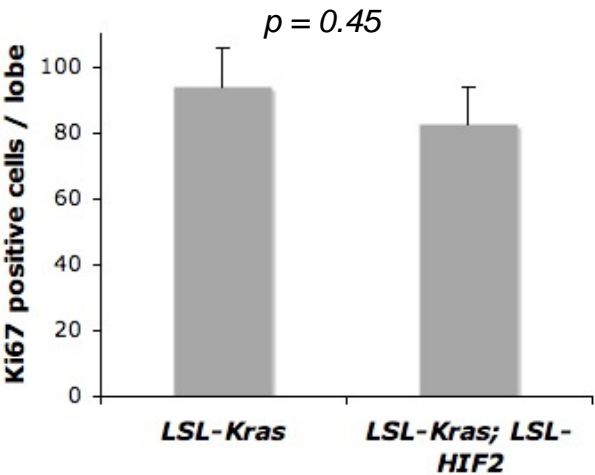
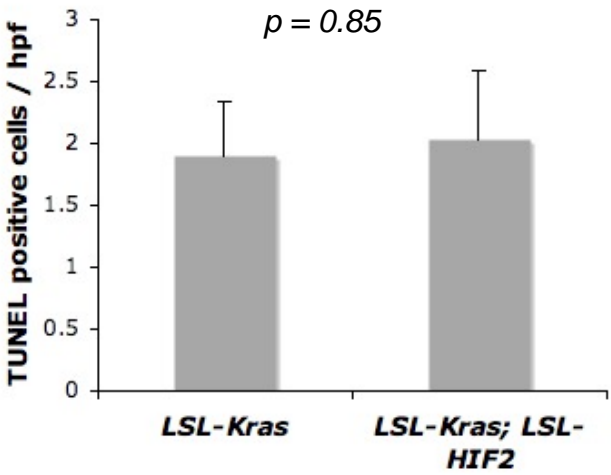


# Supplemental Figure 1.

**A**



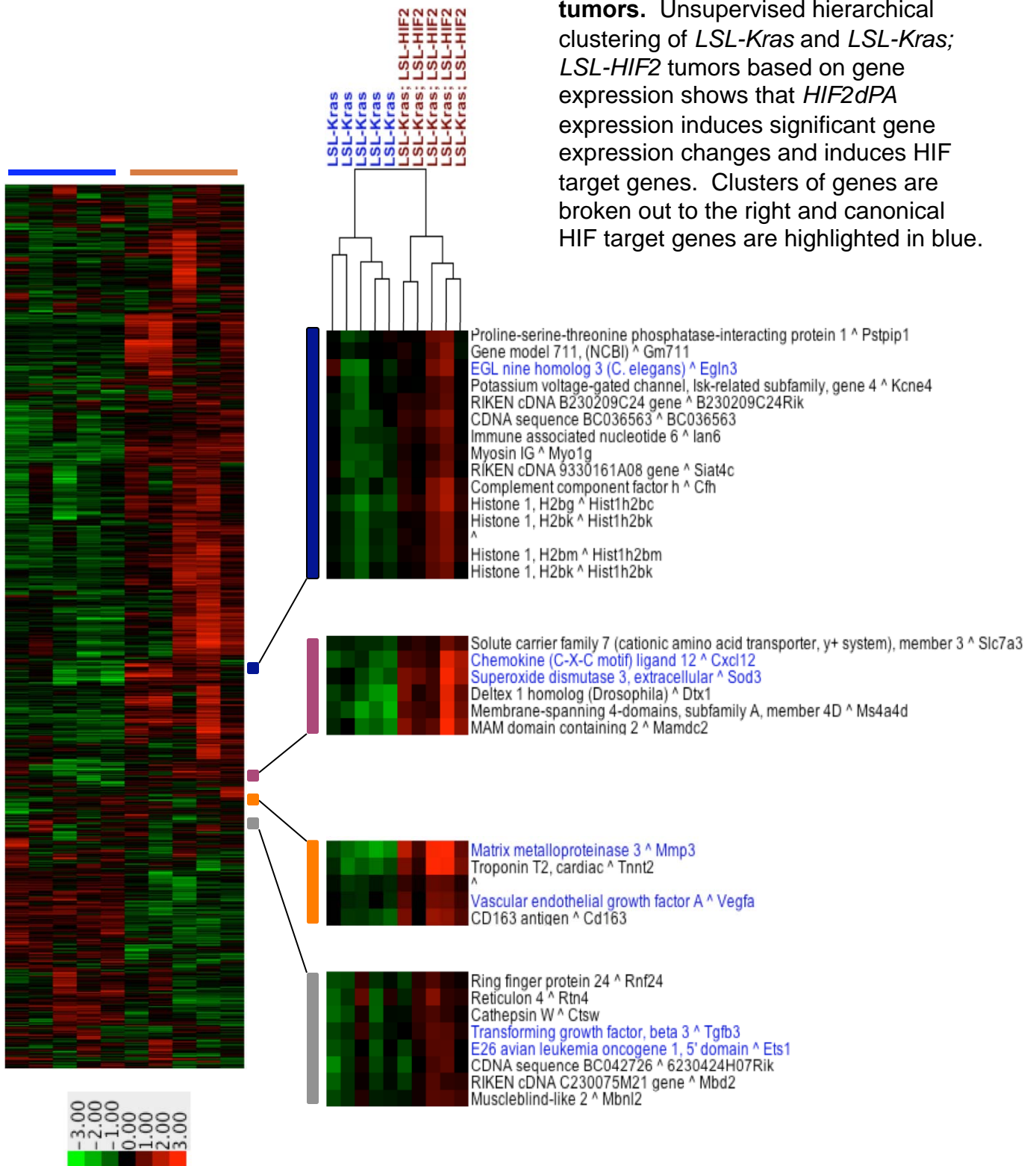
**B**



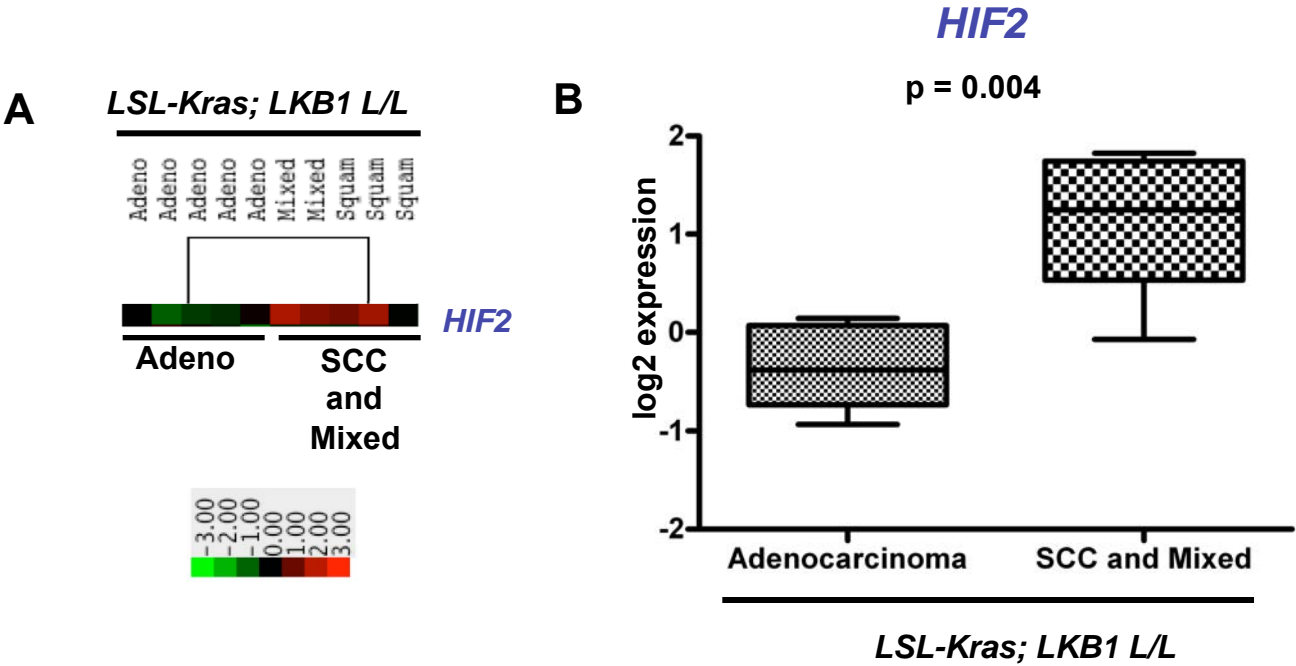
**Supplemental Figure 1. HIF2 $\alpha$  production in tumors does not increase proliferation or apoptosis. A)** Quantification of Ki67+ tumor cells. Error bars = 1 SEM ( $p = 0.45$ ). **B)** Quantification of TUNEL+ tumor cells. Error bars = 1 SEM ( $p = 0.85$ ).

## Supplemental Figure 2.

**Supplemental Figure 2. *HIF2dPA* expression induces gene expression changes in *Kras*-induced lung tumors.** Unsupervised hierarchical clustering of *LSL-Kras* and *LSL-Kras; LSL-HIF2* tumors based on gene expression shows that *HIF2dPA* expression induces significant gene expression changes and induces HIF target genes. Clusters of genes are broken out to the right and canonical HIF target genes are highlighted in blue.



**Supplemental Figure 3.**



**Supplemental Figure 3. HIF2 $\alpha$  is associated with squamous differentiation.**  
**(A,B)** The relative gene expression of HIF2 $\alpha$  in *Kras*-induced, *LKB1*-deficient adenocarcinomas versus squamous cell or mixed (adeno-squamous) carcinomas is shown visually **(A)** and graphically **(B)**, p = 0.004].

## Supplemental Figure 4.

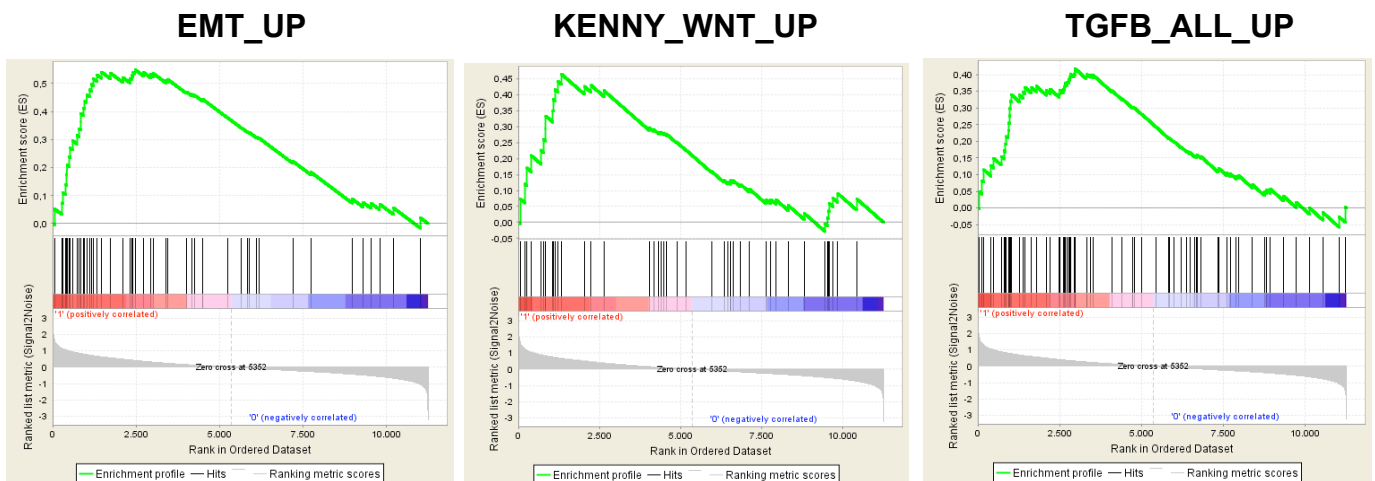
A

### Gene sets enriched in HIF2 $\alpha$ producing tumors

Signature	NOM p-val	FDR q-val
EMT_UP	0.000	0.000
YU_C-MYC_DOWN	0.000	0.000
JECHLINGER_EMT_UP	0.000	0.001
CORDERO_KRAS_KD_VS_CONTROL_UP	0.002	0.002
Coller_Myc_DOWN	0.000	0.004
LEE_E2F1_UP	0.003	0.009
WNT/TGFB_UP	0.000	0.012
STEMCELL_COMMON_DOWN	0.005	0.013
KENNY_WNT_UP	0.007	0.016
Lamb_cyclinD1_DOWN	0.000	0.022
TGFB_ALL_UP	0.005	0.023
COLLER_MYC_DOWN	0.006	0.025
H3K27_targets	0.000	0.032
PRC2_targets	0.001	0.044

Gene sets enriched in LSL-Kras; LSL-HIF2 tumors

B



**Supplemental Figure 4. Gene sets enriched in HIF2 $\alpha$  producing tumors. A)** The fourteen gene signatures that were found to be enriched in HIF2 $\alpha$  producing tumors relative to their mutant *Kras* controls using a false discovery rate (FDR) calculation ( $p < 0.05$ ) to account for multiple hypothesis testing. **B)** Representative GSEA enrichment plots of EMT, b-catenin, and TGFB gene signatures.

<u>HIF2 UP 200genes</u>	<u>EMT UP</u>	<u>KENNY WNT UP</u>	<u>TGFBETA ALL UP</u>	Supplemental Table 1
AAK1	ADA	ACTN4	ADAM9	
ABI3	ADSSL1	AES	ARHGAP1	
ACAS2L	ASNS	AGRN	ARHGDIA	
ACIN1	B2M	ALG3	BSG	
ADAMTS8	BCL3	ARHGDIA	CD44	
ADAMTSL2	CD68	ATP6V0A1	CD59	
ADH1	CDH15	BCAP31	CDH6	
AGA	CDH2	CAPN1	COL16A1	
AIF1	CFH	CCND1	COL1A2	
AMY2	COL6A1	CD99	COL3A1	
ANXA6	COL6A2	CENTB1	COL6A1	
APLP1	CSN3	CPSF4	COL6A3	
APOBEC1	CTSZ	CTDSPL	COL8A1	
ARID5B	CXCL5	EIF5A	CSPG2	
ART3	CXCL6	ETS1	CTNNA1	
ASPN	CXCR7	EVA1	CTNNB1	
ATP6V0E	CYP1B1	FLOT2	DSP	
AW112010	DAB2	GJB1	DVL1	
BC026657	DCN	GLTSCR2	DVL3	
BHC80	DDR2	GNA12	EFNA5	
C1QA	FMO1	HDGF	EPHA2	
C1QB	GALK1	HMG20B	EPHB2	
C1QTNF5	GAS1	HNRPA0	EPHB3	
C1QTNF7	HIF1A	HNRPUL1	EPHB4	
CARD4	HTRA1	HSPE1	FGD1	
CAV3	IFIT1L	IFITM1	FN1	
CCL19	IFIT3	IMPDH2	HSPG2	
CD52	IFITM3	INE1	ICAM1	
CD83	IL11	KIAA0683	IGF2R	
CD86	INHBA	KRT5	IGFBP2	
CDC27	IRF7	KRT7	IGFBP3	
CDH11	ISG15	LMNA	IGFBP4	
CFH	LAMB1	LOC492304	IGFBP5	
CFH	MMP12	LY6E	ITGA3	
CFH	MMP13	MAP3K11	ITGA4	
CILP	MMP2	MMP14	ITGA5	
CKLFSF3	MTHFD2	MTA1	ITGB2	
CLCA3	PCOLCE	PCDH9	ITGB3	
COL14A1	PDGFRA	PCNA	ITGB5	
COL2A1	PDGFRB	PDAP1	ITGB8	
COLEC12	PHGDH	PFN1	JUP	
COMP	PLA2G7	PKP3	LAMA4	
CPXM1	PMP22	POLR2A	LAMB1	
CPXM2	PPIC	POLR2E	LRP1	
CREB3L3	PROCR	PRKCSH	LRRC17	
CRHR2	PTGS1	RAB1B	MARCKSL1	
CSRP3	PTPN22	RPL39L	MMP1	
CX3CR1	RNASET2	SCAP	MMP11	
CXCL10	RRAS	SEC61A1	MMP14	
CXCL13	S100A8	SF3A1	MMP17	
CXCL3	SDC2	SLC1A5	MMP19	
CYGB	SLC3A2	SYK	MMP2	

DAAM1	SLPI	TCF20	MMP3
DEPDC6	SNAI1	TGM2	MTA1
DSCAM	SPARC	UBE1	NEO1
DXBAY18	SRM	ZBTB7A	NID1
EBF2	STAT1		NOTCH2
ETOHI1	TNC		PAK1
ETV1	TNXB		PAK2
EXT1	UPP1		PLAT
FCGR2B	VIM		PXN
FCRL3	VLDLR		RAC1
FGD5			RHOA
FGL2			RHOB
GAL			RHOG
GPR124			RHOQ
GPR65			RND3
GRIT			SEMA3F
HDH			SERPINE1
HEYL			SMO
HIST1H2BC			SPARC
HPS4			TCF7L2
ICA1			THBS1
IFI205			THBS2
IGF1			TIMP1
IL10RA			TNC
IL18BP			TNFRSF1A
IL1B			WNT2B
IL2RG			WNT8B
ITCH			ZYX
ITGA1			
ITGB5			
ITM2C			
JAM3			
KCNMB2			
KCTD12			
KHDRBS3			
KLK11			
LEO1			
LRRC25			
LY86			
LY96			
MAMDC2			
MAN2A1			
MAN2A1			
MATN2			
MB			
MCTS1			
MDK			
MFAP5			
MMP3			
MRPL55			
MS4A4B			
MS4A4D			
MS4A6B			

MS4A6C  
MS4A7  
MTMR7  
MXRA7  
NAT5  
NCOA5  
NEB  
NEBL  
NFKBIE  
NMI  
NNMT  
NOX4  
NR4A2  
NRG1  
OCIL  
OXR1  
PACSIN3  
PAICS  
PDGFRL  
PDZK3  
PENK1  
PHLDB1  
PINX1  
PKIA  
PLAC8  
PLAC9  
PLCD1  
PLSCR4  
PLXDC2  
PPP1R14A  
PPP1R2  
PRG1  
PRICKLE2  
PRSS35  
PTGIR  
PTHR1  
PTPN8  
QPCTL  
RAB11FIP5  
RAD51L1  
RBP1  
RHOJ  
RNASE6  
RPGRIP1  
RTN1  
SERPINA3F  
SERPINA3G  
SLAMF6  
SLC12A6  
SLC16A9  
SLC35A5  
SLC7A2  
SLC7A3

SLC7A7  
SLIT3  
SLN  
SMARCE1  
SMFN  
SPEER4A  
SPEER4F  
SPON1  
STAG1  
STFA1  
STRA6  
SULF1  
TCF4  
TES3  
TFPI  
THY1  
TLR1  
TM4SF6  
TMIE  
TNFAIP6  
TNFAIP8  
TNFRSF5  
TNFSF13B  
TNNI2  
TPI1  
TREM2  
TRIM12  
TRIM16  
TRIM30  
TRIM56  
TRPM2  
TRSPAP1  
TSLPR  
TSPAN18  
UNC5A  
UNC93B1  
VPS37A  
VIM  
VTN  
WDFY4  
ZBP1  
ZFP262  
ZMYND15





LEE_MYC_E2F1_DN	MSigDB (broad.mit.edu/gsea/msigdb)
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LEE_MYC_TGFA_DN	MSigDB (broad.mit.edu/gsea/msigdb)
LEE_MYC_TGFA_UP	MSigDB (broad.mit.edu/gsea/msigdb)
LEE_MYC_UP	MSigDB (broad.mit.edu/gsea/msigdb)
YEN_MYC_MUT	MSigDB (broad.mit.edu/gsea/msigdb)
YEN_MYC_WT	MSigDB (broad.mit.edu/gsea/msigdb)
YU_CMYC_DN	MSigDB (broad.mit.edu/gsea/msigdb)
YU_CMYC_UP	MSigDB (broad.mit.edu/gsea/msigdb)
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CORDERO_KRAS_KD_VS_CONTROL_UP	MSigDB (broad.mit.edu/gsea/msigdb)
METASTASIS_ADENOCARC_DN	MSigDB (broad.mit.edu/gsea/msigdb)
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LEE_MYC_TGFA_UP	MSigDB (broad.mit.edu/gsea/msigdb)
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CHI_HYPOXIA_UP	MSigDB (broad.mit.edu/gsea/msigdb)
CHI_HYPOXIA_DN	MSigDB (broad.mit.edu/gsea/msigdb)
KO_CDH1	Onder et al., 2008
KO_CDH1_BCATENIN	Onder et al., 2009
ES1	Ben-Porath et al., 2008
ES2	Ben-Porath et al., 2008
Myc1_targets	Ben-Porath et al., 2008
Myc2_targets	Ben-Porath et al., 2008

Nanog_targets	Ben-Porath et al., 2008
OCT4_targets	Ben-Porath et al., 2008
Sox2_targets	Ben-Porath et al., 2008
NOS_targets	Ben-Porath et al., 2008
NOSTFs	Ben-Porath et al., 2008
Suz12_targets	Ben-Porath et al., 2008
Eed_targets	Ben-Porath et al., 2008
H3K27_targets	Ben-Porath et al., 2008
PRC2_targets	Ben-Porath et al., 2008
TCF3_Cole	Cole et al., 2008
OCT4_Cole	Cole et al., 2008
NANOG_Cole	Cole et al., 2008
TCF3/OCT4/NANOG_Cole	Cole et al., 2008
CORE9_TFs	Ben-Porath et al., 2008
MYC_NEVINS	Bild et al., 2006
E2F3_NEVINS	Bild et al., 2006
RAS_NEVINS	Bild et al., 2006
SRC_NEVINS	Bild et al., 2006
BCAT_NEVINS	Bild et al., 2006
Cell_cycle_Whitfield	Creighton et al., 2008
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Ras_up_Bild	Creighton et al., 2008
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Bcat_up_Bild	Creighton et al., 2008
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ERBB2_up_Creighton	Creighton et al., 2008
MEK_up_Creighton	Creighton et al., 2008
EGFR_up_Creighton	Creighton et al., 2008
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MAPK_up_Creighton	Creighton et al., 2008
cyclinD1_up_Lamb	Creighton et al., 2008
Akt_up_Majumder	Creighton et al., 2008
Myc_down_Coller	Creighton et al., 2008
Myc_down_Bild	Creighton et al., 2008
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E2F3_down_Bild	Creighton et al., 2008
Bild_down_Bild	Creighton et al., 2008

Src_down_Bild	Creighton et al., 2008
ERBB2_down_Creighton	Creighton et al., 2008
MEK_down_Creighton	Creighton et al., 2008
EGFR_down_Creighton	Creighton et al., 2008
Raf1_down_Creighton	Creighton et al., 2008
MAPK_down_Creighton	Creighton et al., 2008
cyclinD1_down_Lamb	Creighton et al., 2008
Akt_down_Majumder	Creighton et al., 2008

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