Supplementary Table 1 | FXR binding peaks in autophagy related genes

Gene_name	gene_chr	tss-10k	tss+gene size	peak_begin	peak_end	peak size
AMBRA1	chr2	91560294	91759006	91579250	91579840	590
ARNT	chr3	95228311	95301161	95237750	95239090	1340
ARSA	chr15	89302906	89317855	89306070	89308650	2580
ARSB	chr13	94531633	94712971	94591680	94592710	1030
ATF4	chr15	80075613	80087975	80084340	80086650	2310
ATF6	chr1	172634587	172807902	172796940	172798520	1580
ATG10	chr13	91074953	91373592	91362890	91364580	1690
ATG12	chr18	46892070	46911233	46893050	46894100	1050
ATG16L1	chr1	89642585	89689003	89651780	89653130	1350
ATG16L2	chr7	108438129	108460602	108450110	108451610	1500
ATG2A	chr19	6231667	6262304	6235110	6236940	1830
ATG2B	chr12	106851748	106933451	106923437	106923549	112
ATG3	chr16	45148941	45188651	45157990	45160550	2560
ATG4A	chrX	137481455	137598813	137490950	137491660	710
ATG4B	chr1	95641609	95686106	95650710	95652450	1740
ATG4C	chr4	98850837	98926478	98860410	98861960	1550
ATG4D	chr9	21059728	21079281	21059110	21060480	1370
ATG5	chr10	43978163	44084097	43987670	43989920	2250
ATG7	chr6	114583118	114810632	114592790	114593650	860
ATG9A	chr1	75177434	75198584	75188150	75189750	1600
ATG9B	chr5	23889998	23907961	23893690	23894270	580
ATIC	chr1	71593729	71625977	71603360	71604360	1000
BAG1	chr4	40883430	40905327	40893960	40896150	2190
BAG3	chr7	135657096	135690493	135666400	135668950	2550
BAK1	chr17	27156756	27175571	27164450	27165990	1540
BAX	chr7	52717064	52732268	52710980	52717210	6230
BCL2	chr1	108434754	108620867	108526400	108527410	1010
BCL2L1	chr2	152584467	152666453	152652850	152658150	5300
BECN1	chr11	101149580	101173581	101162870	101164110	1240
BID	chr6	120843136	120876838	120853280	120855050	1770
BIRC5	chr11	117700550	117717057	117706040	117711030	4990
BIRC6	chr17	74917634	75102696	74926940	74928390	1450
BNIP1	chr17	26908023	26929466	26917630	26919440	1810
BNIP3	chr7	146082518	146111189	146100860	146102310	1450
BNIP3L	chr14	67604076	67637714	67626380	67627560	1180
CAMKK2	chr5	123181179	123239419	123208530	123209210	680
CANX	chr11	50107458	50149175	50116620	50117660	1040
CAPN10	chr1	94820984	94844525	94832210	94833990	1780
CAPN2	chr1	184397389	184457614	184409020	184409710	690
CAPNS1	chr7	30971960	30990067	30979150	30980760	1610
CASP3	chr8	47692644	47725052	47692150	47692870	720
CASP8	chr1	58842217	58904347	58851680	58853120	1440
CD46	chr1	196868093	196928442	196918140	196918990	850
CDKN1A	chr17	29217930	29237667	29230120	29233070	2950
CDKN1B	chr6	134860418	134875543	134869410	134871800	2390
CFLAR	chr1	58760129	58790071	58768090	58771950	3860
CHMP2B	chr16	65539377	65572942	65562610	65563940	1330
CHMP4B	chr2	154472761	154520519	154482130	154483330	1200
CLN3	chr7	133714913	133737794	133730070	133731180	1110
CTSB	chr14	63731298	63764760	63735500	63737320	1820
CTSD	chr7	149561820	149583775	149572230	149573150	920
CXCR4	chr1	130484775	130498876	130491590	130492070	480
DAPK1	chr13	60693307	60864552	60708600	60709700	1100
DAPK2	chr9	65996032	66120049	66002790	66003820	1030
DDIT3	chr10	126717848	126733344	126723540	126729290	5750
DLC1	chr8	37630792	37806108	37675240	37678160	2920
DNAJB1	chr8	86122073	86135802	86131480	86132800	1320
DNAJB9	chr12	45306883	45321055	45310050	45312290	2240
DRAM1	chr10	87785548	87829820	87789980	87790650	670

Gene_name	gene_chr	tss-10k	tss+gene size	peak_begin	peak_end	peak size
EDEM1	chr6	108768634	108809350	108778080	108780520	2440
EEF2	chr10	80629375	80645254	80630270	80631550	1280
EEF2K	chr7	127976344	128050733	127978610	127979870	1260
EGFR	chr11	16642205	16813910	16641880	16643460	1580
EIF2AK2	chr17	79251889	79291912	79281620	79282490	870
EIF2AK3	chr6	70784520	70855234	70793770	70795230	1460
EIF2S1	chr12	79953058	79987997	79961810	79963880	2070
EIF4EBP1	chr8	28360798	28386128	28370420	28372920	2500
EIF4G1	chr16	20662821	20692956	20671920	20674760	2840
ERN1	chr11	106258933	106359110	106266750	106267770	1020
ERO1L	chr14	45902761	45948247	45937640	45938980	1340
FADD	chr7	151764227	151778341	151767070	151769020	1950
FAS	chr19	34355148	34383840	34364320	34366450	2130
FKBP1A	chr2	151358234	151387427	151367810	151369130	1320
FKBP1B	chr12	4839979	4858401	4849770	4850520	750
FOS	chr12	86804850	86818219	86812620	86815370	2750
FOXO1	chr3	52062258	52154031	52066170	52066850	680
FOXO3	chr10	41905591	42006548	41921830	41923570	1740
GAA	chr11	119119280	119147012	119128330	119130340	2010
GABARAP	chr11	69794871	69808451	69804100	69806640	2540
GABARAPL1	chr6	129473209	129492349	129482310	129484380	2070
GABARAPL2	chr8	114454602	114476815	114463650	114465110	1460
GAPDH	chr6	125111869	125125791	125113520	125115330	1810
GNAI3	chr3	107910192	107959070	107948790	107949600	810
GNB2L1	chr11	48603861	48619743	48612910	48614400	1490
GOPC	chr10	52056829	52111930	52080620	52081780	1160
GRID1	chr14	35623321	36394301	35914320	35915210	890
GRID2	chr6	63196850	64616273	64599930	64600490	560
HDAC1	chr4	129193347	129229890	129219500	129220800	1300
HDAC6	chrX	7507247	7535015	7524780	7525350	570
HGS	chr11	120318948	120345298	120318790	120319930	1140
HIF1A	chr12	74998853	75048517	75008510	75009290	780
HSP90AB1	chr17	45704726	45720210	45709240	45712460	3220
HSPA5	chr2	34617609	34632049	34626830	34628840	2010
HSPA8	chr9	40599355	40613282	40607160	40610640	3480
HSPB8	chr5	116858503	116882873	116869480	116874400	4920
IKBKB	chr8	23769676	23827055	23804030	23805210	1180
IKBKE	chr1	133151178	133186140	133156780	133157460	680
ITGB1	chr8	131199553	131257479	131208920	131211000	2080
ITGB4	chr11	115826038	115869725	115865930	115867810	1880
ITPR1	chr6	108153089	108501110	108376320	108377830	1510
KIF5B	chr18	6201002	6251522	6240900	6241920	1020
KLHL24	chr16	20087626	20127817	20097190	20099000	1810
LAMP2	chrX	35772685	35819632	35775640	35776350	710
MAP1LC3A	chr2	155092099	155103809	155101410	155103520	2110
MAP1LC3B	chr8	124104367	124121947	124100630	124105830	5200
MAP2K7	chr8	4228739	4247897	4237450	4239810	2360
MAPK1	chr16	16973474	17039133	16983040	16984580	1540
MAPK3	chr7	133893139	133909330	133902510	133903440	930
MAPK8	chr14	34191083	34270344	34260220	34261040	820
MAPK8IP1	chr2	92223832	92251420	92229350	92230410	1060
MAPK9	chr11	49650252	49699923	49659790	49661140	1350
MBTPS2	chrX	153985753	154046647	154036360	154037060	700
MLST8	chr17	24610494	24626023	24614880	24616410	1530
MTMR14	chr6	113177836	113231386	113187400	113188700	1300
MTOR	chr4	147812690	147931794	147818030	147819710	1680
MYC	chr15	61806895	61821916	61814810	61817540	2730
NAF1	chr8	69374115	69414463	69383830	69384390	560
NAMPT	chr12	33495199	33538234	33504530	33506480	1950

Gene_name	gene_chr	tss-10k	tss+gene size	peak_begin	peak_end	peak size
NBR1	chr11	101403967	101443265	101413020	101415150	2130
NCKAP1	chr2	80341451	80431122	80401550	80402390	840
NFE2L2	chr2	75513575	75552698	75540670	75543880	3210
NPC1	chr18	12348202	12404895	12391030	12396190	5160
NRG2	chr18	36177311	36366814	36178360	36179000	640
P4HB	chr11	120421617	120444250	120432090	120435430	3340
PARK2	chr17	11023249	12256226	11032710	11033570	860
PARP1	chr1	182489105	182531385	182498600	182499430	830
PELP1	chr11	70206382	70233533	70223280	70224180	900
PEX14	chr4	148334643	148483921	148471780	148474450	2670
PEX3	chr10	13243647	13282948	13272520	13273620	1100
PIK3C3	chr18	30422549	30507774	30432170	30433020	850
PIK3R4	chr9	105535324	105589985	105544960	105545830	870
PINK1	chr4	137869324	137892211	137880920	137883380	2460
PPP1R15A	chr7	52778287	52791638	52781240	52782750	1510
PRKAB1	chr5	116463598	116484437	116473080	116475250	2170
PRKAR1A	chr11	109502262	109530962	109503060	109503880	820
PRKCD	chr14	31408539	31449394	31439260	31439880	620
PTEN	chr19	32822066	32900650	32829230	32832630	3400
PTK6	chr2	180929828	180947494	180931400	180932280	880
RAB11A	chr9	64563106	64595563	64584010	64586410	2400
RAB24	chr13	55420583	55433341	55422700	55425080	2380
RAB33B	chr3	51277887	51300134	51287550	51288640	1090
RAB5A	chr17	53608558	53647003	53617900	53619360	1460
RAC1	chr5	144266348	144298861	144287370	144289770	2400
RAF1	chr6	115568590	115636653	115581000	115581660	660
RB1	chr14	73595308	73735598	73637340	73638900	1560
RB1CC1	chr1	6194742	6266185	6204030	6205770	1740
RELA	chr19	5627489	5648130	5636250	5638200	1950
RHEB	chr5	24308640	24358179	24347540	24349660	2120
RPS6KB1	chr11	86327484	86368309	86358060	86359040	980
RPTOR	chr11	119454308	119760905	119463760	119465480	1720
SAR1A	chr10	61133068	61156045	61142000	61144360	2360
SESN2	chr4	132048721	132076371	132069250	132072390	3140
SH3GLB1	chr3	144349865	144393299	144381270	144384110	2840
SIRT1	chr10	62781752	62811780	62800840	62802830	1990
SIRT2	chr7	29541770	29573684	29546510	29547630	1120
SPNS1	chr7	133513573	133531448	133520380	133521830	1450
SQSTM1	chr11	50013653	50034292	50023180	50025950	2770
ST13	chr15	81195473	81240124	81229520	81231650	2130
STK11	chr10	79569280	79593215	79576260	79579070	2810
TFEB	ch17	46873986	47929365	47873795	47875148	1353
TFEB	ch17	47853986	47929365	47907235	47908235	1000
TBK1	chr10	120983512	121033850	121008510	121009060	550
TM9SF1	chr14	56254802	56272643	56261800	56263030	1230
TNFSF10	chr3	27205998	27238587	27218670	27219230	560
TSC1	chr2	28486752	28546692	28496040	28497430	1390
TSC2	chr17	24732760	24779572	24769340	24770580	1240
TUSC1	chr4	93000838	93012202	93001150	93002390	1240
ULK1	chr5	111213507	111249100	111235610	111239770	4160
ULK2	chr11	61589099	61678594	61667320	61669740	2420
ULK3	chr9	57427258	57444040	57428590	57429270	680
USP10	chr8	122424751	122481457	122425000	122426160	1160
UVRAG	chr7	106035252	106299654	106247820	106251010	3190
VAMP3	chr4	150421413	150442062	150431600	150432870	1270
VEGFA	chr17	46153942	46179326	46167250	46170290	3040
WDFY3	chr5	102261971	102508940	102274710	102275310	600
WDR45	chrX	7289374	7305327	7291680	7292350	670
WIPI1	chr11	109434834	109482703	109472330	109473920	1590
WIPI2	chr5	143095537	143145324	143104620	143106210	1590
ZFYVE1	chr12	84887890	84948097	84936800	84939950	3150

The regions from 10 Kbp upstream of transcription start site (tss-10K) to the transcription end site (tss + gene size) of 230 autophagy related genes were analyzed for FXR binding peaks using FXR liver Chip-seq data. The gene name, chromosome number (gene_chr), the positions of the beginning (peak_begin) and end (peak_end) of the peaks, and the sizes of the peaks are indicated.

Supplementary Table 2 | Transcriptional factor binding motifs in FXR binding peaks near autophagy/lysosome genes

a. Autophagy genes

Motif	chromosome	location start	location end	motif sequence	gene	Potential Transcription Factors (top 10)
No.1	chr6	114523432	114523449	TGTCGTCGCAGTGCTGGG	Atg7	CREB, TLX1_NFIC, PPARG,ESR1,CEBPA,
	chr6	114555772	114555789	TGTCGTCGCAGTGCTGGG	Atg7	STP1, IME1, ESR2, bZIP911, GAL4
	chr6	114567768	114567785	TGTCGTCGCAGTGCTGGG	Atg7	
	chr6	114557884	114557901	TGTCGTCGCAGTGCTGGG	Atg7	
	chr12	106894112	106894129	TGTTGTCAGCTCCCTGTC	Atg2b	
	chr19	6242471	6242488	AGGCAGTGACGCTGTTGT	Atg2a	
	chr19	6254384	6254401	TGGTGGCCTCATACTTAC	Atg2a	
	chr1	89688347	89688364	AGCACTCATGTTGTCCCT	Atg16l1	
No.2	chr6	114534213	114534224	ATGTAGTCAGTT	Atg7	CREB, AP1, FOXO3, CAD1, ARG81,
	chr6	114576214	114576225	ATGTAGTCAGTT	Atg7	MATALPHA2, lbe, CIN5, YAP7, SPI1
	chr6	114586127	114586138	ATGTAGTCAGTT	Atg7	
	chr6	114568770	114568781	ATGTAGTCAGTT	Atg7	
	chr6	114522045	114522056	ATGTAGTCAGTT	Atg7	
	chr6	114527037	114527048	ATGTAGTCAGTT	Atg7	
	chr6	114558894	114558905	ATGTAGTCAGTT	Atg7	
	chr6	114546499	114546510	ATGTAGTCAGTT	Atg7	
	chr6	114554000	114554011	ATGTAGTCAGTT	Atg7	
	chr6	114573767	114573778	ATGTAGTCAGTT	Atg7	
	chr6	114524536	114524547	ATGTAGTCAGTT	Atg7	
	chr6	114581121	114581132	ATGTAGTCAGTT	Atg7	
	chr6	114561352	114561363	ATGTAGTCAGTT	Atg7	
	chr6	114514642	114514653	ATGTAGTCAGTT	Atg7	
	chr12	106894111	106894122	ATGTTGTCAGCT	Atg2b	
	chr10	43891684	43891695	CTGAAGTCAGAT	Atg5	
	chr6	114557950	114557961	CTGAAGTCTCCC	Atg7	
	chr6	114523528	114523539	CTGAAGTCTCCC	Atg7	
	chr6	114555484	114555495	CTGAAGTCTCCC	Atg7	
	chr6	114567834	114567845	CTGAAGTCTCCC	Atg7	
	chr16	45197181	45197192	AATAAGTAACTT	Atg3	
	chr10	44063755	44063766	CTGTTGTCACTC	Atg5	
	chr10	44099494	44099505	CTGAAGTCTGTG	Atg5	
	chr6	114773064	114773075	AGCTAGTCAGCT	Atg7	
	chr8	124113391	124113402	CTGTAATCAGGC	Map1lc3b	
	chr10	43888970	43888981	TTGCAGTAAGCC	Atg5	
	chr6	114716218	114716229	TTGTAATCTGCT	Atg7	
	chr6	114737124	114737135	CTGCAGTTTGCT	Atg7	

b. Lysosome genes

No. 1	chr2	164665959	164665973	ATACGCCACGCCGCA	Ctsa	CREB, Fos, NFE2L2, YDR026C, NHP10,
	chr2	164665783	164665797	AACCACGCGGTAAGT	Ctsa	AP1, sna, SKN7, MOT3, Eip74EF
	chr2	32193717	32193731	ACATAGACGGCAAGA	Dnm1	
	chr6	83704784	83704798	ACTCATCAGGTCCCA	Atp6v1b1	
	chr2	32214034	32214048	TCTCACCAGGGCAGA	Dnm1	
	chr2	32213745	32213759	ACTCCCCCACCCATA	Dnm1	
	chr2	32213818	32213832	ACCCACGCGTCAGTT	Dnm1	

DNA binding motifs within the FXR binding peaks were identified by de novo analysis. Thirty-six motifs with the least motif score, 1.19, were identified using the Gibbs sampling method, with a maximum motif length set to 30 bp. 50,000 iterations for Markov chain Monte Carlo were used, the top 36 motifs were chosen for transcriptional factor identification. The top 10 motifs are listed. Among the identified transcriptions factors, CREB was identified as the top-scoring site in different categories of autophagy-related genes.

Supplementary Table 3 | CREB binding peaks in autophagy related genes

Gene_name	gene_chr	strand	tss	peak_begin	peak_end	peak size	dis_tss
ARNT	chr3	+	95238311	95238013	95238155	142	227
ARSA	chr15	-	89307855	89307861	89307977	116	-64
ARSB	chr13	+	94541633	94592136	94592256	120	-50563
ATF4	chr15	+	80085613	80085541	80085689	148	-2
ATF6	chr1	-	172797902	172797939	172798056	117	-96
ATG10	chr13	-	91363592	91363575	91363734	159	-63
ATG12	chr18	-	46901233	46901190	46901300	110	-12
ATG16L1	chr1	+	89652585	89652466	89652586	120	59
ATG16L2	chr7	-	108450602	108450560	108450671	111	-14
ATG2A	chr19	+	6241667	6235774	6235884	110	5838
ATG2B	chr12	-	106923451	106923437	106923549	112	-42
ATG3	chr16	+	45158941	45159042	45159169	127	-165
ATG4B	chr1	+	95651609	95651506	95651618	112	47
ATG4C	chr4	+	98860837	98860752	98860877	125	23
ATG5	chr10	+	43988163	43988095	43988211	116	10
ATG7	chr6	+	114593118	114593070	114593184	114	-9
ATG9A	chr1	-	75188584	75188585	75188695	110	-56
ATG9B	chr5	-	23897961	23893808	23893918	110	4098
BAG1	chr4	-	40895327	40895375	40895485	110	-103
BAG3	chr7	+	135667096	135667192	135667330	138	-165
BCL2L1	chr2	-	152657464	152657414	152657527	113	-7
BECN1	chr11	-	101163581	101163550	101163670	120	-29
BIRC5	chr11	+	117710550	117710452	117710562	110	43
BIRC6	chr17	+	74927634	74927741	74927851	110	-162
BNIP3	chr7	-	146101189	146101105	146101215	110	29
BNIP3L	chr14	-	67627714	67627693	67627808	115	-37
CAPN10	chr1	+	94830984	94830916	94831026	110	13
CAPN2	chr1	-	184447614	184447644	184447766	122	-91
CAPNS1	chr7	-	30980067	30980070	30980203	133	-70
CDKN1A	chr17	+	29230716	29232340	29232453	113	-1681
CFLAR	chr1	+	58770129	58776156	58776266	110	-6082
CHMP4B	chr2	+	154482761	154482657	154482774	117	46
CTSD	chr7	-	149573775	149573747	149573857	110	-27
DDIT3	chr10	+	126727848	126727615	126727725	110	178
DLC1	chr8	-	37676997	37676951	37677080	129	-19
DNAJB1	chr8	+	86132073	86131998	86132124	126	12
DNAJB9	chr12	-	45311055	45311137	45311247	110	-137
EDEM1	chr6	+	108778634	108778563	108778693	130	6
EEF2	chr10	+	80639375	80630453	80630617	164	8840
EEF2K	chr7	+	127987113	127978582	127978692	110	8476
EGFR	chr11	+	16652205	16700617	16700727	110	-48467
EIF2AK3	chr6	+	70794520	70794375	70794514	139	76
EIF2S1	chr12	+	79963058	79962628	79962738	110	375
FKBP1B	chr12	-	4848401	4850159	4850271	112	-1814
FOS	chr12	+	86814850	86814715	86814833	118	76
FOXO3	chr10	-	41996548	41996509	41996619	110	-16
GAA	chr11	+	119129321	119129200	119129329	129	57
GABARAP	chr11	+	69804871	69804376	69804494	118	436
GABARAPL1	chr6	+	129483209	129483139	129483253	114	13
GABARAPL2	chr8	+	114464602	114464436	114464557	121	106
GAPDH	chr6	-	125116485	125115633	125115745	112	796
GNAI3	chr3	-	107949070	107949009	107949127	118	2
GNB2L1	chr11	+	48613861	48613487	48613597	110	319
HGS	chr11	+	120328948	120319339	120319457	118	9550
HSP90AB1	chr17	-	45710210	45710249	45710391	142	-110
HSPA5	chr2	+	34627609	34627389	34627529	140	150
HSPA8	chr9	+	40609355	40609128	40609251	123	166
IKBKB	chr8	-	23817055	23817010	23817123	113	-12
ITGB1	chr8	+	131209553	131209464	131209584	120	29
ITPR1	chr6	+	108163089	108376841	108376951	110	-213807

Gene_name	gene_chr	strand	tss	peak_begin	peak_end	peak size	dis_tss
KLHL24	chr16	+	20097626	20097551	20097680	129	11
LAMP1	chr8	+	13159134	13159166	13159276	110	-87
MAP1LC3A	chr2	+	155102099	155101974	155102089	115	68
MAP1LC3B	chr8	+	124114367	124109326	124109441	115	4984
MAP2K7	chr8	+	4238739	4238687	4238885	198	-47
MAPK1	chr16	+	16983474	16983387	16983497	110	32
MAPK3	chr7	+	133903139	133902922	133903065	143	146
MAPK8	chr14	-	34260344	34260314	34260433	119	-30
MAPK9	chr11	+	49660252	49660206	49660362	156	-32
MLST8	chr17	-	24616023	24615637	24615747	110	331
MTMR14	chr6	+	113187836	113187678	113187810	132	92
MTOR	chr4	+	147822690	147822378	147822492	114	255
MYC	chr15	+	61816895	61816464	61816574	110	376
NAF1	chr8	+	69384115	69384051	69384161	110	9
NAMPT	chr12	+	33505199	33504332	33504452	120	807
NBR1	chr11	+	101413967	101413360	101413478	118	548
NFE2L2	chr2	-	75542698	75541503	75541613	110	1140
NPC1	chr18	-	12394895	12394999	12395114	115	-162
PARK2	chr17	+	11033249	11033026	11033154	128	159
PELP1	chr11	-	70223533	70223505	70223621	116	-30
PEX14	chr4	-	148473921	148473906	148474016	110	-40
PIK3C3	chr18	+	30432549	30432372	30432498	126	114
PIK3R4	chr9	+	105545324	105545234	105545350	116	32
PPP1R15A	chr7	-	52781638	52781582	52781702	120	-4
PRKAR1A	chr11	+	109512262	109512156	109512272	116	48
PTEN	chr19	+	32832066	32832021	32832133	112	-11
RAB11A	chr9	-	64585563	64585507	64585624	117	-3
RAB24	chr13	-	55423341	55423278	55423388	110	8
RAB33B	chr3	+	51287887	51288126	51288236	110	-294
RAB5A	chr17	+	53618558	53618477	53618595	118	22
RAC1	chr5	-	144288861	144288865	144288983	118	-63
RB1	chr14	-	73605308	73637724	73637834	110	-32471
RELA	chr19	+	5637489	5637663	5637793	130	-239
RHEB	chr5	-	24348179	24348432	24348554	122	-314
RPS6KB1	chr11	-	86358309	86358216	86358326	110	38
SAR1A	chr10	+	61143068	61142939	61143089	150	54
SESN2	chr4	-	132066371	132071451	132071561	110	-5135
SH3GLB1	chr3	-	144383299	144383231	144383341	110	13
SQSTM1	chr11	-	50023653	50023723	50023881	158	-149
TFEB	ch17	+	47873986	47873941	47874089	148	29
ST13	chr15	-	81230124	81230461	81230579	118	-396
STK11	chr10	+	79579280	79578124	79578254	130	1091
TM9SF1	chr14	-	56262643	56262372	56262491	119	212
TSC1	chr2	+	28496752	28496407	28496517	110	290
ULK1	chr5	-	111239100	111237445	111237574	129	1591
ULK2	chr11	-	61668594	61668562	61668684	122	-29
UVRAG	chr7	-	106289654	106249227	106249337	110	40372
VAMP3	chr4	-	150432062	150432043	150432154	111	-37
VEGFA	chr17	-	46169326	46169757	46169867	110	-486
WIPI1	chr11	-	109472703	109472661	109472771	110	-13
WIPI2	chr5	+	143105537	143105412	143105532	120	65
ZFYVE1	chr12	-	84938097	84938148	84938271	123	-113

The region from 10 Kbp upstream of transcription start site (tss) to the transcription end site of 230 autophagy related genes were analyzed for CREB binding peaks using CREB liver Chip-seq data. The gene name, chromosome number (gene_chr), the strand the gene is on, the positions of the tss and the beginning (peak_begin) and end (peak_end) of the peaks, the sizes of the peaks, and the distance of the center of the peak from the tss (dis_tss) are indicated.

Supplementary Table 4 | Autophagy related genes with shared FXR and CREB binding peaks

Gene_name	Gene_chr	FXR center	CREB center	FXR-CREB Distance	Pattern	CREB Motif	P-value
ARNT	chr3	95238420	95238420	586	MA0018.2	TGACGTCA	0.0000147
ATF4	chr15	80085495	80085495	130	MA0018.1	TAGGTTGACGAC	0.000163
ATF6	chr1	172797730	172797730	17	MA0018.1	TCTGCTGACGTC	0.000036
ATG10	chr13	91363735	91363735	331	MA0018.1	CACGGTGACGTC	0.0000052
ATG16L1	chr1	89652455	89652455	179	MA0018.2	TGACGCAA	0.000169
ATG16L2	chr7	108450860	108450860	495	MA0018.2	TGACGTCA	0.0000147
ATG2A	chr19	6236025	6236025	446	MA0018.1	CTCCCTGACGCA	0.000201
ATG3	chr16	45159270	45159270	415	MA0018.2	TGAGGCCT	0.000558
ATG4B	chr1	95651580	95651580	268	MA0018.1	GGCGCTGACGAG	0.000288
ATG4C	chr4	98861185	98861185	621	MA0018.2	TGACATCA	0.000214
ATG7	chr6	114593220	114593220	343	MA0018.2	TGACGTAA	0.0000593
ATG9A	chr1	75188950	75188950	560	MA0018.1	TCGAGTGACGAG	0.000237
BAG1	chr4	40895055	40895055	125	MA0018.2	TGACACCA	0.000377
BAG3	chr7	135667675	135667675	664	MA0018.1	CTGGGTGACGTG	0.00000284
BECN1	chr11	101163490	101163490	130	MA0018.1	CGTCGTGACGTC	0.00000688
BNIP3	chr7	146101585	146101585	675	MA0018.2	TGAGGCCA	0.000196
CAPNS1	chr7	30979955	30979955	69	MA0018.1	GCCGGTGACTCA	0.000836
CHMP4B	chr2	154482730	154482730	265	MA0018.1	TGCCCTGACGCC	0.000213
CTSD	chr7	149573810	149573810	258	MA0018.1	CAGGATGACGCC	0.0000108
DLC1	chr8	37676700	37676700	65	MA0018.1	TGTGCTGACGAC	0.000201
DNAJB1	chr8	86132140	86132140	329	MA0018.1	CTCCGTGACGCA	0.0000626
EDEM1	chr6	108779300	108779300	447	MA0018.1	CCTCGTGACGCA	0.0000211
EEF2	chr10	80630910	80630910	625	MA0018.2	TGACGCGA	0.000236
EEF2K	chr7	127979240	127979240	99	MA0018.1	TGTGATGACGCA	0.0000266
FKBP1B	chr12	4850145	4850145	180	MA0018.2	TGACGTGA	0.000101
GABARAPL1	chr6	129483345	129483345	399	MA0018.1	TCTCGTGACGCC	0.0000308
GABARAPL2	chr8	114464380	114464380	134	MA0018.1	GAGACTGACGTA	0.000201
GNAI3	chr3	107949195	107949195	377	MA0018.1	GCTGTTTACGAC	0.000337
GNB2L1	chr11	48613655	48613655	363	MA0018.2	TGAGGTCA	0.000074
HSP90AB1	chr17	45710850	45710850	270	MA0018.2	TGACGTCA	0.0000147
HSPA5	chr2	34627835	34627835	626	MA0018.2	TGACGTGA	0.000101
HSPA8	chr9	40608900	40608900	39	MA0018.1	CGCGATGACGCA	0.0000247
ITGB1	chr8	131209960	131209960	686	MA0018.1	GCGGCTGACGCG	0.0000734
ITPR1	chr6	108377075	108377075	429	MA0018.1	GCTCATGACGTC	0.0000192
KLHL24	chr16	20098095	20098095	730	MA0018.1	GTGGGTGACGCT	0.0000308
MAP1LC3A	chr2	155102465	155102465	684	MA0018.1	CTGGGTGACGTC	0.000000375
MAP2K7	chr8	4238630	4238630	94	MA0018.2	TGAGGTCG	0.000413
MAPK1	chr16	16983810	16983810	618	MA0018.2	GGACGTCA	0.000125
MAPK3	chr7	133902975	133902975	232	MA0018.2	TGACGTCT	0.0000414
MAPK8	chr14	34260630	34260630	507	MA0018.1	CGCGATGACGTG	0.0000176
MAPK9	chr11	49660465	49660465	431	MA0018.1	CTGGGTGCCGCC	0.000452
MTMR14	chr6	113188050	113188050	556	MA0018.2	TGAGGCCA	0.000196
MYC	chr15	61816175	61816175	94	MA0018.1	GTGCGTGACGCG	0.0000591
NAF1	chr8	69384110	69384110	254	MA0018.1	GCCGGTGACGTC	0.00000237
PARK2	chr17	11033140	11033140	300	MA0018.1	CTCCGTGACGAG	0.000213
PELP1	chr11	70223730	70223730	417	MA0018.1	CGTGATGACGCA	0.00000994
PIK3C3	chr18	30432595	30432595	410	MA0018.2	TGACACCA	0.000377
PIK3R4	chr9	105545395	105545395	353	MA0018.2	TGAGGTCA	0.000074
PPP1R15A	chr7	52781995	52781995	603	MA0018.1	CGGGGTGACGTG	0.00000159
RAB11A	chr9	64585210	64585210	105	MA0018.1	CCCGGTGACGAG	0.0000855
RAB33B	chr3	51288095	51288095	164	MA0018.2	TGACGCCA	0.0000267
RAB5A	chr17	53618630	53618630	344	MA0018.2	TGACGTCA	0.0000147
RAC1	chr5	144288570	144288570	104	MA0018.1	CTCGGTGCCGTC	0.000479
RB1	chr14	73638120	73638120	591	MA0018.2	TGACATCA	0.000214
RHEB	chr5	24348600	24348600	357	MA0018.1	CGCGATGACGCA	0.0000247
RPS6KB1	chr11	86358550	86358550	529	MA0018.1	GGGGGTGAGGCC	0.000509
SAR1A	chr10	61143180	61143180	416	MA0018.1	GGGCGTGACGTA	0.0000211
SQSTM1	chr11	50024565	50024565	495	MA0018.2	CGACGCCA	0.000274
ST13	chr15	81230585	81230585	315	MA0018.1	CCGAGTGACGTC	0.0000131
TFEB*	chr17	47908021	47907735	286	MA0018.2	TGACGTCA	1.47E-05
TFEB	chr17	47874511	47874472	39	MA0018.1	CCGGGGGACGCC	0.000378
TM9SF1	chr14	56262415	56262415	234	MA0018.2	TGAGGCCA	0.000196
ULK2	chr11	61668530	61668530	157	MA0018.1	CGCGCTGACGTC	0.0000406
UVRAG	chr7	106249415	106249415	383	MA0018.2	TGAGGCAA	0.000591
VAMP3	chr4	150432235	150432235	387	MA0018.1	CGTGGTGACGTC	0.000000138
WIPI1	chr11	109473125	109473125	659	MA0018.1	GTGGCTTACGTG	0.000302
ZFYVE1	chr12	84938375	84938375	416	MA0018.1	GTGGGGGACGCG	0.000719

Potential CREB motifs in 78 genes with overlapping FXR-CREB peaks. The gene name, gene chromosome location, the location of FXR and CREB peak centers, the distances between FXR-CREB peak centers are listed. Two position weight matrices for the CREB motif were used to identify CREB motifs within 500 bp of the midpoint between the centers of the overlapping FXR and CREB peaks, and 66 genes with $p < 0.001$ for the CREB motif are listed.

* Tfeb (intron # 1): Intron # 1 region contains a consensus CREB motif. In ChIP-seq analysis, however, CREB binding peak was not detected at the CREB site but gel mobility shift and ChIP assays showed binding of CREB to this region.

Supplementary Table 5 | Potential CREB target autophagy related genes with TFEB binding sites

Gene_name	NCBI_ref_seq	chr:motif_start	Dis_tss	TFEB motif
Atg4b	NM_174874	chr1:95632931	18678	TCACGTGA
Mapk8	NM_016700	chr14:34269208	8863	TCACCTGA
Atg7	NM_001253718	chr6:114586366	6752	TCACGGGA
Gabarapl1	NM_020590	chr6:129471516	11693	TCAGGTGA
Bnip3	NM_009760	chr7:146116514	15324	TCACGTCA
Atg4d	NM_153583	chr9:21046622	23106	TCAGGTGA
Pik3c3	NM_181414	chr18:30410978	21571	TCAGGTGA
Cdkn2a	NM_001040654	chr4:88947399	19302	TCAAGTGA
Atg12	NM_026217	chr18:46913536	12302	TCAGGTGA
Ulk2	NM_013881	chr11:61681870	13275	ACACGTGA
Bcl2l1	NM_009743	chr2:152672371	14906	TCACATGA
Fadd	NM_010175	chr7:151768803	461	TCACATGA
Pik3r4	NM_001081309	chr9:105533277	12047	TGACGTGA
Atg4c	NM_175029	chr4:98853551	7073	GCACGTGA
Htt	NM_010414	chr5:35102805	1583	TCATGTGA
Atg16l1	NM_001205391	chr1:89637610	14975	TCATGTGA
Atg5	NM_053069	chr10:43985195	2968	TCAAGTGA
Arsa	NM_009713	chr15:89308480	624	ACACGTGA
Becn1	NM_019584	chr11:101177257	13675	TCACGTCA
Eif2ak3	NM_010121	chr6:70774630	19890	TCAGGTGA
Map1lc3b	NM_026160	chr8:124114336	31	TCACCTGA
Atg10	NM_025770	chr13:91368438	4845	TCACGTGC
Hgs	NM_008244	chr11:120318142	10806	TCACGTGC
Ulk1	NM_009469	chr5:111258226	19125	TCACCTGA
Gaa	NM_008064	chr11:119112248	17073	TCAGGTGA
Gabarap	NM_019749	chr11:69804520	351	CCACGTGA
Atg3	NM_026402	chr16:45158846	95	TCACGTGT
Gabarapl2	NM_026693	chr8:114442723	21879	TCACGTGC
Sqstm1	NM_011018	chr11:50047000	22707	GCACGTGA
Uvrag	NM_178635	chr7:106289982	327	TCACGTGC
Pten	NM_008960	chr19:32830941	1125	ACACGTGA
Atg9b	NM_001002897	chr5:23922498	24536	TCACGTGA
Rps6kb1	NM_001114334	chr11:86368645	10335	TCACGAGA
Ambra1	NM_172669	chr2:91552843	17451	TTACGTGA

Potential TFEB motifs were identified in the region from the transcription start site (tss) to 25 Kbp upstream in the 112 autophagy-related genes with CREB binding peaks listed in Table S3. Criteria for a TFEB motif were at most a single mismatch with the 8 bp consensus TFEB sequence (GTCACGTGAC). The genes, reference for the sequence (NCBI_ref_seq), the position of the first bp of the TFEB site and the chromosome (chr:motif_star), the distance from the transcriptional start site (distance_tss) and the sequence of the identified TFEB motif (TFEB motif) are indicated. Thirty shared genes were found which may be regulated by both CREB and TFEB.

Supplementary Table 6 |

a List of primer sequences for ChIP-qPCR

No.	Gene	Forward (5'-3')	Reverse (5'-3')
1	Atg2a (+7553/+7664)	TAGCATGTGAGTGT GTA	TCGTTAGATTGATTGACTTAGG
2	Atg2b (-31436/-31321)	TAGATAGAAGATAAGAAGGTCAC	GGAGCACAGTTAGAGAATAG
3	Atg3 (+2006/+2112)	CTCCTGTCACT CTGTAA	TCTAAACCTTCACTTCCTAAC
4	Atg5 (+75312/+75393)	TAAGGTGTGTTACTGTGGA	ATGCCCTGTTACTTCTCA
5	Atg7 (+179805/+179896)	TTAATGACAGACATCAATCCT	TTCTTCCTTCTTTTCCTCAG
6	Atg10 (+58709/+58805)	GTGTCGTTCTTGTCTCTG	AGGGTATAGTAAAGGAATGAAG
7	Atg16l1 (+35785/+35899)	GGTATGTCTGGTCTCACT	CACAGTCCTTTCCTCACA
8	Wipi2 (+17577/+17600)	TTTGTTTGTTTGTTTGTTTGTT	CCTTCTACCCTCCTGTTAT
9	Ulk1 (-22671/-22480)	GACTTACTCTGTGCTCTG	CTCTGCCTTTCATCTACTG
10	Gabarap (+186903/+187001)	CCGAAAGAAATACCCAGAC	TCCCAGACTCAAGCATAG
11	Tfeb (+33598/+33717)	TGAGTGTGATGTGATGTG	ATGGCAAGTCTGAAAGT
12	Ctsa (+181761/+181865)	CACGCACGAAGTTGATAC	AGATGGACTGATGGACAC

b List of primer sequences of promoter region for ChIP-qPCR

No.	Gene	Forward (5'-3')	Reverse (5'-3')
1	Atg2a (-181/-76)	GGAGGTTAAAGGTCCTCCCA	GAGCCTTGAAGAGCG AAA AA
2	Atg2b (-158/-68)	GTTCGCGAGACCCAGACTC	TTTTTCCTGCCTTTCCAGC
3	Atg3 (-219/-100)	CCAGGTGACAGCTGGG	ACAGGGGAGTCAAAAACTGC
4	Atg5 (-48/+67)	AGGTTGGGCCGCGCTC	CAGAGTGAACCGCAGC
5	Atg7 (-48/+65)	CCGCGCTTCCGCGTTT	GGCTTACTTACCGCCGCTCA
6	Atg16l1 (-91/-12)	TTCAAGGTTGCGTCATTTGA	CTCGTAGCCCGACGTCCTAG
7	Ulk1 (-1643/-1534)	AACTGCCGGCTAGAAGGAAT	GCGGGTTTGTTTGTTGACAT
8	Tfeb (-25/+91)	AGGAGGGGCGGGTGCT	CTCCGCTGTCACCTAGCC
9	Lc3a (-243/-142)	TCTGGGTGTTCCATCCTCTC	CCTCCATCCAGTCTCTCGAC
10	Lc3b (-85/+18)	CTGCGGACTGAGACACACAC	CGCTGCTTGAAGGTCTTCTC

c List of primer sequences for ChIP-PCR

No.	Gene	Forward (5'-3')	Reverse (5'-3')
1	Atg7 (+151,719/152,021)	CTTAACCTCTGAGCCATCT	GCCACTACTACCCAACTG
2	Gapdh (+181/+459)	AGTGCCAGCCTCGTCCCGTAGACA	AAGTGGGCCCCGGCCTTCTCCAT

Supplementary Table 7 |

List of primer sequences for q-RTPCR

No.	Gene	Forward (5'-3')	Reverse (5'-3')
1	Atg2a	CACTCTACGCCACTACAT	ATCCAGCACATCCAAGAA
2	Atg2b	CCTCCACTCTCAGAATCA	GTCCATCACACGAACATAA
3	Atg3	TCACAACACAGGTATTACAG	CTTCCTCGTCTTCTTCATC
4	Atg5	ACTTGCTTTACTCTCTATCAG	CATCTTCTTGTCTCATAACCT
5	Atg7	CAGAAGAAGTTGAACGAGTA	CAGAGTCACCATTGTAGTAAT
6	Atg10	GACTGCTGTGCTAAAGAA	ACTCCGATTGTGATGTTG
7	Atg12	GTCTGTCTATGCCTCCAA	TCCACTTCCTCAATGCTA
8	Atg16l1	CCTTCTGGATTCTATCACTAAT	TGGGACTCTCACATCTTTA
9	Becn1	GCGGGAGTATAGTGAGTT	GGTGGCATTGAAGACATT
10	Gabarap	CGTCTATGGTCTGTGAAG	CTGAAGGAGGAACTGGAT
11	Gabarapl1	ATTCATTTCATTTAGGGACTCT	GACGCTCTTCATTGGTAG
12	Map1lc3a	AGAAGGATGAAGACGGATT	TAGTTTAGGAGCCAGGAC
13	Map1lc3b	GCTCTTTGTTGGTGTGTA	TCTTCTGTTGCTGTTGTC
14	Ulk1	ACCATTGTCTACCAGTGT	AGTGTCTTGTTCTTCTCATAA
15	Wipi1	CACAGGATGGAGGAGAAT	GATGGAGGTAAGGAAGGT
16	Wipi2	TCTGCTCACTAACCACAA	TCTCCATACTGCCATCAA
17	Tfeb	CTCAGTTTCTCCTTGTGC	GTATTCATCATCTTCGTAGTCT
18	Atp6v1b1	ATGACGGACGAGTTCTAC	GGGTTCAAGCCATAAAGG
19	Ctsa	AACAGACTTTGGACTTCAC	ACACGGAGCATAGAGATT
20	Dnm1	AAGCGTCCTATTCATCATC	TTCACCAACATCACATCTG
21	Creb	TGCCAACTCCAATTTACCAA	ACCCCATCGGTACCATTGTT
22	Vps18	TGGATGATGGGAGATGGAGTGC	CCAGCAGCAGTAGGAAATGGAAC
23	Vps11	TCCTTCTCGAAGAAAACGAAAC	TGTCACATGACTCGCCTTTC
24	36B4	CGACTCACAGAGCAGGC	CACCGAGGCAACAGTTGG

Supplementary Table 8 |

List of probe sequences containing consensus or variant CREB site used for gel mobility shift assay

No.	Gene	CREB motif	Forward (5'-3')	Reverse (5'-3')
1	Atg7 (-11/+20)	TTACGTCA	GGCTGGGTTATTACGTCATTGGGCCGCGCGG	CCGCGCGGCCCAATGACGTAATAACCCAGCC
2	Ulk1 (-1603/-1575)	TGACGCAG	TTCCAGCCTCTGACGCAGGAGTGGGCTGGGCT	AGCCCAGCCCACTCCTGCGTCAGAGGCTGGAA
3	TFEB (+48/+79)	GGACGCAG	AGCTGCGGGCGGGACGCAGAGAACGGAGACG	CGTCTCCGTTCTCTGCGTCCCGCCCGCAGCT
4	TFEB (intron #1; +34019/+34051)	TGACGTCA	GAAAGCTAGATGTGACGTCAGCTTTGAAGGAT	ATCCTTCAAGCTGACGTCACATCTAGCTTTC
5	Pepck (-31/-58)	TGACGTCA	AGCTCGAGGGCCCCTTACGTCAGAGGCGAGA	AGCTTCTCGCCTCTGACGTAAGGGGCCCTCG