

Supplementary Table 2. A list of modulated biological processes generated by GATHER software following analysis of differential gene expression results from PC3 and DU145 treated with SN30028 for 4, 24 and 96 hours.

<b>Cell lines Times</b>	<b>Biological process</b>	<b>Bayes factor</b>	<b>Differentially expressed genes</b>
PC3 4-hour	Transforming growth factor beta receptor signalling pathway	3.53	BMPR1B, GDF15, HIPK2.
	Eye morphogenesis	3.11	BMPR1B, CYP1B1.
PC3 24-hour	Cyclooxygenase pathway	4.72	PTGS2.
	Arachidonic acid metabolism	3.62	PTGS2.
	Phagocytosis, engulfment	3.34	GULP1.
	Eye morphogenesis	3.11	CYP1B1.
	Embryonic eye morphogenesis	3.11	CYP1B1.
	Eye morphogenesis	3.11	CYP1B1.
PC3 96-hour	Response to nutrients	5.69	OGT, STC1, STC2.
	Response to extracellular stimulus	4.73	OGT, STC1, STC2.
	Epidermis development	3.80	ELF3, KLK5, KRT15, SCLE.
	Nucleobase-containing compound metabolic process	3.80	DDIT3, ELF3, KLF11, MCM6, TNFAIP3.
	Ectoderm development	3.30	ELF3, KLK5, KRT15, SCLE.
DU145 4-hour	Sterol biosynthesis	29.66	DHCR7, HMGCR, HMGCS1, MVK, NSDHL, SC4MOL, SC5DL, SQLE.
	Sterol metabolism	26.51	DHCR7, HMGCR, HMGCS1, LDLR, MVK, NSDHL, SC4MOL, SC5DL, SQLE.
	Steroid biosynthesis	22.06	DHCR7, HMGCR, HMGCS1, MVK, NSDHL, SC4MOL, SC5DL, SQLE.
	Steroid metabolism	19.58	DHCR7, HMGCR, HMGCS1, LDLR, MVK, NSDHL, SC4MOL, SC5DL, SQLE.
	Alcohol metabolism	17.91	DHCR7, HMGCR, HMGCS1, LDLR, MVK, NSDHL, PCK2, SC4MOL, SC5DL, SQLE.
	Cholesterol biosynthesis	15.70	DHCR7, HMGCR, HMGCS1, MVK, NSDHL.
	Lipid biosynthesis	15.64	DHCR7, HMGCR, HMGCS1, MVK, NSDHL, SC4MOL, SC5DL, SCD, SQLE.
	Cholesterol metabolism	14.65	DHCR7, HMGCR, HMGCS1, LDLR, MVK, NSDHL.
	Cellular lipid metabolism	11.59	DHCR7, HMGCR, HMGCS1, LDLR, MVK, NSDHL, SC4MOL, SC5DL, SCD, SQLE.

	Lipid metabolism	9.30	DHCR7, HMGCR, HMGCS1, LDLR, MVK, NSDHL, SC4MOL, SC5DL, SCD, SQLE.
DU145 24-hour	Sterol biosynthesis	51.26	CYP51A1, DHCR7, EBP, FDFT1, FDPS, HMGCR, HMGCS1, IDI1, MVK, NSDHL, SC4MOL, SC5DL, SQLE, TM7SF2.
	Steroid metabolism	49.75	AKR1C2, APOL1, APOL2, CYP51A1, DHCR7, EBP, FDFT1, FDPS, HMGCR, HMGCS1, HSD17B7, IDI1, LDLR, LSS, MVK, NSDHL, SC4MOL, SC5DL, SQLE, STARD4, TM7SF2.
	Sterol metabolism	49.31	APOL1, APOL2, CYP51A1, DHCR7, EBP, FDFT1, FDPS, HMGCR, HMGCS1, IDI1, LDLR, MVK, NSDHL, SC4MOL, SC5DL, SQLE, TM7SF2.
	Steroid biosynthesis	48.99	CYP51A1, DHCR7, EBP, FDFT1, FDPS, HMGCR, HMGCS1, HSD17B7, IDI1, LSS, MVK, NSDHL, SC4MOL, SC5DL, SQLE, STARD4, TM7SF2.
	Lipid biosynthesis	40.15	CYP51A1, DHCR7, EBP, FADS1, FADS2, FDFT1, FDPS, GNE, HMGCR, HMGCS1, HSD17B7, IDI1, LSS, MVK, NSDHL, SC4MOL, SC5DL, SCD, SQLE, STARD4, TM7SF2.
	Cholesterol biosynthesis	38.29	CYP51A1, DHCR7, EBP, FDFT1, FDPS, HMGCR, HMGCS1, IDI1, MVK, NSDHL, TM7SF2.
	Cholesterol metabolism	38.12	APOL1, APOL2, CYP51A1, DHCR7, EBP, FDFT1, FDPS, HMGCR, HMGCS1, IDI1, LDLR, MVK, NSDHL, TM7SF2.
	Cellular lipid metabolism	37.28	AKR1C2, AKR1C3, APOL1, APOL2, CYP51A1, DHCR7, EBP, FADS1, FADS2, FDFT1, FDPS, GNE, HMGCR, HMGCS1, HSD17B7, IDI1, LDLR, LSS, MVK, NSDHL, SC4MOL, SC5DL, SCD, SQLE, STARD4, TM7SF2.
	Alcohol metabolism	35.20	APOL1, APOL2, CYP51A1, DHCR7, EBP, FDFT1, FDPS, HK2, HMGCR, HMGCS1, IDI1, LDLR, MVK, NSDHL, PFKFB2, PFKFB3, SC4MOL, SC5DL, SQLE, TM7SF2.
	Lipid metabolism	33.48	AKR1C2, AKR1C3, APOL1, APOL2, CYP51A1, DHCR7, EBP, FADS1, FADS2, FDFT1, FDPS, GNE, HMGCR, HMGCS1, HSD17B7, IDI1, LDLR, LIPG, LSS, MVK, NSDHL, SC4MOL, SC5DL, SCD, SQLE, STARD4, TM7SF2.

	Isoprenoid biosynthesis	10.51	FDFT1, FDPS, IDI1, MVK.
	Isoprenoid metabolism	9.31	FDFT1, FDPS, IDI1, MVK.
	Fructose 2,6-bisphosphate metabolism	3.91	PFKFB2, PFKFB3.
	Coenzyme A biosynthesis	3.40	PANK1, PANK3.
	Fatty acid desaturation	3.40	FADS1, FADS2.
	Lipid transport	3.13	APOL1, APOL2, LDLR, STARD4.
	Coenzyme A metabolism	3.01	PANK1, PANK3.
DU145 96-hour	Cell proliferation	25.21	AKR1C3, APBB2, ATF5, AURKB, BIRC5, BLM, BRCA1, BRCA2, CABLES1, CCNA1, CCND1, CCNE2, CCNG2, CDC2, CDC25A, CDC25B, CDC27, CDC45L, CDC6, CDCA5, CDKN1B, CDKN1C, CDKN2B, CDKN3, CDT1, CENPF, CHAF1A, CHEK2, CKLF, CLK1, CRIP1, CSPG6, CXCL1, DAB2, DDIT3, DLEU2, DST, DUSP4, DUSP6, E2F1, E2F2, E2F5, E2F7, EDG3, EDN1, EGF, EMP1, ENPEP, ERBB2IP, ERG, ETS1, EXO1, FEN1, FGB, FOSL1, G0S2, GPNMB, HDAC4, HDAC9, HERC5, HIPK2, HMGA1, IGF1R, IGFBP6, IL11, IL15, IL8, ILF3, ING4, IRS2, KIF23, KITLG, KRAS, LRP5, LTBP2, MAD2L1, MCM2, MCM3, MCM4, MCM8, MKI67, MXD4, MYH10, NCK1, NF1, NFIB, NRP1, ORC1L, ORC6L, OSMR, PA2G4, PARD3, PCNA, PDGFA, PKMYT1, PLAGL1, PLCB1, POLA2, POLD4, POLQ, PPP1CB, PRKCA, RAD50, RAD51, RARRES1, RBM14, RECK, RFC3, RFC5, RFP2, RGS2, RRM1, RRM2, SASH1, SEPT10, SEPT4, SEPT6, SESN2, SESN3, SHC1, SIAH1, TACSTD2, TGFBI, TNFSF7, TOP1, TSPAN1, UHRF1.
	Cell cycle	21.49	APBB2, ATF5, AURKB, BIRC5, BLM, BRCA1, BRCA2, CABLES1, CCNA1, CCND1, CCNE2, CCNG2, CDC2, CDC25A, CDC25B, CDC27, CDC45L, CDC6, CDKN1B, CDKN1C, CDKN2B, CDKN3, CDT1, CENPF, CHAF1A, CHEK2, CLK1, CSPG6, DDIT3, DLEU2, DST, DUSP4, DUSP6, E2F1, E2F2, E2F5, E2F7, EGF, ERBB2IP, EXO1, FEN1, G0S2, HDAC4, HDAC9, HERC5, HIPK2, HMGA1, IGF1R, IL8, ILF3, ING4, KIF23, KRAS, LTBP2,

		MAD2L1, MCM2, MCM3, MCM4, MCM8, MKI67, NF1, NFIB, ORC1L, ORC6L, PA2G4, PARD3, PCNA, PDGFA, PKMYT1, PLAGL1, PLCB1, POLA2, POLD4, POLQ, PRKCA, RAD50, RAD51, RBM14, RECK, RFC3, RFC5, RFP2, RGS2, RRM1, RRM2, SASH1, SEPT10, SEPT4, SEPT6, SESN2, SESN3, SHC1, SIAH1, TOP1.
Regulation of cell cycle	13.68	APBB2, ATF5, BRCA1, BRCA2, CCNA1, CCND1, CCNE2, CCNG2, CDC2, CDC25A, CDC25B, CDC45L, CDC6, CDKN1B, CDKN1C, CDKN2B, CDKN3, CDT1, CENPF, CHEK2, CLK1, DDIT3, DLEU2, DST, DUSP4, DUSP6, E2F1, E2F2, E2F5, E2F7, G0S2, HDAC9, HERC5, HIPK2, IGF1R, IL8, ING4, KRAS, LTBP2, MAD2L1, MKI67, NF1, PA2G4, PCNA, PDGFA, PKMYT1, PLAGL1, PLCB1, PRKCA, RECK, RFP2, SASH1, SESN2, SESN3, SHC1.
DNA replication	10.21	BLM, CDC45L, CDC6, CDT1, CHAF1A, EGF, EXO1, FEN1, HMGA1, MCM2, MCM3, MCM4, MCM8, NFIB, ORC1L, ORC6L, PCNA, POLA2, POLD4, POLQ, RAD51, RBM14, RFC3, RFC5, RRM1, RRM2, TOP1.
Neurophysiological process	9.24	ABAT, ALDH7A1, ATRX, CDH3, CDS1, CHRN1, CRY1, CYP1B1, DHRS3, GCH1, OPRL1, PCDHB10, PCLO, SRI, SULT1A3, TACSTD2, TBL1X, TGFBI.
DNA metabolism	9.22	ARID4A, ATRX, BLM, BRCA1, BRCA2, CDC45L, CDC6, CDT1, CHAF1A, CHD2, CHD4, CRY1, CSNK1E, CSPG6, DNMT1, EGF, EXO1, FEN1, GADD45G, GLRX2, H2AFV, H2AFX, HDAC4, HDAC9, HIST1H1C, HIST1H2AC, HIST1H2BD, HIST2H2BE, HMGA1, HMGA2, IFIH1, MCM2, MCM3, MCM4, MCM8, NAV1, NFIB, NP, NT5E, ORC1L, ORC6L, PCGF4, PCNA, POLA2, POLD4, POLQ, PRKDC, RAD50, RAD51, RAD51AP1, RAD51C, RBM14, RECQL, RFC3, RFC5, RRM1, RRM2, SHPRH, SLK, TOP1, TOP2A, WDR33.

DNA replication and chromosome cycle	7.44	BLM, CDC45L, CDC6, CDT1, CENPF, CHAF1A, CSPG6, EGF, EXO1, FEN1, HMGA1, MCM2, MCM3, MCM4, MCM8, NFIB, ORC1L, ORC6L, PCNA, POLA2, POLD4, POLQ, RAD51, RBM14, RFC3, RFC5, RRM1, RRM2, TOP1.
Sensory perception	6.54	ALDH7A1, ATRX, CDH3, CDS1, CRY1, CYP1B1, DHRS3, OPRL1, TACSTD2, TBL1X, TGFBI.
G-protein coupled receptor signalling pathway	5.71	AKAP12, C3, C6orf33, CALCR, CELSR1, CPE, CXCL1, CXCL2, EDG3, EDG8, ENPP2, FZD7, FZD8, GAL, GNAL, GNB4, GNG7, GPR126, GPR39, GPR64, IL8, NMU, OPRL1, OXTR, P2RY6, PARD3, RGS2, SPHK1, WDR5B, XPR1.
Detection of external stimulus	5.67	ALDH7A1, ATRX, CDH3, CDS1, CRY1, CYP1B1, DHRS3, HLA, DMA, OPRL1, PLEKHB1, TACSTD2, TBL1X, TGFBI.
G2/M transition of mitotic cell cycle	3.46	BIRC5, CCNA1, CCNE2, CDC25A, CDC6, CDKN1B, CDKN1C, CDKN2B, CDKN3, HERC5, PKMYT1.
Amino acid and derivative metabolism	3.34	AARS, ABAT, AGMAT, ALDH4A1, ALDH6A1, ARG2, ASMTL, ASNS, ASS, AUH, CBS, CORO2A, CTH, DDAH2, DHFR, ETNK1, GCH1, GCLC, GFPT2, GLS, HIBADH, MTRR, ODC1, PCYOX1, PROSC, PSAT1, SCLY, SLC7A5, SULT1A1, SULT1A2, SULT1A3, TPST2.
Regulation of cyclin-dependent protein serine/threonine kinase activity	3.31	CCNA1, CCNE2, CDC25A, CDC6, CDKN1B, CDKN1C, CDKN2B, CDKN3, HERC5, PKMYT1.
Glutamine family amino acid metabolism	3.31	AGMAT, ALDH4A1, ARG2, ASNS, ASS, CORO2A, DDAH2, GCLC, GFPT2, GLS.
Amine biosynthesis	3.20	AGMAT, ALDH4A1, ASMTL, ASNS, ASS, CBS, CORO2A, CTH, DHFR, ETNK1, MTRR, ODC1, PSAT1, SULT1A2.

---