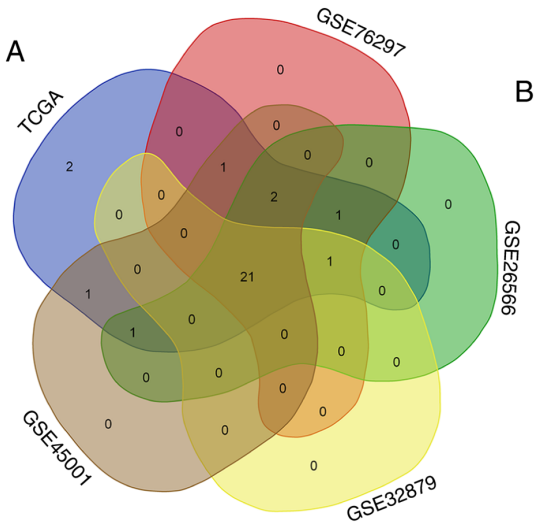
Figure S1. Identification of hub genes by comparison of multiple datasets. (A) Venn diagram indicating the intersection of DEGs obtained from TCGA, GSE76297, GSE26566, GSE32879 and GSE45001. (B) The table lists specific genes for each intersection. TCGA, The Cancer Genome Atlas; DEGs, differentially expressed protein-coding genes.

A



B

Datasets	Total	Genes
TCGA GSE76297 GSE26566 GSE32879 GSE45001	21	FGA MKI67 CDK1 FOXM1 EHHADH ACOX1 APOA1 TOP2A ITGA2 CENPF APOE FGG APOA2 LAMC2 ALB APOB SERPINC1 C3 KNG1 PRC1 AHSG
TCGA GSE76297 GSE26566 GSE32879	1	CCNB2
TCGA GSE76297 GSE26566 GSE454001	2	RRM2 CEP55
TCGA GSE76297 GSE26566	1	KIF2C
TCGA GSE76297 GSE45001	1	SERPINA1
TCGA GSE26566 GSE45001	1	NEK2
TCGA GSE45001	1	UBE2C
TCGA	2	C4A BIRC5

Figure S2. ROC curves for (A) *CDK1*, (B) *MKI67*, (C) *PRC1* and (D) *TOP2A*. The x-axis represents specificity; the y-axis represents sensitivity. AUC is marked in blue. ROC, receiver operating characteristic; AUC, area under the curve; *CDK1*, cyclin dependent kinase 1; *MK167*, marker of proliferation Ki-67; *PRC1*, protein regulator of cytokinesis 1; *TOP2A*, DNA topoisomerase II α.

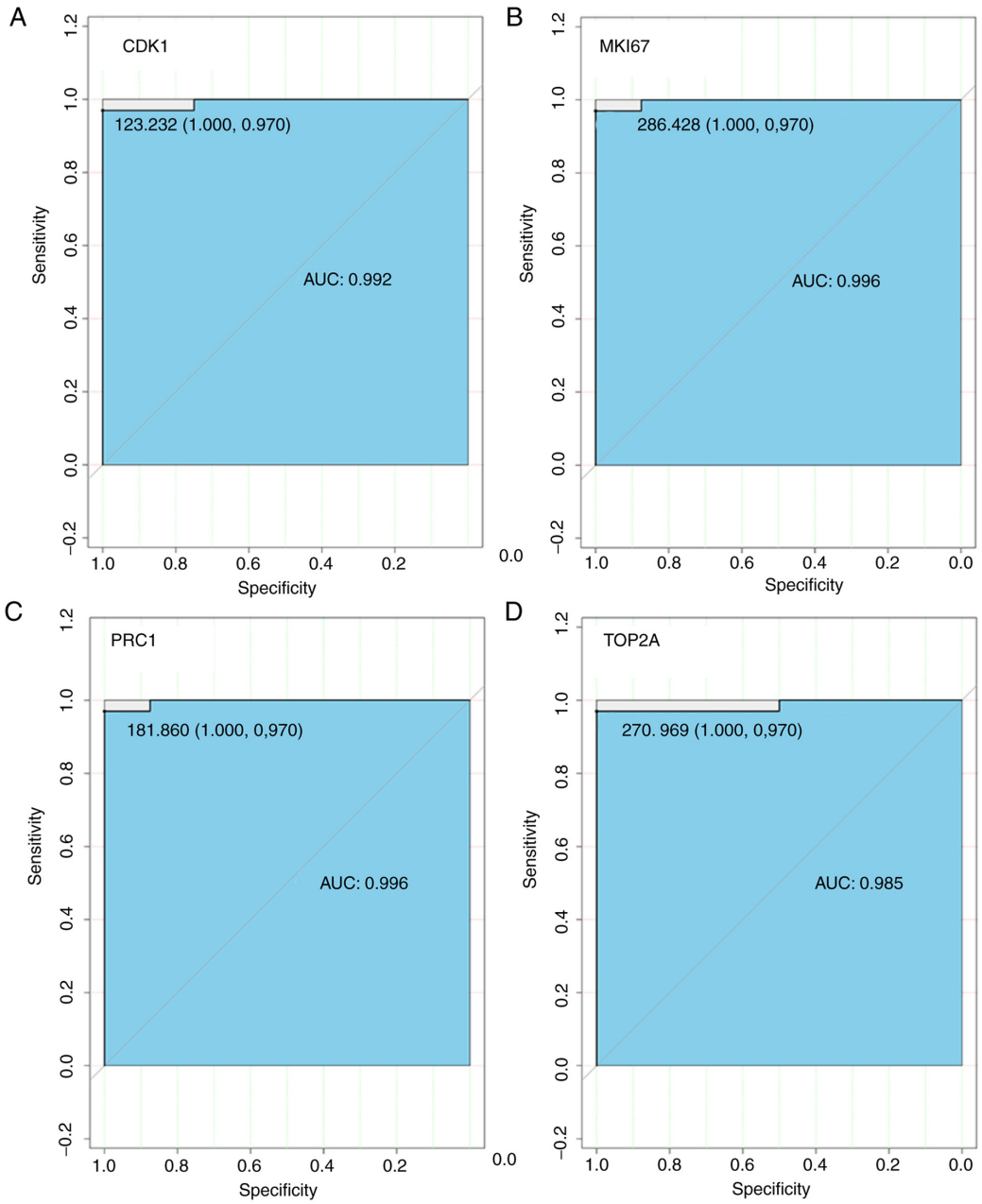


Figure S3. Correlation analysis between gene expression and tumor staging. (A) *ACOX1*, (B) *APOA2*, (C) *APOB*, (D) *FGA* and (E) *FGG*. *ACOX1*, acyl-CoA oxidase 1; *APOA2*, apolipoprotein A2; *APOB*, apolipoprotein B; *FGA*, fibrinogen α chain; *FGG*, fibrinogen γ chain.

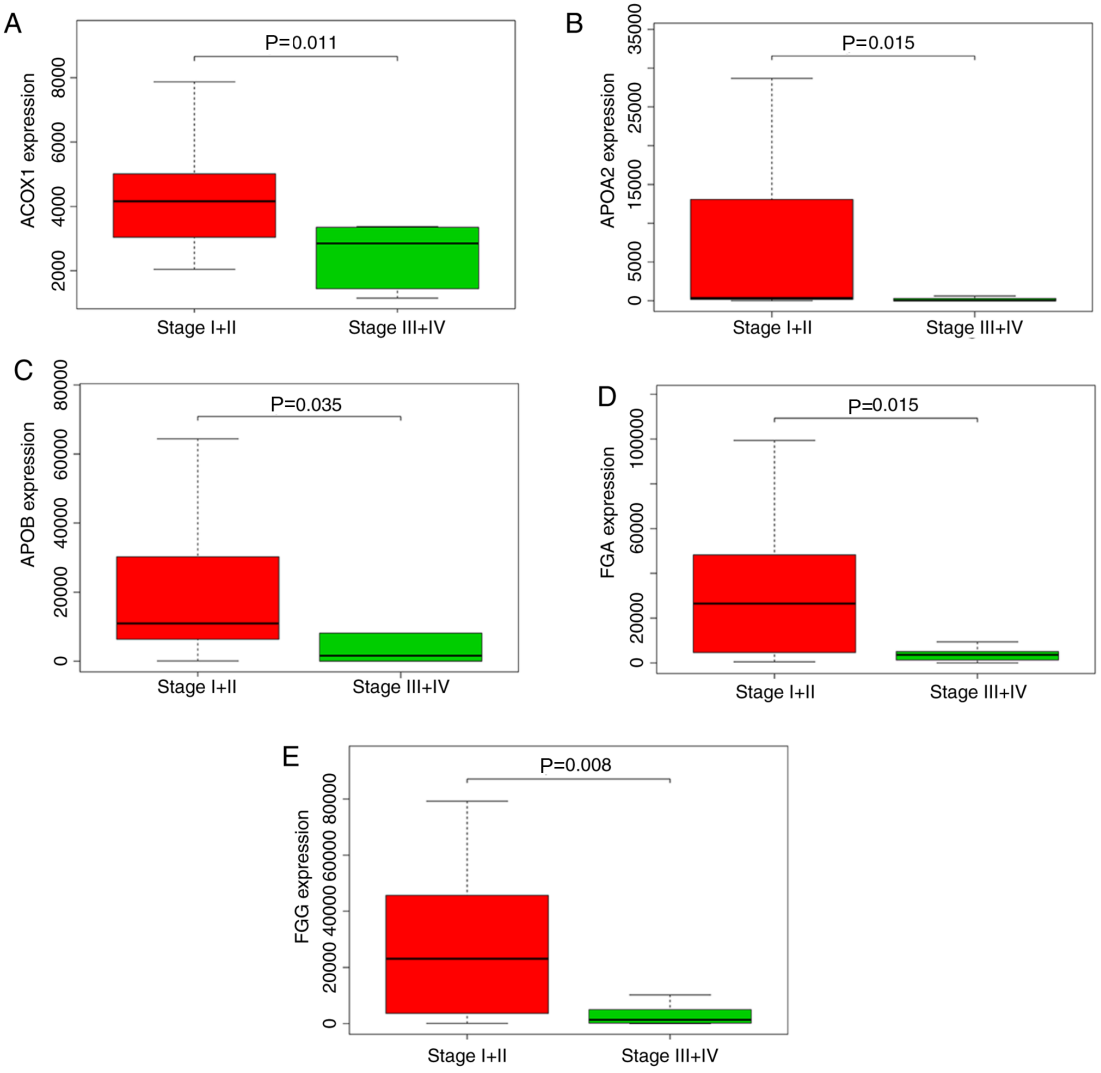


Table SI. Primer sequence for RT-qPCR.

Gene symbol	Primer sequences	Annealing temperature (˚C)	Product length (bp)
β-actin	F: 5'-GTGGCCGAGGACTTTGATTG-3'		
	R: 5'-CCTGTAACAACGCATCTCATATT-3'	60	73
MKI67	F: 5'-TCTGGGTTACCTGGTCTTAGTTC-3'		
	R: 5'-CCCTTTTGAGAGGCGTATTAG-3'	60	163
TOP2A	F: 5'-CAAAAAGTCAGTCTTCCACCTC-3'		
	R: 5'-AGGCTTTTGAGAGACACCAGA-3'	60	104
PRC1	F: 5'-CTATTCTGAGTTTGCGAAGGAT-3'		
	R: 5'-TTCTCAGGACTGGATGTTGGT-3'	60	133
CDK1	F: 5'-GGAACTTCGTCATCCAAAT-3'		
	R: 5'-TGTACTGACCAGGAGGGAT-3'	60	131

MK167, marker of proliferation Ki-67; *TOP2A*, DNA topoisomerase II α; *PRC1*, protein regulator of cytokinesis 1; *CDK1*, cyclin dependent kinase I; F, forward; R, reverse; bp, base pairs.

Table SII. GO enrichment analysis of the upregulated genes.

GO-ID	P-value	Description	Genes
GO:0098641	1.71E-06	Cadherin binding involved in cell-cell adhesion	*ALDOA*, *LAD1*, *PFKP*, *S100A11*, *ANLN*, *SFN*, *FLNA*, *ANXA2*, *NOTCH3*, *PKM*, *EPCAM*, *EVPL*, *CCNB2*, *PKP3*, *CAPG*, *DBN1*, *EPS8L1*
GO:0030198	2.23E-06	Extracellular matrix organization	*COL4A2*, *COL4A1*, *PDGFA*, *NPNT*, *ITGB4*, *ITGA2*, *SPINT1*, *SOX9*, *DDR1*, *LAMB3*, *ITGB8*, *LAMA5*, *LAMC2*, *SPP1*
GO:0005913	6.70E-06	Cell-cell adherens junction	*ALDOA*, *LAD1*, *PFKP*, *S100A11*, *ANLN*, *SFN*, *NECTIN4*, *FLNA*, *ANXA2*, *NOTCH3*, *PKM*, *EVPL*, *CCNB2*, *PKP3*, *CAPG*, *DBN1*, *EPS8L1*
GO:0098609	1.64E-05	Cell-cell adhesion	*ALDOA*, *LAD1*, *PFKP*, *S100A11*, *ANLN*, *SFN*, *ANXA2*, *NOTCH3*, *PKM*, *EPCAM*, *EVPL*, *CCNB2*, *CAPG*, *DBN1*, *EPS8L1*
GO:0070062	2.20E-05	Extracellular exosome	*SLC44A2*, *NPNT*, *MMP7*, *PKM*, *EPCAM*, *DMKN*, *HIST3H2A*, *LOXL4*, *RAB25*, *TUBA1A*, *NQO1*, *TUBB3*, *ADAM9*, *CDK1*, *ZDHHC1*, *EPN3*, *LAD1*, *PFKP*, *SPINT1*, *NECTIN4*, *FLNA*, *DDR1*, *EVPL*, *MELTF*, *ST14*, *SLC38A1*, *MGAT5*, *EPS8L1*, *ALDOA*, *GCNT3*, *PKHD1*, *ITGB4*, *EPHA10*, *SFN*, *TPM4*, *CDH6*, *ITGB8*, *KRT7*, *PAFAH1B3*, *MYOF*, *PHLDA3*, *SPP1*, *PLP2*, *COL4A2*, *TMC4*, *CPNE7*, *S100A11*, *SLC6A14*, *COL15A1*, *ATP1A1*, *TSPAN15*, *HID1*, *ADGRG1*, *ANXA3*, *LGALS9*, *ANXA2*, *WNT7B*, *C1ORF116*, *DSG2*, *LAMA5*, *RAB34*, *CAPG*, *ABCC1*
GO:0007155	4.34E-05	Cell adhesion	*ITGB4*, *COL15A1*, *CTNND2*, *PTK7*, *ITGA2*, *NECTIN4*, *ADGRG1*, *GRHL2*, *CDH6*, *DDR1*, *TNFAIP6*, *LAMB3*, *DSG2*, *ITGB8*, *LAMC2*, *CD24*, *NTM*, *SPP1*, *ADAM9*
GO:0030496	3.21E-04	Midbody	*CDK1*, *PRC1*, *NEK2*, *CENPF*, *BIRC5*, *MTCL1*, *CEP55*, *ECT2*, *ANXA2*
GO:0005198	4.76E-04	Structural molecule activity	*CLDN7*, *LAMB3*, *KRT80*, *EVPL*, *CLDN4*, *LAD1*, *LAMA5*, *KRT7*, *COL15A1*, *JAG1*, *TUBA1A*, *KRT23*
GO:0005911	4.84E-04	Cell-cell junction	*DSG2*, *PDLIM7*, *PKP3*, *IQGAP3*, *PTK7*, *NECTIN4*, *ECT2*, *GRHL2*, *FLNA*, *ANXA2*
GO:0060672	5.22E-04	Epithelial cell morphogenesis involved in placental branching	*SPINT2*, *ST14*, *GRHL2*

The top 10 GO terms are listed. GO, Gene Ontology.

Table SIII. GO enrichment analysis of the downregulated genes.

Term	P-value	Description	Genes
GO:0055114	3.02E-48	Oxidation-reduction process	*CYP3A4, ALDH8A1, SC5D, ALDH1L1, HMGCR, CYP2D7, CYP2D6, LDHD, OSGIN1, HIBADH, BBOX1, GLDC, PECR, AKR7A3, DAO, HIGD1A, ALDH6A1, CYP1A1, PCBD1, FAXDC2, QDPR, CYP26A1, CYP2E1, CYP1A2, CDO1, POR, HSD11B1, XDH, ADHFE1, FDX1, CYP2B6, GLUD1, HSD17B13, KMO, PAH, DHODH, ALDH4A1, PTGR1, MSMO1, CYP2C9, SCD, CYP2C8, HGD, CYP17A1, PRODH2, DIO1, CYP8B1, BCO2, DCXR, TM7SF2, ASPDH, STEAP4, CYP2J2, CYP2C19, CYP2C18, CYP3A43, MTHFD1, TDO2, MSRA, CRYL1, AKR1C4, CYP39A1, GPX3, SRD5A1, SRD5A2, SARDH, HPD, ACADM, AIFM1, CYB5A, GRHPR, ACADL, RDH5, DHRS1, ALDH7A1, DHRS3, DHRS4, CYP27A1, AKR1C8P, CYP2A6, CYP2A7, AKR1D1, ALDH9A1, PHYHD1, SORD, CYP4F22, DHRS4L2, AASS, ADH7, PIPOX, ALDH1A1, FMO4, FMO5, CBR1, CYP4A22, MMACHC, DHCR7, FMO3, HAAO, HSD17B6, DMGDH, PNPO, GSTO1, BDH1, GLRX, HSD17B8, BCKDHB, IDO2, FADS2, MSRB1, CYP4F11, CYP4F12, STAB2, DBH, SOD1, ADI1, FRRS1, CYP4A11, HSDL2, AOX1, PHGDH, KDM8, AGMO, CYP4F3, CP, CYP4F2, DPYD, RDH16, HPGD, MGST1, CBS, RETSAT*
GO:0070062	3.33E-42	Extracellular exosome	*ALDH8A1, ADCY1, A2M, RARRES2, GDF2, ALAD, BTD, MASP2, FAM20A, SELENBP1, SYT7, BBOX1, FAH, GOT2, ATP2B2, APOB, GOT1, APOE, LCAT, APOH, CFH, VNN1, CFI, APOM, FTL, F11, ACAA2, F12, GATM, C4A, ABCB11, C4B, PCBD1, LIFR, F9, CDHR5, SERPING1, RND3, SERPINF1, SERPINF2, PGM1, BHMT, F2, ABAT, RBP5, GC, RBP4, ACADSB, SERPINA10, ENPP3, ALDOC, PTH1R, ALDOB, MST1, MME, ASL, ACAT2, ACAT1, AHSG, ARG1, KLKB1, IDH1, FGL1, SPP2, COL18A1, GPD1, BHMT2, PTGR1, ST6GAL1, CFB, UPB1, GGH, HGD, CD5L, GBE1, PON1, QPRT, GK, SLC46A3, RIDA, PON3, STEAP4, PZP, CYP2J2, ARSF, GPLD1, MTHFD1, CFHR1, EFHD1, CFHR3, MSRA, SERPINA7, SERPINA6, TKFC, SERPINA5, SERPINA4, GPX3, SERPINA1, CETP, NT5E, DPP4, CEACAM1, HYAL1, APCS, PEPD, ACO1, TTC38, SAA4, CYB5A, GRHPR, DECR1, C8G, C8A, AMBP, C8B, HAO2, INHBC, SLC27A2, TF, SORD, C9, C3, ABHD6, C6, C5, DPYS, SEC14L3, SEC14L2, CPN2, GALK1, CBR1, SERPINC1, HAAO, C2, NAT8, CES3, SHMT1, CES2, FTCD, IGF2, SOD1, PCK2, PLG, PCK1, KHK, SDHB, ORM1, AFM, PYGL, AOX1, PHGDH, GFRA1, GAMT, SERPIND1, CP, PSAT1, HPGD, CD14, ORM2, ALDH1L1, THRB, IQGAP2, BPHL, VTN, ENPEP, CXCL12, CMBL, APOA4, TTR, AZGP1, APOA2, SLC16A1, APOA1, SLC25A25, PGLYRP2, PGRMC1, ST3GAL6, AKR7A3, ALDH6A1, QDPR, FBP1, METTL7A, ASS1, FOLH1B, CLU, APOC1, KMO, PAH, AGMAT, ANGPTL6, GALM, FGG, FGA, FGB, ALB, APOC3, ENTPD5, TMEM192, SCARB1, NDRG2, ACY3, SLC6A13, ACMSD, EPHX2, SELENOP, ABHD14B, AK4, ABCB4, TST, LYVE1, DSG1, ALDH2, SLC13A3, FABP1, CPB2, DCXR, SLC5A12, ANO1, SAT2, SORL1, ACOT2, HP, PRDX3, AMN, CRYL1, AKR1C4, ITIH1, ANG, PROZ, ITIH4, RHOB, ACOT13, ITIH2, LBP, CAT, ITIH3, HPD, KNG1, SHBG, PPP2R1B, DDC, ACADM, IGFALS, MAN1A1, SLC9A3R2, HAGH, ALDH7A1, FOLH1, CTH, DHRS4, CFL2, PKLR, DDT, PEBP1, CUX2, AKR1D1, PROS1, UGP2, ALDH9A1, XYLB, ECHS1, ADH6, C1R, C1S, OAF, PLPP3, PBLD, ALDH1A1, LRG1, FCN2, PNPO, ENO3, BDH2, HRG, APMAP, SLC39A5, GSTO1, HBB, GLRX, GSTA1, COBLL1, GSTA2, HPN, RNASE4, FETUB, HOGA1, ISOC1, MAN1C1, HPR, XPNPEP2, ELFN1, A1BG, CYP4A11, GLYAT, HPX, C1RL, SH3BGRL2, GPT, HIBCH, SCP2, IGFBP3, UGT2B7, AQP7P3*
GO:0072562	6.02E-35	Blood microparticle	*A2M, PZP, HP, VTN, APOA4, CFHR1, CFHR3, APOA2, APOA1, ITIH1, APOE, APOA5, ITIH4, CFH, ITIH2, KNG1, APCS, C4A, C4B, SERPING1, C8G, C8A, AMBP, SERPINF2, F2, PROS1, GC, TF, C9, C3, CLU, C1R, C1S, CPN2, AHSG, FGG, FGA, FCN3, FGB, ALB, BCHE, FCN2, SERPINC1, HRG, HBB, ANGPTL4, CFB, CD5L, C4BPA, PLG, HPR, A1BG, ORM1, AFM, HPX, PON1, CP, ORM2*

Table SIII. Continued.

Term	P-value	Description	Genes
GO:0031090	8.59E-28	Organelle membrane	*TM7SF2, CYP3A4, CYP2J2, CYP2C19, CYP2B6, CYP2C18, CYP2D6, CYP4F22, CYP3A43, FMO4, FMO5, CYP39A1, CYP4A22, PGRMC1, FMO3, SLC39A8, SRD5A1, SRD5A2, CYP1A1, CYP2C9, CYP2C8, CYP26A1, EPHX1, CYP4F11, CYP4F12, CYP1A2, AADAC, CYP4A11, TFPI, UGT2B4, CYP2A6, CYP4F3, CYP2A7, UGT2B10, CYP4F2, RDH16, UGT2B15, CYP8B1, UGT2B7, MGST2*
GO:0005759	2.48E-26	Mitochondrial matrix	*ETNPPL, BTD, AMT, OGDHL, ACOT2, BPHL, PRDX3, AGXT, HIBADH, ACSF2, GLDC, GOT2, ALAS1, HADH, DHTKD1, SARDH, GPT2, HMGCL, ACSM2B, AADAT, SUOX, ALDH6A1, ACADM, ACADS, SUCLG2, ALDH5A1, OTC, ACSM2A, DECR1, ACADL, HAGH, ALDH7A1, CYP27A1, ABAT, PCCB, ACADSB, NAGS, ADHFE1, FDX1, CA5A, GLUD1, ECHS1, AASS, ACAT1, GLS2, MTHFS, MUT, IVD, ETFDH, ALDH4A1, DMGDH, BDH1, HSD17B8, GCDH, BCKDHB, AK3, AK4, PCK2, SOD1, CPS1, MMAB, TST, DBT, GLYAT, HMGCS2, MLYCD, ALDH2, AGXT2, HIBCH, ACSM5, BCO2, PC*
GO:0006805	1.48E-23	Xenobiotic metabolic process	*CYP3A4, CYP2J2, CYP2C19, CYP2B6, CYP2C18, CYP2D7, CYP2D6, RORC, BPHL, CMBL, SULT1A1, FMO3, AKR7A3, ACSM2B, CES2, CES1, CYP2C9, ACY3, CYP2C8, NAT2, EPHX2, EPHX1, CYP26A1, CYP2E1, CYP1A2, POR, AADAC, GLYAT, NR1I2, HNF4A, SULT1B1, UGT2B4, UGT2B15, MGST1, MGST2*
GO:0005576	3.26E-23	Extracellular region	*BMP10, PLGLA, GDF2, RARRES2, A2M, CNDP1, MASP1, BTD, MASP2, VTN, NOTUM, CXCL12, DNASE1L3, APOA4, CFP, TTR, AZGP1, APOA2, APOB, LPA, APOA1, APOE, LCAT, APOF, APOA5, CFH, APOH, RGN, CFI, APOM, F11, F12, F10, C4A, C4B, LRCOL1, IL27, COLEC10, F9, SERPING1, F7, COLEC11, FGF21, CLEC4M, SERPINF1, SERPINF2, F2, TFPI, GC, RBP4, LPAL2, HSD17B13, CLU, MST1, APOC1, GREM2, LEAP2, AHSG, F13B, FGG, FGA, ALB, FGB, BCHE, KLKB1, APOC3, GALP, CDA, CDC37L1, SPP2, ANGPTL4, COL18A1, GLT1D1, NTF3, CFB, SELENOP, CD5L, HGF, FAM198A, NPW, PON1, PZP, INS-IGF2, LEPR, HP, ASGR1, CFHR2, CFHR4, SERPINA7, HAMP, ANG, ITIH1, SERPINA5, PROZ, SERPINA4, GPX3, ITIH4, SERPINA1, CETP, ITIH2, LBP, ITIH3, CFHR5, GHR, SHBG, KNG1, APCS, PRG4, SPACA7, SAA4, IGFALS, IL6R, C8G, PROC, C8A, AMBP, C8B, INHBC, PROS1, TF, MBL2, C9, C3, C6, OXT, C5, CXCL2, DHRS4L2, C1R, ADH7, C1S, CPN2, FNDC5, FCN3, LRG1, FCN2, PLA2G12B, SERPINC1, PRAP1, HRG, C2, PLGLB2, HGFAC, PLGLB1, HBB, THPO, ABHD15, RNASE4, FETUB, IGF1, VWCE, C4BPB, IGF2, C4BPA, DBH, SOD1, CCL16, PLG, HPR, A1BG, ORM1, AFM, BMPER, TENM1, HPX, LIPG, SERPIND1, CP, IGFBP1, LIPC, IGFBP3, CD14, ORM2, IGFBP4, ENHO*
GO:0016491	4.95E-22	Oxidoreductase activity	*CYP3A4, ASPDH, SC5D, ALDH1L1, CYP2C19, CYP2D6, ADH1C, ADH1B, OSGIN1, SLC9B2, SARDH, SUOX, CYP1A1, AIFM1, CYP2E1, CYP1A2, POR, DHRS1, ALDH7A1, HAO2, AKR1C8P, HSD11B1, SORD, ADHFE1, HSD17B13, DHRS4L2, AASS, ADH6, ADH7, PIPOX, ALDH1A1, MMACHC, ETFDH, ALDH4A1, DMGDH, HSD17B6, BDH2, HSD17B4, GSTO1, BDH1, PTGR1, MSMO1, CYP2C9, SCD, ADI1, SDHB, HSDL2, AOX1, ALDH2, HPGD, DCXR, RETSAT*
GO:0005615	1.28E-21	Extracellular space	*BMP10, ALAD, GDF2, HFE2, MASP1, BTD, CRHBP, VTN, SELENBP1, CXCL12, APOA4, CFP, AZGP1, TTR, APOB, APOA1, SPX, APOE, LCAT, PPP1R1A, APOA5, CFH, APOH, CFI, VNN3, F11, F12, C4A, C4B, IL27, F9, SERPING1, F7, FGF21, CD36, SERPINF1, SERPINF2, F2, TFPI, GC, C3P1, XDH, RBP4, SERPINA10, SERPINA11, ENPP1, CLU, MST1, GREM2, AHSG, ARG1, FGG, FGA, ALB, FGB, KLKB1, APOC3, ANGPTL3, ANGPTL4, COL18A1, CFB, GGH, SELENOP, CD5L, HGF, ECM2, TST, PON1, CPB2, CHRD, PON3, SORL1, GPLD1, HP, AMN, CFHR1, CFHR3, SERPINA7, SERPINA6, HAMP, ANG, SERPINA5, PROZ, SERPINA4, GPX3, SERPINA1, CETP, LBP, CAT, TSKU, GHR, KNG1, HYAL1, APCS, CES5A, SAA4, IGFALS, IL6R, PROC, C8A, AMBP, C8B, CFL2, INHBC, PROS1, TF, MBL2, SORD, C3, ADAMTS13, OXT, C5, CXCL2, CPN1, LRG1, SERPINC1, ENO3, C2, LECT2, PCSK6, HGFAC, THPO, CES3, CES2, CES1, FETUB, IGF1, C4BPB, IGF2, C4BPA, DBH, SOD1, CCL16, TMPRSS6, PLG, A1BG, ORM1, AFM, BMPER, HPX, CMTM8, LIPG, C1RL, GPT, SERPIND1, CP, IGFBP1, LIPC, IGFBP3, IGFBP4, ORM2, CD14*

Table SIII. Continued.

Term	P-value	Description	Genes
GO:0008152	1.46E-20	Metabolic process	*FTCDNL1, AQP9, EHHADH, ECHDC2, ECHDC3, ACSS2, UGT3A1, ACSS3, ACAT1, ACSF2, AFMID, MUT, ACSL1, UGT1A3, UGT1A4, INSIG1, UGT2A1, GSTO1, FAHD2A, ACSM2B, GSTA1, ECI2, ACAA2, GSTA2, CES1, ACO1, SUCLG2, ACY3, BCKDHB, NAT2, ACSM2A, HOGA1, EPHX2, ISOC1, GRHPR, UGT1A1, MAN1C1, AADAC, DBT, UGT2B4, UGT2B15, SCP2, UGP2, UGT2B7, ACSM5, ACAA1*

The top 10 GO terms are listed. GO, Gene Ontology.

Table SIV. KEGG enrichment analysis of the upregulated genes.

Term	P-value	Description	Genes
hsa04512	7.86E-06	ECM-receptor interaction	*COL4A2*, *LAMB3*, *COL4A1*, *LAMA5*, *ITGB8*, *ITGB4*, *ITGA2*, *LAMC2*, *SPP1*
hsa04510	1.52E-04	Focal adhesion	*COL4A2*, *LAMB3*, *COL4A1*, *LAMA5*, *ITGB8*, *PDGFA*, *ITGB4*, *ITGA2*, *LAMC2*, *FLNA*, *SPP1*
hsa05222	4.93E-04	Small cell lung cancer	*E2F1*, *COL4A2*, *LAMB3*, *COL4A1*, *LAMA5*, *ITGA2*, *LAMC2*
hsa05200	6.86E-04	Pathways in cancer	*E2F1*, *COL4A2*, *CTBP2*, *COL4A1*, *PDGFA*, *ARNT2*, *ITGA2*, *LPAR2*, *BIRC5*, *TGFB2*, *LAMB3*, *WNT7B*, *LAMA5*, *LAMC2*
hsa05410	0.002275	Hypertrophic cardiomyopathy (HCM)	*ITGB8*, *ITGB4*, *ITGA2*, *CACNB3*, *TPM4*, *TGFB2*
hsa04151	0.002451	PI3K-Akt signaling pathway	*COL4A2*, *LAMB3*, *COL4A1*, *LAMA5*, *ITGB8*, *PDGFA*, *ITGB4*, *ITGA2*, *LPAR2*, *LAMC2*, *PPP2R2C*, *SPP1*
hsa05414	0.003147	Dilated cardiomyopathy	*ITGB8*, *ITGB4*, *ITGA2*, *CACNB3*, *TPM4*, *TGFB2*
hsa05412	0.008138	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	*DSG2*, *ITGB8*, *ITGB4*, *ITGA2*, *CACNB3*
hsa05146	0.008433	Amoebiasis	*COL4A2*, *LAMB3*, *COL4A1*, *LAMA5*, *LAMC2*, *TGFB2*
hsa04540	0.020529	Gap junction	*CDK1*, *PDGFA*, *ITPR3*, *TUBA1A*, *TUBB3*
hsa04390	0.033716	Hippo signaling pathway	*WNT7B*, *DLG3*, *TEAD2*, *BIRC5*, *PPP2R2C*, *TGFB2*
hsa05145	0.041832	Toxoplasmosis	*LAMB3*, *LAMA5*, *MAPK13*, *LAMC2*, *TGFB2*
hsa04115	0.045352	p53 signaling pathway	*CDK1*, *CCNB2*, *RRM2*, *SFN*

KEGG, Kyoto Encyclopedia of Genes and Genomes.

Table SV. KEGG enrichment analysis of the downregulated genes.

Term	P-value	Description	Genes
hsa01100	1.58E-62	Metabolic pathways	*CYP3A4, ALAD, SC5D, BTD, EHHADH, HIBADH, GLDC, FAH, GOT2, GOT1, MAT1A, GPT2, ACSM2B, AADAT, ACAA2, CYP1A1, GATM, SUCLG2, FAXDC2, ACSM2A, CYP26A1, CYP1A2, CYP2E1, BHMT, PGM1, HSD11B1, ABAT, ACAA1, ENPP7, ACADSB, NAGS, ENPP1, CYP2B6, ALDOC, ENPP3, ALDOB, HMGCS1, ASL, ACAT2, ACAT1, ARG1, PEMT, CDA, IDH1, ALDH4A1, MOCS1, GCDH, UAP1, ST6GAL1, CYP2C9, CYP2C8, UPB1, HGD, ACACB, CYP17A1, GBE1, HMGCS2, MLYCD, COX6A2, PRODH2, AGXT2, QPRT, GK, IDI1, CYP8B1, NNMT, TM7SF2, CYP2J2, CYP2C19, CYP2C18, MTHFD1, TKFC, GSTZ1, NT5E, SARDH, HYAL1, ACO1, GRHPR, HAO1, G6PC, CYP27A1, SDS, ADK, HAO2, UROC1, SLC27A5, SORD, AASS, DPYS, GCH1, GALK1, CBR1, ACSL1, DHCR7, PLA2G12B, HAAO, HSD17B6, HSD17B4, PAPSS2, AGL, ACSL5, HSD17B8, MOGAT3, SHMT1, CES1, BCKDHB, NAT2, AMACR, FTCD, PCK2, PCK1, GBA3, KHK, SDHB, PYGL, AOX1, PHGDH, GAMT, DPYD, PSAT1, ACSM5, CNDP1, HMGCR, ADH1C, ADH1B, ADH1A, ACSS2, ACSS3, AGXT, CMBL, ST3GAL6, RGN, DAO, HADH, HMGCL, ALDH6A1, SPTLC3, QDPR, HAL, FBP1, CDO1, TAT, PNPLA3, CHPT1, PCCB, XDH, GCLC, ASS1, GNE, GLUD1, CERS4, PAH, KMO, AGMAT, GALM, MUT, CSAD, IVD, DHODH, NADK2, MSMO1, ACMSD, EPHX2, GALT, AK4, CPS1, MMAB, TST, BAAT, ALDH2, DCXR, PC, ETNPPL, ACOX2, ACOX1, KYNU, NDST3, AMT, OGDHL, SAT2, ACOT2, ACOT1, LSS, AFMID, CRYL1, TDO2, ALAS1, AKR1C4, HPD, DDC, ACADM, ACADS, ALDH5A1, OTC, MAN1A1, LPIN2, ACADL, UGT1A1, ALDH7A1, FOLH1, CTH, DHRS3, DHRS4, DGAT2, PANK1, PKLR, CYP2A6, UGT2B10, UGT2B15, AKR1D1, GPAM, ALDH9A1, UGP2, XYLB, DHRS4L2, ADH6, ECHS1, ADH7, PLPP3, PIPOX, GLS2, ALDH1A1, MTHFS, UGT1A3, ADH4, UGT1A4, PNPO, ENO3, UGT2A1, DMGDH, ETNK2, BDH2, BDH1, EBP, HOGA1, IDO2, DBH, MAN1C1, IDNK, ADI1, AMDHD1, DBT, LIPG, UGT2B4, GPT, CYP4F3, HIBCH, CYP4F2, RDH16, LIPC, SCP2, UGT2B7, CBS*
hsa04610	2.15E-31	Complement and coagulation cascades	*MBL2, A2M, C9, MASP1, MASP2, C3, C6, C5, C1R, C1S, F13B, FGG, FGA, FGB, KLKB1, SERPINA5, SERPINC1, CFH, SERPINA1, CFI, C2, KNG1, F11, F12, F10, C4A, C4B, CFB, F9, C4BPB, SERPING1, F7, C4BPA, PLG, C8G, PROC, C8A, C8B, SERPINF2, F2, TFPI, SERPIND1, PROS1, CPB2*
hsa01130	2.74E-26	Biosynthesis of antibiotics	*TM7SF2, SC5D, HMGCR, EHHADH, AMT, OGDHL, LSS, ACSS2, AGXT, CMBL, GLDC, GOT2, GOT1, RGN, DAO, CAT, HADH, AADAT, ACAA2, ACADM, SUCLG2, ACO1, FAXDC2, OTC, FBP1, TAT, HAO1, ALDH7A1, CTH, SDS, PGM1, HAO2, PKLR, PCCB, ALDH9A1, UGP2, ACAA1, ASS1, ALDOC, ALDOB, HMGCS1, ECHS1, AASS, ACAT2, ASL, ACAT1, ARG1, GALM, ENO3, IDH1, PAPSS2, GCDH, SHMT1, UAP1, MSMO1, BCKDHB, AK3, AK4, PCK2, IDNK, PCK1, DBT, SDHB, HMGCS2, PHGDH, ALDH2, IDI1, PSAT1, CBS*
hsa00830	1.66E-18	Retinol metabolism	*CYP3A4, CYP2B6, CYP2C18, DHRS4L2, ADH1C, ADH1B, ADH6, ADH1A, ADH7, ALDH1A1, UGT1A3, ADH4, UGT1A4, UGT2A1, HSD17B6, CYP1A1, CYP2C9, CYP2C8, CYP26A1, CYP1A2, UGT1A1, RDH5, DHRS3, DHRS4, AOX1, CYP2A6, UGT2B4, UGT2B10, RDH16, UGT2B15, UGT2B7, RETSAT*
hsa00071	5.23E-18	Fatty acid degradation	*ACOX1, ACADSB, CPT2, EHHADH, ADH1C, ECHS1, ADH6, ADH1B, ADH7, ADH1A, ACAT2, ACAT1, ACSL1, ADH4, HADH, ACSL5, GCDH, ACAA2, ECI2, ACADM, ACADS, ACADL, ALDH7A1, ALDH2, ALDH9A1, ACAA1*
hsa05204	5.95E-18	Chemical carcinogenesis	*CYP3A4, CYP2C19, CYP2C18, ADH1C, ADH1B, ADH6, ADH1A, ADH7, CYP3A43, CBR1, UGT1A3, SULT1A1, ADH4, UGT1A4, UGT2A1, GSTO1, GSTA1, GSTA2, SULT2A1, CYP1A1, CYP2C9, CYP2C8, NAT2, EPHX1, CYP2E1, CYP1A2, UGT1A1, HSD11B1, CYP2A6, UGT2B4, UGT2B10, UGT2B15, MGST1, UGT2B7, MGST2*
hsa00982	1.52E-17	Drug metabolism-cytochrome P450	*CYP3A4, CYP2C19, CYP2B6, CYP2D6, ADH1C, ADH1B, ADH6, ADH1A, ADH7, FMO4, FMO5, UGT1A3, ADH4, UGT1A4, FMO3, UGT2A1, GSTO1, GSTA1, GSTA2, CYP2C9, CYP2C8, CYP2E1, CYP1A2, UGT1A1, AOX1, CYP2A6, UGT2B4, UGT2B10, UGT2B15, MGST1, UGT2B7, MGST2*

Table SV. Continued.

Term	P-value	Description	Genes
hsa01200	1.56E-17	Carbon metabolism	*ALDOC, GLUD1, AMT, EHHADH, OGDHL, ALDOB, ECHS1, ACAT2, ACSS2, AGXT, ACAT1, GLDC, GOT2, MUT, GOT1, TKFC, RGN, IDH1, ENO3, CAT, GPT2, SHMT1, ALDH6A1, ACADM, ACO1, ACADS, SUCLG2, FBP1, CPS1, IDNK, HAO1, SDHB, SDS, PKLR, HAO2, PHGDH, GPT, HIBCH, PSAT1, PCCB, PC*
hsa00980	3.09E-17	Metabolism of xenobiotics by cytochrome P450	*CYP3A4, CYP2B6, CYP2D6, ADH1C, ADH1B, ADH6, ADH1A, ADH7, CBR1, AKR1C4, UGT1A3, ADH4, UGT1A4, UGT2A1, AKR7A3, GSTO1, GSTA1, GSTA2, SULT2A1, CYP1A1, CYP2C9, EPHX1, CYP2E1, CYP1A2, UGT1A1, HSD11B1, CYP2A6, UGT2B4, UGT2B10, UGT2B15, MGST1, UGT2B7, MGST2*
hsa00280	2.08E-16	Valine, leucine and isoleucine degradation	*ALDH6A1, ACAA2, ACADSB, ACADM, ACADS, EHHADH, BCKDHB, HMGCS1, ECHS1, ACAT2, ACAT1, HIBADH, DBT, ALDH7A1, MUT, HMGCS2, IVD, AOX1, ALDH2, ABAT, HIBCH, HADH, PCCB, HMGCL, ALDH9A1, ACAA1*

The top 10 KEGG terms are listed. KEGG, Kyoto Encyclopedia of Genes and Genomes.