

Table S2. Functional Annotation Clustering of putative BMAL1 targets using DAVID tools.

Cluster 1	Enrichment Score: 7.570281784314562			
Category	Term	#	P	B
INTERPRO	IPR001723:Steroid hormone receptor	18	3.51E-09	5.82E-06
INTERPRO	IPR008946:Nuclear hormone receptor, ligand-binding	18	5.06E-09	4.18E-06
INTERPRO	IPR000536:Nuclear hormone receptor, ligand-binding, core	18	5.06E-09	4.18E-06
GOTERM MF FAT	GO:0003707~steroid hormone receptor activity	18	1.19E-08	1.18E-05
SMART	SM00430:HOLI	18	1.47E-08	4.43E-06
<i>Esrra, Esrrg, Hnf4a, Hnf4g, Nr0b2, Nr1d1, Nr1d2, Nr1h4, Nr1i2, Nr2f2, Nr3c2, Nr5a2, Ppara, Rara, Rarb, Rora, Rorc, Thra</i>				
Cluster 2	Enrichment Score: 5.385647810701173			
Category	Term	#	P	B
GOTERM BP FAT	GO:0006641~triglyceride metabolic process	13	2.02E-06	9.87E-04
GOTERM BP FAT	GO:0006639~acylglycerol metabolic process	14	2.64E-06	1.11E-03
GOTERM BP FAT	GO:0006662~glycerol ether metabolic process	14	4.66E-06	1.52E-03
GOTERM BP FAT	GO:0006638~neutral lipid metabolic process	14	4.66E-06	1.52E-03
GOTERM BP FAT	GO:0018904~organic ether metabolic process	14	1.02E-05	2.14E-03
<i>Agpat6, Apoa5, Dgat2, G6pc, Insig1, Insig2, Mogat2, Pck1, Pcsk9, Pnpla2, Pnpla3, Sirt1, Slc22a4</i>				
Cluster 3	Enrichment Score: 5.076823004927006			
Category	Term	#	P	B
SP PIR KEYWORDS	transcription regulation	156	6.36E-08	1.46E-05
SP PIR KEYWORDS	Transcription	161	1.91E-05	9.73E-04
GOTERM BP FAT	GO:0045449~regulation of transcription	194	3.59E-05	5.54E-03
GOTERM BP FAT	GO:0006350~transcription	157	1.13E-04	1.10E-02
Cluster 4	Enrichment Score: 4.826858791167763			
Category	Term	#	P	B
GOTERM BP FAT	GO:0016481~negative regulation of transcription	51	1.52E-06	1.11E-03
GOTERM BP FAT	GO:0045934~negative regulation of nucleobase, ...	52	4.53E-06	1.66E-03
GOTERM BP FAT	GO:0010629~negative regulation of gene expression	53	5.32E-06	1.56E-03
GOTERM BP FAT	GO:0051172~negative regulation of nitrogen compound ...	52	6.06E-06	1.48E-03
GOTERM BP FAT	GO:0031327~negative regulation of cellular biosynthetic process	54	9.87E-06	2.23E-03
Cluster 5	Enrichment Score: 4.579854703068408			
Category	Term	#	P	B
INTERPRO	IPR004827:Basic-leucine zipper (bZIP) transcription factor	15	6.02E-06	1.99E-03
SMART	SM00338:BRLZ	15	1.38E-05	1.39E-03
UP_SEQ_FEATURE	domain:Leucine-zipper	20	2.19E-04	8.71E-02
Cluster 6	Enrichment Score: 4.172511153755323			
Category	Term	#	P	B
SP PIR KEYWORDS	nucleotide-binding	154	4.33E-06	3.96E-04
SP PIR KEYWORDS	atp-binding	126	6.73E-06	3.85E-04
GOTERM MF FAT	GO:0000166~nucleotide binding	196	3.49E-05	8.60E-03
GOTERM MF FAT	GO:0005524~ATP binding	137	6.36E-05	1.25E-02
GOTERM MF FAT	GO:0030554~adenyl nucleotide binding	143	1.04E-04	1.45E-02

Cluster 7	Enrichment Score: 3.970366701916962			
Category	Term	#	P	B
GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-dependent	52	1.69E-05	3.11E-03
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	52	2.06E-05	3.36E-03
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	56	4.06E-05	5.95E-03
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	57	4.46E-05	5.69E-03
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic ...	68	1.04E-04	1.05E-02
Cluster 8	Enrichment Score: 3.683169135128673			
Category	Term	#	P	B
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	29	6.67E-05	7.50E-03
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	25	3.50E-04	2.67E-02
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	22	3.82E-04	2.84E-02
<i>Aldoat2, Aldob, B4galt1, Car5a, Csgalnact1, Fbp1, G6pc, G6pc3, Gbe1, Gm10481, Gne, Gnptat1, Gys2, Hibadh, Il6st, Ldha, Man2a1, Pck1, Pcx, Pdk1, Pfkfb3, Pfkf, Pgm2l1, Phkb, Ppara, Ppp1r3b, Ppp1r3c, Ugt1a10, Wdtd1</i>				
Cluster 9	Enrichment Score: 3.261796532650017			
Category	Term	#	PValue	B
INTERPRO	IPR001849:Pleckstrin homology	34	1.80E-04	4.85E-02
SMART	SM00233:PH	34	6.37E-04	4.70E-02
UP_SEQ_FEATURE	domain:PH	28	1.43E-03	4.05E-01
Cluster 10	Enrichment Score: 2.760908956897479			
Category	Term	#	P	B
UP_SEQ_FEATURE	zinc finger region:PHD-type 1	11	1.47E-05	2.12E-02
UP_SEQ_FEATURE	zinc finger region:PHD-type 2	10	3.69E-05	3.52E-02
INTERPRO	IPR019787:Zinc finger, PHD-finger	13	5.81E-03	4.53E-01
INTERPRO	IPR001965:Zinc finger, PHD-type	13	1.44E-02	6.63E-01
SMART	SM00249:PHD	13	2.42E-02	4.90E-01
Cluster 11	Enrichment Score: 2.6581652848216746			
Category	Term	#	P	B
GOTERM_BP_FAT	GO:0046463~acylglycerol biosynthetic process	6	6.95E-04	4.75E-02
GOTERM_BP_FAT	GO:0046460~neutral lipid biosynthetic process	6	6.95E-04	4.75E-02
GOTERM_BP_FAT	GO:0046504~glycerol ether biosynthetic process	6	1.07E-03	6.33E-02
GOTERM_BP_FAT	GO:0019432~triglyceride biosynthetic process	5	1.11E-03	6.30E-02
GOTERM_BP_FAT	GO:0045017~glycerolipid biosynthetic process	8	8.97E-02	7.41E-01
<i>Agpat6, Dgat2, Mogat1, Mogat2, Pck1, Pnpla3</i>				
Cluster 12	Enrichment Score: 2.574218919122059			
Category	Term	#	P	B
GOTERM_MF_FAT	GO:0043169~cation binding	307	2.12E-03	1.10E-01
GOTERM_MF_FAT	GO:0043167~ion binding	310	2.38E-03	1.17E-01
GOTERM_MF_FAT	GO:0046872~metal ion binding	302	3.76E-03	1.56E-01
Cluster 13	Enrichment Score: 2.4615864721249996			
Category	Term	#	P	B

GOTERM_BP_FAT	GO:0006094~gluconeogenesis	7	1.49E-03	8.08E-02
GOTERM_BP_FAT	GO:0046364~monosaccharide biosynthetic process	8	3.66E-03	1.51E-01
GOTERM_BP_FAT	GO:0006090~pyruvate metabolic process	7	5.11E-03	1.89E-01
GOTERM_BP_FAT	GO:0019319~hexose biosynthetic process	7	5.11E-03	1.89E-01
<i>Aldob, Car5a, Fbp1, G6pc, G6pc3, Pck1, Pcx</i>				
Cluster 14	Enrichment Score: 2.374480605027989			
Category	Term	#	P	B
INTERPRO	IPR001610:PAC motif	8	1.05E-03	1.75E-01
SMART	SM00086:PAC	8	1.62E-03	7.82E-02
INTERPRO	IPR000014:PAS	8	3.80E-03	3.84E-01
INTERPRO	IPR013655:PAS fold-3	6	4.78E-03	4.33E-01
SMART	SM00091:PAS	8	5.73E-03	2.20E-01
Cluster 15	Enrichment Score: 2.328696704988734			
Category	Term	#	P	B
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	25	3.24E-03	1.43E-01
GOTERM_BP_FAT	GO:0001944~vasculature development	29	4.85E-03	1.82E-01
GOTERM_BP_FAT	GO:0001568~blood vessel development	28	6.57E-03	2.28E-01
Cluster 16	Enrichment Score: 2.2269434033112434			
Category	Term	#	P	B
GOTERM_BP_FAT	GO:0042304~regulation of fatty acid biosynthetic process	5	1.89E-03	9.59E-02
GOTERM_BP_FAT	GO:0019217~regulation of fatty acid metabolic process	6	6.90E-03	2.32E-01
GOTERM_BP_FAT	GO:0010565~regulation of cellular ketone metabolic process	6	1.60E-02	3.48E-01
<i>Hnf4a, Insig1, Insig2, Scap, Wdcl</i>				
Cluster 17	Enrichment Score: 2.02601777896621			
Category	Term	#	P	B
INTERPRO	IPR001841:Zinc finger, RING-type	32	3.49E-03	3.83E-01
SMART	SM00184:RING	32	9.69E-03	3.08E-01
INTERPRO	IPR017907:Zinc finger, RING-type, conserved site	26	2.47E-02	7.60E-01
Cluster 18	Enrichment Score: 2.012102589102119			
Category	Term	#	P	B
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	60	7.08E-03	2.32E-01
GOTERM_BP_FAT	GO:0016310~phosphorylation	65	1.02E-02	2.82E-01
GOTERM_BP_FAT	GO:0006793~phosphorus metabolic process	76	1.11E-02	2.95E-01
GOTERM_BP_FAT	GO:0006796~phosphate metabolic process	76	1.11E-02	2.95E-01

The annotations link the sites to the closest gene irrespective of the distance. In total, 1551 out of 2049 sites have a functional annotation. For details regarding the positions and strength of these sites, we refer to the supplemental file BMAL1_sites.txt. For the small clusters, we list the genes symbols in the most significant subcategory.¹P = p-value, B = Benjamini corrected p-value.