. 2

a



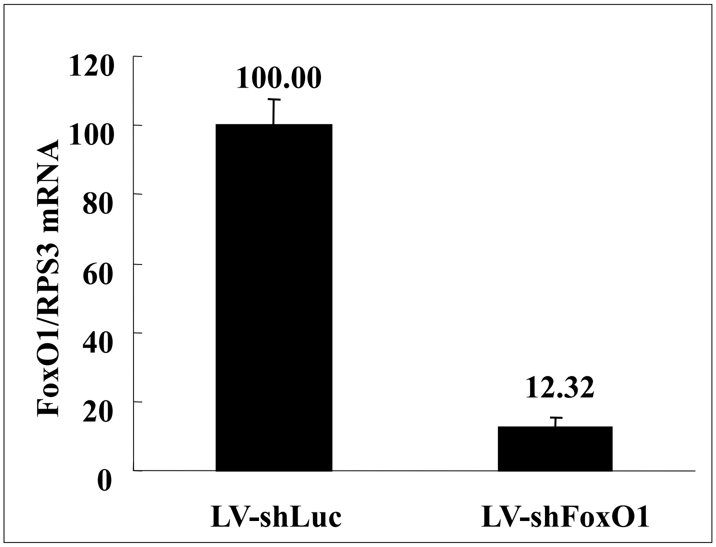
b

mFoxO1-sense | loop | mFoxO1-antisense | Terminator

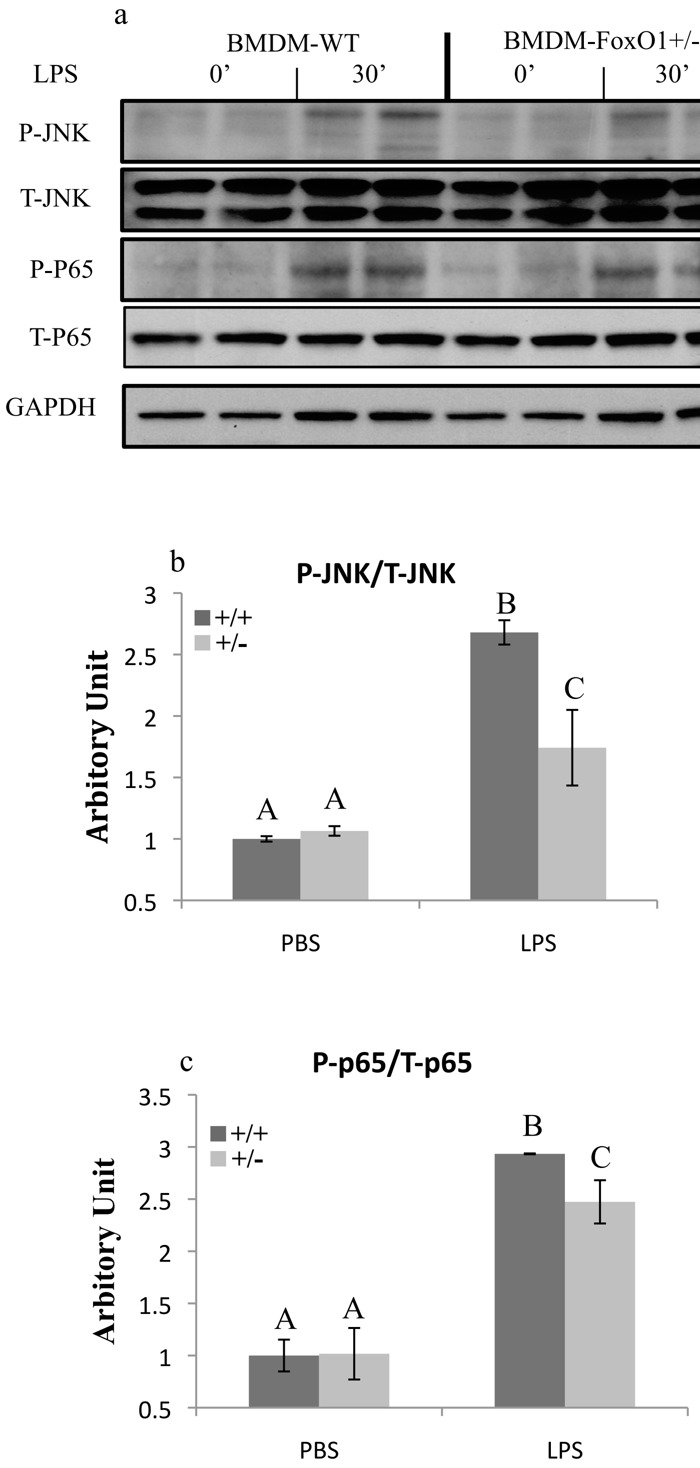
5' TgTacTgaTtttatgagTaacc TTCAAGAGA GGTTGCTCATAAAGTCGGTGC tttttt c 3'

c

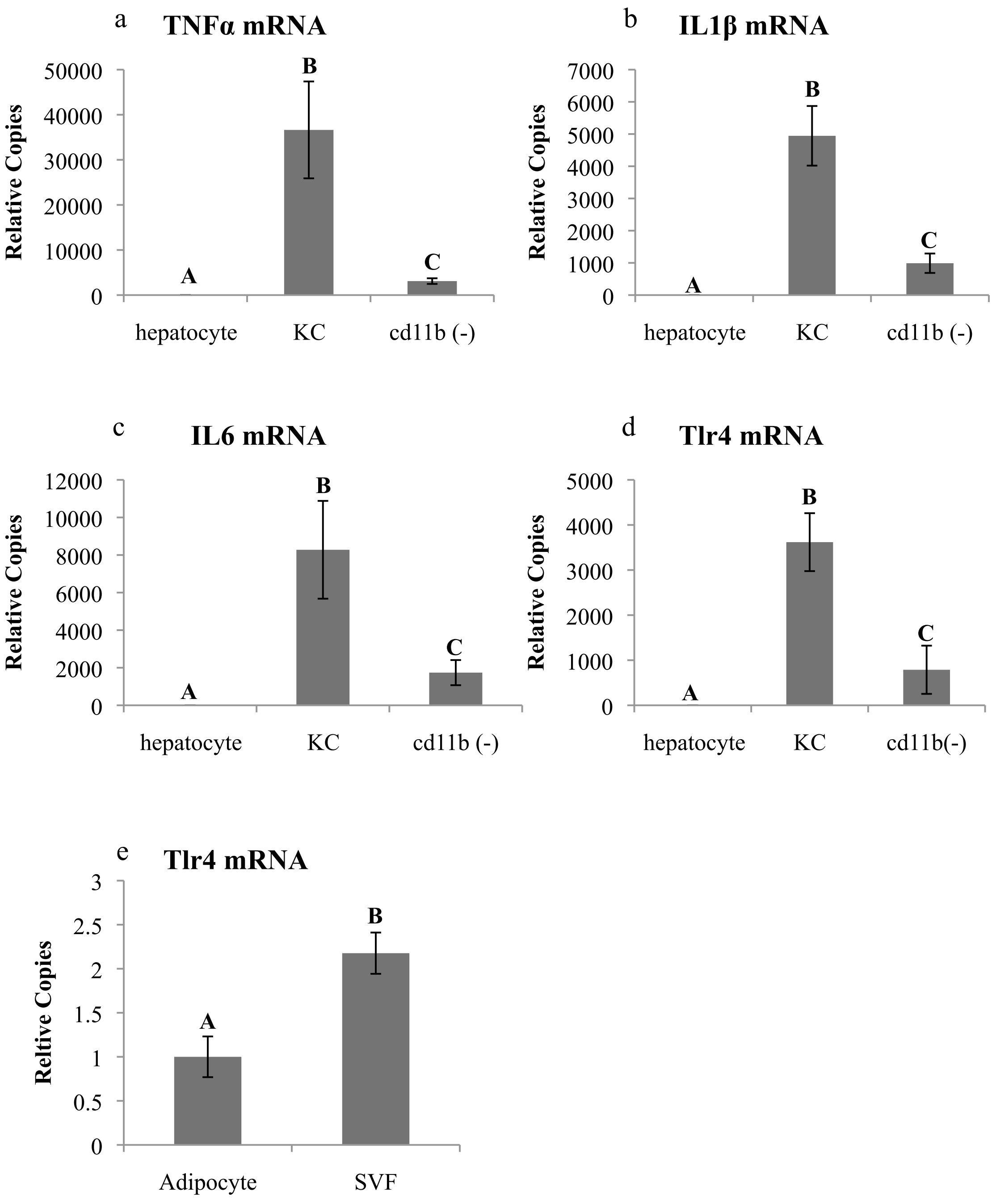
FoxO1 mRNA in
LV-shFoxO1 transduced RAW264.7 cells



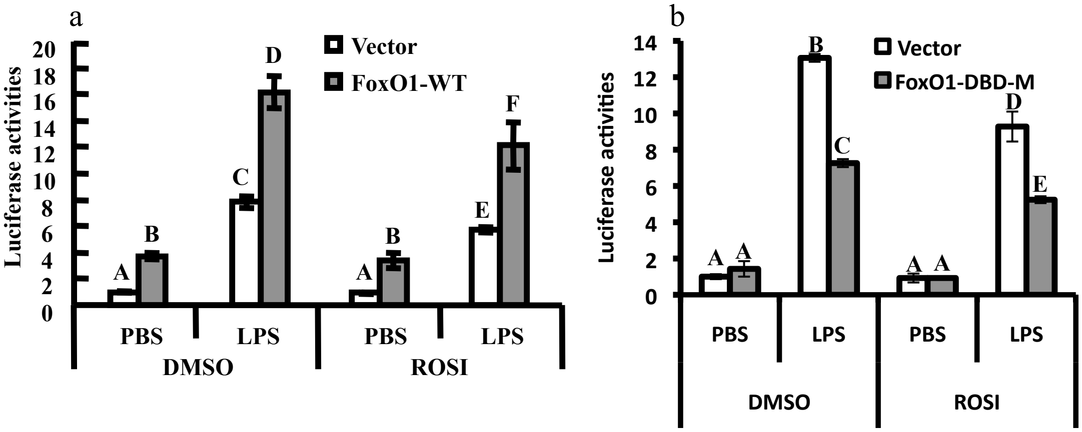
Fan W, et al. Supplemental Fig. 3



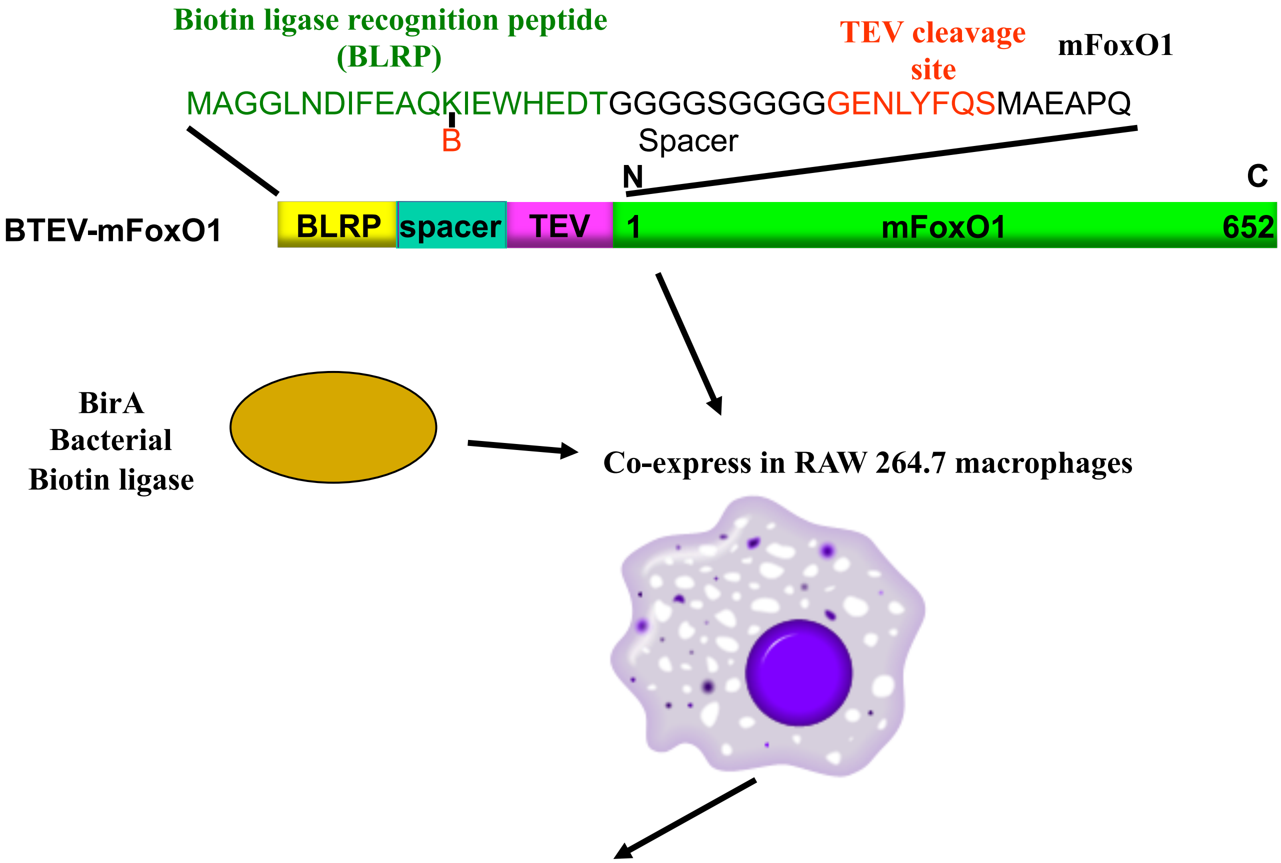
Fan W, et al. Supplemental Fig. 4



Fan W, et al. Supplemental Fig. 5



Fan W, et al. Supplemental Fig. 6



In-vivo biotinylation

↓

Crosslinking/chromatin fragmentation

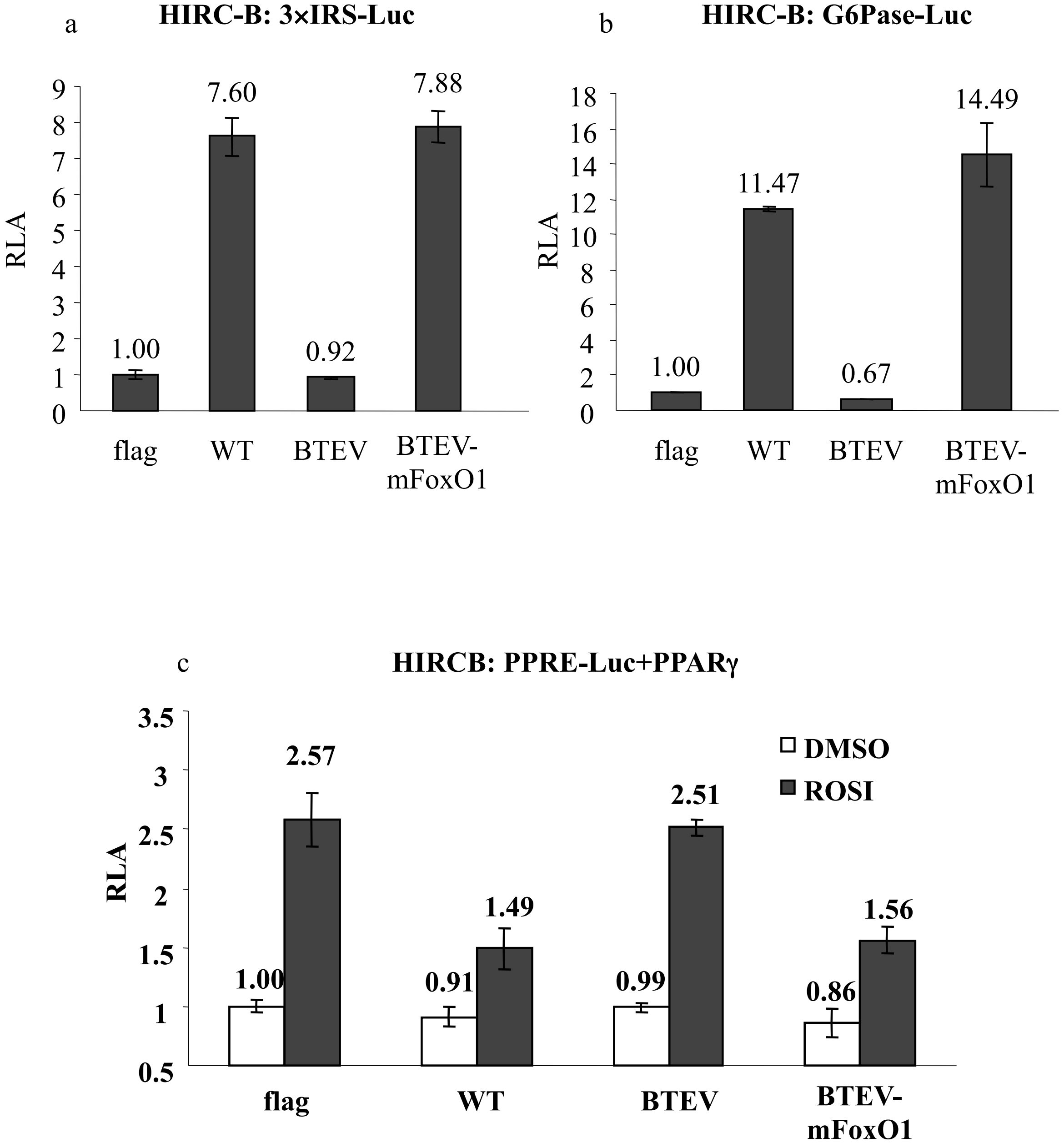
↓

High-affinity purification on streptavidin matrix

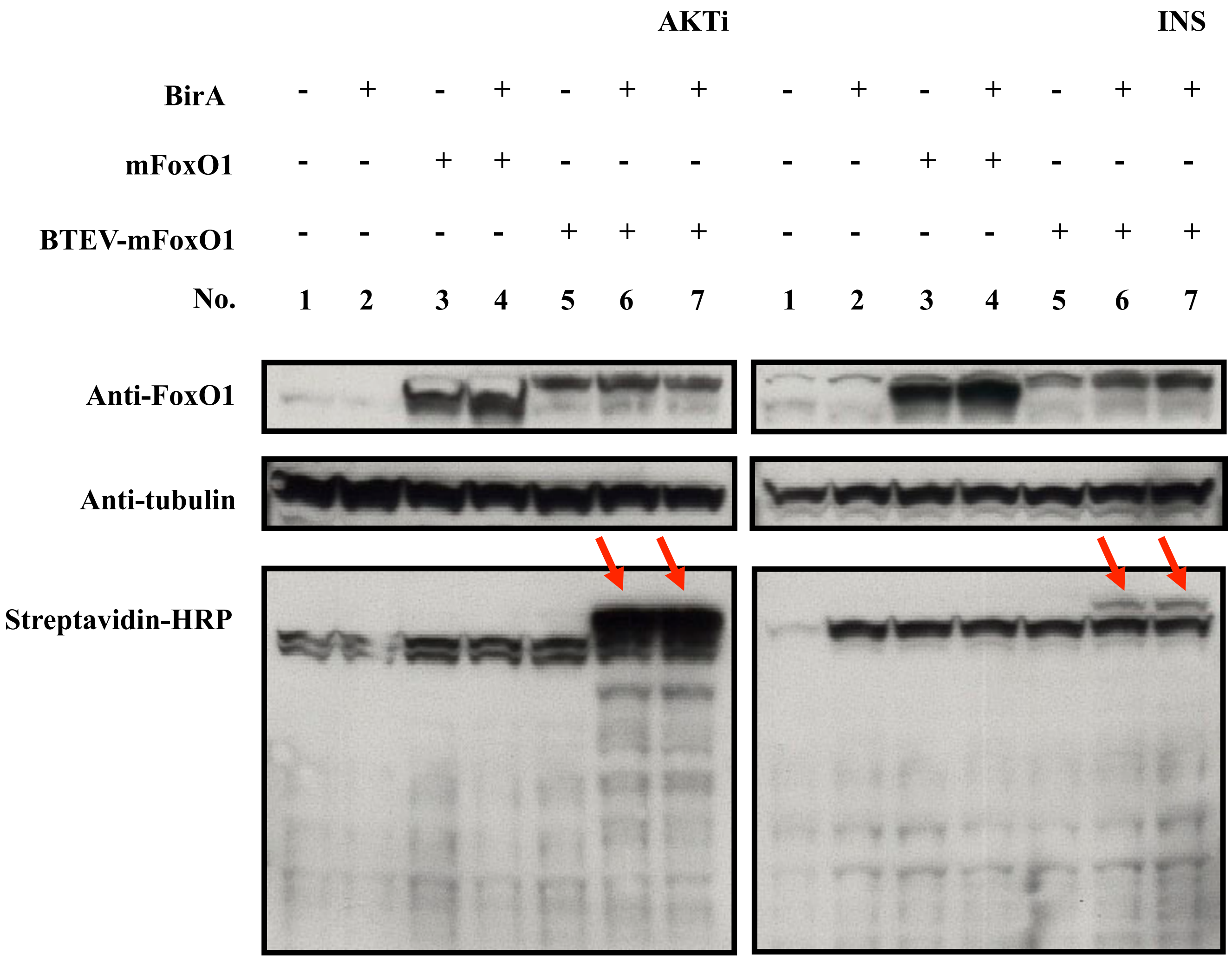
↓

TEV cleavage, reverse crosslinks, sequence

Fan W, et al. Supplemental Fig. 7



Fan W, et al. Supplemental Fig. 8

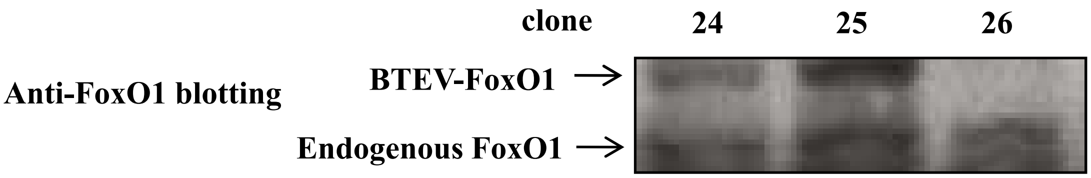


HEK293 cells in 10% FBS medium

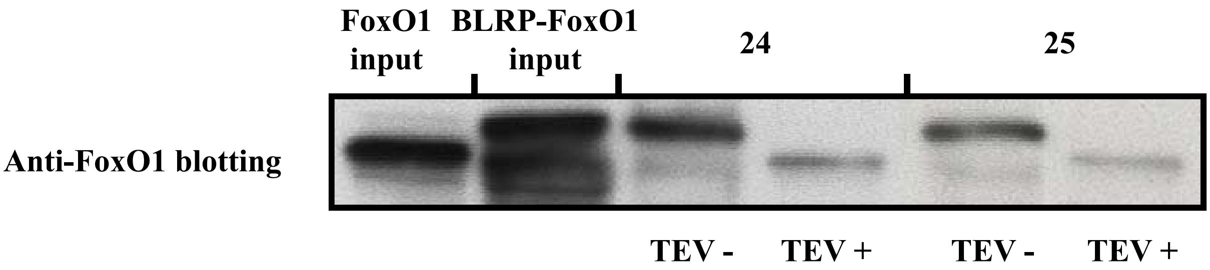
HIRCb cells in 0.1% BSA medium

Fan W, et al. Supplemental Fig. 9

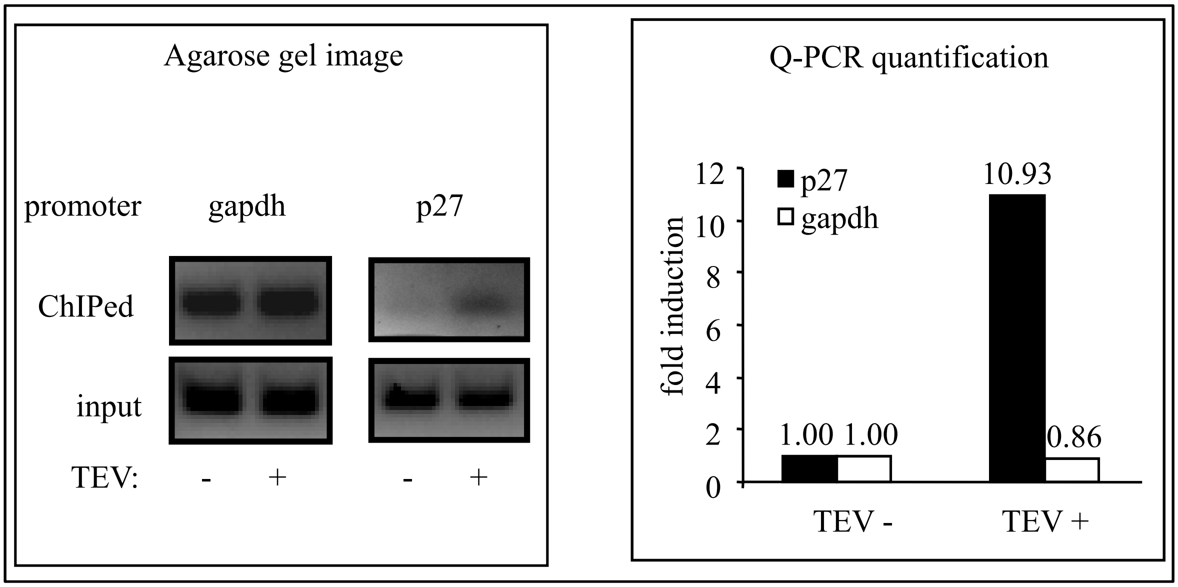
a **RAW264.7 clones exhibiting stable expression of BirA / BLRP-mFoxO1**



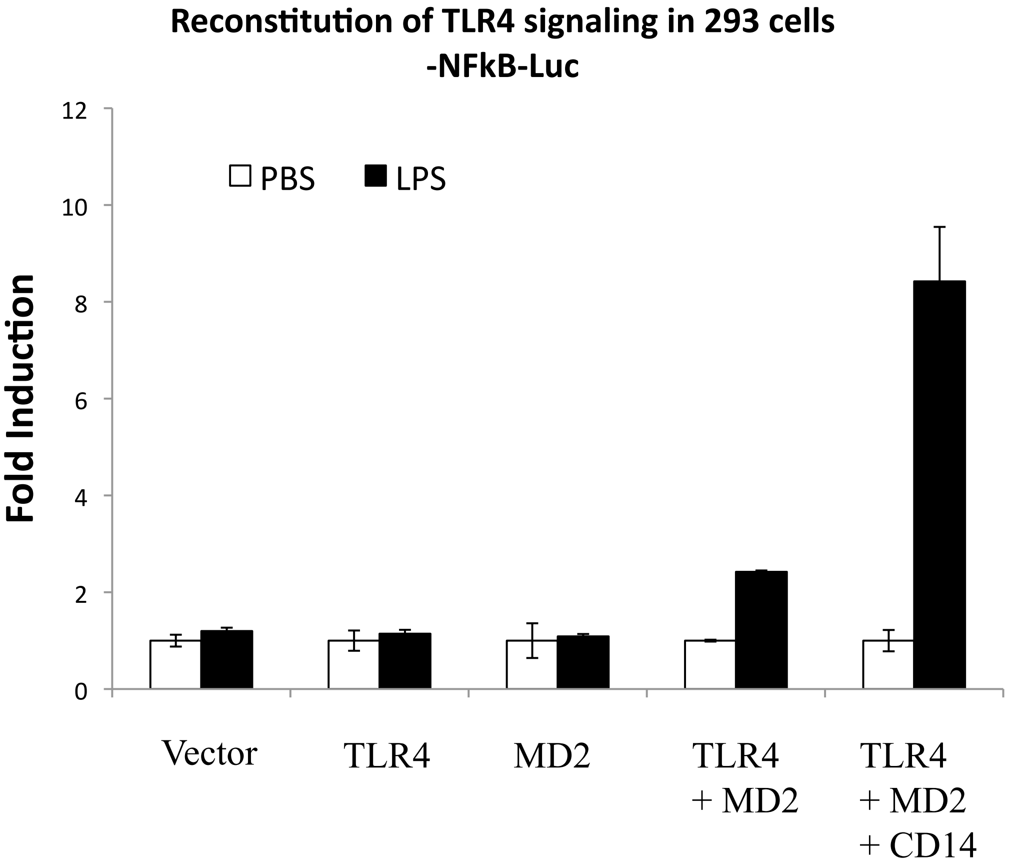
b **TEV cleavage: FoxO1 on beads**



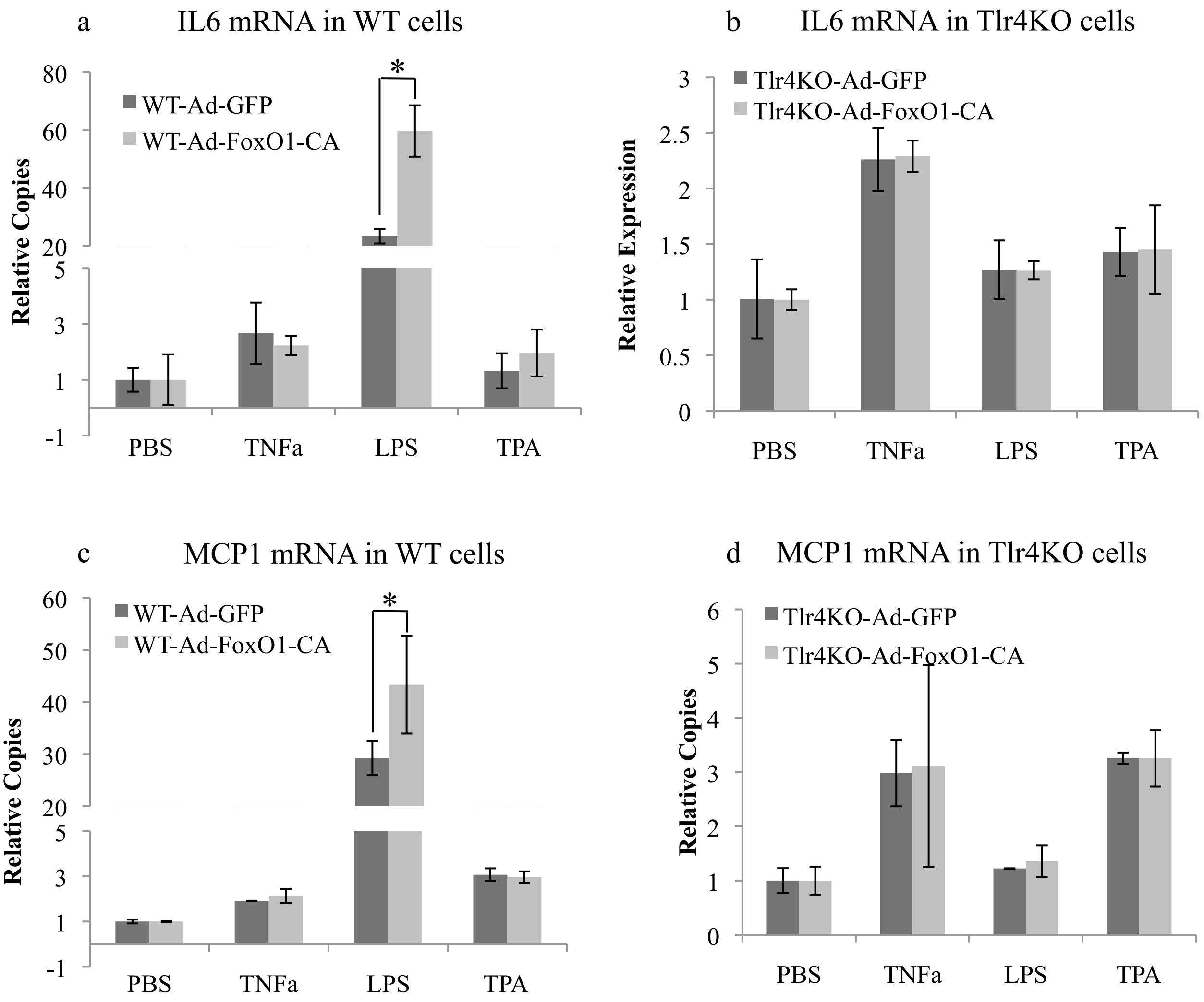
c **Target sequence enrichment**



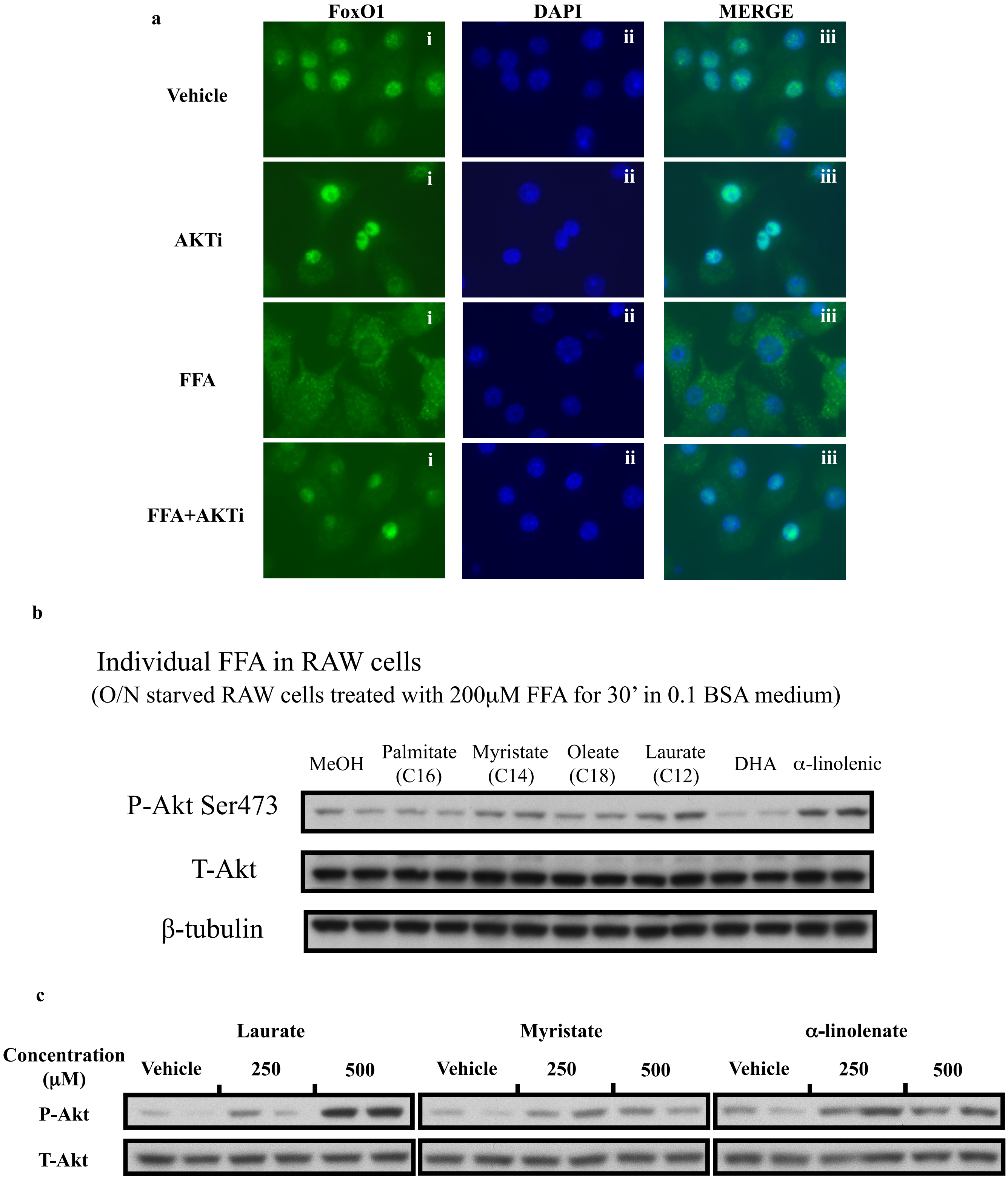
Fan W, et al. Supplemental Fig. 10



Fan W, et al. Supplemental Fig. 11

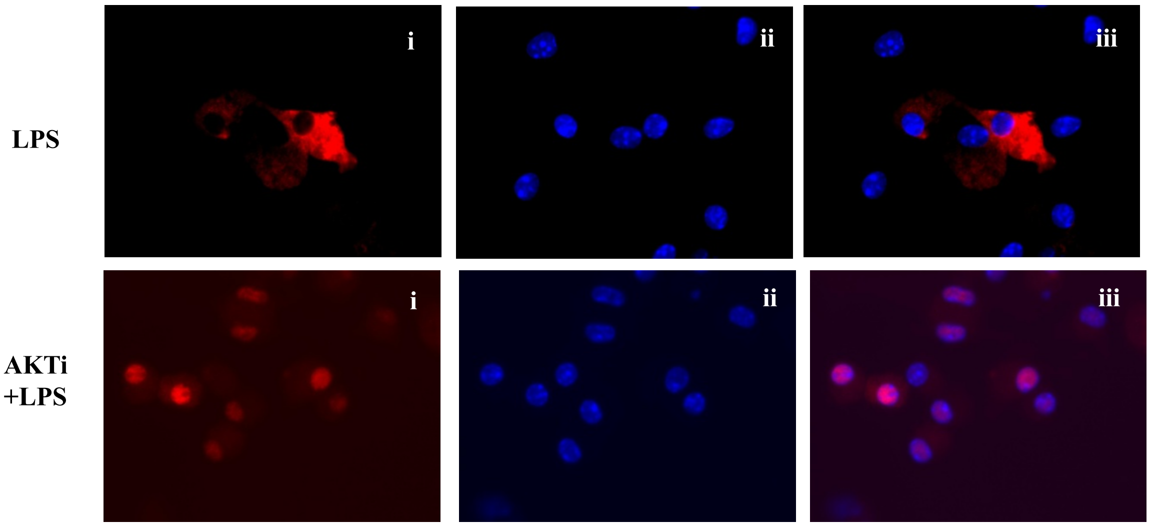


Fan W, et al. Supplemental Fig. 12

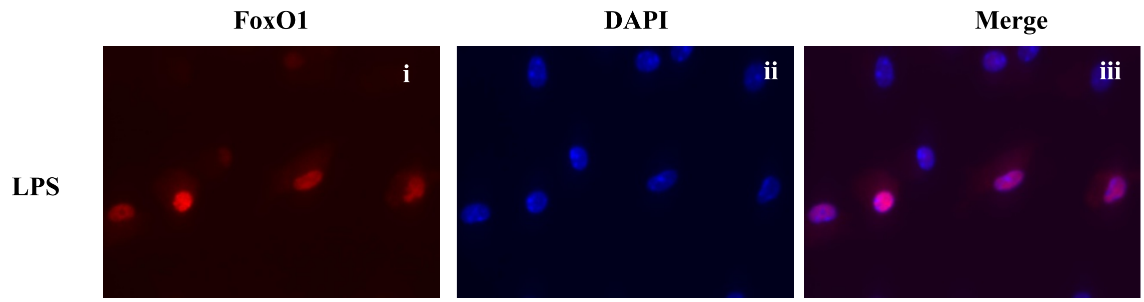


Fan W, et al. Supplemental Fig . 13

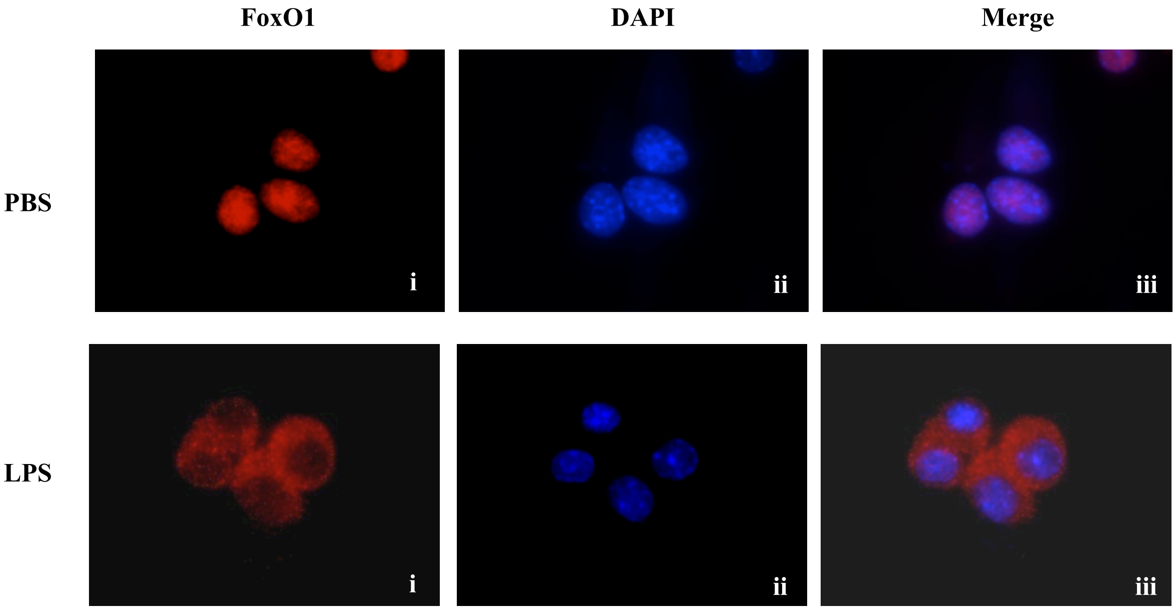
FoxO1-WT in IP-Mac



FoxO1-CA in IP-Mac



Fan W, et al. Supplemental Fig. 14



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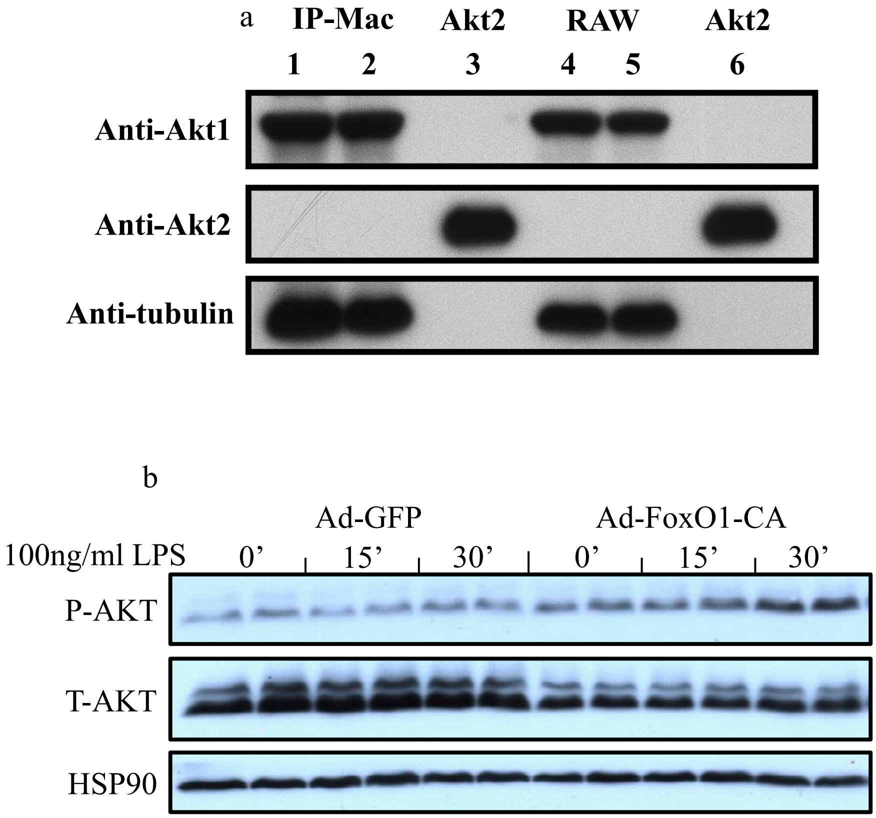
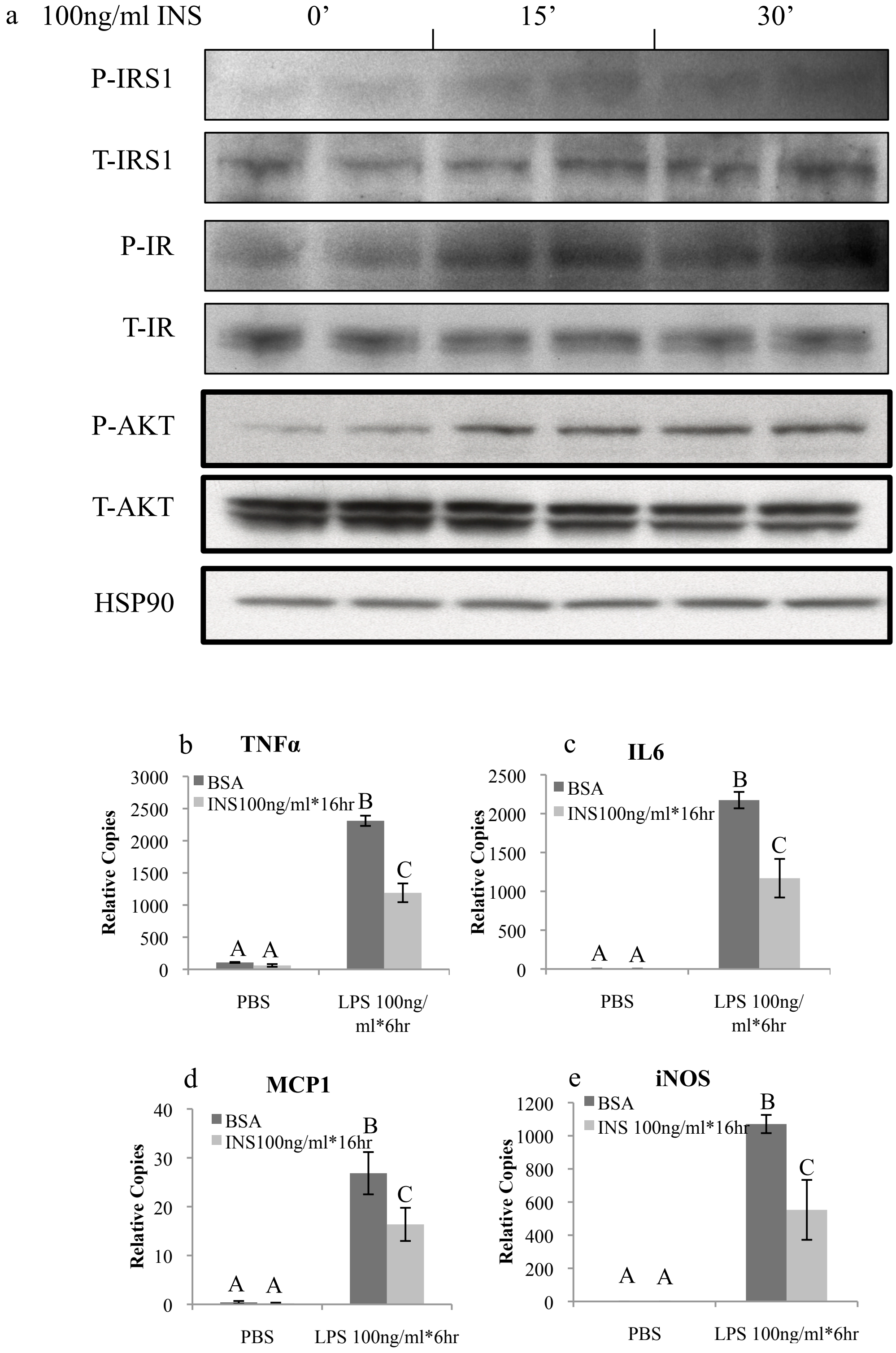
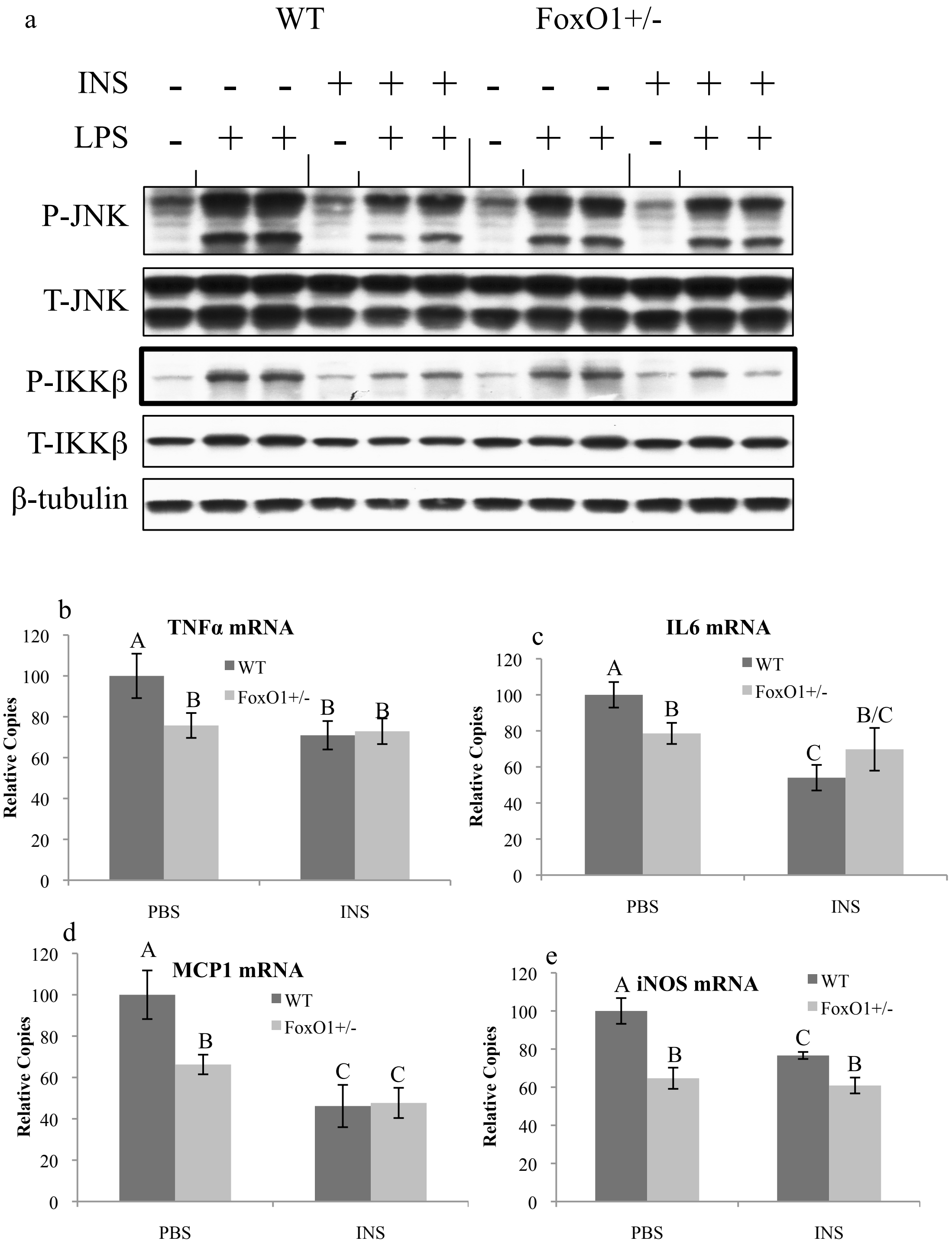


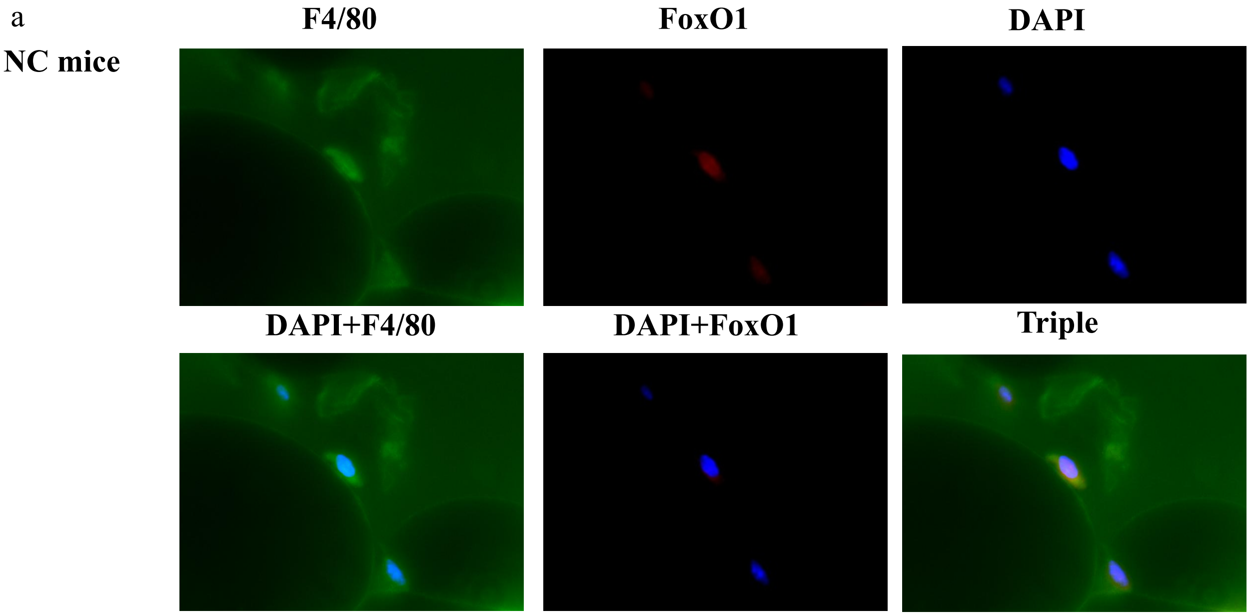
Fan W, et al. Supplemental Fig. 16



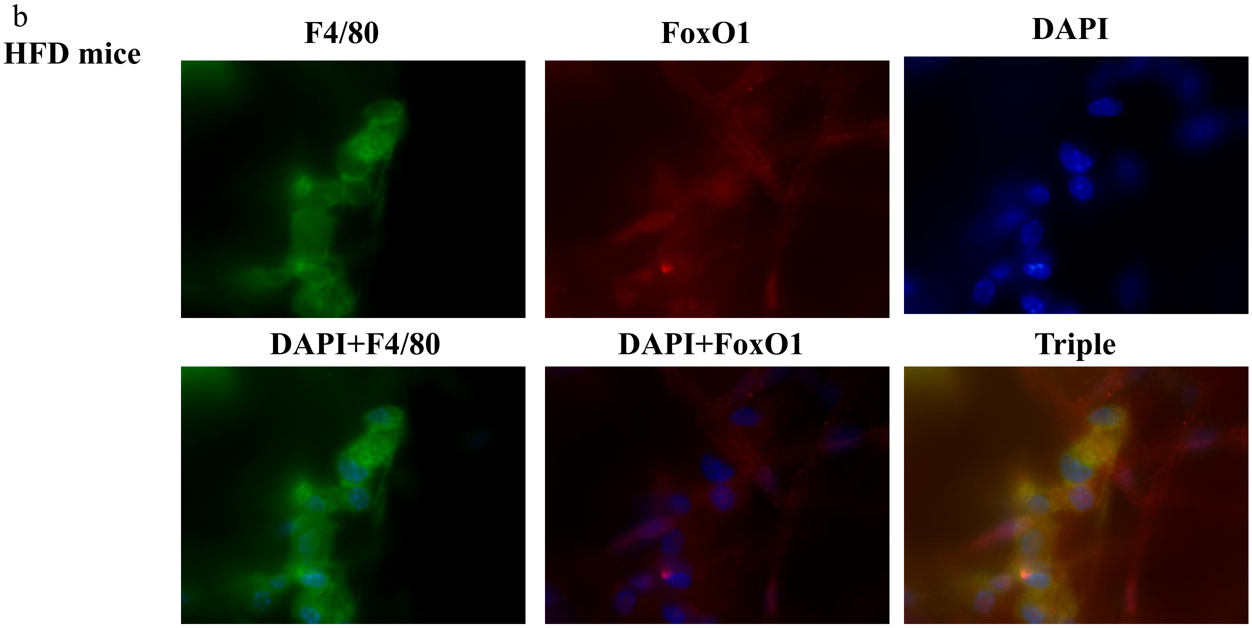
Fan W, et al. Supplemental Fig. 17



Fan W, et al. Supplemental Fig. 18


a

NC mice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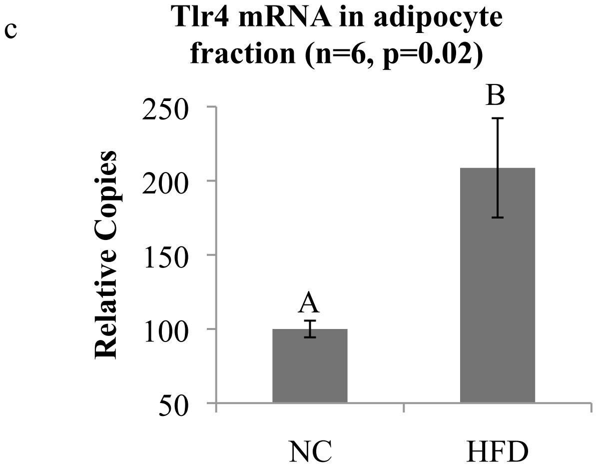
HFD mice


c

Tlr4 mRNA in adipocyte fraction (n=6, p=0.02)

Supplemental table 1- enriched known motif

Motif Name	Consensus	P-value	Log P-value	# of Genes	# of regula	# of Genes	#of regulated genes with Motif
PU.1/ThioMac-PU.1-ChIP-Seq/Homer	AGAGGAAGTG	0.00E+00	-3.47E+03	50000	13334	11338	6626
AP-1/ThioMac-PU.1-ChIP-Seq/Homer	ATGACTCATC	0.00E+00	-3.36E+03	50000	13334	6788	4772
Jun-AP1/K562-cJun-ChIP-Seq/Homer	NATGACTCATNN	0.00E+00	-3.25E+03	50000	13334	5796	4276
Fos/bZIP	GTGAGTCA	0.00E+00	-3.22E+03	50000	13334	7096	4844
ETS/Promoter/Homer	AACCGGAAGT	0.00E+00	-2.58E+03	50000	13334	15511	7502
GABPA/Jurkat-GABPa-ChIP-Seq/Homer	NACCGGAAGT	0.00E+00	-2.56E+03	50000	13334	15028	7334
SPI1/ETS	NGGAAG	0.00E+00	-2.18E+03	50000	13334	27449	10477
SPIB/ETS	AGAGGAA	0.00E+00	-2.06E+03	50000	13334	14012	6667
ETS class/ETS	ACCGGAAG	0.00E+00	-1.95E+03	50000	13334	18490	7941
Ets1-like/CD4+-PolII-ChIP-Seq/Homer	AACAGGAAGT	0.00E+00	-1.93E+03	50000	13334	10577	5438
Eip74EF/ETS	CCGGAAG	0.00E+00	-1.86E+03	50000	13334	17581	7605
ELF5/ETS	TACTTCCTT	0.00E+00	-1.81E+03	50000	13334	19869	8228
NF-E2/K562-NFE2-ChIP-Seq/Homer	GATGACTCAGCA	0.00E+00	-1.65E+03	50000	13334	10225	5115
ETS1/ETS	CTTCCG	0.00E+00	-1.51E+03	50000	13334	24170	9132
GABPA/ETS	ACCGGAAGAG	0.00E+00	-1.35E+03	50000	13334	13979	6092
PU.1-IRF/Bcell-PU.1-ChIP-Seq/Homer	CGGAAGTGAAAC	0.00E+00	-9.20E+02	50000	13334	15542	6141
FOXD1/FORKHEAD	GTAAACAT	0.00E+00	-7.99E+02	50000	13334	2564	1620
TCF11-MafG/bZIP	NATGAC	1.877e-322	-7.41E+02	50000	13334	15012	5777
Foxa2/Liver-Foxa2-ChIP-Seq/Homer	CNTGTTTACATA	2.55E-304	-6.99E+02	50000	13334	6275	2955
Pax2/PAIRED	NGTCACGN	2.55E-287	-6.60E+02	50000	13334	11304	4556
CREB1/bZIP	CNTGGTGACGTN	3.14E-263	-6.04E+02	50000	13334	26330	8720
ELK4/ETS	ACCGGAAGT	2.81E-238	-5.47E+02	50000	13334	11078	4345
MIZF/ZN-FINGER, C2H2	NAACGTCCGC	3.28E-235	-5.40E+02	50000	13334	12376	4731
ELK1/ETS	NNNCCGGAAG	1.12E-234	-5.39E+02	50000	13334	19402	6762
DCE_S_I/Unknown	GCTTCN	1.12E-221	-5.09E+02	50000	13334	7609	3201
Forkhead class/Forkhead	TGTTTATTT	1.74E-214	-4.92E+02	50000	13334	15069	5460
Mafb/bZIP, MAF	GCTGACGN	5.19E-208	-4.77E+02	50000	13334	26732	8636
STAT1/Stat	GGAAAACGAAACTG	1.20E-199	-4.58E+02	50000	13334	15869	5639
CRE/Promoter/Homer	CGGTGACGTCAC	7.06E-197	-4.52E+02	50000	13334	26647	8573
Myf/bHLH	CAGCAGCTGCTG	1.18E-187	-4.30E+02	50000	13334	26916	8608
MAX/bHLH-ZIP	NACCACGTGN	3.63E-183	-4.20E+02	50000	13334	6821	2836
Mycn/bHLH-ZIP	CACGTG	7.13E-180	-4.13E+02	50000	13334	10288	3917
RUNX(AML)/CD4+-PolII-ChIP-Seq/Homer	GCTGTGGTTT	1.50E-173	-3.98E+02	50000	13334	25790	8259
USF1/bHLH-ZIP	CACGTGG	3.11E-173	-3.97E+02	50000	13334	5793	2470
FOXF2/FORKHEAD	NNAACGTAAACAAN	4.43E-169	-3.88E+02	50000	13334	4853	2143
E-box/Promoter/Homer	CCGGTCACGTGA	8.77E-160	-3.66E+02	50000	13334	12994	4655
BRCA1/-	NCAACAC	1.02E-153	-3.52E+02	50000	13334	14452	5056
CEBP/CEBPb-ChIP-Seq/Homer	ATTGCGCAAC	1.15E-153	-3.52E+02	50000	13334	3486	1630
Max/K562-Max-ChIP-Seq/Homer	ACCACGTGGTNN	4.34E-153	-3.51E+02	50000	13334	9180	3485
DCE_S_II/Unknown	NCTGTG	3.10E-150	-3.44E+02	50000	13334	26698	8400
c-Jun-CRE/K562-cJun-ChIP-Seq/Homer	ATGACGTCATCN	1.92E-148	-3.40E+02	50000	13334	4725	2044
n-Myc/mES-nMyc-ChIP-Seq/Homer	NNCCACGTGG	5.18E-145	-3.32E+02	50000	13334	9947	3690
Reverb(DR2)/BLRP(RAW)-Reverba-ChIP-Sec	GTAGGTCACTGGGTCA	1.83E-129	-2.96E+02	50000	13334	26578	8276
MZF1_1-4/ZN-FINGER, C2H2	TGGGGA	6.24E-113	-2.58E+02	50000	13334	26507	8178
CEBP-AP1/ThioMac-CEBPb-ChIP-Seq/Home	NATGTTGCAA	1.73E-111	-2.55E+02	50000	13334	5274	2113
GC-box/Unknown	NGGGGGCGGGGCTN	1.82E-110	-2.53E+02	50000	13334	26478	8158
Cebpa/bZIP	TTNCGCAATNTN	6.01E-108	-2.47E+02	50000	13334	4556	1868
Bapx1/HOMEO	NTAAGTGGN	6.17E-104	-2.38E+02	50000	13334	26449	8117
CTCF/CD4+-CTCF-ChIP-Seq/Homer	ANAGTGCCACCTGGTG	8.95E-104	-2.37E+02	50000	13334	26167	8042
HLF/bZIP	GGTTACGCAATN	1.20E-103	-2.37E+02	50000	13334	4476	1828
ISRE/ThioMac-LPS-exp/HOMER	AGTTTCAGTTTC	1.93E-101	-2.32E+02	50000	13334	17349	5641
c-Myc/cMyc-ChIP-Seq/Homer	NNCCACGTGG	1.63E-99	-2.28E+02	50000	13334	8499	3072
Myb/TRP-CLUSTER	GGCNGTTG	4.57E-98	-2.24E+02	50000	13334	25671	7881
ovo/ZN-FINGER, C2H2	AGTAACNGT	4.96E-96	-2.19E+02	50000	13334	21775	6828
NHLH1/bHLH	NCGCAGCTGCGN	1.29E-95	-2.19E+02	50000	13334	26214	8011
FOXA1/MCF7-FOXA1-ChIP-Seq/Homer	AAAGTAAACA	1.72E-94	-2.16E+02	50000	13334	5151	2015
MYC-MAX/bHLH-ZIP	GACCACGTGGT	1.84E-94	-2.16E+02	50000	13334	20537	6483
bZIP911/bZIP	GATGACGTGGCC	3.32E-94	-2.15E+02	50000	13334	24007	7418
AARE/mES-cMyc-ChIP-Seq/Homer	GATTGCATCA	9.76E-92	-2.10E+02	50000	13334	16923	5471
bZIP cEBP-like subclass/bZIP	ATTGCATAA	6.94E-91	-2.08E+02	50000	13334	5533	2123
GAMYB/TRP-CLUSTER	GACAACCGCC	2.12E-90	-2.07E+02	50000	13334	20293	6394
bHLH(zip) class/bHLH(zip)	ANCACGTG	5.19E-87	-1.99E+02	50000	13334	24654	7550
TRP(MYB) class/TRP	TNTCGGTT	8.59E-86	-1.96E+02	50000	13334	25517	7772
Srebp1a/HepG2-Srebp1a-ChIP-Seq/Homer	ATCACCCCAT	6.92E-85	-1.94E+02	50000	13334	26222	7953
GFY/Promoter/Homer	ACTACAATTCCC	1.73E-84	-1.93E+02	50000	13334	26227	7952
bZIP910/bZIP	ATGACGT	5.38E-82	-1.87E+02	50000	13334	25960	7867
Arnt-Ahr/bHLH	TGCGTG	2.20E-80	-1.83E+02	50000	13334	26273	7940
RUNX1/RUNT	TATTGTGGTTA	2.28E-80	-1.83E+02	50000	13334	4294	1690
RELA/REL	GGGAATTTCC	5.86E-80	-1.82E+02	50000	13334	5059	1932
ARE/LNCAP-AR-ChIP-Seq/Homer	NAGAACAGNNTGTNC	2.70E-78	-1.79E+02	50000	13334	26104	7883
Foxq1/FORKHEAD	NATTGTTTATT	7.84E-74	-1.68E+02	50000	13334	7864	2766
id1/ZN-FINGER, C2H2	TTTTCCTTTTCG	4.25E-71	-1.62E+02	50000	13334	26174	7857
INR/Unknown	TCANTNNN	3.36E-70	-1.60E+02	50000	13334	25602	7700
REL class/REL	GGGGATTTCC	6.39E-70	-1.59E+02	50000	13334	934	502
Tcfcp2l1/mES-Tcfcp2l1-ChIP-Seq/Homer	NAAACCGGTTNNAAC	1.83E-69	-1.58E+02	50000	13334	26134	7836
dl_1/REL	GGGGTTTTTCCN	1.03E-66	-1.52E+02	50000	13334	16023	5075
NF-kappaB/REL	GGGAATTTCC	4.31E-65	-1.48E+02	50000	13334	1137	570
Su(H)/IPT/TIG domain	NTGTGGGAAACGAGA	7.70E-65	-1.48E+02	50000	13334	25957	7759
REL/REL	GGGGNTTTCC	2.32E-64	-1.47E+02	50000	13334	19871	6121
ZNF354C/ZN-FINGER, C2H2	ATCCAC	2.79E-64	-1.46E+02	50000	13334	22337	6789
NFkB(p65,Rel)/LPS-exp/Homer	GGAAATTCCC	1.10E-63	-1.45E+02	50000	13334	10618	3523
NFkB(p50,p52)/p50-ChIP-Chip/Homer	GGGGGAATCCCC	3.91E-63	-1.44E+02	50000	13334	25966	7750
Dl_2/REL	GGGGATTTCC	5.25E-63	-1.43E+02	50000	13334	19937	6130
Znf263/K562-Znf263-ChIP-Seq/Homer	CNGTCCTCCC	1.02E-61	-1.40E+02	50000	13334	26112	7779
NFKB1/REL	GGGGATTCCCC	1.11E-61	-1.40E+02	50000	13334	23531	7092
ERE(IR3)/MCF7-ERa-ChIP-Seq/Homer	NAGGTCACNNTGACC	5.47E-61	-1.39E+02	50000	13334	26044	7756
Tlx/NPC-H3K4me1-ChIP-Seq/Homer	CTGGCAGNCTGCCA	7.23E-61	-1.39E+02	50000	13334	24837	7435
DCE_S_III/Unknown	NAGCN	2.22E-60	-1.37E+02	50000	13334	26056	7755
E2A/proBcell-E2A-ChIP-Seq/Homer	NNACAGCTGC	2.84E-57	-1.30E+02	50000	13334	25866	7683
Arnt/bHLH	CACGTG	3.94E-57	-1.30E+02	50000	13334	21582	6536
Srebp2/HepG2-Srebp2-ChIP-Seq/Homer	CNGTCACGCCAC	5.57E-56	-1.27E+02	50000	13334	25335	7533

bZIP CREB/G-box-like subclass/bZIP	TGACGT	9.69E-56	-1.27E+02	50000	13334	7398	2536
TGA1a/bZIP	TACGTCA	5.64E-55	-1.25E+02	50000	13334	26034	7711
ABI4/AP2	CGGTGCCCCC	2.88E-53	-1.21E+02	50000	13334	26017	7694
TLX1-NFIC/HOMEO/CAAT	TGGCACCATGCCAA	1.21E-52	-1.20E+02	50000	13334	25506	7554
Klf4/ZN-FINGER, C2H2	TAAAGGAAGG	3.35E-52	-1.19E+02	50000	13334	20080	6093
Klf4/mES-Klf4-ChIP-Seq/Homer	GCCACACCCA	4.62E-52	-1.18E+02	50000	13334	21160	6385
ESR1/NUCLEAR RECEPTOR	CCAGGTCACCGTGACC	2.99E-50	-1.14E+02	50000	13334	25936	7650
Pax5/PAIRED	NGNGCACTGAAGCGT	6.12E-50	-1.13E+02	50000	13334	25990	7662
XCPE1/Unknown	GGGCGGGACC	5.06E-48	-1.09E+02	50000	13334	25959	7639
CTCF-SatelliteElement/CD4+-CTCF-ChIP-Se	TGCAGTTCCNNNNNT	1.61E-47	-1.08E+02	50000	13334	25970	7638
IRF2/TRP-CLUSTER	GGAAAGCGAAACCAA	6.63E-47	-1.06E+02	50000	13334	25400	7482
MZF1_5-13/ZN-FINGER, C2H2	GGAGGGGGAA	2.78E-46	-1.05E+02	50000	13334	25950	7623
Stat3/mES-Stat3-ChIP-Seq/Homer	CTTCCNGGAA	4.26E-46	-1.05E+02	50000	13334	25733	7564
TFAP2A/AP2	GCCNNNGGG	2.04E-45	-1.03E+02	50000	13334	25874	7596
FOXC1/FORKHEAD	NNNNAGTA	2.87E-45	-1.03E+02	50000	13334	10572	3396
PPARG/NUCLEAR RECEPTOR	GTAGGTCACNGTGAC	1.43E-44	-1.01E+02	50000	13334	25768	7561
NRF1/MCF7-NRF1-ChIP-Seq/Homer	CTGCGCATGCGC	7.36E-43	-9.70E+01	50000	13334	25715	7533
MTE/Unknown	TTTCGAGCGGAACGGT	1.58E-42	-9.63E+01	50000	13334	24406	7182
SP1/ZN-FINGER, C2H2	GGGGCGGGGT	2.98E-40	-9.10E+01	50000	13334	25839	7544
BREu/Unknown	AGCGCGCC	4.38E-40	-9.06E+01	50000	13334	24288	7130
Sp1/Promoter/Homer	GGCCCCGCCCCC	4.69E-38	-8.60E+01	50000	13334	25609	7464
MEF2A/MADS	CTATTTATAG	9.14E-38	-8.53E+01	50000	13334	847	399
REST/ZN-FINGER, C2H2	GCGCTGTCCATGGTGC	5.54E-37	-8.35E+01	50000	13334	25709	7481
EMBP1/bZIP	ACACGTGG	8.27E-37	-8.31E+01	50000	13334	15937	4836
IRF1/TRP-CLUSTER	GAAAGCGAAACC	4.65E-36	-8.14E+01	50000	13334	1676	679
DPE/Unknown	NAAGATGTN	4.82E-36	-8.13E+01	50000	13334	25116	7315
RORA_2/NUCLEAR RECEPTOR	NATAANTAGGTCAA	1.30E-35	-8.03E+01	50000	13334	25601	7440
EBF1/proBcell-Ebf1-ChIP-Seq/Homer	GTCCCCAGGGGA	2.42E-35	-7.97E+01	50000	13334	25125	7311
Staf/ZN-FINGER, C2H2	GATTTCCCATAATGCC	3.85E-35	-7.92E+01	50000	13334	25828	7496
BREd/Unknown	GTNTNTN	1.50E-34	-7.79E+01	50000	13334	25408	7379
Foxa2/FORKHEAD	CAATATTTACTT	2.61E-34	-7.73E+01	50000	13334	18918	5631
HMG-1/HMG	GTTGTANTC	2.24E-33	-7.52E+01	50000	13334	17791	5315
NRF1/Promoter/Homer	GTGCGCATGCGC	4.99E-33	-7.44E+01	50000	13334	25552	7403
E2F/Cell-Cycle-Exp/Homer	TTCGCGCGAAAA	2.97E-31	-7.03E+01	50000	13334	25503	7373
Ar/NUCLEAR RECEPTOR	NTAAGAACANCNTGT	3.50E-31	-7.01E+01	50000	13334	24942	7223
Spz1/bHLH-ZIP	AGGGTAACAGC	7.88E-30	-6.70E+01	50000	13334	25120	7257
PEND/bZIP	ACTTCTTATT	1.06E-29	-6.67E+01	50000	13334	25670	7402
GLI3/GLI3-ChIP-Chip/Homer	CGTGGGTGGTCC	2.93E-29	-6.57E+01	50000	13334	24316	7037
p53/mES-cMyc-ChIP-Seq/Homer	ACATGCCCGGGCAT	4.37E-28	-6.30E+01	50000	13334	25728	7401
usp/NUCLEAR RECEPTOR	GGGGTCACGG	5.83E-27	-6.04E+01	50000	13334	15435	4608
Ddit3-Cebpa/bZIP	NNATGCAATCCC	1.12E-26	-5.98E+01	50000	13334	25039	7203
MED-1/Unknown	GCTCCG	1.56E-26	-5.94E+01	50000	13334	25714	7381
REST(NRSF)/Jurkat-NRSF-ChIP-Seq/Homer	GGAGCTGTCCATGGT	1.99E-26	-5.92E+01	50000	13334	25703	7377
E2F1/E2F_TDP	TTTGGCGC	3.10E-26	-5.87E+01	50000	13334	23775	6861
AGL3/MADS	CCATAAATAG	2.24E-25	-5.68E+01	50000	13334	956	402
T1ISRE/Ifnb-Exp/Homer	ACTTTCGTTTCT	7.15E-25	-5.56E+01	50000	13334	25661	7349
HMG-IY/HMG	NAACAAATGGAAAAA	1.53E-24	-5.48E+01	50000	13334	24833	7125
CCAAT-box/Unknown	NNTAGCCAATCA	3.57E-24	-5.40E+01	50000	13334	25679	7346
MADS class/MADS	CCATATATGG	1.31E-23	-5.27E+01	50000	13334	1712	642
RXR(DR1)/3T3L1-RXR-ChIP-Seq/Homer	TAGGGCAAAGGTCA	3.47E-23	-5.17E+01	50000	13334	25604	7315
PPARE(DR1)/3T3L1-Pparg-ChIP-Seq/Homer	TGACCTTTGCCCCA	1.17E-22	-5.05E+01	50000	13334	25612	7311
Nuclear Receptor class/Nuclear receptor	AGGTCA	7.22E-22	-4.87E+01	50000	13334	15965	4700
Agamous/MADS	CCAAATNNGGN	3.20E-21	-4.72E+01	50000	13334	20208	5846
NFY/Promoter/Homer	AGCCAATCGG	3.83E-20	-4.47E+01	50000	13334	25349	7211
GFX/Promoter/Homer	ATTCTCGCGAGA	3.25E-19	-4.26E+01	50000	13334	25306	7188
X-box/NPC-H3K4me1-ChIP-Seq/Homer	GGTTGCCATGGCAA	3.53E-19	-4.25E+01	50000	13334	25195	7158
Roaz/ZN-FINGER, C2H2	GGCACCCAGGGGTGC	1.47E-18	-4.11E+01	50000	13334	25499	7231
Sox17/HMG	NNCATTGTC	8.39E-18	-3.93E+01	50000	13334	25551	7235
HMG class/HMG	ATTGTT	2.01E-17	-3.84E+01	50000	13334	21967	6272
Hand1-Tcfe2a/bHLH	NGTCTGGCAT	2.13E-17	-3.84E+01	50000	13334	25485	7212
Sox2/mES-Sox2-ChIP-Seq/Homer	NCCATTGTTC	1.07E-16	-3.68E+01	50000	13334	24601	6967
RREB1/ZN-FINGER, C2H2	CCCCAAACCACCCCCC	4.84E-16	-3.53E+01	50000	13334	25269	7136
LXRE(DR-4)/BLRP(RAW)-LXRb-ChIP-Seq/Ho	GGGTTACTANAGGTC	9.10E-16	-3.46E+01	50000	13334	24387	6897
ZFX/mES-Zfx-ChIP-Seq/Homer	AGGCCTNG	1.62E-15	-3.41E+01	50000	13334	23988	6787
Pax6/PAIRED	TTCACGCATGANTT	1.39E-13	-2.96E+01	50000	13334	24837	6985
SRE/PUER-Srf-ChIP-Seq/Homer	CCATATATGGNA	2.12E-12	-2.69E+01	50000	13334	9472	2797
YY1/Promoter/Homer	CAAGATGGCGGC	1.59E-11	-2.49E+01	50000	13334	25392	7100
STAT1/HelaS3-STAT1-ChIP-Seq/Homer	NATTTCCNGGAAAT	1.07E-10	-2.30E+01	50000	13334	2161	707
TAL1-TCF3/bHLH	NGACCATCTGTT	1.38E-10	-2.27E+01	50000	13334	24320	6798
En1/HOMEO	AAGTAGTGNCC	7.26E-10	-2.10E+01	50000	13334	6150	1839
SRE/ThioMac-Srf-ChIP-Seq/Homer	CCATATATGGNA	1.15E-09	-2.06E+01	50000	13334	12617	3623
NFIL3/bZIP	TTATGTAACNT	1.75E-09	-2.02E+01	50000	13334	1006	353
FOXI1/FORKHEAD	GNNTGTTTGTTT	3.87E-09	-1.94E+01	50000	13334	12840	3675
RORA_1/NUCLEAR RECEPTOR	ATCAAGGTCA	5.34E-09	-1.91E+01	50000	13334	6379	1892
NFYA/CAAT-BOX	NNCAGCCAATCAGNG	6.56E-09	-1.88E+01	50000	13334	357	145
STAT5/mCD4+-Stat5a|b-ChIP-Seq/Homer	NTTTCTNAGAAA	6.94E-08	-1.65E+01	50000	13334	1294	430
TP53/P53	CCGGACATGCCCGGG	7.65E-08	-1.64E+01	50000	13334	23734	6589
PBF/ZN-FINGER, DOF	AAAGC	6.55E-07	-1.42E+01	50000	13334	16856	4722
MNB1A/ZN-FINGER, DOF	AAAGC	6.55E-07	-1.42E+01	50000	13334	16856	4722
Dof3/ZN-FINGER, DOF	AAAGCG	1.29E-06	-1.36E+01	50000	13334	17417	4867
Dof2/ZN-FINGER, DOF	AAAGCN	1.68E-06	-1.33E+01	50000	13334	17386	4856
TEAD1/TEA	CACATTCCTCNG	4.96E-06	-1.22E+01	50000	13334	13776	3870
Nanog/mES-Nanog-ChIP-Seq/Homer	GGCCATTAAC	6.85E-06	-1.19E+01	50000	13334	18423	5121
SRY/HMG	NTAAACAAT	2.21E-05	-1.07E+01	50000	13334	94	44
Broad-complex_4/ZN-FINGER, C2H2	TAGTAAACAAA	4.92E-05	-9.92E+00	50000	13334	243	93
SQUA/MADS	CCAAAAATGGAAAN	1.37E-04	-8.90E+00	50000	13334	1289	402
Esrrb/mES-Esrrb-ChIP-Seq/Homer	NTGACCTTGA	3.08E-04	-8.08E+00	50000	13334	25156	6878
SOX9/HMG	GAACAATGG	7.18E-04	-7.24E+00	50000	13334	279	99
TBP/TATA-box	NTATAAAAGNNNNNN	9.53E-04	-6.96E+00	50000	13334	420	141
TATA-Box/Unknown	NTATAAAAGNNNNNN	9.53E-04	-6.96E+00	50000	13334	420	141
RXRA-VDR/NUCLEAR RECEPTOR	GGGTCAACGAGTTCA	2.91E-03	-5.84E+00	50000	13334	26	14
Oct4/mES-Oct4-ChIP-Seq/Homer	ATTTGCATAA	3.48E-03	-5.66E+00	50000	13334	29	15
NR3C1/NUCLEAR RECEPTOR	GGGAACATTATGTCCT	5.18E-03	-5.26E+00	50000	13334	25011	6797
SRF/MADS	GCCCATATATGG	7.63E-03	-4.88E+00	50000	13334	48	21