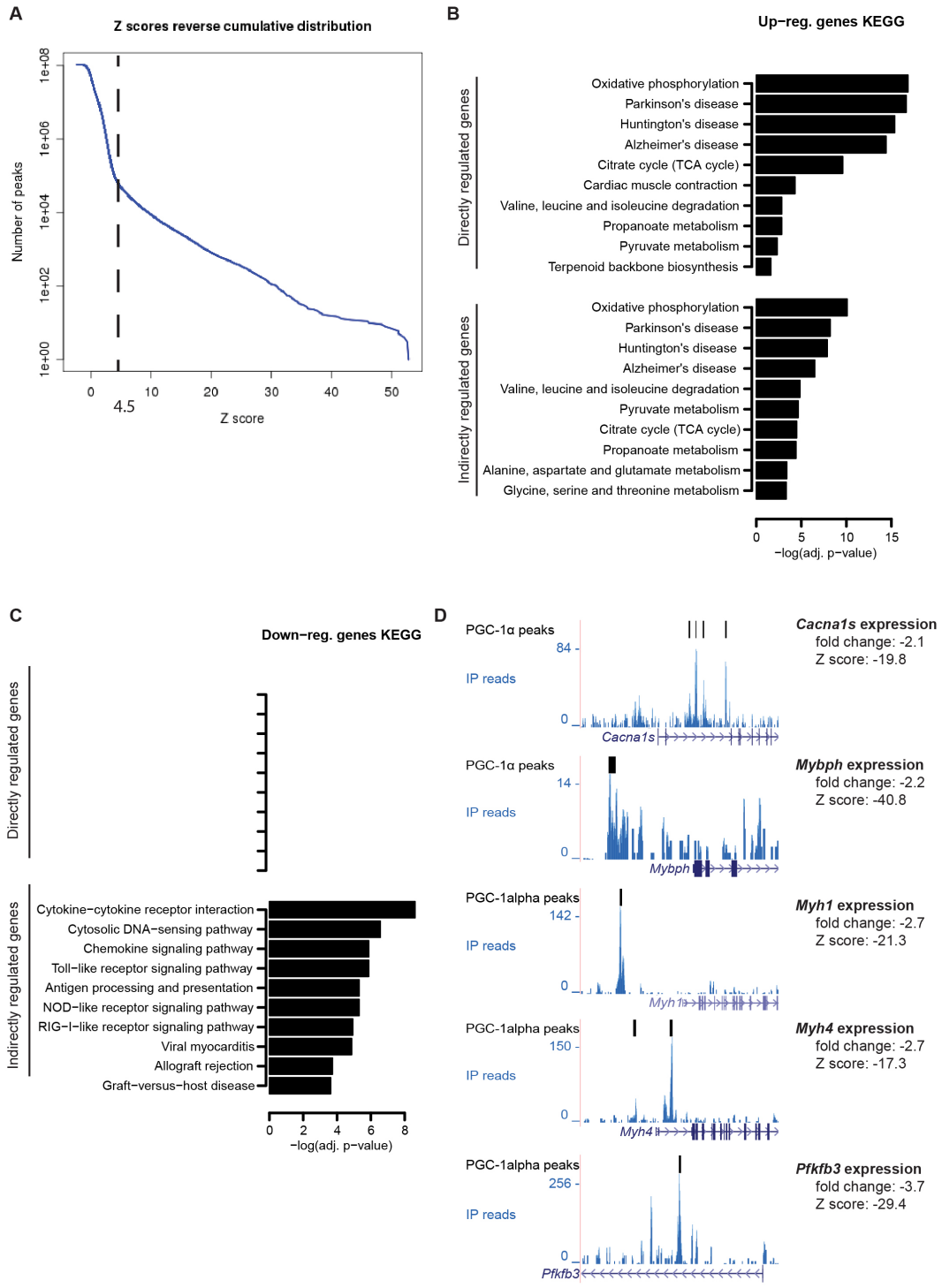
SUPPLEMENTAL FIGURES AND TABLES

Fig.S1



Suppl. Fig. S1. Peak Z score distribution and KEGG functional analysis. Related to Figure 1.

(A) Distribution of the Z scores for all sliding windows considered by the peak-finding algorithm along the mouse genome. The chosen cutoff for peak calling is depicted by the dotted line.

(B) Subset of the top significantly enriched KEGG terms identified for direct and indirect up-regulated PGC-1α target genes.

(C) Subset of the top significantly enriched KEGG terms identified for direct and indirect down-regulated PGC-1α target genes.

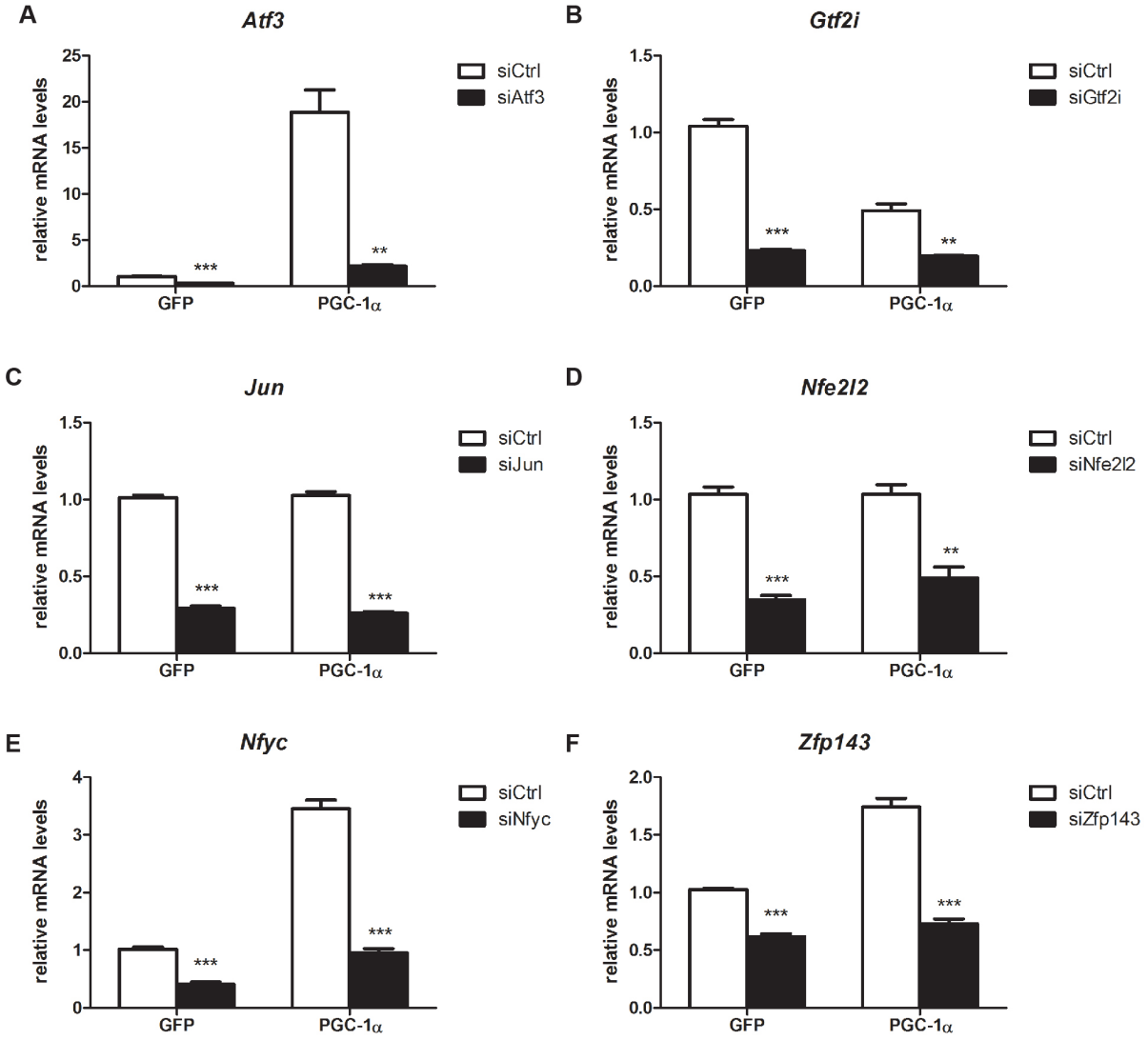
(D) ChIP-Seq signal around the promoter region of the five directly down-regulated genes (*Cacna1s*, *Mybph*, *Myh1*, *Myh4*, *Pfkfb3*) involved in regulating the contractile properties of fast-twitch muscle fibers.

A

Motif name	Z direct	Z indirect	Z avg. direct	Z avg. indirect	Directly activated	Indirectly activated	Directly repressed	Indirectly repressed
Group 1: motifs only directly activated by PGC-1alpha								
SP1.p2	3.99	0.61	9.76	0.33	1	0	0	0
ELF1,2,4.p2	3.11	1.32	7.59	3.13	1	0	0	0
PAX4.p2	2.50	1.53	6.11	-3.68	1	0	0	0
LMO2.p2	2.36	1.65	5.78	3.98	1	0	0	0
HNF4A_NR2F1,2.p2	2.26	1.54	5.52	3.64	1	0	0	0
GTF2I.p2	2.09	2.38	5.10	-5.80	1	0	0	1
Group 2: motifs directly and indirectly activated by PGC-1alpha								
ESRRA.p2	6.04	15.49	14.78	37.94	1	1	0	0
NR5A1,2.p2	3.53	7.73	8.66	17.00	1	1	0	0
ZNF143.p2	2.48	4.65	6.05	9.68	1	1	0	0
NFY{A,B,C}.p2	2.37	3.56	5.80	7.62	1	1	0	0
ESR1.p2	2.33	4.53	5.69	11.04	1	1	0	0
RXR{A,B,G}.p2	2.29	4.30	5.59	10.50	1	1	0	0
Group 3: motifs only indirectly activated by PGC-1alpha								
NRF1.p2	1.60	4.61	3.91	6.21	0	1	0	0
YY1.p2	0.88	2.97	2.09	5.77	0	1	0	0
EHF.p2	0.73	2.77	1.77	6.35	0	1	0	0
RXRA_VDR{dimer}.p2	0.71	2.54	1.71	6.20	0	1	0	0
HES1.p2	0.34	2.52	0.84	6.10	0	1	0	0
FOXO1,3,4.p2	0.46	2.51	1.13	6.12	0	1	0	0
ELK1,4_GABP{A,B1}.p3	1.18	2.46	2.89	5.95	0	1	0	0
NKX3-1.p2	0.60	2.43	1.48	5.93	0	1	0	0
REST.p3	0.48	2.41	1.15	5.70	0	1	0	0
NFE2L1.p2	1.79	2.32	4.36	5.23	0	1	0	0
POU5F1_SOX2{dimer}.p2	0.24	2.32	0.57	5.65	0	1	0	0
AIRE.p2	0.38	2.24	-0.91	5.40	0	1	0	0
RXRG_dimer.p3	1.67	2.01	4.09	4.89	0	1	0	0
Group 4: motifs only indirectly repressed by PGC-1alpha								
IRF1,2,7.p3	1.77	24.23	4.34	-14.48	0	0	0	1
NFKB1_REL_RELA.p2	0.50	6.54	1.19	-16.01	0	0	0	1
TLX1..3_NFIC{dimer}.p2	0.84	4.91	-2.05	-11.97	0	0	0	1
STAT2,4,6.p2	0.35	4.81	0.52	-9.67	0	0	0	1
DMAP1_NCOR{1,2}_SMARC.p	0.25	4.22	-0.60	-8.73	0	0	0	1
RUNX1..3.p2	0.09	3.94	0.11	-9.61	0	0	0	1
NFATC1..3.p2	0.16	3.46	-0.24	-8.42	0	0	0	1
GATA1..3.p2	1.21	3.39	-2.92	-8.04	0	0	0	1
TBP.p2	1.11	3.20	2.71	-4.04	0	0	0	1
ZIC1..3.p2	0.20	2.99	-0.46	-7.24	0	0	0	1
ATF6.p2	0.24	2.97	-0.51	-7.25	0	0	0	1
TLX2.p2	0.57	2.86	1.37	-6.76	0	0	0	1
TFAP2B.p2	1.75	2.72	4.26	-6.61	0	0	0	1
SPI1.p2	1.69	2.70	4.14	-6.19	0	0	0	1
MEF2{A,B,C,D}.p2	0.97	2.67	2.35	-6.51	0	0	0	1
TFCP2.p2	1.07	2.62	2.57	-5.80	0	0	0	1
BPTF.p2	1.38	2.56	3.37	-6.25	0	0	0	1
LEF1_TCF7_TCF7L1,2.p2	0.17	2.55	0.37	-6.11	0	0	0	1
STAT1,3.p3	0.74	2.53	1.79	-6.17	0	0	0	1
RREB1.p2	1.56	2.39	3.82	-5.42	0	0	0	1
GTF2I.p2	2.09	2.38	5.10	-5.80	1	0	0	1
MYFfamily.p2	0.36	2.38	0.79	-5.12	0	0	0	1
ZNF384.p2	0.64	2.34	-1.55	-5.27	0	0	0	1
TGIF1.p2	0.57	2.34	1.34	-5.68	0	0	0	1
TEAD1.p2	0.99	2.23	-2.43	-5.43	0	0	0	1
SOX{8,9,10}.p2	0.16	2.17	0.30	-5.28	0	0	0	1
CEBPA,B_DDIT3.p2	1.03	2.13	2.51	-5.20	0	0	0	1
MYOD1.p2	1.49	2.05	3.65	-4.99	0	0	0	1

Suppl. Fig. S2. Motif activities clustered by Z score in direct/indirect activation/repression. Related to Figure 2.

(A) Motifs showing different types of regulation (1=yes, 0=not).



Suppl. Fig. S3. siRNA knockdown efficiency for the putative PGC-1α partner TFs. Related to Figure 4

(A-F) siRNA knockdown efficiency for ATF3 (A), GTF2I (B), JUN (C), NFE2L2 (D), NFYC (E) and ZFP143 (F) knockdown. Bars represent fold change over GFP/siCtrl levels. Error bars represent SEM. *$p < 0.05$; **$p < 0.01$; ***$p < 0.001$.

Suppl. Table 1. Real-time primer sequences. Semiquantitative real-time PCR primers used for validation experiments.

Real-time PCR primers used for testing the efficiency of the ChIP		
Gene promoter or intron	Forward primer	Reverse primer
Tbp intron	TGTGAGCTCCTTGGCTTTTT	ATAGTTGCCCAGCAATCAGG
promoter of *Aco2*	CACCGATAGTTGCTTTCCAGATAC	AACCATCTGACAGGCATAGTCAAT
promoter of *Cycs*	AAGGGCGCCCTCTGGGCACATC	ATCCCCGTCGCGCGCTCACCG
promoter of *Acadm*	CCTTGCCCGAGCCTAAAC	GTCTGGCTGCGCCCTCT
promoter of *Atp5b*	CTGGAAACTTCCACCCTCACTA	GAGAGGTTTTTGGCGGAACTA
promoter of *Idh3a*	GGACGGCGTCAAGGTCAAG	GCCTAGGTGGCCTGTCTGTG
PGC-1α exon 2	TGAGGACCAGCCTCTTTGCCC A	CGCTACACCACTTCAATCCACCC

Gene or gene promoter	Forward + reverse primer		FOS binding site	Peak position
TGFβ1[*1]	F:	TTTGAGACTTTTCCGCTGCT	chr7:26472349-26472356	(see reference 1)
	R:	GGTCCTGCCTCCTTGCGA		
Nr0b2 promoter	F:	GGTACAGCCTGGGTTAATGAC	chr4:133109008-133109015	chr4:133108962-133109162
	R:	ACTGCCTGGATGCCCTTTAT		
Gprc5a promoter	F:	TGATGTCATGAGCCTCACCC	chr6:135011471-135011478	chr6: 135011398-135011598
	R:	TAGCTGTCATTGAGGGCACT		
Dbt promoter	F:	AAGGGGCAAAGCAATTCAGG	chr3: 116215241-116215248 chr3: 116215242-116215249	chr3: 116215152-116215352 chr3: 116215152-116215352
	R:	CTTAGAAAATGTGGTCAGATGCA		

Real-time PCR primers used for testing the knockdown efficiency by siRNAs		
Gene	Forward primer	Reverse primer
Rn18s	AGTCCCTGCCCTTTGTACACA	CGATCCGAGGGCCTCACTA
Fos	TACTACCATTCCCCAGCCGA	GCTGTCACCGTGGGGATAAA
Jun	TGGGCACATCACCACTACAC	TCTGGCTATGCAGTTCAGCC
Atf3	TCTGCGCTGGAGTCAGTTAC	CCGCCTCCTTTTCCTCTCAT
Gtf2i	TTCGAAGGCTTTGCAAGGAAG	TTCGGGGTCCTCACTGGTTT
Nfe2l2	AGTGGATCCGCCAGCTACTC	ATGGGAATGTCTCTGCCAAA
Nfyc	CCACCAGTTCTACGACCACC	GGCCTGTACAATCTGCACCT
Zfp143	GTGGTCGGTCCTTTACCACA	AAATGCCCTCCCACATCCAG

Real-time primers used for target gene validation		
Gene	Forward primer	Reverse primer
Aim1l	CCTGTTGCGTCCATAAGGGT	GCTCTGAGTTCCACATCCCC
Atp1b1	GCTACGAGGCCTACGTGCTA	TGCCACAGTCCTCGAAAATC
Atp5g1	CAGAGGCCCCATCTAAGCAG	TGTCCCGGGAAATGACACTG
Cdk15	ATGCAGTTGCTACCACCGTT	CCGTGGAACTGGATGCTTCT
Cdr2l	GGAACAGGAAAACGAACGGC	ACCACCGTGTACTCACGTTC
Crb3	CCGGACCCTTTCACAAATAGC	CTCTGTCTGCCGCTTTTCC

Dot1l	TGACCTCAGATGAGGAGCCA	TGTCTTCGGGGGAGATTTGC
Eef1a2	CAAGATGGACTCCACGGAAC	CTGGGTTGTAGCCGATCTTC
Eif2b4	ACGGCAAGACCCAATCAGAG	AAGTTCTGCCTTACTCCGGC
Fa2h	GTGGACTGGCAGAAACCTCT	TCTGAGTGGAAGAGGCGAAT
Fabp3	CATGTGCAGAAGTGGAACGG	CTCACCACACTGCCATGAGT
Fam131c	CTGGCTACGTCATCCCTTGT	TCCAGCCTTTCCACTCGAT
Gabpa	GTCGAGGTGGTCATCGATCC	GTAATGTGCTTGGTGCCGTC
Gdf15	CACGCATGCGCAGATCAAAG	TGTGCATAAGAACCACCGGG
Gtpbp2	TGGAAACCTCAAAGCTCGGG	GTACGGAGGGTTGTTGGCTT
Il1a	TGCAAGCTATGGCTCACTTC	GATACTGTCACCCGGCTCTC
Inpp5j	ACAAGGGCGGAGTAAGTGTG	TGAAAGTTATCCTTGCGCTGT
Jam2	GTATTACTGCGAAGCCCGGA	CAACCGTTGCTATGATGCCG
Kdm5a	GTCTTCCGTGTGTCATCAGC	TTAGTCGGGGCAATTCAGGT
Ldhb	GACTCCGAAAATTGTGGCCG	TTCTCTGCACCAGGTTGAGC
Lpin1	CGGCCCTCAACACCAAAAAG	AATTCACCCCACAGCCAGAG
Lrrc2	GTGGAAGGAGCTGCCTGATT	AACAGCTCGATGTACGTGGG
Met	GCTGAGAAACTCTTCCGGCT	AGCCGGCCCATGAATAAGTC
Ndufa9	TTCTGTGGCTCATCCCATCG	TGTAGCCCCAAACACAGTGG
Nmnat1	GGTCGGTGATGCGTACAAGA	CCACGTATCCACTTCCACCC
Nppb	GGCCTCACAAAAGAACACCC	TGCCCAAAGCAGCTTGAGAT
Nr0b2	CCTCTTCAACCCAGATGTGC	GGGCTCCAAGACTTCACACA
Osbpl1a	TCCCCCAATCAGTGCATTCC	GCTTCTACACTCTTGCCCCA
Qrsl1	GTTGGATCAGGGTGCCCTAC	GGGGTTTCTAACTGGCCCAA
Rasl10b	AGACCTGGAAGTGCGGCTAC	GGCAGCGTGCACGTGTTT
Rrm2	TTGCAGCGAGTGATGGCATA	CCATGGCAATTTGGAAGCCA
Samm50	TTTTGATGGACTTGGGCGGA	TGAGATCGCCGCATTACCTC
Sbno2	AGACATCCCAGACACACCTG	TGAGAAGTGGAGTGCTGGAG
Slc25a4	GGTACTTCCCCACTCAAGCC	AGCAAAGTAGCGCCAGAACT
Slc25a35	TAGTCGTGGCAATGACACCC	TCCAAGATCCCCCGGTACAT
Slc6a19	TCCACTCAACCAGAACCAGAC	TGAGTCACTGATGGAAGTGGAG
Srxn1	CCAGGGTGGCGACTACTACT	AGGTCTGAAAGGGTGGACCTC
Stard7	CTCTACGGCCGCCTGTATTC	CGCCATCAAAACAGAGGCAT
Stk19	GTCCTCACTGTCCGAGATGC	CACCATGCTCAGTACAGCCT
Syt7	ACTGGGCAAACGCTACAAGA	TGCAGGCAACTTGATGGCTT
Tbrg4	AACGACAGCCGTACATTGGT	AGCTCCAGGCACTTGTCTTC
Tfam	GAGCGTGCTAAAAGCACTGG	GCTACCCATGCTGGAAAAACA
Tinagl1	TTCTTGTACCAGCGTGGCAT	CCCCACCCAGTGATCTTGAC
Tomm5	CGGAGGAGATGAAGCGGAAG	TATGGAGTGACTCGCAGCAG
Trak2	GCTGAAGAGACGTTCCGCTA	ATCTCGATCCCTCTCTGCCA
Trmt61a	GCTCCTTCTCTCCGTGCATT	TGCGCACATTGTAGACCTGT
Trp53inp2	TACCCCTCCCGCCTGTTTTA	CTGCCGGTGACATAAACGGA
Ttc7b	TGCTCCCCACGATCAAGAAC	ATCTCCCGACTCCTCTCGTC
Tusc2	GCAGTGCCTCCCTTCGTATT	CTGCCCATTCTTGGTGACGA
Twf2	TGCTACCTCCTCTTCCGACT	ATAGCATCTTCAGCCGCACC
VEGFα	CACGACAGAAGGAGAGCAGA	GGGCTTCATCGTTACAGCAG
Wnt7b	TTTCTCTGCTTTGGCGTCCT	GGCCAGGAATCTTGTTGCAG

SUPPLEMENTAL REFERENCES

[1] Liu, G., Ding, W., Liu, X., and Mulder, K.M. (2006). c-Fos is required for TGFbeta1 production and the associated paracrine migratory effects of human colon carcinoma cells. Mol Carcinog *45*, 582-593