

Clinical relevance of cell proliferation-related pathways in pancreatic cancer

Table S1. Member genes of the Hallmark proliferation-related pathway gene sets

G2M checkpoint: ABL1, AC027237.1, AC091021.1, AMD1, ARID4A, ATF5, ATRX, AURKA, AURKB, BARD1, BCL3, BIRC5, BRCA2, BUB1, BUB3, CASP8AP2, CBX1, CCNA2, CCNB2, CCND1, CCNF, CCNT1, CDC20, CDC25A, CDC25B, CDC27, CDC45, CDC6, CDC7, CDK1, CDK4, CDKN1B, CDKN2C, CDKN3, CENPA, CENPE, CENPF, CHAF1A, CHEK1, CHMP1A, CKS1B, CKS2, CTCF, CUL1, CUL3, CUL4A, CUL5, DBF4, DDX39A, DKC1, DMD, DR1, DTYMK, E2F1, E2F2, E2F3, E2F4, EFNA5, EGFR, ESLP1, EWSR1, EXO1, EZH2, FANCC, FBXO5, FOXN3, G3BP1, GINS2, GSPT1, H2AFV, H2AFX, H2AFZ, HIF1A, HIRA, HIST1H2BK, HMGA1, HMGB3, HMGN2, HMMR, HNRNP, HNRNPU, HOXC10, HSPA8, HUS1, ILF3, INCENP, JPT1, KATNA1, KIF11, KIF15, KIF20B, KIF22, KIF2C, KIF4A, KIF5B, KMT5A, KNL1, KPNA2, KPNA2, LBR, LIG3, LMNB1, MAD2L1, MAP3K20, MAPK14, MARCKS, MCM2, MCM3, MCM5, MCM6, MEIS1, MEIS2, MKI67, MNAT1, MT2A, MT2B, MYBL2, MYC, NASP, NCL, NDC80, NEK2, NOLC1, NOTCH2, NSD2, NUMA1, NUP50, NUP98, NUSAP1, ODC1, ODF2, ORC5, ORC6, PAFAH1B1, PBK, PDS5B, PLK1, PLK4, PML, POLA2, POLE, POLQ, PRC1, PRIM2, PRMT5, PRPF4B, PTTG1, PTTG3P, PURA, RACGAP1, RAD21, RAD23B, RAD54L, RASAL2, RBL1, RBM14, RPA2, RPS6KA5, SAP30, SFPQ, SLC12A2, SLC38A1, SLC7A1, SLC7A5, SMAD3, SMARCC1, SMC1A, SMC2, SMC4, SNRPD1, SQLE, SRSF10, SRSF2, STAG1, STIL, STMN1, SUV39H1, SYNCRI, TACC3, TENT4A, TFPD1, TGFB1, TLE3, TMPO, TNPO2, TOP1, TOP2A, TPX2, TRA2B, TRAIP, TTK, UBE2C, UBE2S, UCK2, UPF1, WRN, XPO1, YTHDC1
E2F Targets: AK2, ANP32E, ASF1A, ASF1B, ATAD2, AURKA, AURKB, BARD1, BIRC5, BRCA1, BRCA2, BRMS1L, BUB1B, CBX5, CCNB2, CCNE1, CCP110, CDC20, CDC25A, CDC25B, CDC3A, CDCA8, CDK1, CDK4, CDKN1A, CDKN1B, CDKN2A, CDKN2C, CDKN3, CENPE, CENPM, CHEK1, CHEK2, CIT, CKS1B, CKS2, CNOT9, CSE1L, CTCF, CTPS1, DCK, DCLRE1B, DCTPP1, DDX39A, DEK, DEPDIC1, DIAPH3, DLGAP5, DNMT1, DONSON, DSCC1, DUT, E2F8, EED, EIF2S1, ESLP1, EXOSC8, EZH2, GINS1, GINS3, GINS4, GSPT1, H2AFX, H2AFZ, HELLS, HMGA1, HMGB2, HMGB3, HMMR, HNRNP, HUS1, ILF3, ING3, IP07, JPT1, KIF18B, KIF22, KIF2C, KIF4A, KPNA2, LBR, LIG1, LMNB1, LUC7L3, LYAR, MAD2L1, MCM2, MCM3, MCM5, MCM6, MELK, MKI67, MLH1, MMS22L, MRE11, MSH2, MTHFD2, MXD3, MYBL2, MYC, NAA38, NAP1L1, NASP, NBN, NCAPD2, NME1, NOLC1, NOP56, NUDT21, NUP107, NUP153, NUP205, ORC2, ORC6, PA2G4, PAICS, PAN2, PCNA, PDS5B, PHF5A, PLK1, PLK4, PMS2, PNN, POLA2, POLD1, POLD2, POLD3, POLE, POLE4, POP7, PPP1D, PRDX4, PRIM2, PRKD2, PSIP1, PSMC3IP, PTTG1, RACGAP1, RAD1, RAD21, RAD50, RAD51AP1, RAD51C, RAN, RANBP1, RBBP7, RFC1, RFC2, RFC3, RNASEH2A, RPA1, RPA2, RPA3, RRM2, SHMT1, SLBP, SMC1A, SMC3, SMC4, SMC6, SNRPB, SPAG5, SPC24, SPC25, SRSF1, SRSF2, SRRP1, STAG1, STMN1, SUV39H1, SYNCRI, TACC3, TBRG4, TCF19, TFRC, TIMELESS, TIPIN, TK1, TMPO, TOP2A, TP53, TRA2B, TRIP13, TUBB, TUBG1, UBE2S, UBE2T, UBR7, UNG, USP1, WDR90, WEE1, XPO1, XRCC6, ZW10
MYC Targets V1: ABCE1, AC004086.1, ACP1, AIM2P, AP3S1, APEX1, BUB3, C1QBP, CAD, CANX, CBX3, CCNA2, CCT2, CCT3, CCT4, CCT5, CCT7, CDC20, CDC45, CDK2, CDK4, CLNS1A, CNBP, COP5, COX5A, CSTF2, CTPS1, CUL1, CYC1, DDX18, DDX21, DEK, DHX15, DUT, EEF1B2, EIF1AX, EIF2S1, EIF2S2, EIF3B, EIF3D, EIF3J, EIF4A1, EIF4E, EIF4G2, EIF4H, EPRS, ERH, ETF1, EXOSC7, FAM120A, FBL, G3BP1, GLO1, GNL3, GOT2, GSPT1, H2AFX, HDAC2, HDDC2, HDGF, HNRNPA1, HNRNPA2B1, HNRNPA3, HNRNPC, HNRNPD, HNRNPR, HNRNPU, HPRT1, HSP90AB1, HSPD1, HSPE1, IARS, IFRD1, ILF2, IMPDH2, KARS, KPNA2, KPNB1, LDHA, LSM2, LSM7, MAD2L1, MCM2, MCM4, MCM5, MCM6, MCM7, MRPL23, MRPL9, MRPS18B, MYC, NAP1L1, NCBP1, NCBP2, NDUFAF1, NH2P, NME1, NOLC1, NOP16, NOP56, NPM1, ODC1, ORC2, PA2G4, PABPC1, PABPC4, PCBP1, PCNA, PGK1, PHB, PHB2, POLD2, POLE3, PPIA, PPM1G, PRDX3, PRDX4, PRPF31, PRPS2, PSMA1, PSMA2, PSMA4, PSMA6, PSMA7, PSMB2, PSMB3, PSMC4, PSMC6, PSMD1, PSMD3, PSMD7, PSMD8, PTGES3, PWL1, RACK1, RAD23B, RAN, RANBP1, RFC4, RNPS1, RPL14, RPL18, RPL22, RPL34, RPLP0, RPS10, RPS2, RPS3, RPS5, RPS6, RRM1, RRP9, RSL1D1, RUVBL2, SERBP1, SET, SF3A1, SF3B3, SLC25A3, SMARCC1, SNRPA1, SNRPA1, SNRPA2, SNRPD1, SNRPD2, SNRPD3, SNRPG, SRM, SRPK1, SRSF1, SRSF2, SRSF3, SRSF7, SSB, SSBP1, STARD7, SYNCRI, TARDBP, TCP1, TFPD1, TOMM70, TRA2B, TRIM28, TUFM, TXNL4A, TYMS, U2AF1, UBA2, UBE2E1, UBE2L3, USP1, VBP1, VDAC1, XPO1, XPOT, XRCC6, YWHAE, YWHAQ
MYC Targets V2: AIMP2, BYSL, CBX3, CDK4, DCTPP1, DDX18, DUSP2, EXOSC5, FARSA, GNL3, GRWD1, HK2, HSPD1, HSPE1, IMP4, IPO4, LAS1L, MAP3K6, MCM4, MCM5, MPHOSPH10, MRT04, MYBBP1A, MYC, NDUFAF4, NIP7, NOC4L, NOLC1, NOP16, NOP2, NOP56, NPM1, PA2G4, PES1, PHB, PLK1, PLK4, PPAN, PPRC1, PRMT3, PUS1, RABEPK, RCL1, RRP12, RRP9, SLC19A1, SLC29A2, SORD, SRM, SUPV3L1, TBRG4, TCOF1, TFB2M, TMEM97, UNG, UTP20, WDR43, WDR74
Mitotic spindle: ABI1, ABL1, ABR, AC027237.1, ACTN4, AKAP13, ALMS1, ALS2, ANLN, APC, ARAP3, ARF6, ARFGEF1, ARFIP2, ARHGAP10, ARHGAP27, ARHGAP29, ARHGAP4, ARHGAP5, ARHGDIA, ARHGEF11, ARHGEF2, ARHGEF3, ARHGEF7, ARL8A, ATG4B, AURKA, BCAR1, BCL2L11, BCR, BIN1, BIRC5, BRCA2, BUB1, CAPZB, CCDC88A, CCNB2, CD2AP, CDC27, CDC42, CDC42BPA, CDC42EP1, CDC42EP2, CDC42EP4, CDK1, CDK5RAP2, CENPE, CENPF, CEP131, CEP192, CEP250, CEP57, CEP72, CKAP5, CLASP1, CLIP1, CLIP2, CNTRL, CNTROB, CSNK1D, CTTN, CYTH2, DLG1, DLGAP5, DOCK2, DOCK4, DST, DYNC1H1, DYNLL2, ECT2, EPB41, EPB41L2, ESLP1, EZR, FARP1, FBXO5, FGD4, FGD6, FLNA, FLNB, FSCN1, GEMIN4, GSN, HDAC6, HOOK3, INCENP, ITSN1, KATNA1, KATNB1, KIF11, KIF15, KIF1B, KIF20B, KIF22, KIF2C, KIF3B, KIF3C, KIF4A, KIF5B, KIFAP3, KLC1, KNTC1, KPTN, LAT51, LLGL1, LMNB1, LRPPRC, MAP1S, MAP3K11, MAPRE1, MARCKS, MARK4, MID1, MID1P1, MYH10, MYH9, MYO1E, MYO9B, NCK1, NCK2, NDC80, NEDD9, NEK2, NET1, NF1, NIN, NOTCH2, NUMA1, NUSAP1, OPNH1, PAFAH1B1, PALLD, PCGF5, PCM1, PCNT, PDLM5, PIF1, PKD2, PLEKHG2, PLK1, PPP4R2, PRC1, PREX1, PXN, RAB3GAP1, RABGAP1, RACGAP1, RALBP1, RANBP9, RAPGEF5, RAPGEF6, RASA1, RASA2, RASAL2, RFC1, RHOF, RHOT2, RICTOR, ROCK1, SAC3D1, SASS6, SEPT9, SHROOM1, SHROOM2, SMC1A, SMC3, SMC4, SORBS2, SOS1, SPTAN1, SPTBN1, SSH2, STAU1, STK38L, SUN2, SYNPO, TAOK2, TBCD, TIAM1, TLK1, TOP2A, TPX2, TRIO, TSC1, TTK, TUBA4A, TUBD1, TUBGCP2, TUBGCP3, TUBGCP5, TUBGCP6, UXT, VCL, WASF1, WASF2, WASL, YWHAE
p53 pathway: ABAT, ABCC5, ABHD4, ACVR1B, ADA, AEN, AK1, ALOX15B, ANKRA2, APAF1, APP, ATF3, BAIAP2, BAK1, BAX, BLCAP, BMP2, BTG1, BTG2, CASP1, CCND2, CCND3, CCNG1, CCNK, CCP110, CD81, CD82, CDH13, CDK5R1, CDKN1A, CDKN2A, CDKN2AIP, CDKN2B, CEBPA, CGRRF1, CLCA2, COQ8A, CSRNP2, CTSD, CYFIP2, DCXR, DDB2, DDT3, DDT4, DEF6, DGKA, DNNTIP2, DRAM1, EI24, ELP1, EPHA2, EPHX1, EPS8L2, ERCC5, F2R, FAM162A, FAS, FBXW7, FDXR, FGF13, FOS, FOXO3, FUCA1, GADD45A, GLS2, GM2A, GPX2, H2AFJ, HBEGF, HDAC3, HEXIM1, HINT1, HIST1H1C, HIST3H2A, HMOX1, HRAS, HSPA4L, IER3, IER5, IFI30, IL1A, INHBB, IP6K2, IRAK1, ISCU, ITGB4, JAG2, JUN, KIF13B, KLF4, KLF8, KRT17, LDHB, LIF, LRMP, MAPKAPK3, MDM2, MKN2, MXD1, MXD4, NDRG1, NHLH2, NINJ1, NOL8, NOTCH1, NUDT15, NUPR1, OSGN1, PCNA, PDGFA, PERP, PHLDA3, PIDD1, PITPN1, PLK2, PLK3, PLXNB2, PMM1, POLH, POM121, PPP1D, PPP1R15A, PRKAB1, PRMT2, PROCR, PTPN14, PTPRE, PVT1, RAB40C, RACK1, RAD51C, RAD9A, RALGDS, RAP2B, RB1, RCHY1, RETSAT, RGS16, RHBDF2, RNF19B, RPL18, RPL36, RPS12, RPS27L, RRAD, RRP8, RXRA, S100A10, S100A4, SAT1, SDC1, SEC61A1, SERPINB5, SERTAD3, SESN1, SFN, SLC19A2, SLC35D1, SLC3A2, SLC7A11, SOCS1, SP1, SPHK1, ST14, STEAP3, STOM, TAP1, TAX1BP3, TCHH, TCN2, TGFA, TGFB1, TM4SF1, TM7SF3, TNFSF9, TNNI1, TOB1, TP53, TP63, TPD52L1, TPRKB, TRAF4, TRAFD1, TRIAP1, TRIB3, TSC22D1, TSPYL2, TXNIP, UPP1, VAMP8, VDR, VWA5A, WRAP73, WWP1, XPC, ZBTB16, ZFP36L1, ZMAT3, ZNF365

Clinical relevance of cell proliferation-related pathways in pancreatic cancer

Table S2. Association of other hallmark gene sets scores and patient survival in pancreatic cancer in the TCGA cohort. Cox proportional hazard analyses were used to estimate hazard ratio (HR), 95% CI, and p-value. The median value was used as a cut-off to divide low and high groups within cohorts

Category	Pathway	TCGA (OS)				TCGA (DFS)				TCGA (DSS)			
		HR	95% CI	P	HR	95% CI	p	HR	95% CI	P			
Cellular Component	APJ	1.28	0.85	1.94	0.24	1.86	0.79	4.35	0.15	1.68	1.04	2.71	0.03 *
	APS	1.70	1.11	2.61	0.01 *	2.04	0.85	4.88	0.11	2.04	1.26	3.31	0.00 *
	PER	1.12	0.74	1.69	0.61	0.94	0.41	2.18	0.89	1.21	0.76	1.93	0.43
Development	ADI	1.37	0.90	2.08	0.14	1.18	0.51	2.73	0.70	1.48	0.92	2.38	0.10
	ANG	1.44	0.95	2.18	0.09	2.67	1.11	6.46	0.03 *	1.76	1.10	2.83	0.02 *
	EMT	1.51	0.99	2.29	0.06	4.34	1.65	11.39	0.00 *	1.73	1.08	2.78	0.02 *
	MYO	0.88	0.58	1.34	0.56	1.07	0.47	2.46	0.87	1.13	0.71	1.79	0.62
	PAN	0.83	0.55	1.26	0.38	0.40	0.17	0.95	0.04 *	0.98	0.62	1.56	0.94
	SPE	0.93	0.62	1.41	0.74	0.67	0.29	1.52	0.34	1.01	0.64	1.62	0.95
	DNA	1.37	0.90	2.08	0.14	0.60	0.26	1.38	0.23	1.37	0.86	2.19	0.19
DNA damage	UVU	1.43	0.94	2.16	0.09	2.46	1.03	5.91	0.04	1.49	0.94	2.39	0.09
	UVU	1.53	1.00	2.32	0.05 *	1.13	0.49	2.62	0.77	1.69	1.05	2.73	0.03 *
	ALL	1.21	0.80	1.83	0.37	1.16	0.49	2.76	0.73	1.27	0.80	2.02	0.31
Immune	COA	1.47	0.97	2.24	0.07	1.27	0.55	2.90	0.58	1.87	1.15	3.02	0.01 *
	COM	1.82	1.20	2.77	0.01 *	1.40	0.59	3.34	0.45	1.97	1.22	3.17	0.01 *
	IFA	1.68	1.11	2.55	0.01 *	1.34	0.58	3.09	0.49	1.60	1.00	2.56	0.05 *
	IFG	1.31	0.86	1.98	0.21	0.95	0.41	2.22	0.91	1.26	0.79	2.01	0.32
	IL6	1.40	0.92	2.12	0.12	1.35	0.56	3.23	0.51	1.57	0.98	2.52	0.06
	INF	1.44	0.95	2.19	0.09	1.12	0.47	2.67	0.79	1.74	1.08	2.80	0.02 *
	BIL	0.86	0.57	1.30	0.46	0.82	0.36	1.91	0.65	0.87	0.54	1.38	0.55
Metabolic	CHO	1.68	1.10	2.56	0.02 *	1.17	0.52	2.66	0.71	1.62	1.01	2.60	0.04 *
	FAT	1.39	0.92	2.12	0.12	0.89	0.39	2.03	0.78	1.37	0.86	2.19	0.19
	GLY	1.76	1.15	2.69	0.01 *	1.90	0.82	4.40	0.13	2.08	1.27	3.39	0.00 *
	HEM	1.29	0.85	1.95	0.23	0.72	0.32	1.64	0.43	1.40	0.88	2.25	0.16
	OXI	0.95	0.63	1.44	0.81	0.73	0.31	1.72	0.47	0.87	0.54	1.38	0.54
	XEN	1.67	1.10	2.54	0.02 *	1.35	0.59	3.08	0.48	1.72	1.07	2.75	0.02 *
	APO	1.88	1.22	2.88	0.00 *	2.18	0.92	5.19	0.08	2.17	1.33	3.53	0.00 *
Pathway	HYP	1.93	1.26	2.97	0.00 *	2.23	0.97	5.10	0.06	2.22	1.36	3.63	0.00 *
	PRO	1.49	0.98	2.27	0.06	1.15	0.50	2.66	0.75	1.56	0.97	2.51	0.07
	REA	1.10	0.73	1.66	0.66	0.78	0.34	1.77	0.55	1.05	0.66	1.67	0.83
	UNF	1.14	0.75	1.74	0.53	0.74	0.32	1.70	0.48	1.17	0.73	1.88	0.52
	AND	1.86	1.22	2.84	0.00 *	2.43	1.02	5.83	0.05 *	1.97	1.22	3.18	0.01 *
Signaling	ERE	1.95	1.28	2.99	0.00 *	2.15	0.93	4.94	0.07	2.18	1.34	3.55	0.00 *
	ERL	2.22	1.45	3.41	0.00 *	1.09	0.48	2.49	0.84	2.43	1.49	3.96	0.00 *
	HED	0.79	0.52	1.20	0.27	1.25	0.54	2.91	0.60	1.00	0.63	1.60	0.99
	IL2	1.35	0.89	2.04	0.16	1.49	0.62	3.55	0.37	1.44	0.90	2.30	0.12
	KRD	0.98	0.65	1.49	0.94	1.51	0.65	3.50	0.34	1.07	0.67	1.70	0.78
	KRU	1.47	0.97	2.23	0.07	1.85	0.76	4.49	0.17	1.70	1.06	2.73	0.03 *
	MTO	1.56	1.02	2.38	0.04 *	1.79	0.76	4.23	0.18	1.70	1.05	2.76	0.03 *
	NOT	1.51	1.00	2.29	0.05	2.25	0.97	5.23	0.06	1.79	1.11	2.89	0.02 *
	PI3	1.56	1.02	2.37	0.04 *	1.16	0.51	2.64	0.73	1.68	1.04	2.70	0.03 *
	TGF	1.67	1.10	2.54	0.02 *	3.21	1.32	7.85	0.01 *	2.15	1.31	3.51	0.00 *
	TNF	1.56	1.03	2.37	0.04 *	2.01	0.86	4.69	0.11	1.85	1.15	2.97	0.01 *
	WNT	1.29	0.85	1.95	0.23	1.87	0.80	4.34	0.15	1.43	0.90	2.29	0.13

ADI, Adipogenesis; ALL, Allograft rejection; AND, Androgen response; ANG, Angiogenesis; APO, Apoptosis; APS, Apical surface; APJ, Apical junction; BIL, Bile acid metabolism; CHO, Cholesterol homeostasis; COA, Coagulation; COM, Complement; DNA, DNA repair; EMT, Epithelial mesenchymal transition; ERE, Estrogen response early; ERL, Estrogen response late; FAT, Fatty acid metabolism; GLY, Glycolysis; HED, Hedgehog signaling; HEM, Heme metabolism; HYP, Hypoxia; IFA, Interferon alpha response; IFG, Interferon gamma response; IL2, IL2/JAK/STAT5 signaling; IL6, IL6/JAK/STAT3 signaling; INF, Inflammatory response; KRD, KRAS signaling down; KRU, KRAS signaling up; MTO, MtorC1 signaling; MYO, Myogenesis; NOT, Notch signaling; OXI, Oxidative phosphorylation; PAN, Pancreas beta cell; PER, Peroxisome; PI3, PI3K/AKT/MTOR signaling; PRO, Protein secretion; REA, Reactive oxygen species pathway; SPE, Spermatogenesis; TGF, TGF beta signaling; TNF, TNFa signaling via NFkB; UNF, Unfolded protein response; UVD, UV response down; UVU, UV response up; XEN, Xenobiotic metabolism; WNT, WNT beta catenin signaling.

Clinical relevance of cell proliferation-related pathways in pancreatic cancer

Table S3. Association of other hallmark gene sets scores and patient survival in pancreatic cancer in the GSE57495 and GSE62452 cohorts. Cox proportional hazard analyses were used to estimate hazard ratio (HR), 95% CI, and *p*-value. The median value was used as a cut-off to divide low and high groups within cohorts

Category	Pathway	GSE57495 (OS)				GSE62452 (OS)				
		HR	95% CI	P	*	HR	95% CI	P		
Cellular Component	APJ	2.44	1.29	4.61	0.01	*	1.14	0.65	2.00	0.64
	APS	1.39	0.75	2.58	0.29		1.61	0.91	2.84	0.10
	PER	1.12	0.61	2.05	0.72		0.98	0.55	1.74	0.94
Development	ADI	0.99	0.54	1.82	0.98		1.03	0.58	1.81	0.92
	ANG	0.90	0.49	1.65	0.74		0.86	0.49	1.51	0.60
	EMT	1.25	0.68	2.29	0.48		1.04	0.59	1.83	0.89
	MYO	0.59	0.32	1.10	0.10		0.96	0.54	1.70	0.88
	PAN	0.76	0.41	1.39	0.37		0.61	0.35	1.08	0.09
	SPE	1.14	0.62	2.10	0.66		1.06	0.60	1.86	0.85
DNA damage	DNA	0.72	0.39	1.32	0.29		1.49	0.84	2.64	0.17
	UVD	1.44	0.78	2.66	0.24		1.07	0.61	1.90	0.81
	UVU	0.96	0.52	1.76	0.89		1.05	0.60	1.84	0.87
Immune	ALL	0.94	0.52	1.73	0.85		1.16	0.65	2.04	0.62
	COA	1.06	0.58	1.94	0.85		0.77	0.44	1.37	0.37
	COM	0.98	0.53	1.79	0.94		1.07	0.61	1.88	0.82
	IFA	1.39	0.75	2.56	0.30		1.94	1.05	3.58	0.03
	IFG	0.82	0.45	1.51	0.53		1.23	0.69	2.18	0.48
	IL6	0.87	0.47	1.59	0.64		1.21	0.68	2.14	0.52
Metabolic	INF	0.98	0.54	1.80	0.95		1.15	0.65	2.04	0.62
	BIL	0.77	0.42	1.42	0.40		0.45	0.25	0.80	0.01
	CHO	1.53	0.83	2.84	0.18		0.99	0.56	1.73	0.96
	FAT	1.39	0.76	2.55	0.29		0.83	0.47	1.46	0.53
	GLY	1.72	0.93	3.20	0.08		1.88	1.05	3.34	0.03
	HEM	1.09	0.59	1.99	0.79		1.41	0.80	2.48	0.24
Pathway	OXI	1.01	0.55	1.86	0.96		0.98	0.54	1.75	0.94
	XEN	0.94	0.51	1.73	0.85		0.85	0.48	1.49	0.57
	APO	2.41	1.29	4.50	0.01	*	1.03	0.59	1.82	0.92
	HYP	1.43	0.77	2.62	0.26		1.42	0.81	2.49	0.22
	PRO	1.87	1.00	3.48	0.05		1.28	0.72	2.25	0.40
	REA	1.25	0.68	2.29	0.47		1.01	0.58	1.79	0.96
Signaling	UNF	0.97	0.53	1.78	0.92		1.91	1.07	3.42	0.03
	AND	1.54	0.83	2.85	0.17		1.28	0.72	2.28	0.40
	ERE	1.01	0.55	1.85	0.98		1.05	0.59	1.84	0.88
	ERL	1.13	0.62	2.08	0.69		0.95	0.54	1.68	0.87
	HED	1.20	0.65	2.21	0.56		0.63	0.36	1.10	0.11
	IL2	0.85	0.47	1.57	0.61		1.00	0.57	1.77	0.99
	KRD	0.67	0.36	1.23	0.19		0.74	0.42	1.29	0.28
	KRU	0.88	0.48	1.62	0.69		0.98	0.56	1.73	0.95
	MTO	2.01	1.08	3.76	0.03	*	1.94	1.08	3.51	0.03
	NOT	1.05	0.57	1.92	0.89		0.90	0.51	1.59	0.72
	PI3	1.63	0.88	3.00	0.12		1.55	0.88	2.75	0.13
	TGF	1.26	0.69	2.31	0.45		0.86	0.49	1.51	0.60
	TNF	0.89	0.48	1.63	0.70		0.84	0.48	1.47	0.54
	WNT	0.93	0.50	1.70	0.80		1.05	0.60	1.85	0.86

ADI, Adipogenesis; ALL, Allograft rejection; AND, Androgen response; ANG, Angiogenesis; APO, Apoptosis; APS, Apical surface; APJ, Apical junction; BIL, Bile acid metabolism; CHO, Cholesterol homeostasis; COA, Coagulation; COM, Complement; DNA, DNA repair; EMT, Epithelial mesenchymal transition; ERE, Estrogen response early; ERL, Estrogen response late; FAT, Fatty acid metabolism; GLY, Glycolysis; HED, Hedgehog signaling; HEM, Heme metabolism; HYP, Hypoxia; IFA, Interferon alpha response; IFG, Interferon gamma response; IL2, IL2/JAK/STAT5 signaling; IL6, IL6/JAK/STAT3 signaling; INF, Inflammatory response; KRD, KRAS signaling down; KRU, KRAS signaling UP; MTO, Mtorc1 signaling; MYO, Myogenesis; NOT, Notch signaling; OXI, Oxidative phosphorylation; PAN, Pancreas beta cell; PER, Peroxisome; PI3, PI3K/AKT/MTOR signaling; PRO, Protein secretion; REA, Reactive oxygen species pathway; SPE, Spermatogenesis; TGF, TGF beta signaling; TNF, TNFα signaling via NFκB; UNF, Unfolded protein response; UVD, UV response down; UVU, UV response up; XEN, Xenobiotic metabolism; WNT, WNT beta catenin signaling.