Table S1. Clinical parameters in the GSE14520 cohort of HBV-related HCC patients

Variables	Patients (n=212)	RFS				OS			
		No. of events	MST (months)	HR (95% CI)	P	No. of events	MST (months)	HR (95% CI)	P
Age(years)									
≤60	175	96	45	1		69	NA	1	
>60	37	20	48	0.974(0.602-1.578)	0.916	13	NA	0.864(0.478-1.564)	0.63
Gender									
Female	29	10	NA	1		8	NA	1	
Male	183	106	40	2.143(1.120-4.100)	0.021	74	NA	1.704(0.821-3.534)	0.152
Multinodular									
Single	167	90	49	1		59	NA	1	
Multiple	45	26	28	1.216(0.785-1.883)	0.382	23	47	1.607(0.992-2.604)	0.054
Tumor Size &									
≤5cm	137	73	51	1		46	NA	1	
>5cm	74	43	28	1.409(0.966-2.056)	0.075	36	53	1.975(1.274-3.060)	0.002
Cirrhosis									
NO	17	5	NA	1		2	NA	1	
Yes	195	111	37	2.612(1.066-6.402)	0.036	80	NA	4.335(1.065-17.638)	0.041
BCLC stage									
0	20	6	NA	1		2	NA	1	
A	143	74	51	2.050(2.892-4.711)	0.091	48	NA	4.119(1.001-16.951)	0.05
B	22	15	26	4.019(1.550-10.421)	0.004	12	46	8.992(2.005-40.320)	0.004
C	27	21	8	6.163(2.477-15.333)	<0.001	20	13	18.993(4.419-81.632)	<0.001
Serum AFP φ									
≤300 ng/ml	115	62	48	1		39	NA	1	
>300 ng/ml	94	54	35	1.200(0.833-1.728)	0.328	43	NA	1.546(1.002-2.385)	0.049

Notes: &Information of tumor size was unavailable in 1 patients; φ Information of serum AFP was unavailable in 3 patients.

Table S2. Clinical parameters of HBV-related HCC patients in the First Affiliated Hospital of Guangxi Medical University cohort

Variables	Patients(n=474)	No. of events	MST(months)	HR (95% CI)	Log-rank P
Age (years)					0.517
≤60	420	197	65	1	
>60	54	25	44	1.147(0.756-1.740)	
Gender					0.259
Male	419	202	57	1	
Female	55	20	80	0.769(0.486-1.218)	
Ethnicity					0.464
Han	298	140	71	1	
Minority	176	82	51	1.107(0.841-1.458)	
BMI					0.885
≤25	375	171	58	1	
>25	99	51	57	0.977(0.712-1.340)	
Smoking status					0.272
None	311	143	71	1	
Ever	163	79	44	1.166(0.885-1.537)	
Drinking status					0.135
None	285	127	71	1	
Ever	189	95	48	1.224(0.937-1.598)	
Child–Pugh §					
A	385	175	63	1	0.247
B	59	32	39	1.247(0.855-1.819)	
Cirrhosis £					0.326
No	57	2	82	1	
Yes	416	198	52	1.235(0.808-1.887)	
Radical resection ƀ					0.04
Yes	264	114	74	1	
No	200	104	41	1.320(1.011-1.723)	
Pathological diagnosis ƙ					0.559
Well differentiated	26	10	79	1	
Moderately differentiated	364	174	51	1.351(0.714-2.558)	
Poorly differentiated	12	4	NA	1.016(0.318-3.242)	
Tumor size					<0.001
≤5 cm	191	62	123	1	
>5 cm	283	160	40	2.207(1.642-2.966)	
Tumor number					0.002
Single	350	150	68	1	
Multiple	124	72	35	1.536(1.159-2.036)	
BCLC					<0.001
A	279	97	96	1	
B	75	41	71	1.808(1.252-2.610)	
C	120	84	24	3.435(2.548-4.629)	
portal vein tumor thrombus ƕ					<0.001

No	387	158	79	1	
Yes	86	64	18	3.310(2.461-4.453)	
Serum AFP ƛ					0.048
AFP ≤400 (ng/mL)	243	103	68	1	
AFP >400 (ng/mL)	197	98	42	1.319(1.000-1.741)	

Notes: § Information of Child–Pugh was unavailable in 30 patients; £ Information of cirrhosis was unavailable in 1 patients; ƀ Information of radical resection was unavailable in 10 patients; ƙ Information of Pathological diagnosis was unavailable in 72 patients; ƕ Information of PVTT was unavailable in 1 patients; ƛ Information of AFP was unavailable in 34 patients;

Table S3. Genome-wide co-expression analysis of ACBD4 gene in HBV-related HCC tumor tissues of GSE14520 cohort

ID	ID	r	P Value
ACBD4	SUMO2	-0.64	0.005229
ACBD4	HNRPA3P1	-0.637	0.005449
ACBD4	RPL9	-0.616	0.007229
ACBD4	CLIC1	-0.612	0.007622
ACBD4	SNRPG	-0.593	0.009764
ACBD4	HNRPH3	-0.59	0.010147
ACBD4	RPS3	-0.573	0.012582
ACBD4	MAPRE1	-0.569	0.013226
ACBD4	HMGB2	-0.568	0.013391
ACBD4	MARCKS	-0.567	0.013558
ACBD4	NPM1	-0.567	0.013558
ACBD4	RPS3A	-0.567	0.013558
ACBD4	EEF1E1	-0.566	0.013727
ACBD4	CKAP4	-0.564	0.014071
ACBD4	SNRPF	-0.564	0.014071
ACBD4	GYG1	-0.561	0.0146
ACBD4	RPL17	-0.561	0.0146
ACBD4	HDAC2	-0.56	0.01478
ACBD4	RPL7	-0.559	0.014963
ACBD4	ANP32B	-0.558	0.015147
ACBD4	GNL3	-0.557	0.015333
ACBD4	NUP62	-0.553	0.016099
ACBD4	KHDRBS1	-0.551	0.016494
ACBD4	FUBP1	-0.548	0.017103
ACBD4	SAE2	-0.546	0.01752
ACBD4	UBE2E1	-0.546	0.01752
ACBD4	HNRPK	-0.542	0.01838
ACBD4	CPSF6	-0.541	0.018601
ACBD4	GTPBP9	-0.541	0.018601
ACBD4	HNRPU	-0.541	0.018601
ACBD4	EWSR1	-0.54	0.018824
ACBD4	TDG	-0.54	0.018824
ACBD4	CBX3	-0.539	0.019049
ACBD4	MMD	-0.539	0.019049
ACBD4	UBE2D1	-0.538	0.019277
ACBD4	SSB	-0.535	0.019974
ACBD4	NAP1L1	-0.533	0.020452
ACBD4	HIST1H4C	-0.532	0.020694
ACBD4	MTHFD2	-0.532	0.020694
ACBD4	SET	-0.532	0.020694
ACBD4	NUP43	-0.531	0.020939
ACBD4	NCL	-0.53	0.021186
ACBD4	CCT6A	-0.529	0.021436

ACBD4	IRAK1BP1	-0.529	0.021436
ACBD4	MARCKSL1	-0.529	0.021436
ACBD4	KIF15	-0.528	0.021688
ACBD4	SNRPD1	-0.525	0.022461
ACBD4	RPS10	-0.524	0.022724
ACBD4	TFAM	-0.524	0.022724
ACBD4	TNFRSF21	-0.524	0.022724
ACBD4	XRCC6	-0.524	0.022724
ACBD4	ACTG1	-0.523	0.02299
ACBD4	PABPC3	-0.52	0.023803
ACBD4	PABPC1	-0.519	0.024079
ACBD4	RPS7	-0.518	0.024359
ACBD4	NOL5A	-0.517	0.024641
ACBD4	SLC4A7	-0.517	0.024641
ACBD4	LOC646912	-0.512	0.026094
ACBD4	PHIP	-0.512	0.026094
ACBD4	ACTR3	-0.511	0.026393
ACBD4	CDCA4	-0.511	0.026393
ACBD4	SPHK1	-0.511	0.026393
ACBD4	KIF11	-0.51	0.026695
ACBD4	CCL20	-0.509	0.027001
ACBD4	SEMA4D	-0.509	0.027001
ACBD4	PTGES3	-0.508	0.027309
ACBD4	CCNB1	-0.506	0.027935
ACBD4	FAM60A	-0.504	0.028573
ACBD4	CALM2	-0.503	0.028897
ACBD4	HNRPC	-0.503	0.028897
ACBD4	MCM6	-0.499	0.030223
ACBD4	UBAP2	-0.499	0.030223
ACBD4	PPP1R12A	-0.498	0.030563
ACBD4	PTMA	-0.498	0.030563
ACBD4	SLC1A5	-0.498	0.030563
ACBD4	IARS	-0.497	0.030906
ACBD4	C12orf48	-0.495	0.031602
ACBD4	GMIP	-0.495	0.031602
ACBD4	CKAP2	-0.494	0.031955
ACBD4	PLEKHO1	-0.494	0.031955
ACBD4	RAN	-0.494	0.031955
ACBD4	DDX50	-0.493	0.032311
ACBD4	SAE1	-0.493	0.032311
ACBD4	SMARCA5	-0.493	0.032311
ACBD4	YWHAQ	-0.493	0.032311
ACBD4	LMNB2	-0.492	0.032671
ACBD4	LOC642741	-0.492	0.032671
ACBD4	SMC4	-0.491	0.033034
ACBD4	ZNF74	-0.489	0.033771

ACBD4	EIF3S6	-0.488	0.034144
ACBD4	FBXO5	-0.488	0.034144
ACBD4	KPNA2	-0.488	0.034144
ACBD4	PCNP	-0.488	0.034144
ACBD4	RPL23	-0.488	0.034144
ACBD4	SFRS10	-0.488	0.034144
ACBD4	CCT3	-0.486	0.034902
ACBD4	CTSC	-0.486	0.034902
ACBD4	SLC7A1	-0.486	0.034902
ACBD4	CCR6	-0.485	0.035286
ACBD4	FLJ16542	-0.485	0.035286
ACBD4	NACA	-0.485	0.035286
ACBD4	BUB1B	-0.484	0.035674
ACBD4	ELF4	-0.483	0.036066
ACBD4	SNRPD2	-0.481	0.03686
ACBD4	TRAF5	-0.481	0.03686
ACBD4	RALA	-0.48	0.037262
ACBD4	DDX1	-0.479	0.037668
ACBD4	PTPN2	-0.479	0.037668
ACBD4	DKK1	-0.478	0.038078
ACBD4	RPL39	-0.478	0.038078
ACBD4	ARID3A	-0.477	0.038492
ACBD4	DKC1	-0.477	0.038492
ACBD4	ESF1	-0.477	0.038492
ACBD4	SNRPD3	-0.477	0.038492
ACBD4	TPM4	-0.477	0.038492
ACBD4	SUB1	-0.476	0.03891
ACBD4	DENND3	-0.475	0.039331
ACBD4	HNRPA2B1	-0.475	0.039331
ACBD4	MRPL9	-0.475	0.039331
ACBD4	RPL13A	-0.475	0.039331
ACBD4	RPL37	-0.474	0.039757
ACBD4	SNRPA1	-0.474	0.039757
ACBD4	BZW2	-0.473	0.040186
ACBD4	INTS8	-0.473	0.040186
ACBD4	RPL6	-0.473	0.040186
ACBD4	HELLS	-0.472	0.040619
ACBD4	HIF1A	-0.472	0.040619
ACBD4	ZC3H15	-0.472	0.040619
ACBD4	ARPC2	-0.47	0.041497
ACBD4	RPL22	-0.47	0.041497
ACBD4	FLJ20105	-0.469	0.041942
ACBD4	PWCR1	-0.469	0.041942
ACBD4	TMSB10	-0.469	0.041942
ACBD4	CEP135	-0.468	0.042392
ACBD4	GTF2H2	-0.468	0.042392

ACBD4	HK2	-0.468	0.042392
ACBD4	GALNT7	-0.467	0.042845
ACBD4	KIF18A	-0.467	0.042845
ACBD4	PTP4A3	-0.467	0.042845
ACBD4	TMEM165	-0.467	0.042845
ACBD4	GTF3C2	-0.466	0.043302
ACBD4	RPL24	-0.466	0.043302
ACBD4	TOP2A	-0.466	0.043302
ACBD4	ARID5B	-0.465	0.043763
ACBD4	CEP55	-0.465	0.043763
ACBD4	GTSE1	-0.465	0.043763
ACBD4	IER3	-0.465	0.043763
ACBD4	PTPRE	-0.465	0.043763
ACBD4	BAT2D1	-0.464	0.044229
ACBD4	DBF4	-0.464	0.044229
ACBD4	PELI1	-0.463	0.044699
ACBD4	SEC61G	-0.463	0.044699
ACBD4	SFRS3	-0.463	0.044699
ACBD4	PDCL	-0.461	0.045651
ACBD4	RPS6	-0.461	0.045651
ACBD4	SMURF2	-0.46	0.046133
ACBD4	LAMC1	-0.458	0.047111
ACBD4	LRRC1	-0.458	0.047111
ACBD4	SOX4	-0.458	0.047111
ACBD4	HNRPR	-0.457	0.047606
ACBD4	KIAA0133	-0.457	0.047606
ACBD4	NUP107	-0.456	0.048106
ACBD4	RPL4	-0.455	0.04861
ACBD4	RPS24	-0.455	0.04861
ACBD4	LBR	-0.454	0.049119
ACBD4	LOC146909	-0.454	0.049119
ACBD4	TM4SF1	-0.454	0.049119
ACBD4	EEF1B2	-0.453	0.049632
ACBD4	LIMS1	-0.453	0.049632
ACBD4	LOC643287	-0.453	0.049632
ACBD4	LARGE	0.432	0.049736
ACBD4	SLC13A4	0.432	0.049736
ACBD4	C19orf4	0.433	0.049222
ACBD4	EZH1	0.433	0.049222
ACBD4	MGMT	0.433	0.049222
ACBD4	HERC1	0.434	0.048713
ACBD4	LEPR	0.434	0.048713
ACBD4	PERLD1	0.434	0.048713
ACBD4	ALAD	0.435	0.048208
ACBD4	DBNDD1	0.435	0.048208
ACBD4	GNMT	0.435	0.048208

ACBD4	HSF4	0.435	0.048208
ACBD4	SPR	0.435	0.048208
ACBD4	UGT2B15	0.435	0.048208
ACBD4	APOC1	0.436	0.047707
ACBD4	PQLC1	0.436	0.047707
ACBD4	ALDOB	0.437	0.047211
ACBD4	FCN2	0.437	0.047211
ACBD4	GFRA4	0.437	0.047211
ACBD4	GRHPR	0.437	0.047211
ACBD4	LPPR2	0.437	0.047211
ACBD4	RNF123	0.437	0.047211
ACBD4	HPX	0.438	0.046719
ACBD4	LARP4	0.438	0.046719
ACBD4	NR1I3	0.438	0.046719
ACBD4	PER1	0.438	0.046719
ACBD4	SERPING1	0.438	0.046719
ACBD4	TM7SF4	0.438	0.046719
ACBD4	E4F1	0.439	0.046231
ACBD4	LOC339457	0.439	0.046231
ACBD4	POU6F1	0.439	0.046231
ACBD4	GRPR	0.44	0.045748
ACBD4	KIF1B	0.44	0.045748
ACBD4	BHMT2	0.441	0.045269
ACBD4	ECHS1	0.441	0.045269
ACBD4	LANCL2	0.441	0.045269
ACBD4	NAT6	0.441	0.045269
ACBD4	SLC6A13	0.441	0.045269
ACBD4	SOX15	0.441	0.045269
ACBD4	BDH1	0.442	0.044794
ACBD4	CLDN17	0.442	0.044794
ACBD4	PPP2R5B	0.442	0.044794
ACBD4	TNFRSF12A	0.442	0.044794
ACBD4	LOC649115	0.443	0.044324
ACBD4	GLI3	0.444	0.043857
ACBD4	SAA4	0.444	0.043857
ACBD4	AGXT	0.445	0.043395
ACBD4	ATF7IP2	0.445	0.043395
ACBD4	BMP1	0.445	0.043395
ACBD4	SS18L1	0.445	0.043395
ACBD4	SULT1A1	0.445	0.043395
ACBD4	CDC37L1	0.446	0.042937
ACBD4	CSAD	0.446	0.042937
ACBD4	MGC4172	0.446	0.042937
ACBD4	OCEL1	0.446	0.042937
ACBD4	CES1	0.447	0.042483
ACBD4	MGAT4B	0.447	0.042483

ACBD4	PLCG2	0.447	0.042483
ACBD4	PNPLA2	0.447	0.042483
ACBD4	GRAMD1C	0.448	0.042033
ACBD4	MASP1	0.448	0.042033
ACBD4	CCDC25	0.449	0.041587
ACBD4	SOD1	0.449	0.041587
ACBD4	LOC200383	0.45	0.041145
ACBD4	MRPL34	0.45	0.041145
ACBD4	PNPLA4	0.45	0.041145
ACBD4	CCDC44	0.451	0.040707
ACBD4	SH3BGR	0.451	0.040707
ACBD4	STK11	0.451	0.040707
ACBD4	TCTA	0.451	0.040707
ACBD4	F9	0.452	0.040273
ACBD4	LLGL1	0.452	0.040273
ACBD4	GBA3	0.453	0.039843
ACBD4	NOS1	0.453	0.039843
ACBD4	TMEM16A	0.453	0.039843
ACBD4	UBOX5	0.453	0.039843
ACBD4	CLDN14	0.454	0.039417
ACBD4	CPB2	0.454	0.039417
ACBD4	GHR	0.454	0.039417
ACBD4	MYL5	0.454	0.039417
ACBD4	PBEF1	0.454	0.039417
ACBD4	BCKDHB	0.455	0.038995
ACBD4	FBXO31	0.455	0.038995
ACBD4	LIME1	0.455	0.038995
ACBD4	XDH	0.455	0.038995
ACBD4	PEMT	0.456	0.038576
ACBD4	PPP5C	0.456	0.038576
ACBD4	SLC22A14	0.456	0.038576
ACBD4	ZNF442	0.456	0.038576
ACBD4	DHRS12	0.457	0.038162
ACBD4	HADH	0.457	0.038162
ACBD4	CYP2C8	0.458	0.037751
ACBD4	FXR2	0.458	0.037751
ACBD4	RARA	0.458	0.037751
ACBD4	KIR3DX1	0.459	0.037344
ACBD4	OGFOD2	0.459	0.037344
ACBD4	PDE6G	0.459	0.037344
ACBD4	VRK3	0.459	0.037344
ACBD4	ACACB	0.46	0.036941
ACBD4	FBXO2	0.46	0.036941
ACBD4	PAX5	0.46	0.036941
ACBD4	TFR2	0.46	0.036941
ACBD4	SULT2A1	0.461	0.036541

ACBD4	ABCB11	0.462	0.036145
ACBD4	ABTB2	0.462	0.036145
ACBD4	ACAT1	0.462	0.036145
ACBD4	ASMTL	0.462	0.036145
ACBD4	HMGCL	0.462	0.036145
ACBD4	ROGDI	0.462	0.036145
ACBD4	C6	0.463	0.035753
ACBD4	SLC35D1	0.463	0.035753
ACBD4	AZGP1	0.464	0.035364
ACBD4	BCKDK	0.464	0.035364
ACBD4	EPB42	0.464	0.035364
ACBD4	KLK5	0.464	0.035364
ACBD4	CYB5A	0.465	0.034979
ACBD4	DIO1	0.465	0.034979
ACBD4	GCKR	0.465	0.034979
ACBD4	ECM2	0.466	0.034598
ACBD4	GENX-3414	0.466	0.034598
ACBD4	KHK	0.466	0.034598
ACBD4	PGM1	0.466	0.034598
ACBD4	SIRT2	0.466	0.034598
ACBD4	TMEM8	0.466	0.034598
ACBD4	C14orf172	0.467	0.03422
ACBD4	DUS1L	0.467	0.03422
ACBD4	PRB1	0.467	0.03422
ACBD4	ALDH5A1	0.468	0.033846
ACBD4	FARP2	0.468	0.033846
ACBD4	MPPED1	0.468	0.033846
ACBD4	OTC	0.468	0.033846
ACBD4	SLC27A2	0.468	0.033846
ACBD4	SORL1	0.468	0.033846
ACBD4	UGP2	0.468	0.033846
ACBD4	APOC3	0.469	0.033475
ACBD4	ARFRP1	0.469	0.033475
ACBD4	CRADD	0.47	0.033108
ACBD4	ELAVL3	0.47	0.033108
ACBD4	SMCP	0.47	0.033108
ACBD4	CTPS	0.471	0.032744
ACBD4	CYP2A13	0.471	0.032744
ACBD4	HAO2	0.471	0.032744
ACBD4	MAOA	0.471	0.032744
ACBD4	TBXA2R	0.471	0.032744
ACBD4	AASS	0.472	0.032383
ACBD4	ACYP2	0.472	0.032383
ACBD4	ANGPTL4	0.472	0.032383
ACBD4	C2orf18	0.472	0.032383
ACBD4	DUX1	0.472	0.032383

ACBD4	ZBTB16	0.472	0.032383
ACBD4	ATP6V0E2	0.473	0.032026
ACBD4	C16orf58	0.473	0.032026
ACBD4	IGFALS	0.473	0.032026
ACBD4	MSRA	0.473	0.032026
ACBD4	PCTP	0.473	0.032026
ACBD4	ARSA	0.474	0.031673
ACBD4	HYAL1	0.474	0.031673
ACBD4	ALAS1	0.475	0.031322
ACBD4	PIPOX	0.475	0.031322
ACBD4	DOC2B	0.476	0.030976
ACBD4	SCN4A	0.476	0.030976
ACBD4	ALDH6A1	0.477	0.030632
ACBD4	HPR	0.477	0.030632
ACBD4	KLKB1	0.477	0.030632
ACBD4	LOC222070	0.477	0.030632
ACBD4	CRYL1	0.478	0.030291
ACBD4	ASB13	0.479	0.029954
ACBD4	PSKH1	0.479	0.029954
ACBD4	SLC25A20	0.479	0.029954
ACBD4	DEXI	0.48	0.02962
ACBD4	LOC643641	0.481	0.02929
ACBD4	TOLLIP	0.481	0.02929
ACBD4	TST	0.481	0.02929
ACBD4	VIPR1	0.481	0.02929
ACBD4	CHRNA3	0.482	0.028962
ACBD4	EPHX1	0.482	0.028962
ACBD4	C11orf32	0.483	0.028638
ACBD4	CDK5	0.483	0.028638
ACBD4	DAK	0.483	0.028638
ACBD4	HAAO	0.483	0.028638
ACBD4	ZMYM6	0.483	0.028638
ACBD4	C8B	0.484	0.028317
ACBD4	FLJ21736	0.484	0.028317
ACBD4	TMEM142C	0.484	0.028317
ACBD4	POR	0.485	0.027999
ACBD4	CD14	0.486	0.027684
ACBD4	GOT2	0.486	0.027684
ACBD4	GPT	0.486	0.027684
ACBD4	DECR2	0.487	0.027372
ACBD4	EPOR	0.487	0.027372
ACBD4	MLYCD	0.487	0.027372
ACBD4	MPDZ	0.487	0.027372
ACBD4	PLD2	0.487	0.027372
ACBD4	ABHD6	0.488	0.027063
ACBD4	NNT	0.488	0.027063

ACBD4	PRKAG2	0.488	0.027063
ACBD4	HSD17B4	0.489	0.026757
ACBD4	MPG	0.489	0.026757
ACBD4	RAB17	0.489	0.026757
ACBD4	SLC25A10	0.49	0.026454
ACBD4	SLCO2B1	0.49	0.026454
ACBD4	UQCRQ	0.49	0.026454
ACBD4	GAS8	0.491	0.026154
ACBD4	COPZ2	0.492	0.025857
ACBD4	FLJ21865	0.492	0.025857
ACBD4	FTS	0.492	0.025857
ACBD4	PON3	0.492	0.025857
ACBD4	SLC6A1	0.493	0.025563
ACBD4	SUCLG2	0.493	0.025563
ACBD4	CBS	0.494	0.025272
ACBD4	MAP3K14	0.494	0.025272
ACBD4	ZG16	0.494	0.025272
ACBD4	CRYAA	0.495	0.024983
ACBD4	FUT7	0.495	0.024983
ACBD4	LOC283537	0.495	0.024983
ACBD4	LOC654056	0.495	0.024983
ACBD4	RBKS	0.495	0.024983
ACBD4	TGM5	0.495	0.024983
ACBD4	CXorf1	0.496	0.024698
ACBD4	NPPA	0.497	0.024415
ACBD4	TPMT	0.497	0.024415
ACBD4	DCI	0.498	0.024135
ACBD4	F8	0.498	0.024135
ACBD4	HDAC6	0.498	0.024135
ACBD4	OGDHL	0.498	0.024135
ACBD4	PON1	0.498	0.024135
ACBD4	FTCD	0.499	0.023858
ACBD4	HGD	0.499	0.023858
ACBD4	C1orf160	0.5	0.023584
ACBD4	DHRS4	0.5	0.023584
ACBD4	GFRA1	0.5	0.023584
ACBD4	HRSP12	0.5	0.023584
ACBD4	FETUB	0.501	0.023313
ACBD4	CYP3A5	0.502	0.023044
ACBD4	GCGR	0.502	0.023044
ACBD4	GPLD1	0.502	0.023044
ACBD4	PMS2L11	0.502	0.023044
ACBD4	RANBP10	0.504	0.022514
ACBD4	TSC2	0.504	0.022514
ACBD4	JMJD5	0.505	0.022253
ACBD4	C9orf95	0.506	0.021995

ACBD4	SDC1	0.506	0.021995
ACBD4	SEC31B	0.506	0.021995
ACBD4	TG	0.506	0.021995
ACBD4	CCL16	0.507	0.02174
ACBD4	LGP2	0.508	0.021487
ACBD4	NDUFS7	0.508	0.021487
ACBD4	C16orf45	0.509	0.021236
ACBD4	CCS	0.509	0.021236
ACBD4	KIAA0265	0.509	0.021236
ACBD4	PGRMC1	0.509	0.021236
ACBD4	RAB40C	0.509	0.021236
ACBD4	SERPINC1	0.51	0.020988
ACBD4	CHRNB2	0.511	0.020743
ACBD4	COQ3	0.511	0.020743
ACBD4	EHHADH	0.511	0.020743
ACBD4	NIT1	0.511	0.020743
ACBD4	PECI	0.511	0.020743
ACBD4	THRA	0.511	0.020743
ACBD4	TTC31	0.511	0.020743
ACBD4	ZHX3	0.511	0.020743
ACBD4	CYP3A43	0.512	0.0205
ACBD4	SPSB3	0.512	0.0205
ACBD4	AR	0.513	0.02026
ACBD4	CAT	0.513	0.02026
ACBD4	CTF1	0.513	0.02026
ACBD4	CYP4F12	0.514	0.020022
ACBD4	HAO1	0.514	0.020022
ACBD4	HSD17B6	0.514	0.020022
ACBD4	OASL	0.514	0.020022
ACBD4	CTH	0.515	0.019787
ACBD4	MGC10334	0.515	0.019787
ACBD4	DKFZP564J102	0.516	0.019554
ACBD4	FDX1	0.516	0.019554
ACBD4	FLJ10986	0.516	0.019554
ACBD4	IPO13	0.516	0.019554
ACBD4	C11orf71	0.517	0.019323
ACBD4	GCDH	0.517	0.019323
ACBD4	SDS	0.517	0.019323
ACBD4	ABCC6	0.518	0.019095
ACBD4	MTHFD1	0.518	0.019095
ACBD4	REPS2	0.518	0.019095
ACBD4	F11	0.519	0.018869
ACBD4	GADD45A	0.519	0.018869
ACBD4	CBR1	0.52	0.018645
ACBD4	SLC16A2	0.52	0.018645
ACBD4	SHMT1	0.521	0.018424

ACBD4	CPT2	0.522	0.018205
ACBD4	CYP4A11	0.522	0.018205
ACBD4	ACADL	0.523	0.017989
ACBD4	CRAT	0.523	0.017989
ACBD4	C8A	0.524	0.017774
ACBD4	KIAA0251	0.524	0.017774
ACBD4	LONP2	0.524	0.017774
ACBD4	NCR2	0.524	0.017774
ACBD4	RPIB9	0.524	0.017774
ACBD4	CRY2	0.526	0.017352
ACBD4	BAAT	0.527	0.017145
ACBD4	BLVRB	0.527	0.017145
ACBD4	IVD	0.527	0.017145
ACBD4	KIAA1772	0.527	0.017145
ACBD4	LRP16	0.527	0.017145
ACBD4	PNPO	0.527	0.017145
ACBD4	FBP1	0.528	0.016939
ACBD4	C21orf6	0.529	0.016736
ACBD4	DHRS3	0.529	0.016736
ACBD4	EPHX2	0.529	0.016736
ACBD4	LHPP	0.529	0.016736
ACBD4	RSAD1	0.529	0.016736
ACBD4	TAT	0.531	0.016335
ACBD4	TMPRSS2	0.531	0.016335
ACBD4	IGFBP4	0.532	0.016138
ACBD4	PCAF	0.532	0.016138
ACBD4	TCEA2	0.532	0.016138
ACBD4	BHMT	0.533	0.015944
ACBD4	BPHL	0.533	0.015944
ACBD4	METTL7A	0.533	0.015944
ACBD4	SCP2	0.534	0.015751
ACBD4	AQP9	0.535	0.01556
ACBD4	CYP4F2	0.535	0.01556
ACBD4	SLC17A4	0.535	0.01556
ACBD4	ACY1	0.536	0.015371
ACBD4	FAM82C	0.539	0.014817
ACBD4	MASP2	0.539	0.014817
ACBD4	NR1I2	0.539	0.014817
ACBD4	BTD	0.54	0.014636
ACBD4	CUTL2	0.541	0.014458
ACBD4	HSD11B1	0.541	0.014458
ACBD4	APBB3	0.544	0.013933
ACBD4	PEBP1	0.545	0.013761
ACBD4	SELENBP1	0.545	0.013761
ACBD4	RARG	0.546	0.013592
ACBD4	SRD5A1	0.546	0.013592

ACBD4	CYP2J2	0.549	0.013095
ACBD4	PDK2	0.549	0.013095
ACBD4	RDH16	0.55	0.012933
ACBD4	STARD5	0.55	0.012933
ACBD4	FLJ20581	0.551	0.012773
ACBD4	CYP4F3	0.552	0.012614
ACBD4	HSD17B8	0.552	0.012614
ACBD4	CPN2	0.553	0.012457
ACBD4	RGN	0.555	0.012149
ACBD4	GSTZ1	0.557	0.011847
ACBD4	PINK1	0.557	0.011847
ACBD4	MUCDHL	0.558	0.011699
ACBD4	MMACHC	0.559	0.011552
ACBD4	PCK2	0.56	0.011407
ACBD4	CYP4F11	0.561	0.011264
ACBD4	SORBS2	0.561	0.011264
ACBD4	KIAA0427	0.562	0.011122
ACBD4	ABCA6	0.563	0.010982
ACBD4	RAB26	0.565	0.010706
ACBD4	TNFAIP1	0.566	0.010571
ACBD4	CIDEB	0.567	0.010437
ACBD4	IL17RC	0.567	0.010437
ACBD4	MYCL1	0.567	0.010437
ACBD4	RDH5	0.567	0.010437
ACBD4	AFM	0.569	0.010173
ACBD4	FAHD2A	0.569	0.010173
ACBD4	HPD	0.569	0.010173
ACBD4	SLC22A1	0.573	0.009664
ACBD4	ABAT	0.575	0.009418
ACBD4	DCXR	0.575	0.009418
ACBD4	FAH	0.575	0.009418
ACBD4	ALDH2	0.576	0.009297
ACBD4	GYS2	0.578	0.00906
ACBD4	NAT2	0.58	0.008827
ACBD4	ETNK2	0.581	0.008713
ACBD4	CYP2A6	0.583	0.008489
ACBD4	HMOX2	0.583	0.008489
ACBD4	PAFAH2	0.587	0.008056
ACBD4	APOC4	0.588	0.007951
ACBD4	LOC123876	0.588	0.007951
ACBD4	ETFDH	0.589	0.007847
ACBD4	SIRT3	0.589	0.007847
ACBD4	SUOX	0.589	0.007847
ACBD4	ABCB4	0.59	0.007744
ACBD4	CCL14	0.591	0.007643
ACBD4	CRYM	0.595	0.007249

ACBD4	FAAH	0.597	0.007058
ACBD4	SLC28A1	0.599	0.006873
ACBD4	COQ9	0.601	0.006692
ACBD4	ELK1	0.602	0.006603
ACBD4	AKR7A3	0.605	0.006342
ACBD4	PXMP2	0.612	0.005769
ACBD4	TREX1	0.617	0.005389
ACBD4	POL3S	0.618	0.005316
ACBD4	AGXT2L1	0.619	0.005244
ACBD4	GPD1	0.62	0.005173
ACBD4	HAGH	0.622	0.005032
ACBD4	GSTK1	0.625	0.004828
ACBD4	ACAA2	0.626	0.004762
ACBD4	DHTKD1	0.627	0.004697
ACBD4	CES2	0.631	0.004443
ACBD4	GLYAT	0.633	0.004321
ACBD4	PFKFB1	0.633	0.004321
ACBD4	ECHDC2	0.641	0.003862
ACBD4	DHRS1	0.643	0.003754
ACBD4	SLC27A5	0.648	0.003497
ACBD4	DAO	0.649	0.003448
ACBD4	SLC10A1	0.661	0.002902
ACBD4	SEC14L2	0.662	0.00286
ACBD4	FMO4	0.669	0.002583
ACBD4	ACBD4	1	7.41E-06

Table S4. GO term analysis results of ACBD4 and its co-expressed genes

Term	Count	%	P Value	Genes
GO:0055114~oxidation-reduction process	63	12.70161	2.18E-19	DHRS12, AKR7A3, ACADL, SPR, NNT, OGFOD2, NOS1, LBR, AASS, GSTK1, CBR1, HGD, DCXR, RSAD1, CYP4A11, CYP3A43, DIO1, BCKDHB, PIPOX, CYP2A6, POR, F8, NDUFS7, MTHFD1, BDH1, MTHFD2, FDX1, BLVRB, RDH5, HPD, MAOA, HAAO, HSD17B6, HSD17B8, HSD11B1, CYP2A13, CBS, RDH16, PNPO, CRYM, DECR2, XDH, CYP2J2, CYB5A, SRD5A1, CYP4F2, CYP4F3, FMO4, DHRS1, CYP4F11, CYP4F12, DHRS3, DHRS4, SOD1, MSRA, GRHPR, CYP2C8, ALDH6A1, CCS, DAO, CRYL1, DUS1L, MMACHC
GO:0005829~cytosol	166	33.46774	1.67E-17	RPL4, NUP107, TPMT, UBE2D1, PEBP1, BUB1B, OGDHL, GBA3, SMC4, RPL9, RPL6, ACTG1, RPL7, EEF1B2, STK11, AKR7A3, HERC1, SNRPD2, SNRPD1, RPL37, FBXO5, SNRPD3, KPNA2, RPL39, GTSE1, RPS10, GYG1, SULT2A1, IER3, STARD5, CEP135, TPM4, HGD, RPS7, FBXO2, RPL23, RPL22, RPS6, UBE2E1, TSC2, MYL5, AR, MTHFD1, MTHFD2, GPD1, SNRPG, RPL24, TFAM, SNRPF, HPD, CES1, PFKFB1, KHDRBS1, SET, SHMT1, HIF1A, ACACB, SULT1A1, CCNB1, PNPO, PLCG2, LHPP, GCKR, XRCC6, CRADD, SMURF2, EPHX2, TREX1, ZBTB16, CIDEB, FBXO31, CCT6A, MSRA, GRHPR, KIF18A, BHMT, PPP5C, DAO, ARPC2, CDK5, NAT2, TOLLIP, RANBP10, PDCL, CRYL1, IARS, DUS1L, SAE1, CALM2, MAP3K14, RPS24, ACY1, THRA, TAT, PRKAG2, GPT, PCTP, KIF11, HK2, FTCD, GLI3, KIF15, OASL, KHK, DHTKD1, GYS2, ALAD, SPR, YWHAQ, SEC61G, NOS1, PGM1, CCT3, ACTR3, CBR1, PPP1R12A, SPHK1, BHMT2, PPP2R5B, COPZ2, RPL13A, RPS3A, BAAT, GMIP, SIRT2, EHHADH, TRAF5, CAT, PELI1, LANCL2, RGN, BLVRB, PABPC1, HAGH, ALDOB, EEF1E1, MAPRE1, FBP1, HAAO, NR1I3, HDAC6, SELENBP1, ARFRP1, UGP2, CBS, RPS3, NUP43, XDH, RPL17, SH3BGR, FARP2, NPM1, PTGES3, FAH, GNMT, SOD1, GSTZ1, CCS, PINK1, ETNK2, CTH, PNPLA4, MMACHC, RAN, PNPLA2, LIMS1
GO:0070062~extracellular exosome	148	29.83871	3.09E-17	RPL4, FCN2, ACAA2, TPMT, PEBP1, ABAT, ACTG1, RPL7, STK11, AKR7A3, SCP2, SNRPD2, SNRPD3, RPS10, GYG1, ARSA, GSTK1, TPM4, HGD, RPS7, FBXO2, RPL23, RPL22, SLC6A13, AZGP1, BTD, MTHFD1, NCL, SUB1, GPD1, RPL24, FETUB, SERPING1, PHIP, MASP2, IGFALS, HPD, SLC27A2, GPLD1, CES2, CPB2, SHMT1, ABCB4, CCDC25, ABHD6, GLYAT, SLC1A5, HPR, ACAT1, SEC14L2, HPX, FXR2, C6, PNPO, PLCG2, CD14, HAO2, PCK2, CYP2J2, EPHX2, GOT2, CCT6A, MSRA, GRHPR,

				BHMT, ALDH6A1, ARPC2, NACA, TOLLIP, CRYL1, SDC1, ANP32B, IARS, HIST1H4C, NIT1, CALM2, ACY1, GPT, LAMC1, C8B, C8A, FTCD, KHK, ALAD, SPR, ALDH2, YWHAQ, HYAL1, CLIC1, CTSC, PGM1, CCT3, ACTR3, CBR1, BHMT2, DCXR, CYP4A11, RPS3A, GFRA1, CKAP4, GFRA4, F9, TST, CAT, BLVRB, PABPC3, PABPC1, HAGH, ALDOB, EEF1E1, CRYAA, PTMA, FBP1, RBKS, PON3, RALA, ECHS1, SERPINC1, HAAO, PON1, SAA4, AFM, TMPRSS2, ABCB11, BPHL, CPN2, SELENBP1, PGRMC1, UGP2, RPS3, METTL7A, CRYM, GALNT7, CYB5A, MARCKSL1, PTGES3, F11, APOC3, FAH, SORL1, DHRS4, SOD1, MARCKS, CTH, APOC1, RAB17, KLKB1, RAN
GO:0005759~mitochondrial matrix	42	8.467742	1.16E-16	GCDH, ALAS1, ECHS1, ETFDH, OGDHL, ABAT, GLYAT, BPHL, HSD17B8, ACAT1, DHTKD1, HMGCL, ALDH2, ACADL, RPS3, MLYCD, HADH, PDK2, AASS, PCK2, GSTK1, BCKDHB, GOT2, SUOX, SIRT3, SOD1, BCKDK, COQ3, ALDH6A1, ALDH5A1, BTD, NDUFS7, TST, BDH1, MTHFD2, IVD, FDX1, SUCLG2, TFAM, HAGH, AGXT, OTC
GO:0005739~mitochondrion	81	16.33065	4.47E-12	ACAA2, ALAS1, TAT, ABAT, OGDHL, MRPL34, ELK1, DHTKD1, GHR, STK11, ACADL, SCP2, YWHAQ, CPT2, NNT, KIF1B, NOS1, MRPL9, MLYCD, HADH, CLIC1, SOX4, PDK2, AASS, GSTK1, SDS, STARD5, RSAD1, BCKDHB, ACYP2, SIRT3, POR, ALDH5A1, MTHFD1, TST, BDH1, MTHFD2, IVD, EHHADH, CRY2, GPD1, FDX1, CAT, SUCLG2, TFAM, SLC27A2, GCDH, ECHS1, MAOA, SHMT1, HSD17B4, ABHD6, GLYAT, BPHL, ACACB, ACAT1, HMGCL, SLC25A20, CRYM, HAO2, PCK2, SMCP, GCKR, GOT2, COQ9, SUOX, DHRS4, SOD1, GSTZ1, BCKDK, MSRA, COQ3, ALDH6A1, PINK1, UQCRQ, PNPLA4, ECHDC2, NIT1, CRAT, MMACHC, OTC
GO:0005782~peroxisomal matrix	15	3.024194	8.39E-12	PIPOX, HSD17B4, BAAT, GRHPR, DAO, SCP2, EHHADH, CAT, LONP2, HAO1, MLYCD, CRYM, AGXT, CRAT, HAO2
GO:0031090~organelle membrane	19	3.830645	1.20E-11	CYP2J2, FAAH, SRD5A1, CYP4F2, FBXO2, EPHX1, UGT2B15, CYP4A11, CYP3A43, CYP4F3, CYP4F11, FMO4, CYP3A5, CYP4F12, PGRMC1, CYP2A6, CYP2C8, CYP2A13, RDH16
GO:0005777~peroxisome	19	3.830645	2.72E-10	GSTK1, EPHX2, PIPOX, HSD17B4, BAAT, DHRS4, SOD1, HMGCL, DAO, SCP2, EHHADH, CAT, LONP2, HAO1, MLYCD, AGXT, CRAT, XDH, HAO2
GO:0019083~viral transcription	20	4.032258	3.29E-10	RPL4, NUP107, RPS7, RPL23, RPL22, RPS6, RPL13A, RPS3A, RPL9, RPL6, RPL7, NUP62, RPS3, RPL24, NUP43, RPL37, RPL39, RPL17, RPS10, RPS24

GO:0006805~xenobiotic metabolic process	17	3.427419	4.48E-10	CYP2J2, ACY1, EPHX2, EPHX1, UGT2B15, NR1I2, GLYAT, CYP3A5, BPHL, SULT1A1, POR, CYP2C8, AKR7A3, CYP2A13, NAT2, CES2, CES1
GO:0006614~SRP-dependent cotranslational protein targeting to membrane	17	3.427419	7.89E-09	RPL4, RPS7, RPL23, RPL22, RPS6, RPL13A, RPS3A, RPL9, RPL6, RPL7, RPS3, RPL24, RPL37, RPL39, RPL17, RPS10, RPS24
GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	18	3.629032	4.09E-08	RPL4, RPS7, RPL23, RPL22, RPS6, RPL13A, RPS3A, RPL9, RPL6, RPL7, RPS3, RPL24, PABPC1, RPL37, RPL39, RPL17, RPS10, RPS24
GO:0020037~heme binding	19	3.830645	5.69E-08	CYP2J2, CYB5A, CYP4F2, CYP4A11, CYP3A43, CYP4F3, SUOX, CYP4F11, CYP3A5, CYP4F12, PGRMC1, CYP2A6, CYP2C8, CYP2A13, CBS, CAT, NOS1, KLKB1, HMOX2
GO:0006413~translational initiation	18	3.629032	3.31E-07	RPL4, RPS7, RPL23, RPL22, RPS6, RPL13A, RPS3A, RPL9, RPL6, RPL7, RPS3, RPL24, PABPC1, RPL37, RPL39, RPL17, RPS10, RPS24
GO:0019373~epoxygenase P450 pathway	8	1.612903	3.37E-07	CYP2J2, CYP2C8, CYP2A6, CYP2A13, CYP4F2, EPHX2, CYP4A11, CYP4F12
GO:0016705~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	12	2.419355	4.47E-07	CYP2J2, CYP2C8, CYP2A6, CYP4F2, CYP3A43, CYP4F3, CYP4A11, OGFOD2, CYP4F11, CYP4F12, CYP3A5, KLKB1
GO:0030529~intracellular ribonucleoprotein complex	17	3.427419	7.07E-07	RPL4, NPM1, CPSF6, SSB, RPS7, DDX1, RPL22, RPS6, RPL13A, RPS3A, RPL7, SNRPD1, NCL, NUP62, RPS3, SNRPA1, PABPC1
GO:0016020~membrane	96	19.35484	1.13E-06	RPL4, NUP107, KIF11, DOC2B, SLC6A1, BZW2, C8B, C8A, RPL9, HK2, RPL6, KIF15, LRRC1, OASL, ACTG1, RPL7, STK11, SCP2, YWHAQ, HERC1, NNT, SLCO2B1, SEC61G, LEPR, LONP2, KPNA2, CLIC1, GYG1, GTSE1, RPS10, LBR, CTSC, CEP55, ACTR3, GSTK1, TPM4, RPS7, MMD, RPL23, RPS6, TSC2, RPL13A, DDX50, CKAP4, GNL3, POR, MTHFD1, NCL, CAT, RPL24, PABPC1, KHDRBS1, DDX1, ABCB4, SLC22A1, HSD17B4, SLC1A5, ABCB11, SLC7A1, SELENBP1, HSD11B1, ARFRP1, PGRMC1, CCNB1, FXR2, FUT7, RPS3, METTL7A, C16ORF58, ATP6V0E2, HMOX2, SLC17A4, GALNT7, CYB5A, NPM1, XRCC6, CPSF6, MGMT, GCGR, F11, NAP1L1, LARP4, SORL1, MSRA, PINK1, CDK5, MGAT4B, PXMP2, PNPLA4, SDC1, IARS, HIST1H4C, SLC28A1, RAN, RPS24, PNPLA2
GO:0009055~electron carrier activity	14	2.822581	1.34E-06	GCDH, SRD5A1, HAAO, ETFDH, HSD17B6, DHRS3, POR, AKR7A3, ACADL, ALDH2,

				IVD, FDX1, RDH16, XDH
GO:0022625~cytosolic large ribosomal subunit	12	2.419355	1.68E-06	RPL4, FXR2, RPL23, RPL22, RPL13A, RPL24, RPL37, RPL9, RPL39, RPL17, RPL6, RPL7
GO:0008392~arachidonic acid epoxygenase activity	7	1.41129	1.94E-06	CYP2J2, CYP2C8, CYP2A6, CYP2A13, CYP4F2, CYP4A11, CYP4F12
GO:0006572~tyrosine catabolic process	5	1.008065	3.09E-06	GSTZ1, HGD, TAT, FAH, HPD
GO:0006635~fatty acid beta-oxidation	10	2.016129	3.16E-06	ACAA2, ECHS1, CPT2, ACADL, EHHADH, ECHDC2, HSD17B4, HADH, SLC27A2, ACAT1
GO:0006412~translation	23	4.637097	3.25E-06	RPL4, RPS7, RPL23, RPL22, RPS6, RPL13A, RPS3A, GTF2H2, MRPL34, RPL9, RPL6, RPL7, NACA, RPS3, RPL24, SLC25A10, MRPL9, SLC25A20, RPL37, RPL39, RPL17, RPS10, RPS24
GO:0030170~pyridoxal phosphate binding	11	2.217742	3.73E-06	SDS, ALAS1, CBS, TAT, CTH, SHMT1, GOT2, ABAT, GPT, CSAD, AGXT
GO:0003735~structural constituent of ribosome	21	4.233871	4.95E-06	RPL4, RPS7, RPL23, RPL22, RPS6, RPL13A, RPS3A, MRPL34, RPL9, RPL6, RPL7, RPS3, RPL24, SLC25A10, MRPL9, SLC25A20, RPL37, RPL39, RPL17, RPS10, RPS24
GO:0044822~poly(A) RNA binding	59	11.89516	6.08E-06	RPL4, TOP2A, ACAA2, HMGB2, PEBP1, RPL6, OASL, RPL7, SNRPD2, SNRPD1, SUMO2, SNRPD3, MRPL9, KPNA2, RPS10, LBR, CCT3, RPS7, RPL23, RPL22, RPS6, RPL13A, RPS3A, DDX50, CKAP4, GNL3, DKC1, EWSR1, SUB1, NCL, SNRPG, RPL24, TFAM, SNRPA1, PABPC1, MAPRE1, KHDRBS1, HDAC2, DDX1, FXR2, RPS3, RPL17, ZC3H15, NPM1, XRCC6, CPSF6, SSB, GOT2, SORBS2, NAP1L1, LARP4, CCT6A, ALDH6A1, FUBP1, ESF1, UBAP2, HIST1H4C, RAN, RPS24
GO:0005506~iron ion binding	17	3.427419	6.67E-06	CYP2J2, HAAO, CYP4F2, CYP4A11, CYP3A43, CYP4F3, CYP4F11, CYP3A5, CYP4F12, CYP2A6, CYP2C8, CYP2A13, FDX1, OGFOD2, NOS1, XDH, KLKB1
GO:0005840~ribosome	17	3.427419	9.79E-06	RPL4, RPS7, RPL23, RPL22, RPS6, RPL13A, RPS3A, MRPL34, RPL9, RPL6, RPL7, RPS3, RPL24, MRPL9, RPL37, RPS10, RPS24
GO:0008202~steroid metabolic process	9	1.814516	2.35E-05	SULT1A1, CYP2C8, CYP2A6, UGT2B15, NR1I2, HSD17B6, CYP3A5, DHRS4, SULT2A1
GO:0005102~receptor binding	26	5.241935	2.41E-05	HSD17B4, HMGCL, SCP2, NPPA, LONP2, HAO1, MLYCD, DECR2, HAO2, GSTK1, SEMA4D, IGFBP4, EPHX2, PIPOX, GFRA1, BAAT, IL17RC, DHRS4, AR, DAO, EHHADH, CAT, RARA, AGXT, CRAT, SLC27A2
GO:0006094~gluconeogenesis	9	1.814516	2.80E-05	PFKFB1, SDS, GPD1, GOT2, SLC25A10, ALDOB, FBP1, PGM1, PCK2
GO:0004497~monooxygenase activity	10	2.016129	3.21E-05	CYP2J2, CYP2C8, CYP4F2, CYP3A43, CYP4F3, CYP4A11, CYP4F11, CYP4F12,

				CYP3A5, KLKB1
GO:0003857~3-hydroxyacyl-CoA dehydrogenase activity	5	1.008065	3.96E-05	EHHADH, CRYL1, HSD17B4, HADH, HSD17B8
GO:0045471~response to ethanol	13	2.620968	4.11E-05	CHRNB2, ARSA, MGMT, GOT2, ABAT, SOD1, EEF1B2, ALAD, TBXA2R, CAT, RARA, PEMT, CD14
GO:0016491~oxidoreductase activity	18	3.629032	5.29E-05	DHRS12, MAOA, DCXR, ETFDH, PIPOX, HSD17B4, HSD17B6, SUOX, DHRS1, CYP3A5, HSD11B1, POR, F8, BDH1, ALDH2, HAO2, MMACHC, AASS
GO:0030532~small nuclear ribonucleoprotein complex	6	1.209677	6.27E-05	SNRPD2, SNRPD1, SNRPG, SNRPA1, SNRPD3, SNRPF
GO:0046487~glyoxylate metabolic process	7	1.41129	7.06E-05	GRHPR, DAO, BCKDHB, HAO1, AGXT, GNMT, DHTKD1
GO:0050051~leukotriene-B4 20-monooxygenase activity	4	0.806452	8.67E-05	CYP4F2, CYP4F3, CYP4A11, CYP4F12
GO:0008152~metabolic process	16	3.225806	8.74E-05	ARSA, ACAA2, EPHX2, UGT2B15, AQP9, BCKDHB, FAHD2A, ACAT1, GRHPR, UGP2, SCP2, NAT2, EHHADH, SUCLG2, ECHDC2, CES1
GO:0036101~leukotriene B4 catabolic process	4	0.806452	8.81E-05	CYP4F2, CYP4F3, CYP4A11, CYP4F12
GO:0017144~drug metabolic process	7	1.41129	8.86E-05	CBR1, CYP2C8, CYP2A6, CYP4F2, EPHX2, FMO4, CYP4F12
GO:0005615~extracellular space	60	12.09677	1.10E-04	ECM2, HMGB2, PRKAG2, GPT, LAMC1, C8B, C8A, ACTG1, GHR, ALAD, HYAL1, NPPA, RPL39, CLIC1, CTSC, ARSA, IGFBP4, LIME1, DKK1, GFRA4, GNL3, AZGP1, F8, BTD, F9, TST, MTHFD2, CAT, SERPING1, FETUB, MASP1, IGFALS, ANGPTL4, GPLD1, CES2, CES1, CCL14, PON3, CPB2, CTF1, SERPINC1, SAA4, PON1, AFM, KLK5, SELENBP1, HPX, CD14, XDH, CCL16, SEMA4D, CCL20, F11, APOC3, SORL1, SOD1, BMP1, TG, ESF1, KLKB1
GO:0006364~rRNA processing	18	3.629032	1.29E-04	RPL4, RPS7, RPL23, RPL22, RPS6, RPL13A, RPS3A, RPL9, RPL6, RPL7, DKC1, RPS3, RPL24, RPL37, RPL39, RPL17, RPS10, RPS24
GO:0009636~response to toxic substance	11	2.217742	1.40E-04	PON3, MGMT, EPHX2, EPHX1, PON1, SDC1, GLYAT, SLC6A1, BPHL, HDAC6, CES1
GO:0005687~U4 snRNP	5	1.008065	1.42E-04	SNRPD2, SNRPD1, SNRPG, SNRPD3, SNRPF
GO:0005925~focal adhesion	25	5.040323	1.42E-04	RPL4, RALA, RPL9, RPL6, ACTG1, RPL7, YWHAQ, RPS3, RPS10, ACTR3, NPM1, PPP1R12A, TPM4, RPS7, RPL23, RPL22, RPL13A, SORBS2, RPS3A, MARCKS, ARPC2,

				CAT, SDC1, PABPC1, LIMS1
GO:0000062~fatty-acyl-CoA binding	7	1.41129	1.61E-04	HMGCL, GCDH, ALDH6A1, ACBD4, ACADL, SCP2, IVD
GO:0006559~L-phenylalanine catabolic process	5	1.008065	1.78E-04	GSTZ1, HGD, TAT, FAH, HPD
GO:0042803~protein homodimerization activity	39	7.862903	2.07E-04	TOP2A, PON3, SHMT1, PON1, SLC22A1, HSD17B4, ABAT, ACAT1, RPL7, GHR, GYS2, HMGCL, FXR2, CBS, TDG, CRYM, XDH, PDK2, LHPP, NPM1, ZHX3, SDS, EPHX2, TREX1, ZBTB16, GOT2, TSC2, ARID3A, COQ9, SOD1, GSTZ1, GRHPR, ALDH5A1, GPD1, CAT, CRYL1, MASP1, AGXT, MMACHC
GO:0034709~methylosome	5	1.008065	2.09E-04	SNRPD2, SNRPD1, SNRPG, SNRPD3, SNRPF
GO:0006699~bile acid biosynthetic process	6	1.209677	2.48E-04	SCP2, HSD17B4, ABCB11, BAAT, SLC27A2, SLC27A5
GO:0051289~protein homotetramerization	9	1.814516	2.72E-04	ALDH5A1, ACADL, CTH, SHMT1, DCXR, CAT, ACACB, FBP1, GNMT
GO:0034715~pICln-Sm protein complex	4	0.806452	3.55E-04	SNRPD2, SNRPD1, SNRPD3, SNRPF
GO:0050661~NADP binding	7	1.41129	3.90E-04	POR, SPR, NNT, CAT, NOS1, CRYM, FMO4
GO:0050660~flavin adenine dinucleotide binding	9	1.814516	4.12E-04	GCDH, POR, ACADL, IVD, ETFDH, DUS1L, NOS1, FMO4, XDH
GO:0010181~FMN binding	5	1.008065	6.60E-04	POR, PNPO, HAO1, NOS1, HAO2
GO:1990446~U1 snRNP binding	4	0.806452	7.12E-04	SNRPD2, SNRPD1, SNRPG, SNRPD3
GO:0046500~S-adenosylmethionine metabolic process	4	0.806452	7.23E-04	BHMT, BHMT2, PEMT, GNMT
GO:0070330~aromatase activity	6	1.209677	8.35E-04	CYP2J2, CYP2C8, CYP2A13, CYP3A43, CYP4F12, CYP3A5
GO:0003824~catalytic activity	15	3.024194	8.97E-04	ARSA, ALAS1, EPHX2, BCKDHB, HSD17B6, FAHD2A, FTCD, PLD2, GSTZ1, ALAD, EHHADH, LANCL2, SUCLG2, ECHDC2, DUS1L
GO:0034719~SMN-Sm protein complex	5	1.008065	9.02E-04	SNRPD2, SNRPD1, SNRPG, SNRPD3, SNRPF
GO:0005789~endoplasmic reticulum membrane	40	8.064516	9.30E-04	FAAH, SLC35D1, CYP3A5, PLD2, HSD11B1, PGRMC1, CYP2A13, SEC61G, RDH16, HMOX2, SEC31B, PSKH1, CYP2J2, CYB5A, SRD5A1, TREX1, CYP4F2, EPHX1, DIO1, UGT2B15, CYP4F3, CYP4A11, CYP3A43, ABCC6, COPZ2, FMO4, CYP4F11, CYP4F12, CKAP4, DHRS3, DHRS4, POR, CYP2A6, CYP2C8, RDH5, PEMT, HPD, SLC27A2,

				SLC27A5, PNPLA2
GO:0016655~oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor	4	0.806452	0.001116	CBR1, NDUFS7, DCXR, DHRS4
GO:0046951~ketone body biosynthetic process	4	0.806452	0.001133	HMGCL, BDH1, SLC27A5, ACAT1
GO:0019899~enzyme binding	21	4.233871	0.00127	TOP2A, CYB5A, HDAC2, CBX3, GOT2, PEBP1, HIF1A, HDAC6, ACAT1, SIRT3, AR, POR, CYP2A6, CBS, EHHADH, CAT, RPS3, RARA, LONP2, SNRPD3, SLC27A2
GO:0005685~U1 snRNP	5	1.008065	0.001408	SNRPD2, SNRPD1, SNRPG, SNRPD3, SNRPF
GO:0007597~blood coagulation, intrinsic pathway	5	1.008065	0.001411	F8, F9, F11, SERPING1, KLKB1
GO:0051170~nuclear import	5	1.008065	0.001411	SNRPD2, SNRPD1, SNRPG, SNRPD3, SNRPF
GO:0006853~carnitine shuttle	4	0.806452	0.001664	CPT2, PRKAG2, SLC25A20, ACACB
GO:0005686~U2 snRNP	5	1.008065	0.001723	SNRPD2, SNRPD1, SNRPG, SNRPA1, SNRPD3
GO:0009083~branched-chain amino acid catabolic process	5	1.008065	0.001748	BCKDK, ALDH6A1, IVD, BCKDHB, ACAT1
GO:0003723~RNA binding	29	5.846774	0.001787	RPL4, KHDRBS1, RPL9, RPL6, ELAVL3, RPL7, FXR2, SNRPD1, RPS3, RPL37, RPL39, NPM1, SSB, CPSF6, RPS7, RPL22, RPS3A, DDX50, PPP5C, DKC1, EWSR1, NCL, FUBP1, ZNF74, SNRPG, RPL24, PABPC3, PABPC1, SNRPF
GO:0005743~mitochondrial inner membrane	24	4.83871	0.001806	GSTK1, ACAA2, GOT2, ETFDH, COQ9, DHRS1, MRPL34, ACAT1, SIRT3, HMGCL, COQ3, PINK1, CPT2, NDUFS7, TST, NNT, UQCRQ, RPS3, SLC25A10, MRPL9, SLC25A20, HADH, CRAT, OTC
GO:0019825~oxygen binding	7	1.41129	0.001942	CYP2C8, CYP2A13, CBS, CYP4F3, CYP4A11, CYP4F12, CYP3A5
GO:0006000~fructose metabolic process	4	0.806452	0.002327	PFKFB1, ALDOB, FBP1, KHK
GO:0003095~pressure natriuresis	3	0.604839	0.002351	CYP4F2, CYP4A11, CYP4F12
GO:0006096~glycolytic process	6	1.209677	0.002506	PFKFB1, OGDHL, ALDOB, PGM1, HK2, DHTKD1
GO:0072562~blood microparticle	12	2.419355	0.002572	FCN2, HPX, SERPINC1, PON1, AFM, SERPING1, HPR, ANGPTL4, CLIC1, C8A, CPN2, ACTG1
GO:2000378~negative regulation of reactive oxygen species metabolic	5	1.008065	0.002581	PINK1, HIF1A, SIRT2, HK2, SIRT3

process				
GO:0070932~histone H3 deacetylation	5	1.008065	0.002581	PER1, HDAC2, SIRT2, HDAC6, SIRT3
GO:0001676~long-chain fatty acid metabolic process	5	1.008065	0.002581	CYP4F2, CYP4A11, CYP4F12, SLC27A2, SLC27A5
GO:0005654~nucleoplasm	98	19.75806	0.002944	NUP107, MPG, UBE2D1, SMC4, ELK1, STK11, SCP2, SNRPD2, SNRPD1, FBXO5, SNRPD3, HADH, KPNA2, GTSE1, RPS10, SOX4, PDK2, RPS7, RPS6, UBE2E1, ARID5B, AR, DKC1, NCL, SNRPG, IGFALS, SNRPF, KHDRBS1, SET, DDX1, HIF1A, CCNB1, PNPO, E4F1, LHPP, GCKR, XRCC6, CPSF6, SMURF2, GADD45A, SMARCA5, ABTB2, MSRA, PPP5C, ALDH6A1, CDK5, FUBP1, IARS, SAE1, HIST1H4C, CALM2, INTS8, RPS24, EZH1, TOP2A, RARG, ALAS1, THRA, HMGB2, PRKAG2, GLI3, SPR, CPT2, SUMO2, ZMYM6, ZHX3, PPP1R12A, RPS3A, GNL3, DBF4, BDH1, ELF4, IVD, RARA, RGN, BLVRB, SNRPA1, MCM6, PTMA, GTF3C2, HDAC2, NR1I3, NR1I2, BPHL, TDG, RPS3, HSF4, NPM1, MGMT, PTGES3, ARID3A, GTF2H2, SOD1, ZNF74, TCEA2, ESF1, RAN, PTPN2
GO:0016597~amino acid binding	5	1.008065	0.003027	TAT, SHMT1, GOT2, AGXT, OTC
GO:0005778~peroxisomal membrane	7	1.41129	0.003048	DAO, PXMP2, CAT, HSD17B4, DECR2, SLC27A2, DHRS4
GO:0005737~cytoplasm	168	33.87097	0.003175	IPO13, RPL4, UBE2D1, BUB1B, BZW2, SMC4, RPL9, RPL7, EEF1B2, STK11, SCP2, HERC1, SOX15, MLYCD, FBXO5, SNRPD3, TGM5, HADH, KPNA2, TMSB10, SOX4, PDK2, SULT2A1, SDS, RPS7, FBXO2, RPL23, RPL22, RPS6, TSC2, VRK3, AR, RNF123, EWSR1, DKC1, RPL24, GPLD1, LLGL1, SET, SHMT1, DDX1, ABCB4, HIF1A, SEC14L2, CCNB1, FXR2, PNPO, E4F1, MPDZ, ZC3H15, LHPP, SMCP, GCKR, XRCC6, CRADD, SMURF2, GADD45A, EPHX2, CYP4F2, CYP4F12, PAFAH2, CCT6A, ABTB2, NAT6, MSRA, PTPRE, GRHPR, KIF18A, IRAK1BP1, BHMT, PPP5C, ARPC2, CDK5, NACA, TOLLIP, PXMP2, PDCL, CRYL1, SDC1, ANP32B, IARS, CALM2, MAP3K14, RPS24, TOP2A, ALAS1, ACY1, ATF7IP2, HMGB2, TNFAIP1, KIF11, DOC2B, FTCD, GLI3, LRRC1, OASL, KHK, GYS2, SPR, YWHAQ, HYAL1, NUP62, ZMYM6, NOS1, CLIC1, PGM1, CCT3, PPP1R12A, SPHK1, BHMT2, CYP4A11, PPP2R5B, CKAP2, ASMTL, RPL13A, RPS3A, SIRT2, PTP4A3, BDH1, EHHADH, TRAF5, CRY2, RARA, LANCL2, RGN, BLVRB, PABPC3, PLEKHO1, PABPC1, HAGH, EEF1E1, CRYAA, MAPRE1, PTMA, FBP1, RBKS, HDAC2, NR1I3, BPHL, HDAC6, UGP2, CBS, RPS3, CDC37L1, REPS2, SLC25A20, METTL7A, CRYM, APBB3, FARP2, CYB5A, NPM1,

				MARCKSL1, PTGES3, ARID3A, GNMT, SOD1, GSTZ1, PER1, DBNDD1, CCS, PINK1, CTH, PNPLA4, UBAP2, MMACHC, RAN, PNPLA2
GO:0042738~exogenous drug catabolic process	4	0.806452	0.00409	CYP2C8, CYP2A6, NR1I2, NOS1
GO:0006554~lysine catabolic process	4	0.806452	0.00409	GCDH, PIPOX, CRYM, AASS
GO:0008334~histone mRNA metabolic process	4	0.806452	0.00409	SSB, SNRPG, SNRPD3, SNRPF
GO:0018685~alkane 1-monooxygenase activity	3	0.604839	0.004566	CYP4F2, CYP4A11, CYP4F12
GO:0006565~L-serine catabolic process	3	0.604839	0.004613	SDS, CBS, SHMT1
GO:0055088~lipid homeostasis	6	1.209677	0.004619	GCDH, ACADL, IVD, ABCB4, PNPLA4, PNPLA2
GO:0005689~U12-type spliceosomal complex	5	1.008065	0.004687	SNRPD2, SNRPD1, SNRPG, SNRPD3, SNRPF
GO:0007067~mitotic nuclear division	16	3.225806	0.004825	HELLS, PPP1R12A, RPS6, BUB1B, KIF11, SIRT2, KIF15, PPP5C, NUP62, RPS3, NUP43, E4F1, FBXO5, MAPRE1, RAN, CEP55
GO:0006749~glutathione metabolic process	7	1.41129	0.004873	GSTZ1, GSTK1, ALDH5A1, EEF1E1, MMACHC, CLIC1, SOD1
GO:0001889~liver development	8	1.612903	0.004877	HMGCL, SRD5A1, SLCO2B1, RARA, ARID5B, BAAT, OTC, ACAT1
GO:0008143~poly(A) binding	4	0.806452	0.00513	KHDRBS1, DDX1, PABPC3, PABPC1
GO:0070403~NAD+ binding	4	0.806452	0.00513	CRYL1, HADH, SIRT2, SIRT3
GO:0051262~protein tetramerization	6	1.209677	0.005159	HMGCL, CPSF6, SHMT1, CAT, AASS, DHRS4
GO:0031641~regulation of myelination	4	0.806452	0.005206	RARG, TG, RARA, SIRT2
GO:0000245~spliceosomal complex assembly	5	1.008065	0.005767	SNRPD2, SNRPD1, DDX1, SNRPG, SNRPD3
GO:0005978~glycogen biosynthetic process	5	1.008065	0.005767	GYS2, UGP2, PTGES3, GYG1, PGM1
GO:0006606~protein import into nucleus	7	1.41129	0.005795	IPO13, NUP107, CRY2, NUP62, TSC2, KPNA2, RAN
GO:0042493~response to drug	18	3.629032	0.006088	CPB2, HDAC2, SRD5A1, MGMT, ABCB4, ABCC6, HMGB2, ABAT, ACACB, SOD1, ALAD, POR, CCNB1, TBXA2R, CAT, PEMT, HADH, OTC
GO:0000038~very long-chain fatty acid	4	0.806452	0.006488	CYP4F2, HSD17B4, CYP4F12, SLC27A5

metabolic process				
GO:0097526~spliceosomal tri-snRNP complex	3	0.604839	0.006728	SNRPD1, SNRPG, SNRPD3
GO:0042802~identical protein binding	34	6.854839	0.007423	PFKFB1, KHDRBS1, ALAS1, ACY1, SHMT1, ACTG1, ALAD, UGP2, AKR7A3, FXR2, CBS, CTSC, HGD, SMURF2, CBX3, ZBTB16, DCXR, GOT2, CIDEB, EPOR, SOD1, PPP5C, CLDN14, EWSR1, CTH, NCL, TRAF5, CLDN17, MCM6, ALDOB, ANGPTL4, CRYAA, MAPRE1, FBP1
GO:0051005~negative regulation of lipoprotein lipase activity	3	0.604839	0.007545	APOC1, APOC3, ANGPTL4
GO:0019346~transsulfuration	3	0.604839	0.007545	MTHFD1, CBS, CTH
GO:0019439~aromatic compound catabolic process	3	0.604839	0.007545	PON3, EPHX1, PON1
GO:0000387~spliceosomal snRNP assembly	5	1.008065	0.007555	SNRPD2, SNRPD1, SNRPG, SNRPD3, SNRPF
GO:0042593~glucose homeostasis	9	1.814516	0.007877	STK11, GCGR, CRY2, RPS6, LEPR, HIF1A, SOX4, PTPN2, PDK2
GO:0006977~DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	7	1.41129	0.00801	NPM1, CCNB1, CRADD, GADD45A, ARID3A, GTSE1, SOX4
GO:0003684~damaged DNA binding	7	1.41129	0.008438	XRCC6, MPG, MGMT, TDG, CRY2, RPS3, HMGB2
GO:0022627~cytosolic small ribosomal subunit	6	1.209677	0.008811	RPS7, RPS6, RPS3, RPS3A, RPS10, RPS24
GO:0005682~U5 snRNP	4	0.806452	0.009702	SNRPD2, SNRPD1, SNRPG, SNRPD3
GO:0004300~enoyl-CoA hydratase activity	3	0.604839	0.010994	ECHS1, EHHADH, ECHDC2
GO:0006555~methionine metabolic process	3	0.604839	0.011106	MSRA, MTHFD1, GNMT
GO:0009086~methionine biosynthetic process	3	0.604839	0.011106	BHMT, MTHFD1, BHMT2
GO:0020027~hemoglobin metabolic process	3	0.604839	0.011106	HPX, EPB42, CAT
GO:0006266~DNA ligation	3	0.604839	0.011106	TOP2A, XRCC6, MGMT

GO:0005881~cytoplasmic microtubule	6	1.209677	0.011329	CYP2A6, DCXR, CKAP2, MAPRE1, GTSE1, HDAC6
GO:0070542~response to fatty acid	4	0.806452	0.011383	ALAD, HMGCL, PON1, CAT
GO:0032868~response to insulin	7	1.41129	0.011563	PFKFB1, CRY2, NPPA, CAT, HADH, OTC, KHK
GO:0005515~protein binding	273	55.04032	0.011649	IPO13, RPL4, FAAH, VIPR1, NUP107, SMC4, ELK1, RPL9, RPL7, SCP2, SNRPD2, SNRPD1, SOX15, LONP2, FBXO5, SNRPD3, RPS10, GTSE1, SOX4, SULT2A1, IER3, ARSA, GSTK1, FBXO2, RPL23, RPL22, DKK1, AR, AZGP1, POR, MTHFD1, EWSR1, TFR2, SUB1, RPL24, SERPING1, TFAM, ZG16, LLGL1, SET, EPB42, CDCA4, ABCB4, SHMT1, SLC22A1, KLK5, HIF1A, SULT1A1, HPX, C6, FXR2, PLCG2, CD14, HMOX2, PCK2, SMCP, XRCC6, CRADD, GADD45A, TREX1, CYP4F2, SS18L1, SMARCA5, CIDEB, CCT6A, PPP5C, FUBP1, TOLLIP, SDC1, ANP32B, HIST1H4C, CALM2, INTS8, TOP2A, RARG, ACY1, GLI3, KIF15, KHK, SEC61G, KIF1B, CCR6, CLIC1, CTSC, CEP55, CCT3, HELLS, ZHX3, TNFRSF12A, SPHK1, PAX5, BAAT, GMIP, SIRT2, GNL3, SIRT3, F8, RARA, PELI1, PLEKHO1, ALDOB, PABPC1, ANGPTL4, EEF1E1, CRYAA, MAPRE1, PTMA, GRAMD1C, ECHS1, CTF1, SERPINC1, HAAO, NR1I2, TMPRSS2, HSD17B8, SLC7A1, PCNP, ARFRP1, PGRMC1, RPS3, APBB3, RPL17, NPM1, CCL20, PTGES3, F11, SORBS2, GTF2H2, DHRS1, FAH, GNMT, SPSB3, TCEA2, KLKB1, LIMS1, FCN2, ACAA2, MPG, UBE2D1, BUB1B, PEBP1, OGDHL, DUX1, ACTG1, EEF1B2, STK11, AKR7A3, NPPA, LEPR, KPNA2, GYG1, TMSB10, PSKH1, CHRNB2, CEP135, TPM4, HGD, RPS7, RPS6, UBE2E1, PIPOX, TSC2, ARID5B, ACYP2, VRK3, DKC1, NCL, SNRPG, PHIP, MASP2, MASP1, SNRPF, PFKFB1, KHDRBS1, DDX1, CCDC25, GLYAT, SLC1A5, ACACB, PLD2, CCNB1, TBXA2R, E4F1, MPDZ, ZC3H15, GCKR, CPSF6, SMURF2, CBX3, ZBTB16, COQ9, PTPRE, KIF18A, IRAK1BP1, UBOX5, DAO, BMP1, ARPC2, CDK5, NAT2, PXMP2, PDCL, C16ORF45, IARS, SAE1, MAP3K14, ALAS1, THRA, HMGB2, PCTP, TNFAIP1, HK2, FTCD, GHR, YWHAQ, NUP62, SUMO2, NOS1, MRPL9, LBR, PGM1, ACTR3, PPP1R12A, BCKDHB, PPP2R5B, ASMTL, RPS3A, NDUFS7, ELF4, EHHADH, TRAF5, CRY2, LANCL2, SLC25A10, SNRPA1, MCM6, HAGH, AGXT, FBP1, RBKS, TNFRSF21, FAM60A, RALA, HDAC2, ASB13, HDAC6, SELENBP1, UGP2, RAB26, CBS, TDG, CDC37L1, REPS2, NUP43, CRYM, MARCKSL1, SSB, SEMA4D, PDE6G, NAP1L1, ARID3A, SORL1, EPOR, SOD1, BCKDK, GSTZ1, CCS, PINK1, CTH, RAB17, MMACHC, PTPN2, RAN
GO:0004745~retinol dehydrogenase	4	0.806452	0.013189	RDH16, RDH5, HSD17B6, DHRS3

activity				
GO:0051536~iron-sulfur cluster binding	4	0.806452	0.013189	NDUFS7, RPS3, ETFDH, ABAT
GO:0033539~fatty acid beta-oxidation using acyl-CoA dehydrogenase	4	0.806452	0.013377	GCDH, ACADL, IVD, ETFDH
GO:0005683~U7 snRNP	3	0.604839	0.013637	SNRPG, SNRPD3, SNRPF
GO:0005579~membrane attack complex	3	0.604839	0.013637	C6, C8B, C8A
GO:0001867~complement activation, lectin pathway	3	0.604839	0.015259	FCN2, MASP2, MASP1
GO:0010870~positive regulation of receptor biosynthetic process	3	0.604839	0.015259	HDAC2, HIF1A, HDAC6
GO:0034983~peptidyl-lysine deacetylation	3	0.604839	0.015259	SIRT2, HDAC6, SIRT3
GO:0046689~response to mercury ion	3	0.604839	0.015259	ALAD, TAT, AQP9
GO:0071806~protein transmembrane transport	3	0.604839	0.015259	AZGP1, SEC61G, RAN
GO:0006631~fatty acid metabolic process	6	1.209677	0.015475	GHR, EHHADH, CYP4A11, CRYL1, HADH, BAAT
GO:0048814~regulation of dendrite morphogenesis	4	0.806452	0.015558	CHRNB2, CHRNA3, STK11, SEMA4D
GO:0032259~methylation	7	1.41129	0.017141	COQ3, TPMT, BHMT2, PEMT, ASMTL, METTL7A, GNMT
GO:0034366~spherical high-density lipoprotein particle	3	0.604839	0.017864	PON1, APOC3, HPR
GO:0032183~SUMO binding	3	0.604839	0.01977	TDG, TOLLIP, RPS3
GO:0004887~thyroid hormone receptor activity	3	0.604839	0.01977	THRA, NR1I3, NR1I2
GO:0034364~high-density lipoprotein particle	4	0.806452	0.019916	SAA4, PON1, APOC1, APOC4
GO:0042135~neurotransmitter catabolic process	3	0.604839	0.019968	ALDH5A1, MAOA, ABAT

GO:0006690~icosanoid metabolic process	3	0.604839	0.019968	CYP2J2, CYP4F2, CYP4F3
GO:0003707~steroid hormone receptor activity	6	1.209677	0.020348	AR, RARG, THRA, NR1I3, NR1I2, RARA
GO:0019835~cytolysis	4	0.806452	0.020484	C6, MMD, C8B, C8A
GO:0021766~hippocampus development	6	1.209677	0.020764	CDK5, UQCRQ, SRD5A1, RARA, EZH1, GLI3
GO:0005730~nucleolus	34	6.854839	0.022133	RPL4, TOP2A, ATF7IP2, HMGB2, TNFAIP1, RPL9, RPL7, OASL, SELENBP1, PGRMC1, CPT2, RPS3, RPS10, ZC3H15, NPM1, XRCC6, RPS7, RPL23, ZBTB16, RPS6, SMARCA5, RPL13A, ARID3A, RPS3A, DDX50, GNL3, DKC1, EWSR1, NCL, SUB1, CRYL1, ESF1, ANP32B, RAN
GO:0006637~acyl-CoA metabolic process	4	0.806452	0.023231	HMGCL, GLYAT, MLYCD, BAAT
GO:0010906~regulation of glucose metabolic process	4	0.806452	0.023231	IGFBP4, MLYCD, ACACB, PDK2
GO:0016746~transferase activity, transferring acyl groups	5	1.008065	0.023411	ACAA2, CPT2, GLYAT, BAAT, CRAT
GO:0016747~transferase activity, transferring acyl groups other than amino-acyl groups	3	0.604839	0.024951	ACAA2, SCP2, ACAT1
GO:0097267~omega-hydroxylase P450 pathway	3	0.604839	0.025198	CYP2C8, CYP4F2, CYP4A11
GO:0006544~glycine metabolic process	3	0.604839	0.025198	SHMT1, GLYAT, BAAT
GO:0006111~regulation of gluconeogenesis	3	0.604839	0.025198	FBP1, PDK2, GNMT
GO:0006520~cellular amino acid metabolic process	5	1.008065	0.025886	SDS, ACY1, TAT, GOT2, BPHL
GO:0051439~regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	4	0.806452	0.026168	CCNB1, UBE2E1, UBE2D1, FBXO5
GO:0046835~carbohydrate	4	0.806452	0.026168	PFKFB1, RBKS, HK2, KHK

phosphorylation				
GO:0045892~negative regulation of transcription, DNA-templated	23	4.637097	0.027078	KHDRBS1, XRCC6, HDAC2, ZHX3, SET, SMURF2, THRA, CBX3, NR1I3, ZBTB16, NR1I2, HMGB2, ARID5B, GLI3, SIRT2, HDAC6, PER1, YWHAQ, CDK5, CRY2, LANCL2, RARA, LIMS1
GO:0036464~cytoplasmic ribonucleoprotein granule	4	0.806452	0.028053	NCL, RPS6, PABPC1, RPL6
GO:0071011~precatalytic spliceosome	4	0.806452	0.028053	SNRPD2, SNRPD1, SNRPG, SNRPD3
GO:0032024~positive regulation of insulin secretion	5	1.008065	0.028064	ABAT, DOC2B, SOX4, SIRT3, PCK2
GO:0031012~extracellular matrix	15	3.024194	0.028098	RPS7, RPL23, RPL22, RPS3A, LAMC1, RPL9, CKAP4, ACTG1, SOD1, CCT6A, RPS3, ZG16, HIST1H4C, RPS10, RAN
GO:0019104~DNA N-glycosylase activity	3	0.604839	0.030615	MPG, TDG, RPS3
GO:0046653~tetrahydrofolate metabolic process	3	0.604839	0.030916	MTHFD2, SHMT1, PIPOX
GO:0006476~protein deacetylation	3	0.604839	0.030916	SIRT2, HDAC6, SIRT3
GO:0035999~tetrahydrofolate interconversion	3	0.604839	0.030916	MTHFD1, SHMT1, FTCD
GO:0006105~succinate metabolic process	3	0.604839	0.030916	GHR, ALDH5A1, SUCLG2
GO:0007569~cell aging	4	0.806452	0.032608	NPM1, NUP62, LIMS1, SOD1
GO:0002181~cytoplasmic translation	4	0.806452	0.032608	RPL22, RPL9, RPL6, RPL7
GO:0046686~response to cadmium ion	4	0.806452	0.032608	ALAD, CYB5A, HAAO, CAT
GO:0019369~arachidonic acid metabolic process	4	0.806452	0.032608	FAAH, CYP4F2, CYP4A11, CYP4F12
GO:0006913~nucleocytoplasmic transport	4	0.806452	0.032608	NPM1, SET, CDK5, RAN
GO:0008022~protein C-terminus binding	11	2.217742	0.033446	TOP2A, XRCC6, CEP135, YWHAQ, NCL, ZBTB16, SDC1, PABPC1, MAPRE1, SAE1, MPDZ
GO:0005543~phospholipid binding	7	1.41129	0.03424	SEC14L2, NUP62, PON1, GOT2, APOC3, PAFAH2, OTC
GO:0006879~cellular iron ion	5	1.008065	0.035235	HPX, TFR2, HIF1A, HMOX2, SOD1

homeostasis				
GO:0008395~steroid hydroxylase activity	4	0.806452	0.035631	CYP2J2, CYP2C8, CYP2A6, CYP2A13
GO:0070328~triglyceride homeostasis	4	0.806452	0.036109	GCKR, APOC4, APOC3, ANGPTL4
GO:0006259~DNA metabolic process	4	0.806452	0.036109	IGFBP4, TREX1, KPNA2, RAN
GO:0071013~catalytic step 2 spliceosome	7	1.41129	0.036405	SNRPD2, SNRPD1, SNRPG, SNRPA1, PABPC1, SNRPD3, SNRPF
GO:0060326~cell chemotaxis	6	1.209677	0.036621	CCL14, CCL20, SAA4, HMGB2, CCR6, CCL16
GO:0051384~response to glucocorticoid	6	1.209677	0.036621	ALAD, GHR, PFKFB1, TAT, SDC1, AGXT
GO:0006979~response to oxidative stress	8	1.612903	0.036625	ALAD, MSRA, PINK1, TAT, RPS3, ETFDH, HAO1, HMOX2
GO:0016811~hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	3	0.604839	0.036733	BTD, SIRT2, SIRT3
GO:0055078~sodium ion homeostasis	3	0.604839	0.03709	CYP4F2, CYP4A11, CYP4F12
GO:0051879~Hsp90 protein binding	4	0.806452	0.039272	NUP62, RPS3, HIF1A, HDAC6
GO:0015721~bile acid and bile salt transport	4	0.806452	0.039795	SLC10A1, SLCO2B1, ABCB11, SLC27A5
GO:0008203~cholesterol metabolic process	6	1.209677	0.043196	PON1, APOC1, FDX1, CAT, LEPR, SORL1
GO:0032041~NAD-dependent histone deacetylase activity (H3-K14 specific)	3	0.604839	0.043273	HDAC2, HDAC6, SIRT3
GO:0009755~hormone-mediated signaling pathway	4	0.806452	0.043664	GHR, THRA, GCGR, NUP62
GO:0010033~response to organic substance	4	0.806452	0.043664	AQP9, CTSC, HDAC6, SOD1
GO:0042446~hormone biosynthetic process	3	0.604839	0.04369	TG, DIO1, FDX1
GO:0045717~negative regulation of fatty acid biosynthetic process	3	0.604839	0.04369	ACADL, APOC1, APOC3

GO:0006107~oxaloacetate metabolic process	3	0.604839	0.04369	GHR, GOT2, PCK2
GO:0043231~intracellular membrane-bounded organelle	23	4.637097	0.044859	GSTK1, PON3, CYB5A, ABCA6, CYP4F2, PON1, UGT2B15, CYP4A11, AQP9, HSD17B4, CYP3A5, CYP4F12, BPHL, TMEM165, DHRS4, PPP5C, POR, SCP2, CAT, NUP62, RDH16, GPLD1, AASS
GO:0006099~tricarboxylic acid cycle	4	0.806452	0.047713	NNT, SUCLG2, OGDHL, DHTKD1

Table S5. KEGG analysis results of ACBD4 and its co-expressed genes

Term	Count	%	PValue	Genes
hsa01100:Metabolic pathways	103	20.76613	2.91E-12	ACAA2, ABAT, OGDHL, GBA3, SCP2, MLYCD, HADH, SDS, HGD, UGT2B15, PIPOX, BTD, MTHFD1, MTHFD2, SUCLG2, HPD, SLC27A5, CES1, GCDH, MAOA, SHMT1, ACACB, ACAT1, PLD2, HSD11B1, FUT7, PNPO, RDH16, PLCG2, HAO1, HAO2, PCK2, CYP2J2, EPHX2, CYP4F2, CYP4F3, GOT2, PAFAH2, COQ3, GRHPR, CYP2C8, BHMT, ALDH6A1, DAO, NAT2, UQCRQ, CRYL1, PEMT, ALAS1, ACY1, TAT, GPT, CSAD, HK2, FTCD, KHK, ALAD, ACADL, SPR, ALDH2, HYAL1, NNT, NOS1, PGM1, AASS, CBR1, SPHK1, DCXR, BCKDHB, BAAT, CYP2A6, ALDH5A1, NDUFS7, TST, BDH1, IVD, EHHADH, RGN, ALDOB, AGXT, FBP1, ECHS1, HAAO, HSD17B4, HSD17B6, CYP3A5, HSD17B8, HMGCL, UGP2, CBS, ATP6V0E2, XDH, GALNT7, PTGES3, FAH, DHRS3, DHRS4, GSTZ1, ETNK2, CTH, MGAT4B, PNPLA2, OTC
hsa04146:Peroxisome	21	4.233871	2.23E-10	GSTK1, EPHX2, PIPOX, HSD17B4, BAAT, DHRS4, SOD1, HMGCL, DAO, SCP2, EHHADH, PXMP2, CAT, HAO1, MLYCD, DECR2, AGXT, CRAT, XDH, HAO2, SLC27A2
hsa01130:Biosynthesis of antibiotics	32	6.451613	1.92E-09	GCDH, ACAA2, ECHS1, ACY1, SHMT1, TAT, OGDHL, HK2, ACAT1, UGP2, ALDH2, CBS, HAO1, HADH, HAO2, AASS, PGM1, PCK2, SDS, BCKDHB, GOT2, PAFAH2, DAO, CTH, EHHADH, CAT, RGN, SUCLG2, ALDOB, AGXT, FBP1, OTC
hsa00260:Glycine, serine and threonine metabolism	12	2.419355	5.08E-07	GRHPR, BHMT, SDS, ALAS1, DAO, MAOA, CBS, CTH, SHMT1, PIPOX, AGXT, GNMT
hsa01200:Carbon metabolism	18	3.629032	6.71E-06	ECHS1, SDS, SHMT1, GOT2, OGDHL, GPT, HK2, ACAT1, ALDH6A1, EHHADH, CAT, RGN, SUCLG2, HAO1, ALDOB, AGXT, HAO2, FBP1
hsa03010:Ribosome	19	3.830645	2.22E-05	RPL4, RPS7, RPL23, RPL22, RPS6, RPL13A, RPS3A, MRPL34, RPL9, RPL6, RPL7, RPS3, RPL24, MRPL9, RPL37, RPL39, RPL17, RPS10, RPS24
hsa00280:Valine, leucine and isoleucine degradation	11	2.217742	2.64E-05	HMGCL, ALDH6A1, ACAA2, ECHS1, ALDH2, IVD, EHHADH, BCKDHB, ABAT, HADH, ACAT1
hsa00380:Tryptophan metabolism	10	2.016129	4.19E-05	GCDH, ECHS1, ALDH2, MAOA, EHHADH, HAAO, CAT, OGDHL, HADH, ACAT1
hsa00650:Butanoate metabolism	8	1.612903	1.17E-04	HMGCL, ECHS1, ALDH5A1, BDH1, EHHADH, ABAT, HADH, ACAT1
hsa00640:Propanoate metabolism	8	1.612903	1.50E-04	ALDH6A1, ECHS1, EHHADH, SUCLG2, ABAT, MLYCD, ACACB, ACAT1
hsa05204:Chemical carcinogenesis	13	2.620968	1.59E-04	GSTK1, CBR1, EPHX1, UGT2B15, CYP3A43, CYP3A5, SULT1A1, HSD11B1,

				CYP2A6, CYP2C8, CYP2A13, NAT2, SULT2A1
hsa04610:Complement and coagulation cascades	12	2.419355	1.71E-04	CPB2, F8, C6, F9, SERPINC1, F11, SERPING1, MASP2, MASP1, C8B, KLKB1, C8A
hsa00071:Fatty acid degradation	9	1.814516	3.84E-04	GCDH, ACAA2, ECHS1, CPT2, ACADL, ALDH2, EHHADH, HADH, ACAT1
hsa00630:Glyoxylate and dicarboxylate metabolism	7	1.41129	8.91E-04	GRHPR, SHMT1, CAT, HAO1, AGXT, HAO2, ACAT1
hsa00310:Lysine degradation	9	1.814516	0.001679	GCDH, ECHS1, ALDH2, EHHADH, PIPOX, OGDHL, HADH, AASS, ACAT1
hsa00830:Retinol metabolism	10	2.016129	0.001682	CYP2C8, CYP2A6, UGT2B15, RDH16, PNPLA4, RDH5, HSD17B6, CYP3A5, DHRS3, DHRS4
hsa00350:Tyrosine metabolism	7	1.41129	0.003643	GSTZ1, HGD, MAOA, TAT, GOT2, FAH, HPD
hsa01230:Biosynthesis of amino acids	10	2.016129	0.003833	SDS, ACY1, CBS, TAT, CTH, SHMT1, GOT2, GPT, ALDOB, OTC
hsa00980:Metabolism of xenobiotics by cytochrome P450	10	2.016129	0.004614	HSD11B1, GSTK1, CBR1, CYP2A6, AKR7A3, CYP2A13, EPHX1, UGT2B15, CYP3A5, SULT2A1
hsa00360:Phenylalanine metabolism	5	1.008065	0.005376	MAOA, TAT, GOT2, GLYAT, HPD
hsa00270:Cysteine and methionine metabolism	7	1.41129	0.005553	BHMT, SDS, TST, CBS, TAT, CTH, GOT2
hsa00620:Pyruvate metabolism	7	1.41129	0.007179	GRHPR, ALDH2, ACYP2, HAGH, ACACB, PCK2, ACAT1
hsa03320:PPAR signaling pathway	9	1.814516	0.008279	CPT2, ACADL, SCP2, EHHADH, APOC3, ANGPTL4, SLC27A2, SLC27A5, PCK2
hsa04976:Bile secretion	9	1.814516	0.009848	SLC10A1, ABCB4, EPHX1, SLC22A1, AQP9, ABCB11, BAAT, SLC27A5, SULT2A1
hsa00220:Arginine biosynthesis	5	1.008065	0.009872	ACY1, GOT2, GPT, NOS1, OTC
hsa00410:beta-Alanine metabolism	6	1.209677	0.010194	ALDH6A1, ECHS1, ALDH2, EHHADH, ABAT, MLYCD
hsa00983:Drug metabolism - other enzymes	7	1.41129	0.014093	CYP2A6, TPMT, NAT2, UGT2B15, XDH, CES2, CES1
hsa05020:Prion diseases	6	1.209677	0.015013	C6, LAMC1, C8B, ELK1, C8A, SOD1
hsa01212:Fatty acid metabolism	7	1.41129	0.017176	ACAA2, ECHS1, CPT2, ACADL, EHHADH, HADH, ACAT1
hsa00232:Caffeine metabolism	3	0.604839	0.017368	CYP2A6, NAT2, XDH
hsa00120:Primary bile acid biosynthesis	4	0.806452	0.035465	SCP2, HSD17B4, BAAT, SLC27A5
hsa00030:Pentose phosphate pathway	5	1.008065	0.035641	RGN, ALDOB, FBP1, RBKS, PGM1
hsa04152:AMPK signaling pathway	11	2.217742	0.041741	GYS2, PFKFB1, STK11, LEPR, PPP2R5B, TSC2, PRKAG2, MLYCD, ACACB, FBP1, PCK2
hsa00590:Arachidonic acid metabolism	7	1.41129	0.048769	CYP2J2, CBR1, CYP2C8, CYP4F2, EPHX2, PTGES3, CYP4F3
hsa00051:Fructose and mannose metabolism	5	1.008065	0.048783	PFKFB1, ALDOB, FBP1, HK2, KHK

Table S6. Differentially expressed genes between high- and low-ACBD4 expression groups in HBV-related HCC tumor tissues

ID	log2FC	AveExpr	t	P Value	FDR
ACBD4	-1.25266	5.145237	-19.168	3.32E-48	4.33E-44
FMO4	-1.58568	6.378221	-11.1381	5.44E-23	3.54E-19
SEC14L2	-1.52346	5.31878	-10.4422	7.23E-21	3.14E-17
SLC10A1	-2.89859	8.041443	-10.3601	1.28E-20	4.09E-17
CYP4F11	-1.48451	5.871592	-10.168	4.84E-20	9.37E-17
DAO	-1.57569	6.077899	-10.138	5.95E-20	9.70E-17
GLYAT	-2.03174	5.808095	-10.0199	1.34E-19	1.75E-16
CES2	-1.76886	8.937062	-9.97655	1.81E-19	2.14E-16
AKR7A3	-1.72162	6.494085	-9.88784	3.32E-19	3.49E-16
ABAT	-1.15344	7.95932	-9.8809	3.48E-19	3.49E-16
ABCA6	-1.51885	6.930738	-9.83407	4.79E-19	4.46E-16
LOC123876	-1.97044	8.191822	-9.80972	5.66E-19	4.91E-16
SLC27A5	-1.91679	7.338316	-9.60453	2.28E-18	1.48E-15
DHTKD1	-1.01615	7.993549	-9.57053	2.87E-18	1.78E-15
PXMP2	-1.1025	7.510747	-9.55021	3.29E-18	1.95E-15
AGXT2L1	-2.34715	7.540065	-9.46144	5.99E-18	3.25E-15
HAGH	-1.18924	7.757918	-9.30841	1.67E-17	7.77E-15
CTH	-1.80225	6.325104	-9.30117	1.75E-17	7.88E-15
ETFDH	-1.0802	5.722271	-9.23926	2.65E-17	1.08E-14
DHRS1	-1.23325	7.726745	-9.16475	4.35E-17	1.62E-14
DCXR	-1.49818	9.559617	-9.14577	4.94E-17	1.79E-14
RGN	-1.15699	8.402178	-8.91262	2.30E-16	7.31E-14
FLJ10986	-1.96132	6.724714	-8.87351	2.97E-16	9.22E-14
MASP2	-1.10148	5.732834	-8.84488	3.59E-16	1.04E-13
CPN2	-1.2854	8.025686	-8.83734	3.77E-16	1.07E-13
APOC4	-1.98991	8.362903	-8.74994	6.66E-16	1.77E-13
ABCB4	-1.93833	7.609965	-8.71242	8.51E-16	2.17E-13
PCK2	-1.18236	9.052714	-8.68531	1.01E-15	2.45E-13
AFM	-2.0833	6.86282	-8.62196	1.53E-15	3.47E-13
ETNK2	-1.1726	6.058521	-8.57795	2.03E-15	4.49E-13
PFKFB1	-1.22304	5.166731	-8.56801	2.17E-15	4.58E-13
HAO1	-1.66008	8.395726	-8.5671	2.18E-15	4.58E-13
CYP4F3	-1.16506	7.577653	-8.47027	4.06E-15	7.68E-13
CRYM	-1.08879	5.872419	-8.417	5.72E-15	1.06E-12
HPD	-2.74035	8.473735	-8.39161	6.73E-15	1.22E-12
HSD17B6	-2.12777	9.436527	-8.37633	7.42E-15	1.31E-12
AQP9	-2.14389	8.322899	-8.34436	9.09E-15	1.54E-12
CBR1	-1.13531	8.036129	-8.32643	1.02E-14	1.68E-12
GYS2	-1.88685	6.25735	-8.24337	1.73E-14	2.74E-12
RPIB9	-1.2032	4.790572	-8.24	1.76E-14	2.76E-12
DKK1	2.539628	5.555949	8.231643	1.86E-14	2.85E-12
FLJ20581	-1.56778	6.815825	-8.22094	1.99E-14	3.02E-12
AASS	-1.19099	4.702534	-8.21137	2.11E-14	3.17E-12

SLC22A1	-2.47866	6.358986	-8.17764	2.62E-14	3.79E-12
CIDEB	-1.08687	8.583835	-8.1004	4.25E-14	6.00E-12
BAAT	-1.59867	8.982378	-8.09245	4.47E-14	6.20E-12
CYP4F2	-1.32666	7.797647	-8.08033	4.83E-14	6.50E-12
FAM60A	1.12934	7.074484	8.079909	4.84E-14	6.50E-12
TAT	-1.3797	6.235319	-8.06297	5.38E-14	7.15E-12
HSD11B1	-2.58818	7.779858	-8.0516	5.78E-14	7.60E-12
EHHADH	-1.17837	8.355389	-8.01262	7.37E-14	9.32E-12
MMD	1.008487	7.685096	8.000735	7.94E-14	9.95E-12
OGDHL	-1.32866	6.319545	-7.96728	9.78E-14	1.16E-11
MUCDHL	-1.11055	5.577592	-7.94947	1.09E-13	1.28E-11
SDS	-2.53138	6.847577	-7.89987	1.49E-13	1.60E-11
SELENBP1	-1.10218	8.733003	-7.88023	1.68E-13	1.74E-11
TNFRSF21	1.080664	5.47248	7.845036	2.09E-13	2.08E-11
NAT2	-1.43659	5.195785	-7.84436	2.10E-13	2.08E-11
LOC283537	-1.43938	6.252418	-7.82417	2.37E-13	2.29E-11
CBS	-1.29018	7.741646	-7.82325	2.39E-13	2.29E-11
CCL16	-1.46914	7.243689	-7.69386	5.29E-13	4.47E-11
RDH16	-1.58371	7.021418	-7.60823	8.91E-13	7.04E-11
BHMT	-1.9013	8.920819	-7.59616	9.59E-13	7.53E-11
ARID3A	1.102278	4.475953	7.562714	1.17E-12	8.74E-11
EPHX2	-1.22596	6.848464	-7.53574	1.38E-12	1.01E-10
ATP6V0E2	-1.04515	7.265057	-7.48289	1.90E-12	1.35E-10
CUTL2	-1.39671	6.012531	-7.47334	2.01E-12	1.42E-10
CYP2J2	-1.109	7.369588	-7.44205	2.43E-12	1.67E-10
OTC	-1.74981	7.764211	-7.42458	2.70E-12	1.81E-10
PWCR1	1.237239	4.711568	7.391971	3.28E-12	2.12E-10
CCL20	1.948793	7.276674	7.391109	3.30E-12	2.12E-10
CYP2C8	-1.11849	6.095355	-7.3852	3.42E-12	2.18E-10
C6	-1.61599	8.935164	-7.37676	3.60E-12	2.28E-10
C8A	-1.45531	8.114645	-7.37505	3.63E-12	2.30E-10
PON1	-1.20126	7.046695	-7.34881	4.25E-12	2.63E-10
CYP2A6	-1.86746	6.797622	-7.34518	4.34E-12	2.66E-10
MTHFD2	1.049879	4.543816	7.307994	5.42E-12	3.21E-10
CYP4A11	-1.40077	7.036607	-7.27031	6.77E-12	3.85E-10
SLC17A4	-1.43547	6.83152	-7.24174	8.02E-12	4.43E-10
HGD	-1.21943	8.280587	-7.23372	8.41E-12	4.57E-10
HRSP12	-1.10741	9.692893	-7.21857	9.20E-12	4.93E-10
HPR	-1.80406	7.616379	-7.20527	9.95E-12	5.31E-10
F13B	-1.41917	7.433842	-7.20273	1.01E-11	5.37E-10
INSIG1	-1.24971	8.713562	-7.17154	1.21E-11	6.27E-10
ECM2	-1.10186	6.452112	-7.16114	1.29E-11	6.62E-10
CRYL1	-1.01732	7.757398	-7.07377	2.15E-11	1.05E-09
SERPINC1	-1.52332	10.9578	-7.0466	2.52E-11	1.19E-09
SLC6A1	-1.33088	8.519134	-6.9565	4.25E-11	1.92E-09
CD14	-1.21519	8.465587	-6.91234	5.48E-11	2.38E-09

CDO1	-1.33778	9.442393	-6.90097	5.85E-11	2.53E-09
LRRC1	1.007278	5.003467	6.895614	6.04E-11	2.60E-09
FMO3	-1.75051	8.822553	-6.89281	6.14E-11	2.63E-09
PON3	-1.24164	9.328873	-6.87421	6.83E-11	2.88E-09
BDH1	-1.16454	7.698996	-6.84448	8.09E-11	3.37E-09
FLJ10159	1.411494	5.62146	6.842079	8.21E-11	3.39E-09
UGT2B15	-1.13359	6.877853	-6.80553	1.01E-10	4.04E-09
C8B	-1.26344	8.878935	-6.80448	1.02E-10	4.05E-09
ANGPTL4	-1.13823	6.693636	-6.80144	1.04E-10	4.10E-09
EPHX1	-1.18401	11.74839	-6.79014	1.10E-10	4.34E-09
IGF2BP2	1.390769	7.096283	6.77409	1.21E-10	4.69E-09
SULT2A1	-1.5401	8.648061	-6.72319	1.61E-10	6.01E-09
HAO2	-1.69502	6.223365	-6.62375	2.83E-10	9.52E-09
AZGP1	-1.16289	9.487139	-6.60998	3.05E-10	1.02E-08
CTSC	1.004023	7.709894	6.565128	3.92E-10	1.28E-08
SLC2A2	-1.29988	9.530739	-6.54296	4.44E-10	1.42E-08
CYP7A1	-1.97945	5.777102	-6.48588	6.09E-10	1.84E-08
TOP2A	1.132828	6.687422	6.479057	6.33E-10	1.90E-08
ACOX2	-1.07869	8.079855	-6.47889	6.33E-10	1.90E-08
ADH1B	-1.73927	9.636713	-6.47845	6.35E-10	1.90E-08
FBP1	-1.1962	7.482052	-6.46143	6.98E-10	2.05E-08
ADH1A	-1.41029	8.30048	-6.44765	7.53E-10	2.20E-08
AFP	2.730334	6.978337	6.442206	7.76E-10	2.26E-08
ECHDC3	-1.22118	6.67722	-6.44169	7.78E-10	2.26E-08
DIO1	-1.72681	8.10208	-6.43492	8.08E-10	2.31E-08
SLC27A2	-1.22625	8.046473	-6.41211	9.16E-10	2.56E-08
ZBTB16	-1.0434	6.097912	-6.37927	1.10E-09	2.98E-08
GBA3	-1.31841	4.951862	-6.37594	1.12E-09	3.02E-08
PFKFB3	1.094636	5.789954	6.375355	1.12E-09	3.02E-08
FABP5	1.090992	6.379256	6.368821	1.16E-09	3.11E-08
CFHR5	-1.72606	8.65229	-6.36406	1.19E-09	3.17E-08
ALDOB	-1.57	10.13799	-6.32064	1.51E-09	3.87E-08
LEPR	-1.37725	6.98074	-6.31405	1.57E-09	3.99E-08
PIPOX	-1.18931	9.141665	-6.28995	1.78E-09	4.52E-08
PDK4	-1.09196	5.255135	-6.25664	2.14E-09	5.26E-08
IER3	1.231825	7.398804	6.232271	2.44E-09	5.92E-08
SOX9	1.222951	6.585554	6.22998	2.47E-09	5.95E-08
TTR	-1.35546	11.18085	-6.21892	2.62E-09	6.25E-08
NR1I3	-1.30046	6.386906	-6.21555	2.67E-09	6.34E-08
SLC25A15	-1.09915	7.942842	-6.16615	3.48E-09	8.00E-08
GNMT	-1.64691	6.399407	-6.15082	3.78E-09	8.62E-08
KCNJ8	-1.09359	6.074137	-6.14339	3.93E-09	8.91E-08
ACSL1	-1.01633	9.009321	-6.11521	4.57E-09	1.02E-07
CES1	-1.30348	11.07282	-6.11495	4.57E-09	1.02E-07
SLCO1B1	-1.14992	7.65214	-6.09331	5.13E-09	1.13E-07
GHR	-1.35064	7.421662	-6.08783	5.29E-09	1.16E-07

SAA4	-1.48876	8.398068	-6.0855	5.35E-09	1.17E-07
CYP3A4	-1.15043	7.475567	-6.06265	6.04E-09	1.29E-07
MYRIP	-1.21799	5.202299	-6.05	6.46E-09	1.37E-07
FTCD	-1.1332	7.299212	-6.03117	7.14E-09	1.48E-07
HPX	-1.03691	11.01297	-6.0309	7.15E-09	1.48E-07
APOC3	-1.0092	12.25664	-5.9874	8.99E-09	1.82E-07
SERPINA4	-1.17119	7.613573	-5.93176	1.20E-08	2.35E-07
PDZK1IP1	-1.52158	5.54291	-5.91446	1.32E-08	2.55E-07
COL5A2	1.044298	6.545728	5.890032	1.50E-08	2.84E-07
MAGED4	1.194677	4.737058	5.832545	2.01E-08	3.70E-07
HRG	-1.4496	10.64855	-5.83137	2.03E-08	3.71E-07
KLKB1	-1.03807	7.058461	-5.79506	2.44E-08	4.35E-07
TESC	1.117473	4.977835	5.7884	2.53E-08	4.47E-07
ANXA10	-1.07142	5.922316	-5.78626	2.56E-08	4.51E-07
KNG1	-1.01859	11.98102	-5.75867	2.95E-08	5.12E-07
ACSL4	1.390431	7.21037	5.734657	3.33E-08	5.70E-07
PCK1	-1.68427	9.344688	-5.69706	4.03E-08	6.73E-07
HMGCS2	-1.05733	10.91736	-5.6952	4.07E-08	6.78E-07
F9	-1.60697	9.321608	-5.68538	4.28E-08	7.07E-07
TMEM16A	-1.24093	5.561714	-5.67099	4.61E-08	7.50E-07
CFHR4	-1.53774	8.597148	-5.67023	4.62E-08	7.52E-07
CYP2C9	-1.07347	7.387742	-5.62599	5.78E-08	9.13E-07
IL32	-1.0373	8.806057	-5.57635	7.42E-08	1.13E-06
AGXT	-1.12897	8.034335	-5.52038	9.81E-08	1.43E-06
SLC1A1	-1.00112	5.577977	-5.51727	9.96E-08	1.45E-06
G0S2	-1.25812	6.388885	-5.5161	1.00E-07	1.45E-06
GLS2	-1.3216	5.755525	-5.35673	2.20E-07	2.90E-06
PEG3	1.44331	5.104623	5.344641	2.33E-07	3.04E-06
HMGA2	1.136061	4.19492	5.310778	2.75E-07	3.51E-06
ABCB1	-1.09527	7.787271	-5.28802	3.07E-07	3.85E-06
PLG	-1.05319	10.29159	-5.27583	3.25E-07	4.04E-06
ROBO1	1.177546	8.748362	5.169771	5.40E-07	6.30E-06
SLC38A4	-1.12568	8.597868	-5.09433	7.71E-07	8.66E-06
DPYS	-1.10181	9.38255	-5.08659	8.00E-07	8.92E-06
MMP12	1.158497	4.615301	5.082121	8.17E-07	9.09E-06
UGT1A4	-1.19079	10.18245	-5.03822	1.00E-06	1.08E-05
SERPINE2	1.109171	6.999469	5.030345	1.04E-06	1.11E-05
COL1A2	1.082745	7.968147	5.017333	1.11E-06	1.17E-05
UPB1	-1.22098	8.127285	-4.99843	1.21E-06	1.26E-05
UGT1A6	-1.17041	10.12103	-4.98168	1.30E-06	1.35E-05
G6PC	-1.11584	8.304966	-4.97267	1.36E-06	1.40E-05
LYZ	1.001606	9.968117	4.867403	2.20E-06	2.09E-05
ALDH8A1	-1.04062	8.392931	-4.86405	2.24E-06	2.12E-05
ABCA8	-1.25797	6.361696	-4.76909	3.44E-06	3.05E-05
TACSTD1	1.745215	6.145478	4.725084	4.18E-06	3.62E-05
DLK1	2.186712	5.764323	4.71575	4.36E-06	3.74E-05

ARG1	-1.07081	10.30573	-4.6499	5.83E-06	4.81E-05
RGS2	1.01281	6.384129	4.627947	6.42E-06	5.23E-05
FXYD1	-1.04235	6.686936	-4.55907	8.67E-06	6.75E-05
CD24	1.083838	7.965138	4.502956	1.10E-05	8.34E-05
CPS1	-1.44887	10.18513	-4.43825	1.46E-05	0.000106
LGALS4	-1.48928	8.424398	-4.43505	1.48E-05	0.000107
SPP1	1.422677	8.494728	4.35151	2.10E-05	0.000144
PEG10	1.413498	7.412252	4.343253	2.17E-05	0.000148
GPC3	1.37861	9.793988	4.126232	5.30E-05	0.000317
RELN	1.23165	7.091277	4.117879	5.48E-05	0.000327
IGF2	1.611052	7.35955	3.982908	9.35E-05	0.000515
KRT23	1.058911	5.560642	3.937935	0.000111	0.000597
S100P	1.506036	6.467515	3.925905	0.000117	0.000622
SLPI	-1.19513	7.878514	-3.78785	0.000198	0.000975
APCS	-1.00335	10.43007	-3.77819	0.000205	0.001006
SAA1	-1.07057	7.349179	-3.77364	0.000209	0.00102
SPP2	-1.10383	7.779109	-3.77319	0.000209	0.001021
SPINK1	1.360573	9.481919	3.411163	0.000774	0.003065
NTS	1.091271	4.701384	3.27213	0.001246	0.004581

Table S7. GO term analysis results of DEGs between low- and high-ACBD4 expression groups

Term	Count	%	P Value	Genes
GO:0055114~oxidation-reduction process	32	17.1123	1.99E-13	HSD17B6, CYP3A4, CYP7A1, HSD11B1, AKR7A3, CBS, RDH16, CRYM, AASS, CYP2J2, CBR1, HGD, CYP4F2, DCXR, DIO1, CYP4F3, CYP4A11, PIPOX, FMO3, FMO4, DHRS1, CYP4F11, CYP2C9, CYP2A6, CYP2C8, DAO, BDH1, MTHFD2, CRYL1, ALDH8A1, CDO1, HPD
GO:0031090~organelle membrane	15	8.02139	2.13E-13	CYP2J2, CYP4F2, EPHX1, UGT2B15, CYP4A11, CYP4F3, FMO3, CYP3A4, CYP4F11, FMO4, CYP7A1, CYP2C9, CYP2A6, CYP2C8, RDH16
GO:0070062~extracellular exosome	70	37.43316	2.53E-13	DPYS, ABAT, C8B, C8A, SERPINA4, FTCD, AKR7A3, CTSC, CBR1, SPINK1, HGD, ARG1, DCXR, CYP4A11, ACSL4, UPB1, AZGP1, F9, SLPI, MASP2, HAGH, ALDOB, FBP1, HPD, SLC27A2, CES2, APCS, PON3, ABCB1, SERPINC1, ABCB4, SAA4, PON1, SLC1A1, AFM, PLG, GLYAT, HPR, CPN2, KNG1, SELENBP1, SEC14L2, HPX, C6, TTR, GPC3, SPP1, SPP2, CD14, CRYM, PCK1, HAO2, UGT1A6, PCK2, CYP2J2, EPHX2, IGF2, APOC3, PDZK1IP1, LYZ, BHMT, COL1A2, FABP5, CTH, SAA1, CRYL1, S100P, ALDH8A1, HRG, KLKB1
GO:0006805~xenobiotic metabolic process	14	7.486631	1.92E-12	CYP2J2, EPHX2, EPHX1, UGT2B15, GLYAT, FMO3, CYP3A4, CYP2C9, CYP2C8, AKR7A3, NAT2, CES2, CES1, UGT1A6
GO:0005615~extracellular space	44	23.52941	1.00E-11	APCS, PON3, ECM2, SERPINE2, SERPINC1, PON1, SAA4, AFM, PLG, AFP, C8B, C8A, SERPINA4, KNG1, GHR, SELENBP1, LGALS4, HPX, RELN, TTR, GPC3, SPP1, CD14, CCL16, CTSC, IL32, SPINK1, CCL20, ARG1, IGF2, APOC3, LYZ, DKK1, DLK1, AZGP1, F9, COL1A2, SLPI, MTHFD2, SAA1, ANGPTL4, KLKB1, CES2, CES1
GO:0017144~drug metabolic process	9	4.812834	2.78E-10	CYP2C9, CBR1, CYP2C8, CYP2A6, CYP4F2, EPHX2, ADH1A, CYP3A4, FMO4
GO:0016705~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	10	5.347594	8.87E-09	CYP2J2, CYP2C9, CYP2C8, CYP2A6, CYP4F2, CYP4F3, CYP4A11, CYP3A4, CYP4F11, KLKB1
GO:0004497~monooxygenase activity	10	5.347594	1.04E-08	CYP2J2, CYP2C9, CYP2C8, CYP4F2, CYP4F3, CYP4A11, FMO3, CYP3A4, CYP4F11, KLKB1
GO:0005782~peroxisomal matrix	9	4.812834	1.82E-08	DAO, ACOX2, EHHADH, PIPOX, HAO1, CRYM, BAAT, AGXT, HAO2

GO:0019373~epoxygenase P450 pathway	7	3.743316	2.33E-08	CYP2J2, CYP2C9, CYP2C8, CYP2A6, CYP4F2, EPHX2, CYP4A11
GO:0005576~extracellular region	42	22.45989	2.74E-08	APCS, SERPINE2, SERPINC1, PON1, SAA4, AFM, PLG, HPR, C8B, NTS, C8A, SERPINA4, CPN2, KNG1, GHR, HPX, C6, TTR, SPP1, LEPR, SPP2, CD14, CCL16, CCL20, IGF2, APOC3, LYZ, DKK1, MMP12, AZGP1, F9, COL1A2, CFHR4, COL5A2, RGN, SAA1, CFHR5, F13B, MASP2, ANGPTL4, HRG, KLKB1
GO:0020037~heme binding	13	6.951872	2.78E-08	CYP2J2, CYP4F2, CYP4A11, CYP4F3, CYP3A4, CYP4F11, CYP7A1, CYP2C9, CYP2A6, CYP2C8, CBS, HRG, KLKB1
GO:0008152~metabolic process	13	6.951872	2.64E-07	ACSL1, EPHX2, INSIG1, UGT2B15, AQP9, ACSL4, LYZ, NAT2, EHHADH, UGT1A4, ECHDC3, CES1, UGT1A6
GO:0008202~steroid metabolic process	8	4.278075	3.37E-07	CYP2C9, CYP2C8, CYP2A6, G6PC, UGT2B15, HSD17B6, CYP3A4, SULT2A1
GO:0008392~arachidonic acid epoxygenase activity	6	3.208556	3.69E-07	CYP2J2, CYP2C9, CYP2C8, CYP2A6, CYP4F2, CYP4A11
GO:0072562~blood microparticle	12	6.417112	4.39E-07	APCS, HPX, SERPINC1, PON1, AFM, PLG, HPR, ANGPTL4, HRG, C8A, KNG1, CPN2
GO:0005759~mitochondrial matrix	16	8.55615	1.30E-06	GLS2, ETFDH, OGDHL, ABAT, GLYAT, DHTKD1, BDH1, CPS1, MTHFD2, PDK4, HAGH, HMGCS2, AGXT, AASS, OTC, PCK2
GO:0005789~endoplasmic reticulum membrane	26	13.90374	2.20E-06	INSIG1, CYP3A4, CYP7A1, HSD11B1, RDH16, UGT1A4, UGT1A6, CYP2J2, G6PC, ACSL1, CYP4F2, EPHX1, DIO1, UGT2B15, CYP4F3, CYP4A11, ACSL4, FMO3, FMO4, CYP4F11, CYP2C9, CYP2A6, CYP2C8, HPD, SLC27A2, SLC27A5
GO:0001676~long-chain fatty acid metabolic process	6	3.208556	2.37E-06	ACSL1, CYP4F2, CYP4A11, ACSL4, SLC27A2, SLC27A5
GO:0005506~iron ion binding	11	5.882353	5.98E-06	CYP2J2, CYP2C9, CYP2C8, CYP2A6, CYP4F2, CYP4F3, CYP4A11, CYP3A4, CYP4F11, KLKB1, CYP7A1
GO:0006094~gluconeogenesis	7	3.743316	7.03E-06	PFKFB1, SDS, G6PC, ALDOB, PCK1, FBP1, PCK2
GO:0016491~oxidoreductase activity	12	6.417112	1.07E-05	HSD11B1, CYP2C9, BDH1, ADH1B, DCXR, ETFDH, PIPOX, HSD17B6, CYP3A4, DHRS1, HAO2, AASS
GO:0005777~peroxisome	9	4.812834	1.09E-05	DAO, ACOX2, EPHX2, EHHADH, PIPOX, HAO1, BAAT, AGXT, HAO2
GO:0009636~response to toxic substance	8	4.278075	3.53E-05	PON3, CPS1, EPHX2, EPHX1, PON1, GLYAT, SLC6A1, CES1
GO:0006699~bile acid biosynthetic process	5	2.673797	6.63E-05	ACOX2, BAAT, SLC27A2, CYP7A1, SLC27A5
GO:0019835~cytolysis	5	2.673797	6.63E-05	C6, MMD, LYZ, C8B, C8A

GO:0097267~omega-hydroxylase P450 pathway	4	2.139037	9.70E-05	CYP2C9, CYP2C8, CYP4F2, CYP4A11
GO:0005102~receptor binding	14	7.486631	1.15E-04	SERPINE2, EPHX2, PIPOX, PLG, BAAT, KNG1, DAO, ACOX2, EHHADH, HAO1, HRG, AGXT, HAO2, SLC27A2
GO:0006000~fructose metabolic process	4	2.139037	1.38E-04	PFKFB1, PFKFB3, ALDOB, FBP1
GO:0019825~oxygen binding	6	3.208556	1.43E-04	CYP2C9, CYP2C8, CBS, CYP4F3, CYP4A11, CYP3A4
GO:0046487~glyoxylate metabolic process	5	2.673797	1.59E-04	DAO, HAO1, AGXT, GNMT, DHTKD1
GO:0008395~steroid hydroxylase activity	5	2.673797	1.59E-04	CYP2J2, CYP2C9, CYP2C8, CYP2A6, CYP3A4
GO:0000050~urea cycle	4	2.139037	2.48E-04	SLC25A15, CPS1, ARG1, OTC
GO:0042738~exogenous drug catabolic process	4	2.139037	2.48E-04	CYP2C9, CYP2C8, CYP2A6, CYP3A4
GO:0004467~long-chain fatty acid-CoA ligase activity	4	2.139037	3.20E-04	ACSL1, ACSL4, SLC27A2, SLC27A5
GO:0030170~pyridoxal phosphate binding	6	3.208556	3.58E-04	SDS, CBS, TAT, CTH, ABAT, AGXT
GO:0006641~triglyceride metabolic process	5	2.673797	5.16E-04	G6PC, ACSL1, INSIG1, APOC3, ACSL4
GO:0019448~L-cysteine catabolic process	3	1.604278	6.76E-04	CBS, CDO1, AGXT
GO:0036101~leukotriene B4 catabolic process	3	1.604278	6.76E-04	CYP4F2, CYP4F3, CYP4A11
GO:0050051~leukotriene-B4 20-monooxygenase activity	3	1.604278	6.76E-04	CYP4F2, CYP4F3, CYP4A11
GO:0034875~caffeine oxidase activity	3	1.604278	6.76E-04	CYP2C9, CYP2C8, CYP3A4
GO:0006855~drug transmembrane transport	4	2.139037	0.001034	ABCB1, ABCB4, SLC22A1, ABCA8
GO:0019439~aromatic compound catabolic process	3	1.604278	0.001119	PON3, EPHX1, PON1
GO:0006572~tyrosine catabolic process	3	1.604278	0.001119	HGD, TAT, HPD
GO:0008559~xenobiotic-transporting ATPase activity	3	1.604278	0.001119	ABCB1, ABCB4, ABCA8
GO:0034364~high-density lipoprotein particle	4	2.139037	0.001375	SAA4, PON1, SAA1, APOC4
GO:0016597~amino acid binding	4	2.139037	0.001607	TAT, DPYS, AGXT, OTC
GO:0042737~drug catabolic process	3	1.604278	0.001666	CYP2C9, CYP3A4, FMO4
GO:0010951~negative regulation of endopeptidase activity	7	3.743316	0.001939	SERPINE2, SLPI, SERPINC1, SPP2, HRG, SERPINA4, KNG1
GO:0005579~membrane attack complex	3	1.604278	0.002082	C6, C8B, C8A
GO:0005739~mitochondrion	26	13.90374	0.002093	GLS2, TAT, OGDHL, ABAT, GLYAT, DHTKD1, GHR, RGS2, PDK4, HMGCS2, CRYM, HAO2, AASS, PCK2, SDS, KCNJ8, ACSL1, G0S2, ANXA10, BDH1, ACOX2, MTHFD2, EHHADH, ECHDC3, SLC27A2, OTC
GO:0005778~peroxisomal membrane	5	2.673797	0.002188	DAO, ACSL1, PXMP2, ACSL4, SLC27A2

GO:0042803~protein homodimerization activity	18	9.625668	0.002236	TOP2A, PON3, SDS, EPHX2, TESC, ZBTB16, PON1, SLC22A1, ABAT, ARID3A, GHR, GYS2, CBS, UGT1A4, CRYL1, CRYM, AGXT, UGT1A6
GO:0016311~dephosphorylation	6	3.208556	0.002314	PON3, PFKFB1, PFKFB3, EPHX2, PON1, FBP1
GO:0006631~fatty acid metabolic process	5	2.673797	0.002315	GHR, EHHADH, CYP4A11, CRYL1, BAAT
GO:0042908~xenobiotic transport	3	1.604278	0.002316	ABCB1, ABCB4, ABCA8
GO:0034366~spherical high-density lipoprotein particle	3	1.604278	0.002757	PON1, APOC3, HPR
GO:0006690~icosanoid metabolic process	3	1.604278	0.003067	CYP2J2, CYP4F2, CYP4F3
GO:0046951~ketone body biosynthetic process	3	1.604278	0.003067	BDH1, HMGCS2, SLC27A5
GO:0102391~decanoate--CoA ligase activity	3	1.604278	0.003068	ACSL1, ACSL4, SLC27A2
GO:0007596~blood coagulation	8	4.278075	0.003731	F9, COL1A2, SERPINE2, SERPINC1, CYP4F2, F13B, PLG, CYP4F11
GO:0051289~protein homotetramerization	5	2.673797	0.003902	CTH, DCXR, DPYS, FBP1, GNMT
GO:0004867~serine-type endopeptidase inhibitor activity	6	3.208556	0.003902	SPINK1, SERPINE2, SLPI, SERPINC1, HRG, SERPINA4
GO:0070327~thyroid hormone transport	3	1.604278	0.003915	SLCO1B1, TTR, CRYM
GO:0003824~catalytic activity	8	4.278075	0.004203	PFKFB3, ACSL1, EPHX2, EHHADH, ECHDC3, ACSL4, HSD17B6, FTCD
GO:0043231~intracellular membrane-bounded organelle	14	7.486631	0.004666	PON3, ABCA6, CYP4F2, PON1, UGT2B15, CYP4A11, AQP9, FMO3, CYP3A4, CYP7A1, CYP2C9, ACOX2, RDH16, AASS
GO:0031957~very long-chain fatty acid-CoA ligase activity	3	1.604278	0.004862	ACSL4, SLC27A2, SLC27A5
GO:0042632~cholesterol homeostasis	5	2.673797	0.004919	G6PC, EPHX2, APOC3, CD24, CYP7A1
GO:0002576~platelet degranulation	6	3.208556	0.00503	IGF2, SPP2, PLG, HRG, SERPINA4, KNG1
GO:0051384~response to glucocorticoid	5	2.673797	0.005199	GHR, PFKFB1, TAT, CDO1, AGXT
GO:0005829~cytosol	49	26.20321	0.005343	SERPINE2, DPYS, TAT, OGDHL, GBA3, FTCD, DHTKD1, GYS2, LGALS4, RGS2, AKR7A3, SULT2A1, IER3, CBR1, HGD, ARG1, BAAT, UPB1, MTHFD2, EHHADH, RGN, HAGH, ALDOB, FBP1, HPD, CES1, PFKFB1, PFKFB3, ADH1B, NR1I3, ADH1A, SELENBP1, CBS, IGF2BP2, PCK1, IL32, EPHX2, ZBTB16, CIDEB, GNMT, BHMT, DAO, FABP5, NAT2, ETNK2, CTH, CRYL1, CDO1, ALDH8A1
GO:0006096~glycolytic process	4	2.139037	0.005678	PFKFB1, OGDHL, ALDOB, DHTKD1
GO:0006006~glucose metabolic process	5	2.673797	0.005789	FABP5, DCXR, IGF2, PDK4, PCK1

GO:0006559~L-phenylalanine catabolic process	3	1.604278	0.005898	HGD, TAT, HPD
GO:0070989~oxidative demethylation	3	1.604278	0.007028	CYP2C9, CYP2C8, CYP3A4
GO:0015908~fatty acid transport	3	1.604278	0.007028	ACSL1, ACSL4, SLC27A2
GO:0006107~oxaloacetate metabolic process	3	1.604278	0.007028	GHR, PCK1, PCK2
GO:0006554~lysine catabolic process	3	1.604278	0.007028	PIPOX, CRYM, AASS
GO:0042301~phosphate ion binding	3	1.604278	0.007031	G6PC, MTHFD2, OTC
GO:0006957~complement activation, alternative pathway	3	1.604278	0.008247	CFHR5, C8B, C8A
GO:0044267~cellular protein metabolic process	6	3.208556	0.008847	APCS, TTR, SAA1, IGF2, PLG, LYZ
GO:0006520~cellular amino acid metabolic process	4	2.139037	0.008947	SLC25A15, SDS, GLS2, TAT
GO:0006869~lipid transport	5	2.673797	0.008998	ABCA6, CFHR4, APOC4, APOC3, ABCA8
GO:0006691~leukotriene metabolic process	3	1.604278	0.010947	CYP4F2, CYP4F3, CYP4A11
GO:0042626~ATPase activity, coupled to transmembrane movement of substances	4	2.139037	0.011634	ABCB1, ABCA6, ABCB4, ABCA8
GO:0052695~cellular glucuronidation	3	1.604278	0.012423	UGT2B15, UGT1A4, UGT1A6
GO:0006810~transport	10	5.347594	0.012898	SEC14L2, SLC25A15, ABCB1, TTR, SLC10A1, ABCB4, AQP9, AFP, ABCA8, SLC6A1
GO:0005543~phospholipid binding	5	2.673797	0.013732	SEC14L2, CPS1, PON1, APOC3, OTC
GO:0005788~endoplasmic reticulum lumen	7	3.743316	0.013756	F9, COL1A2, COL5A2, SLC27A2, CTSC, CES2, CES1
GO:0042802~identical protein binding	16	8.55615	0.015016	PFKFB1, HGD, DCXR, ZBTB16, CIDEB, LYZ, ROBO1, AKR7A3, TTR, COL1A2, CBS, CTH, ALDOB, ANGPTL4, FBP1, CTSC
GO:0007597~blood coagulation, intrinsic pathway	3	1.604278	0.01562	F9, KLKB1, KNG1
GO:0004745~retinol dehydrogenase activity	3	1.604278	0.015627	ADH1A, RDH16, HSD17B6
GO:0009055~electron carrier activity	5	2.673797	0.015991	AKR7A3, ACOX2, RDH16, ETFDH, HSD17B6
GO:0001501~skeletal system development	6	3.208556	0.016079	COL1A2, ZBTB16, COL5A2, IGF2, SPP2, SOX9
GO:0055085~transmembrane transport	8	4.278075	0.016365	AZGP1, ABCB1, ABCA6, SLC10A1, ABCB4, ABCA8, SLC6A1, SLC17A4
GO:0031093~platelet alpha granule lumen	4	2.139037	0.018353	IGF2, PLG, HRG, KNG1
GO:0009813~flavonoid biosynthetic process	3	1.604278	0.019127	UGT2B15, UGT1A4, UGT1A6
GO:0030234~enzyme regulator activity	3	1.604278	0.019137	RGN, APOC3, CPN2
GO:0042730~fibrinolysis	3	1.604278	0.020994	PLG, HRG, KLKB1
GO:0032094~response to food	3	1.604278	0.020994	GHR, G6PC, CPS1

GO:0006954~inflammatory response	10	5.347594	0.02124	CCL20, EPHX2, SPP1, CD14, LYZ, CYP4F11, CDO1, KNG1, CCL16, TNFRSF21
GO:0055081~anion homeostasis	2	1.069519	0.021325	CPS1, OTC
GO:0046395~carboxylic acid catabolic process	2	1.069519	0.021325	PON3, PON1
GO:0042361~menaquinone catabolic process	2	1.069519	0.021325	CYP4F2, CYP4F11
GO:0042377~vitamin K catabolic process	2	1.069519	0.021325	CYP4F2, CYP4F11
GO:0006116~NADH oxidation	2	1.069519	0.021325	ALDOB, PCK2
GO:0046226~coumarin catabolic process	2	1.069519	0.021325	PON3, CYP2A6
GO:0032305~positive regulation of icosanoid secretion	2	1.069519	0.021325	CYP4F2, CYP4A11
GO:0004613~phosphoenolpyruvate carboxykinase (GTP) activity	2	1.069519	0.02133	PCK1, PCK2
GO:0052853~long-chain-(S)-2-hydroxy-long-chain-acid oxidase activity	2	1.069519	0.02133	HAO1, HAO2
GO:0052854~medium-chain-(S)-2-hydroxy-acid oxidase activity	2	1.069519	0.02133	HAO1, HAO2
GO:0052871~alpha-tocopherol omega-hydroxylase activity	2	1.069519	0.02133	CYP4F2, CYP4F3
GO:0097259~20-aldehyde-leukotriene B4 20-monooxygenase activity	2	1.069519	0.02133	CYP4F2, CYP4F3
GO:0097258~20-hydroxy-leukotriene B4 omega oxidase activity	2	1.069519	0.02133	CYP4F2, CYP4F3
GO:0003973~(S)-2-hydroxy-acid oxidase activity	2	1.069519	0.02133	HAO1, HAO2
GO:0052852~very-long-chain-(S)-2-hydroxy-acid oxidase activity	2	1.069519	0.02133	HAO1, HAO2
GO:0004063~aryldialkylphosphatase activity	2	1.069519	0.02133	PON3, PON1
GO:0005215~transporter activity	7	3.743316	0.021802	SEC14L2, SLCO1B1, ABCB1, FABP5, ABCA6, AQP9, ABCA8
GO:0052696~flavonoid glucuronidation	3	1.604278	0.022933	UGT2B15, UGT1A4, UGT1A6
GO:0001972~retinoic acid binding	3	1.604278	0.024954	UGT2B15, UGT1A4, UGT1A6
GO:0006629~lipid metabolic process	6	3.208556	0.027099	FABP5, ABCB4, RDH16, APOC4, ACSL4, CYP3A4
GO:0019899~enzyme binding	9	4.812834	0.027405	TOP2A, CYP2A6, SLPI, CBS, EHHADH, UGT1A4, CYP3A4, SLC27A2, UGT1A6

GO:0008201~heparin binding	6	3.208556	0.02911	ECM2, SERPINE2, SERPINC1, SAA1, HRG, KNG1
GO:0019433~triglyceride catabolic process	3	1.604278	0.029167	FABP5, CPS1, APOC3
GO:0071356~cellular response to tumor necrosis factor	5	2.673797	0.030667	CCL20, PCK1, CCL16, TNFRSF21, PCK2
GO:0050660~flavin adenine dinucleotide binding	4	2.139037	0.031352	ACOX2, ETFDH, FMO3, FMO4
GO:0061621~canonical glycolysis	3	1.604278	0.031378	PFKFB1, PFKFB3, ALDOB
GO:0070328~triglyceride homeostasis	3	1.604278	0.031378	APOC4, APOC3, ANGPTL4
GO:0003095~pressure natriuresis	2	1.069519	0.031817	CYP4F2, CYP4A11
GO:0042376~phylloquinone catabolic process	2	1.069519	0.031817	CYP4F2, CYP4F11
GO:0032787~monocarboxylic acid metabolic process	2	1.069519	0.031817	CYP2C9, GLYAT
GO:0019343~cysteine biosynthetic process via cystathionine	2	1.069519	0.031817	CBS, CTH
GO:0102007~acyl-L-homoserine-lactone lactonohydrolase activity	2	1.069519	0.031825	PON3, PON1
GO:0047374~methylumbelliferyl-acetate deacetylase activity	2	1.069519	0.031825	CES2, CES1
GO:0008431~vitamin E binding	2	1.069519	0.031825	SEC14L2, AFM
GO:0032496~response to lipopolysaccharide	6	3.208556	0.031874	KCNJ8, CPS1, SLPI, PCK1, TNFRSF21, PCK2
GO:0015721~bile acid and bile salt transport	3	1.604278	0.033654	SLCO1B1, SLC10A1, SLC27A5
GO:0042056~chemoattractant activity	3	1.604278	0.03367	SAA4, SAA1, CCL16
GO:0070330~aromatase activity	3	1.604278	0.03367	CYP2J2, CYP2C8, CYP3A4
GO:0048247~lymphocyte chemotaxis	3	1.604278	0.035992	CCL20, SAA1, CCL16
GO:0010033~response to organic substance	3	1.604278	0.035992	AQP9, S100P, CTSC
GO:0015020~glucuronosyltransferase activity	3	1.604278	0.03841	UGT2B15, UGT1A4, UGT1A6
GO:0071347~cellular response to interleukin-1	4	2.139037	0.040732	CCL20, SOX9, PCK1, CCL16
GO:0030449~regulation of complement activation	3	1.604278	0.04085	C6, C8B, C8A
GO:0016758~transferase activity, transferring hexosyl groups	3	1.604278	0.040869	UGT2B15, UGT1A4, UGT1A6
GO:0051919~positive regulation of fibrinolysis	2	1.069519	0.042197	PLG, KLKB1
GO:1903052~positive regulation of proteolysis involved in cellular protein catabolic process	2	1.069519	0.042197	RGN, CTSC
GO:0070814~hydrogen sulfide biosynthetic process	2	1.069519	0.042197	CBS, CTH

GO:0019344~cysteine biosynthetic process	2	1.069519	0.042197	CBS, CTH
GO:0009605~response to external stimulus	2	1.069519	0.042197	PON3, PON1
GO:0006565~L-serine catabolic process	2	1.069519	0.042197	SDS, CBS
GO:0006534~cysteine metabolic process	2	1.069519	0.042197	CTH, CDO1
GO:0019240~citrulline biosynthetic process	2	1.069519	0.042197	CPS1, OTC
GO:0004591~oxoglutarate dehydrogenase (succinyl-transferring) activity	2	1.069519	0.042207	OGDHL, DHTKD1
GO:0003873~6-phosphofructo-2-kinase activity	2	1.069519	0.042207	PFKFB1, PFKFB3
GO:0018685~alkane 1-monooxygenase activity	2	1.069519	0.042207	CYP4F2, CYP4A11
GO:0090554~phosphatidylcholine-translocating ATPase activity	2	1.069519	0.042207	ABCB1, ABCB4
GO:0004301~epoxide hydrolase activity	2	1.069519	0.042207	EPHX2, EPHX1
GO:0043200~response to amino acid	3	1.604278	0.043366	CPS1, ARG1, CDO1
GO:0022617~extracellular matrix disassembly	4	2.139037	0.04822	MMP12, SPP1, PLG, KLKB1
GO:0015758~glucose transport	3	1.604278	0.048565	G6PC, FABP5, SLC2A2
GO:0045252~oxoglutarate dehydrogenase complex	2	1.069519	0.049742	OGDHL, DHTKD1

Table S8. KEGG analysis results of DEGs between low- and high-ACBD4 expression groups

Term	Count	%	PValue	Genes
hsa01100:Metabolic pathways	63	33.68984	3.73E-16	DPYS, TAT, ABAT, OGDHL, GBA3, FTCD, HMGCS2, AASS, CBR1, G6PC, SDS, HGD, ACSL1, ARG1, DCXR, UGT2B15, PIPOX, ACSL4, BAAT, UPB1, CYP2A6, BDH1, ACOX2, MTHFD2, EHHADH, RGN, ALDOB, AGXT, FBP1, HPD, SLC27A5, CES1, GLS2, ADH1B, ADH1A, HSD17B6, CYP3A4, CYP7A1, HSD11B1, CBS, RDH16, UGT1A4, HAO1, ATP6V0E2, PCK1, HAO2, UGT1A6, PCK2, CYP2J2, EPHX2, CYP4F2, CYP4F3, CYP2C9, CYP2C8, BHMT, DAO, CPS1, NAT2, ETNK2, CTH, CRYL1, CDO1, OTC
hsa05204:Chemical carcinogenesis	14	7.486631	1.56E-09	CBR1, ADH1B, ADH1A, EPHX1, UGT2B15, CYP3A4, HSD11B1, CYP2C9, CYP2A6, CYP2C8, NAT2, UGT1A4, SULT2A1, UGT1A6
hsa00980:Metabolism of xenobiotics by cytochrome P450	13	6.951872	7.06E-09	CBR1, ADH1B, ADH1A, EPHX1, UGT2B15, CYP3A4, HSD11B1, CYP2C9, CYP2A6, AKR7A3, UGT1A4, SULT2A1, UGT1A6
hsa03320:PPAR signaling pathway	12	6.417112	2.71E-08	ACOX2, FABP5, ACSL1, EHHADH, APOC3, ACSL4, ANGPTL4, PCK1, SLC27A2, CYP7A1, SLC27A5, PCK2
hsa04146:Peroxisome	13	6.951872	2.71E-08	ACSL1, EPHX2, PIPOX, ACSL4, BAAT, DAO, ACOX2, EHHADH, PXMP2, HAO1, AGXT, HAO2, SLC27A2
hsa01130:Biosynthesis of antibiotics	19	10.16043	4.52E-08	SDS, ARG1, TAT, OGDHL, DAO, CBS, EHHADH, CTH, RGN, HAO1, ALDOB, HMGCS2, PCK1, AGXT, HAO2, FBP1, AASS, OTC, PCK2
hsa00983:Drug metabolism - other enzymes	10	5.347594	1.08E-07	CYP2A6, NAT2, DPYS, UGT2B15, UGT1A4, CYP3A4, UPB1, CES2, UGT1A6, CES1
hsa00830:Retinol metabolism	11	5.882353	1.95E-07	CYP2C9, CYP2C8, CYP2A6, ADH1B, ADH1A, UGT2B15, RDH16, UGT1A4, HSD17B6, CYP3A4, UGT1A6
hsa00982:Drug metabolism - cytochrome P450	11	5.882353	3.52E-07	CYP2C9, CYP2C8, CYP2A6, ADH1B, ADH1A, UGT2B15, UGT1A4, FMO3, CYP3A4, FMO4, UGT1A6
hsa04976:Bile secretion	11	5.882353	4.05E-07	SLCO1B1, ABCB1, SLC10A1, ABCB4, EPHX1, SLC22A1, AQP9, BAAT, CYP7A1, SLC27A5, SULT2A1
hsa04610:Complement and coagulation cascades	10	5.347594	3.91E-06	C6, F9, SERPINC1, F13B, MASP2, PLG, C8B, KLKB1, C8A, KNG1
hsa00260:Glycine, serine and threonine metabolism	8	4.278075	5.53E-06	BHMT, SDS, DAO, CBS, CTH, PIPOX, AGXT, GNMT
hsa01200:Carbon metabolism	10	5.347594	2.09E-04	SDS, CPS1, EHHADH, RGN, OGDHL, HAO1, ALDOB, AGXT, FBP1, HAO2

hsa01230:Biosynthesis of amino acids	8	4.278075	3.21E-04	SDS, CPS1, CBS, ARG1, TAT, CTH, ALDOB, OTC
hsa00270:Cysteine and methionine metabolism	6	3.208556	5.89E-04	BHMT, SDS, CBS, TAT, CTH, CDO1
hsa00140:Steroid hormone biosynthesis	7	3.743316	6.22E-04	HSD11B1, UGT2B15, UGT1A4, HSD17B6, CYP3A4, CYP7A1, UGT1A6
hsa00590:Arachidonic acid metabolism	7	3.743316	8.16E-04	CYP2J2, CYP2C9, CBR1, CYP2C8, CYP4F2, EPHX2, CYP4F3
hsa00010:Glycolysis / Gluconeogenesis	7	3.743316	0.001342	G6PC, ADH1B, ADH1A, ALDOB, PCK1, FBP1, PCK2
hsa00040:Pentose and glucuronate interconversions	5	2.673797	0.002911	DCXR, UGT2B15, UGT1A4, CRYL1, UGT1A6
hsa00120:Primary bile acid biosynthesis	4	2.139037	0.003382	ACOX2, BAAT, CYP7A1, SLC27A5
hsa00350:Tyrosine metabolism	5	2.673797	0.003621	HGD, ADH1B, TAT, ADH1A, HPD
hsa00220:Arginine biosynthesis	4	2.139037	0.005447	CPS1, GLS2, ARG1, OTC
hsa00071:Fatty acid degradation	5	2.673797	0.007016	ACSL1, ADH1B, EHHADH, ADH1A, ACSL4
hsa04152:AMPK signaling pathway	8	4.278075	0.007185	GYS2, PFKFB1, PFKFB3, G6PC, LEPR, PCK1, FBP1, PCK2
hsa04920:Adipocytokine signaling pathway	6	3.208556	0.008917	G6PC, ACSL1, LEPR, ACSL4, PCK1, PCK2
hsa00650:Butanoate metabolism	4	2.139037	0.012735	BDH1, EHHADH, ABAT, HMGCS2
hsa00053:Ascorbate and aldarate metabolism	4	2.139037	0.012735	UGT2B15, RGN, UGT1A4, UGT1A6
hsa04931:Insulin resistance	7	3.743316	0.014035	GYS2, G6PC, SLC2A2, PCK1, SLC27A2, SLC27A5, PCK2
hsa00591:Linoleic acid metabolism	4	2.139037	0.015493	CYP2J2, CYP2C9, CYP2C8, CYP3A4
hsa00410:beta-Alanine metabolism	4	2.139037	0.018562	EHHADH, DPYS, ABAT, UPB1
hsa00051:Fructose and mannose metabolism	4	2.139037	0.020214	PFKFB1, PFKFB3, ALDOB, FBP1
hsa00250:Alanine, aspartate and glutamate metabolism	4	2.139037	0.02564	CPS1, GLS2, ABAT, AGXT
hsa04922:Glucagon signaling pathway	6	3.208556	0.034758	GYS2, PFKFB1, G6PC, SLC2A2, PCK1, PCK2
hsa00360:Phenylalanine metabolism	3	1.604278	0.037831	TAT, GLYAT, HPD
hsa05146:Amoebiasis	6	3.208556	0.04458	COL1A2, ARG1, COL5A2, CD14, C8B, C8A
hsa02010:ABC transporters	4	2.139037	0.046117	ABCB1, ABCA6, ABCB4, ABCA8

Table S9. GSEA results between low- and high-ACBD4 expression groups by using c2 reference gene set.

NAME	SIZE	ES	NES	NOM p-val	FDR q-val
KEGG_CITRATE_CYCLE_TCA_CYCLE	30	0.684246	1.701258	0.017964	0.143114
REACTOME_GAMMA_CARBOXYLATION_HYPUSINE_FORMATION_AND_ARYLSULFATASE_ACTIVATION	31	0.61831	1.67699	0.012072	0.143506
LEE_LIVER_CANCER_DENA_DN	72	0.774205	1.709192	0.002049	0.143665
REACTOME_THE_PHOTOTRANSDUCTION_CASCADE	30	0.428149	1.68462	0.020121	0.144099
KEGG_TRYPTOPHAN_METABOLISM	30	0.792638	1.688628	0.00611	0.144152
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	62	0.550098	1.71033	0.004202	0.144388
SHEN_SMARCA2_TARGETS_DN	266	0.392519	1.682721	0.032193	0.144799
BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN	36	0.811455	1.701741	0.006048	0.144821
BOYAULT_LIVER_CANCER_SUBCLASS_G3_DN	47	0.804704	1.677312	0.014894	0.144931
WP_NUCLEAR_RECEPTORS_IN_LIPID_METABOLISM_AND_TOXICITY	32	0.782606	1.678269	0.008333	0.145427
CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_UP	51	0.837356	1.688965	<0.01	0.145715
ACEVEDO_LIVER_CANCER_DN	382	0.619411	1.684762	0.006369	0.145944
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	66	0.581405	1.678896	0.049383	0.146402
LEE_LIVER_CANCER_SURVIVAL_UP	145	0.842902	1.702217	<0.01	0.146564

LEE_LIVER_CANCER_CIPROFIBRATE_DN	63	0.739	1.679	<0.01	0.146
		238	96		721
CAIRO_HEPATOBLASTOMA_DN	239	0.857	1.712	<0.01	0.146
		501	308		768
ANDERSEN_LIVER_CANCER_KRT19_DN	64	0.875	1.685	<0.01	0.146
		115	521		871
CAIRO_HEPATOBLASTOMA_CLASSES_DN	182	0.737	1.705	<0.01	0.146
		888	323		933
HSIAO_LIVER_SPECIFIC_GENES	234	0.820	1.710	0.002	0.147
		141	353	049	014
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	306	0.486	1.703	0.014	0.147
		24	54	433	119
REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	50	0.546	1.719	0.012	0.147
		51	112	295	288
WOO_LIVER_CANCER_RECURRENCE_DN	75	0.883	1.689	<0.01	0.147
		952	091		662
CAIRO_LIVER_DEVELOPMENT_DN	207	0.654	1.693	0.010	0.147
		68	388	661	717
REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	116	0.490	1.726	0.033	0.148
		651	082	597	498
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	48	0.595	1.689	0.012	0.148
		338	895	346	615
MIKKELSEN_MEF_LCP_WITH_H3K27ME3	37	0.554	1.732	0.010	0.148
		241	078	373	727
STEIN_ESRRA_TARGETS_UP	318	0.470	1.734	<0.01	0.148
		849	134		781
REACTOME_GLYOXYLATE_METABOLISM_AND_GLYCINE_DEGRADATION	28	0.764	1.672	0.014	0.148
		125	024	675	919
REACTOME_PHASE_I_FUNCTIONALIZATION_OF_COMPOUNDS	86	0.735	1.691	0.002	0.148
		677	094	11	979
KEGG_TYROSINE_METABOLISM	36	0.731	1.712	<0.01	0.149

		059	326		494
BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_48HR_UP	18	0.599	1.719	0.008	0.149
		715	507	18	635
WP_EICOSANOID_METABOLISM_VIA_LIPO_OXYGENASES_LOX	24	0.687	1.693	0.010	0.149
		379	477	823	913
REACTOME_THE_CANONICAL_RETINOID_CYCLE_IN_RODS_TWILIGHT_VISION_	18	0.707	1.735	0.005	0.150
		414	313	988	181
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	68	0.491	1.726	0.052	0.150
		905	966	023	231
REACTOME_RECYCLING_OF_BILE_ACIDS_AND_SALTS	16	0.879	1.742	<0.01	0.150
		433	3		608
REACTOME_DEFECTS_IN_VITAMIN_AND_COFACTOR_METABOLISM	17	0.682	1.720	0.012	0.150
		515	766	739	776
REACTOME_METABOLISM_OF_STEROID_HORMONES	28	0.711	1.737	<0.01	0.151
		184	066		236
SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM4	218	0.613	1.722	<0.01	0.151
		043	438		236
WP_METAPATHWAY_BIOTRANSFORMATION_PHASE_I_AND_II	134	0.715	1.739	<0.01	0.151
		953	448		288
REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE	55	0.746	1.669	0.008	0.151
		473	149	23	367
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	57	0.843	1.712	<0.01	0.151
		679	985		468
LEE_LIVER_CANCER_ACOX1_DN	62	0.760	1.693	0.002	0.151
		911	84	075	697
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	30	0.660	1.659	0.006	0.152
		878	879	135	482
KEGG_PYRUVATE_METABOLISM	33	0.709	1.727	0.002	0.152
		636	569	083	58
WP_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	36	0.499	1.743	<0.01	0.152
		67	311		945

WP_TRYPTOPHAN_METABOLISM	34	0.740	1.658	0.008	0.153
		446	147	386	143
RUAN_RESPONSE_TO_TNF_TROGLITAZONE_DN	35	0.612	1.653	0.011	0.153
		298	341	013	51
CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_DN	147	0.923	1.654	<0.01	0.153
		096	375		575
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE_	21	0.698	1.660	0.018	0.153
		029	206	868	672
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	53	0.816	1.656	<0.01	0.153
		558	529		924
REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	40	0.767	1.713	<0.01	0.154
		495	144		263
WP_MELATONIN_METABOLISM_AND_EFFECTS	35	0.593	1.654	0.011	0.154
		367	932	811	39
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN	486	0.552	1.764	<0.01	0.154
		898	742		683
KEGG_RETINOL_METABOLISM	45	0.837	1.660	0.002	0.155
		039	52	079	063
WP_OXIDATION_BY_CYTOCHROME_P450	50	0.765	1.662	0.006	0.155
		875	956	173	256
OHGUCHI_LIVER_HNF4A_TARGETS_DN	112	0.763	1.648	0.004	0.155
		451	841	175	351
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_	72	0.457	1.665	0.069	0.155
HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_		044	271	903	451
WP_CONSTITUTIVE_ANDROSTANE_RECEPTOR_PATHWAY	26	0.870	1.661	<0.01	0.155
		22	401		533
REACTOME_SIGNALING_BY_RETINOIC_ACID	36	0.574	1.649	0.008	0.155
		721	536	299	722
KEGG_BETA_ALANINE_METABOLISM	21	0.757	1.744	0.006	0.155
		594	112	224	771
KEGG_FATTY_ACID_METABOLISM	35	0.773	1.650	0.010	0.156

		312	22	46	334
REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	45	0.593	1.787	<0.01	0.156
		98	642		515
MEBARKI_HCC_PROGENITOR_FZD8CRD_DN	270	0.672	1.766	<0.01	0.156
		399	694		862
VANTVEER_BREAST_CANCER_METASTASIS_UP	34	0.621	1.663	0.002	0.157
		685	046	012	038
MOOTHA_GLYCOGEN_METABOLISM	20	0.663	1.642	0.006	0.157
		3	877	186	724
LUCAS_HNF4A_TARGETS_UP	51	0.622	1.643	0.015	0.157
		471	821	284	898
WP_ONE_CARBON_METABOLISM_AND_RELATED_PATHWAYS	45	0.636	1.645	0.008	0.157
		149	989	493	921
WP_PREGNANE_X_RECEPTOR_PATHWAY	28	0.821	1.644	0.002	0.158
		825	236	092	796
REACTOME_FATTY_ACID_METABOLISM	135	0.640	1.768	0.002	0.158
		316	641	105	947
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODEL_OXPHOS_SYSTEM	34	0.495	1.639	0.067	0.159
		771	748	864	11
WP_AMINO_ACID_METABOLISM	77	0.627	1.640	0.016	0.159
		729	807	26	202
VILLANUEVA_LIVER_CANCER_KRT19_DN	47	0.851	1.744	<0.01	0.159
		528	45		477
LEE_LIVER_CANCER_MYC_E2F1_DN	58	0.752	1.636	0.002	0.160
		365	912	024	228
XU_GH1_EXOGENOUS_TARGETS_DN	82	0.446	1.637	0.006	0.160
		271	466	036	925
PARENT_MTOR_SIGNALING_UP	484	0.423	1.770	<0.01	0.161
		301	538		164
BOYAULT_LIVER_CANCER_SUBCLASS_G123_DN	48	0.901	1.630	<0.01	0.161
		914	466		236

REACTOME_CLASS_I_PEROXISOMAL_MEMBRANE_PROTEIN_IMPORT	17	0.708259	1.773969	<0.01	0.161356
FONTAINE_PAPILLARY_THYROID_CARCINOMA_DN	58	0.522175	1.757603	<0.01	0.161564
WP_FATTY_ACID_BETA_OXIDATION	31	0.644621	1.630 86	0.021231	0.162005
WP_LEPTIN_INSULIN_OVERLAP	17	0.606921	1.631652	0.029821	0.162289
REACTOME_ARACHIDONIC_ACID_METABOLISM	49	0.662345	1.633511	0.006036	0.162371
REACTOME_PHASE_II_CONJUGATION_OF_COMPOUNDS	71	0.724 18	1.745293	0.002024	0.162 65
ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_DN	248	0.565721	1.788268	0.002045	0.162724
RUAN_RESPONSE_TO_TNF_DN	72	0.570968	1.632278	0.016949	0.162822
KEGG_PHENYLALANINE_METABOLISM	16	0.755637	1.620095	0.014344	0.162849
REACTOME_SULFUR_AMINO_ACID_METABOLISM	21	0.871568	1.792805	<0.01	0.162939
REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATION	16	0.685432	1.620895	0.005976	0.163034
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS	31	0.743585	1.622 56	0.010684	0.163255
BIOCARTA_STRESS_PATHWAY	24	0.502567	1.621464	0.023061	0.163 52
DESERT_PERIPORTAL_HEPATOCELLULAR_CARCINOMA_SUBCLASS_UP	147	0.894889	1.633 67	<0.01	0.163708
REACTOME_BIOLOGICAL_OXIDATIONS	162	0.735123	1.805731	<0.01	0.163 92
BOCHKIS_FOXA2_TARGETS	318	0.552	1.750	<0.01	0.164

		962	234		187
KEGG_INSULIN_SIGNALING_PATHWAY	127	0.400	1.618	0.007	0.164
		764	131	874	368
RODWELL_AGING_KIDNEY_NO_BLOOD_DN	114	0.502	1.622	0.012	0.164
		751	635	195	544
MIKKELSEN_NPC_LCP_WITH_H3K4ME3	38	0.587	1.746	<0.01	0.165
		857	724		381
KEGG_ABC_TRANSPORTERS	36	0.623	1.622	0.016	0.165
		432	986	129	454
DURCHDEWALD_SKIN_CARCINOGENESIS_UP	58	0.555	1.751	<0.01	0.166
		627	95		489
MOOTHA_FFA_OXYDATION	20	0.823	1.778	<0.01	0.166
		288	359		62
KEGG_PEROXISOME	67	0.746	1.774	<0.01	0.166
		54	759		653
KEGG_GLYCOLYSIS_GLUCONEOGENESIS	53	0.597	1.622	0.007	0.166
		561	999	921	877
LEE_LIVER_CANCER_E2F1_DN	57	0.695	1.625	0.004	0.167
		781	738	049	029
SERVITJA_ISLET_HNF1A_TARGETS_DN	76	0.567	1.611	0.014	0.167
		94	429	493	749
KIM_LIVER_CANCER_POOR_SURVIVAL_DN	43	0.867	1.610	0.006	0.167
		723	561	342	829
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	27	0.801	1.614	0.010	0.167
		543	793	504	886
REACTOME_COMPLEX_I_BIOGENESIS	36	0.506	1.612	0.067	0.168
		884	856	073	252
IIZUKA_LIVER_CANCER_PROGRESSION_G2_G3_UP	23	0.706	1.623	0.025	0.168
		224	034	157	297
KEGG_LYSINE_DEGRADATION	35	0.695	1.794	<0.01	0.168
		53	452		404

WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_WITH_H4K20ME1_MARK	100	0.488639	1.62382	0.012552	0.168507
BIOCARTA_NUCLEARRS_PATHWAY	32	0.750105	1.611586	0.016736	0.168878
REACTOME_ABC_TRANSPORTERS_IN_LIPID_HOMEOSTASIS	15	0.67377	1.61315	0.02045	0.169131
VARELA_ZMPSTE24_TARGETS_DN	34	0.745651	1.608564	0.006316	0.169605
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION	23	0.793147	1.807567	0.002128	0.17008
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	38	0.774951	1.606933	0.010549	0.170743
WP_TCA_CYCLE_AKA_KREBS_OR_CITRIC_ACID_CYCLE	18	0.675674	1.605995	0.033473	0.170794
REACTOME_RA_BIOSYNTHESIS_PATHWAY	16	0.720269	1.602006	0.012605	0.17562
KAAB_HEART_ATRIUM_VS_VENTRICLE_DN	231	0.431828	1.600073	0.00202	0.175991
BIOCARTA_INTRINSIC_PATHWAY	23	0.757754	1.600913	0.010616	0.176075
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN	40	0.630933	1.794679	0.004141	0.177341
SU_LIVER	57	0.868958	1.598056	0.006329	0.177811
YAMASHITA_LIVER_CANCER_STEM_CELL_DN	71	0.801252	1.587472	0.002075	0.180416
RODWELL_AGING_KIDNEY_DN	108	0.480697	1.587975	0.018145	0.180896
WP_NUCLEAR_RECEPTORS	38	0.538806	1.586416	0.023305	0.180924
KEGG_PROPANOATE_METABOLISM	26	0.788	1.807	0.002	0.181

		171	626	058	418
REACTOME_PLASMA_LIPOPROTEIN_ASSEMBLY	18	0.697	1.588	0.033	0.181
		466	203	264	834
REACTOME_GLUCONEOGENESIS	33	0.621	1.594	0.021	0.182
		544	672	825	
CHANGOLKAR_H2AFY_TARGETS_DN	29	0.616	1.588	0.023	0.182
		734	629	576	366
KEGG_STEROID_HORMONE_BIOSYNTHESIS	46	0.768	1.593	0.004	0.182
		989	412	237	636
WP_TAMOXIFEN_METABOLISM	20	0.917	1.589	<0.01	0.182
		761	208		772
REACTOME_GLUTATHIONE_CONJUGATION	25	0.696	1.591	0.011	0.183
		047	381	858	122
LEE_LIVER_CANCER_MYC_TGFA_DN	59	0.719	1.590	0.004	0.183
		285	461	124	408
SERVITJA_LIVER_HNF1A_TARGETS_DN	126	0.647	1.591	0.012	0.183
		623	821	146	83
VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN	92	0.589	1.589	0.012	0.183
		837	325	295	895
WP_PPAR_SIGNALING_PATHWAY	59	0.626	1.583	0.025	0.184
		39	45	157	374
WP_NUCLEAR_RECEPTORS_METAPATHWAY	255	0.517	1.579	0.004	0.187
		756	834	184	258
REACTOME_METABOLISM_OF_PORPHYRINS	24	0.712	1.580	0.023	0.187
		315	499	256	455
REACTOME_DEFECTS_OF_CONTACT_ACTIVATION_SYSTEM_CAS_AND_KALLIKREIN_KININ_SYSTEM_KKS_	16	0.805	1.577	0.012	0.189
		447	473	766	88
WONG_MITOCHONDRIA_GENE_MODULE	175	0.424	1.575	0.055	0.190
		321	946	441	77
HOEGERKORP_CD44_TARGETS_DIRECT_UP	23	0.552	1.572	0.037	0.191
		08	962	344	816

ONDER_CDH1_TARGETS_1_UP	117	0.483711	1.571315	0.009615	0.191988
KEGG_BUTANOATE_METABOLISM	31	0.772551	1.808 64	0.002088	0.192024
KEGG_PPAR_SIGNALING_PATHWAY	60	0.620 26	1.574275	0.022965	0.192099
LEE_LIVER_CANCER_MYC_DN	54	0.637794	1.573306	0.008 13	0.192472
MEBARKI_HCC_PROGENITOR_WNT_DN_BLOCKED_BY_FZD8CRD	32	0.593639	1.571445	0.023301	0.193054
REACTOME_GLYCOGEN_METABOLISM	24	0.571882	1.568388	0.028 34	0.194312
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	28	0.732069	1.569022	0.024 44	0.194441
CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_UP	58	0.680532	1.566 8	0.019231	0.195759
REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS_VIA_7ALPHA_HYDROXYCHOLESTEROL	22	0.809297	1.563002	0.016771	0.198152
WP_MITOCHONDRIAL_LCFATTY_ACID_BETAOXIDATION	15	0.751 19	1.563486	0.037578	0.198626
WENG_POR_TARGETS_LIVER_DN	17	0.733855	1.562005	0.012397	0.198 63
WP_GABA_RECEPTOR_SIGNALING	28	0.486928	1.564021	0.019608	0.199078
BURTON_ADIPOGENESIS_6	155	0.574513	1.811431	0.002096	0.200722
MOOTHA_VOXPHOS	68	0.412996	1.557542	0.077071	0.203432
REACTOME_NA_CL_DEPENDENT_NEUROTRANSMITTER_TRANSPORTERS	16	0.647027	1.557626	0.028455	0.204483
HOSHIDA_LIVER_CANCER_SUBCLASS_S3	247	0.828	1.816	<0.01	0.204

		786	159		8
REACTOME_DISEASES_ASSOCIATED_WITH_GLYCOSYLATION_PRECURSOR_BIOSYNTHESIS	15	0.652	1.555	0.061	0.205
		09	572	602	497
YANG_BREAST_CANCER_ESR1_LASER_UP	25	0.596	1.551	0.031	0.209
		331	169	25	196
REACTOME_METABOLISM_OF_ANGIOTENSINOGEN_TO_ANGIOTENSINS	17	0.684	1.552	0.029	0.209
		291	358	412	673
WP_DRUG_INDUCTION_OF_BILE_ACID_PATHWAY	15	0.910	1.551	<0.01	0.209
		883	534		773
SMID_BREAST_CANCER_LUMINAL_B_UP	145	0.479	1.545	0.001	0.212
		199	341	931	755
DOANE_BREAST_CANCER_CLASSES_UP	62	0.560	1.548	0.012	0.213
		16	174	5	089
KEGG_STARCH_AND_SUCROSE_METABOLISM	36	0.704	1.545	0.016	0.213
		593	576	842	584
WP_OXYSTEROLS_DERIVED_FROM_CHOLESTEROL	16	0.739	1.546	0.026	0.213
		238	99	804	624
REACTOME_FOXO_MEDIATED_TRANSCRIPTION_OF_OXIDATIVE_STRESS_METABOLIC_AND_NEURONAL_GENES	22	0.640	1.546	0.032	0.213
		91	213	258	667
LANDIS_ERBB2_BREAST_PRENEOPLASTIC_DN	49	0.547	1.544	0.028	0.213
		304	152	747	697
REACTOME_PEROXISOMAL_LIPID_METABOLISM	23	0.872	1.819	<0.01	0.215
		575	105		357
KOHOUTEK_CCNT2_TARGETS	32	0.562	1.541	0.014	0.216
		425	217	257	33
WP_UREA_CYCLE_AND_ASSOCIATED_PATHWAYS	19	0.781	1.541	0.020	0.216
		629	777	661	543
REACTOME_PYRUVATE_METABOLISM	26	0.575	1.534	0.037	0.217
		475	859	624	708
ACEVEDO_LIVER_TUMOR_VS_NORMAL_ADJACENT_TISSUE_DN	201	0.599	1.535	0.030	0.218
		785	22	55	247

REACTOME_SUMOYLATION_OF_INTRACELLULAR_RECEPTORS	30	0.536681	1.536626	0.041237	0.218297
REACTOME_SYNTHESIS_OF_LEUKOTRIENES_LT_AND_EOXINS_EX_	17	0.632106	1.538512	0.038229	0.218749
REACTOME_PLASMA_LIPOPROTEIN_ASSEMBLY_REMODELING_AND_CLEARANCE	58	0.547241	1.535626	0.035941	0.21875
WP_COMPLEMENT_AND_COAGULATION_CASCADES	55	0.666028	1.539011	0.022869	0.219082
MINGUEZ_LIVER_CANCER_VASCULAR_INVASION_DN	18	0.923321	1.536785	<0.01	0.219172
WP_CLASSICAL_PATHWAY_OF_STEROIDOGENESIS_INCLUDING_DISEASES	15	0.741136	1.537187	0.023404	0.219748
MOOTHA_TCA	15	0.658347	1.532866	0.061983	0.219915
HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_DN	63	0.510798	1.531707	0.027542	0.220935
WANG_CLASSIC_ADIPOGENIC_TARGETS_OF_PPARG	23	0.670943	1.526143	0.0375	0.227353
REACTOME_DISEASES_OF_CARBOHYDRATE_METABOLISM	33	0.555154	1.526415	0.058116	0.228113
REACTOME_METABOLISM_OF_STEROIDS	133	0.525838	1.524643	0.032854	0.228893
REACTOME_INTRINSIC_PATHWAY_OF_FIBRIN_CLOT_FORMATION	23	0.70551	1.526589	0.057026	0.229057
WENG_POR_TARGETS_GLOBAL_DN	21	0.650083	1.52042	0.03112	0.230279
REACTOME_XENOBIOTICS	20	0.837158	1.52209	0.020534	0.230914
HOUSTIS_ROS	34	0.60308	1.522729	0.050813	0.23099
ST_GA13_PATHWAY	36	0.455	1.520	0.033	0.231

		013	618	403	136
MIKKELSEN_MCV6_LCP_WITH_H3K4ME3	104	0.502	1.520	0.04	0.231
		529	956		682
BIOCARTA_AKT_PATHWAY	19	0.515	1.518	0.055	0.232
		55	785	666	002
KEGG_LINOLEIC_ACID_METABOLISM	25	0.725	1.516	0.040	0.232
		834	713	241	183
REACTOME_ENDOGENOUS_STEROLS	23	0.617	1.517	0.038	0.232
		386	927	697	368
WP_ANGIOPOIETIN_LIKE_PROTEIN_8_REGULATORY_PATHWAY	122	0.397	1.516	0.006	0.233
		608	808	41	128
MOOTHA_HUMAN_MITODB_6_2002	391	0.512	1.820	0.004	0.233
		614	402	158	736
GUO_TARGETS_OF_IRS1_AND_IRS2	79	0.509	1.513	0.028	0.234
		626	341	398	551
FERREIRA_EWINGS_SARCOMA_UNSTABLE_VS_STABLE_DN	68	0.443	1.514	0.026	0.235
		548	327	871	201
BIOCARTA_GH_PATHWAY	25	0.453	1.513	0.041	0.235
		373	541	667	388
UEDA_PERIFERAL_CLOCK	124	0.476	1.509	0.030	0.239
		018	934	55	521
NADLER_OBESITY_DN	45	0.498	1.507	0.039	0.242
		89	913	095	022
CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_UP	120	0.743	1.504	0.053	0.247
		615	152	305	562
REACTOME_INFLUENZA_INFECTION	146	-0.58	-2.19	0.002	0.008
		1	882	075	36
REACTOME_REGULATION_OF_EXPRESSION_OF_SLITS_AND_ROBOS	160	-0.51	-2.21	<0.01	0.010
		379	214		637
REACTOME_NONSENSE_MEDIATED_DECAY_NMD_	110	-0.61	-2.16	0.002	0.011
		388	11	11	31

REACTOME_SIGNALING_BY_ROBO_RECEPTORS	203	-0.49624	-2.23542	<0.01	0.014203
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	107	-0.60456	-2.08686	0.004274	0.030917
MALONEY_RESPONSE_TO_17AAG_DN	60	-0.6008	-2.03481	<0.01	0.046933
REACTOME_EUKARYOTIC_TRANSLATION_INITIATION	104	-0.5937	-2.01613	0.004175	0.052259
REACTOME_RESPONSE_OF_EIF2AK4_GCN2_TO_AMINO_ACID_DEFICIENCY	97	-0.5844	-1.9607	0.008421	0.095952
WP_MRNA_PROCESSING	86	-0.54475	-1.96571	0.009921	0.102023
ANDERSEN_LIVER_CANCER_KRT19_UP	29	-0.73268	-1.94745	<0.01	0.102314
REACTOME_METABOLISM_OF_RNA	491	-0.4594	-1.90461	0.004132	0.126455
SHEPARD_CRUSH_AND_BURN_MUTANT_DN	137	-0.66105	-1.90864	<0.01	0.12859
MATTIOLI_MGUS_VS_PCL	86	-0.59724	-1.88643	<0.01	0.134746
LEE_LIVER_CANCER_SURVIVAL_DN	137	-0.75642	-1.91003	<0.01	0.137333
REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION	91	-0.60754	-1.89354	0.006356	0.137462
BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVE_GENES	58	-0.59802	-1.87853	0.010504	0.140424
REACTOME_RRNA_PROCESSING	159	-0.51958	-1.8878	0.020747	0.140888
HSIAO_HOUSEKEEPING_GENES	352	-0.41694	-1.86417	0.014463	0.142099
SHEPARD_BMYB_TARGETS	55	-0.80	-1.87	<0.01	0.143

		176	249		637
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND	46	-0.59	-1.86	0.010	0.146
_SUBSEQUENT_BINDING_TO_43S		58	576	46	968
WP_CYTOPLASMIC_RIBOSOMAL_PROTEINS	87	-0.60	-1.91	0.004	0.147
		313	114	283	658
KEGG_RIBOSOME	84	-0.61	-1.85	0.006	0.147
		976	365	356	824
JISON_SICKLE_CELL_DISEASE_DN	147	-0.45	-1.85	0.004	0.150
		478	517	107	74
RHODES_CANCER_META_SIGNATURE	58	-0.71	-1.84	<0.01	0.153
		611	721		831
TOMIDA_METASTASIS_UP	18	-0.70	-1.84	<0.01	0.154
		532	043		616
WANG_TUMOR_INVASIVENESS_UP	307	-0.42	-1.84	<0.01	0.157
		632	22		717
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	36	-0.57	-1.83	0.004	0.157
		773	292	32	821
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	162	-0.49	-1.83	0.010	0.157
		871	544	163	888
DESERT_STEM_CELL_HEPATOCELLULAR_CARCINOMA_SUBCLASS_UP	204	-0.85	-1.82	<0.01	0.172
		717	022		34
LE_NEURONAL_DIFFERENTIATION_DN	16	-0.80	-1.82	0.001	0.177
		048	073	992	261
HOLLEMAN_VINCRISTINE_RESISTANCE_ALL_DN	19	-0.63	-1.81	0.008	0.179
		934	096	299	832
SANA_RESPONSE_TO_IFNG_DN	73	-0.56	-1.81	<0.01	0.181
		293	269		607
REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION	43	-0.54	-1.79	0.005	0.202
		6	961	988	601
HOLLEMAN_ASPARAGINASE_RESISTANCE_B_ALL_UP	20	-0.68	-1.79	0.004	0.210
		264	374	082	408

MODY_HIPPOCAMPUS_NEONATAL	28	-0.66587	-1.78217	0.004032	0.235013
KEGG_SPLICEOSOME	85	-0.50637	-1.77863	0.017964	0.238075
HAHTOLA_MYCOSIS_FUNGOIDES_CD4_DN	97	-0.50385	-1.77145	0.010395	0.239214
POMEROY_MEDULLOBLASTOMA_PROGNOSIS_DN	41	-0.63823	-1.77353	0.004219	0.239962
REACTOME_POSITIVE_EPIGENETIC_REGULATION_OF_RRNA_EXPRESSION	39	-0.56219	-1.77399	0.008351	0.245126

Table S10. GSEA results between low- and high-ACBD4 expression groups by using c5 reference gene set.

NAME	SIZE	ES	NES	NOM p-val	FDR q-val
GO_ORGANIC_HYDROXY_COMPOUND_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	32	0.7322294	1.757228	<0.01	0.1527779
HP_AMINOACIDURIA	109	0.62968	1.7558088	0.005988	0.1529866
HP_NEONATAL_ONSET	23	0.6724449	1.75266	0.001946	0.1536368
GO_NEGATIVE_REGULATION_OF_BLOOD_PRESSURE	41	0.5158156	1.75761	0.012121	0.1544455
GO_POLYSACCHARIDE_CATABOLIC_PROCESS	22	0.6086922	1.747514	0.00818	0.1535345
HP_FETAL_DISTRESS	25	0.5583366	1.7528889	0.005837	0.1555551
GO_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	396	0.4833366	1.75837	0.002	0.1563562
GO_POSITIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	20	0.5516518	1.74829	0.015595	0.1546311
HP_ELEVATED_HEPATIC_TRANSAMINASE	176	0.49991	1.76229	<0.01	0.15672

		7	5		5
GO_NEGATIVE_REGULATION_OF_LIPID_CATABOLIC_PROCESS	19	0.63	1.74	0.00	0.15
		061	903	410	736
		7	3	7	1
HP_LETHARGY	107	0.62	1.75	0.00	0.15
		587	881	608	739
			7	5	4
GO_TETRAPYRROLE_BINDING	111	0.61	1.74	<0.0	0.15
		309	233	1	787
			5		7
GO_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	247	0.60	1.74	0.00	0.15
		463	333	197	825
		5	7	2	8
HP_REDUCED_CONSCIOUSNESS_CONFUSION	254	0.46	1.74	<0.0	0.15
		317	438	1	858
		3	8		6
HP_ABNORMAL_CIRCULATING_CARBOXYLIC_ACID_CONCENTRATION	99	0.71	1.73	0.00	0.15
		179	921	395	899
		5	6	3	7
GO_POSITIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	37	0.66	1.76	<0.0	0.15
		072	415	1	902
		5	1		8
HP_ABNORMAL_CIRCULATING_FATTY_ACID_CONCENTRATION	34	0.66	1.76	0.00	0.15
		288	233	798	933
		1	2	4	
HP_LACTIC_ACIDOSIS	103	0.57	1.73	0.00	0.15
		005	775	804	934
		9	4	8	2
HP_PRIMARY_ADRENAL_INSUFFICIENCY	46	0.57	1.75	0.00	0.15
		537	913	782	946
		6	4	8	3

GO_RESPONSE_TO_XENOBIOTIC_STIMULUS	104	0.72697	1.74002	<0.01	0.15972
GO_REGULATION_OF_CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	110	0.50432	1.73145	<0.01	0.15991
GO_ORGANIC_HYDROXY_COMPOUND_METABOLIC_PROCESS	441	0.52501	1.73455	0.00193	0.16045
GO_AEROBIC_RESPIRATION	69	0.52861	1.73200	0.02890	0.16087
HP_NAUSEA_AND_VOMITING	327	0.44929	1.73540	<0.01	0.16110
HP_EPISODIC_HYPERHIDROSIS	20	0.62815	1.73306	0.00970	0.16112
GO_REGULATION_OF_DOPAMINE_SECRETION	25	0.55045	1.76957	0.00396	0.16124
GO_GAMMA_AMINOBUTYRIC_ACID_TRANSPORT	15	0.74140	1.77270	0.00194	0.16143
GO_POSITIVE_REGULATION_OF_ANION_TRANSPORT	53	0.61725	1.76429	<0.01	0.16168
GO_HORMONE_METABOLIC_PROCESS	179	0.57266	1.71154	0.00198	0.16308
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_CH_OH_GROUP_OF_DONORS	99	0.68	1.77	<0.0	0.16

		812	322	1	349
		5	8		9
GO_STEROID_HORMONE_BIOSYNTHETIC_PROCESS	42	0.65	1.76	<0.0	0.16
		614	998	1	351
			1		6
GO_MONOCARBOXYLIC_ACID_TRANSPORT	131	0.56	1.68	0.00	0.16
		122	516	202	362
		9	7	8	9
GO_LIPID_MODIFICATION	188	0.54	1.80	<0.0	0.16
		831	373	1	369
			6		1
HP_ARACHNOID_HEMANGIOMATOSIS	15	0.67	1.76	0.01	0.16
		118	472	197	382
		2	8	6	8
GO_VERY_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS	22	0.78	1.71	0.00	0.16
		619	18	390	433
		8		6	2
GO_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS	88	0.69	1.72	<0.0	0.16
		198	287	1	461
		6	8		9
GO_ORGANIC_ACID_BIOSYNTHETIC_PROCESS	267	0.58	1.68	0.00	0.16
		201	529	196	468
		5	6	1	5
GO_N_ACYLTRANSFERASE_ACTIVITY	47	0.48	1.72	0.01	0.16
		974	396	158	485
		6	2	3	5
GO_ALCOHOL_CATABOLIC_PROCESS	46	0.61	1.71	0.00	0.16
		673	518	588	531
		9	7	2	1
GO_PORPHYRIN_CONTAINING_COMPOUND_METABOLIC_PROCESS	31	0.66	1.68	0.01	0.16
		822	814	174	533

		5	9	2	2
GO_NEUROTRANSMITTER_METABOLIC_PROCESS	25	0.60	1.72	0.01	0.16
		512	685	162	543
		5	9	8	9
GO_FLAVIN_ADENINE_DINUCLEOTIDE_BINDING	67	0.67	1.72	0.00	0.16
		805	468	400	546
		3	7	8	1
GO_MICROBODY_LUMEN	41	0.82	1.76	<0.0	0.16
		557	546	1	548
		8	1		2
HP_ABNORMAL_CIRCULATING_ASPARTATE_FAMILY_AMINO_ACID_CONCENTRATION	15	0.85	1.68	<0.0	0.16
		637	964	1	551
		3	5		
GO_TRICARBOXYLIC_ACID_CYCLE	30	0.70	1.71	0.01	0.16
		089	306	181	551
		1		1	8
GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_NADH_TO_UBIQUINONE	41	0.54	1.65	0.05	0.16
		373	622	371	564
		8		9	7
GO_ARACHIDONIC_ACID_METABOLIC_PROCESS	46	0.74	1.68	0.00	0.16
		861	546	198	572
		5	5	4	6
GO_THIOESTER_METABOLIC_PROCESS	69	0.65	1.65	0.00	0.16
		064	117	808	58
		5	2	1	
HP_ABNORMALITY_OF_URINE_HOMEOSTASIS	478	0.44	1.65	0.00	0.16
		391	796	193	581
		2	2	8	5
GO_NUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	95	0.61	1.65	0.00	0.16
		576	543	608	585
		1	8	5	9

GO_BENZENE_CONTAINING_COMPOUND_METABOLIC_PROCESS	18	0.87 471 6	1.70 722 2	<0.0 1	0.16 585 9
HP_ABNORMAL_METABOLISM	79	0.55 49	1.71 185 8	<0.0 1	0.16 594 5
GO_RETINOL_METABOLIC_PROCESS	34	0.80 909 3	1.77 368 8	<0.0 1	0.16 595 8
GO_CELLULAR_GLUCAN_METABOLIC_PROCESS	57	0.56 779 2	1.66 889 1	0.00 2	0.16 599 2
GO_ALPHA_AMINO_ACID_CATABOLIC_PROCESS	81	0.74 937 8	1.65 659 4	0.00 967 1	0.16 610 1
GO_HEME_METABOLIC_PROCESS	24	0.66 695 1	1.65 909 5	0.01 383 4	0.16 614 5
GO_CELLULAR_RESPONSE_TO_GLUCAGON_STIMULUS	23	0.65 210 2	1.65 460 8	0.01 976 3	0.16 620 9
HP_HYPERCHOLESTEROLEMIA	41	0.56 348 2	1.65 838	0.01	0.16 621 1
GO_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN	82	0.49 021 2	1.71 355 4	0.04 624 3	0.16 635 4
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OXO_GROUP_OF_DONORS	38	0.73 042 3	1.71 552 9	0.00 191 6	0.16 643 9
GO_CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	220	0.43	1.65	0.00	0.16

		922	949	404	645
		2	7		2
GO_POSITIVE_REGULATION_OF_CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	45	0.51	1.65	0.00	0.16
		685	133	976	647
		5	5	6	5
HP_ABNORMAL_TISSUE_METABOLITE_CONCENTRATION	27	0.60	1.68	0.01	0.16
		768	824	227	652
		4	5		2
HP_INCREASED_MUSCLE_FATIGUABILITY	15	0.60	1.65	0.01	0.16
		764	686	414	664
		2	8	1	1
HP_SPASTIC_PARAPARESIS	33	0.53	1.68	0.01	0.16
		065	566	140	673
		3	6	7	8
GO_PYRUVATE_METABOLIC_PROCESS	131	0.51	1.66	0.00	0.16
		164	913	411	673
		7	3	5	9
GO_MONOCARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	36	0.75	1.68	<0.0	0.16
		899	970	1	675
		9	8		5
GO_SOLUTE_SODIUM_SYMPORTER_ACTIVITY	58	0.57	1.65	0.00	0.16
		284	177	596	675
		4	4	4	8
GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS	20	0.68	1.78	0.00	0.16
		956	651	196	679
		2	5	1	4
HP_LIPID_ACCUMULATION_IN_HEPATOCYTES	84	0.60	1.79	0.00	0.16
		809	974	413	682
			9	2	
GO_PRIMARY_ALCOHOL_CATABOLIC_PROCESS	15	0.83	1.68	0.00	0.16
		408	641	197	691

		7	5	2	
GO_HORMONE_BIOSYNTHETIC_PROCESS	60	0.58	1.70	0.00	0.16
		365	855	401	691
		7	8	6	3
GO_ACETYL_COA_METABOLIC_PROCESS	30	0.68	1.65	0.00	0.16
		349	984	8	695
		5	7		6
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_SULFUR_CONTAINING_GROUPS	48	0.53	1.64	0.00	0.16
		383	970	792	696
		9	6	1	9
GO_ELECTRON_TRANSFER_ACTIVITY	88	0.58	1.71	0.00	0.16
		339	616	195	7
			5	3	
HP_ABNORMAL_URINE_CARBOXYLIC_ACID_LEVEL	20	0.81	1.65	0.00	0.16
		284	216	571	708
		5	5	4	
GO_HORMONE_BINDING	74	0.52	1.68	0.01	0.16
		369	043	006	711
			8		8
GO_ALCOHOL_METABOLIC_PROCESS	300	0.51	1.66	0.00	0.16
		009	040	193	713
		9	6	8	9
GO_PEROXISOME_ORGANIZATION	70	0.71	1.80	<0.0	0.16
		109	441	1	716
			9		6
GO_GLUCOSE_METABOLIC_PROCESS	166	0.51	1.70	<0.0	0.16
		860	739	1	724
		4	8		
HP_ABNORMALITY_OF_THE_GALLBLADDER	74	0.47	1.68	0.00	0.16
		947	200	591	726
			4	7	9

GO_STEROID_DEHYDROGENASE_ACTIVITY	27	0.810943	1.724717	<0.01	0.16733
GO_CARBOHYDRATE_CATABOLIC_PROCESS	167	0.462506	1.669445	0.002033	0.167364
GO_MICROBODY	98	0.667433	1.774587	<0.01	0.167446
HP_HYPERAMMONEMIA	41	0.723678	1.678548	0.008	0.167666
GO_POSITIVE_REGULATION_OF_LIPID_LOCALIZATION	76	0.502118	1.648011	0.003929	0.167748
GO_CATECHOLAMINE_SECRETION	45	0.477915	1.652301	0.011472	0.167835
GO_CARBOXYLIC_ESTER_HYDROLASE_ACTIVITY	82	0.539599	1.660634	0.006048	0.167936
HP_ADRENAL_HYPERPLASIA	17	0.622212	1.680677	0.017045	0.167957
GO_MONOSACCHARIDE_METABOLIC_PROCESS	225	0.497817	1.679129	0.002028	0.168003
GO_REGULATION_OF_LIPID_CATABOLIC_PROCESS	49	0.5885	1.689801	0.007952	0.168018
HP_KETOACIDOSIS	23	0.62	1.71	0.00	0.16

		483	647	961	813
		7	3	5	3
HP_ABNORMAL_BASAL_GANGLIA_MRI_SIGNAL_INTENSITY	28	0.54	1.66	0.01	0.16
		743	122	840	814
		3	7	5	8
GO_ENDOPLASMIC_RETICULUM_EXIT_SITE	22	0.57	1.66	0.02	0.16
		049	966	321	820
		2	8	1	2
HP_CEREBRAL_EDEMA	20	0.76	1.81	<0.0	0.16
		175	155	1	826
		3	3		5
GO_CELLULAR_AMINO_ACID_CATABOLIC_PROCESS	98	0.75	1.69	0.00	0.16
		116	131	588	827
		1	8	2	3
GO_CELLULAR_POLYSACCHARIDE_CATABOLIC_PROCESS	20	0.64	1.77	0.00	0.16
		014	988	602	828
		8	8	4	4
GO_REGULATION_OF_GLUCONEOGENESIS	28	0.63	1.65	0.00	0.16
		141	262	994	829
		5	6		8
HP_DEVELOPMENTAL_REGRESSION	226	0.37	1.64	<0.0	0.16
		844	807	1	852
		3	7		5
GO_LYASE_ACTIVITY	134	0.52	1.66	0.00	0.16
		127	161	784	861
		8	4	3	7
GO_AROMATIC_AMINO_ACID_FAMILY_METABOLIC_PROCESS	27	0.79	1.66	0.01	0.16
		638	219	149	865
		8	5	4	1
HP_HYPERTENSION_ASSOCIATED_WITH_PHEOCHROMOCYTOMA	18	0.58	1.67	0.03	0.16
		500	698		868

		6	3		1
HP_COMA	75	0.64	1.79	<0.0	0.16
		292	640	1	873
		7	6		1
GO_VITAMIN_BINDING	103	0.58	1.70	0.00	0.16
		893	151	387	886
		8	6	6	1
GO_NEUROTRANSMITTER_BINDING	18	0.64	1.69	0.00	0.16
		718	262	766	891
		4	2	3	2
GO_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	86	0.54	1.71	<0.0	0.16
		954	925	1	899
		8	8		1
HP_ELEVATED_CALCITONIN	17	0.63	1.78	0.01	0.16
		155	737	165	908
		5	1		3
GO_VITAMIN_BIOSYNTHETIC_PROCESS	19	0.66	1.66	0.01	0.16
		497	981	361	911
		1	4	9	4
HP_ABNORMALITY_OF_COAGULATION	150	0.50	1.67	0.00	0.16
		318	048	392	928
		4	1	2	4
GO_CELLULAR_KETONE_METABOLIC_PROCESS	210	0.51	1.68	0.00	0.16
		346	983	4	937
		8	5		6
HP_ABNORMAL_LARYNX_PHYSIOLOGY	45	0.51	1.66	0.00	0.16
		229	243	621	942
		1		1	1
HP_STATUS_EPILEPTICUS	92	0.45	1.69	0.00	0.16
		595	294	396	964
		3	6		

HP_DICARBOXYLIC_ACIDURIA	27	0.77 457 8	1.77 522	0.00 203 3	0.16 967 8
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR	45	0.56 717	1.69 133 6	0.02 115 4	0.16 969 6
GO_DEACETYLASE_ACTIVITY	29	0.54 585 7	1.71 663 1	0.00 821 4	0.16 974 4
GO_ORGANIC_HYDROXY_COMPOUND_TRANSPORT	195	0.48 281 5	1.79 363 2	<0.0 1	0.16 975
HP_DELAYED_CNS_MYELINATION	21	0.65 780 1	1.66 352 2	0.01 394 4	0.16 984 9
GO_VITAMIN_B6_BINDING	35	0.71 631	1.66 280 3	0.01 132 1	0.16 991 9
GO_MONOSACCHARIDE_BIOSYNTHETIC_PROCESS	77	0.60 262	1.66 482	0.01 222	0.17 012 1
HP_DECREASED_CIRCULATING_ALDOSTERONE_LEVEL	15	0.66 631 7	1.70 266 3	0.00 598 8	0.17 017 1
GO_CELLULAR_RESPIRATION	137	0.50 049	1.77 699 7	0.01 380 7	0.17 021 6
HP_FLUSHING	21	0.68 174	1.80 524 9	0.00 601 2	0.17 027 6
GO_POSITIVE_REGULATION_OF_AMINE_TRANSPORT	35	0.58	1.70	<0.0	0.17

		095	154	1	043
		3	2		9
GO_CELLULAR_RESPONSE_TO_CAMP	45	0.56	1.66	0.01	0.17
		967	387	550	046
		1	1	4	
HP_PROLONGED_PARTIAL_THROMBOPLASTIN_TIME	16	0.83	1.67	0.00	0.17
		741	049	201	046
		1	1	2	1
HP_RETINAL_HAMARTOMA	20	0.59	1.78	0.00	0.17
		908	253	796	064
		7	3	8	3
HP_ABNORMAL_CIRCULATING_LONG_CHAIN_FATTY_ACID_CONCENTRATION	16	0.69	1.64	0.03	0.17
		810	206	483	076
		6	9	6	2
HP_RHABDOMYOLYSIS	27	0.54	1.63	0.03	0.17
		395	513	762	079
		9		4	3
GO_FATTY_ACID_DERIVATIVE_METABOLIC_PROCESS	129	0.59	1.64	0.00	0.17
		081	318	197	085
		9	1	6	7
GO_IRON_ION_BINDING	108	0.60	1.67	0.00	0.17
		589	156	389	097
		1	6	9	7
GO_NOREPINEPHRINE_TRANSPORT	23	0.58	1.71	0.00	0.17
		952	708	611	098
		8	1		7
GO_CELLULAR_CARBOHYDRATE_CATABOLIC_PROCESS	36	0.55	1.69	0.01	0.17
		808	303	008	099
		8	4	1	6
GO_LIPID_TRANSPORTER_ACTIVITY	90	0.62	1.70	0.00	0.17
		827	313	198	100

		7	2	4	1
GO_PHENOL_CONTAINING_COMPOUND_METABOLIC_PROCESS	91	0.49	1.64	0.00	0.17
		864	363	594	101
		2	7	1	2
HP_ABNORMAL_CIRCULATING_LIPID_CONCENTRATION	174	0.49	1.63	0.00	0.17
		289	727	396	105
		9			9
HP_ABNORMAL_CSF_METABOLITE_LEVEL	66	0.47	1.66	0.02	0.17
		049	490	409	113
		8	7	6	
HP_DROWSINESS	27	0.57	1.78	0.00	0.17
		424	031	198	114
		2	7	4	2
GO_CELLULAR_HORMONE_METABOLIC_PROCESS	106	0.62	1.67	<0.0	0.17
		598	076	1	120
		6	1		9
GO_MONOCARBOXYLIC_ACID_BIOSYNTHETIC_PROCESS	181	0.58	1.67	0.00	0.17
		767	202	199	138
			3	6	8
GO_NAD_BINDING	51	0.58	1.67	0.00	0.17
		265	358	982	143
		4	5	3	9
HP_CHOLELITHIASIS	58	0.49	1.63	0.01	0.17
		178	756	153	149
		7	9	8	2
GO_POSITIVE_REGULATION_OF_LIPID_TRANSPORT	61	0.50	1.64	0.00	0.17
		552	220	383	149
			6	1	3
GO_REGULATION_OF_FATTY_ACID_BETA_OXIDATION	15	0.73	1.63	0.00	0.17
		499	523	202	150
		8	5		7

GO_QUINONE_METABOLIC_PROCESS	28	0.70861	1.62241	0.01818	0.171597
GO_INTERMEMBRANE_LIPID_TRANSFER	26	0.61345	1.62556	0.00606	0.171698
HP_TACHYPNEA	53	0.48478	1.64378	0.00611	0.171725
GO_UNSATURATED_FATTY_ACID_METABOLIC_PROCESS	93	0.63500	1.67258	<0.01	0.171733
GO_PURINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	338	0.45569	1.64499	0.00201	0.171741
GO_REGULATION_OF_HORMONE_LEVELS	422	0.42851	1.63797	<0.01	0.171763
HP_ABNORMAL_GLUCOSE_HOMEOSTASIS	429	0.39949	1.64431	<0.01	0.171838
HP_ABNORMALITY_OF_THE_COAGULATION_CASCADE	96	0.55115	1.69341	0.01153	0.171858
GO_RESPONSE_TO_CAMP	84	0.54462	1.63553	0.00584	0.171991
GO_CELLULAR_MODIFIED_AMINO_ACID_METABOLIC_PROCESS	142	0.54586	1.63611	0.00396	0.172002
GO_ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	39	0.67	1.62	0.00	0.17

		705	31	590	205
		7		6	7
GO_COPII_VESICLE_COAT	15	0.59	1.62	0.02	0.17
		346	256	661	212
		4	9	6	5
GO_REGULATION_OF_ANION_TRANSPORT	91	0.48	1.62	0.00	0.17
		702	149	193	221
		4	3	8	5
HP_KETONURIA	18	0.74	1.62	0.00	0.17
		450	576	588	221
		5	9	2	6
GO_LIGAND_ACTIVATED_TRANSCRIPTION_FACTOR_ACTIVITY	50	0.51	1.62	0.01	0.17
		443	621	402	230
		8	8	8	7
HP_PHEOCHROMOCYTOMA	21	0.55	1.67	0.02	0.17
		217	383	559	232
		4		1	5
HP_SEVERE_MUSCULAR_HYPOTONIA	48	0.50	1.63	0.01	0.17
		818	983	8	237
		7	6		7
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS	47	0.75	1.78	<0.0	0.17
		145	779	1	238
		8	4		3
GO_RESPIRASOME	66	0.46	1.63	0.07	0.17
		720	807	114	247
		9	6	6	
HP_ABNORMAL_CALCIUM_PHOSPHATE_REGULATING_HORMONE_LEVEL	34	0.44	1.63	0.02	0.17
		945	355	912	250
		2	4	6	6
HP_EMOTIONAL_LABILITY	93	0.41	1.63	0.01	0.17
		797	859		252

		7	2		2
GO_ICOSANOID_METABOLIC_PROCESS	91	0.60	1.62	0.01	0.17
		156	335	149	254
		7	3	4	1
GO_POSITIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	66	0.47	1.62	0.01	0.17
		347	017	008	257
		7	3	1	3
GO_POSITIVE_REGULATION_OF_STEROL_TRANSPORT	23	0.64	1.63	0.00	0.17
		484	909	809	262
		7	2	7	4
GO_LIPOPROTEIN_METABOLIC_PROCESS	89	0.47	1.62	0.01	0.17
		029	707	178	264
		3	5	8	2
GO_CALMODULIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	23	0.49	1.62	0.03	0.17
		938	436	149	267
		8	3	6	4
GO_SOLUTE_CATION_SYMPORTER_ACTIVITY	76	0.52	1.63	0.00	0.17
		079	290	389	272
		6	1	1	8
HP_EEG_WITH_ABNORMALLY_SLOW_FREQUENCIES	44	0.48	1.64	0.01	0.17
		609	014	553	278
		9	4	4	9
HP_INCREASED_SERUM_LACTATE	102	0.48	1.62	0.03	0.17
		616	639	455	286
		2	8	3	8
GO_STEROID_BINDING	89	0.53	1.63	<0.0	0.17
		274	165	1	289
		7	5		
HP_HEMANGIOBLASTOMA	17	0.57	1.62	0.02	0.17
		229	366	135	294
		8	2	9	1

HP_ABNORMAL_CIRCULATING_SULFUR_AMINO_ACID_CONCENTRATION	15	0.80526	1.62041	0.00399	0.17297
GO_ENERGY_RESERVE_METABOLIC_PROCESS	66	0.52120	1.62785	0.00408	0.17299
GO_AMINE_TRANSPORT	83	0.47263	1.69363	<0.01	0.17301
GO_MITOCHONDRIAL_MATRIX	319	0.56985	1.81185	0.00781	0.17308
HP_ABNORMAL_URINE_PH	137	0.67429	1.81779	0.00401	0.17321
HP_HYPOGLYCEMIC_COMA	16	0.71634	1.62714	0.02028	0.17338
GO_MONOAMINE_TRANSPORT	69	0.43767	1.69524	0.00192	0.17342
GO_FAT_SOLUBLE_VITAMIN_METABOLIC_PROCESS	40	0.59584	1.63074	0.00573	0.17345
GO_PROTEIN_QUALITY_CONTROL_FOR_MISFOLDED_OR_INCOMPLETELY_SYNTHESIZED_PROTEINS	20	0.50510	1.62859	0.03320	0.17346
GO_ELECTRON_TRANSPORT_CHAIN	139	0.55573	1.81464	0.00195	0.17352
GO_HYDRO_LYASE_ACTIVITY	41	0.61	1.63	0.02	0.17

		215	181	204	355
		1	2	4	7
GO_MONOOXYGENASE_ACTIVITY	79	0.67	1.62	0.00	0.17
		856	796	386	366
		5	2	1	3
GO_LIPID_TRANSFER_ACTIVITY	25	0.62	1.61	0.00	0.17
		202	689	808	368
		7	7	1	4
GO_SULFUR_COMPOUND_METABOLIC_PROCESS	262	0.54	1.69	0.00	0.17
		825	794	410	369
		1	7	7	5
HP_CHOLECYSTITIS	17	0.66	1.69	0.00	0.17
		058	596	793	384
		4	5	7	5
GO_FATTY_ACID_METABOLIC_PROCESS	285	0.62	1.78	<0.0	0.17
		866	923	1	392
		9	3		4
GO_REGULATION_OF_ORGANIC_ACID_TRANSPORT	59	0.52	1.61	0.00	0.17
		503	720	386	399
		4	6	8	1
GO_ALPHA_AMINO_ACID_METABOLIC_PROCESS	156	0.65	1.69	0.00	0.17
		410	685	779	406
		8	6	7	6
GO_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	28	0.57	1.62	0.00	0.17
		953	861	789	427
		2	6		6
HP_ABNORMAL_MITOCHONDRIA_IN_MUSCLE_TISSUE	20	0.56	1.61	0.05	0.17
		766	595	823	433
		9	7	3	2
GO_LIPID_LOCALIZATION	302	0.46	1.61	0.00	0.17
		168	802	197	437

		9	5	2	1
GO_STEROID_METABOLIC_PROCESS	273	0.55	1.61	0.00	0.17
		256	850	388	445
		5	9	3	9
GO_CELLULAR_RESPONSE_TO_PH	15	0.72	1.69	0.00	0.17
		326	364	202	457
		2	1	4	7
GO_DOPAMINE_METABOLIC_PROCESS	36	0.53	1.61	0.00	0.17
		835	722	576	474
		6	3	9	9
GO_CATECHOLAMINE_METABOLIC_PROCESS	47	0.53	1.62	0.01	0.17
		676	868	354	503
		3	3		5
GO_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	163	0.41	1.62	<0.0	0.17
		425	917	1	506
		6	6		3
HP_ORGANIC_ACIDURIA	47	0.77	1.80	<0.0	0.17
		769	543	1	519
		5	7		5
GO_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	162	0.44	1.60	0.01	0.17
		042	008	402	603
		3		8	3
GO_TRIGLYCERIDE_LIPASE_ACTIVITY	18	0.72	1.60	0.01	0.17
		885	049	209	608
		3	4	7	8
GO_PROTEIN_TRANSMEMBRANE_IMPORT_INTO_INTRACELLULAR_ORGANELLE	24	0.56	1.59	0.04	0.17
		074	809	480	640
		8	5	7	6
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULA	110	0.59	1.60	0.00	0.17
R_OXYGEN		695	059	781	662
		2	1	3	3

GO_POSITIVE_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	18	0.57872	1.591	0.03807	0.176759
GO_SERINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	31	0.75806	1.596	0.00776	0.176882
GO_BILE_ACID_BIOSYNTHETIC_PROCESS	29	0.74807	1.598	0.00996	0.17057
GO_HYDROLASE_ACTIVITY_HYDROLYZING_O_GLYCOSYL_COMPOUNDS	59	0.49751	1.596	0.00412	0.17074
GO_MITOCHONDRIAL_ENVELOPE	471	0.39514	1.589	0.01195	0.17711
GO_NEGATIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	18	0.69979	1.592	0.01636	0.17237
GO_RESPONSE_TO_DEXAMETHASONE	33	0.59333	1.606	0.01162	0.17258
GO_TRIGLYCERIDE_METABOLIC_PROCESS	70	0.60916	1.599	0.02544	0.17491
GO_LIPID_HOMEOSTASIS	114	0.57012	1.598	0.00601	0.17647
GO_RESPONSE_TO_GLUCAGON	32	0.60389	1.609	0.01949	0.17758
GO_TRIGLYCERIDE_RICH_PLASMA_LIPOPROTEIN_PARTICLE	16	0.73	1.60	0.00	0.17

		761	071	784	777
		4	9	3	
HP_EXPRESSIVE_LANGUAGE_DELAY	18	0.53	1.59	0.02	0.17
		972	100	834	784
		2	3		3
GO_NADH_DEHYDROGENASE_COMPLEX_ASSEMBLY	39	0.48	1.59	0.07	0.17
		513	436	010	797
		2	1	3	3
HP_PROXIMAL_MUSCLE_WEAKNESS_IN_UPPER_LIMBS	30	0.45	1.60	0.01	0.17
		760	104	622	799
		8	4	7	
HP_METABOLIC_ACIDOSIS	102	0.63	1.81	0.00	0.17
		509	841	197	805
		9	9	6	4
GO_THIOLESTER_HYDROLASE_ACTIVITY	20	0.61	1.60	0.00	0.17
		854	946	835	811
		6	2	1	7
GO_CELLULAR_RESPONSE_TO_STEROL	21	0.66	1.60	0.00	0.17
		957	231	823	815
		3	2		4
GO_SULFUR_AMINO_ACID_METABOLIC_PROCESS	34	0.69	1.60	0.01	0.17
		656	178	167	824
		1	7	3	8
HP_WEAKNESS_OF_THE_INTRINSIC_HAND_MUSCLES	18	0.53	1.61	0.03	0.17
		27	124	151	832
			4	3	6
GO_CARBOHYDRATE_METABOLIC_PROCESS	479	0.41	1.61	0.00	0.17
		210	220	209	832
		4	8	6	6
GO_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	254	0.43	1.59	0.00	0.17
		723	283	198	835

		2	9	8	3
GO_PEROXISOMAL_MEMBRANE_TRANSPORT	19	0.59	1.59	0.04	0.17
		949	196	674	835
		2	9	8	4
GO_BILE_ACID_METABOLIC_PROCESS	38	0.69	1.59	0.01	0.17
		676	454	388	835
		3	6	9	5
GO_KETONE_BIOSYNTHETIC_PROCESS	38	0.56	1.61	0.00	0.17
		384	165	813	843
		4	3		5
GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCESS	438	0.43	1.60	0.00	0.17
		607	973	414	843
		5	9	9	6
HP_GLYCOSURIA	34	0.58	1.59	0.02	0.17
		163	143	564	844
		9	7	1	7
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OXO_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEP	30	0.65	1.59	0.02	0.17
TOR		707	101	641	847
		8	3	5	3
GO_NEGATIVE_REGULATION_OF_AMYLOID_PRECURSOR_PROTEIN_CATABOLIC_PROCESS	16	0.55	1.59	0.03	0.17
		551	319	632	848
		3		9	5
GO_NEGATIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION	44	0.48	1.60	0.01	0.17
		037	580	242	855
		7	7	2	1
HP_ENCEPHALOPATHY	171	0.41	1.59	0.00	0.17
		832	222	965	858
		4	8	3	7
HP_ALKALOSIS	27	0.64	1.60	0.02	0.17
		810	243	890	866
		1	2	2	7

HP_DECREASED_ACTIVITY_OF_THE_PYRUVATE_DEHYDROGENASE_COMPLEX	24	0.55375	1.61242	0.05952	0.178727
HP_CEREBRAL_PALSY	33	0.50695	1.60279	0.01976	0.178862
GO_NEUTRAL_LIPID_METABOLIC_PROCESS	88	0.57229	1.60605	0.01574	0.178902
GO_PROTEIN_HOMOTETRAMERIZATION	52	0.51599	1.60640	0.01050	0.179021
GO_SYMPORTER_ACTIVITY	100	0.50456	1.60979	0.00387	0.179096
GO_ORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	15	0.64393	1.61026	0.02880	0.179144
GO_RESPONSE_TO_PURINE_CONTAINING_COMPOUND	132	0.46094	1.60301	0.00197	0.179256
GO_FATTY_ACID_BIOSYNTHETIC_PROCESS	127	0.54494	1.60331	0.00404	0.179539
GO_DRUG_METABOLIC_PROCESS	38	0.79923	1.60653	0.00392	0.179551
GO_ANDROGEN_METABOLIC_PROCESS	26	0.69391	1.60367	0.00978	0.179678
GO_CATECHOLAMINE_UPTAKE	15	0.57	1.60	0.02	0.17

		663	779	615	985
		3	7	7	4
GO_SULFUR_COMPOUND_BIOSYNTHETIC_PROCESS	137	0.49	1.60	0.00	0.18
		621	668	601	004
		3	3	2	8
GO_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	98	0.43	1.60	0.00	0.18
		578	370	409	037
		4	2		4
GO_BILE_ACID_AND_BILE_SALT_TRANSPORT	22	0.77	1.60	0.00	0.18
		941	677	389	065
		8	7	9	
HP_HEPATIC_NECROSIS	16	0.65	1.60	0.05	0.18
		169	377	395	098
		2	9		7
GO_STEROID_HORMONE_RECEPTOR_ACTIVITY	22	0.58	1.81	0.00	0.18
		757	947	595	193
		6	4	2	3
GO_TETRAPYRROLE_METABOLIC_PROCESS	47	0.55	1.58	0.01	0.18
		292	698	606	254
		4	7	4	1
GO_FAD_BINDING	28	0.68	1.58	0.01	0.18
		395	700	612	316
		6	1	9	8
HP_PARAGANGLIOMA	19	0.52	1.58	0.03	0.18
		813	514	703	466
		8	6	7	6
HP_PIGMENTARY_RETINOPATHY	101	0.36	1.58	0.02	0.18
		398	456	409	495
		4	2	6	6
GO_RIBOSE_PHOSPHATE_METABOLIC_PROCESS	311	0.42	1.58	0.00	0.18
		127	164	411	809

		2	5	5	7
GO_GLANDULAR_EPITHELIAL_CELL_DEVELOPMENT	24	0.53	1.58	0.03	0.18
		538	205	765	815
		9	1	7	7
GO_BRANCHED_CHAIN_AMINO_ACID_METABOLIC_PROCESS	22	0.80	1.81	<0.0	0.18
		603	975	1	834
		5			7
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULA	29	0.83	1.58	0.00	0.18
R_OXYGEN_REDUCED_FLAVIN_OR_FLAVOPROTEIN_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_OF_OXYGEN		874	098	400	847
		5	5	8	2
HP_OPTIC_NEUROPATHY	32	0.50	1.57	0.04	0.18
		430	980	8	957
		6	5		3
GO_NEGATIVE_REGULATION_OF_SMALL_MOLECULE_METABOLIC_PROCESS	73	0.51	1.57	0.00	0.19
		111	813	196	168
		9	5	9	9
HP_INFANTILE_ONSET	335	0.33	1.57	<0.0	0.19
		312	736	1	223
			9		1
GO_VITAMIN_METABOLIC_PROCESS	106	0.51	1.57	0.00	0.19
		093	654	587	286
		9	8	1	6
GO_AROMATIC_AMINO_ACID_FAMILY_CATABOLIC_PROCESS	17	0.86	1.57	0.01	0.19
		661	587	343	325
		4	3	6	
HP_ABNORMAL_CIRCULATING_NITROGEN_COMPOUND_CONCENTRATION	93	0.54	1.57	0.02	0.19
		888	435	191	496
		4	6	2	8
GO_PRIMARY_ALCOHOL_METABOLIC_PROCESS	74	0.75	1.82	<0.0	0.19
		125	009	1	520
		2	7		1

HP_ABNORMAL_LDL_CHOLESTEROL_CONCENTRATION	26	0.63	1.57	0.01	0.19
		571	289	988	531
		2	9	1	6
HP_LEUKODYSTROPHY	61	0.44	1.57	0.03	0.19
		721	331	549	533
		7	9	1	2
HP_HYPERCOAGULABILITY	17	0.66	1.57	0.02	0.19
		222	352	755	568
		6	5	9	7
HP_FAT_MALABSORPTION	30	0.56	1.57	0.01	0.19
		818	132	183	653
		5		4	7
GO_ACIDIC_AMINO_ACID_TRANSPORT	63	0.43	1.57	0.00	0.19
		693	16	197	676
		9		2	1
GO_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	206	0.49	1.82	<0.0	0.19
		597	953	1	785
		6	7		2
GO_SECONDARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	165	0.44	1.56	0.00	0.19
		671	963	776	848
			6	7	5
GO_ORGANELLE_INNER_MEMBRANE	316	0.40	1.56	0.03	0.19
		089	869	339	865
		6	7	9	
GO_REGULATION_OF_STEROL_TRANSPORT	38	0.56	1.56	0.02	0.19
		149	894	061	893
		4	7	9	6
HP_ABNORMAL_URINE_PHOSPHATE_CONCENTRATION	26	0.58	1.56	0.01	0.19
		084	803	581	911
		9	7		7
GO_STEROL_TRANSPORT	79	0.47	1.56	0.01	0.19

		877	732	018	959
		9	7	3	2
HP_ABNORMALITY_OF_ACID_BASE_HOMEOSTASIS	248	0.56	1.82	0.00	0.20
		530	122	397	008
		6	9	6	1
GO_ISOPRENOID_METABOLIC_PROCESS	111	0.55	1.56	0.01	0.20
		341	582	346	144
		1	5	2	
HP_DEATH_IN_CHILDHOOD	20	0.57	1.56	0.04	0.20
		877	004	135	382
		5	5	3	3
GO_NEUROPEPTIDE_BINDING	21	0.50	1.56	0.04	0.20
		226	144	109	402
		7	6	6	7
GO_DIOXYGENASE_ACTIVITY	45	0.52	1.56	0.01	0.20
		527	098	185	415
		6	5	8	2
GO_BLOOD_COAGULATION_INTRINSIC_PATHWAY	18	0.77	1.56	0.02	0.20
		592	254	941	423
		5	6	2	4
HP_ABNORMAL_CNS_MYELINATION	148	0.40	1.56	0.01	0.20
		700	010	792	438
		9	3	8	4
HP_EPISODIC_ABDOMINAL_PAIN	35	0.57	1.83	<0.0	0.20
		094	916	1	45
		4	7		
GO_ORGANIC_ACID_TRANSPORT	264	0.45	1.56	0.00	0.20
		518	041	608	450
			4	5	6
GO_CELLULAR_RESPONSE_TO_DEXAMETHASONE_STIMULUS	25	0.60	1.56	0.01	0.20
		865	146	185	465

		9	1	8	7
GO_TERPENOID_METABOLIC_PROCESS	96	0.57	1.56	0.01	0.20
		608	181	904	472
		2	7	8	4
HP_AMYOTROPHIC_LATERAL_SCLEROSIS	35	0.48	1.56	0.01	0.20
		716	264	821	472
			5	9	9
GO_ORGANIC_ACID_CATABOLIC_PROCESS	218	0.74	1.83	0.00	0.20
		989	432	198	507
			4		2
GO_DEMETHYLATION	40	0.55	1.56	0.02	0.20
		989	283	941	509
		5	6	2	6
GO_GLUTATHIONE_TRANSFERASE_ACTIVITY	18	0.73	1.56	0.01	0.20
		741	304	596	544
		9	8	8	1
GO_PEROXISOMAL_TRANSPORT	65	0.73	1.83	<0.0	0.20
		472	022	1	546
		9	7		9
HP_RENAL_TUBULAR_DYSFUNCTION	70	0.46	1.55	0.02	0.20
		958	535	686	574
		5			8
GO_NADH_DEHYDROGENASE_COMPLEX	34	0.49	1.55	0.11	0.20
		111	547	226	618
		9	1	6	9
GO_DRUG_CATABOLIC_PROCESS	21	0.84	1.55	0.00	0.20
		863	456	607	645
		5	3	3	2
GO_ALDO_KETO_REDUCTASE_NADP_ACTIVITY	19	0.70	1.55	0.02	0.20
		529	606	857	653
		8	5	1	6

HP_EEG_WITH_MULTIFOCAL_SLOW_ACTIVITY	30	0.51	1.55	0.03	0.20
		431	805	294	662
		8	1	6	1
GO_AMINO_ACID_BINDING	45	0.61	1.55	0.03	0.20
		405	639	346	667
		9	9	5	
GO_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	77	0.51	1.55	0.00	0.20
		965	553	803	672
		6	5	2	7
GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	69	0.44	1.55	0.09	0.20
		670	386	523	697
		6	7	8	3
GO_NADP_BINDING	49	0.59	1.55	0.02	0.20
		594	738	092	702
		3	9	1	7
GO_CELLULAR_AMINO_ACID_BIOSYNTHETIC_PROCESS	64	0.63	1.55	0.01	0.20
		458	641	535	730
		1	1	5	2
GO_ETHANOL_METABOLIC_PROCESS	17	0.84	1.55	0.00	0.20
		045	644	201	790
		7	1	6	2
GO_MONOCARBOXYLIC_ACID_CATABOLIC_PROCESS	107	0.77	1.84	<0.0	0.20
		662	232	1	823
		6	6		7
HP_ABNORMALITY_OF_THE_INTRINSIC_PATHWAY	26	0.74	1.82	<0.0	0.20
		349	129	1	860
		5	1		3
GO_POSITIVE_REGULATION_OF_FATTY_ACID_TRANSPORT	19	0.60	1.55	0.01	0.20
		969	241	171	878
		1	4	9	8
GO_FLUID_TRANSPORT	24	0.55	1.55	0.03	0.20

		933	165	030	942
		6	3	3	3
GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS_IN_LINEAR_AMIDES	47	0.51	1.55	0.01	0.21
		067	002	239	009
		1	5	7	5
GO_HYDROLASE_ACTIVITY_ACTING_ON_GLYCOSYL_BONDS	90	0.42	1.54	0.00	0.21
		412	800	617	022
		8	2	3	5
GO_SYNAPTIC_TRANSMISSION_DOPAMINERGIC	23	0.49	1.55	0.04	0.21
		042	022	329	037
		3	1	9	7
HP_PROXIMAL_TUBULOPATHY	26	0.54	1.54	0.04	0.21
		914	809	140	070
		4	5	8	9
GO_MICROBODY_MEMBRANE	47	0.55	1.54	0.04	0.21
		881	879	175	086
		4	2		2
GO_CELLULAR_RESPONSE_TO_CHOLESTEROL	17	0.61	1.54	0.02	0.21
		701	911	702	094
		8		7	2
HP_HYPERLIPIDEMIA	86	0.50	1.55	0.01	0.21
		910	025	818	097
		8	3	2	4
HP_ABNORMALITY_OF_THE_MITOCHONDRION	99	0.44	1.54	0.06	0.21
		226	820	981	116
		6	2	5	3
GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	41	0.50	1.54	0.01	0.21
		760	610	626	274
		9	7		4
GO_ENTEROENDOCRINE_CELL_DIFFERENTIATION	25	0.51	1.54	0.04	0.21
		342	329	670	367

		2	8	9	3
GO_GLUTATHIONE_DERIVATIVE_METABOLIC_PROCESS	17	0.75	1.54	0.02	0.21
		398	401	226	373
		7	2	7	6
HP_ENURESIS	17	0.54	1.54	0.05	0.21
		322	282	576	381
		3	2	9	
GO_ENERGY_HOMEOSTASIS	24	0.57	1.54	0.03	0.21
		433	237	232	384
		6	7	3	2
GO_ORGANIC_ANION_TRANSPORT	373	0.43	1.54	0.00	0.21
		570	357	816	386
		7	9	3	2
GO_RESPONSE_TO_PH	31	0.54	1.53	0.02	0.21
		940	891	840	419
		8	7	9	
GO_REGULATION_OF_FATTY_ACID_OXIDATION	25	0.65	1.54	0.00	0.21
		863	444	990	424
		6	6	1	2
GO_PHOSPHOLIPID_TRANSPORTER_ACTIVITY	26	0.56	1.54	0.02	0.21
		806	407	929	429
		3		7	3
HP_ABNORMALITY_OF_HEPATOBILIARY_SYSTEM_PHYSIOLOGY	145	0.43	1.54	0.00	0.21
		351	155	207	460
		3	5	5	4
GO_RESPONSE_TO_ORGANOPHOSPHORUS	118	0.44	1.53	0.01	0.21
		919	897	176	470
		3	6	5	9
GO_STEROID_HYDROXYLASE_ACTIVITY	32	0.78	1.54	0.01	0.21
		387	447	789	482
		5	7	3	

GO_RESPIRATORY_CHAIN_COMPLEX	55	0.45	1.53	0.10	0.21
		166	912	750	505
		2	7	5	8
GO_ALDITOL_METABOLIC_PROCESS	17	0.67	1.53	0.03	0.21
		805	940	339	516
		8	2	9	9
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH_GROUP_OF_DONORS	20	0.73	1.53	0.01	0.21
		974	960	386	545
		4	1	1	8
HP_ABNORMAL_ACTIVITY_OF_MITOCHONDRIAL_RESPIRATORY_CHAIN	43	0.45	1.53	0.08	0.21
		259	994	739	55
		7	8	8	
HP_POLYNEUROPATHY	38	0.48	1.53	0.05	0.21
		836	998	01	608
		4	9		5
GO_AROMATASE_ACTIVITY	21	0.85	1.54	0.00	0.21
		909	029	396	622
		8	3		7
GO_POSITIVE_REGULATION_OF_AMINO_ACID_TRANSPORT	19	0.62	1.53	0.02	0.21
		945	729	828	623
		6	8	3	5
HP_ABNORMAL_CIRCULATING_CHOLESTEROL_CONCENTRATION	72	0.49	1.53	0.03	0.21
		745	686	891	636
		3	1	1	
HP_CEREBRAL_HEMORRHAGE	53	0.47	1.53	0.02	0.21
		131	592	982	734
			1	1	
HP_IRREGULAR_MENSTRUATION	21	0.54	1.53	0.02	0.21
		927	433		745
		5	2		1
HP_ABNORMALITY_OF_VITAMIN_METABOLISM	43	0.54	1.53	0.02	0.21

		3574	5329	5591	7691
HP_ABNORMALITY_OF_CIRCULATING_GLUCOCORTICOID_LEVEL	42	0.47829	1.53447	0.02862	0.217826
HP_LARYNGOSPASM	37	0.46629	1.53482	0.02208	0.217883
GO_CATECHOLAMINE_BIOSYNTHETIC_PROCESS	20	0.60367	1.5337	0.03106	0.21789
HP_ABNORMALITY_OF_THE_COMMON_COAGULATION_PATHWAY	40	0.51394	1.53293	0.02907	0.21802
HP_INTERICTAL_EEG_ABNORMALITY	159	0.37315	1.53325	0.01188	0.21810
HP_HAMARTOMA_OF_THE_EYE	24	0.56965	1.84321	0.00392	0.21825
GO_ASPARTATE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	17	0.79956	1.53087	0.02381	0.21907
GO_ORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	152	0.49854	1.53124	0.01926	0.21908
GO_RESPONSE_TO_MISFOLDED_PROTEIN	19	0.48086	1.53049	0.04863	0.21912
HP_ATTENUATION_OF_RETINAL_BLOOD_VESSELS	27	0.48300	1.53154	0.05996	0.21914

		9	9	1	3
GO_MALE_GENITALIA_DEVELOPMENT	19	0.60	1.53	0.01	0.21
		252	169	810	950
		2	6	9	3
GO_GLUTATHIONE_METABOLIC_PROCESS	39	0.61	1.52	0.03	0.22
		454	917	901	071
		6	3	4	9
GO_COPII_COATED_VESICLE_BUDDING	58	0.43	1.52	0.02	0.22
		886	636	952	074
		6	5	8	2
GO_ORGANIC_ACID_SODIUM_SYMPORTER_ACTIVITY	23	0.61	1.52	0.02	0.22
		759	653	539	107
		1	7	1	2
GO_ACETYL_COA_BIOSYNTHETIC_PROCESS	16	0.67	1.52	0.04	0.22
		480	752	123	115
		9	8	7	1
GO_ASPARTATE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	18	0.60	1.52	0.03	0.22
		979	711	619	124
		2	8		4
GO_CELLULAR_METABOLIC_COMPOUND_SALVAGE	23	0.57	1.52	0.03	0.22
		496	672	519	132
		7		7	1
GO_EXPLORATION_BEHAVIOR	21	0.48	1.52	0.06	0.22
		561	769	285	15
		6	1	7	
GO_ORGANIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	106	0.54	1.52	0.02	0.22
		798	787	285	178
		8	9	7	4
GO_THYROID_HORMONE_METABOLIC_PROCESS	21	0.59	1.52	0.02	0.22
		799	797	286	220
			8	9	7

GO_NEGATIVE_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	21	0.63987	1.52435	0.02419	0.22351
GO_CELL_DEATH_IN_RESPONSE_TO_HYDROGEN_PEROXIDE	20	0.53082	1.52135	0.03933	0.22390
GO_REGULATION_OF_TRIGLYCERIDE_METABOLIC_PROCESS	23	0.63386	1.52098	0.05294	0.22397
GO_CARBON_OXYGEN_LYASE_ACTIVITY	54	0.51857	1.52192	0.03265	0.22417
HP_TREMOR	347	0.32835	1.52149	0.00604	0.22428
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_NAD_P_H_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_OF_OXYGEN	41	0.70917	1.52206	0.01778	0.22452
GO_STEROL_TRANSFER_ACTIVITY	17	0.62061	1.52035	0.03225	0.22454
GO_STEROID_BIOSYNTHETIC_PROCESS	158	0.51147	1.52339	0.02119	0.22456
HP_INTRACRANIAL_HEMORRHAGE	106	0.45131	1.52227	0.04125	0.22475
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_SINGLE_DONORS_WITH_INCORPORATION_OF_MOLECULAR_OXYGEN	19	0.68357	1.52257	0.02761	0.22482
GO_NEGATIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	38	0.52	1.52	0.02	0.22

		830	271	282	518
		9	7	2	9
HP_IRRITABILITY	118	0.45	1.51	0.02	0.22
		423	816	414	693
		1	8	5	4
HP_HYPERLIPOPROTEINEMIA	22	0.63	1.51	0.03	0.22
		691	849	522	701
			7	5	2
HP_NEOPLASM_OF_THE_PERIPHERAL_NERVOUS_SYSTEM	50	0.40	1.51	0.01	0.22
		827	282	8	958
		5	1		8
GO_NEGATIVE_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA	18	0.51	1.51	0.05	0.22
		770	201	220	979
		3	1	9	9
GO_ACYL_COA_BINDING	16	0.66	1.51	0.03	0.22
		942	303	8	984
		3	4		6
HP_HYPOPHOSPHATEMIA	39	0.47	1.51	0.04	0.22
		124	231	780	986
		4	6	9	9
GO_REGULATION_OF_CELLULAR_KETONE_METABOLIC_PROCESS	154	0.41	1.51	0.00	0.22
		986	595	795	995
		1	8	2	8
GO_DICARBOXYLIC_ACID_METABOLIC_PROCESS	74	0.56	1.51	0.04	0.23
		179	309	125	031
		5	4	7	8
HP_GENERALIZED_MUSCLE_WEAKNESS	92	0.40	1.51	0.01	0.23
		395	473	792	032
			1	8	6
GO_CARBOHYDRATE_TRANSPORT	99	0.42	1.51	0.00	0.23
		628	421	579	068

		7	1	2	3
GO_PIGMENT_METABOLIC_PROCESS	57	0.50	1.51	0.02	0.23
		657	478	970	080
		7	5	3	7
HP_NEPHROLITHIASIS	82	0.47	1.51	0.01	0.23
		923	316	785	081
			5	7	
GO_METAL_CLUSTER_BINDING	49	0.50	1.51	0.04	0.23
		101	379	819	081
		3	9	3	8
HP_MOTOR_NEURON_ATROPHY	42	0.42	1.51	0.01	0.23
		940	336	419	101
		9	7	9	6
HP_HYPSARRHYTHMIA	106	0.38	1.51	0.02	0.23
		913	485	161	131
		1	9	1	
GO_AMINO_ACID_SODIUM_SYMPORTER_ACTIVITY	15	0.64	1.50	0.03	0.23
		299	944	977	132
		9		3	3
HP_ACUTE_KIDNEY_INJURY	19	0.58	1.50	0.03	0.23
		008	895	740	156
		1	9	2	9
HP_MACULAR_THICKENING	18	0.59	1.84	0.00	0.23
		882	330	808	172
		7	2	1	1
HP_APLASIA_HYPOPLASIA_OF_THE_UTERUS	45	0.41	1.51	0.03	0.23
		149	052	898	174
		7	6	6	7
GO_LIPOPROTEIN_BIOSYNTHETIC_PROCESS	61	0.43	1.50	0.03	0.23
		540	715	061	178
		5	7	2	8

GO_REVERSE_CHOLESTEROL_TRANSPORT	17	0.71	1.50	0.03	0.23
		972	945	968	187
		5	8	3	
GO_POSITIVE_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	28	0.55	1.50	0.03	0.23
		471	677	137	187
		2	6	3	2
GO_ACYLGLYCEROL_HOMEOSTASIS	24	0.67	1.50	0.04	0.23
		542	805	216	196
		9	8	9	7
HP_NAUSEA	53	0.46	1.50	0.03	0.23
		493	831	777	206
		7	8	3	1
GO_EPOXYGENASE_P450_PATHWAY	16	0.91	1.50	0.00	0.23
		199	729	404	211
			8		4
GO_RETINOIC_ACID_METABOLIC_PROCESS	23	0.71	1.50	0.02	0.23
		099	955	739	225
		6	8	7	4
HP_RETINAL_DEGENERATION	144	0.34	1.50	0.01	0.23
		424	622	127	230
		8	8	8	6
GO_CARBOHYDRATE_HOMEOSTASIS	180	0.37	1.50	0.00	0.23
		743	750	388	233
		5	7	3	2
GO_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	241	0.41	1.50	0.00	0.23
		348	583	585	238
		5	2	9	1
GO_OXIDATIVE_PHOSPHORYLATION	88	0.41	1.50	0.08	0.23
		075	956	669	280
		8	8	4	9
HP_ABNORMAL_ATRIOVENTRICULAR_CONDUCTION	55	0.44	1.50	0.06	0.23

		728	506	521	319
		8	8	7	4
GO_NADH_DEHYDROGENASE_ACTIVITY	32	0.46	1.50	0.13	0.23
		796	460	645	341
			4	6	1
GO_REGULATION_OF_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	69	0.42	1.50	0.03	0.23
		290	337	048	392
		7		8	
GO_POLYSACCHARIDE_METABOLIC_PROCESS	86	0.42	1.50	0.01	0.23
		818	352	405	420
		2		6	2
GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	115	0.42	1.50	0.02	0.23
		666	37	231	443
		7		2	5
GO_PROTEIN_LIPID_COMPLEX	33	0.67	1.50	0.02	0.23
		966	264	352	448
		2	9	9	2
HP_ENLARGED_OVARIES	18	0.54	1.50	0.04	0.23
		933	140	823	613
			2	7	
HP_MOTOR_AXONAL_NEUROPATHY	17	0.53	1.49	0.06	0.23
		915	970	666	732
		9	3	7	
GO_ARACHIDONIC_ACID_MONOOXYGENASE_ACTIVITY	15	0.91	1.50	0.01	0.23
		495	032	587	733
		9	9	3	7
GO_MULTIVESICULAR_BODY	44	0.44	1.49	0.02	0.23
		326	884	348	768
		3	4	3	1
GO_NEGATIVE_REGULATION_OF_ATP_METABOLIC_PROCESS	23	0.59	1.49	0.02	0.23
		060	973	489	783

		7	2	6	8
GO_RESPONSE_TO_COCAINE	43	0.42	1.49	0.01	0.23
		979	899	949	799
		7		3	8
GO_NEUTRAL_LIPID_CATABOLIC_PROCESS	34	0.63	1.49	0.04	0.23
		500	739	6	947
		3	7		4
GO_XENOBIOTIC_TRANSPORT	28	0.65	1.49	0.03	0.24
		953	565	434	077
		2	2	3	6
HP_ABNORMALITY_OF_EXTRAPYRAMIDAL_MOTOR_FUNCTION	188	0.34	1.49	0.00	0.24
		384	630	790	080
		6	9	5	2
GO_URONIC_ACID_METABOLIC_PROCESS	16	0.87	1.49	0.00	0.24
		619	590	619	094
		2	5	8	2
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE	86	0.42	1.49	0.03	0.24
		214	501	305	132
		6	2	8	3
HP_EPILEPTIC_ENCEPHALOPATHY	70	0.41	1.49	0.05	0.24
		373	467	038	139
		6	5	8	9
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ALKYL_OR_ARYL_OTHER_THAN_METHYL_GROUPS	45	0.51	1.49	0.02	0.24
		366	200	510	268
		4	9	5	
HP_DYSTONIA	285	0.33	1.49	0.00	0.24
		346	166	782	275
		3	4	8	1
GO_MITOPHAGY	18	0.49	1.49	0.07	0.24
		915	244	385	300
		4		2	4

HP_INCREASED_CIRCULATING_RENIN_LEVEL	15	0.58597	1.49211	0.05964	0.24303
HP_ABNORMAL_RETINAL_VASCULAR_MORPHOLOGY	155	0.34038	1.49261	0.01949	0.24321
HP_BILATERAL_TONIC_CLONIC_SEIZURE_WITH_GENERALIZED_ONSET	17	0.57300	1.49318	0.03006	0.24334
GO_STEROID_CATABOLIC_PROCESS	27	0.68661	1.49093	0.01785	0.24340
HP_HYPERKINETIC_MOVEMENTS	20	0.47372	1.48769	0.05566	0.24349
GO_REGULATION_OF_LIPID_METABOLIC_PROCESS	323	0.41314	1.49265	0.00772	0.24371
GO_STEROL_HOMEOSTASIS	72	0.55718	1.49040	0.02952	0.24381
GO_MONOVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	263	0.35208	1.48777	0.01529	0.24388
GO_ACID_THIOL_LIGASE_ACTIVITY	17	0.68364	1.48781	0.03359	0.24435
HP_VOMITING	166	0.57431	1.84432	<0.01	0.24461
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	83	0.45	1.48	0.06	0.24

		2581	7911	3584	4746
HP_INCREASED_CSF_LACTATE	48	0.45800	1.48803	0.10505	0.24509
GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS	85	0.42543	1.48849	0.01209	0.24544
GO_RESPONSE_TO_EPINEPHRINE	15	0.62068	1.48812	0.05501	0.24548
GO_REGULATION_OF_ICOSANOID_SECRETION	19	0.55044	1.48859	0.03614	0.24584
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_DONORS	37	0.48911	1.48599	0.06	0.24588
GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE_REMODELING	17	0.69798	1.48882	0.03854	0.24605
GO_LONG_CHAIN_FATTY_ACID_BIOSYNTHETIC_PROCESS	31	0.63356	1.48556	0.02952	0.24607
GO_NOREPINEPHRINE_SECRETION	16	0.53312	1.48523	0.05118	0.24612
HP_NEOPLASM_OF_THE_TRACHEOBRONCHIAL_SYSTEM	18	0.58729	1.48460	0.04526	0.24667
GO_REGULATION_OF_CAMP_MEDIATED_SIGNALING	39	0.37759	1.48281	0.04323	0.24697

		9	1	3	6
HP_INCREASED_LDL_CHOLESTEROL_CONCENTRATION	19	0.61	1.48	0.04	0.24
		289	309	125	703
		6	5	7	1
GO_NUCLEOBASE_METABOLIC_PROCESS	27	0.64	1.48	0.04	0.24
		411	246	970	704
		1		2	6
GO_C4_DICARBOXYLATE_TRANSPORT	20	0.58	1.48	0.03	0.24
		039	313	379	751
		6	3	7	1
GO_OXIDOREDUCTASE_COMPLEX	83	0.42	1.48	0.08	0.24
		650	153	097	759
		4	9	2	4
HP_HYPERKALEMIA	26	0.48	1.48	0.05	0.24
		823	179	954	770
			1	8	6
GO_ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	489	0.32	1.48	0.00	0.24
		140	317	998	798
		6	3		4
GO_PYRIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	19	0.66	1.48	0.02	0.24
		296	348	964	803
		8	3	4	
HP_JOINT_HEMORRHAGE	16	0.72	1.48	0.04	0.24
		803	038	807	912
		3	9	7	7
GO_POSITIVE_REGULATION_OF_GLYCOLYTIC_PROCESS	23	0.55	1.47	0.05	0.24
		723	821	304	965
		7	4	5	
GO_ANION_TRANSPORT	483	0.37	1.47	0.00	0.24
		606	880	796	965
		7	3	8	1

HP_ESOPHAGEAL_VARIX	17	0.54233	1.47844	0.05870	0.24978
GO_ORGANIC_CATION_TRANSPORT	38	0.44363	1.47746	0.04008	0.24985
GO_PORE_COMPLEX	18	0.69103	1.47776	0.05576	0.24989
HP_XANTHOMATOSIS	23	0.65917	1.47957	0.06835	0.24993
GO_VIRAL_GENE_EXPRESSION	171	-0.5227	-2.2091	<0.01	0.01250
GO_TRANSLATIONAL_INITIATION	151	-0.5448	-2.2291	<0.01	0.01709
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	109	-0.6128	-2.1520	<0.01	0.02469
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS	158	-0.5065	-2.1072	0.00796	0.04505
GO_PROTEIN_TARGETING_TO_MEMBRANE	151	-0.4434	-2.0384	0.00196	0.05950
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	123	-0.5049	-2.0392	0.00611	0.06702
GO_RNA_CATABOLIC_PROCESS	305	-0.4	-2.0	<0.0	0.07

		318	586	1	134
		3	8		7
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	103	-0.6	-2.0	<0.0	0.07
		022	407	1	616
		3	5		2
GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	93	-0.6	-1.9	0.00	0.13
		204	721	205	206
		1	2	8	5
HP_ACUTE_LEUKEMIA	82	-0.4	-1.9	<0.0	0.19
		914	383	1	108
		2	1		3
GO_CATALYTIC_STEP_2_SPLICEOSOME	57	-0.5	-1.8	0.01	0.22
		397	340	556	954
		1	4	4	3
GO_PRECATALYTIC_SPLICEOSOME	41	-0.5	-1.8	0.01	0.23
		875	365	367	003
		1	9	2	9
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	249	-0.3	-1.8	0.00	0.23
		757	518	384	072
		2		6	6
HP_POINTED_CHIN	57	-0.5	-1.8	<0.0	0.23
		264	379	1	388
		6	7		6
GO_REGULATION_OF_TELOMERE_MAINTENANCE	58	-0.5	-1.8	0.01	0.23
		017	087	359	827
		4	8	2	9
GO_SM_LIKE_PROTEIN_FAMILY_COMPLEX	55	-0.5	-1.8	0.00	0.23
		560	525	391	853
		4		4	9
GO_RNA_LOCALIZATION	165	-0.4	-1.8	0.00	0.24
		921	385	790	075

		3	5	5	
GO_MRNA_EXPORT_FROM_NUCLEUS	77	-0.5	-1.8	0.01	0.24
		194	101	380	075
		6	7	7	9
GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	97	-0.4	-1.8	0.00	0.24
		755	122	196	096
		7	4	1	5
GO_SMALL_NUCLEAR_RIBONUCLEOPROTEIN_COMPLEX	47	-0.5	-1.8	0.00	0.24
		852	450	967	126
		5	1	1	
GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE	39	-0.5	-1.8	0.01	0.24
		376	273	372	156
		2	9	5	
GO_SPLICEOSOMAL_TRI_SNRNP_COMPLEX	28	-0.6	-1.8	0.01	0.24
		368	415	162	228
		4	2	8	3
GO_CAJAL_BODY	37	-0.5	-1.8	0.00	0.24
		561	138	393	343
		4		7	6
GO_SYNAPSE_MATURATION	19	-0.6	-1.8	0.00	0.24
		263	539	193	517
			2	8	8
GO_RNA_EXPORT_FROM_NUCLEUS	96	-0.5	-1.8	0.00	0.24
		289	577	980	547
		7	4	4	4
GO_MRNA_BINDING	189	-0.4	-1.8	0.00	0.24
		123	230	386	605
		3	2	1	5
GO_NUCLEOSOME_ORGANIZATION	81	-0.5	-1.8	0.00	0.24
		698	139	785	974
		4	9	9	6

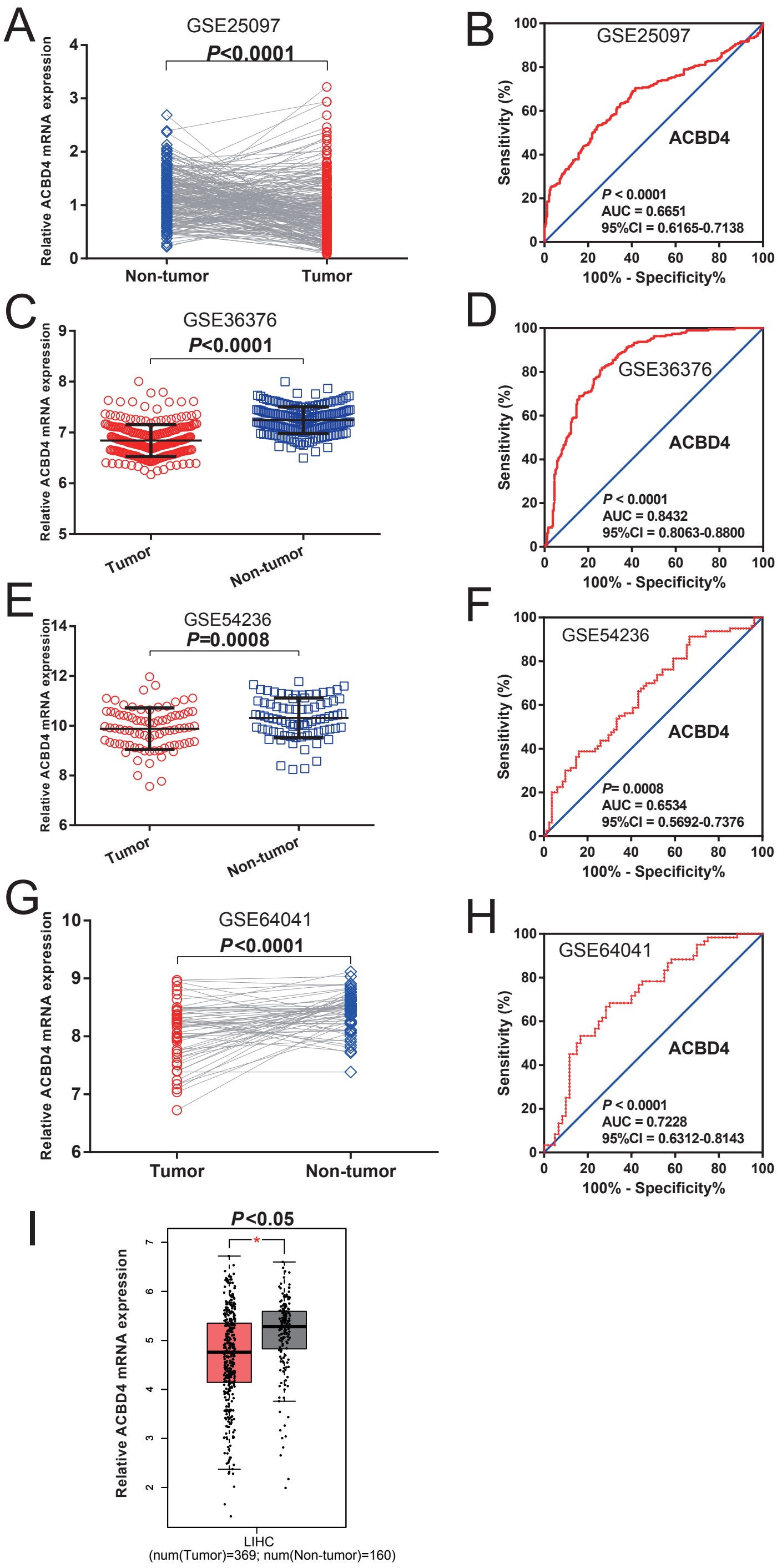

Figure S1. The expression distribution of ACBD4 gene in HCC tumor and non-tumor tissues.
(A) Scatter plot of ACBD4 gene expression in HCC tumor and paired non-tumor tissues of GSE25097 cohort;
(B) The ROC curve of ACBD4 gene in distinguished HCC tumor and paired non-tumor tissues of GSE25097 cohort;
(C) Scatter plot of ACBD4 gene expression in HCC tumor and adjacent non-tumor tissues of GSE36376 cohort;
(D) The ROC curve of ACBD4 gene in distinguished HCC tumor and adjacent non-tumor tissues of GSE36376 cohort;
(E) Scatter plot of ACBD4 gene expression in HCC tumor and adjacent non-tumor tissues of GSE54236 cohort;
(F) The ROC curve of ACBD4 gene in distinguished HCC tumor and adjacent non-tumor tissues of GSE54236 cohort;
(G) Scatter plot of ACBD4 gene expression in HCC tumor and paired non-tumor tissues of GSE64041cohort;
(H) The ROC curve of ACBD4 gene in distinguished HCC tumor and paired non-tumor tissues of GSE64041 cohort;
(I) Box plot of ACBD4 gene expression in HCC tumor and non-tumor tissues of TCGA cohort. Note:* represents P<0.05.

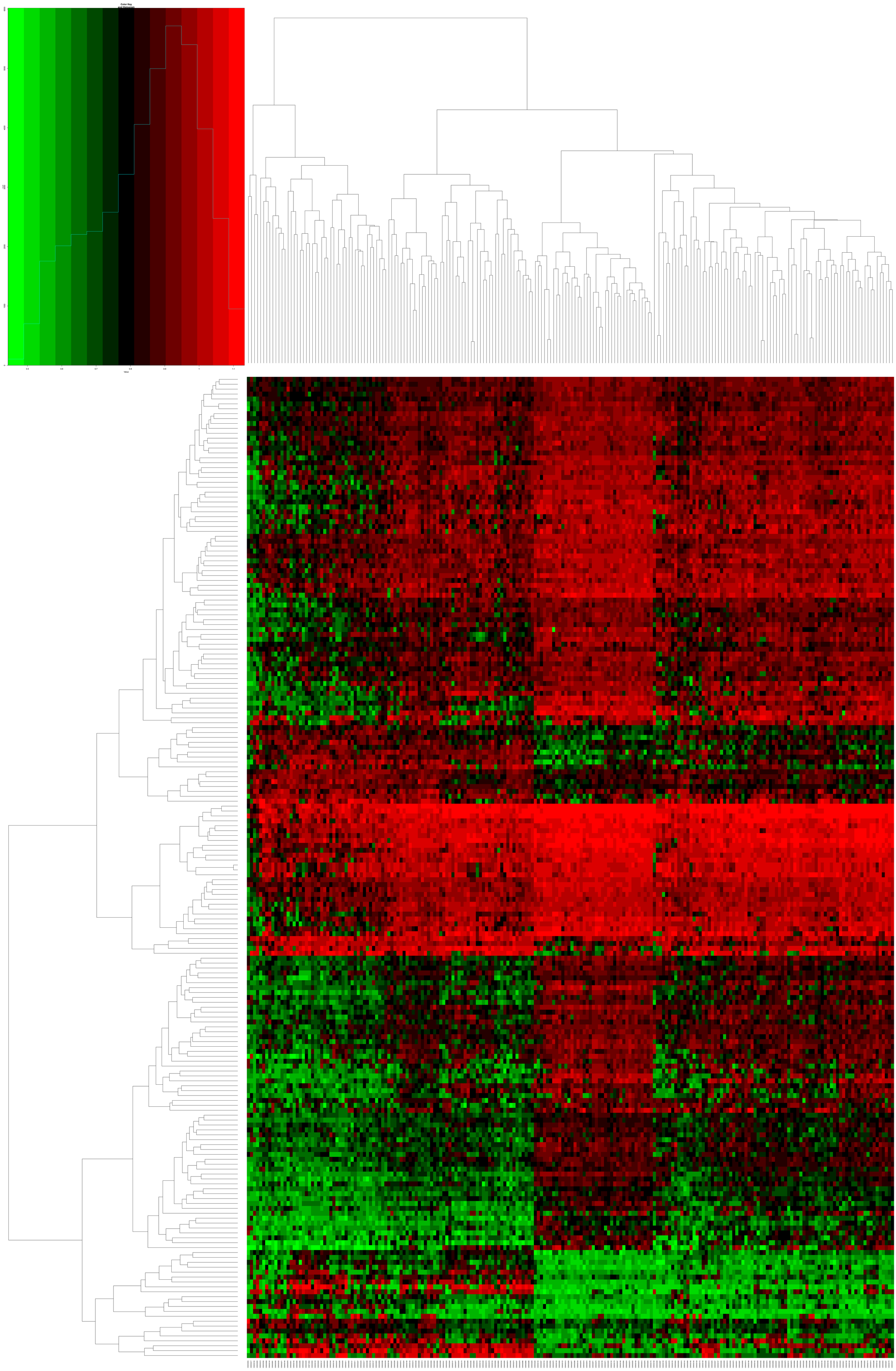

Figure S2. Heatmap of differentially expressed genes between high- and low-ACBD4 expression groups in HBV-related HCC tumor tissues.