

PKC δ regulates integrin $\alpha_v\beta_3$ expression and transformed growth of K-ras dependent lung cancer cells

Supplementary Material

Table S1: Shared genes regulated by PKC δ in K-ras dependent or independent NSCLC cells. Data is the average change in expression of significant genes in both K-ras dependent (H2009 and H441) or K-ras independent (A549 and H460) cell lines ($p < 0.05$). Only genes that were increased or decreased in both cell lines are included for each K-ras subpopulation.

K-ras Dependent				K-ras Independent			
Down (fold change)		Up (fold change)		Down (fold change)		Up (fold change)	
PRKCD	-4.11	CD274	2.61	PRKCD	-3.05	OR51B4	2.34
PI3	-3.58	CALB2	2.54	GPRC5B	-2.24	HBE1	2.24
SPINK6	-3.45	TRPA1	2.49	ADA	-2.09	STC1	2.03
ALDH1A1	-2.72	GFPT2	2.01	RAB23	-1.97	BDKRB1	2.01
RAB23	-2.42	LCP1	1.97	HOXA2	-1.83	CYP1B1	1.99
C9orf5	-2.38	SLC1A3	1.86	CP	-1.82	SLC16A6	1.99
PON2	-2.03	DYNLRB1	1.84	FERMT2	-1.77	TFF1	1.92
CFL1	-2.02	HSD17B10	1.84	TMEM47	-1.72	EDIL3	1.86
GALC	-2.01	MUC13	1.83	C9orf5	-1.70	HHIPL2	1.80
ADA	-1.95	TIMP3	1.79	HOXA3	-1.67	SMOC1	1.76
CALU	-1.93	HOXB9	1.77	TERF2IP	-1.63	TRPA1	1.74
RBM9	-1.91	NROB1	1.74	RNF157	-1.62	HSD17B10	1.69
SAMD9	-1.87	RELN	1.70	FAM171A1	-1.61	DYNLRB1	1.67
STK38	-1.85	CLU	1.65	SCARA3	-1.59	SLC4A4	1.65
FSTL1 MIR198	-1.82	TMED4	1.64	SNX27	-1.58	GLRX	1.65
CROT	-1.78	BMP6	1.64	LIFR	-1.56	SYTL3	1.61
TERF2IP	-1.77	WARS	1.62	NRP2	-1.56	SCARNA7	1.60

VAMP7	-1.74	GBP1 GBP3	1.61	DGKA	-1.52	MDM2	1.57
ASCC3	-1.74	PMP22	1.61	RBM9	-1.51	ELL2	1.56
LIFR	-1.73	FERMT3	1.59	CTSH	-1.49	IGFBP3	1.55
ITGA3	-1.72	NID2	1.58	CDK6	-1.47	MT1X	1.54
C1orf85	-1.71	B3GALNT2	1.56	NDRG2	-1.46	MCTP1	1.50
SNX27	-1.71	TNC	1.54	RNF185	-1.46	DKFZp686O24166	1.50
TSPAN1	-1.71	HBA1 HBA2	1.52	HMOX1	-1.46	KATNAL1	1.45
HIRA	-1.65	GLP2R	1.52	EDA2R	-1.45	NF2	1.45
NRAS CSDE1	-1.65	HBA2 HBA1	1.51	PSME3	-1.44	TMED4	1.44
GPRC5A	-1.64	GPT2	1.51	FBLN1	-1.43	SPRY4	1.44
NEK7	-1.64	CENPV	1.50	TULP3	-1.42	CCDC68	1.41
ELF4	-1.64	ANKRD36B	1.49	C5orf25	-1.42	B3GALNT2	1.41
ELF3	-1.64	RPIA	1.49	STRA6	-1.42	SCARNA9L	1.41
AMIGO2	-1.60	MYC	1.48	MRC2	-1.42	ATP2B1	1.39
IL6ST	-1.59	C9orf37	1.48	PON2	-1.40	SLC25A32 DCAF1 3	1.37
PSME3	-1.59	MTHFD2	1.48	UGP2	-1.40	KRT17	1.35
SMAD5	-1.58	KIAA1804	1.46	TLR3	-1.39	SLC9A2	1.35
RAB5B	-1.57	KCNG1	1.46	JAK1	-1.39	CLGN	1.34
DHRS3	-1.56	LYRM1	1.46	PDK3	-1.39	FOS	1.33
TNFRSF10D	-1.56	COX10	1.45	PLK2	-1.39	SS18	1.33
TM9SF1	-1.55	ADD2	1.44	ARRB1	-1.38	IL20RB	1.33
RBP4	-1.55	PRKD1	1.44	ANKRD54	-1.38	GBA2 CREB3	1.32
GOLIM4	-1.54	NPM3	1.44	PQLC3	-1.38	MAP2K3	1.31
BNIP3L	-1.53	FAM27E3	1.44	SMAD5	-1.38	ZC3HAV1L	1.31
WDR45L	-1.53	MAFG	1.44	BNIP3L	-1.37	IRS2	1.31
YIPF6	-1.53	FAM27E3	1.43	ATP6V1C1	-1.37	CABYR	1.28

FERMT2	-1.53	CUTC	1.42	TMEM139	-1.37	FAM83A	1.28
LCOR	-1.52	TYW3 CRYZ	1.42	CLMN	-1.37	FURIN	1.27
PODXL	-1.51	CABYR	1.42	PLAC8	-1.37	PYGB	1.27
SEPX1	-1.51	PDP2	1.42	ZNF281	-1.36	PLIN3	1.27
F11R TSTD1	-1.50	NEIL3	1.40	PBK	-1.36		
ASAH1	-1.50	DOT1L	1.40	ZDHHC13	-1.35		
AGRN	-1.50	SLC43A1	1.40	PLA2R1	-1.35		
FYTDD1	-1.50	CREB5	1.39	TSPAN6	-1.35		
NRIP1	-1.49	SPRYD3	1.39	TSPAN33	-1.35		
SFT2D2	-1.49	CPVL	1.39	RNF170	-1.34		
ICAM2	-1.49	PALLD	1.39	C1S	-1.34		
LOC554202	-1.47	UPP1	1.39	PTBP2	-1.34		
EPGN	-1.47	RAP1GAP2	1.38	C6orf72	-1.33		
DGKA	-1.47	CBLB	1.38	IRF2	-1.33		
ITGAV	-1.47	SH3PXD2B	1.38	TM2D2	-1.33		
DAG1	-1.46	PCID2	1.37	C3	-1.32		
ID2	-1.45	SDCCAG3	1.37	AADAC	-1.32		
CCNYL1	-1.45	C17orf75	1.37	ERBB2	-1.32		
SLC39A11	-1.45	MTIF2	1.36	GALC	-1.32		
C6orf72	-1.45	AKT3	1.36	FIG4	-1.32		
FUCA1	-1.45	IL32	1.35	CIB2	-1.32		
NRP2	-1.44	CNRIP1	1.34	NFKBIA	-1.31		
SGMS2	-1.43	MED24	1.34	GLIS3	-1.31		
C4orf34	-1.43	CRLF3	1.34	NRAS CSDE 1	-1.31		
FAM171A1	-1.42	SHISA3	1.33	CNTNAP1	-1.31		
TMBIM4 LOC10013332 2	-1.42	ZYX	1.33	ARL15	-1.30		

MET	-1.42	CENPH	1.33	SCML2	-1.30		
TAF10	-1.41	NCRNA0015 2	1.32	SEPX1	-1.29		
TP53	-1.41	DPH5	1.32	DIRC2	-1.29		
C20orf3	-1.41	RSL24D1	1.31	IL6ST	-1.29		
ITGB3	-1.41	MPZ	1.31	CSF1	-1.28		
ATXN1	-1.41	SLC16A3	1.31	SEMA4B	-1.27		
ATF6B TNXB	-1.40	SLC16A9	1.31	NAB1	-1.26		
HOXA2	-1.40	METTL3	1.31	LHFP	-1.26		
ATF6B TNXB	-1.40	TMEM120B	1.31				
ENTPD7	-1.40	THOC6	1.31				
SYT14	-1.39	POLR3D	1.31				
TMEM63B	-1.38	DNMT3B	1.31				
UBE3B	-1.38	JUND	1.30				
REEP3	-1.38	AKAP12	1.30				
RNF185	-1.36	DTD1	1.30				
FUT8	-1.36	SNRNP27	1.29				
HOXA3	-1.35	STAC	1.29				
EAF1	-1.35	ATG4D KRI1	1.28				
ATP6V1C1	-1.35	OSBPL1A	1.28				
SLC9A7	-1.35	FKBP11	1.28				
RNF141	-1.34	MRPS23	1.28				
ANPEP	-1.34	SMAP2	1.27				
KIAA1370	-1.34	RPUSD3	1.26				
TMEM56	-1.34	MRPL47	1.26				
DCTN5	-1.34	ZBTB11	1.26				
GPATCH8	-1.34						

GGCX	-1.34						
MYLIP	-1.33						
SSR1	-1.33						
LRRC16A	-1.33						
LTBP3	-1.33						
PPIC	-1.32						
SLC35B4	-1.32						
MAP3K7	-1.32						
PIGQ	-1.31						
MST1R	-1.30						
SLC9A6	-1.30						
YIPF3	-1.30						
SEMA3C	-1.29						
EXOC6B	-1.29						
TMCO3	-1.29						
TMEM9B	-1.29						
DNAJC3	-1.28						
NEU1	-1.27						
C10orf118 MIR2110	-1.26						
HS2ST1	-1.26						
MYD88	-1.26						

Table S2: Validation of Focal adhesion and ECM-receptor interaction gene expression in K-ras mutant NSCLC cells. Gene expression was validated by qRT-PCR in cell lines expressing $\delta 193$ and $\delta 203$ and compared to expression in cells expressing δscr (see Materials and Methods). Values represent fold change relative to δscr cells. nc= no change with PKC δ depletion; nc*=predicted down by microarray; nc**=predicted up by microarray.

Gene	K-ras dependent		K-ras independent	
	H2009	H441	H460	A549
CFL1	-1.48	-1.97	-1.44	-1.33
COL5A2	1.48	nc*	nc	nc
CPA4	-1.80	-42.49	-3.21	-1.58
DAG	-1.33	-2.29	nc*	-1.43
DUSP5	nc**	5.06	1.28	nc
FN1	nc	-2.30	nc	1.79
ITGA2	-2.42	-2.69	1.28	-1.93
ITGA5	nc	nc	1.74	1.50
ITGA6	nc	-1.73	nc	nc
ITGAV	-1.81	-2.53	-1.33	nc
ITGB1	nc	nc*	nc	nc
ITGB3	-2.78	-2.78	nc	nc
ITGB4	nc	-2.85	1.20	1.91
JUND	1.76	nc*	2.03	nc
LAMA1	1.55	nc	-1.58	nc
LAMA4	-1.87	-3.32	-3.85	7.78
LAMB2	-1.48	-2.88	-1.86	-1.39
LAMC1	nc	nc	nc	nc
LAMC2	-2.04	-2.28	nc	-2.07
LXN	nc	-56.94	nc*	nc
MMP16	1.73	nc	-1.56	nc
MMP19	-	-1.93	-1.80	nc
MMP2	1.12	-2.19	-1.58	2.92
RELN	1.32	nc**	nc	nc
TNC	1.69	1.23	11.79	1.46
TNXB	-2.72	-2.03	2.53	nc
VTN	-1.62	-6.37	nc	nc

Table S3: Primers used for qRT-PCR.

Gene	Forward (5' to 3')	Reverse (5' to 3')
CD274	TGCCGACTACAAGCGAATTACTG	CTGCTTGTCCAGATGACTTCGG
CFL1	GCAACCTATGAGACCAAGGAGAG	TCTTGATGGCGTCCTTGGAGCT
COL5A2	GAAGCCTCCCAGAACATCACTTAC	TTGCCCTTTGAGAACCACAGC
CPA4	CAATGAAGGGCAAGAACGGAGC	GGTCAGGAAAGTCTGCGGCAAT
DAG	CCACAGTGGTTGGCATTCTGA	CCAAGATGGCAAAGCCTCCTTC
DUSP5	CAGCATCCTGATTTGAACCCTG	TCCAGAAAAGCCAACATCTTGC
FN1	TGTCTATGCTCAGAATCCAAGCG	CCACATCAGTGAATGCCAGTCC
GAPDH	GCCAAATATGATGACATCAAGAAGG	GGTGTGCGTGTTGAAGTCAGAG
ITGA2	TGTTACCTGCTGGTTGAAAGACG	TGATGCGAAAGTCCCCTTCC
ITGA5	CTCCTTCTTCGGATTCTCAGTGG	TGGTATTAGCCTTGGGTGCTCC
ITGA6	CGAGGTTATGGAACAGCACATTTT	TTTCGGCAGCAGCAGTCACATC
ITGAV	AGGAGAAGGTGCCTACGAAGCT	GCACAGGAAAGTCTTGCTAAGGC
ITGB1	GCCCTCCAGATGACATAGAAAATCC	TGCTGTTCTTTGCTACGGTTG
ITGB3	AAGCAGAGTGTGTACGGAACC	CCTCCAGCCAATCTTTTCATCAC
ITGB4	CTCGCCAAGCACAACATCATC	CAGTGAGGAGACAGGGAAATAGGTG
JUND	ATCGACATGGACACGCAGGAGC	CTCCGTGTTCTGACTCTTGAGG
LAMA1	TGGCAGGGAAAAGGTGTGACAG	TCGCAGGTATTCTGAGTGTGTGGG
LAMA4	TGGCTCACCAATCAGTGCTCAG	TCCACATCTCTATCCACCCTGG
LAMB2	ACGGCACTGGGATGATGTAGTC	AGCACACGATAGATGACCTCGC
LAMC1	TGTTCCCAAGACAAAGGAGGTG	CCAAAGTAGCCATCATCACAGAGC
LAMC2	CTGGGAAACTGGAAGAAGAAGC	TTTAGCAAGATTGGCACGGG
LTX	GCGACTTTTCCGCCTCGGCA	TGGGTAGTTGGTCGGCGGGA
MAP3K7	CAGAGCAACTCTGCCACCAGTA	CATTTGTGGCAGGAAGTCTGCTCC
MET	TGCACAGTTGGTCTGCCATGA	CAGCCATAGGACCGTATTTCCGG
MMP16	GCAGCACAAGCACATCACTTACAG	CATCAAAGGCACGGCGAATAG
MMP19	CAGTGCCACAGAACCCAGTC	TGAAAGCATAGGTCTTCCCACG
MMP2	GTGTCTTCCCCTTCACTTTCCTG	ACCACATCTTCCGTCAGTCCG
MYC	GCTCGCCCTCCTACGTTGCG	TGGTCGGCCGTGGAGAAGCT
RELN	GTCTACCTTCCACTCTCCACCA	GTCCAGCATCACAAATCCCTCG
TNC	ATGTCCTCCTGACAGCCGAGAA	AGTCACGGTGAGGTTTTCCAGC
TNXB	CTGGAATCCGACCACAGATACC	TGGGAGGTTCTGAAGGCTTCTC
VTN	TGGACGAAAAGGCAGTGAGG	TGACAGTTGATGCGGGTGAAGG