

TABLE S1. ChIP-chip, Fold change > 5.0

Chromosome (human)	Start	End	Length	Gene Name	Fold Change
chr.1	148520227	148522337	2110	C1orf51	31.91
chr.2	10099988	10100991	1003	KLF11	5.16
chr.2	112448688	112449959	1271	MERTK	6.14
chr.2	238861341	238862907	1566	PER2	20.49
chr.2	241147655	241148661	1006	DUSP28	6.8
chr.3	40473162	40473982	820	RPL14	5.07
chr.5	137576312	137577308	996	CDC23	5.08
chr.7	881939	882974	1035	C7orf20	5.72
chr.7	91995562	91996733	1171	DKFZP564O0523	5.04
chr.7	101999590	102000401	811	POLR2J3	5.1
chr.9	94126803	94128215	1412	CENPP NOL8	33.46
chr.9	134895475	134896616	1141	GTF3C5	6.11
chr.11	45824896	45826057	1161	CRY2	5.81
chr.11	49788712	49789371	659	-	5.22
chr.11	66482051	66483307	1256	PC	5.8
chr.12	106011061	106012251	1190	CRY1	8.75
chr.12	130760999	130762208	1209	SFRS8	7.19
chr.14	19999153	20000370	1217	NP TMEM55B	6.39
chr.16	3490488	3491478	990	CLUAP1 LOC646174	7.28
chr.16	82543694	82544490	796	OSGIN1	5.04
chr.17	7999189	8001347	2158	PER1	87.65
chr.17	35508235	35511375	3140	NR1D1	10.3
chr.17	71174456	71175594	1138	SAP30BP RECQL5	5.43
chr.18	9126014	9127303	1289	ANKRD12	5.81
chr.19	10390953	10392266	1313	PDE4A	14.46
chr.19	50372888	50374335	1447	BLOC1S3 TRAPPC6A	53.86
chr.19	53832125	53833487	1362	DBP	9.07
chr.19	59310158	59311328	1170	PRPF31 TFPT	5.12
chr.22	30016274	30017176	902	PIK3IP1	5.87
chr.22	37113723	37114362	639	-	5.37
chr.22	40106486	40108174	1688	TEF	5.02
chr.X	103287543	103288643	1100	MCART6	7.71

TABLE S2. ChIP-seq, Tag < 10.0 (nonconsecutive), ChIP-chip, Fold change > 3.0

Gene name	Chromosome (mouse)	Start	End	Distribution	Tag number	ChIP-chip Fold change
Coq4	chr.2	29643201	29643300	promoter	7	3.34
Trub2	chr.2	71384901	71385000	exon1	5	3.13
Dlx2	chr.2	93850901	93851000	promoter	7	4.38
Alkbh3	chr.2	144353401	144353500	intron1	6	3.7
Polr3f	chr.2	107552301	107552400	promoter	5	3.33
C20orf12	chr.4	124023001	124023100	promoter, exon1	5	3.94
Magoh	chr.5	13159201	13159300	intron1	6	4.24
Vps33a	chr.8	87549101	87549200	promoter	6	3.42
Lamp1	chr.8	44169701	44169800	promoter, exon1	5	3.05
Asna1	chr.8	126500501	126500600	promoter	5	3.69
C19orf43	chr.9	3232201	3232300	promoter, exon1	7	7
Vps11	chr.10	8911001	8911100	intergenic	6	4.33
March9	chr.11	97176901	97177000	exon3,intron3	5	3.13
Cdk4	chr.11	32635401	32635500	exon1	7	3.38
Pik3ip1	chr.12	21167301	21167400	promoter	7	3.09
Hus1	chr.14	43291201	43291300	promoter	7	4.97
Mrpl45	chr.15	55388801	55388900	intergenic	7	4.22
Hbp1	chr.15	66426401	66426500	promoter	9	5.81
Ecd	chr.17	73185601	73185700	promoter, exon1	5	3
Ttc35	chr.17	32996801	32996900	promoter	5	3.41
Mtbp	chr.18			promoter		
Mrpl13						
Ankrd12						
Ypel5						
Wdr36						

TABLE S3. ChIP-seq, Tag > 10.0 (consecutive), ChIP-chip, Fold change > 5.0

Gene name	Chromosome (mouse)	Start	End	Distribution	Tag number	E-box	E like-box	CATTGG	ChIP-chip Fold change
Per2	chr.1	93355701	93355800	exon 1 intron 1	10	0	0	0	20.49
		93355801	93355900	exon 1	52	0	TTGCAC	0	
		93355901	93356000	promoter	34	0	1	1	
		93356001	93356100	promoter	50	0	1	0	
Cry2	chr.2	92264001	92264100	intron 3	10	(*)	0	0	5.81
		92274301	92274400	promoter	28	0	1	(**1)	
		92274401	92274500	promoter	13	0		0	
Gm129	chr.3	95686101	95686200	promoter exon 1	19	1	0	0	31.91
		95686201	95686300	promoter	17	2	1	1	
Dbp	chr.7	52960101	52960200	promoter	20	0	1	0	9.07
		52960201	52960300	promoter	7	0	0	2	
		52960301	52960400	promoter	5	0	0	1	
		52960401	52960500	promoter	10	0	0	0	
		52961401	52961500	intron 1	11	0	1	0	
		52963001	52963100	intron 2	11	1	1	0	
		52963101	52963200	intron 2	15	1	0	0	
Cry1	chr.10	84647801	84647900	promoter	19	(***1)	0	1	8.75
		84647901	84648000	promoter	5	0	0	0	
		84648001	84648100	promoter	16	0	0	0	
		84648101	84648200	promoter	27	0	0	1	
Per1	chr.11	68908301	68908400	intergenic	52	1	0	0	87.65
		68908401	68908500	intergenic	24	0	0	0	
		68908501	68908600	intergenic	15	1	0	0	
		68908601	68908700	intergenic	22	0	0	2	
		68908701	68908800	intergenic	8	0	0	0	
		68912201	68912300	promoter	12	1	0	1	
		68912301	68912400	promoter	10	0	0	1	
		68912401	68912500	exon 1	10	0	0	0	
Rev-erb α	chr.11	98635101	98635200	intron 1	81	2	0	0	10.3
		98635201	98635300	intron 1	18	0	0	0	
		98635301	98635400	intron 1	5	0	0	0	
		98635401	98635500	intron 1	32	1	1	1	
		98636501	98636600	promoter exon 1	12	0	0	0	N.D.
		98636601	98636700	promoter	27	0	1	0	
		98644601	98644700	intergenic	17	0	0	0	
		98644701	98644800	intergenic	50	0	2	0	
		98644801	98644900	intergenic	19	1	1	0	
Tef	chr.15	81641301	81641400	intron 1	64	1	0	0	5.02
		81641401	81641500	intron 1	69	1	0	1	
		81641501	81641600	intron 1	10	0	0	0	
		81641601	81641700	intron 1	24	0	1	0	

*Rat: CACATG, **Human : ATTGG, ***Human : CTCGTG, N.D.: Not detected

TABLE S4. Genomic signatures that correlate with the Bmal1-regulating genes

Gene ontology term	Count	%	P -Value
Biological Process			
rhythmic process	9	17.0	2.55E-11
circadian rhythm	7	13.2	9.00E-11
gene expression	24	45.3	2.18E-08
nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	23	43.4	7.02E-07
RNA metabolic process	20	37.7	1.28E-06
cellular metabolic process	31	58.5	4.08E-06
macromolecule metabolic process	29	54.7	5.09E-06
regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	18	34.0	5.73E-06
transcription	18	34.0	6.95E-06
biopolymer metabolic process	25	47.2	8.10E-06
regulation of transcription, DNA-dependent	17	32.1	1.16E-05
transcription, DNA-dependent	17	32.1	1.35E-05
RNA biosynthetic process	17	32.1	1.38E-05
regulation of cellular metabolic process	18	34.0	1.82E-05
regulation of transcription	17	32.1	2.22E-05
primary metabolic process	30	56.6	2.29E-05
regulation of metabolic process	18	34.0	3.02E-05
regulation of gene expression	17	32.1	5.08E-05
metabolic process	31	58.5	6.42E-05
regulation of cellular process	20	37.7	2.56E-04
regulation of biological process	21	39.6	2.87E-04
biological regulation	21	39.6	1.07E-03
cellular process	35	66.0	1.52E-02
Molecular Function			
sequence-specific DNA binding	7	13.2	6.45E-04
nucleic acid binding	17	32.1	9.21E-04
DNA binding	12	22.6	3.45E-03
transcription factor activity	8	15.1	3.61E-03
transcription regulator activity	9	17.0	5.99E-03
signal transducer activity	8	15.1	5.84E-01
molecular transducer activity	8	15.1	5.84E-01
Cellular Component			
nucleus	25	47.2	8.52E-06

TABLE S5. Primer list

Primer pair		Sequence (5'- 3')	Primer pair		Sequence (5'- 3')
Bmal1	Fw	GCAGTGCCACTGACTACCAAGA	Pus10	Fw	ATGGTGCTGTTTTTGTCTGCTG
	Rv	TCCTGGACATTGCATTGCAT		Rv	CCACCGAAGATTCCATTTTCCT
Per1	Fw	CAGGCTAACCAGGAATATTACCAGC	Pex13	Fw	TCTTTGCTGTTATCCTTGCGC
	Rv	CACAGCCACAGAGAAGGTGTCCTGG		Rv	ATCCTCACCACCTTGCCCAGTT
Per2	Fw	CGCCTAGAATCCCTCCTGAGA	Klf11	Fw	GGCAAATGGCTTACTCGTCACT
	Rv	CCACCGGCCTGTAGGATCT		Rv	GCCATCCTGTCTGTTGACCTTT
Cry1	Fw	CCCAGGCTTTTCAAGGAATGGAACA	Ccde85b	Fw	ATTTCATCTGTGCCAAAGCCTC
	Rv	TCTCATCATGGTCATCAGACAGAGG		Rv	CTAACTCCCCACTGGCAAGCTA
Cry2	Fw	GGGACTCTGTCTATTGGCATCTG	Ankrd12	Fw	CTGTACTGGCATGCGCAATAA
	Rv	GTCACCTAGCCCGCTTGGT		Rv	TTTCTGGCCCCATGCAAT
Dbp	Fw	TGCCCCGAAGAACGTCATGA	Pik3ip1	Fw	AGGTGACAAAGAGGCACAGGTG
	Rv	CCCAACATGCTAAGAGCACACA		Rv	TCACAAGCTGACTGATCCCGA
Rev-erb α	Fw	CGTTTCGCATCAATCGCAACC	Asna1	Fw	GATCAGCCCCCTTCATCTCACAG
	Rv	GATGTGGAGTAGGTGAGGTC		Rv	GGATGACAGGCAACGTCTCTTC
Tef	Fw	AAGGAAAGGAGTCTGCCAGCTC	Coq4	Fw	TGCCCAGATTCTACAAGAGCGT
	Rv	CAAGGACGATTCTGTGCTGGAC		Rv	CCAGGAAGCGAAGATACTCACG
Gm129	Fw	TGGTGTTCATCCTTGTCTCTCCA	Dlx2	Fw	TTCCAGCTCTCCCAACTCTTCC
	Rv	CGCCAGGCAGTTTCTTCAGAT		Rv	CCGCAAAGGCACCTAAACTTTT
Rev-erb β	Fw	ACGGATTCCCAGGAACATGG	Hus1	Fw	GCACCTTCCTACCCATCATCAG
	Rv	CCTCCAGTGTTGCACAGGTA		Rv	CGCCCCAGAACTAATGTTGAAC
Crispld2	Fw	CACCCCTCTTAGTTGTGGCTGA	Lamp1	Fw	GATTTCAGTCTTGTGTTGGCG
	Rv	AAGGCCTGTACTCCACAGACCA		Rv	TACAACCCACCTACGCTGCAA
2310035K24Rik	Fw	GGCCCCGAATTTGGAAGATA	Mrpl45	Fw	ACCGAACACTGTTTTCCGGAC
	Rv	TCCCTTTCTGCACCATGTGAC		Rv	CAACGGACATGAACCACTTGG
Igsf8	Fw	TGTGCATGTGAGAGAAGAAGGC	Mrpl13	Fw	GCATCTTTTCCCAGACGAGGA
	Rv	CCCGCACAGATATGTTGCATAG		Rv	TGTACTCGTCCAGCCGTTTAGG
Nptn	Fw	TGACATCACTGGCCATAAACGA	Mtbp	Fw	AATCCTCTGGAATGGCCAGAA
	Rv	TCTTGCGCCATATCCACTCTG		Rv	TCAGACGAACGCGGTAATGAG
Hlf	Fw	ACTGAGTGTTGGAGGCAGGTGA	Trub2	Fw	TCACCAAGGATTACACAGTGCG
	Rv	TTTCGTGTTCTCAGTGCCGAC		Rv	TCTCTGGTCACGTGGTCATACG
Dec2	Fw	TGAACCCAGCATTCCTTCCA	Vps33a	Fw	ATTTTTTTGGTCAGACCCAGGC
	Rv	AGCATCGCTTACTCTTCCTCCC		Rv	GCGAGGCACAAACAAAATATGG
Ighmbp2	Fw	CCCGAATCACCCAAAAATCA	Vps11	Fw	TCGAGCAAGCGGAGAGTAACA
	Rv	GACATCGTTGGCAAGCTTCA		Rv	CGATAGTCAGTGCAGAGGCCTT
Mrpl21	Fw	GGACCCTGTTGAAGAGACGAGA	Wdr36	Fw	TGGCCTCTCTTCAGGAGCTGTA
	Rv	AAGTGCACGACAGCAAAGAGC		Rv	TCCACGGCAACACCTCTAACA
Rsad1	Fw	TTGGATGAAAGAGGTGACGCTC	Ypel5	Fw	GCTGGCAGGTTAAGCAACAAAC
	Rv	AACATCAGTACGCAGCCCCATA		Rv	TCACACACAGGTCTTCCAGCAC
Cops7b	Fw	TGCTGCTGAAAGACCTGGAGAT	Trappe6a	Fw	TGATCCAGAAGTCCTGAGGACC
	Rv	TGATTTTCGCTGGTCCAGTTTG		Rv	TTCAAGGCGACCTGCAAAG
Per3	Fw	CTGCTCCAACCTCAGCTTCCTTT	Bloc1s3	Fw	CTGCCTCTTGGTGAACATTTCGT
	Rv	TTAGACAGCAAGGCTCTGGTTCT		Rv	GCTTCTGTCTGGCATTGATCAA
C030048B08Rik	Fw	ATTTTCATCTGTGCCAAAGCCTC	Cenpp	Fw	TGGATCTTCTCACCAAAGTCCC
	Rv	CTAACTCCCCACTGGCAAGCTA		Rv	AAGTACACCTAGCAGGCTTCGG
Pex1	Fw	CGAAGAGGCCATGACAACACA	Nol8	Fw	GCCAAAATTCCAGGCCTTCA
	Rv	CAGCCAGCACATAAACTCCCTG		Rv	TGCCCACCGCCAGTATTAAAG
Krr1	Fw	TTGATGTGGCTGCTATCAAGGA	G3-PDH	Fw	ACGGGAAGCTCACTGGCATGGCCTT
	Rv	TTCTGTCAGCCTCCATCTTGAG		Rv	CATGAGGTCCACCACCCTGTTGCTG
Thra	Fw	GTCCCCTGAAAAGCAGCATGT			
	Rv	ACAGCGGTAGTGATAACCGGTG			

Table S1. Result of ChIP-chip (Fold change > 5.0).

These sites are extracted from ChIP-chip with more than 5.0 fold changes from human fibroblasts. The start and end indicate the position of start and end site in the Integrated Genome Browser of Affymetrix.

Table S2. Results of ChIP-seq and ChIP-chip.

Twenty-five genes are extracted from ChIP-seq with less than 10 tags (nonconsecutive) and ChIP-chip with more than 3.0-fold change. The 2 kb region upstream of transcription start site is defined as the promoter. Chromosome, Start, End, Distribution and Tag number show ChIP-seq data from mouse fibroblasts. ChIP-chip Fold change shows ChIP-chip data from human fibroblasts.

Table S3. Results of ChIP-seq and ChIP-chip.

Eight genes are overlapped from ChIP-seq with high tags and ChIP-chip with more than 5.0-fold change. The 2 kb region upstream of transcription start site is defined as the promoter. E-box and E-box like sequences are defined as CACGTG and CANNTG, respectively. Chromosome, Start, End, Distribution and Tag number show ChIP-seq data from mouse fibroblasts. Number of E-box, E like-box and CATTGG element are from mouse genome. ChIP-chip Fold change shows ChIP-chip data from human fibroblasts.

Table S4. Result of Gene Ontology.

Genes identified in Table 1 and Supplementary Table 2 are analyzed by DAVID for associations with particular Gene Ontology terms. The *P*-values refer to how significant an association a particular gene ontology term has with the gene list.

Table S5. Primers for RT-PCR.