

Supplemental Data

A Gene Expression Signature Associated with “K-Ras Addiction” Reveals Regulators of EMT and Tumor Cell Survival

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Supplemental Experimental Procedures

RT-PCR analysis

To assess *ANKRD22* mRNA levels, total RNA was extracted from cells using Trizol Reagent (Invitrogen). RNA was reverse transcribed utilizing random primers with Stratagene's AffinityScript Multiple Temperature Reverse Transcriptase cDNA Synthesis kit (cat#200436). RT-PCR was performed according the QuantiTect® SYBR® Green I (Qiagene cat#204143) Master Mix protocol on ABI 7500 system using the following primers for *ANKRD22*: Forward: CCCCTTTGAGTATTGAGCA; Reverse: CACACTCACCGCTGACACTT. For the housekeeping gene GAPDH: Forward: GGTCTCCTCTGACTTCAAACA; Reverse: GTGAGGGTCTCTCTCTTCCT.

In-cell western assay for PARP cleavage

Cells were plated at a density of 6×10^3 cells per well in 96-well plates. The following day, cells were infected with lentiviruses expressing control or K-RasB or C shRNAs. Twenty-four h post-infection, cells were treated with 1 μ g/ml puromycin. Forty-eight h later, cells were fixed in 4% paraformaldehyde and permeabilized with 0.1% Tx-100 in the presence of 10% goat serum. Cells were then blocked with 1% non-fat dairy milk for 15 min. Cells were then incubated with Cleaved

PARP antibody (Cell Signaling) for 24h at 4°C. Cells were then incubated with Li-Cor IR-Dye 800 conjugated goat anti-mouse secondary for 1 h plus Syto-60 dye, as a loading control. Cell staining was then visualized with Li-Cor Odyssey scanner and quantitated.

Parameters used for the PAM algorithm

Note: PAM is a module for the R program package.

Tab-delimited text files were created for training and test data. CSV files from SGD1 were opened in Excel, sorted in probeset id order, then exported as tab-delimited text.

Filename	Columns	Probe Sets
AllGenes_PAMTrain.txt	15	52,920
AllGenes_PAMTest.txt	30	52,920

I. Start Up PAM

- From **Packages** menu, select **Load**, pamr.
- From **File** menu, select **Change dir...**, and browse to the directory containing the data files.

II. Read the Training Set Data

```
data <- pamr.from.excel("AllGenes_AnuragPAMTrain.txt", 15,  
sample.labels=TRUE)
```

III. Train the Data

```
trainedData <- pamr.train(data)
```

IV. Cross-Validate

```
set.seed(120)  
  
results <- pamr.cv(trainedData, data)  
  
pamr.plotcv(results)
```

- Examine the error curve and choose an appropriate threshold value.

```
pamr.plotcvprob(results, data, threshold=x.x)
```

V. Estimate False Discovery Rates

```
fdr.obj <- pamr.fdr(trainedData, data, threshold=x.x)

pamr.plotfdr(fdr.obj)
```

- Examine the FDR curve and verify threshold value falls within an acceptable false discovery rate (around 2.5).

VI. Get the Gene List

```
pamr.plotcen(trainedData, data, threshold=x.x)

pamr.geneplot(trainedData, data, threshold=x.x)

pamr.listgenes(trainedData, data, threshold=x.x, fitcv=results,
genenames=TRUE)
```

VII. Predict Class of Test Data

```
testData <- pamr.from.excel("AllGenes_AnuragPAMTest.txt", 30,
sample.labels=TRUE)

classPredict <- pamr.predict(trainedData, testData$x, threshold=x.x,
type="class")

probPredict <- pamr.predict(trainedData, testData$x, threshold=x.x,
type="posterior")

prediction <- cbind(testData$samplelabels, classPredict,
probPredict)

write.table(prediction, file="predicition.txt", col.names=TRUE,
quote=FALSE, sep="\t")
```

Supplementary Figures and Legends

Singh et al. Supplementary Figure 1

A

Anova: Single Factor

SUMMARY

Groups	Number of Lines	Mean RDI	Variance
RAS-INDEPENDENT	17	1.383	0.0904
RAS-DEPENDENT	17	5.316	5.0858

ANOVA

Source of Variation	SS	df	MS	F	P-value	F crit
Between Groups	131.482	1	131.482	50.801	4.35E-08	4.149
Within Groups	82.821	32	2.588			
Total	214.303	33				

B

	RDI	RelativeCasp3 Cleavage
A549	0.612271443	0.539464105
SW1573	0.747458815	0.896674369
H23	0.779526361	0.726880852
H460	0.793419084	0.524686733
SK-LU-1	0.989259859	0.821241591
H727	1.840453722	1.336308068
H441	2.072743821	2.428367012
H358	2.102978438	2.28017945
H2009	2.351490754	2.392729846
PANC-1	0.918843158	0.331383659
PA-TU-8988T	1.021180446	0.539464105
SW1990	1.641141131	1.02953976
YAPC	3.727096814	2.398895665
HPAF-II	4.699546041	2.727118654
PA-TU-8902	8.78477499	2.718306788
Capan-1	9.955879487	2.921120209

n 15
 r* 0.77
 df 13
 t* 4.351
2-tailedp 0.0008

Figure S1. (A) ANOVA calculations were performed on RDI values for cell lines that were classified as K-Ras-dependent or K-Ras-independent based on an apoptotic

response to K-Ras depletion by RNAi or a defined “Dependency Threshold” of 2.0. (B) Student T-Test showing a statistically significant correlation between RDI values and relative caspase-3 cleavage values ($P=0.0008$).

Singh et al. Supplementary Figure 2

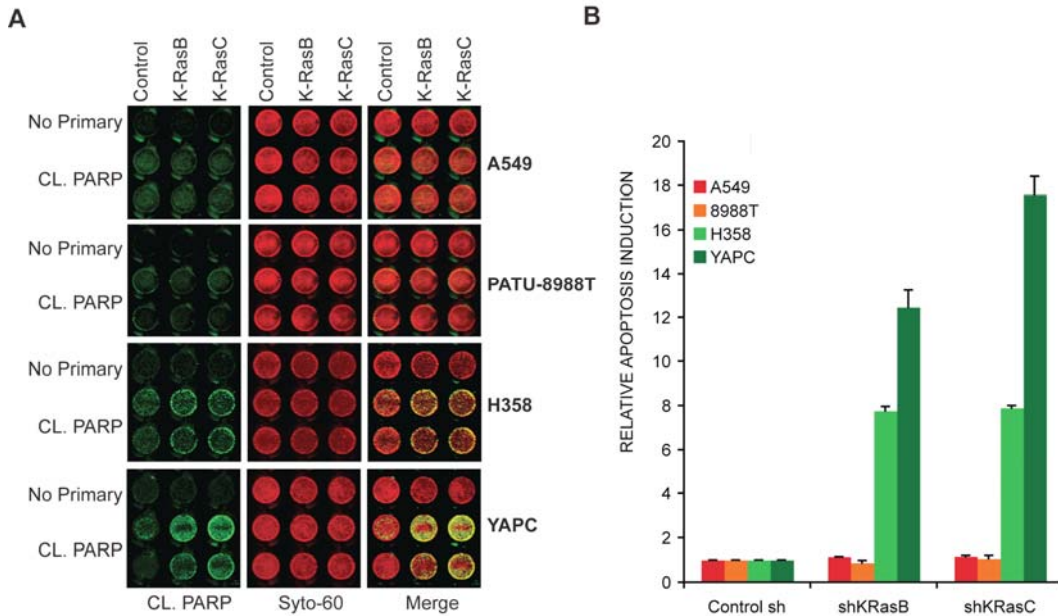
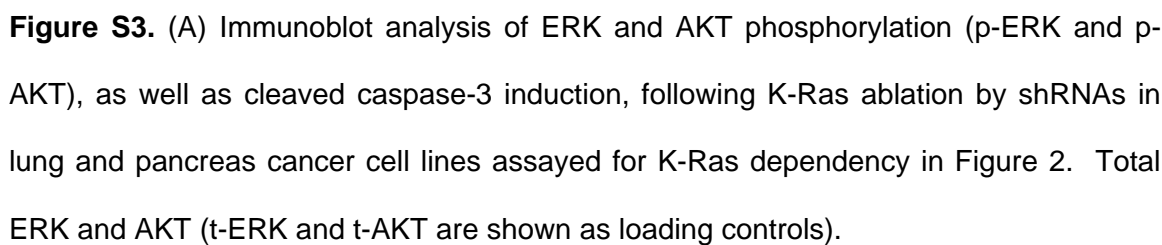


Figure S2. (A) Induction of PARP cleavage following K-Ras ablation in K-Ras-independent (A549 and PATU-8988T) and K-Ras-dependent cells (H358 and YAPC) as measured by In-Cell Western (ICW) assay. Cleaved PARP was detected by staining with a specific antibody, corresponding to the green signal. Syto-60 nuclear dye is shown in red as a loading control. (B) Quantitation of PARP cleavage corresponding to Relative Apoptosis Induction. Data are presented as the mean + SD.



(B) Immunoblot analysis of total tyrosine phosphorylated proteins as well as ERK and AKT phospho-activation, and PTEN expression in K-Ras-dependent (green) versus K-Ras-independent (red) cancer cell lines. GAPDH is shown as a protein loading control.

Singh et al. Supplementary Figure 4

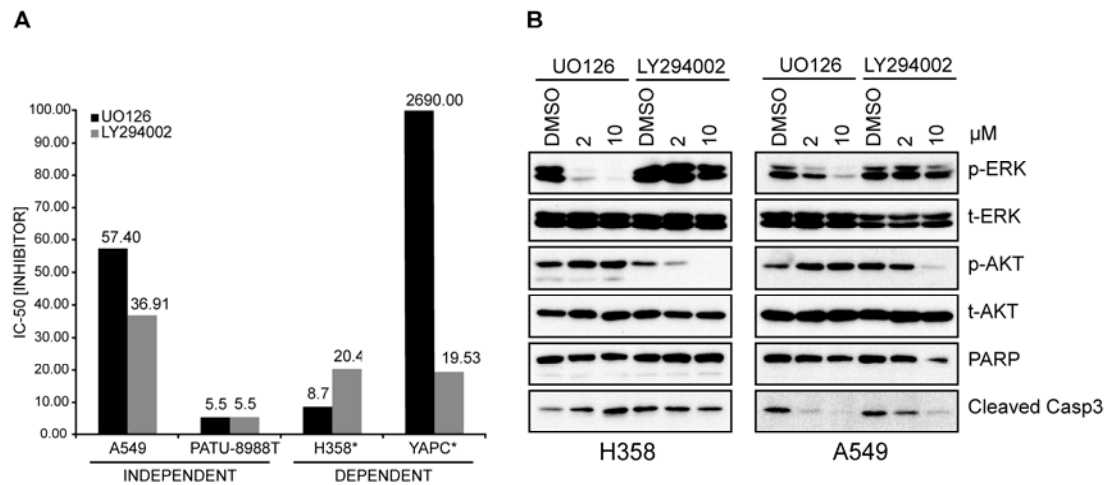


Figure S4. (A) IC-50 values for Mek (UO126 – black bars) and PI3K (LY294002 – gray bars) inhibitors in K-Ras-independent and K-Ras-dependent cell lines. (B) Erk and Akt phosphorylation as well as caspase-3 cleavage following treatment with Mek and PI3K inhibitors. Total ERK and AKT (t-ERK and t-AKT) are shown as loading controls.

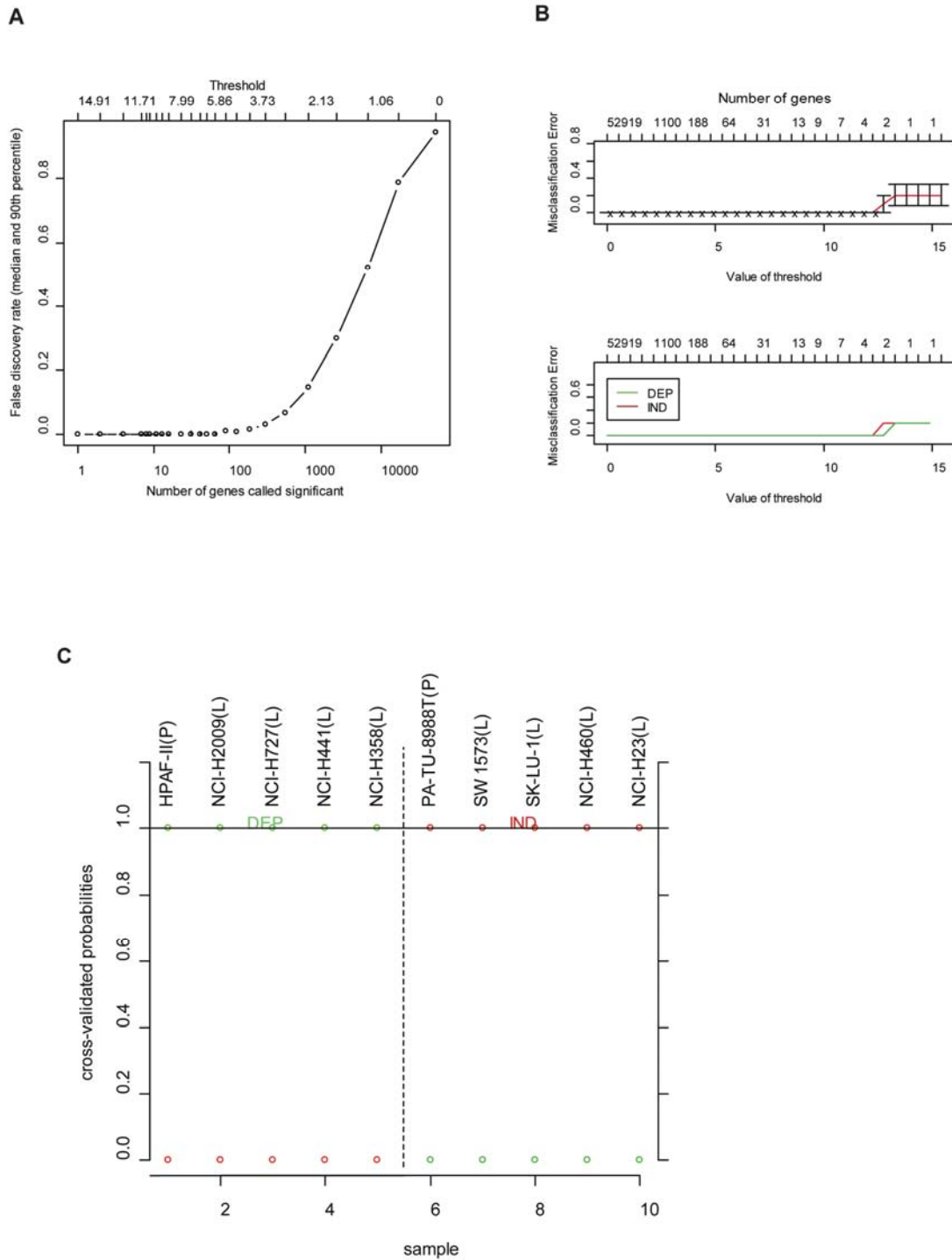


Figure S5. (A) False Discovery Rate as a function of the number of genes and/or the threshold parameter for the K-Ras dependency signature. (B) Misclassification errors as

a function of the threshold parameter. (C) Cross-validated probabilities for the training set of cell lines used to generate the K-Ras dependency signature and for generating prediction assignments for the “test-set” of cell lines. Green= K-Ras-dependent (DEP) and Red= K-Ras-independent (IND).

Singh et al. Supplementary Figure 6

Category	Term	Count	%	P-Value
GOTERM_CC_ALL	intercellular junction	8	8.4	6.40E-06
GOTERM_CC_ALL	cell junction	11	11.6	1.10E-05
GOTERM_CC_ALL	membrane	52	54.7	1.50E-05
SP_PIR_KEYWORDS	membrane	41	43.2	4.30E-05
GOTERM_BP_ALL	cell adhesion	12	12.6	9.20E-05
GOTERM_BP_ALL	biological adhesion	12	12.6	9.20E-05
GOTERM_CC_ALL	plasma membrane part	22	23.2	1.90E-04
GOTERM_CC_ALL	tight junction	5	5.3	3.00E-04
INTERPRO	Myelin P0 protein	3	3.2	3.50E-04
GOTERM_CC_ALL	membrane part	43	45.3	4.20E-04
GOTERM_BP_ALL	cell-cell adhesion	7	7.4	6.20E-04
GOTERM_CC_ALL	apical junction complex	5	5.3	6.30E-04
GOTERM_CC_ALL	apicolateral plasma membrane	5	5.3	6.80E-04
SP_PIR_KEYWORDS	glycoprotein	30	31.6	9.70E-04
GOTERM_CC_ALL	integral to membrane	38	40	1.50E-03
GOTERM_CC_ALL	intrinsic to membrane	38	40	1.60E-03
SP_PIR_KEYWORDS	tight junction	4	4.2	1.70E-03
SP_PIR_KEYWORDS	cell junction	7	7.4	2.20E-03
UP_SEQ_FEATURE	topological domain:Cytoplasmic	23	24.2	2.60E-03
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	26	27.4	2.70E-03
SP_PIR_KEYWORDS	transmembrane	32	33.7	2.80E-03
UP_SEQ_FEATURE	transmembrane region	26	27.4	4.80E-03
GOTERM_CC_ALL	apical plasma membrane	4	4.2	5.20E-03
SP_PIR_KEYWORDS	cell adhesion	7	7.4	6.90E-03
GOTERM_CC_ALL	plasma membrane	25	26.3	9.50E-03
GOTERM_CC_ALL	apical part of cell	4	4.2	1.00E-02
GOTERM_BP_ALL	epithelial cell differentiation	3	3.2	1.00E-02
SP_PIR_KEYWORDS	calcium	9	9.5	1.50E-02
SP_PIR_KEYWORDS	serine protease	4	4.2	1.60E-02
GOTERM_BP_ALL	homophilic cell adhesion	4	4.2	1.60E-02
GOTERM_BP_ALL	epidermis development	4	4.2	1.70E-02
UP_SEQ_FEATURE	topological domain:Extracellular	18	18.9	1.70E-02
GOTERM_BP_ALL	anatomical structure development	15	15.8	2.00E-02
GOTERM_BP_ALL	ectoderm development	4	4.2	2.00E-02
GOTERM_BP_ALL	anatomical structure morphogenesis	10	10.5	2.00E-02
INTERPRO	Low density lipoprotein-receptor, class A	3	3.2	2.20E-02
SP_PIR_KEYWORDS	signal	21	22.1	2.40E-02
INTERPRO	Epidermal growth factor receptor ligand	2	2.1	2.50E-02
UP_SEQ_FEATURE	active site:Charge relay system	4	4.2	2.70E-02
KEGG_PATHWAY	Leukocyte transendothelial migration	4	4.2	2.80E-02
INTERPRO	Cadherin prodomain like	2	2.1	2.90E-02
SP_PIR_KEYWORDS	carcinogenesis	2	2.1	3.00E-02
SMART	LDLa	3	3.2	3.10E-02
GOTERM_BP_ALL	cell-cell signaling	7	7.4	3.30E-02
	region of interest:Interactions with TJP1, TJP2 and TJP3	2	2.1	3.30E-02
UP_SEQ_FEATURE	Cell adhesion molecules (CAMs)	4	4.2	3.50E-02
KEGG_PATHWAY	Tight junction	4	4.2	3.80E-02
GOTERM_BP_ALL	morphogenesis of an epithelium	3	3.2	3.80E-02

Figure S6. Term enrichment analysis of the K-Ras dependency signature genes using the EASE algorithm from The Database for Annotation, Visualization and Integrated Discovery (DAVID).

Supplementary Figure 7.

Cell Line	Tissue	Prediction	DEP	IND
SW 1116	Intestine	DEP	1	3.50E-93
Panc 08.13	Pancreas	DEP	1	5.62E-122
RCM-1	Intestine	DEP	1	2.22E-91
NCI-H1573	Lung	DEP	1	1.09E-69
NCI-H1734	Lung	DEP	1	1.76E-25
NCI-H2122	Lung	DEP	1	9.44E-81
GP5D	Intestine	DEP	1	1.39E-67
KYSE-410	Esophagus	DEP	1	2.06E-74
AGS	Stomach	DEP	1	6.60E-64
HuCCT1	Liver	DEP	1	3.97E-81
LS174T	Intestine	DEP	1	1.90E-67
SW 1463	Intestine	DEP	1	5.32E-80
T84	Intestine	DEP	1	1.78E-79
HCT 116	Intestine	DEP	1	1.31E-14
SW837	Intestine	DEP	1	8.58E-75
HUP-T4	Pancreas	DEP	1	1.07E-105
LU99A	Lung	IND	1.82E-73	1
SNG-M	Uterus	IND	4.67E-44	1
A-427	Lung	IND	1.84E-39	1
SW 900	Lung	IND	2.54E-05	0.999974636
NCI-H1155	Lung	IND	5.07E-27	1
LU65	Lung	IND	2.53E-56	1
Calu-1	Lung	IND	5.96E-72	1
NOMO-1/ADM	Blood	IND	5.04E-24	1
KP-1N	Pancreas	IND	4.72E-81	1
SUIT-2	Pancreas	IND	3.65E-29	1
HEC-1	Uterus	IND	3.55E-81	1
TCO-1	Thymus	IND	9.34E-76	1
KP-4	Pancreas	IND	2.93E-81	1
NCI-H1792	Lung	IND	7.48E-76	1

Figure S7. Table showing prediction of Ras dependencies for a large panel of *K-Ras* mutant cell lines as assigned by the PAM algorithm. DEP = predicted to be K-Ras-dependent; IND = predicted to K-Ras-independent. Cell lines in green were experimentally determined to be K-Ras-dependent whereas those in red were found to be K-Ras-independent.

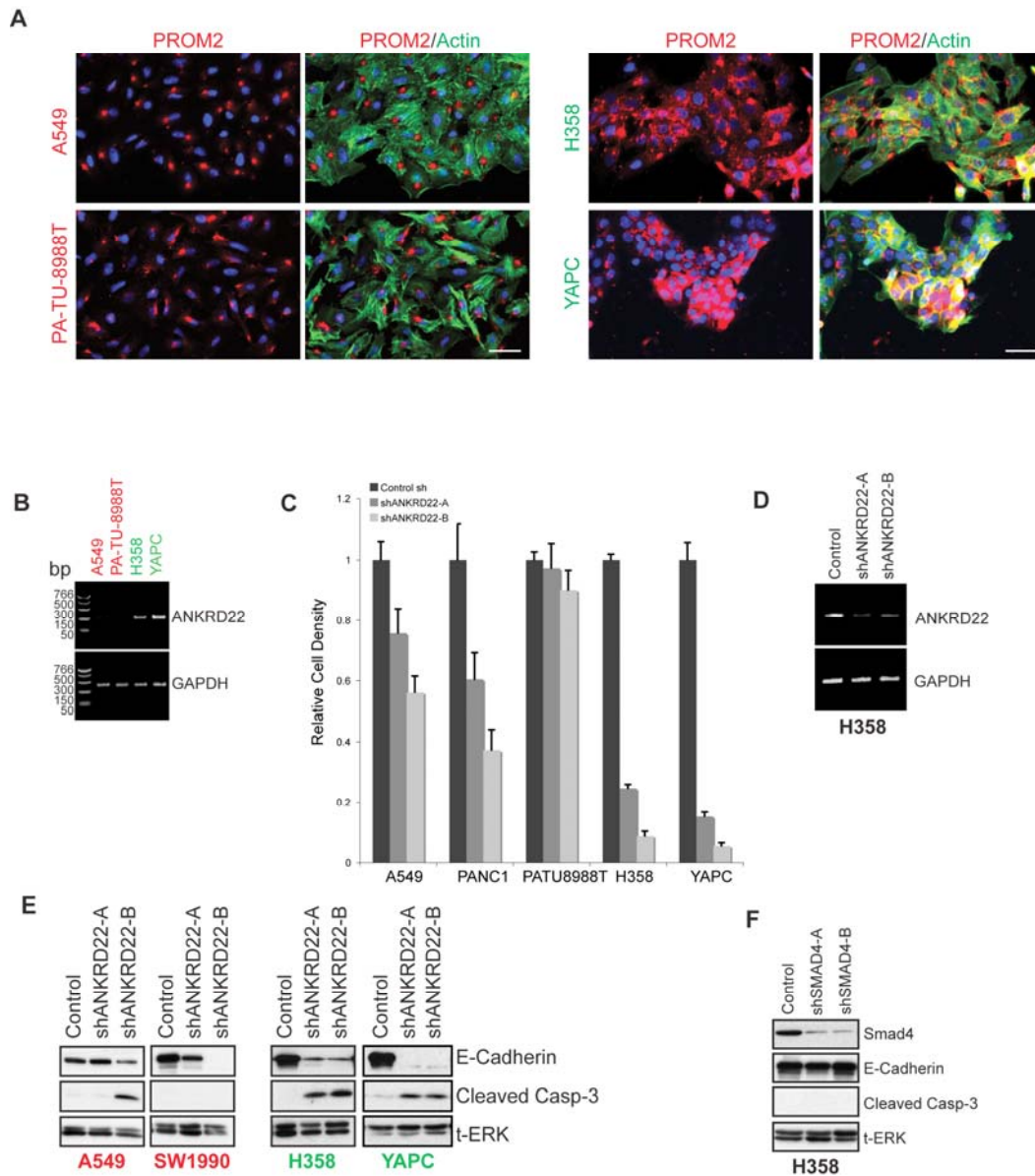


Figure S8. (A) Fluorescence microscopy analysis of expression of PROM2 (red signal), a K-Ras dependency signature gene, in K-Ras-dependent (H358 and YAPC) and K-Ras-independent (PA-TU-8988T and A549) cell lines. Green signal corresponds to F-actin, as revealed by phalloidin staining. Scale bar = 15µM.

(B) *ANKRD22* mRNA levels in a subset of K-Ras-dependent (green) and K-Ras-independent (red) cell lines as assessed by RT-PCR. DNA size markers are shown in the leftmost lane in base pairs (bp).

(C) Differential growth inhibitory effects of *ANKRD22* ablation in K-Ras-dependent (H358 and YAPC) versus K-Ras-independent cell lines (A549, PANC1 and PATU8988T). Data are represented as the mean + SD.

(D) Reduced RNAi-mediated *ANKRD22* mRNA levels in H358 cells.

(E) Ablation of *ANKRD22* in K-Ras-dependent cells and effects on E-Cadherin expression and cleaved caspase-3 associated cell death, as assessed by western blotting. Total ERK (t-ERK) is shown as a loading control.

(F) ShRNA-mediated ablation of SMAD4 in H358 cells and effects on E-Cadherin expression and cleaved caspase-3 induction. Total ERK (t-ERK) is shown as a loading control.

Singh et al. Supplementary Figure 9

LUNG

	K-Ras	PIK3CA	CTNNB1	MADH4	RB1	TP53	p16/INK4A
A549	G12S (HOMO)	WT	WT	WT	WT	WT	HD
NCI-H460	Q61H (HOMO)	WT	WT	WT	WT	WT	HD
NCI-H23	G12C (HET)	WT	WT	WT	WT	M246I	WT
SW1573	G12C	K111E (HET)	S33F (HET)	HD	WT	WT	HD
SK-LU-1	G12D	WT	WT	WT	WT	WT	HD
NCI-H358	G12C (HET)	WT	T75A (HET)	WT	WT	WT	WT
NCI-H2009	G12A (HET)	WT	WT	WT	HD	R273L	WT
NCI-H727	G12V (HOMO)	WT	WT	WT	WT	Q165 S166insYKQ	WT
NCI-H441	G12V (HET)	WT	WT	WT	WT	WT	WT

PANCREAS

	K-Ras	MADH4	TP53	INK4A
PANC-1	G12D (HET)	WT	H273	HD
PA-TU-8988T	G12V (HOMO)			
SW1990	G12D (HOMO)	WT	WT	HD
PA-TU-8902	G12V			
YAPC	G12V (HOMO)	HD	H179R	HD
Capan-1	G12V (HOMO)	pS343*	A159V	HD
HPAF II	G12D (HET)	WT	P151S	HD

Figure S9. Mutational status of known oncogenes and tumor suppressor genes in *K-Ras* mutant lung and pancreatic cancer cell lines used in this study.

Supplementary Table1. K-Ras dependency signature genes and corresponding Affymetrix probeset IDs. The top 250 probes were used to generate the heatmap in Figure 5E. Genes verified to be expressed in K-Ras dependent cells are highlighted in green, whereas those expressed in independent cells are highlighted in red.

Affymetrix Probe ID	Gene Symbol	DEP-score	IND-score
g4507328_3p_a_at	SYK	4.0281	-4.0281
Hs.24743.1.A1_3p_at	RBM35A	3.3478	-3.3478
g8923166_3p_a_at	RBM35A	3.0155	-3.0155
Hs.56937.1.S1_3p_a_at	ST14	2.8812	-2.8812
Hs.85335.0.A1_3p_at	TMEM30B	2.7817	-2.7817
g4504328_3p_at	SPINT1	2.7352	-2.7352
Hs.74101.2.S1_3p_at	SYK	2.6864	-2.6864
Hs.74101.2.S1_3p_a_at	SYK	2.3608	-2.3608
g9966860_3p_at	RAB25	2.2896	-2.2896
Hs.188881.0.A1_3p_at	C1orf172	2.159	-2.159
g13376381_3p_at	GRHL2	2.1037	-2.1037
Hs.278611.0.S1_3p_a_at	GALNT3	1.963	-1.963
g4506814_3p_at	SCNN1A	1.909	-1.909
g9392652_3p_at	EVA1	1.7071	-1.7071
Hs.57664.0.S1_3p_at	ITGB6	1.7038	-1.7038
Hs.11801.0.S2_3p_at	C1orf74	1.6883	-1.6883
g13528968_3p_at	INPP4B	1.6168	-1.6168
g4505630_3p_s_at	PCDH1	1.5484	-1.5484
Hs2.98573.1.S1_3p_s_at	C6orf141	1.5167	-1.5167
g4826763_3p_a_at	HS3ST1	1.5134	-1.5134
g4502756_3p_a_at	CDS1	1.5125	-1.5125
Hs.76853.0.S1_3p_at	DNAJA4	1.5051	-1.5051
g11065890_3p_a_at	F11R	1.4376	-1.4376
Hs2.145582.1.S1_3p_s_at	PROM2	1.4203	-1.4203
g10835007_3p_at	CLDN7	1.4171	-1.4171
g13129133_3p_at	UNKNOWN/INVALID SYMBOL:(653098)	1.4038	-1.4038
Hs.115166.1.S1_3p_at	SCEL	1.3739	-1.3739
g5031844_3p_at	LAD1	1.356	-1.356
g4506798_3p_a_at	SCEL	1.3383	-1.3383
Hs2.210473.1.S2_3p_at	SCIN	1.3156	-1.3156
g11415039_3p_x_at	ST14	1.2894	-1.2894
g10190711_3p_at	S100A14	1.2733	-1.2733
Hs.268362.0.A1_3p_at	ANKRD22	1.2731	-1.2731
g4505630_3p_x_at	PCDH1	1.2459	-1.2459
Hs.76550.0.S1_3p_at	MAL2	1.2422	-1.2422
Hs.52620.2.S1_3p_at	CDS1	1.2381	-1.2381
Hs.8364.1.A1_3p_at	EHF	1.1968	-1.1968
g11967980_3p_s_at	RAB17	1.1724	-1.1724
g8922753_3p_at	C1orf106	1.1536	-1.1536
1552575_3p_a_at	C6orf141	1.1522	-1.1522
Hs.79170.0.S1_3p_at	TTC9	1.0957	-1.0957

Hs.43355.0.A1_3p_at	DENND1C	1.0869	-1.0869
Hs.52620.2.S2_3p_at	CDS1	1.0731	-1.0731
g189084_3p_at	CEACAM6	1.0344	-1.0344
g12653328_3p_s_at	MAPK13	1.0334	-1.0334
g5032246_3p_a_at	EVA1	1.0298	-1.0298
Hs.15396.0.A1_3p_at	LOC196264	1.005	-1.005
Hs.108502.0.S1_3p_a_at	BSPRY	0.9841	-0.9841
g13027607_3p_at	C1orf116	0.9626	-0.9626
Hs2.98573.2.S1_3p_at	C6orf141	0.9472	-0.9472
g8923147_3p_a_at	BSPRY	0.9266	-0.9266
Hs.177164.0.A1_3p_at	VSIG1	0.9141	-0.9141
Hs.323439.0.A1_3p_at	KIAA0703	0.9092	-0.9092
g7705976_3p_at	TMPRSS4	0.8894	-0.8894
g12653328_3p_at	MAPK13	0.8637	-0.8637
g4507460_3p_at	TGFA	0.8383	-0.8383
g8923677_3p_at	EPN3	0.8373	-0.8373
g4503596_3p_a_at	ERBB3	0.8309	-0.8309
Hs2.158963.1.S1_3p_x_at	C1orf210	0.8269	-0.8269
Hs.283552.0.S1_3p_a_at	TMEM45B	0.8066	-0.8066
Hs.220745.0.S1_3p_at	RALGPS2	0.8051	-0.8051
g11386156_3p_at	CDA	0.7775	-0.7775
g4757959_3p_a_at	CDH1	0.7627	-0.7627
Hs.97774.0.A1_3p_at	SYTL5	0.7543	-0.7543
g4503786_3p_a_at	FRK	0.7479	-0.7479
g13544025_3p_s_at	OVOL2	0.7362	-0.7362
Hs.170673.0.A1_3p_at	RDHE2	0.7337	-0.7337
g12583651_3p_at	LOC653857	0.7324	-0.7324
g7657171_3p_at	B3GNT3	0.7276	-0.7276
g7662255_3p_s_at	KIAA0703	0.7213	-0.7213
g4503366_3p_at	DPP4	0.7093	-0.7093
g11545838_3p_at	PRSS22	0.7011	-0.7011
g9944939_3p_s_at	EPS8L1	0.6975	-0.6975
g13435148_3p_at	RBM35B	0.6964	-0.6964
g902370_3p_a_at	EFNB2	0.6864	-0.6864
Hs.10119.0.S1_3p_at	CGNL1	0.6753	-0.6753
g4557710_3p_a_at	LAMA3	0.6655	-0.6655
Hs.182704.0.A1_3p_at	PGM2L1	0.658	-0.658
g2338755_3p_at	ELF3	0.6548	-0.6548
Hs.12332.0.A1_3p_at	PLEKHA7	0.6397	-0.6397
g1841524_3p_a_at	ELF3	0.6387	-0.6387
g4759231_3p_at	TIAF1	0.6285	-0.6285
Hs.97013.0.A1_3p_at	C11orf52	0.6281	-0.6281
Hs.49397.0.A1_3p_at	EPB41L5	0.6199	-0.6199
Hs.283552.0.S1_3p_x_at	TMEM45B	0.6138	-0.6138
g7657171_3p_x_at	B3GNT3	0.6085	-0.6085
Hs.59509.0.A1_3p_at	KRTCAP3	0.605	-0.605
Hs.199067.2.A1_3p_at	ERBB3	0.5812	-0.5812
Hs.3454.0.A1_3p_at	RAB11FIP4	0.5761	-0.5761
g4505992_3p_at	PPL	0.5751	-0.5751
g13435365_3p_a_at	DSC2	0.5719	-0.5719
g4505058_3p_a_at	TACSTD1	0.5707	-0.5707
Hs.72222.1.S1_3p_a_at	FER1L4	0.5615	-0.5615
Hs2.11801.1.S1_3p_s_at	IRF6	0.5612	-0.5612
g340184_3p_a_at	CDH1	0.5595	-0.5595

g6434903_3p_at	TSPAN1	0.5552	-0.5552
g4557734_3p_a_at	MAOA	0.5516	-0.5516
g5457118_3p_s_at	F11R	0.5504	-0.5504
g4502876_3p_at	CLDN4	0.5494	-0.5494
Hs.120219.0.A1_3p_at	TMEM154	0.531	-0.531
Hs.168953.0.A1_3p_at	EVA1	0.5287	-0.5287
Hs.39871.0.S1_3p_at	MYO1D	0.5276	-0.5276
Hs.79170.0.S2_3p_at	TTC9	0.514	-0.514
Hs.57887.0.A1_3p_at	GPR115	0.5077	-0.5077
Hs.192822.0.A1_3p_at	PPP1R14C	0.5049	-0.5049
g12655880_3p_at	PKIB	0.4898	-0.4898
g6912529_3p_at	TSPAN15	0.4824	-0.4824
g4885524_3p_s_at	SH2D3A	0.4816	-0.4816
g4502078_3p_a_at	AMPD3	0.4789	-0.4789
Hs.217484.0.A1_3p_x_at	ANKRD22	0.4781	-0.4781
g5454143_3p_a_at	UBD	0.4762	-0.4762
Hs2.57787.1.S1_3p_s_at	MTAC2D1	0.4692	-0.4692
Hs.145807.0.S1_3p_a_at	TMC5	0.4607	-0.4607
Hs.13337.0.A1_3p_at	PGM2L1	0.4517	-0.4517
Hs.161002.0.S1_3p_at	AIM1	0.4314	-0.4314
g7705954_3p_at	ACP6	0.4276	-0.4276
Hs.188881.0.A1_3p_x_at	C1orf172	0.4224	-0.4224
g4502198_3p_at	AREG	0.4201	-0.4201
Hs.111334.4.S1_3p_at	FAM102A	0.4178	-0.4178
Hs.93738.0.S1_3p_at	ZNF608	0.4175	-0.4175
Hs.187646.0.A1_3p_at	TMEM65	0.411	-0.411
Hs.322735.0.A1_3p_at	KIAA1522	0.4062	-0.4062
4861120_3p_s_at	C5orf4	0.4041	-0.4041
Hs.172674.4.A1_3p_at	NFATC3	0.4041	-0.4041
Hs2.21599.2.S1_3p_s_at	KLF7	0.399	-0.399
Hs.173334.2.S1_3p_at	ELL2	0.3982	-0.3982
g12962938_3p_a_at	OTUB2	0.3953	-0.3953
Hs.51965.0.S1_3p_at	PLEKHG1	0.3897	-0.3897
g12804894_3p_a_at	FUT2	0.3862	-0.3862
g4505264_3p_x_at	MST1R	0.3855	-0.3855
Hs.82845.0.S1_3p_at	SORL1	0.3854	-0.3854
g4505264_3p_at	MST1R	0.3821	-0.3821
g6325473_3p_at	SORL1	0.3817	-0.3817
Hs.159115.0.S1_3p_at	IKZF2	0.3793	-0.3793
g12803726_3p_x_at	KRT7	0.3783	-0.3783
Hs.122489.0.S1_3p_at	C4orf34	0.378	-0.378
Hs.224012.0.S1_3p_at	JAG1	0.3744	-0.3744
g7705414_3p_at	HOOK1	0.3711	-0.3711
Hs.11101.0.S1_3p_at	DLG3	0.3674	-0.3674
g12803726_3p_at	KRT7	0.3556	-0.3556
g7799987_3p_a_at	KCNMB4	0.3542	-0.3542
Hs.293902.0.A1_3p_at	C12orf46	0.3533	-0.3533
Hs.95549.0.A1_3p_a_at	FLJ20273	0.3521	-0.3521
g13477106_3p_s_at	CEACAM6	0.3453	-0.3453
Hs.301175.1.S1_3p_s_at	RAC2	0.3367	-0.3367
Hs.50841.0.A1_3p_at	Gcom1	0.336	-0.336
Hs.299254.0.S1_3p_at	HOOK1	0.3296	-0.3296
Hs.283552.1.S1_3p_a_at	TMEM45B	0.3223	-0.3223
Hs.21554.0.S1_3p_at	KIAA1107	0.3211	-0.3211

g12653994_3p_a_at	STAP2	0.32	-0.32
Hs.23582.0.A2_3p_a_at	TACSTD2	0.3171	-0.3171
g5031630_3p_a_at	SCARB2	0.3114	-0.3114
g8308175_3p_a_at	CGN	0.3079	-0.3079
g4506152_3p_at	PRSS8	0.3059	-0.3059
g13376137_3p_a_at	TMC5	0.301	-0.301
g4759083_3p_at	DHRS3	0.3004	-0.3004
g13325163_3p_a_at	C1orf34	0.2976	-0.2976
Hs.153028.2.S2_3p_at	CYB561	0.2954	-0.2954
g439225_3p_at	FBP1	0.2898	-0.2898
Hs.23240.0.S1_3p_at	ZNF468	0.286	-0.286
g13236539_3p_a_at	GDPD3	0.2856	-0.2856
g11545786_3p_a_at	EGLN3	0.2847	-0.2847
Hs.9598.1.S1_3p_a_at	SEMA4B	0.2822	-0.2822
g9506400_3p_at	ARHGEF3	0.2808	-0.2808
g4507864_3p_at	VAMP8	0.2784	-0.2784
Hs.236894.0.A1_3p_at	LOC146795	0.2746	-0.2746
Hs.18376.0.S1_3p_a_at	CGN	0.2741	-0.2741
g10190675_3p_a_at	RIPK4	0.2734	-0.2734
Hs.226562.0.S1_3p_at	EHF	0.2725	-0.2725
Hs.2.351442.2.S1_3p_at	RASEF	0.2689	-0.2689
g13129041_3p_at	PRKCH	0.2679	-0.2679
g9507120_3p_a_at	SLC37A1	0.2676	-0.2676
g13876385_3p_s_at	EPPK1	0.2674	-0.2674
Hs.30942.0.S3_3p_at	EFNB2	0.2614	-0.2614
Hs.2.145582.3.S1_3p_s_at	PROM2	0.2613	-0.2613
Hs.23071.0.A1_3p_at	STON2	0.2613	-0.2613
Hs.105959.0.A1_3p_at	PGM2L1	0.2538	-0.2538
g12056467_3p_a_at	JUP	0.2526	-0.2526
g4758287_3p_at	EPHB3	0.2494	-0.2494
Hs.18878.0.A1_3p_a_at	EGLN3	0.245	-0.245
Hs.184581.0.A1_3p_at	RPS6KA2	0.2442	-0.2442
g340300_3p_a_at	VEGF	0.2406	-0.2406
g4502040_3p_at	ALDH1A3	0.2349	-0.2349
g4826983_3p_a_at	ROD1	0.2288	-0.2288
Hs.21420.0.S2_3p_s_at	PAK6	0.226	-0.226
Hs.2.2719.5.A1_3p_s_at	WFDC2	0.2252	-0.2252
Hs.23317.0.A1_3p_at	TMEM87B	0.2243	-0.2243
Hs.201661.0.A1_3p_at	PLEKHA7	0.2226	-0.2226
g9964114_3p_a_at	SP110	0.2222	-0.2222
Hs.2.98573.1.S1_3p_x_at	C6orf141	0.2184	-0.2184
Hs.71779.0.S1_3p_at	C19orf21	0.2183	-0.2183
g7328555_3p_a_at	TNFSF13	0.2182	-0.2182
g5901560_3p_s_at	VEGF	0.2135	-0.2135
Hs.77348.0.S1_3p_a_at	HPGD	0.2122	-0.2122
Hs.25740.0.S1_3p_a_at	ERO1L	0.2112	-0.2112
Hs.137313.0.A1_3p_at	SPINT1	0.2096	-0.2096
Hs.200412.0.S1_3p_at	EPPK1	0.2059	-0.2059
g4557252_3p_a_at	ADAM8	0.2051	-0.2051
Hs.67928.0.A1_3p_at	ELF3	0.2035	-0.2035
Hs.19978.5.S1_3p_a_at	ARSD	0.2033	-0.2033
Hs.23881.1.A1_3p_at	KRT7	0.2029	-0.2029
g1203981_3p_a_at	HPGD	0.2027	-0.2027
g12804234_3p_a_at	CYB561	0.2017	-0.2017

Hs.49136.0.A1_3p_at	FAM84B	0.1993	-0.1993
209771_3p_x_at	CD24	0.1973	-0.1973
g13236537_3p_at	FA2H	0.1947	-0.1947
g13124448_3p_a_at	F11R	0.1935	-0.1935
g4557296_3p_a_at	ALAD	0.1927	-0.1927
Hs.135643.0.A1_3p_at	EMG1	0.1908	-0.1908
Hs.95612.0.A1_3p_at	DSC2	0.1901	-0.1901
g1695875_3p_s_at	IL13RA1	0.1896	-0.1896
Hs.286124.0.A2_3p_s_at	CD24	0.1862	-0.1862
g7706171_3p_at	TNFRSF21	0.1858	-0.1858
Hs.296259.0.S1_3p_at	PON3	0.1837	-0.1837
1554246_3p_at	C1orf210	0.1817	-0.1817
Hs.67776.0.A1_3p_at	FAM83H	0.1815	-0.1815
g4504038_3p_at	GNA15	0.1806	-0.1806
g3719220_3p_a_at	VEGF	0.1801	-0.1801
g899458_3p_a_at	YWHAZ	0.1788	-0.1788
g13111771_3p_a_at	ARHGEF10L	0.1787	-0.1787
g12053164_3p_at	SLC41A2	0.1727	-0.1727
Hs.122244.0.A1_3p_at	C1orf116	0.1717	-0.1717
Hs.234786.0.A1_3p_at	ACOT11	0.1711	-0.1711
g4505198_3p_at	NR3C2	0.1711	-0.1711
Hs2.149377.1.S1_3p_at	KIAA1217	0.1691	-0.1691
g2047312_3p_a_at	HPGD	0.167	-0.167
g6382072_3p_at	GCHFR	0.1647	-0.1647
Hs.162189.1.S1_3p_at	KALRN	0.163	-0.163
g4504706_3p_at	INPP4B	0.1621	-0.1621
g4506954_3p_a_at	ST3GAL5	0.1596	-0.1596
Hs.65641.1.A1_3p_at	SAMD9	0.1589	-0.1589
g7657308_3p_at	LMCD1	0.1589	-0.1589
208651_3p_x_at	CD24	0.1586	-0.1586
Hs.149018.0.S1_3p_at	WFDC3	0.1577	-0.1577
Hs2.397084.1.S1_3p_at	TMEM49	0.1559	-0.1559
g7657036_3p_at	DOC1	0.1535	-0.1535
L33930_3p_s_at	CD24	0.1535	-0.1535
Hs.57876.0.A1_3p_at	AMDD	0.1475	-0.1475
Hs.166011.3.A1_3p_a_at	CTNND1	0.1458	-0.1458
Hs2.14894.2.S1_3p_at	TGOLN2	0.1453	-0.1453
g8922916_3p_a_at	MCTP2	0.1451	-0.1451
g4503112_3p_at	CST6	0.143	-0.143
Hs.81800.4.A1_3p_a_at	CSPG2	0.1414	-0.1414
g12654424_3p_s_at	EPN3	0.1406	-0.1406
Hs.145078.1.A1_3p_at	ROD1	0.139	-0.139
218779_3p_x_at	EPS8L1	0.139	-0.139
Hs.19978.5.S2_3p_at	ARSD	0.1364	-0.1364
Hs.323164.0.S1_3p_a_at	CHCHD7	0.1361	-0.1361
g7305226_3p_at	TMC6	0.1328	-0.1328
g9506670_3p_a_at	FLJ20273	0.1324	-0.1324
Hs.104476.0.A1_3p_at	TMEM125	0.1323	-0.1323
208083_3p_s_at	ITGB6	0.1304	-0.1304
Hs.25978.0.A1_3p_at	PRRG4	0.1264	-0.1264
g4504164_3p_a_at	GSN	0.1258	-0.1258
g7705942_3p_a_at	C5orf4	0.124	-0.124
Hs.6390.1.A1_3p_at	DKFZP779L1068	0.1235	-0.1235
Hs.50964.3.S2_3p_at	CEACAM1	0.1182	-0.1182

g4929600_3p_a_at	CAB39	0.1176	-0.1176
Hs.109012.1.A1_3p_x_at	MXD1	0.1145	-0.1145
Hs.278628.0.S1_3p_at	SHROOM3	0.1138	-0.1138
g7656943_3p_at	LYPD3	0.1108	-0.1108
Hs.174104.0.S1_3p_at	RALGPS2	0.1101	-0.1101
g5031846_3p_at	LAMC2	0.1095	-0.1095
g7657068_3p_a_at	ERO1L	0.1082	-0.1082
g4557424_3p_at	ENTPD3	0.1077	-0.1077
228531_3p_at	SAMD9	0.1038	-0.1038
g4758287_3p_x_at	EPHB3	0.1024	-0.1024
Hs.272556.0.S2_3p_s_at	PADI1	0.1022	-0.1022
g11496995_3p_at	ADAM28	0.1021	-0.1021
Hs.112184.1.A1_3p_at	TMC4	0.1012	-0.1012
Hs.197751.0.A1_3p_at	DAAM1	0.1009	-0.1009
g7706701_3p_at	IL23A	0.1006	-0.1006
g3978241_3p_at	SNN	0.0992	-0.0992
Hs.83484.0.S1_3p_at	SOX4	0.0987	-0.0987
g5454161_3p_a_at	TXNIP	0.0982	-0.0982
Hs.57787.0.A1_3p_at	MTAC2D1	0.0978	-0.0978
Hs.2.14894.2.S1_3p_x_at	TGOLN2	0.0974	-0.0974
g9845499_3p_at	LAMC2	0.0974	-0.0974
g4758679_3p_a_at	LLGL2	0.097	-0.097
g5031992_3p_a_at	PRSS16	0.0954	-0.0954
Hs.172458.4.S1_3p_a_at	IDS	0.0922	-0.0922
1553114_3p_a_at	PTK6	0.0917	-0.0917
Hs.197751.2.S1_3p_a_at	DAAM1	0.0904	-0.0904
g4502722_3p_at	CDH3	0.0903	-0.0903
Hs.61311.0.A1_3p_at	CAPN8	0.0903	-0.0903
Hs.7946.0.S3_3p_a_at	MTUS1	0.088	-0.088
Hs.160483.0.S2_3p_a_at	STOM	0.0873	-0.0873
Hs.45008.0.S1_3p_at	CEACAM19	0.0863	-0.0863
207291_3p_at	PRRG4	0.0853	-0.0853
Hs.738.3.A1_3p_at	S100A16	0.081	-0.081
Hs.323567.0.A2_3p_at	SCARB2	0.0799	-0.0799
g7019410_3p_at	HOOK2	0.0786	-0.0786
g4502748_3p_at	CDKN2A	0.0771	-0.0771
Hs.193341.0.A1_3p_at	APRIN	0.075	-0.075
g8272417_3p_a_at	KLF5	0.0725	-0.0725
Hs.62643.0.S1_3p_a_at	DAPP1	0.0717	-0.0717
g7662329_3p_s_at	ABLIM3	0.0715	-0.0715
Hs.159651.0.S2_3p_x_at	TNFRSF21	0.071	-0.071
Hs.2.210473.1.S1_3p_s_at	SCIN	0.0691	-0.0691
g13129073_3p_at	PRRG4	0.0651	-0.0651
Hs.16578.0.A1_3p_at	PDE5A	0.0635	-0.0635
g4758943_3p_at	REPS2	0.0627	-0.0627
g8922660_3p_at	LRRC1	0.0611	-0.0611
g4504808_3p_s_at	JUNB	0.0603	-0.0603
Hs.217484.0.A1_3p_at	ANKRD22	0.0583	-0.0583
g12053382_3p_at	SLC40A1	0.0581	-0.0581
Hs.49657.1.A2_3p_at	ZNRF1	0.0568	-0.0568
g6912705_3p_at	PSD4	0.0567	-0.0567
Hs.62643.0.S2_3p_a_at	DAPP1	0.0555	-0.0555
g13487920_3p_a_at	KIAA1815	0.0547	-0.0547
g1256421_3p_a_at	PAK1	0.0546	-0.0546

g8922142_3p_at	KIF21B	0.0541	-0.0541
g13129073_3p_x_at	PRRG4	0.0541	-0.0541
Hs.234101.0.A1_3p_at	SLC44A3	0.0534	-0.0534
Hs.154365.0.S1_3p_at	ELF1	0.0527	-0.0527
Hs.73793.2.S2_3p_a_at	VEGF	0.0505	-0.0505
g10518500_3p_a_at	F5	0.0494	-0.0494
g2598967_3p_a_at	SPINT2	0.0492	-0.0492
g4826753_3p_at	FGFBP1	0.048	-0.048
Hs.40342.2.S1_3p_a_at	TRIOBP	0.0479	-0.0479
Hs.49657.0.A1_3p_at	ZNRF1	0.047	-0.047
g4826867_3p_a_at	ROR1	0.0461	-0.0461
Hs.44343.0.A1_3p_at	ATP8B1	0.0461	-0.0461
Hs.279607.3.A1_3p_at	ROD1	0.0442	-0.0442
Hs.184050.1.A1_3p_a_at	KRAS	0.043	-0.043
Hs.83484.0.S3_3p_x_at	SOX4	0.0423	-0.0423
g11545921_3p_at	IFIH1	0.0422	-0.0422
Hs.45192.0.S1_3p_at	TSGA10	0.0422	-0.0422
Hs.169238.3.A1_3p_a_at	FUT3	0.0419	-0.0419
Hs.83484.1.S1_3p_a_at	SOX4	0.0408	-0.0408
g2735848_3p_a_at	EDG4	0.0399	-0.0399
Hs.22902.0.A1_3p_at	ZBTB25	0.0397	-0.0397
Hs.289005.0.S1_3p_at	TJP2	0.0388	-0.0388
224558_3p_s_at	MALAT1	0.0386	-0.0386
Hs.101799.0.A1_3p_s_at	B3GNT5	0.0379	-0.0379
g4503802_3p_at	FUCA1	0.0377	-0.0377
g8923080_3p_a_at	SAMD9	0.0375	-0.0375
g12043713_3p_a_at	FOXP1	0.0373	-0.0373
Hs.183109.1.S1_3p_at	MAOA	0.0366	-0.0366
g625085_3p_s_at	MET	0.0358	-0.0358
g6996011_3p_at	GBP2	0.0347	-0.0347
1557448_3p_a_at	RPL41	0.0342	-0.0342
g11907929_3p_a_at	NRP2	0.0339	-0.0339
g4502174_3p_at	SHROOM2	0.0333	-0.0333
Hs.179526.0.S2_3p_a_at	TXNIP	0.0323	-0.0323
g4505792_3p_a_at	SERPINA1	0.0321	-0.0321
Hs.57837.0.A1_3p_at	TMTC2	0.0319	-0.0319
g4885348_3p_a_at	GRK5	0.0304	-0.0304
Hs.83484.0.S3_3p_at	SOX4	0.0292	-0.0292
g12006357_3p_a_at	TRIOBP	0.0272	-0.0272
Hs.183765.0.A1_3p_at	UCA1	0.0259	-0.0259
g5174646_3p_at	PTK6	0.0251	-0.0251
Hs.159651.0.S2_3p_at	TNFRSF21	0.0246	-0.0246
Hs.26765.0.S1_3p_at	LOC58489	0.0239	-0.0239
g11386170_3p_at	CEACAM5	0.0234	-0.0234
Hs.21599.0.S2_3p_at	KLF7	0.0233	-0.0233
Hs.6975.2.A2_3p_s_at	MALAT1	0.0185	-0.0185
g4959037_3p_at	RASD1	0.0177	-0.0177
g5817105_3p_s_at	TSC22D3	0.017	-0.017
Hs.81800.0.S2_3p_a_at	CSPG2	0.0169	-0.0169
Hs2.352326.1.S1_3p_a_at	CBR3	0.0166	-0.0166
g10835001_3p_at	ARHGDIB	0.0161	-0.0161
Hs.96427.0.S1_3p_x_at	FRMD4B	0.0157	-0.0157
g9845517_3p_at	S100A6	0.0153	-0.0153
Hs2.334568.1.S1_3p_at	ZNF626	0.0152	-0.0152

g10518499_3p_at	F3	0.0141	-0.0141
Hs.172458.0.S2_3p_s_at	IDS	0.0138	-0.0138
g4885208_3p_a_at	EPHA1	0.0135	-0.0135
g4505896_3p_at	PLS1	0.0133	-0.0133
Hs.124740.0.A1_3p_at	TAF9	0.0123	-0.0123
g13477352_3p_s_at	RPH3AL	0.0116	-0.0116
Hs.105509.1.S2_3p_at	SLC44A2	0.0113	-0.0113
Hs.272068.0.S1_3p_at	FAM83A	0.0096	-0.0096
Hs.109012.1.A1_3p_at	MXD1	0.0088	-0.0088
g5453622_3p_at	CNKSR1	0.0085	-0.0085
Hs.170218.0.A1_3p_at	KIAA0251	0.0079	-0.0079
Hs.125343.0.A1_3p_at	GPR110	0.0071	-0.0071
Hs.286124.1.A1_3p_s_at	CD24	0.0062	-0.0062
g9845517_3p_x_at	S100A6	0.0062	-0.0062
g13376358_3p_a_at	DENND2D	0.0046	-0.0046
207517_3p_at	LAMC2	0.0038	-0.0038
g7262371_3p_at	BIK	0.0037	-0.0037
Hs.182536.0.S1_3p_s_at	KIAA0284	0.002	-0.002
Hs.238030.1.S1_3p_x_at	SCAMP2	0.0011	-0.0011
g220150_3p_x_at	AZGP1	9.00E-04	-9.00E-04
Hs.44021.0.S1_3p_at	BMF	8.00E-04	-8.00E-04
Hs.183861.0.S1_3p_at	CHMP4C	7.00E-04	-7.00E-04
Hs.6616.0.A1_3p_at	HNRPU	-8.00E-04	8.00E-04
Hs.89868.0.A1_3p_at	SLC39A14	-0.003	0.003
4876811C_3p_x_at	PARVB	-0.0039	0.0039
g4885454_3p_at	SH2B3	-0.0068	0.0068
Hs.88045.0.A1_3p_at	FLJ45482	-0.0073	0.0073
Hs.1565.0.S1_3p_at	NEDD4	-0.0077	0.0077
Hs.5151.0.S5_3p_at	IPO7	-0.0089	0.0089
g13540568_3p_s_at	SGPP1	-0.0106	0.0106
g12652938_3p_a_at	USP47	-0.0107	0.0107
Hs.136857.0.S1_3p_at	HIST1H1D	-0.0118	0.0118
Hs.748.8.A1_3p_at	FGFR1	-0.0127	0.0127
4902565C_3p_at	MRC2	-0.0198	0.0198
Hs.1494.1.A1_3p_at	MSX1	-0.0199	0.0199
g4503698_3p_s_at	FGF2	-0.0224	0.0224
g4507426_3p_s_at	TEAD4	-0.0287	0.0287
Hs.281895.0.S1_3p_x_at	AGPAT5	-0.029	0.029
Hs.72160.0.S2_3p_at	WDHD1	-0.0292	0.0292
Hs.201769.0.A1_3p_at	B4GALT6	-0.0296	0.0296
Hs.11390.0.S1_3p_at	TTC28	-0.0322	0.0322
Hs.184771.1.S1_3p_x_at	NFIC	-0.0326	0.0326
Hs.9195.1.S1_3p_x_at	RAPGEF1	-0.0343	0.0343
g11065969_3p_at	ZIC2	-0.0366	0.0366
Hs.26797.0.S1_3p_at	RAB6IP1	-0.0372	0.0372
Hs.201769.0.A1_3p_x_at	B4GALT6	-0.0398	0.0398
Hs2.389054.1.A1_3p_at	RECK	-0.041	0.041
g5031864_3p_at	LHFP	-0.0472	0.0472
Hs.48793.1.S2_3p_at	ST3GAL3	-0.0474	0.0474
Hs2.376912.1.S1_3p_at	MSRB3	-0.0482	0.0482
Hs.26425.0.A1_3p_at	HNRPU	-0.0493	0.0493
Hs.302738.0.S1_3p_at	SLC26A2	-0.0493	0.0493
g182984_3p_a_at	PMP22	-0.0548	0.0548
g7661529_3p_at	MAGEH1	-0.0559	0.0559

g4809281_3p_s_at	BMP6	-0.0588	0.0588
g11641296_3p_at	ROBO3	-0.0596	0.0596
Hs.43761.1.A1_3p_at	GJA7	-0.0609	0.0609
Hs.134069.0.A1_3p_at	TMEM20	-0.0616	0.0616
230110_3p_at	MCOLN2	-0.062	0.062
Hs.301957.0.A2_3p_at	SEC61A2	-0.0642	0.0642
g4758593_3p_at	IL11RA	-0.0645	0.0645
g7705982_3p_at	COPZ2	-0.0646	0.0646
Hs.117929.0.A1_3p_at	UNKNOWN/INVALID SYMBOL:(642705)	-0.0648	0.0648
Hs.12772.0.S1_3p_at	NIN	-0.0657	0.0657
Hs.42927.0.S1_3p_at	ANTXR1	-0.0677	0.0677
g8922910_3p_at	RSAD1	-0.0721	0.0721
Hs.259855.0.S3_3p_at	EEF2K	-0.0722	0.0722
Hs.238272.0.A2_3p_at	ITPR2	-0.0728	0.0728
Hs2.321261.1.S1_3p_s_at	C14orf135	-0.0756	0.0756
g8922811_3p_a_at	CWF19L1	-0.0826	0.0826
Hs.32556.0.S1_3p_at	ANKRD28	-0.0861	0.0861
241864_3p_x_at	PPP4R2	-0.1032	0.1032
Hs.18653.0.S2_3p_at	TMEM118	-0.1078	0.1078
Hs.24678.0.S2_3p_at	SGPP1	-0.1137	0.1137
g12653240_3p_x_at	TSPAN4	-0.1145	0.1145
g7657497_3p_at	RAGE	-0.1163	0.1163
Hs.35092.0.A1_3p_at	MSRB3	-0.1199	0.1199
Hs.17154.0.S1_3p_at	DYRK4	-0.1212	0.1212
Hs.100292.0.A1_3p_at	FLJ36166	-0.1261	0.1261
Hs.55950.0.S1_3p_at	ALPK2	-0.1308	0.1308
Hs.31685.0.A1_3p_at	BCAP29	-0.1315	0.1315
g13375863_3p_at	C14orf139	-0.1316	0.1316
4858229C_3p_at	CSPG5	-0.1317	0.1317
Hs.19762.0.S1_3p_at	TTC7B	-0.1323	0.1323
Hs.12896.0.S1_3p_at	SATB2	-0.1357	0.1357
Hs.232068.2.A1_3p_s_at	TCF8	-0.1358	0.1358
37966_3p_at	PARVB	-0.1451	0.1451
g4505266_3p_at	MSX1	-0.1497	0.1497
4876812C_3p_x_at	PARVB	-0.1546	0.1546
Hs.173051.0.A2_3p_x_at	SLC35B4	-0.1567	0.1567
Hs.29019.0.A1_3p_at	OSTM1	-0.1575	0.1575
Hs.134156.0.A1_3p_at	IKIP	-0.1622	0.1622
Hs.21255.0.A1_3p_at	SFXN1	-0.1634	0.1634
g12407394_3p_at	TRIM7	-0.1652	0.1652
g8922402_3p_a_at	KIAA1212	-0.1653	0.1653
Hs.30936.0.A1_3p_at	MGC39900	-0.1693	0.1693
Hs.35841.2.S1_3p_at	NFIX	-0.173	0.173
g12654386_3p_at	PDLIM3	-0.1804	0.1804
Hs.34892.0.S4_3p_at	MIB1	-0.1858	0.1858
Hs.288368.0.A2_3p_at	MLSTD2	-0.2038	0.2038
g11863155_3p_at	RECK	-0.2051	0.2051
Hs2.385650.1.S1_3p_at	LOC401068	-0.2107	0.2107
Hs.12319.0.S1_3p_x_at	ALS2CR4	-0.2192	0.2192
g4506044_3p_at	PRG1	-0.2212	0.2212
4876812C_3p_at	PARVB	-0.2214	0.2214
Hs.303084.0.S3_3p_at	APLN	-0.249	0.249
g7661737_3p_at	OSTM1	-0.2662	0.2662
Hs.124707.0.A1_3p_at	FAM101B	-0.2671	0.2671

Hs.50724.1.A1_3p_s_at	LOC541471	-0.2795	0.2795
Hs.71523.0.A1_3p_at	IKIP	-0.2827	0.2827
Hs.232400.1.S1_3p_s_at	HNRPA2B1	-0.2901	0.2901
Hs.99263.0.A1_3p_at	RHOT1	-0.3145	0.3145
Hs.159475.0.S1_3p_at	LOC153346	-0.323	0.323
g10441414_3p_a_at	DYRK3	-0.3376	0.3376
Hs.12451.0.S2_3p_at	EML1	-0.3496	0.3496
Hs.158923.0.S1_3p_at	RYK	-0.3512	0.3512
g7661737_3p_x_at	OSTM1	-0.3576	0.3576
Hs.171637.0.A3_3p_at	KCTD15	-0.3619	0.3619
Hs.65264.0.A1_3p_at	PAX6	-0.3767	0.3767
g4505866_3p_a_at	PLCB4	-0.3869	0.3869
Hs.145365.0.S2_3p_at	WDR35	-0.3869	0.3869
g1458119_3p_a_at	CHRNA7	-0.3871	0.3871
Hs.97600.0.A1_3p_at	PPP4R2	-0.3898	0.3898
Hs.187932.0.A1_3p_at	FAM101B	-0.3906	0.3906
Hs.303090.1.A1_3p_at	LIX1L	-0.3965	0.3965
Hs.283006.0.S2_3p_at	PLCB4	-0.4027	0.4027
g4501882_3p_s_at	ACTA2	-0.4113	0.4113
Hs.12319.0.S1_3p_at	ALS2CR4	-0.4134	0.4134
g4506140_3p_at	HTRA1	-0.4142	0.4142
Hs.105621.0.S1_3p_at	ABP1	-0.4243	0.4243
Hs.8966.0.A1_3p_at	ANTXR1	-0.4492	0.4492
g4809274_3p_a_at	ANXA6	-0.4636	0.4636
Hs.12385.1.S1_3p_at	HSPA12A	-0.4694	0.4694
Hs2.407360.1.A1_3p_s_at	MAGEE1	-0.4877	0.4877
216272_3p_x_at	SYDE1	-0.4892	0.4892
218196_3p_at	OSTM1	-0.4901	0.4901
g4758267_3p_a_at	EML1	-0.5204	0.5204
Hs.128751.0.S1_3p_at	TUB	-0.5238	0.5238
g4507086_3p_at	SMARCD3	-0.5303	0.5303
g8922558_3p_at	NUDT11	-0.5377	0.5377
g12653878_3p_a_at	SYNGR1	-0.5578	0.5578
g4505614_3p_s_at	PAX6	-0.5814	0.5814
Hs.86178.1.S1_3p_a_at	MPHOSPH9	-0.6728	0.6728
Hs.123022.0.S2_3p_at	ADRA2C	-0.7053	0.7053
Hs.170337.0.A1_3p_at	TXNRD1	-0.7162	0.7162
Hs2.399761.1.S1_3p_at	MPHOSPH9	-0.7232	0.7232
Hs.35092.0.A2_3p_at	MSRB3	-0.7408	0.7408
Hs.6728.0.S1_3p_at	EPB41L5	-0.7513	0.7513
Hs.154145.3.A1_3p_at	MPPE1	-0.8687	0.8687
g4759125_3p_at	SLC1A3	-0.8725	0.8725
Hs.9291.0.S1_3p_s_at	SYDE1	-0.9064	0.9064
Hs.133878.0.A1_3p_s_at	MSRB3	-1.1698	1.1698
Hs.46919.0.S1_3p_at	LOC439949	-1.4256	1.4256
g8922708_3p_at	FLJ10847	-1.6416	1.6416

Supplementary Table 2. The RNAi Consortium (TRC) Clone Names and target sequences for shRNA vectors used in this study.

Clone Name	Designation	Sequence	Target Region
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NM_002485.3-705s1c1	Control sh	CCTCTTGATGAACCATCTATT	CDS
NM_004985.3-570s1c1	shK-RasA	CTCAGGACTTAGCAAGAAGTT	CDS
NM_033360.2-269s1c1	shK-RasB	GACGAATATGATCCAACAATA	CDS
NM_004985.x-1160s1c1	shK-RasC	CAGTTGAGACCTTCTAATTGG	3' UTR
NM_000888.3-2128s1c1	shITGB6-A	GCCTCCAAACATTCCCATGAT	CDS
NM_000888.3-659s1c1	shITGB6-B	CCATTGACAAATGATGCTGAA	CDS
NM_144590.1-917s1c1	shANKRD22-A	CCATGGCCGTAATCCTTCTAA	CDS
NM_144590.1-504s1c1	shANKRD22-B	CTTGTACGAATGCTACTTGAT	CDS
NM_003177.3-245s1c1	shSYK-A	GCATGAGTGATGGGCTTTATT	CDS
NM_003177.x-579s1c1	shSYK-B	GCAGGCCATCATCAGTCAGAA	CDS
NM_002447.x-609s1c1	shMST1R-A	CCTCCTATTTCTACGTGGCAT	CDS
NM_002447.x-4136s1c1	shMST1R-B	GAGATGAATGTGCGTCCAGAA	CDS
NM_030751.2-3706s1c1	shZeb1	GCAACAATACAAGAGGTAAA	3' UTR
