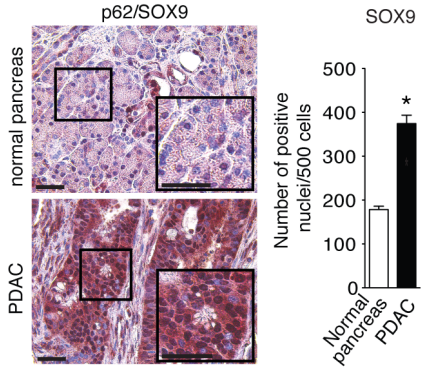
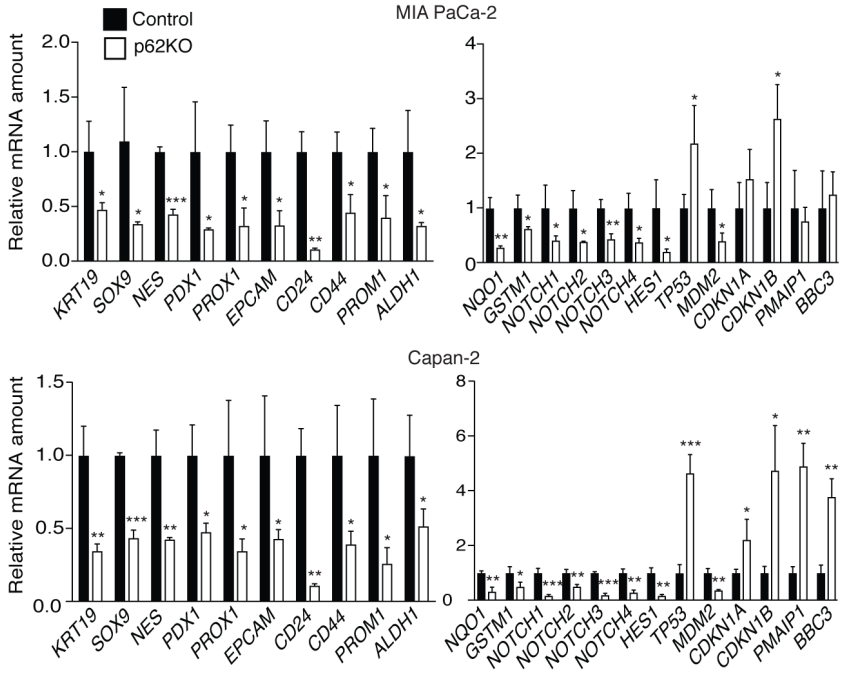
A

		Expression Intensity				
		negative	weak	intermediate	strong	
IKKα	Normal	0/64; 0%	6/64; 9%	23/64; 36%	35/64; 55%	*
	PDAC	8/79; 10%	21/79; 27%	42/79; 53%	8/79; 10%	
p62	Normal	19/82; 23%	19/82; 23%	37/82; 45%	7/82; 9%	*
	PDAC	5/87; 6%	12/87; 14%	29/87; 33%	41/87; 47%	
NQO1	Normal	19/47; 41%	8/47; 17%	18/47; 38%	2/47; 4%	*
	PDAC	1/64; 2%	4/64; 6%	34/64; 53%	25/64; 39%	
NRF2	Normal	12/67; 18%	30/67; 45%	21/67; 31%	4/67; 6%	*
	PDAC	0/86; 0%	15/86;17%	29/86; 34%	42/86; 49%	
MDM2	Normal	10/59; 17%	20/59; 33%	28/59; 47%	2/59; 3%	*
	PDAC	1/65; 2%	10/65;15%	25/65; 38%	29/65; 45%	

B



C



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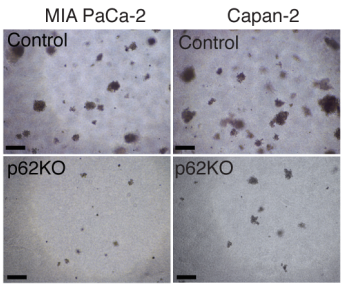
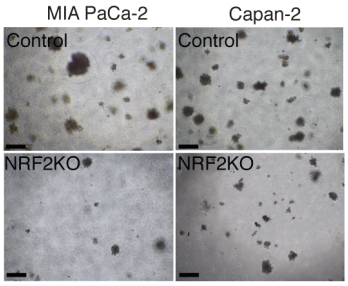
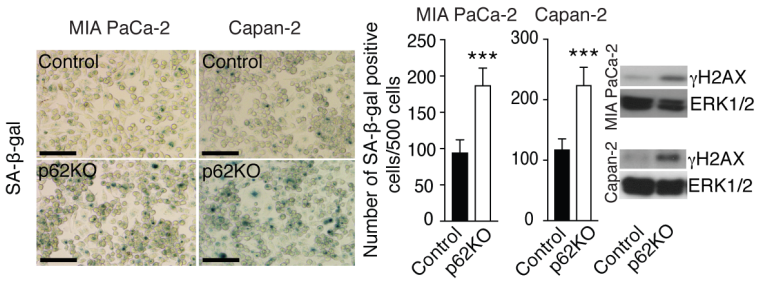


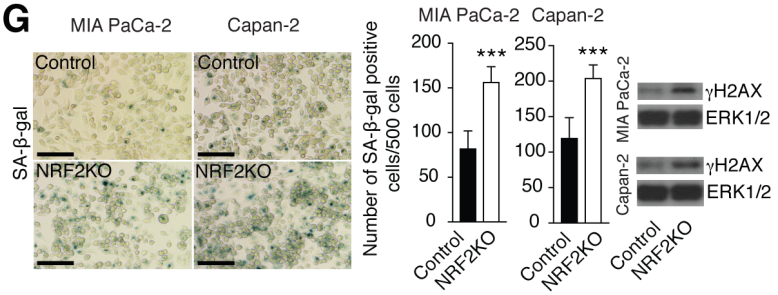
E



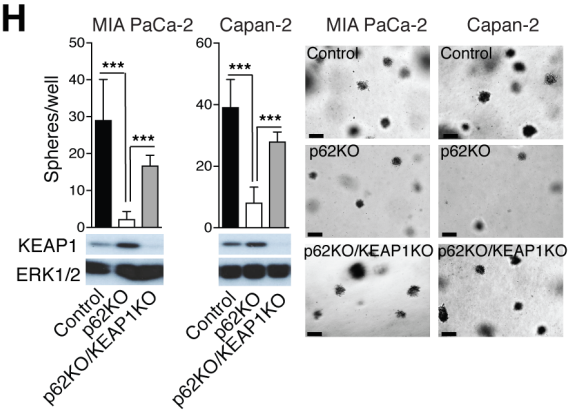
F



G



H



I

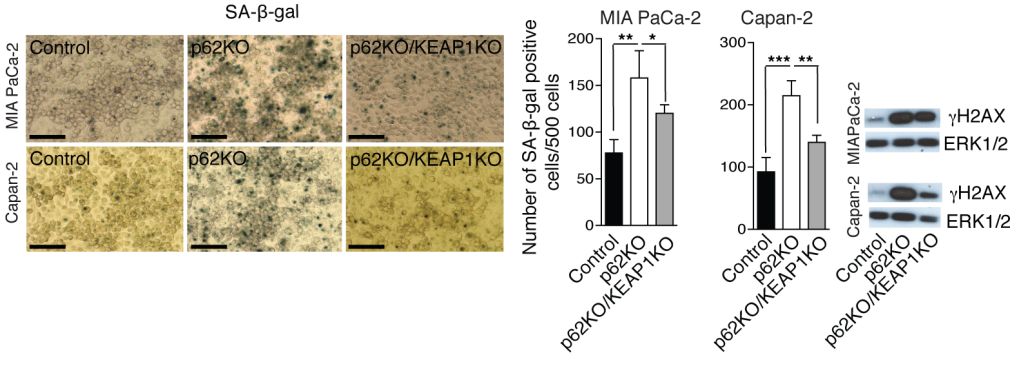


Figure S1 p62 Accumulates in Human PDAC and Its Depletion Decreases Progenitor and Cancer Stem Cell Markers, Related to Figure 1

(A) The table depicts the numbers and percentages of human cancerous (n = 64-87) or healthy (n = 47-82) pancreatic tissues with relative staining intensities (arbitrarily indicated as negative, weak, intermediate or strong) of the indicated markers. *, $p < 0.001$, normal vs. PDAC. (B) Sox9 and p62 double IHC staining of normal human pancreas and PDAC. Sox9 positive nuclei were visualized with DAB in brown and cytoplasmic p62 was stained with AEC (reddish). Quantitation of Sox9 staining is shown to the right (n = 52). Scale bars: 25 μm. (C) RNA was extracted from MIA PaCa-2 and Capan-2 cells in which p62 was ablated or not (n = 3). Expression of the indicated genes was analyzed by Q-RT-PCR. (D) Representative images of spheres formed by WT or p62-ablated MIA PaCa-2 and Capan-2 cells. Scale bars: 100 μm (E) Representative images of spheres formed by WT or NRF2-ablated MIA PaCa-2 and Capan-2 cells. Scale bars: 100 μm. (F) SA-β-gal staining of control and p62-ablated MIA PaCa-2 and Capan-2 cells (n = 6) and IB analysis of γ-H2AX. Scale bars: 100 μm. (G) SA-β-gal staining of control and NRF2-ablated MIA PaCa-2 and Capan-2 cells (n = 6) and IB analysis of γ-H2AX. Scale bars: 100 μm. (H) Quantification and representative images of spheres formed by WT and p62-ablated MIA PaCa-2 and Capan-2 cells with or without ablated KEAP1 and IB analysis of KEAP1. Scale bars: 100 μm. (I) Quantification and images of SA-β-gal staining of WT and p62-ablated MIA PaCa-2 and Capan-2 cells with or without ablated KEAP1 and γ-H2AX IB. Scale bars: 100 μm. (I). Results in B, C and F-I are mean ± SEM; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$. Statistical significance was calculated using Student's t test.

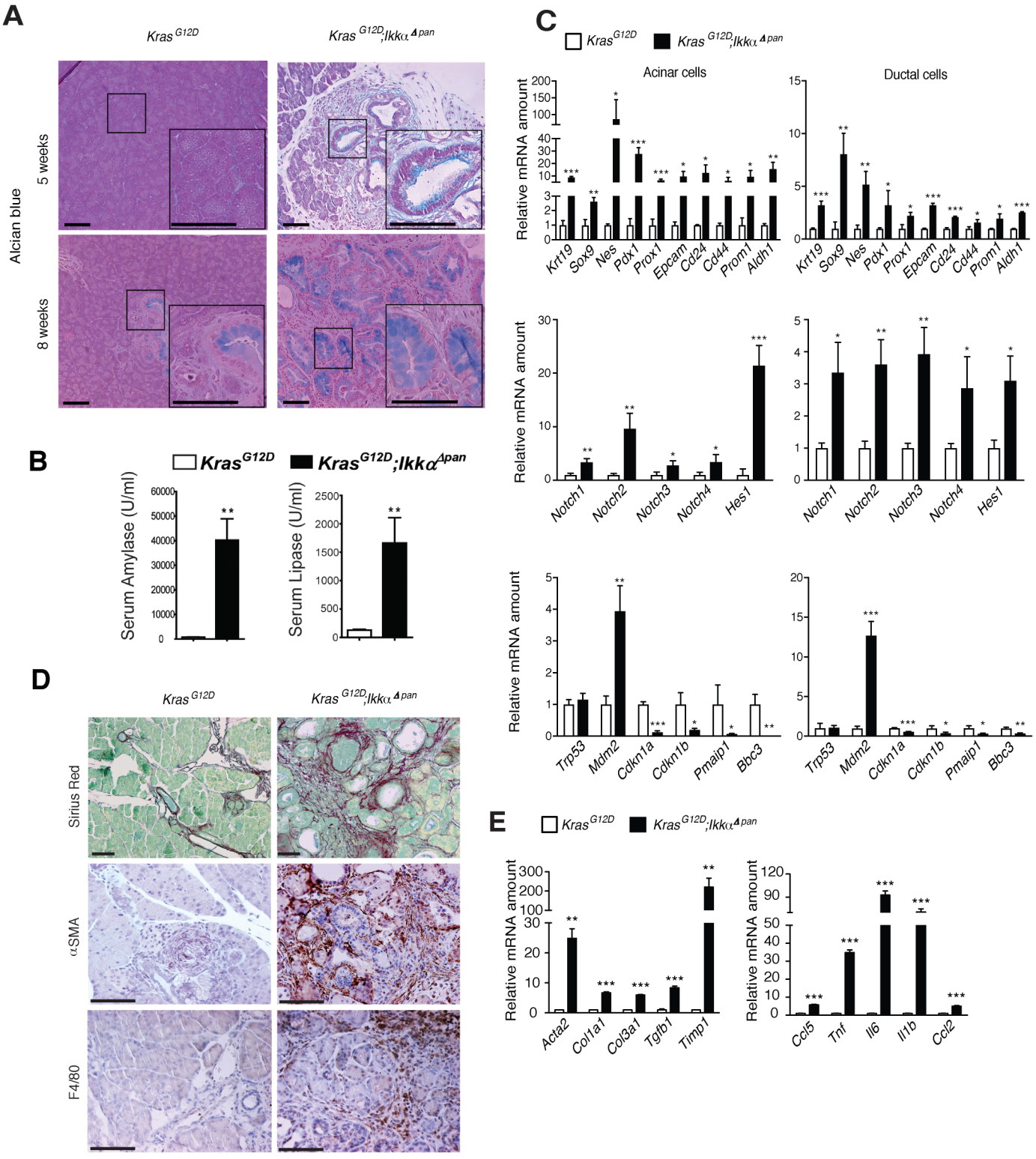

A
Kras G12D
Kras G12D;Ikkα Δpan
Alcian blue
5 weeks
8 weeks
B
Kras G12D
Kras G12D;Ikkα Δpan
Serum Amylase (U/ml)
Serum Lipase (U/ml)
C
Kras G12D
Kras G12D;Ikkα Δpan
Acinar cells
Ductal cells
Relative mRNA amount
Krt19
Sox9
Nes
Pdx1
Prox1
Epcam
Cd24
Cd44
Prom1
Aldh1
Notch1
Notch2
Notch3
Notch4
Hes1
Trp53
Mdm2
Cdkn1a
Cdkn1b
Pmaip1
Bbc3
D
Kras G12D
Kras G12D;Ikkα Δpan
Sirius Red
αSMA
F4/80
E
Kras G12D
Kras G12D;Ikkα Δpan
Relative mRNA amount
Acta2
Col1a1
Col3a1
Tgfb1
Timp1
Ccl5
Tnf
Il6
Il1b
Ccl2

Figure S2 Loss of Pancreatic IKKα in *Kras^{G12D}* Mice Leads to Acinar Cell Damage, Fibrosis, Inflammation and Up-regulation of Progenitor and Stem Cell Markers, Related to Figure 2

(A) Alcian Blue staining of pancreatic sections from indicated mouse strains. Scale bars: 50 μm. (B) Analysis of serum amylase and lipase in 5-week-old *Kras^{G12D}* and *Kras^{G12D};Ikkα^{Δpan}* mice (n = 4). (C) Q-RT-PCR analysis of ductal, progenitor, stem cell and senescence markers and Notch and p53 pathway genes in acinar and ductal cell fractions obtained from 5-week-old *Kras^{G12D}* and *Kras^{G12D};Ikkα^{Δpan}* mice (n = 6). (D) Sirius Red staining and αSMA and F4/80 IHC of pancreatic tissue sections from 5-week-old *Kras^{G12D}* and *Kras^{G12D};Ikkα^{Δpan}* mice. Scale bars: 50 μm. (E) Q-RT-PCR analysis of cytokine, chemokine and fibrosis-related genes in pancreata of 5-week-old mice (n = 6). Results in B, C and E are mean ± SEM; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$. Statistical significance was calculated using Student's t test.

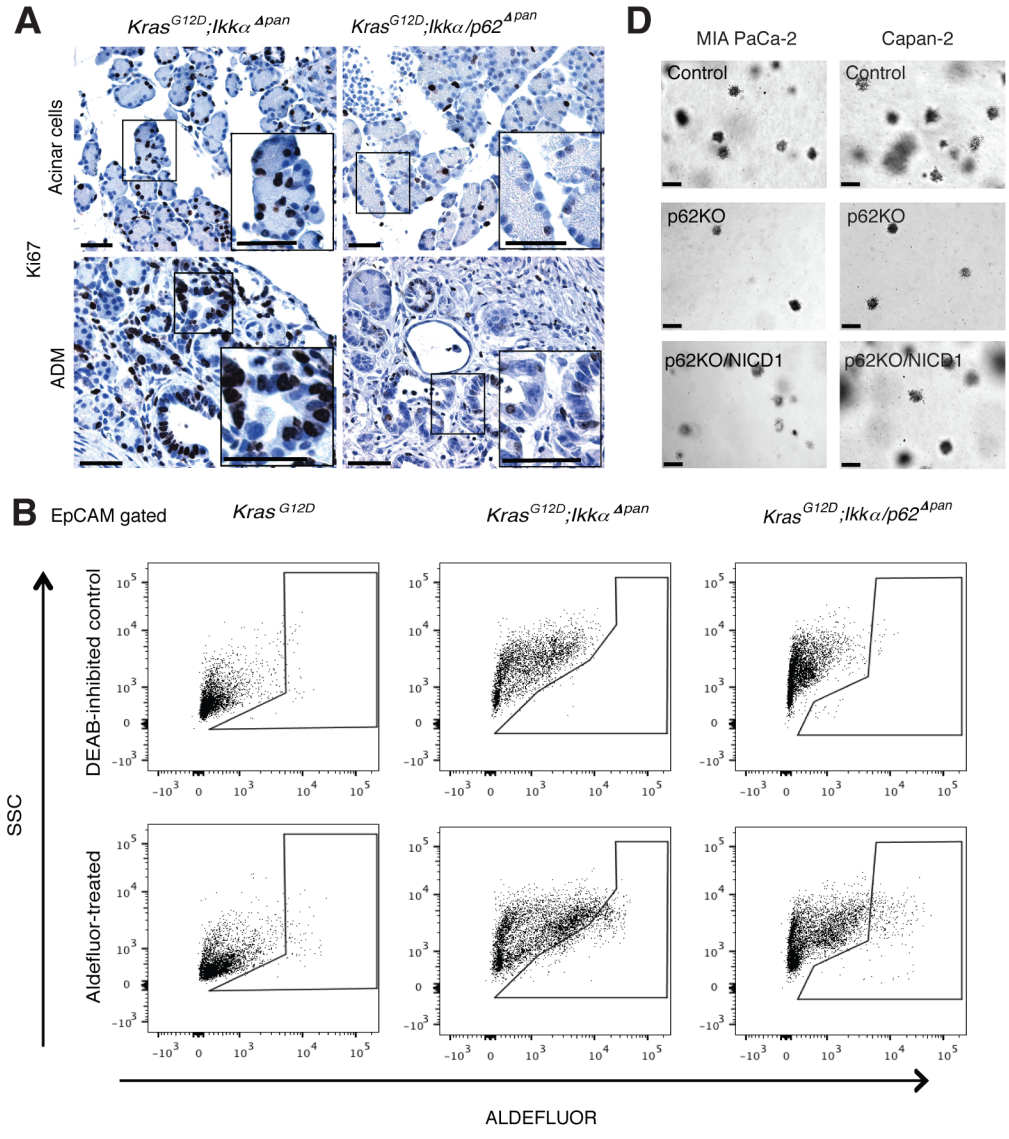

A
Kras G12D;Ikkα Δpan
Kras G12D;Ikkα/p62 Δpan
Acinar cells
Ki67
ADM
D
MIA PaCa-2
Capan-2
Control
Control
p62KO
p62KO
p62KO/NICD1
p62KO/NICD1
B
EpCAM gated
Kras G12D
Kras G12D;Ikkα Δpan
Kras G12D;Ikkα/p62 Δpan
DEAB-inhibited control
Aldefluor-treated
SSC
ALDEFLUOR
C
Kras G12D
Kras G12D;Ikkα Δpan
Kras G12D;Ikkα/p62 Δpan
ALDH+
ALDH+
ALDH+

Figure S3 Pathologies Caused by IKKα Loss are Rescued by p62 Ablation, Related to Figure 3

(A) Ki67 IHC of acinar cells and ADM of $Kras^{G12D}$ and $Kras^{G12D};p62^{\Delta pan}$ mice. Scale bars: 25 μm. (B) Representative FACS plots showing frequency of ALDH expression in $EpCAM^{+}$ cells from 8-week-old $Kras^{G12D}$ (n = 3), $Kras^{G12D};Ikk\alpha^{\Delta pan}$ (n = 7), and $Kras^{G12D};Ikk\alpha/p62^{\Delta pan}$ (n = 4) mice. (C) Representative light microscopy images of spheres formed by sorted $ALDH^{+}$ cell fractions from B. Scale bars: 100 μm. (D) Representative images of control and p62-ablated MIA PaCa-2 and Capan-2 cells with or without NICD1 overexpression. Scale bars: 100 μm.

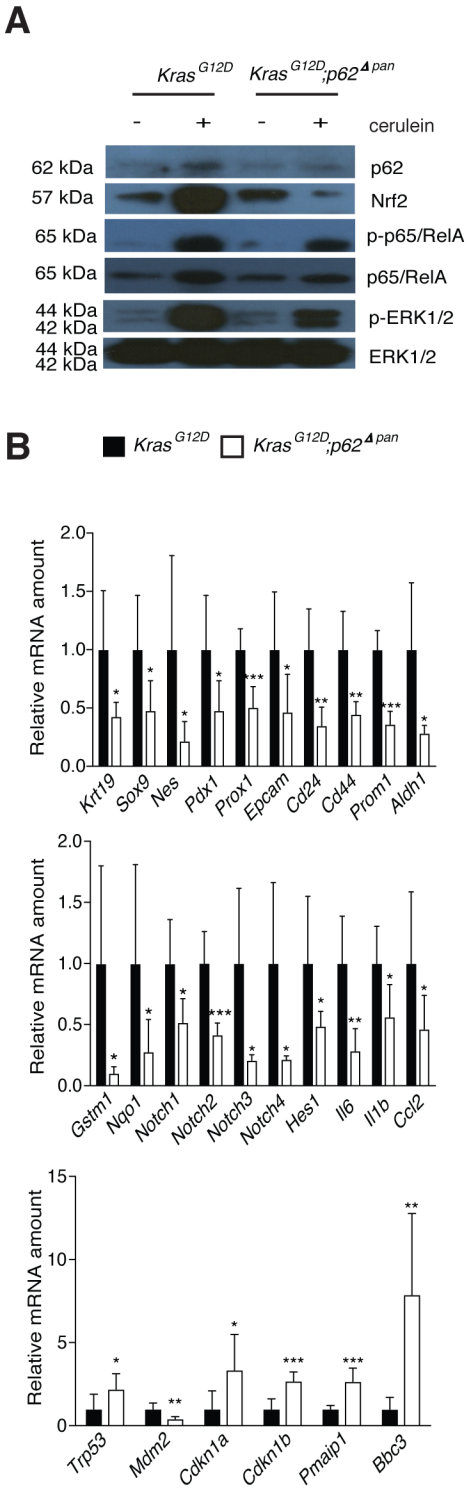

A
KrasG12D
KrasG12D;p62Δpan
- + - +
cerulein
62 kDa
57 kDa
65 kDa
65 kDa
44 kDa
42 kDa
44 kDa
42 kDa
p62
Nrf2
p-p65/RelA
p65/RelA
p-ERK1/2
ERK1/2
B
KrasG12D
KrasG12D;p62Δpan
Relative mRNA amount
2.0
1.5
1.0
0.5
0.0
Krt19
Sox9
Nes
Pdx1
Prox1
Epcam
Cd24
Cd44
Prom1
Aldh1
Gstm1
Nqo1
Notch1
Notch2
Notch3
Notch4
Hes1
Il6
Il1b
Ccl2
15
10
5
0
Trp53
Mdm2
Cdkn1a
Cdkn1b
Pmaip1
Bbc3

Figure S4 p62 Ablation Inhibits NRF2 Activation, Transcription of Ductal, Progenitor and Stemness Markers and *Mdm2* in Cerulein-Induced Acinar-to-Ductal Metaplasia, Related to Figure 4 (A) IB analysis of pancreatic lysates from $Kras^{G12D}$ and $Kras^{G12D};p62^{\Delta pan}$ mice prepared 3 days after treatment with PBS or cerulein. (B) Q-RT-PCR analysis of pancreatic RNA from cerulein-treated $Kras^{G12D}$ and $Kras^{G12D};p62^{\Delta pan}$ mice (n = 3). Results in B are mean ± SEM; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$. Statistical significance was calculated using Student's t test.

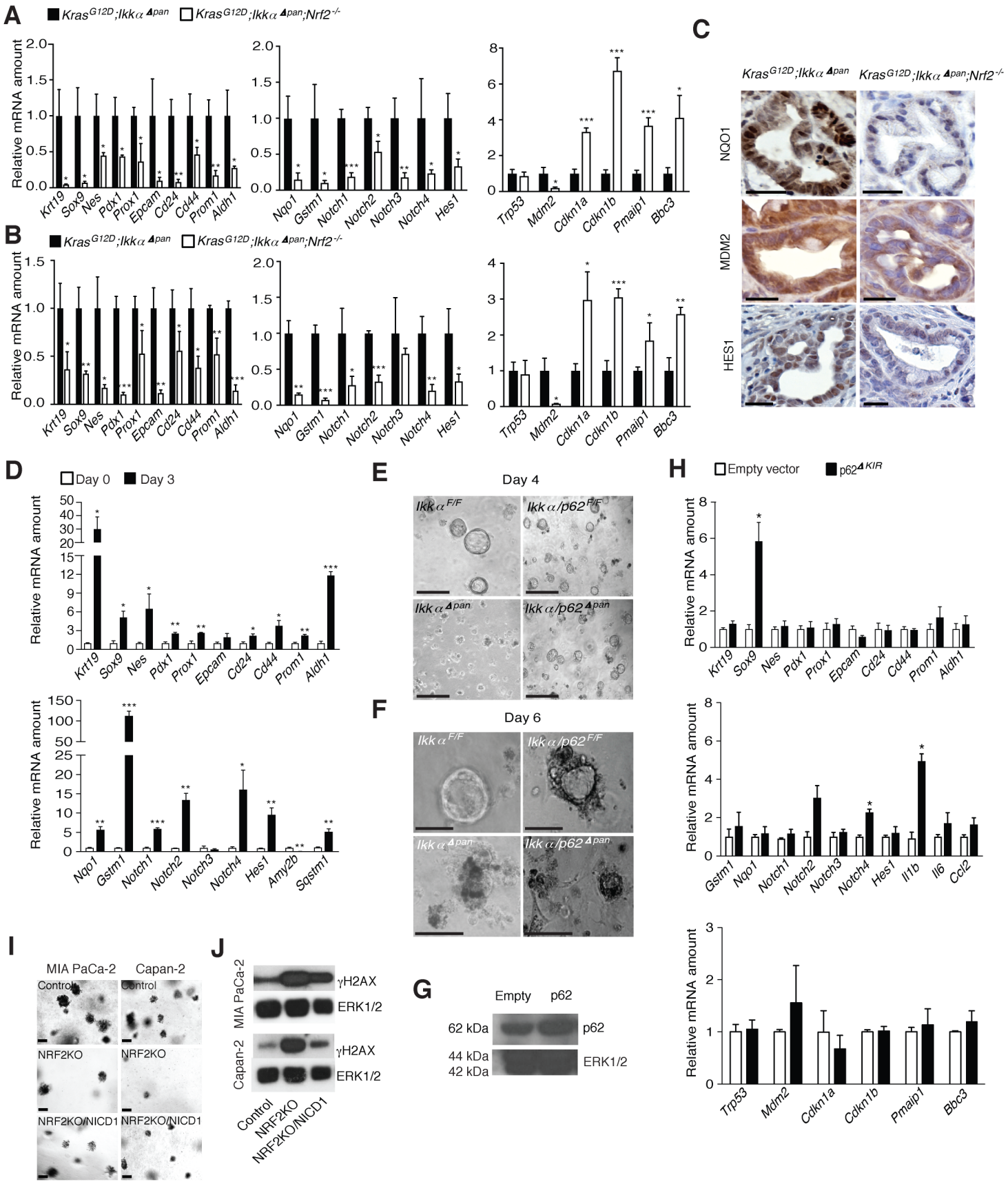

A
KrasG12D;Ikkα Δpan
KrasG12D;Ikkα Δpan;Nrf2-/-
Relative mRNA amount
Krt19 Sox9 Nes Pdx1 Prox1 Epcam Cd24 Cd44 Prom1 Aldh1
Nqo1 Gstm1 Notch1 Notch2 Notch3 Notch4 Hes1
Trp53 Mdm2 Cdkn1a Cdkn1b Pmaip1 Bbc3
B
KrasG12D;Ikkα Δpan
KrasG12D;Ikkα Δpan;Nrf2-/-
Relative mRNA amount
Krt19 Sox9 Nes Pdx1 Prox1 Epcam Cd24 Cd44 Prom1 Aldh1
Nqo1 Gstm1 Notch1 Notch2 Notch3 Notch4 Hes1
Trp53 Mdm2 Cdkn1a Cdkn1b Pmaip1 Bbc3
C
KrasG12D;Ikkα Δpan
KrasG12D;Ikkα Δpan;Nrf2-/-
NQO1
MDM2
HES1
D
Day 0
Day 3
Relative mRNA amount
Krt19 Sox9 Nes Pdx1 Prox1 Epcam Cd24 Cd44 Prom1 Aldh1
Relative mRNA amount
Nqo1 Gstm1 Notch1 Notch2 Notch3 Notch4 Hes1 Amy2b Sqstm1
E
Day 4
Ikkα F/F
Ikkα/p62 F/F
Ikkα Δpan
Ikkα/p62 Δpan
F
Day 6
Ikkα F/F
Ikkα/p62 F/F
Ikkα Δpan
Ikkα/p62 Δpan
G
Empty
p62
62 kDa
44 kDa
42 kDa
p62
ERK1/2
H
Empty vector
p62Δ KIR
Relative mRNA amount
Krt19 Sox9 Nes Pdx1 Prox1 Epcam Cd24 Cd44 Prom1 Aldh1
Relative mRNA amount
Gstm1 Nqo1 Notch1 Notch2 Notch3 Notch4 Hes1 Il1b Il6 Ccl2
Relative mRNA amount
Trp53 Mdm2 Cdkn1a Cdkn1b Pmaip1 Bbc3
I
MIA PaCa-2
Capan-2
Control
NRF2KO
NRF2KO/NICD1
J
MIA PaCa-2
Capan-2
γH2AX
ERK1/2
Control
NRF2KO
NRF2KO/NICD1

Figure S5 Effects of NRF2, p62 and Matrigel Culture on Gene Expression and Ductal Structure Formation, Related to Figure 5 (A, B) Q-RT-PCR analysis of indicated mRNAs in acinar (A) and ductal (B) pancreatic cells isolated from 5-week-old $Kras^{G12D};Ikk\alpha^{\Delta pan}$ and $Kras^{G12D};Ikk\alpha^{\Delta pan};Nrf2^{-/-}$ mice (n = 5). (C) NQO1, MDM2 and HES1 IHC of pancreatic tissue sections from 5-week-old mice (ductal lesions are shown). Scale bars: 25 μm. (D) Q-RT-PCR analysis indicated mRNAs in freshly isolated acinar cells (d0) and ductal structures formed after 3 days in Matrigel (d3) by the same cells (n = 5). (E, F) Images of ductal structures formed by the indicated acinar cell genotypes after 4 (E) and 6 (F) days in Matrigel. Scale bar: 50 μm (E), 20 μm (F). (G) p62 IB analysis of WT acinar cells transfected with either empty or p62 expression vectors. (H) Q-RT-PCR analysis of acinar cells transfected with p62 KIR^- ($p62^{\Delta KIR}$) or empty expression vectors (n = 3). (I) Representative images of spheres formed by WT or NRF2-ablated MIA PaCa-2 and Capan-2 cells with or without NICD1 overexpression. Scale bars: 100 μm. (J) IB analysis of indicated proteins in whole cell lysates. All results depicted by bar graphs are mean ± SEM *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$. Statistical significance was calculated using Student's t test.

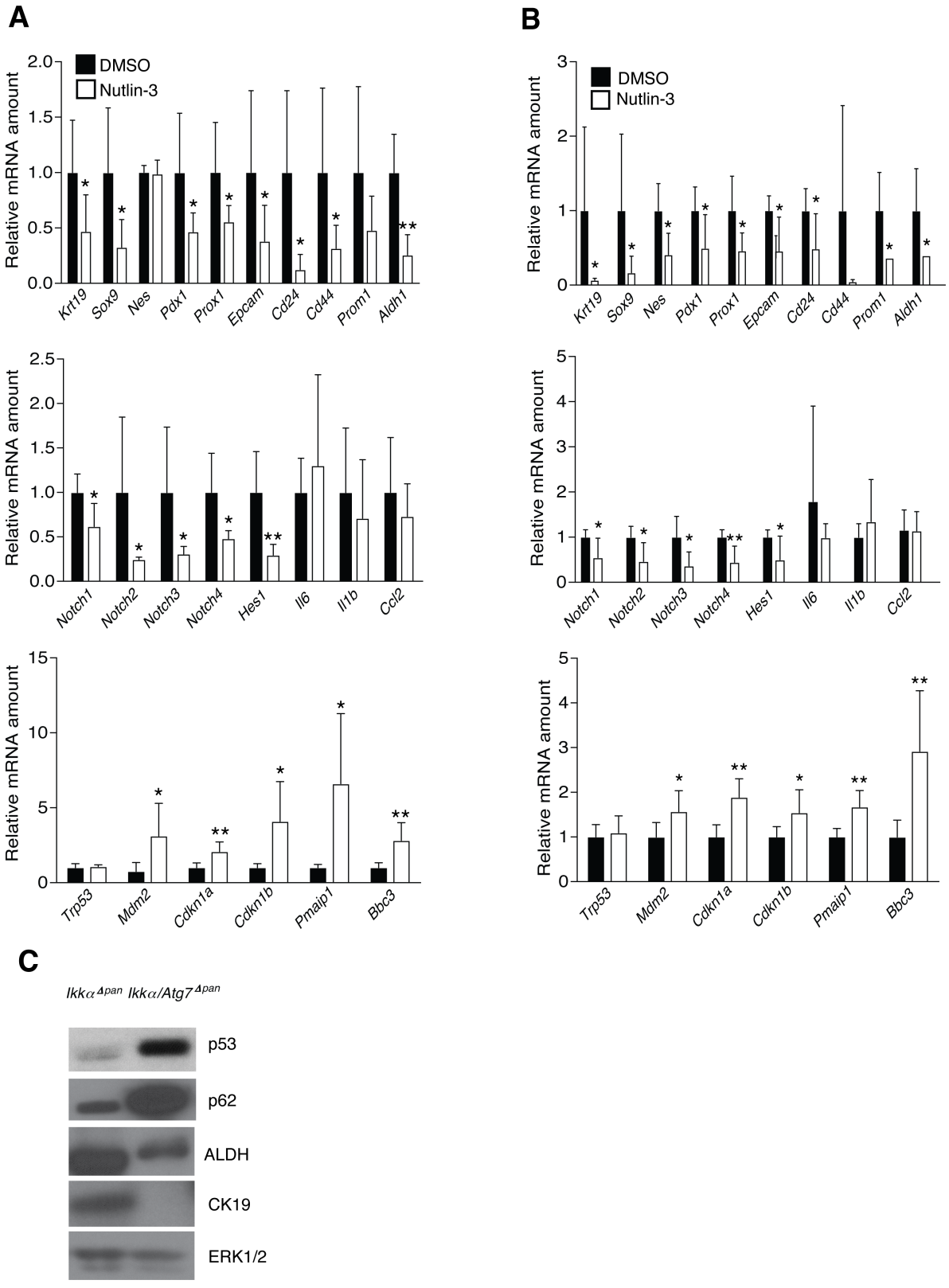

A
B
DMSO
Nutlin-3
Relative mRNA amount
Krt19
Sox9
Nes
Pdx1
Prox1
Epcam
Cd24
Cd44
Prom1
Aldh1
Notch1
Notch2
Notch3
Notch4
Hes1
Il6
Il1b
Ccl2
Trp53
Mdm2
Cdkn1a
Cdkn1b
Pmaip1
Bbc3
C
Ikkα Δpan
Ikkα/Atg7 Δpan
p53
p62
ALDH
CK19
ERK1/2

Figure S6 In Vivo Nutlin-3 Treatment Impairs Expression of Ductal, Progenitor and Stemness Markers, Related to Figure 6 (A, B) Q-RT-PCR analysis of mRNAs isolated from pancreata of $Kras^{G12D}$ (A) and $Kras^{G12D};Ikk\alpha^{\Delta pan}$ (B) mice (n = 7 each group) treated as indicated. (C) IB analysis of the indicated proteins in pancreatic lysates from $Ikk\alpha^{\Delta pan}$ and $Ikk\alpha/Atg7^{\Delta pan}$ mice (n = 4 each group). Results in A and B are mean ± SEM *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$ by Student's t test.

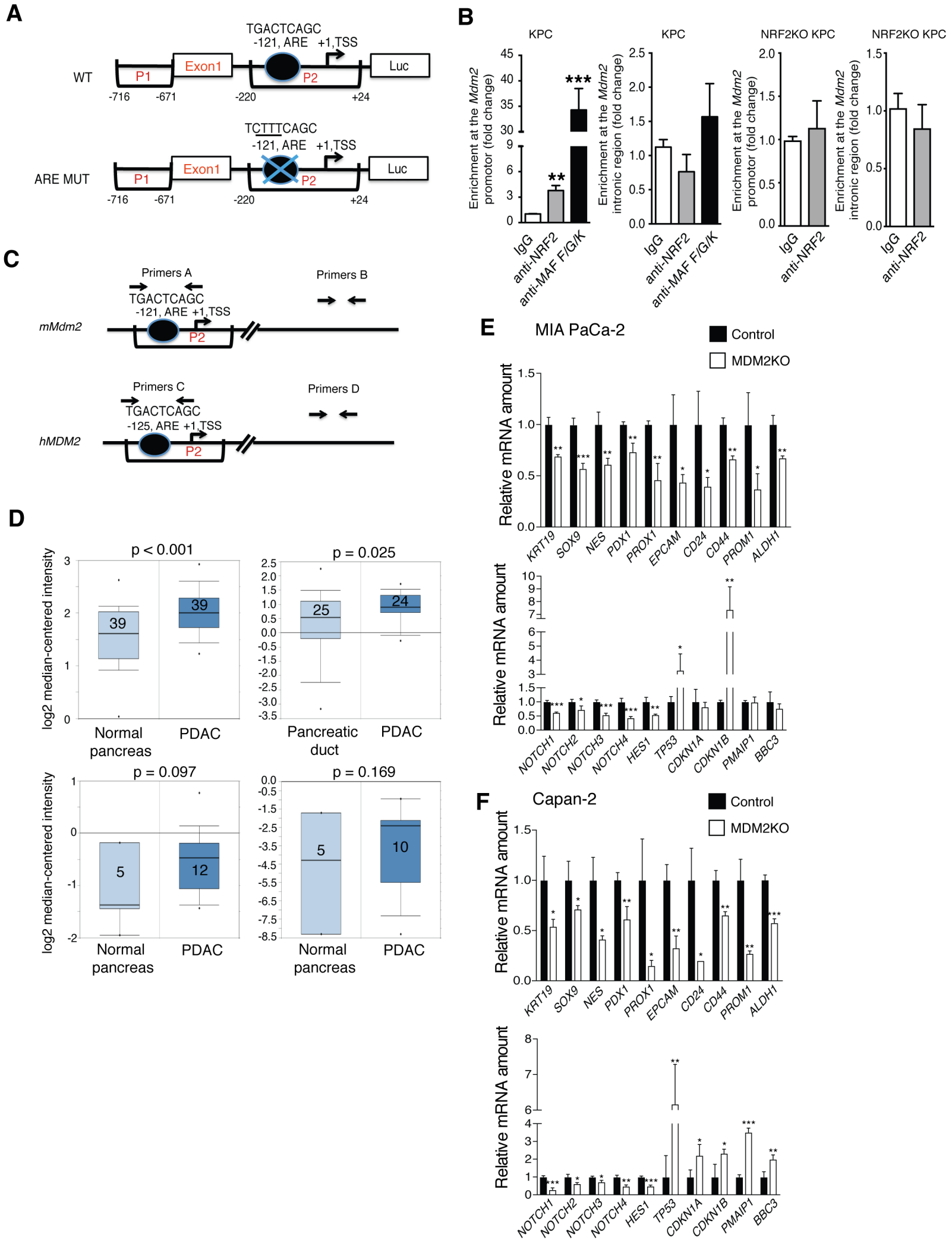

A
TGACTCAGC
-121, ARE +1,TSS
WT
P1
Exon1
P2
Luc
-716
-671
-220
+24
TCTTTCAGC
-121, ARE +1,TSS
ARE MUT
P1
Exon1
P2
Luc
-716
-671
-220
+24
B
KPC
KPC
NRF2KO KPC
NRF2KO KPC
Enrichment at the Mdm2 promotor (fold change)
Enrichment at the Mdm2 intronic region (fold change)
Enrichment at the Mdm2 promotor (fold change)
Enrichment at the Mdm2 intronic region (fold change)
***
**
IgG
anti-NRF2
anti-MAF F/G/K
IgG
anti-NRF2
anti-MAF F/G/K
IgG
anti-NRF2
IgG
anti-NRF2
C
Primers A
Primers B
TGACTCAGC
-121, ARE +1,TSS
mMdm2
P2
Primers C
Primers D
TGACTCAGC
-125, ARE +1,TSS
hMDM2
P2
D
p < 0.001
p = 0.025
log2 median-centered intensity
39
39
Normal pancreas
PDAC
25
24
Pancreatic duct
PDAC
p = 0.097
p = 0.169
log2 median-centered intensity
5
12
Normal pancreas
PDAC
5
10
Normal pancreas
PDAC
E
MIA PaCa-2
Control
MDM2KO
Relative mRNA amount
KRT19
SOX9
NES
PDX1
PROX1
EPCAM
CD24
CD44
PROM1
ALDH1
Relative mRNA amount
NOTCH1
NOTCH2
NOTCH3
NOTCH4
HES1
TP53
CDKN1A
CDKN1B
PMAIP1
BBC3
F
Capan-2
Control
MDM2KO
Relative mRNA amount
KRT19
SOX9
NES
PDX1
PROX1
EPCAM
CD24
CD44
PROM1
ALDH1
Relative mRNA amount
NOTCH1
NOTCH2
NOTCH3
NOTCH4
HES1
TP53
CDKN1A
CDKN1B
PMAIP1
BBC3

Figure S7. NRF2 Directly Controls *MDM2* Transcription in PDAC, Related to Figure 7 (A) Reporter constructs used to assess the functionality of the NRF2 binding site/ARE upstream to the *Mdm2* promoter 2 (P2). (B) Chromatin immunoprecipitation assays probing NRF2 and small MAF protein recruitment to the *Mdm2/MDM2* promoters in WT and NRF2 ablated KPC (n = 3) cells. (C) Positions of the ChIP primer sets used to assess NRF2 binding to the *Mdm2/MDM2* control region, including the P2 promoter with the adjacent NRF2 binding site. (D) Relative *MDM2* mRNA amounts in normal and cancerous pancreatic tissue were obtained from www.oncomine.org and expressed as log2 median-centered intensity. Numbers within the bars represent study participants. p values were obtained from public datasets. (E, F) Q-RT-PCR mRNA analysis of MIA PaCa-2 cells (E) and Capan-2 cells (F), transfected with either MDM2 KO CRISPR/Cas9 or control vector (n = 3). Results in B, E and F are mean ± SEM; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$ by Student's t test.

Table S1, related to the STAR Methods. Primers used for analyzing changes in gene expression levels.

Gene name (Forward-F; Reverse-R;)	**Primer sequences**
mAldh1(Aldh1a1)_F	CTGTGAAGGCTGCAAGACAGG
mAldh1(Aldh1a1)_R	GTCAGCCAGCTTGTTCAGCAG
mAmy2b_F	TGGTGACAAGGTGCAACAATG
mAmy2b_R	GATTGCCTGAGCCACACATG
mαSma (Acta2)_F	GTTCAGTGGTGCCTCTGTCA
mαSma (Acta2)_R	ACTGGGACGACATGGAAAAG
mCcl2_F	GCCAGCTCTCTCTTCCTCCA
mCcl2_R	CCCAGAAGCATGACAGGGAC
mCcl5_F	AATCCCCTACTCCCACTCGG
mCcl5_R	TTCTTGGGTTTGCTGTGCAG
mCd3(Cd3e)_F	GAGAGACATCGCCTTCTGTGG
mCd3(Cd3e)_R	GCTGAAGAGCAAGCTGTGGAG
mCd19_F	TATGCAGCTCCTCAGCTCCAC
mCd19_R	CCATGCTGGTTCTAGGTCGTC
mCd24(Cd24a)_F	TGACCGATAAGGCCATAGTGC
mCd24(Cd24a)_R	CGCCTGGTAGTTCCTTCCAAC
mCd44_F	CGGAATCTGCAGAGTGTGGAC
mCd44_R	CAGGAATGACGTCTCCAATCG
mCd133(Prom1)_F	AATTCGCTCAGCAGCAGTGAC
mCd133(Prom1)_R	TGCTTAGGCTTGGTCTGATGC
Ck19 (Krt19)_F	GGGGGTTCAGTACGCATTGG
*Ck19 (Krt19)*_R	GAGGACGAGGTCACGAAGC
mCola1a_F	TAGGCCATTGTGTATGCAGC
mCola1a_R	ACATGTTCAGCTTTGTGGACC
mCola13_F	TAGGACTGACCAAGGTGGCT
mCola13_R	GGAACCTGGTTTCTTCTCACC
mEmr1(Adgre1):_F	GACTGACAACCAGACGGCTTG
mEmr1(Adgre1):_R	TCACTGCCTCCACTAGCATCC
mEpcam_F	TTAATGCCTAGCCGTGCTGAG
mEpcam_R	TCTGCAGTCCGAGCTCTTCTG
mGclc_F	TTCATGATCGAAGGACACCA
mGclc_R	CTGCACATCTACCACGCAGT
mGclm_F	GGCTGATTTGGGAACTCCAT
mGclm_R	CGGGAACCTGCTCAACTG
mGgt1_F	GGTGGCGTAGAACTCAGAGC
mGgt1_R	TTTGCCTATGCCAAGAGGAC
mGsta1_F	CTGGACTGTGAGCTGAGTGG
mGsta1_R	CATTGAAGTGGTGAAGCACG
mGstm1_F	CTACCTTGCCCGAAAGCAC
mGstm1_R	ATGTCTGCACGGATCCTCTC
mHes1_F	TCTACACCAGCAACAGTG
mHes1_R	TCAAACATCTTTGGCATCAC
mHey1_F	GCGGACGAGAATGGAAACTTG
mHey1_R	GCTCAGATAACGGGCAACTTC
mHmox1_F	CCTTCAAGGCCTCAGACAAA
mHmox1_R	GAGCCTGAATCGAGCAGAAC
mIl1-β (Il1b)_F	CAACCAACAAGTGATATTCTCCATG
mIl1-β (Il1b)_R	GATCCACACTCTCCAGCTGCA
mIl6_F	GAGGATACCACTCCCAACAGACC
mIl6_R	AAGTGCATCATCGTTGTTCATACA

mJag1_F	GCCACCTGTGTGGATGAGATC
mJag1_R	GGCACTTGGCACCACTATGTC
mMdm2_F	TTCGTGAGAACTGGCTTCCAG
mMdm2_R	AGGCACATCCAAGCCTTCTTC
mMmp7_F	CCCGGTACTGTGATGTACCC
mMmp7_R	AATGGAGGACCCAGTGAGTG
mMuc5ac_F	CAGGACTCTCTGAAATCGTACCA
mMuc5ac_R	AAGGCTCGTACCACAGGGA
mMuc6_F	CGGCTGCGTCTGTCCTAAG
mMuc6_R	GCATAGTCACATGGGCATTCCT
*mNes_*F	CCCTGAAGTCGAGGAGCTG
*mNes_*R	CTGCTGCACCTCTAAGCGA
mNotch1_F	GATGGCCTCAATGGGTACAAG
mNotch1_R	TCGTTGTTGTTGATGTCACAGT
mNotch2_F	AACGAGAAGGTCCAGCTGTCC
mNotch2_R	ATGTGGCATCGGAGACATACG
mNotch3_F	AGTCAATGGCTTCAGCTGCAC
mNotch3_R	GGAGTGCTTGCACACTCATCC
mNotch4_F	CTGGACCAGAATGCGAGACAG
mNotch4_R	GTTGTAGCCAGATGGCTGTGG
mNoxa (Pmaip1)_F	TACCACCTGAGTTCGCAGCTC
mNoxa (Pmaip1)_R	CAGTTATGTCCGGTGCACTCC
mNqo1_F	AGCGTTCGGTATTACGATCC
mNqo1_R	AGTACAATCAGGGCTCTTCTCG
mPdx1_F	TTAACCTAGGCGTCGCACAAG
mPdx1_R	TTCCAGAAGTCTGCCAGCATC
mProx1_F	GGAGATGGCTGAGAACAAGC
mProx1_R	AGACTTTGACCACCGTGTCC
mPuma (Bbc3)_F	CGAAGACTCCAGAAGCAGCAG
mPuma (Bbc3)_R	TGCTATTGAGGCACCTTGCTG
mp21 (Cdkn1a)_F	TGAGGAGGAGCATGAATGGAG
mp21 (Cdkn1a)_R	CATCACCAGGATTGGACATGG
mp27 (Cdkn1b)_F	GCCTGACTCGTCAGACAATCC
mp27 (Cdkn1b)_R	CTTCTGCAGCAGGTCGCTTC
mp53 (Trp53)_F	GACCATCCTGGCTGTAGGTAGC
mp53 (Trp53)_R	CAGTCTTCGGAGAAGCGTGAC
mp62 (Sqstm1)_F	GCTGCCCTATACCCACATCT
mp62 (Sqstm1)_R	CGCCTTCATCCGAGAAAC
mSox9_F	CGGAACAGACTCACATCTCTCC
mSox9_R	GCTTGCACGTCGGTTTTGG
mTgfb1_F	TTGCTTCAGCTCCACAGAGA
mTgfb1_R	TGGTTGTAGAGGGCAAGGAC
mTimp1_F	AGGTGGTCTCGTTGATTTCT
mTimp1_R	GTAAGGCCTGTAGCTGTGCC
mTnf_F	GCACAGAAAGCATGACCCG
mTnf_R	GCCCCCCATCTTTTGGG
m18s_F	AGCCCCTGCCCTTTGTACACA
m18s_R	CGATCCGAGGGCCTCACTA
hALDH1 (ALDH1a1)_F	TTAGCTGATGCCGACTTGGAC
hALDH1 (ALDH1a1)_R	TCCTGGATGCGGCTATACAAC
hCD24_F	AGTGCAGTGGTGCGATCTCAG
hCD24_R	GTGGCAGGTGCCTGTAATCC
hCD44_F	TTGCATTGCAGTCAACAGTCG

hCD44_R	CTGTCCTCCACAGCTCCATTG
hCD133 (PROM1)_F	GCGTTGGAGAACATGAACAGC
hCD133 (PROM1)_R	TGAGAGATGACCGCAGGCTAG
hCK19 (KRT19)_F	ATCCTGAGTGACATGCGAAGC
hCK19 (KRT19)_R	AACCAGGCTTCAGCATCCTTC
hEPCAM_F	GATCCTGACTGCGATGAGAGC
hEPCAM_R	GCAGTGTTCACACACCAGCAC
hGSTM1_F	AGCAACGCCATCTTGTGCTAC
hGSTM1_R	TGGTTGTCCATGGTCTGGTTC
hHES1_F	CCGGAGCTGGTGCTGATAAC
hHES1_R	TCAGTAGCGCTGTTCCAGGAC
hNES_F	AGGACCAAGAACTGGCTCAGG
hNES_R	CCAGTGAAGCCATCCTGCTC
hNFE2L2_F	GCCTGTAAGTCCTGGTCATCG
hNFE2L2_R	TTGTGAGATGAGCCTCCAAGC
hNOTCH1_F	GATGCCAACATCCAGGACAAC
hNOTCH1_R	CCGGATCAGGATCTGGAAGAC
hNOTCH2_F	CACTGTGGCCAACCAGTTCTC
hNOTCH2_R	CTGGCAGTGTCCTGGAATGTC
hNOTCH3_F	ATCTGGTTGCTGCTGACATCC
hNOTCH3_R	ATTGACATCCATGCCATCAGC
hNOTCH4_F	CACTAGGCGAGGACAGCATTG
hNOTCH4_R	GCCTGAGCACATCACAACTCC
hNQO1_F	CTGGAGTGCAGTGGTGTGATC
hNQO1_R	AGGCAGGAGAATTGCTGGAAC
hPDX1_F	TCCTACAGCACTCCACCTTGG
hPDX1_R	GGAGCCTTCCAATGTGTATGG
hPROX1_F	CGAAGCGAGAAGGCAACAAC
hPROX1_R	CGACATGGCAGTGTTCAGTTC
hP27 (CDKN1B)_F	TCCGGCTAACTCTGAGGACAC
hP27 (CDKN1B)_R	TGCAGGTCGCTTCCTTATTCC
hP53 (TP53)_F	CCTTGCTTGCAATAGGTGTGC
hP53 (TP53)_R	AGTGCAGGCCAACTTGTTCAG
hP62 (SQSTM1)_F	GAAGAGCAGCTCACAGCCAAG
hP62 (SQSTM1)_R	AAGGCGATCTTCCTCATCTGC
hSOX9_F	CATCAAGACGGAGCAGCTGAG
hSOX9_R	GGCTGTAGGCGATCTGTTGG
h18S_F	GGACACGGACAGGATTGACAG
h18S_R	CAACTAAGAACGGCCATGCAC