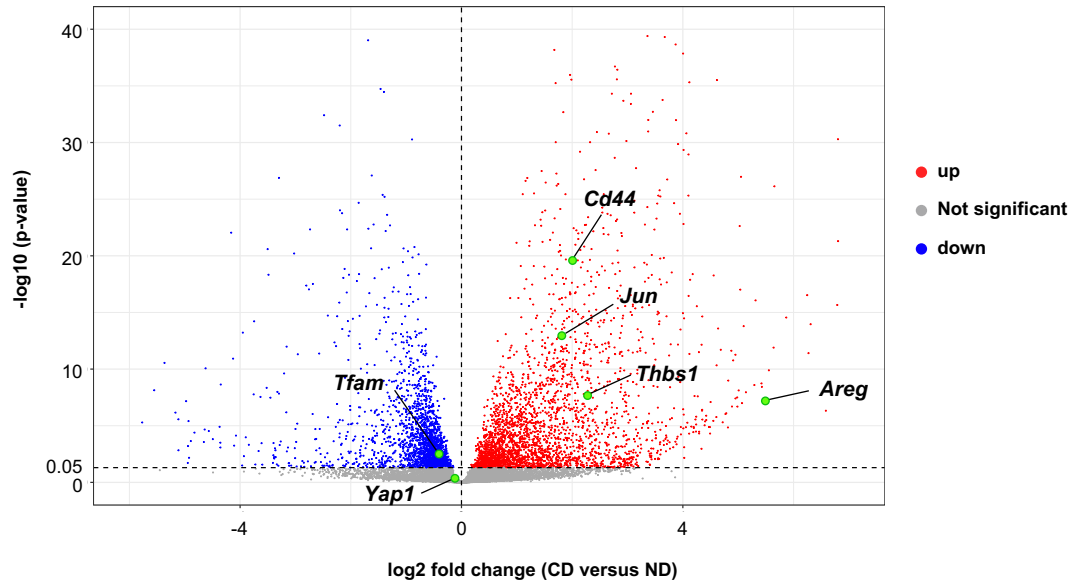
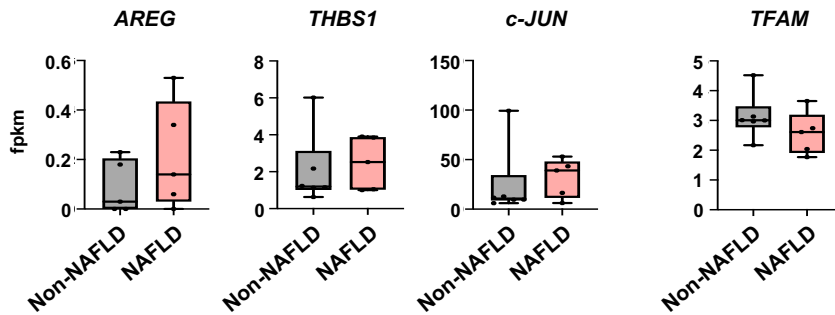


Supplementary Figure S1.

(A) Protein and mRNA levels of TFAM were analyzed 72 h after TFAM-KD (siTFAM #1, #2) or control-KD (siCtrl). 10 μg of total protein was used for the western blot analysis. mRNA expression was normalized by the *RPLP0* gene and indicated as mean ± SD ($n = 3$).

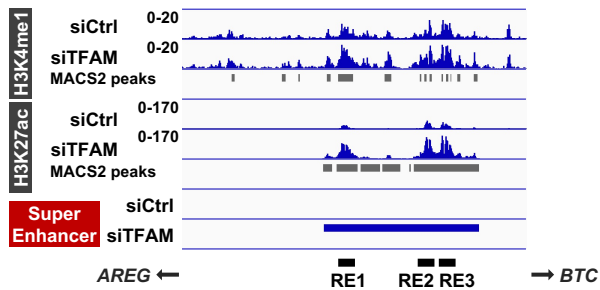
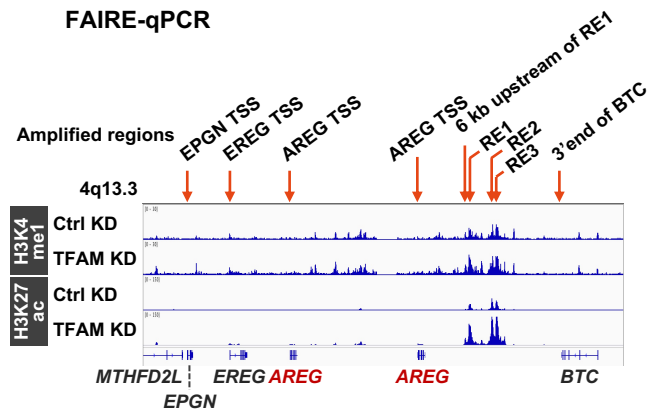
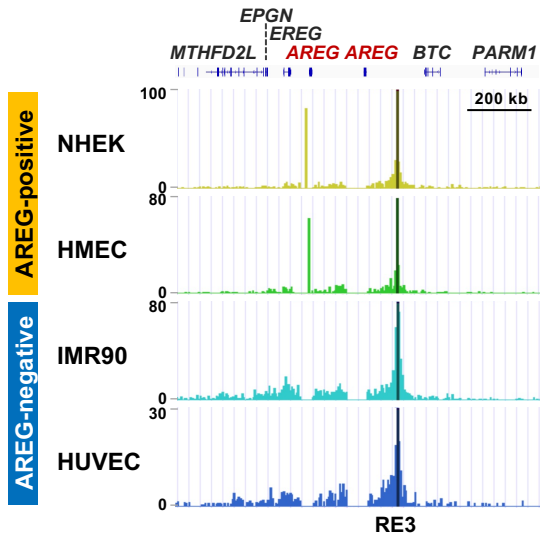
(B) Effect of TFAM-KD on the OXPHOS and glycolysis capacity in HepG2 and HeLa cells. OXPHOS activity was determined by measuring the OCR using the XF24 Analyzer. During the real-time measurement, respiratory chain inhibitors were added to the culture at the indicated time points. Values are mean ± SD of five assay wells.

(C) Effect of TFAM-KD on ATP production. Intracellular ATP concentrations in HepG2 cells were measured 48 h after control and TFAM-KD (siTFAM #1). ATP concentration was normalized to the cell number. $n = 3$, data are represented as mean ± SD. * $p < 0.05$.

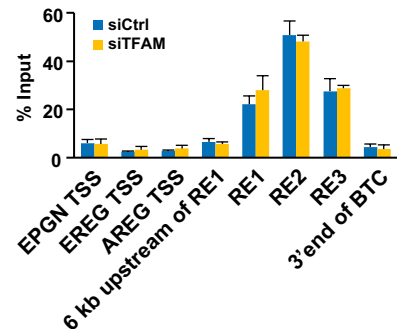
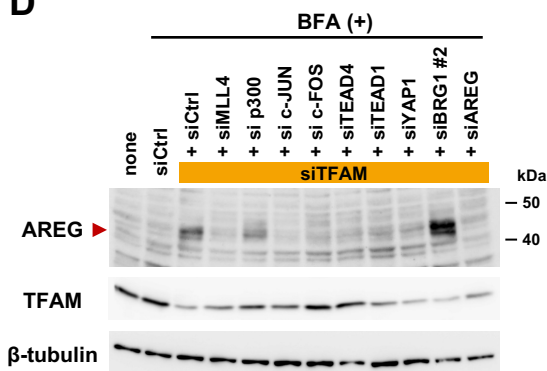
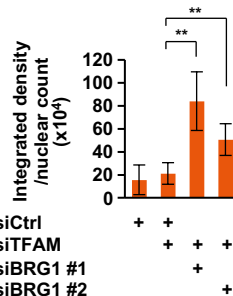
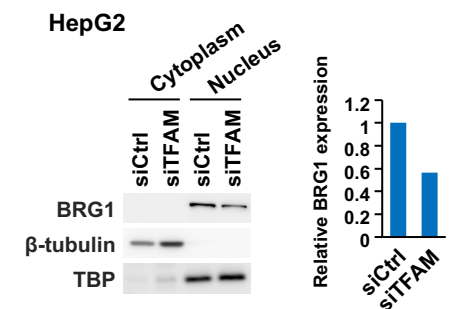
A**B****Supplementary Figure S2.**

(A) Volcano-plot of RNA sequencing data from NASH model mice (Heintz et al. 2020). Up-regulated and down-regulated genes are indicated.

(B) Expression of AREG, THBS1, and mitochondrial stress-related genes in liver tissues of 5 NAFLD patients and 6 non-NAFLD donors (Hou et al., 2021).

A**B****C**

KD for 24 h

**D****E****F****Supplementary Figure S3.**

(A) Detection of super-enhancers using H3K27ac ChIP-seq data in TFAM KD or Control KD HepG2 cells by Homer algorithm.

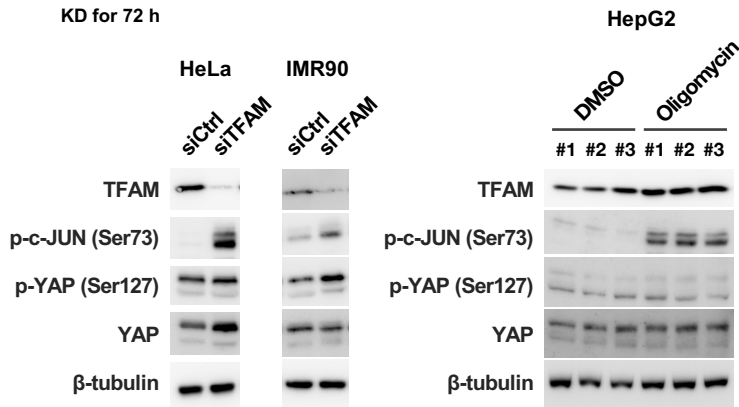
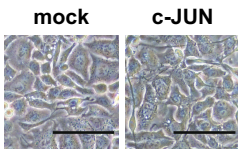
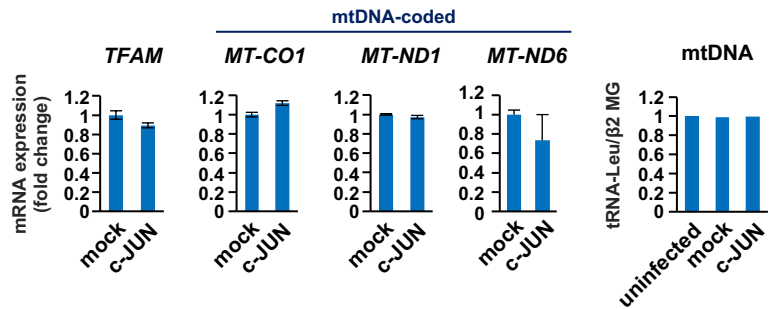
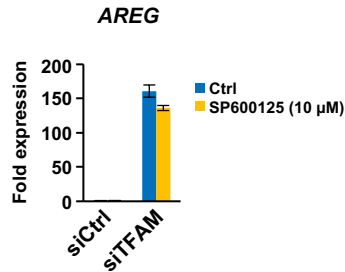
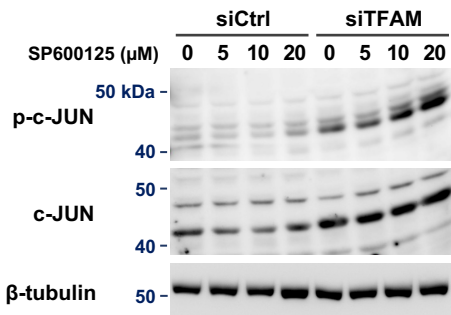
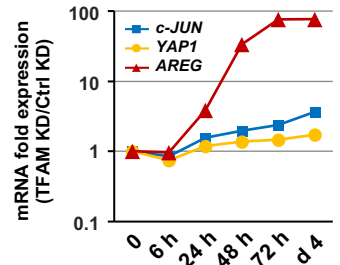
(B) Target sites of FAIRE-qPCR in the EGF family gene cluster (upper) and the results of FAIRE-qPCR of HepG2 cells under TFAM KD for 24 h ($n = 3$) (lower).

(C) ChromContact (Sato and Suyama, 2015) revealed long-range chromatin interactions between RE3 and promoter of the *AREG* gene in AREG-positive cells but not in AREG-negative cells. The black bar at RE3 indicates the reference site.

(D) Western blot analysis of HepG2 cells under the combined knockdown of TFAM and RE-associated factors for 72 h. For AREG detection, cells were treated with 5 $\mu\text{g}/\text{mL}$ of brefeldin A (BFA) for 6 h.

(E) Quantitative intensity analysis of AREG signals in TFAM and Brg1 double knockdown HepG2 cells (Figure 3F). Four to five immunofluorescence images were randomly examined for the density of AREG signals per image, using Image J software and correction by the number of nuclei.

(F) Representative western blot images of decreased BRG1 in the TFAM-KD HepG2 cells. The band intensity of BRG1 was normalized to TFIID (TBP). Three independent BRG1 experiments were done with similar results.

A**B****C****D****E****Supplementary Figure S4.**

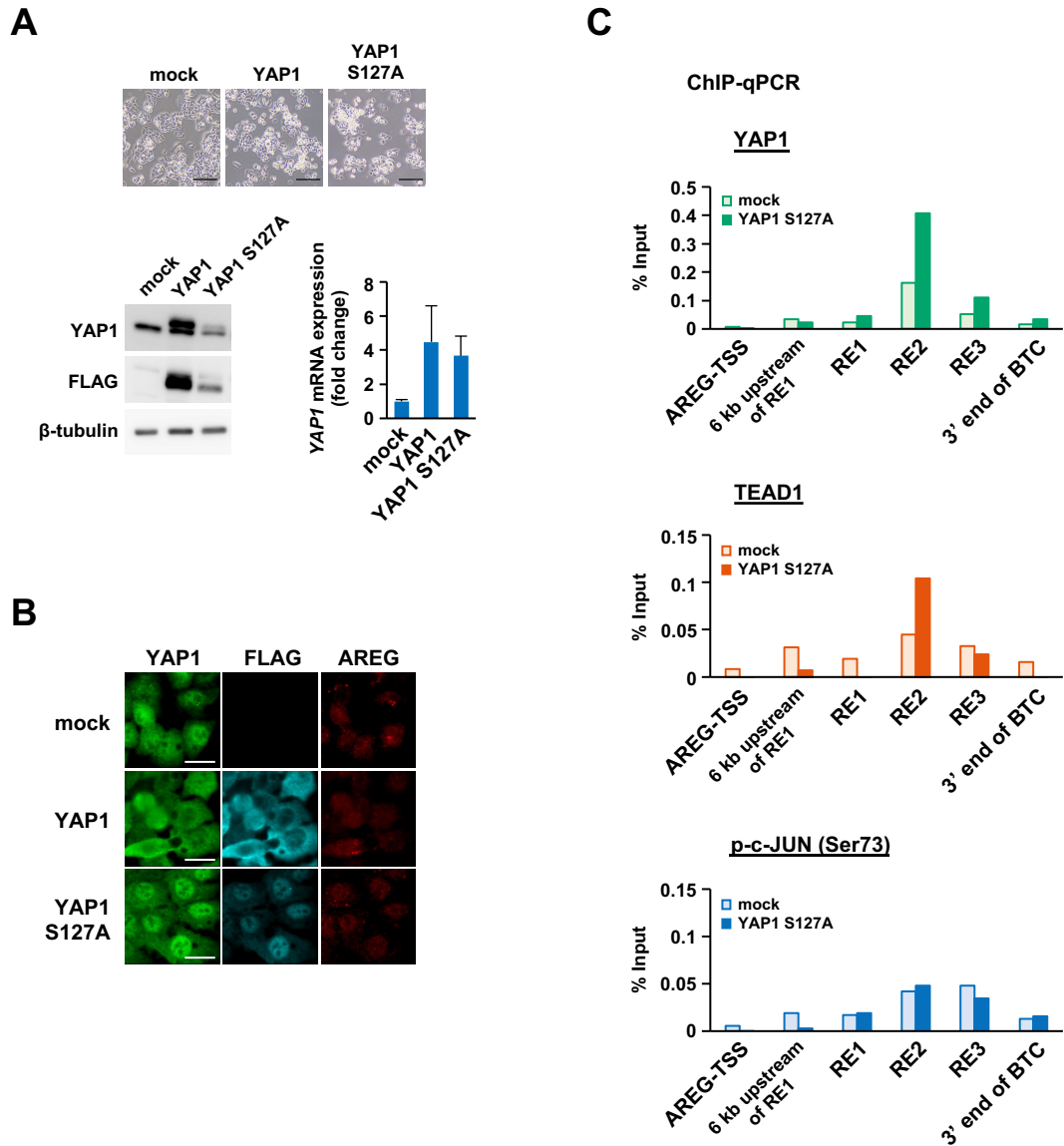
(A) Western blot analysis of phosphorylated c-JUN and YAP1 using whole cell extracts of TFAM-depleted HeLa or IMR90 cells, and three independent HepG2 cells treated with 0.5 μg/mL oligomycin A for 24 hours.

(B) Representative images of mock and c-JUN-expressing virus infected HepG2 cells (day 7). Scale bar, 100 μm.

(C) Expression of *TFAM*, and mitochondrial DNA (mtDNA)-coded genes such as cytochrome c oxidase subunit 1 (*MT-CO1*), NADH dehydrogenase 1 (*MT-ND1*) and NADH dehydrogenase 6 (*MT-ND6*) in c-JUN overexpressing cells (n=3). Quantification of relative mtDNA copy numbers in c-JUN overexpressing cells.

(D) Western blot analysis (left) or qPCR analysis (right) of SP600125-treated TFAM-depleted HepG2 cells. SP600125 was added to the medium at the indicated concentrations 4 hours after siRNA transfection and cells were cultured for additional 68 hours.

(E) Time-course expression of *AREG*, *c-JUN*, and *YAP1* genes after TFAM KD in HepG2 cells. The fold expression shows a relative value to control KD.

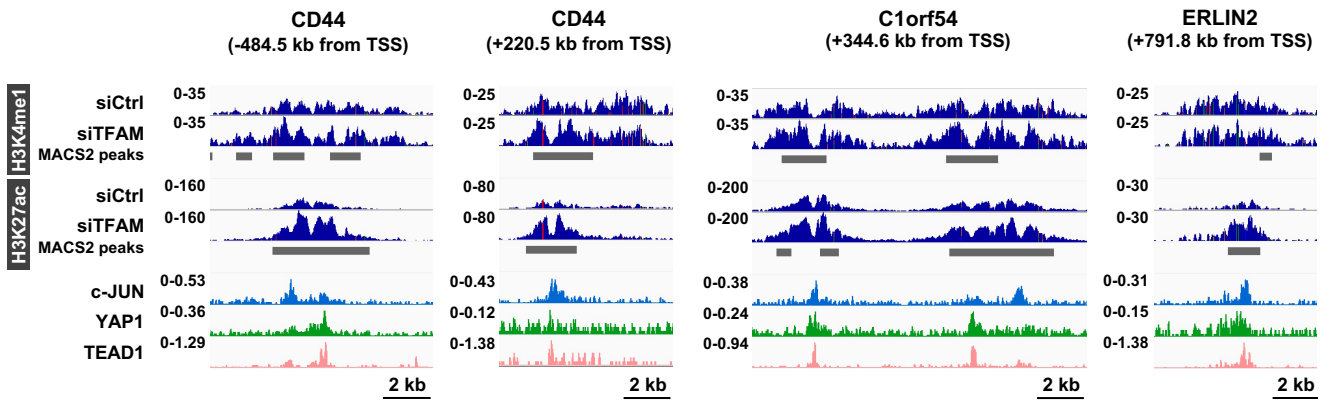


Supplementary Figure S5.

(A) Overexpression of FLAG-tagged YAP1 and its constitutively active/unstable mutant YAP1(S127A) using lentivirus vectors in HepG2 cells. Representative images of mock, YAP1, and YAP1(S127A)-expressing virus infected cells (day 4). Scale bar, 200 μ m. Western blot analysis of total YAP1 and FLAG-tagged YAP1 (day 22). RT-qPCR analysis of *YAP1* and *YAP1(S127A)* mRNAs (n=3, day 22 to 36).

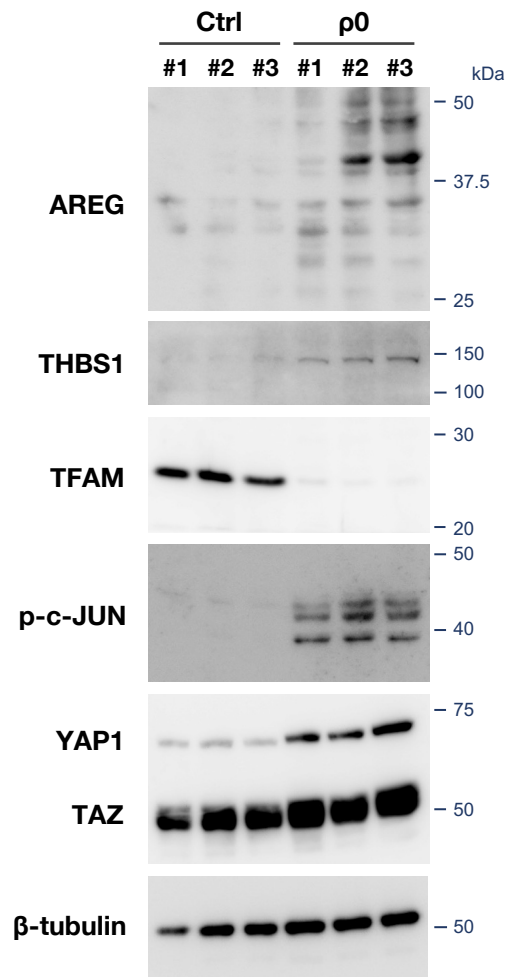
(B) Immunofluorescence staining of YAP1/FLAG and AREG in mock and YAP1-overexpressing HepG2 cells (day 22). Scale bar, 20 μ m.

(C) ChIP-qPCR analysis of mock and YAP1-overexpressing HepG2 cells (day 33). The values were corrected for IgG control.



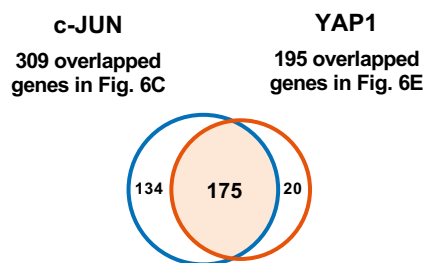
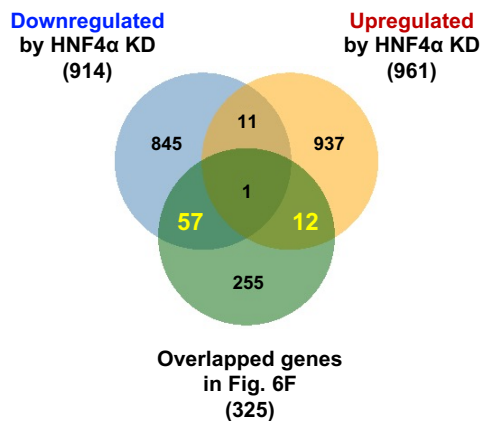
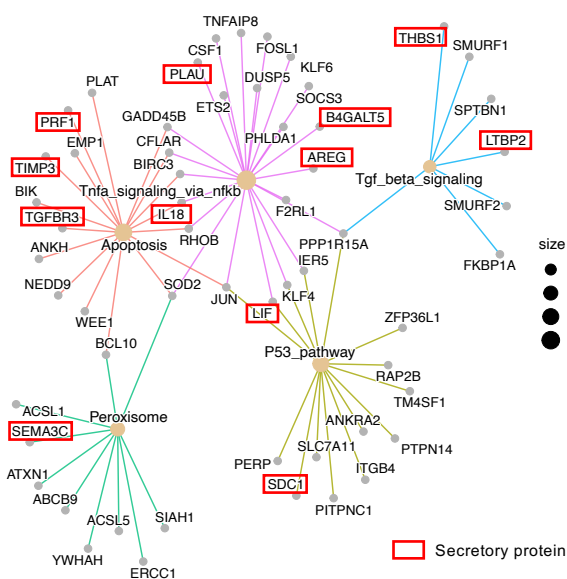
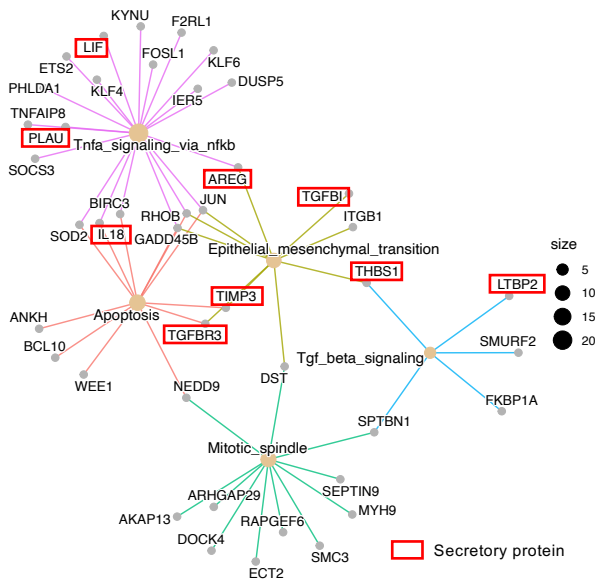
Supplementary Figure S6.

Enrichment of active enhancer marks and transcription factors at the enhancer sites of secretory protein genes upregulated by TFAM KD. ChIP-seq data are from GSM1700784 for c-JUN, GSM1614029 for YAP1, and GSM1667161 for TEAD1.



Supplementary Figure S7.

Western blot analysis of AREG and related proteins using whole cell extracts of three independent ρ0 cell lines induced from HepG2 for 10 days. For detection of AREG and THBS1, 0.5 μg/mL of brefeldin A was added to the medium for 6 hr.

A**D****B****c-JUN targets****C****YAP1 targets****Supplementary Figure S8.****(A)** Overlap between genes regulated by c-JUN and YAP1 under TFAM-KD.**(B, C)** Gene-concept network plots of enriched Hallmark gene sets from MSigDB in Fig. 6D.**(D)** Comparison of 325 overlapped genes in Fig. 6F with up-regulated or down-regulated genes by HNF4α KD in HepG2 cells (Bolontin et al., 2010).

Supplementary Table S1. List of siRNAs used in this study.

siRNAs	Sequence (5' → 3')
siGL3	cuuacgcugaguacuucga
siTFAM #1	guuguccaaagaaccugu
siTFAM #2	gauugagauguguucacaa
siAREG	cuucgacaagagauggaa
siYAP1	gacaucuucuggucagaga
siTEAD1	ggccgauuuguauaccgaa
siSMARCA4 #1	gucugauagugaagaaagu
siSMARCA4 #2	ccaucauggaagauuacuu
siGENOME Human JUN siRNA	M-003268-03

Supplementary Table S2. List of primers used in this study.

Primers	Sequence (5' → 3')	experiment
hTFAM-F	TTCCAAGAAGCTAAGGGTGATT	qRT-PCR
hTFAM-R	CGAGTTTCGTCCTCTTTAGCA	qRT-PCR
mTfam-F	GCATACAAAGAAGCTGTGAG	qRT-PCR
mTfam-R	GTTATATGCTGAACGAGGTC	qRT-PCR
hAREG-F	TCTAGTAGTGAACCGTCCTCG	qRT-PCR
hAREG-R	TTTGGGGGGGCTTAACTACC	qRT-PCR
mAreG-F	AACTCTCCACAGGGGACTACG	qRT-PCR
mAreG-R	CTTCTGTCTTGTITTTCTTGGGC	qRT-PCR
hmJUN-F	CCTCAACGCCTCGTTCTCT	qRT-PCR
hmJUN-R	AGTTCTTGGCGCGGAGGT	qRT-PCR
YAP1-F	CCAAGGCTTGACCCTCGTTT	qRT-PCR
YAP1-R	GTTGCTGCTGTTGGAGTTG	qRT-PCR
TEAD1-F	GCCTCCCAACATCCATAGCA	qRT-PCR
TEAD1-R	TCTGTCCACCAGCCGAGATT	qRT-PCR
hRPLP0-F	GATGCCAGGGGAAGACAG	qRT-PCR
hRPLP0-R	TCTGCTCCACAATGAAACAT	qRT-PCR
mRplp0-F	GCGTCCTGGCATTGTCTGT	qRT-PCR
mRplp0-R	GCAAATGCAGATGGATCAGCC	qRT-PCR
SMARCA4-F	CTGCCGAGAACTCTCCCTC	qRT-PCR
SMARCA4-R	TGAGCTGACGTCCACTGCTG	qRT-PCR
THBS1-F	GAACCACACCAAGAAGACATCC	qRT-PCR
THBS1-R	GTGGCCAATGTAGTTAGTGCG	qRT-PCR
mCD44-F	CCAATGAAGTTGGCCCTGAGC	qRT-PCR
mCD44-R	TGGTTGGCTGCACAGATAGCG	qRT-PCR
hMT-COI-reF	GACGTAGACACACGAGCATATTTCA	qRT-PCR
hMT-COI-reR	AGGACATAGTGGAAGTGAGCTACAAC	qRT-PCR
hMT-ND1-reF	CCACCTTAGCCCTAGCCGTTTA	qRT-PCR
hMT-ND1-reR	GGGTCATGATGGCAGGAGTAAT	qRT-PCR
hMT-ND6-reF	GCGATGGCTATTGAGGAGTATCC	qRT-PCR
hMT-ND6-reR	CACAGCACCAATCCTACCTCCA	qRT-PCR
tRNA-Leu (UUR)-F	CACCCAAGAACAGGGTTTGT	qRT-PCR
tRNA-Leu (UUR)-R	TGGCCATGGGTATGTTGTTA	qRT-PCR
B2-microglobulin-F	TGCTGTCTCCATGTTTATGTATCT	qRT-PCR
B2-microglobulin-R	TCTCTGCTCCCCACCTCTAAGT	qRT-PCR
AREG TSS-F	AAACGGCTTGCAGCTAGAGG	ChIP, FAIRE
AREG TSS-R	AGAAGGTGCTACCCGAAAACC	ChIP, FAIRE
6 kb upstream of RE 1-F	TGTGAGGCAGAACCTACCAG	ChIP, FAIRE
6 kb upstream of RE 1-R	GGTAAGGGTGCAAGTGGTGG	ChIP, FAIRE
RE 1_center-F	AGTCACTAAAGGGAACTGGGGA	ChIP, FAIRE
RE 1_center-R	GGGCCTTTGTATAGGAGAGAGAA	ChIP, FAIRE
RE 2_center-F	GCAGCGAAAATCCTACAGCA	ChIP, FAIRE
RE 2_center-R	TAGACCGAGAAGGAATCCAGC	ChIP, FAIRE
RE 3_center-F	TGGGGAGTGAATCAGCCATTT	ChIP, FAIRE
RE 3_center-R	AAAATGTGTGGCAGTTGTGACG	ChIP, FAIRE
RE 1_side-F	AAGGATTGTAGCCTAGGTTTGC	ChIP
RE 1_side-R	TCCTGTTCTTCTTACCACCAA	ChIP
RE 2_side-F	ATGAGACATAACATGCAGGTCCG	ChIP
RE 2_side-R	CATGGACTGAGGGGTATGT	ChIP
RE 3_side-F	CTCCATGGTTGGCCATTGAAC	ChIP
RE 3_side-R	TTTGCCTGTGCTCTGCTGAA	ChIP
EPGN TSS-F	TAAGAAGTCCAGATGACGCTT	FAIRE
EPGN TSS-R	TCTAGACTGACGGGTGGAAGG	FAIRE
EREG TSS-F	GGATGACTTCTGACGGTCC	FAIRE
EREG TSS-R	GAGCTCAACTGTCTGGTGTCT	FAIRE
3' end of BTC-F	TAAGTGCCACCTCAGACCA	ChIP, FAIRE
3' end of BTC-R	TCTGGGAGTGTGTTGGACATC	ChIP, FAIRE
JUN TSS-F	TCTGCTACCAGTCAACCCCT	ChIP
JUN TSS-R	CCTGAGAGCGACGCGAG	ChIP
RE 1_EcoRV-F	NNGATATCAATAATGGTGAGGCACCACTGG	Luciferase reporter assay
RE 1_BglII-R	NNAGATCTGTGAGGCCATGAAGAATGATGC	Luciferase reporter assay
RE 2_XhoI-F	NNNCTCGAGTACCTTTCCAGGTGAGAG	Luciferase reporter assay
RE 2_EcoRV-R	NNGATATCGAGTCAAAATTCATTTGCCCC	Luciferase reporter assay
RE 3_NheI-F	NNNGCTAGCCTGTAATCCCAGCTACTGG	Luciferase reporter assay
RE 3_XhoI-R	NNNCTCGAGTCACTACTCTGTTTCTC	Luciferase reporter assay
c-JUN_EcoRI-F	GACGAATTCATGACTGCAAAGATGGAAAC	CSII-EF-3xFLAG-JUN-IRES2-Bsd
c-JUN_BamHI-R	NNNGGATCCTCAAAATGTTTGCAACTGC	CSII-EF-3xFLAG-JUN-IRES2-Bsd
YAP1_EcoRI-F	GCAGAATTCATGGATCCCGGGCAGCA	CSII-EF-3xFLAG-YAP1-IRES2-Bsd
YAP1_NotI-R	TCAGTCTGCCGCGCCGCTATAACCATGTAAGAAAGC	CSII-EF-3xFLAG-YAP1-IRES2-Bsd

Supplementary Table S3. List of genes upregulated or downregulated more than 1.5-fold in TFAM knockdown HepG2 cells.

Upregulated genes					Downregulated genes				
Gene	HepG2		HeLa		Gene	HepG2		HeLa	
	siTFAM #1	#2	#1	#2		siTFAM #1	#2	#1	#2
AREG	48.5	6.7	3.5	3.0	TFAM	-13.9	-33.0	-30.0	-53.4
THBS1	9.7	13.9	2.0	7.4	PRKAA2	-2.5	-4.5	-2.1	-3.4
TNFRSF10D	1.6	1.6	10.2	15.5	RG9MTD3	-2.1	-5.6	-1.9	-4.5
GRIPAP1	13.0	8.0	2.4	2.3	EGR1	-2.1	-2.3	-4.1	-2.2
CD44	4.3	7.4	1.6	4.2	LOC100289079	-2.1	-1.7	-3.7	-3.0
TMEM8A	2.2	1.6	4.0	5.5	KLHL23	-3.7	-2.3	-2.2	-1.8
TIMM17A	2.0	2.3	3.0	3.7	SEC14L2	-2.1	-1.6	-2.9	-3.4
JUN	2.5	2.8	3.2	2.3	SUFU	-20.6	-1.7	-1.7	-1.9
CDC42SE2	2.8	2.3	2.3	3.1	FAM69A	-2.4	-2.4	-2.3	-2.1
PREPL	2.7	4.3	1.6	1.9	PIAS2	-2.4	-1.8	-2.9	-2.3
NARG2	4.5	1.8	2.0	2.1	SHB	-2.6	-5.7	-1.6	-1.6
PEX13	2.5	2.6	2.5	2.8	GLE1	-3.3	-1.9	-1.7	-2.6
CRLF3	3.4	2.0	2.8	2.1	ACADSB	-2.6	-1.5	-2.1	-2.6
PLK2	2.2	2.2	2.5	3.4	COBLL1	-2.4	-1.8	-2.9	-1.7
SPTLC1	1.7	2.0	1.7	4.4	BCAP29	-2.9	-2.2	-2.2	-1.5
IFNGR1	1.5	2.7	2.2	3.2	PLEKHA3	-3.1	-2.3	-1.8	-1.5
C10RF54	2.2	3.0	2.4	1.9	ZNF721	-2.2	-1.9	-1.9	-2.0
MSI2	1.6	2.7	1.8	3.3	EI24	-2.6	-1.7	-1.9	-1.9
ALG13	2.2	3.4	1.7	1.9	TADA2A	-2.2	-1.6	-1.7	-2.2
LOC100507375	2.5	2.0	1.9	2.5	PDK3	-2.1	-1.5	-1.6	-2.5
FARP1	2.5	3.1	1.7	1.5	WTAP	-2.0	-1.6	-1.6	-2.2
TM4SF1	2.2	1.6	1.6	3.5	C5ORF44	-2.1	-1.9	-1.7	-1.7
C6ORF120	1.6	2.2	1.9	2.9	TMCC1	-2.3	-1.5	-1.7	-1.9
ZNF782	1.6	1.5	3.9	1.6					
ERLIN2	1.6	1.7	1.7	3.6					
TATDN3	1.8	2.0	2.0	2.7					
ZNF281	1.8	1.5	2.6	2.5					
TRAPPC10	2.1	1.5	1.8	2.7					
MANEA	2.4	1.8	1.7	2.2					
ROD1	1.5	1.5	2.3	2.8					
APAF1	1.7	2.0	1.6	2.8					
ZNF451	2.0	2.1	1.5	2.3					
ZKSCAN3	2.5	2.0	1.6	1.5					
RHOB	1.6	1.6	1.7	2.7					
HIST1H2AK	1.5	2.3	1.8	1.9					
TNFRSF21	1.8	1.8	1.6	2.3					
MREG	1.6	2.1	2.0	1.6					
MYO6	1.9	1.5	2.0	1.8					
EXOC5	2.1	1.6	1.9	1.6					
LOC254128	2.1	2.0	1.6	1.5					
ZNF891	1.8	1.6	1.6	2.2					
RNF4	1.8	1.8	1.5	1.9					
TMEM80	1.6	2.1	1.8	1.5					
LRRC57	1.9	1.9	1.6	1.5					
CFL1	1.6	1.8	1.5	1.9					
TRIM38	1.8	1.6	1.6	1.8					
SGK494	1.8	1.5	1.7	1.7					
YIPF4	1.5	1.6	2.0	1.5					
C5ORF41	1.5	1.7	1.6	1.8					
C16ORF57	1.5	1.6	1.9	1.5					
MTX3	1.5	1.7	1.5	1.8					
SENP7	1.5	1.7	1.5	1.7					

Supplementary Table S4. ChIP-Atlas analysis of REs-associated transcriptional regulators in TFAM knockdown HepG2 cells.

Rank	ID	Antigen	Cell	Log P-val	Log Q-val	Fold Enrichment
1	SRX1123964	SMARCA4/BRG1	HCT 116	-23.769	-22.961	85.00
2	SRX1569429	BRD4	HCT 116	-23.470	-22.665	84.00
3	SRX360377	EP300/p300	HCT 116	-152.461	-151.041	67.50
4	SRX360376	KMT2D/MLL4	HCT 116	-170.244	-168.775	60.60
5	SRX084521	ETV4	PC-3	-13.965	-13.268	52.00
6	SRX1044411	JUN/c-Jun	MDA-MB-231	-226.538	-224.947	47.88
7	SRX2020849	STAT3	HCC1143	-49.442	-48.457	46.25
8	SRX398302	CDK8	SW 480	-48.846	-47.863	45.75
9	SRX1384029	ATF3	HCT 116	-132.765	-131.416	41.25
10	SRX2585779	FOSL1	MDA-MB-231	-324.000	-324.000	40.97
11	SRX1531785	MED1	A549	-20.956	-20.175	40.00
12	SRX1123965	SMARCC1	HCT 116	-20.956	-20.175	40.00
13	SRX1538803	JUND	HT-29	-205.865	-204.318	39.89
14	SRX366167	SMAD3	NCI-H441	-215.315	-213.753	34.96
15	SRX1650401	NR3C1	A549	-99.253	-98.028	34.64
16	SRX092306	FOS/c-Fos	K-562	-156.595	-155.162	33.17
17	SRX825397	IRF1	CFPAC-1	-215.662	-214.098	32.52
18	SRX092300	JUNB	K-562	-143.944	-142.555	32.47
19	SRX190228	TEAD4	HCT 116	-202.956	-201.417	32.04
20	SRX883577	YAP1	MDA-MB-231	-44.014	-43.059	29.17
21	SRX190308	CEBPB	HCT 116	-324.000	-324.000	27.08
22	SRX883578	WWTR1/TAZ	MDA-MB-231	-73.849	-72.741	26.91
23	SRX1389378	ELF3	CFPAC-1	-209.387	-207.835	19.95
24	SRX359886	ETV5	LoVo	-56.574	-55.551	18.77
25	SRX1011298	TEAD1	HuCCT1	-138.022	-136.655	18.34

Cutoff $p < 1e-5$
Rank by Fold Enrichment
Excluded AREG negative cells
(CCLE RNA-seq <1)

Supplementary Table S5. List of AP-1 and TEAD binding motifs at RE sequences.

Seq. name	Detailed Matrix Information	Anchor position	Strand	Matrix sim.	Sequence
3.6 kb region around RE1	AP1	1347	-	0.961	tgatGAGTaatgc
	AP1	1761	+	0.990	caatgAGTCacta
	AP1	1761	-	0.964	tagtgACTCattg
3 kb region around RE2	AP1	288	-	0.907	aattGAGTaagaa
	AP1	694	+	0.880	ttctGAGTtagaa
	TEAD 1,3,4,5	843	+	0.956	cgctCATTccacaa
	AP1	1130	-	0.886	tcctGAGTtatta
	AP1	1801	+	0.955	ttctgACTCagat
	AP1	1801	-	0.978	atctgAGTCagaa
	AP1	2185	+	0.896	acatGAGTaaaaa
	AP1	2555	+	0.975	ccttgAGTCatag
	AP1	2555	-	0.963	ctatgACTCaagg
3 kb region around RE3	AP1	934	+	1.000	ggctGAGtcagga
	AP1	934	-	0.976	tccTGACTcagcc
	AP1	1246	+	0.962	gagtgAATCagcc
	Jun dimerization protein 2	1246	-	0.888	ggctgaTTCActc
	AP1	1282	-	0.978	ttctgAGTCagtc
	AP1	1282	+	0.956	gacTGACTcagaa
	AP1	1348	+	0.997	atatgAGTCataa
	AP1	1348	-	0.973	ttatgACTCatat
	TEAD 1,3,4,5	2355	-	0.911	ttcCATTccaagc
	TEAD 1,3,4,5	2372	-	0.905	ttcCATTccaagt
AP1	2714	+	0.940	tgctGAGTaatta	
AP1	2881	+	0.896	aaatGAGTaatg	
ChIP-qPCR amplified regions					
RE1	1760-1838				
RE2	1454-1525				
RE3	1236-1301				

Supplementary Table S6. List of overlapped genes in Figure 6 (C), (E) and (F).

HepG2 siTFAM #1 Proximal active enhancer mark Proximal binding transcription factor	genes in Fig. 6C (309 genes)				genes Fig. 6E (195 genes)				genes in Fig. 6F (325 genes)			
	≥ 1.5 fold increased c-JUN				≥ 1.5 fold increased YAP1				< 0.67 fold reduced HNF4a			
ABC9	DTWD1	LIMS1	RAP2B	ABTB2	FLJ10661	PHLDA1	ABCC11	DDC	KIFC3	RTEL1		
ABTB2	DUSP3	LIPC	RAPGEF2	ACSL5	FLJ32255	PION	ABCC3	DEPDC6	KLHL23	RXRA		
ACP6	DUSP5	LIPH	RAPGEF6	ADAM19	FLJ42351	PLAU	ABCC6	DIDD1	KYNU	SAMHD1		
ACSL1	E2F7	LOC100499467	RHBDD1	AGPAT9	FOSL1	PLS1	ABCC6P1	DIO1	LASS6	SAR1B		
ACSL5	EFHD2	LOC100506860	RHOB	AKAP12	FOXP1	PLXNC1	ACADSB	DLGAP4	LCA5	SC5DL		
ACSS1	EIF2C2	LOC149086	RHOV	AKAP13	FRMD5	POLA2	ACSL6	DLX1	LGALS2	SCFD2		
ACTR5	ELK3	LOC401233	RNF128	ANK1	FRYL	PPP1R1C	ACSM3	DNAH1	LGALS3	SCML4		
ADAM19	EMP1	LOC730755	RNF144B	ANKH	GADD45B	PRKCA	ADAT2	DNAJB2	LGALS8	SEC24A		
AGA	ENAH	LPP	RNF145	ANKRA2	GALNT10	PRSS23	ADCK3	DNAJB12	LIME1	SEPP1		
AGPAT9	EPB41	LRP6	RNF145	ANKRD28	GAP43	PSD3	ADH6	DNAJB4	LOC100288198	SERPINC1		
AK2	ERCC1	LTBP1	S100A2	ANKRD5	GRAMD1A	PTPN14	AGT	DOCK5	LOC400960	SERPIND1		
AKAP13	ETS2	LTBP2	S100A3	ANXA3	GRAMD1C	PTPRS	AGXT	DPEP1	LOC729970	SGMS1		
AKR1C1	EXOC1	LYST	S100A6	AREG	GRAMD3	PYGB	AGXT2	DPYSL4	LPP	SH3BP2		
ANK1	EZR	LZTS2	SDC1	ARHGAP29	GRB10	RAH4	AK2	ECH1	LPPR1	SH3D9		
ANKH	F2RL1	MALAT1	SDPR	ARID3B	GRB14	RAPGEF2	AK4	EIF4EBP2	LTK	SH3TC1		
ANKRA2	F5	MAS74	SEMA3C	ATG16L1	HS3ST3A1	RAPGEF6	AKR1D1	ELL	MAD1L1	SH3YL1		
ANKRD28	FAM107B	MCC	SEPTIN9	ATPB81	HSPH1	RBMS2	AKT2	ELP3	MAP4K4	SHANK2		
ANKRD5	FAM110B	MCCC2	SERPINE2	ATXN7L1	IER5	RHOB	ALAD	EMLE	MAT1A	SIK2		
ANTXR2	FAM172A	MCTP1	SH2D4A	AVL9	IL18	RHOJ	AMACR	EPB41L1	MB	SIL1		
ANXA3	FAM201A	MECOM	SH2D5	BBS10	IPMK	RNF144B	ANKRD55	EPHX2	MCFD2	SKI		
AREG	FGD6	MET	SH3BGR13	BCL10	ITGA6	RNF43	ANKRD57	ETV5	MEGF9	SLC13A5		
ARG2	FHL3	METT5D1	SH3BP4	BIRC3	ITGB1	RUNX1	ANKS4B	FARP1	MERTK	SLC26A3		
ARHGAP29	FKBP1A	METTL13	SH3BP1	C12orf75	ITGB4	S100A2	ANPEP	FAH	MFSD9	SLC27A2		
ARID3B	FLJ10661	MGC11082	SH2D4A	C1GALT1	ITPRIPL2	SDPR	ANTXR1	FAM117A	MLANA	SLC39A5		
ATG16L1	FLJ32255	MICAL2	SLC22A16	C1orf107	JUN	SEMA3C	ANXA6	FAM13A	MPRIP	SLC44A1		
ATP8B1	FLJ42351	MKLN1	SLC35D2	C3orf65	KIAA0226	SEPTIN9	AOX1	FAM176B	MRPL35	SLC46A1		
ATXN1	FMNL2	MREG	SLC7A11	C9orf3	KIAA0754	SH2D4A	APOH	FAM178A	MTRF1	SLC47A1		
ATXN7L1	FOSL1	MRPL51	SLFN5	C9orf30	KIAA0802	SH2D5	APOL6	FAM20A	MTSS1	SLC6A4		
AVL9	FOXP1	MYH9	SMC3	CAPN2	KLF4	SH3BP4	ARHGAP26	FAM3B	MYO7A	SLC7A9		
B4GALT5	FRMD5	MYO6	SMURF1	CBLB	KLF5	SLC22A16	ARHGAP10L	FAM69A	NBR2	SLC02B1		
BAZ1A	FRYL	MYOF	SMURF2	CCDC148	KLF6	SLC7A11	ASAP3	FAM8A1	NDUFC2	SMAD6		
BBS10	GADD45B	MYSM1	SOC3	CLDN1	KLHL31	SMC3	ASH2L	FARP1	NEDD4L	SNX24		
BCL10	GALNT10	NAA30	SOC5	CLIP4	KLRC3	SMURF2	ASRGL1	FBXO31	NEDD9	SNX29		
BFSF1	GAP43	NAV2	SOD2	CP	KYNU	SOC3	ATP2C2	FGFR4	NELF	SOAT2		
BIK	GATA6	NCRNA00162	SPATS2L	CPLX2	LIF	SOD2	ATP7B	FITM1	NEU4	SOD2		
BIRC3	GCOM1	NEDD4L	SPTNB1	CPXCR1	LOC730755	SPATS2L	ATXN1L	FOXN3	NFATC3	SORL1		
C12orf75	GJC1	NEDD9	SSFA2	CREB5	LPP	SPTBN1	ATXN2	FRMD3	NFE2L2	SPAG9		
C14orf128	GLS	NR1D2	STAMBPL1	CSGALNACT1	LRP6	STK4	AURKAIP1	FRS2	NQO1	SPIRE1		
C16orf45	GNAI1	NRP1	STK17A	CSTF2T	LRR6	SVIL	B9D1	FSD1L	NR1H4	SPOCK2		
C1GALT1	GPR56	NRP2	SVIL	CYP24A1	LTBP2	TBC1D8	BATF2	FTH1	NTSC2	SPTLC3		
C1orf107	GPRC5A	NUAK1	SYTL4	DCAF5	LYST	TCF11L2	BCL2L13	GALM	OSTalpha	SSBP3		
C3orf65	GRAMD1C	OSBPL3	TAF1B	DCBLD2	MALAT1	TEAD1	BCR	GANC	OSTBETA	ST3GAL1		
C9orf3	GRAMD3	OTUD1	TANC1	DCP2	MCC	TGFB1	BDH1	GAPVD1	PARP12	STK11		
C9orf30	GRB10	PAK6	TBC1D8	DFNA5	MCTP1	TGFBR3	C10orf58	GCNT2	PCSK6	STOX1		
CAMTA1	GRB14	PAQR5	TCF7L2	DKFZp686O1327	MECOM	THBS1	C11orf75	GFPT1	PCSK9	STXBPA		
CAPN2	HAS3	PARD3	TCF11L2	DOCK4	MET	TIMP3	C12orf72	GLRX	PDE11A	SUSD2		
CB1	HS3ST3A1	PARP11	TEAD1	DOCK9	MGC11082	TLE1	C16orf87	GNAQ	PDE4D	TASP1		
CBLB	HSPH1	PAWR	TGFB1	DOPEY2	MKLN1	TMEM106B	C17orf89	GNG4	PDE4DIP	TGC1D22A		
CD9	HTR7	PDLM3	TGFBR3	DST	MRPL51	TMEM156	C18orf45	GNNPAT1	PDXDC1	TGOLN2		
CD97	IER5	PDLM4	THBS1	DTNA	MYH9	TNFAIP8	C1orf113	GOSR2	PDZK1	THADA		
CFLAR	IER5L	PDP1	TIMP3	DTWD1	MYOF	TNFRSF21	C1orf115	GPD1	PER2	TKT		
CHGB	IL18	PEAR1	TLE1	DUSP5	NAA30	TRIL	C20orf112	GPR107	PEX14	TLE4		
CHST3	IPMK	PERP	TM4SF1	E2F7	NAV2	TTC32	C22orf36	GPR160	PHLPP1	TMCC1		
CLIP4	IRF2BP2	PFKP	TMEM45B	ECT2	NCRNA00162	UBASH3B	C2orf72	GREB1	PIK3P1	TMEM106A		
CMTM7	ITGA6	PHLDA1	TNFAIP8	EFHD2	NEDD4L	VRK2	C3orf32	GRTP1	PLA2G1B	TMEM127		
COBLL1	ITGB1	PION	TNFRSF21	ELF5	NEDD9	WDFY3	C4orf34	GTPBP1	PLEKHA6	TMEM17		
COL27A1	ITGB4	PITPNC1	TPBG	ELK3	NR1D2	WEE1	C7orf30	H1FX	PLEKHA7	TMEM37		
CP	ITPR3	PKN2	TRIL	ENAH	NRP1	ZAK	ADAM4	HAL	PLLP	TNFSF10		
CPLX2	ITPRIPL2	PLAT	TTC32	ETS2	NUAK1	ZBTB20	CALML4	HAVCR1	PLXNA2	TNS1		
CREB5	JUN	PLAU	TTC39C	EXOC6B	OSBPL3	ZFH3	CAMK2D	HDHD3	PMVK	TOR3A		
CSDA	KIAA0226	PLEKHF2	UBASH3B	F2RL1	OTUD1	ZFP36L1	CAPN12	HES6	POLR3H	TP53INP2		
CSF1	KIAA0802	PLXNC1	VRK2	FAM107B	PARD3	ZG16B	CAPN3	HGD	PPA2	TRAPPPC10		
CSGALNACT1	KIAA1217	POLA2	WDFY3	FAM172A	PEAR1	ZMIZ2	CCDC34	HIPK2	PPARA	TRIM2		
CTSC	KIAA1549	PPFIBP1	WEE1	FAM201A	PELO	ZNF608	CCDC58	HKDC1	PPARGC1B	TSKU		
CWF19L2	KIF2A	PPP1R15A	YAP1	FKBP1A	PFKP	ZSCAN20	CEP57L1	HPR	PPM1H	TLL11		
CYP24A1	KIF3C	PPP1R1C	YWHAH				CHST13	HSDL2	PPP6R2	TULP4		
DCAF5	KLF4	PRF1	ZAK				CHST15	IDH1	PRICKLE2	UBA5		
DCBLD2	KLF5	PRKCA	ZBTB20				CHST9	IFT88	PRKAR1A	UBE2O		
DCP2	KLF6	PROX1	ZBTB38				CNNM2	IKZF4	PRLR	UNC45A		
DFNA5	KLHL31	PRSS23	ZDHHC14				CNNM3	IL1R1	PRR5	USP18		
DHX32	KLRC3	PSD3	ZFH3				COMT	IL1RAP	PTK7	USP2		
DKFZp686O1327	KRT12	PTPN14	ZFP36L1				COQ9	INPP5F	PTP4A2	VASH2		
DOCK4	KRT19	PTPN3	ZG16B				CPLX1	IQSEC1	PTPRA	VDR		
DOCK9	KRT23	PTPRS	ZMIZ2				CRYBB2P1	ITIH3	QKI	VEGFA		
DOPEY2	LARP6	PYGB	ZNF193				CRYL1	ITPR1	QPRT	VIL1		
DSG2	LEKR1	RAH4	ZNF608				CSNK2A1	ITPR2	RAB36	WNK1		
DST	LIF	RALB	ZSCAN20				CTAGE5	KHK	RAD52	ZCCHC14		
DTNA							CTGF	KIAA1161	RAP1GAP	ZFYVE20		
							CYP19A1	KIAA1919	RIN3	ZHX3		
							CYP4F12	KIF16B	RNF103	ZNF556		
							CYP4F3	KIF9	RPRD2	ZNF787		
							CYTH1					