

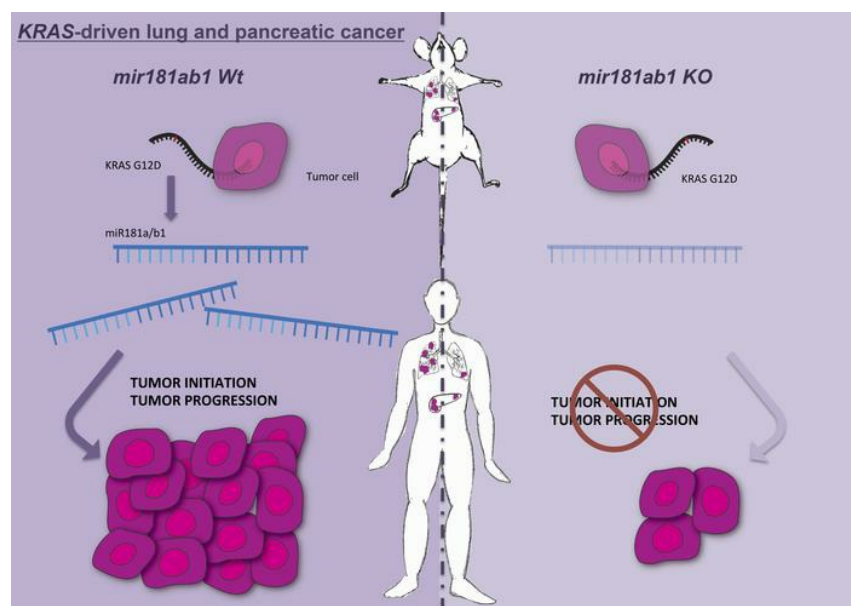
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THE MIR181AB1 CLUSTER PROMOTES KRAS-DRIVEN ONCOGENESIS AND PROGRESSION IN LUNG AND PANCREAS

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KRAS, miRNAs, miR181ab1, lung cancer, pancreatic cancer

ABSTRACT

Few therapies are currently available for patients with *KRAS*-driven cancers, highlighting the need to identify new molecular targets that modulate central downstream effector pathways. Here we found the miRNA cluster including miR181ab1 as a key modulator of *KRAS*-driven oncogenesis. Ablation of *Mir181ab1* in genetically-engineered mouse models of *Kras-driven* lung and pancreatic cancer was deleterious to tumor initiation and progression. Expression of both resident miRNAs in the *Mir181ab1* cluster, miR181a1 and miR181b1, was necessary to rescue the *Mir181ab1*-loss phenotype underscoring their non-redundant role. In human cancer cells, depletion of miR181ab1 impaired proliferation and 3D growth, whereas overexpression provided a proliferative advantage. Lastly, we unveiled miR181ab1-regulated genes responsible for this phenotype. These studies identified what we believe to be a previously unknown role for miR181ab1 as a potential therapeutic target in two highly aggressive and difficult to treat *KRAS*-mutated cancers.

INTRODUCTION

KRAS is one of the most commonly mutated oncogenes in human cancer (1) and is a key oncogenic driver in many lung and most pancreatic cancers (2-5). *KRAS* induces the coordinated action of several downstream effector pathways to induce a transcriptional response that sustains a pro-oncogenic phenotype (1). Prior work has identified genes that are transcriptionally regulated as a consequence of *KRAS* activation (6-10), fostering strategies for the discovery of critical transcriptional regulators within the *KRAS* signaling pathway (11, 12). An alternative mechanism for regulation of gene expression is via microRNAs (miRNAs) (13). However, the role of miRNAs functionally regulating the consequences of *KRAS* activation is still limited (14-17). The study of miRNA function is an alternative strategy to yield molecular insights necessary for the development of novel therapies against *KRAS*-driven tumors.

miRNAs are small, non-coding RNAs that act largely by fine-tuning post-transcriptional gene expression (13). Many miRNAs are differentially expressed in human tumors (18-22) and a few have been confirmed to have either oncogenic or tumor suppressive effects across tumor types (23-25). Some miRNAs are themselves regulated by oncogenic pathways. For example, pioneering studies described overexpression of *MYC* (26) or mutations in *TP53* (27-31) as drivers of miRNA expression. Comparatively fewer studies have focused on miRNAs with a pro-oncogenic role in the context of mutant *KRAS* tumorigenesis (14, 15, 32, 33), in contrast with the wealth of information about tumor-suppressive miRNAs reported to downregulate *KRAS* expression (34, 35). In addition, functional validation of miRNAs involved in *KRAS*-driven oncogenesis has focused primarily on the role of such miRNAs

in tumor initiation (14, 15) with less attention on their role in tumor progression. To our knowledge no miRNAs clearly functioning in tumor maintenance in KRAS-driven cancers have definitively been identified. Understanding the role of miRNAs sustaining *KRAS* oncogene tumorigenesis might unveil new targets amenable to intervention strategies.

We identified miR181ab1 as a miRNA cluster upregulated by oncogenic KRAS and used multiple genetically-engineered mouse models (GEMMs) to demonstrate a role for this cluster in both initiation and maintenance of lung and pancreatic cancer. We extended these results to human cells where we show that miR181ab1 plays an important role in early and late stages of KRAS-driven oncogenesis. Our findings support the value of mouse genetics for the identification of functionally relevant elements of the KRAS signaling network and justify further efforts to develop inhibitory strategies against members of the miR181ab1 cluster as a possible therapeutic opportunity in *KRAS*-mutated tumors.

RESULTS

Deletion of *Mir181ab1* impairs *Kras*-driven lung cancer development

We used mouse embryo fibroblasts (MEFs) carrying a conditionally activatable allele to identify miRNAs upregulated by oncogenic KRAS (36). Differentially expressed miRNAs were profiled using a bead-based flow cytometric method (37). Fifty-three upregulated and five downregulated miRNAs were identified in MEFs expressing oncogenic KRAS compared to controls ($\log_{2}FC \pm 1$) (**Suppl. Figure 1A**). The miR181 family (miR181a, miR181b, miR181c and miR181d) were among the top upregulated miRNAs (**Suppl. Figure 1A and B**). Thus, we focused on this miRNA family for subsequent experiments.

To evaluate the role of miR181ab1 in tumor initiation, *Mir181ab1*^{-/-} mice (38) were crossed to *Kras*^{LSL-G12D/+} mice to generate *Kras*^{LSL-G12D/+}; *Mir181ab1*^{-/-}. Compound mutant *Kras*^{LSL-G12D/+}; *Mir181ab1*^{+/+} (K181^{+/+}) and *Kras*^{LSL-G12D/+}; *Mir181ab1*^{-/-} (K181^{-/-}) mice were treated with intranasal instillation of adCre to evaluate the function of *Mir181ab1* in KRAS-driven oncogenesis. Histological analysis of hematoxylin-eosin (H-E) stained sections of mouse lungs 20 weeks after adCre revealed that *Mir181ab1* deletion significantly reduced overall tumor burden (**Figure 1A and B**) with both tumor number and tumor size decreased in K181^{-/-} mice (**Figure 1C and D**). The effect on both tumor number and size suggested an effect on both tumor initiation and progression, possibly due to impaired proliferative capacity as indicated by fewer Ki67+ cells (**Figure 1E**). Analysis of individual tumors by laser microdissection showed a significant reduction in both miR181a and miR181b in K181^{-/-} mice, with no compensatory increase in miR181c or miR181d (**Suppl. Figure 1C and D**). As miR181

can be expressed from 3 different clusters in mouse chromosomes 1, 2 and 8 (chromosomes 1, 9, 19 in human) (**Supplementary Figure 1E**), these data suggest that neither the *Mir181ab2* nor the *Mir181cd8* clusters compensate for the loss of miR181ab1 in this model. Furthermore, *Mir181ab1* loss significantly increased overall survival in mice harboring *Kras* mutations (**Figure 1F**). Taken together, these results demonstrate that the *Mir181ab1* cluster has a prominent role in *Kras*-dependent lung tumorigenesis.

Intranasal administration of adCre to *Kras*^{LSL-G12D/+} mice produces an inflammatory response involving the recruitment of T and B cells, and this reaction is essential for the development of lung adenomas (39). Importantly, *Mir181ab1*^{-/-} mice show severe defects in lymphoid development and in T cell homeostasis and function (38, 40-42). Therefore, it is possible that the effect of *Mir181ab1* depletion could be due to modulation of the tumor immune microenvironment. To determine whether the differences in tumor development between K181^{+/+} and K181^{-/-} mice were due to loss of miR181ab1 expression in T cells or other non-cell autonomous effects, we conditionally deleted the *Mir181ab1* cluster in lung epithelial cells using *Mir181ab1*^{flox/flox} mice (38). *Kras*^{LSL-G12D/+} mice were bred to *Mir181ab1*^{flox/flox} mice to yield compound K181^{+/+} and *Kras*^{LSL-G12D/+}; *Mir181ab1*^{flox/flox} mice (K181^{f/f}). Twenty weeks following adCre, analysis of H-E stained sections revealed a significant decrease in the K181^{f/f} mice compared to the K181^{+/+} group (**Figure 2A and B**), similar to that observed in K181^{-/-} mice. A reduction in the average number of tumors and tumor size was also found (**Figure 2C and D**). Conditional deletion of *Mir181ab1* in lung epithelial cells also increased mice survival (**Figure 2E**). Taken together, these results demonstrate that miR181ab1

expression in lung epithelial tumor cells contributes to formation of *Kras* oncogene-initiated tumors.

Deletion of *Mir181ab1* impairs *Kras*-driven pancreatic ductal adenocarcinoma tumorigenesis

To determine if miR181ab1 played a functional role in other oncogenic KRAS-driven cancers, we evaluated its role in pancreatic ductal adenocarcinoma (PDAC), a highly lethal cancer in which *KRAS* mutations are present in over 90% of cases. PDAC shows overexpression of miR181a, miR181b and miR181c relative to benign pancreatic tissue (43, 44) and expression of miR181b negatively correlates with PDAC patient survival (45). We studied the effect of miR181ab1 in early stages of pancreatic tumorigenesis by deleting the cluster and activating expression of oncogenic *Kras*^{LSL-G12D/+} in mouse pancreas using a *Ptf1a*^{Cre/+} strain (46). In the *Ptf1a*^{Cre/+}; *Kras*^{LSL-G12D/+} mice, pancreatic intra-epithelial neoplasia (PanIN) are observed around 6 months of age (**Figure 3A**). Cohorts of *Ptf1a*^{Cre/+}; *Kras*^{LSL-G12D/+} (KC181^{+/+}) and *Ptf1a*^{Cre/+}; *Kras*^{LSL-G12D}, *Mir181ab1*^{flox/flox} (KC181^{f/f}) mice were obtained. Deletion of *Mir181ab1* greatly reduced tumor weight and decreased PanIN lesions (assessed by MUC5AC) (**Figure 3B-D**). Immunohistochemistry (IHC) revealed a decrease in the number of proliferating cells without changes in the number of apoptotic cells in KC181^{f/f} mice compared to controls (**Figure 3B and E-F**).

Next, we assessed miR181ab1 function in pancreatic tumor development using the *Ptf1a*^{+/-Cre}; *Kras*^{+/-LSL-G12D}; *Trp53*^{flox/flox} (KPC181^{f/f}) mutant model in which PDAC develops with 100% penetrance 6-8 weeks after birth (**Figure 3G**) (47). Magnetic Resonance Imaging (MRI) revealed that tumor volume in *Mir181ab1* knockouts was

significantly reduced compared to age-matched control mice (**Figure 3H-I**), consistent with a reduced pancreas weight (**Figure 3J**). At autopsy, pancreatic tissue from control KPC181^{+/+} mutant mice was entirely occupied by transformed cells, whereas in KPC181^{ff} mutant mice areas of normal pancreatic tissue remained with decreased signal for Ki67 and elevated number of cleaved caspase 3 (CC3) positive cells compared to control animals (**Figure 3K-M**). Furthermore, *Mir181ab1* ablation prolonged overall survival in this aggressive model (**Figure 3N**). Together these data support a key *in vivo* role for *Mir181ab1* in oncogenic *Kras*-driven pancreatic tumorigenesis.

The *Mir181ab1* cluster is required for *Kras*-mutated lung and pancreatic cancer progression

To assess the role of miR181ab1 in tumor maintenance, we turned to a model system that allows for the deletion of the *Mir181ab1* cluster in already established cancers. The *Kras*^{LA2-G12D/+} allele spontaneously recombines to initiate lung tumors (4). We crossed these mice to the *Rosa26*^{CreERT2/+}; *Mir181ab1*^{ff} mice to generate KR181^{ff} mice in which whole-body deletion of *Mir181ab1* floxed alleles occurs upon tamoxifen administration (48). At 8 weeks of age, when adenomas are already spontaneously developing in the lungs (4), KR181^{ff} mice were given tamoxifen or vehicle for 1 week. Lungs were harvested 8 weeks after the last dose of tamoxifen and subjected to histological analyses. A significant decrease in the average tumor burden of KR181^{ff} mice treated with tamoxifen was observed (**Figure 4A and B**), with a reduction in lung tumors size and number (**Figure 4C and D**). Therefore, depletion of the *Mir181ab1* cluster not only interferes with tumor initiation but also affects the development of

established tumors, nominating the transcriptional regulon of this cluster as a potential therapeutic target in this disease.

We also investigated whether miR181ab1 is required for pancreatic cancer progression and maintenance by generating *Kras*^{FSF-G12D/+}, *Trp53*^{Frt/Frt}, *Rosa26*^{CreERT2/+}, *Mir181ab1*^{flox/flox} (KPR181^{f/f}) mice. In these mice activation of *Kras* oncogene, deletion of *Trp53*, and expression of CreER is achieved by administration of an adenovirus expressing the FLP recombinase (adFlp) directly into the pancreatic parenchyma (49). KPR181^{f/f} mice were administered adFlp to initiate tumorigenesis. Upon PDAC development (~50 days after infection) tumors were harvested and allografted into immunodeficient mice. Ablation of *Mir181ab1* in this model is achieved by intraperitoneal injection of tamoxifen, which triggers CreER-recombination of the *Mir181ab1*^{flox/flox} alleles (**Figure 4E**). *Mir181ab1* deletion resulted in decreased tumor volume (**Figure 4F**) indicating an important role for miR181ab1 in established PDAC growth.

Mir181ab1-loss in mutant *Kras* cancer cells adversely impacts cell proliferation

The above findings in multiple GEMMs of tumor initiation and progression indicate that the effect of miR181ab1 on mutant *Kras*-driven tumorigenesis is likely cell-autonomous and not tissue specific. However, they do not rule out whether cancer cells can influence the surrounding microenvironment to foster tumor progression. To determine the role of miR181ab1 exclusively in cancer cells, cell lines were isolated from lung and pancreatic cancer mouse models. KLA cells derived from KR181^{f/f} mice carry the oncogenic KRAS allele but are wild-type for *Mir181ab1* until delivery of Cre using adenoviral infection (**Suppl. Figure 2A-C**). Loss of *Mir181ab1* led to significant

reduction in the number of cells (**Figure 5A**) and impaired cell growth in a 3D organoid assay (**Figure 5B**). Moreover, cells xenografted after *Mir181ab1* deletion originated smaller tumors (**Figure 5C**), paralleling the results obtained in the GEMM. Of note, the tumors that did develop retained expression of miR181a and miR181b due to incomplete recombination of the *Mir181ab1* allele (**Suppl. Figure 2D and E**), suggesting selective pressure for the *Mir181ab1* cluster expression in oncogenic KRAS-driven tumors.

In mouse PDAC cell lines (KPC181^{wt} and KPC181^{ko}) (**Suppl. Figure 2F**) analysis of the growth kinetics showed that KPC181^{ko} cells had a slower proliferation rate than KPC181^{wt} cells (**Figure 5D**). Moreover, growth of 3D organoids from KPC181^{ko} cells was much lower than the wild-type counterparts (**Figure 5E**). Lastly, KPC181^{ko} cells grew smaller tumors in immunodeficient mice than KPC181^{wt} ones (**Figure 5F**). Collectively, these data suggest that expression of both members of the *Mir181ab1* cluster favors a pro-oncogenic phenotype in epithelial lung and pancreatic cancer cells with *Kras* mutations.

Dual miR181a and miR181b expression is necessary to rescue the *Mir181ab1*-loss phenotype

The *Mir181ab1* cluster contains two miRNA genes, *Mir181a1* and *Mir181b1*. To dissect the contribution of each miRNA to the *Mir181ab1*-knockout phenotype, we took advantage of the cellular models to manipulate miR181a1 and miR181b1 expression. First, *Mir181a*, *Mir181b* or both were transduced in the KLA cell line using retroviral vectors (38) (**Suppl. Figure 3A**). These vectors included the genomic region spanning *Mir181ab1* on chromosome 1 yet differed in that the seed-sequence binding the

mRNA's 3'UTR is wild type in *Mir181a1* and *Mir181b1* (wt/wt), mutated in *Mir181a1* (mut/wt), mutated in *Mir181b1* (wt/mut) or mutated in both (mut/mut), abrogating single- or dual-miRNA function. Reconstitution of both miR181a1 and miR181b1 rescued the cell proliferation rate impaired by the cluster deletion, whereas individual expression of each miRNA was unable to fully recover the normal phenotype (**Figure 6A**). Likewise, only simultaneous expression of miR181a1 and miR181b1 successfully recovered cell growth in 3D (**Figure 6B and Suppl. Figure 3B**) and in a xenograft model (**Figure 6C and Suppl. Figure 3C**).

Additionally, the miR181 constructs were overexpressed in pancreatic cancer cells (**Suppl. Figure 3D**). Dual expression of miR181a1 and miR181b1 enhanced organoid growth in 3D assays compared to miR181ab1-deficient cells (**Figure 6D and Suppl. Figure 3E**). Additionally, combined miR181a1 and miR181b1 expression yielded significantly larger tumors in a xenograft model at the earlier time points (15 and 18 days), although this growth advantage was lost to miR181a1- or miR181b1-overexpressing cells at the end of the experiment (day 22) (**Figure 6E and Suppl. Figure 3F**). Mouse lung and pancreatic cancer cells expressing miR181ab1 underwent mitosis more efficiently than miR181ab1-deficient cells (**Figure 6F and G**). Consistent with these results, combined miR181a1 and miR181b1 overexpression shortened progression time through cell cycle of both mouse lung and pancreatic cancer cells, indicative of an increased proliferation, as shown by a significant percentage of cells reaching G2/M phase with regard to *Mir181ab1*-knockout cells (**Suppl. Figure 3G and H**). Taken together, these observations support that both miR181a1 and miR181b1 are

necessary for proficient induction of tumorigenesis by mutant *Kras*, in part by regulating cell cycle progression.

Mir181ab1 expression enhances proliferation of lung and pancreas epithelial cells

To investigate the potential role of miR181ab1 in human cancer, we queried its association with oncogenic *KRAS* expression *in vitro*. For these experiments, we used immortalized bronchio-epithelial cells (3KT), wild-type (H2126) and mutant (H1792) *KRAS* lung cancer cells (**Suppl. Figure 4A**). Upregulation of both miR181a and miR181b in wild-type *KRAS* lung cancer cells was observed upon expression of oncogenic *KRAS* (**Suppl. Figure 4B and C**). 3KT cells transduced with mutant *KRAS* proliferated faster than control cells in 2D and 3D (**Suppl. Figure 4D and E**).

Next, we investigated if miR181ab1 plays a role in malignant transformation. First, we constructed immortalized lung 3KT cells expressing *Mir181a1*, *Mir181b1* or both (**Figure 7A**). Simultaneous overexpression of both miRNAs increased proliferation of 3KT cells, while each individual miRNA had little or no effect (**Figure 7B**). Likewise, only combined overexpression of miR181a1 and miR181b1 enhanced growth of 3KT cells in 3D cultures compared to single miRNA overexpression (**Figure 7C and Suppl. Figure 4F**). These results were partially recapitulated in immortalized human pancreatic ductal epithelial cells (H6c7) transduced with the miR181 constructs (**Figure 7D**). In these cells, dual miR181a1 and miR181b1 overexpression induced the highest proliferation rate among the different constructs in 2D (**Figure 7E**). Interestingly, in 3D cultures the effect of the combined miRNAs overexpression was similar to that of miR181a expression alone (**Figure 7F and Suppl. Figure 4G**), suggesting distinct functional relevance of these two miRNAs depending on growth conditions.

Mir181ab1 plays a functionally-relevant role in human oncogenesis

To determine if miR181a1 and miR181b1 influence homeostasis of mutant *KRAS* cancer cells, we used a CRISPR/Cas9-based knockout strategy using sgRNAs flanking the genomic region spanning the miR181ab1 cluster (**Suppl. Figure 5A**). Clonal expansion of CRISPR- engineered lung cancer cells (H1792) was used to isolate two clones with partial knockout of the cluster (#1#2 and #1#4) (**Suppl. Figure 5B**) that led to >50% decreased expression of both miR181a and miR181b (**Figure 8A**). Of note, proliferation between parental cells and single cell-derived wild-type clones was very similar (**Suppl. Figure 5C**). Partial deletion of the mir181ab1 cluster decreased proliferation, colony formation ability and 3D growth (**Figure 8B-D and Suppl. Figure 5D**). These findings were associated with a decreased percentage of mitotic cells in partially mir181ab1 cluster-knockedout cells compared to wild-type ones (**Figure 8E**) as well as a delayed cell cycle progression, evidenced by larger percentage of control cells reaching G1 phase (**Suppl. Figure 5E**). Consistent with a critical role for miR181ab1, we were unable to obtain clones with full knockout (data not shown). Indeed, subsequent reintroduction of sgRNAs in the two partial knockout clones yielded no clones with full abrogation of miR181ab1, although analysis of these pools of cells did reveal greater and more efficient knockout of the cluster (**Suppl. Figure 5F**). Overall these results suggest that the miR181ab1 cluster is required for maintenance of the oncogenic phenotype in *KRAS*-driven human NSCLC.

Effective targeting of mutant *KRAS* tumors likely requires concomitant inhibition of different effector pathway. To ascertain whether miR181ab1 inhibition would enhance the effect of targeted therapies, we screened a series of inhibitors available in the clinic

or in late clinical phases. Murine lung cancer cells lacking the *Mir181ab1* cluster were more sensitive to the multi-tyrosine kinase (BCR-ABL, SRC, c-KIT) inhibitor dasatinib than those cells where *Mir181ab1* was reconstituted (**Figure 8F**). These results were recapitulated in a human lung cancer cell line expressing oncogenic KRAS where *mir181ab1* was partially knocked-out (**Figure 8G**). Taken together, these observations suggest that *miR181ab1* plays an important role in human *KRAS*-mutated oncogenesis and that its ablation could cooperate with targeted agents to improve therapeutic efficacy in *KRAS*-mutated cancers.

Mir181ab1 expression is regulated by TGF β in mutant *KRAS* lung and pancreatic cancer cells

To determine the molecular mechanisms of *Mir181ab1* regulation, we first evaluated the role of specific effector pathways using pharmacological inhibition in mouse lung and pancreatic cancer cells. *Mir181a* and *mir181b* expression levels were assessed 3 and 12 h after inhibition. Effector inactivation did not decrease either *mir181a* or *mir181b* levels, suggesting that *Mir181ab1* is not directly regulated through these effectors by KRAS (**Suppl. Figure 6A and B**).

As an additional means for *Mir181ab1* regulation, we explored the potential involvement of TGF β , a growth factor previously described to increase *miR181a* and *miR181b* expression in hepatocellular carcinoma (50). Of note, *miR181a* and *miR181b* expression was upregulated 3 h after exogenous addition of TGF β in both mouse lung and pancreatic cancer cells (**Figure 9A**). These results suggest that the TGF β signaling cascade could be involved in *Mir181ab1* regulation in both tumor types.

To ascertain potential transcriptional regulators of the *Mir181ab1* cluster, we carried out a 3-step analysis (**Figure 9B**). First, we scanned a 2 Kb region of the promoter of the mouse and human miR181ab1 gene to uncover transcription factors (TFs) binding to specific motifs in this genomic region. Next, we identified those TFs conserved across species. Lastly, we focused on those TFs that had been previously linked to RAS signaling (*Cebpa*, *Cebpb*, *Cmyb*, *Evi1*, *Meis1*, *Gata2*, *Gata3* and *Foxa2*) (51-58). Q-PCR analysis of the TFs revealed upregulation of *Gata3* in both mouse lung and pancreatic cancer cell lines after TGF β treatment for 3 h (**Figure 9C**), while no consistent upregulation in the two cell lines was found for the remaining TFs (**Suppl. Figure 6C and D**).

The similar expression pattern of *Gata3* and miR181a/miR181b, and the presence of regulatory elements in the *Mir181ab1* promoter suggested that miR181a1 and miR181b1 could be regulated by *Gata3*. To substantiate this potential association, further analysis of *GATA3* expression was done in immortalized lung epithelial cells expressing mutant *KRAS* where miR181a and miR181b levels increased upon oncogene expression (**Suppl. Figure 4C**). The results showed that *GATA3* is also overexpressed upon oncogenic *KRAS* expression (**Figure 9D**). These findings suggest that *GATA3* upregulation by *KRAS* oncogene may mediate miR181a and miR181b expression.

A miR181ab1 signature predicting poor prognosis in KRAS-driven cancers includes genes with a tumor suppressive role

Next, to define key miR181ab1 targets we first evaluated protein expression levels of *KRAS* and *RASSF1A*, previously reported as miR181 targets (59, 60). No

differential expression of either KRAS or RASSF1A was observed upon genetic mir181ab1 manipulation in our mouse and human cellular systems (**Suppl. Figure 7A and B**), suggesting no direct involvement in the miR181ab1 loss of function phenotype. We then undertook an unbiased approach to identify potential miR181ab1 targets. RNA sequencing was performed on mouse lung cancer cells (KLA) expressing wild-type (wt/wt) or seed-mutated (mut/mut) versions of *Mir181ab1*. Both cell lines were treated with adCre to deplete endogenous miR181a1 and miR181b1 in order to obtain homogeneous cell pools for comparison since single-cell qPCR revealed that expression of miR181a and miR181b is highly heterogeneous in the parental cell pool (**Suppl. Figure 8A and B**). The heterogeneous expression observed is consistent with previous studies reporting heterogeneous expression of this miRNA in cancer cell populations of distinct tissue types (50, 61, 62). A list of 111 differentially expressed genes (54 downregulated and 57 upregulated) was obtained ($B > 0$ and $\log FC / 0.5$) (**Suppl. Figure 8C and Suppl. Table 1**) and queried for molecular functions using Ingenuity Pathways Analysis (IPA). The top 10 processes associated with this gene list are cellular movement, molecular transport, carbohydrate metabolism, cell cycle, cell morphology, cell-to-cell signaling and interaction, cellular development, cellular growth and proliferation, cellular function and maintenance, and cell death and survival (**Figure 10A**). These findings are consistent with data above indicating that miR181ab1 regulates cell proliferation and cell cycle progression.

Next, we focused on those genes whose expression decreased upon exogenous reconstitution of miR181ab1, as they could include putative direct targets of the miRNA cluster. First, the list of downregulated genes was queried against the Molecular

Signature Database (MSigDB) to search for miRNAs involved in the regulation of this gene set. The top miRNA predicted to regulate genes in the downregulated list was the miR181 family (**Suppl. Table 2**), suggesting that our reconstitution approach provides an optimal model to unveil miR181ab1 direct targets. The expression decrease of these miR181ab1 putative targets (*C77370/Kiaa2022/Nexmif*, *Fbxo33*, *Meaf6*, *Med8*, *Mfsd6*, *Plekhj1*, *Rbbp7* and *Scoc*) was validated by qPCR in independent samples (**Suppl. Figure 8D**). Review of the known activity of the proteins encoded by these genes provides a potential mechanism for the effect of miR181ab1 in *KRAS*-driven oncogenesis. For example, *Fbx033* is known to promote degradation of the oncoprotein YB-1 (63), and *Rbbp7* has been reported to function similarly to the Ras negative regulator MSI1 in yeast (64), suggesting an overall tumor suppressive function.

Next, to test the clinical relevance of miR181ab1 targets in mutant *KRAS* patients, we unveiled an accurate list of putative targets in human cancer. To do this, we used a conservative approach by identifying genes for which a seed sequence in the 3'UTR was predicted to exist by at least 3 independent prediction algorithms (65). This analysis yielded a 10-gene set of downregulated genes with a seed sequence predicted to be bound by miR181a1 or miR181b1 which included (*NEXMIF*, *DEK*, *DTX4*, *FBXO33*, *MEAF6*, *MED8*, *MFSD6*, *PLEKHJ1*, *RBBP7* and *SCOC*) (**Suppl. Table 3**). The 10-gene set was interrogated against the human lung (TCGA) and pancreatic (ICGC) cancer data sets. Low expression levels of the 10-gene set were associated with poor survival in lung cancer (lung adenocarcinoma: LUAD) patients harboring *KRAS* mutations ($p=0.035$), whereas no association was found in wild-type *KRAS* LUAD patients ($p=0.958$) (**Figure 10B**). A similar trend was obtained in the analysis of

pancreatic cancer (pancreatic ductal adenocarcinoma: PDAC) patients, where low expression of the putative miR181ab1 targets was a marker of poor prognosis ($p=0.018$) (**Figure 10C**). Collectively, these data suggest that the miR181ab1 regulates a series of genes involved in the induction of the tumor phenotype whose expression associates with lung and pancreatic cancer patients' survival, in line with its strong functional role in both types of mutant *KRAS*-driven cancers.

To ascertain the role of the identified genes as direct *mir181ab1* targets, we focused on *Nexmif*, whose expression was largely decreased upon miR181ab1 overexpression. First, luciferase assays in miR181ab1-proficient mouse lung cancer cells were performed. Mutation of the miR181ab1 seed sequence in the 3'UTR of *Nexmif* led to an enhanced signal due to impaired miRNA binding (**Figure 10D**). Next, the functional implication of *Nexmif* was queried through ectopic expression in mouse lung cancer cells (**Figure 10E**). Overexpression of *Nexmif* significantly reduced cell proliferation and clone-forming capacity (**Figure 10F and G**), consistent with a predicted tumor suppressive role of miR181ab1 targets. Lastly, the clinical value of NEXMIF was investigated in human LUAD and PDAC data sets. Low levels of *NEXMIF* expression associated with a worse survival outcome in LUAD patients with *KRAS* mutations (**Suppl. Figure 8E**), with a similar trend observed for PDAC patients (**Suppl. Figure 8F**). Furthermore, NEXMIF expression was lower in LUAD patients harboring *KRAS* mutations (**Suppl. Figure 8G**).

Collectively, our data indicate that miR181ab1 is a *KRAS* effector with functional and clinical implications in *KRAS*-mutated lung and pancreatic tumorigenesis, whose expression regulation may rely on non-canonical *KRAS* downstream pathways. A

proposed model for miR181ab1 regulation and function in the context of *KRAS* mutations is illustrated in **Figure 10H**.

DISCUSSION

KRAS is a key oncogene in the development of lung and pancreatic cancer. Understanding how *KRAS* signaling leads to gene expression changes that ultimately result in tumorigenesis is of paramount importance for the development of effective therapies. Given the complexity of the effector output downstream of *KRAS*, it is likely that small changes in the expression of multiple proteins can impact the relative strength of this output and thus strongly regulate oncogenesis. Here we demonstrate that miR181ab1 is a critical mediator of *KRAS* oncogenic effects in mouse and human. While alterations such as gene amplification, deletion and translocation are common events in genomic regions hosting miRNAs and can influence their expression in cancer (66), direct regulation by oncogenes and tumor suppressors can also significantly influence miRNA expression levels (27-31). Previous studies have suggested upregulation and functional roles for miR21, miR450b-5p and miR30c in response to oncogenic *KRAS* in cancer (14-17). Here we used primary mouse embryonic fibroblasts with conditional expression of oncogenic *KRAS* (36) to identify key dysregulated miRNAs. This approach likely identifies different microRNAs compared to over-expression of *KRAS* which is known to lead to a distinct outcome in primary cells. Having first identified miR181 RNAs in MEFs, we then utilized several genetically engineered mouse models to determine the phenotype of loss of function of the *Mir181ab1* cluster in epithelial cells of the lung or pancreas. These studies convincingly demonstrate a key role for miR181ab1 in regulating the pro-oncogenic transcriptional output of oncogenic *KRAS*, a finding with potentially profound implications for the search of novel approaches to target *KRAS*-mutant cancers.

MiR181 was first described as a miRNA preferentially expressed in B-lymphoid cells of mouse bone marrow (67), and subsequent studies underscored a role for the *Mir181ab1* cluster in natural killer T cell development and T cell homeostasis (38, 40, 41). In cancer, the miR181 family is upregulated in several cancer types including T-cell acute lymphoblastic leukemia (T-ALL) (68), pancreatic cancer (43, 44) and high-risk neuroblastoma (69). Moreover, early studies in T-ALL, hepatocellular carcinoma and breast cancer demonstrated a potential functional oncogenic role for the miR181 family in cancer (38, 50, 61, 62). However, members of the miR181 family have been reported as tumor suppressors in other cancers such as AML (70), colorectal cancer (71) and lung cancer (72) and *KRAS* was recently proposed as a direct target of miR181a in AML (73). While tissue-specific differences may account for some of these discrepancies in miR181ab1 expression and function, the data described here unequivocally demonstrate that miR181ab1 functions as a pro-oncogenic miRNA in lung and pancreatic tumors where *KRAS* oncogene is expressed. The miR181ab1 cluster is highly conserved across human-mouse species. Genetic ablation of this cluster in mouse and human models showed a consistent deleterious phenotype via a similar cellular mechanism, involving regulation of cell cycle, strongly favoring a conserved mechanism of action across species. Moreover, our results provide evidence suggesting that the main contributor of the miR181 family to the tumor phenotype induced by mutant *KRAS* is miR181ab1, similarly to what have been reported previously in a GEMM of Notch-induced T-ALL (38). The differential expression of the different miR181 clusters may be explained by the presence of distinct transcriptional regulatory elements in the promoter region of each cluster. Moreover, regulation of *Mir181ab1* by

specific transcriptional regulators, such as GATA3, may require the action of non-canonical KRAS downstream pathways involving TGF β activity. Nonetheless, genetic inhibition of the remaining two miR181 clusters, *Mir181ab2* and *Mir181cd* would be required to definitively resolve their functional implication in mutant *KRAS*-driven oncogenesis. More importantly, despite the fact that the cellular systems deployed in this study suggest a cell-intrinsic effect of miR181ab1, further analyses to investigate how miR181ab1-depleted cells may influence other cell types to foster tumor formation and progression may shed more light into the mechanism of action of this miRNA cluster in *KRAS*-driven oncogenesis.

Mechanistically, we provide data indicating that expression of both members of the *Mir181ab1* cluster, *Mir181a1* and *Mir181b1*, is necessary to induce a complete oncogenic phenotype in *KRAS*-mutated tumors. Our current findings suggest a non-redundant function of miR181a1 and miR181b1, however they do not completely rule out the possibility that both resident miRNAs may be needed to generate a threshold level of miR181 RNA required for the full oncogenic phenotype, especially given that they target the same target 3'UTR sequence.

We also provide functional evidence that the miR181ab1 target *Nexmif* (*KIAA2022/KIDLIA*) has a functional role in *KRAS*-mutated tumors. NEXMIF is a nuclear protein that has been implicated in N-Cadherin and δ -catenin signaling (74). To our knowledge, this gene has not previously been implicated in *KRAS* signaling or in oncogenesis. It is likely that miR181ab1 functions to dysregulate a large number of genes and that together these impact on *KRAS* oncogenesis. Among other miR181ab1 targets, *FBXO33* mediates degradation of the oncoprotein YB-1 upon apoptosis (63).

Additionally, *RBBP7* polyubiquitinates HUWE1 (75), an E3 ubiquitin ligase that interacts with PCNA to alleviate replication stress (76), a type of stress that characterizes mutant *KRAS* tumors (77). These findings suggest that miR181ab1 may sustain *KRAS* oncogene action in part by stabilizing the expression of cancer-promoting genes. Further efforts beyond this study will be required to address these molecular relationships.

Our studies identify miR181ab1 as a novel molecular target whose inhibition could be exploited to treat lung and pancreatic cancer patients. This is particularly significant as our data suggest that inhibition of this cluster is relevant not only to tumor initiation but also for tumor progression and maintenance. Furthermore, functional testing of miR181ab1's function in other mutant *KRAS* tumors beyond lung and pancreatic cancer would be highly interesting, as those could also benefit from direct inhibition of this miRNA cluster. Given the limited number of effective treatments for patients harboring *KRAS* mutations, strategies based on miR181ab1 inhibition could represent a valuable therapeutic approach. Indeed, we showed that combinatorial approaches involving concomitant inhibition of miR181ab1 and dasatinib administration yielded a larger antitumor response in mutant *KRAS* tumors. In this regard, *Mir181ab1* knockout mice as well as triple knockout mice without *Mir181ab1*, *Mir181ab2*, and *Mir181cd8* mice are normal and viable (38), what suggests that at least inhibition of *KRAS*-driven tumors by targeting miR181ab1 could be achieved without significant toxicity. Efforts to develop miRNA inhibitors are currently underway and various miRNA therapeutics, including anti-oncomiRs, have reached phase I and II clinical trials (78). Although challenges related to effective route of administration, long-lasting action, and

potential adverse reactions are yet to be addressed, miR181ab1 inhibition could represent a new paradigm for the treatment of *KRAS*-mutated tumors.

METHODS

Cell lines. Early passage MEFs (p3-4) from e13.5 embryos were used for experiments. Mouse lung cancer (KLA -KR181^{ff/-}) and pancreatic cancer (KPC181^{wt} and KPC181^{ko}) cell lines were isolated from corresponding GEMMs. MEFs and mouse cancer cell lines were grown in DMEM supplemented with 10% FBS and 1% Penicillin-Streptomycin. Human non-small cell lung cancer used were either wild-type *KRAS* (NCI-H2126) or mutant *KRAS* (NCI-H1792) were grown in RPMI1640 supplemented with 10% FBS and 1% Penicillin-Streptomycin and were acquired from ATCC. 3KT cells were a kind gift by John Minna (79). 3KT and H6c7 cells (Kerafast Inc.) were grown in keratinocyte medium (GIBCO). Human cancer cell lines were authenticated by the Genomics Unit at CIMA using Short Tandem Repeat profiling (AmpFLSTR® Identifier® Plus PCR Amplification Kit). Cell lines were tested with the MycoAlert Mycoplasma Detection Kit (LONZA). Only mycoplasma negative cells were used.

3D cultures. Previously-published protocols for the generation of pancreatic cancer organoids were followed (80). Organoids images were taken using an inverted microscope DMI3000 from Leica at 10x. Diameter quantification was done with ImageJ.

Luminex-based miRNA profiling. Characterization of miRNA profiles in wild-type and mutant *Kras* MEFs was done following previously-described protocols (37).

Mouse work. For lung cancer experiments, *Kras*^{LSLG12D/+}; *Mir181ab1*^{-/-} mice were in a mixed 129/Sv and C57bl/6 background whereas *Kras*^{LSLG12D/+}; *Mir181ab1*^{flox/flox} mice were in a C57bl/6 background. *Kras*^{LA2/+}; *Mir181ab1*^{flox/flox}; *Rosa26Cre*^{ERT2} compound mice were in a mixed 129/Sv and C57bl/6 background. For pancreatic cancer experiments, *Ptf1a*^{Cre/+}, *Kras*^{LSLG12D/+}; *Trp53*^{ff} and *Mir181ab1*^{-/-} mice were on a C57bl/6

background. Mice on a mixed background were backcrossed for at least 4 generations. Male and female mice were used indistinctively for mouse genetics experiments. Only Rag2^{-/-} female mice were used for allograft experiments. Further details of mouse work can be found in Supplementary Methods.

Magnetic Resonance Imaging. Magnetic Resonance Imaging (MRI) experiments were performed on *Ptf1a*^{Cre/+}; *Kras*^{LSL-G12D/+}; *Trp53*^{flox/flox} and *Ptf1a*^{Cre/+}; *Kras*^{LSL-G12D/+}; *Trp53*^{flox/flox}; *Mir181ab1*^{flox/flox} mutant mice at the age of 7 weeks. MRI was performed using the Biospec USR70/30 (Bruker Biospin MRI, Billerica, MA). MR images were analyzed using open source Horos processing software. Tumor volume (V) was assessed, using three-dimensional volumetric measurements according to the modified Simpson rule

$$V = T_s \times \left(\sum_{i=1}^n A_i \right)$$

where Ts is the thickness of each slice, i is the individual slice number and n is the total number of slices.

Tumor area analysis. Micrographs of H-E slides from multiple lung sections for each sample were obtained and pictures taken at 20X magnification. Bioquant software was used to montage the entire lung sections and to calculate tumor area for each sample. Tumor area was calculated with the manual measurement feature in Bioquant.

Histology and immunohistochemistry. Immunohistochemistry (IHC) was performed on formalin-fixed, paraffin-embedded mouse and human tissue sections using a biotin-avidin method as described before (81). The following antibodies were used: cleaved caspase 3 (1:200), Ki67 (1:1.000) and MUC5AC (1:500). Sections were developed with

DAB and counterstained with hematoxylin. Pictures were taken using a Leica microscope equipped with the LAX software. IHC analysis was performed using ImageJ software.

Quantitative PCR (qPCR) analysis. RNA was analyzed as previously published (82). MEFs were treated for 72 h with adenoviruses and grown in fresh medium for additional 72 h. Then, MEFs were plated and RNA harvested after 24 h with TRIzol reagent (Invitrogen). KLA cells were treated for 48 h with adenoviruses and then fresh medium was added for 24 h before RNA isolation. cDNA was synthesized with a DyNAmo cDNA synthesis kit (F470, New England Biolabs) and qRT-PCR was performed using SYBRGreen (Applied Biosystems). GAPDH and HPRT were used as housekeeping genes. For miRNA analyses, taqman assays were used (miR181a: ID 000480; miR181b: ID 001098). RNU6 and sno135 were reference genes in mouse cell lines. RNU6 and RNU48 were used as housekeeping genes in human cell lines.

Northern blot. The non-radioactive miRNA Northern Blot Assay Kit including 2 gels (NB-0001), miR181a-5p(HS) (HP-0081) and miR181b-5p(HS) (HP-0082) (Signosis) was used to study miR181a1 and miR181b1 expression in mouse lung tumor cells KLA following the instructions from the manufacturer. 10 µg of RNA from KLA cells treated with adEmpty or adCre for 48 h was used. A ChemiDoc™ Gel Imaging System (Bio-Rad) was utilized to acquire Northern blot images.

Cell proliferation assay. Cell proliferation in 2D was assessed using the CellTiter 96® AQueous Non-Radioactive Cell Proliferation Assay, MTS (Promega). Experiments were read on the indicated days according to manufacturer's instructions and normalized to

day 1 post-seeding. Cell proliferation in 3D was measured by the CellTiterGLO (Promega) and normalized to day 1 post-seeding.

Clonogenic assay. Two thousand H1792 cells were seeded in a 6-well plate for 10 days. Then, wells were washed with DPBS and fixed for 10-15 minutes with 4% formaldehyde. Fixed cells were dyed with 0.5% crystal violet for 5 minutes. Crystal violet was diluted in DPBS-Acetic Acid 10% and absorbance was measured at 570nm.

CRISPR-Cas9 strategy. SgRNAs complementary to 5' and 3' flanks of mir181ab1 gDNA were designed using a crispr.mit.edu tool. Then, a combination of 5'-3' guides was cloned in pX333 from addgene (83). Cells were transduced with 10:1 ratio of pX333:pMax GFP (Lonza). Single GFP positive cells were sorted in a p96 plate using FACSARIA IIU (Becton Dickinson) and expanded for experiments.

Phospho-histone 3 (p-H3) immunofluorescence. KLA wt/wt and KLA mut/mut adCre-treated (10000 cells/well), KPC181ko wt/wt and KPC181ko mut/mut, H1792 control and CRISPR'ed miR181 cells were seeded in 8 chamber polystyrene vessel, tissue culture Treated Glass Slides (354108; Falcon) and cultured for 72 h. Then, phospho-Histone 3 (p-H3) immunofluorescence was performed using P-H3 (S10) antibody (1:800, 9701, Cell Signaling) and Alexa-594 Goat anti-rabbit (A11037; Life Technologies). Nuclei were dyed with dapi (1:1000). Images were taken at 5x and 20x using a fluorescence microscope (Axioimager M1; Zeiss) and percentage of p-H3 positive cells was analyzed using FiJi software.

Pharmacological inhibitor and TGF β treatment. For dasatinib (Selleck) treatment, KLA wt/wt and KLA mut/mut cells treated with adCre or H1792 control and CRISPR-knockedout cells were seeded in 96-well plates. After overnight culture, dasatinib was added at the indicated concentrations for 72 h. For TGF β treatment, KLA and KPC cells were seeded and treated for 3 h at a concentration of 10 ng/mL of recombinant human TGF β (Preprotech).

RNA sequencing (RNAseq) analysis. Samples were prepared with Illumina TruSeq Stranded mRNA kit as per manufacturer's indications and sequenced as reverse paired-end (100 bp) on the HiSeq-4000 sequencer. Details of RNAseq analysis are provided in Supplementary Methods. The GEO accession number is GSE128478.

Pathway analysis. The biological knowledge extraction and network representation was complemented through the use of Ingenuity Pathway Analysis (Ingenuity Systems, <http://www.ingenuity.com>).

Luciferase assay. Complementary oligonucleotides containing the wild-type or a mutated sequence of the *Nexmif* 3'UTR were cloned into the psiCHECKTM-2 vector using XhoI and NotI restriction sites. KLA wt/wt and mut/mut cells pretreated with adCre (48 h) were seeded in a 24-well plate. Cells were transfected with 0.5 μ g of plasmids using the X-tremeGENETM HP DNA Transfection Reagent (6366244001; Roche) for 72 h. Media was refreshed for 24 h and renilla and luciferase were measured using the Dual Luciferase Report Assay System (Promega), following manufacturers' instructions, and a plate reader (Berthold).

Wild-type 3'UTR primers:

Forward (5'-3')

aagttctcgaggctgcctacagagtttgaatgtacttactagactttagttagagacccttttatgaatgtaacctgtttctgttg
tttaaatatttgtagctgaatgtatggtgaaactgtcatgcggccgcttgaa

Reverse (5'-3')

ttcaagcggccgcatgacagtttcaccatacattcagtcacaaatatttaacaaacagaaacaggttacattcataaaaa
gggtctctaactaaagtctagtaagtacattcaaaactctgtaggcagcctcgagaactt

Mutated 3'UTR primers:

Forward (5'-3')

5'aagttctcgaggctgcctacagagttggggggacttactagactttagttagagacccttttaggggggaacctgtttctg
ttgtttaaatatttgtagcggggggatggtgaaactgtcatgcggccgcttgaa

Reverse (5'-3')

5'ttcaagcggccgcatgacagtttcaccatcccccgtcacaaatatttaacaaacagaaacaggttccccctaaaa
agggtctctaactaaagtctagtaagtccccccaaactctgtaggcagcctcgagaactt

Nexmif overexpression. Nexmif ORF (NM_001077354.2) was used to replace Nanog in the pSIN-EF2-Nanog-Puro vector (<https://www.addgene.org/16578/>) using SpeI and EcoRI. Lentiviruses were produced in HEK293T cells. KLA cells were infected and selected with 5 µg/ml puromycin.

Survival Analyses. Survival analysis was conducted on the selected gene set using RNAseq datasets of LUAD patients (TCGA) and PDAC (ICGC) (3). Log-rank test was used to calculate the statistical significance of differences observed among Kaplan-Meier curves as previously described (84).

Statistics. Sample size was chosen using <http://www.biomath.info/power/ttest.htm> or based on similar experiments previously published by the authors. For comparison of two groups, samples were explored for normality (Shapiro–Wilk test) and variance (Levene test). Groups with normal distribution of samples followed a *t*-test. Non-normal samples were analyzed using a Mann–Whitney test (equal variances) or a Median test (unequal variances). For more than two groups comparison, a residual test was performed to study normality and Levene test assessed homoscedasticity. ANOVA, Brown Forsythe, Kruskal Wallis or Median tests were performed depending on data distribution. A post-hoc test (Dunnet) explored paired comparisons. All analyses were two-tailed. Error bars correspond to either standard deviation (SD, $n < 8$) or standard error of the mean (SEM, $n \geq 8$) for parametric variables, and interquartile range for non-parametric variables, as indicated for each experiment. Statistical analyses were done using SPSS software.

Study approval. All experiments in mice were performed according to MDACC Institutional Animal Care and Use Committee (IACUC 00001636), UCSF Committee on Animal Care (APLAC) and to University of Navarra Ethical Committee on Animal Research (CEEA; protocol # 068-13). Regarding human data, only normalized/processed data of coded clinical information was made available to this study to preserve patients' anonymity.

AUTHORS' CONTRIBUTION

A.S-C. and S.V. conceived the project. C-Z.C., P.K.M, A.S-C and S.V. designed and planned the experiments. P.K.M, A.S-C and S.V. supervised the work. E.G. and A.L. carried out computational analyses. K.V, O.E., K.K., S.H., A.T., L.C.S., N.M.F., R.F., A.V., M.R., R. E-C., I.M., F.L., J.L. and M.P-S. contributed to experimental design and execution. C-Z.C. provided *Mir181^{-/-}* and *Mir181^{ff}* mice. K.V., O.E., K.K., S.H., C-Z.C., P.K.M. A.S-C., S.V. were responsible for the data analysis and interpretation. K.V., O.E., P.K.M., A.S-C., S.V. wrote the manuscript and were in charge of the manuscript preparation. All the authors reviewed and edited the manuscript.

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FIGURES AND FIGURE LEGENDS

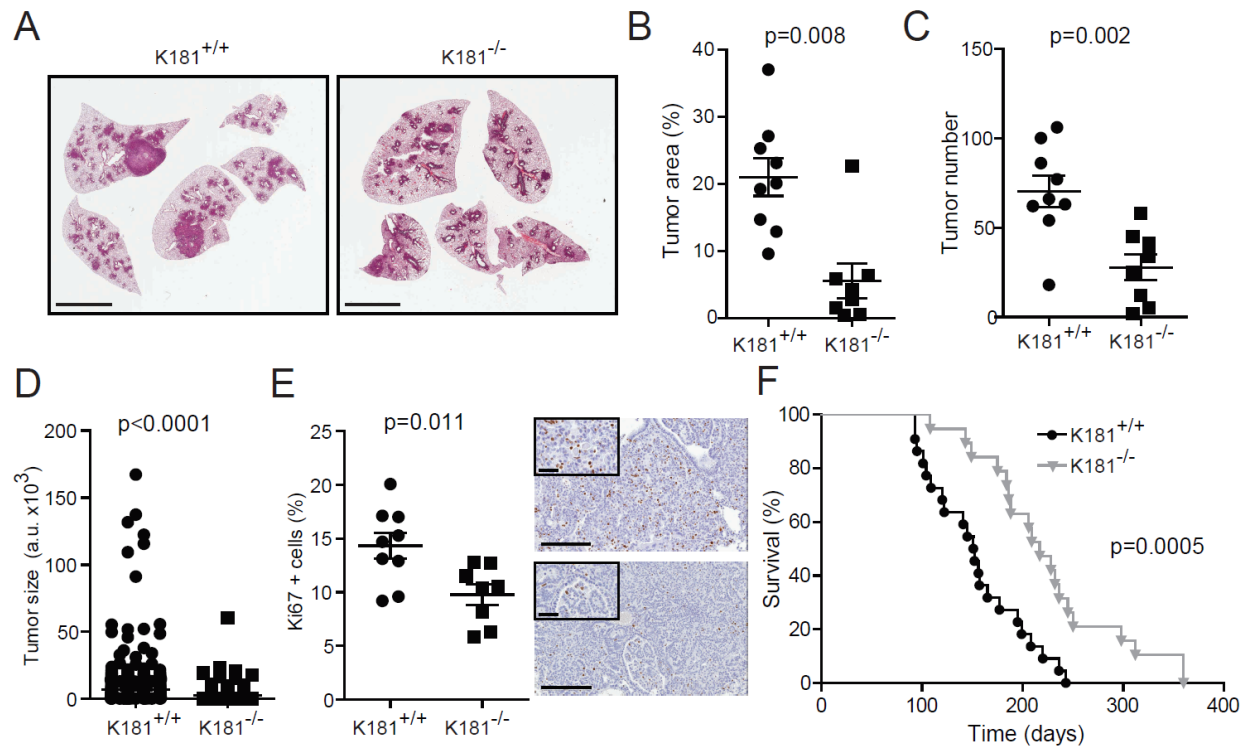


Figure 1. Systemic *Mir181ab1* ablation impairs *Kras*-driven lung cancer. (A) Representative H-E-stained sections of *K181*^{+/+} and *K181*^{-/-} lungs 20 weeks post-adCre infection. Scale bar is 5 mm. (B) Average tumor area percentage in *K181*^{+/+} (n=9) and *K181*^{-/-} (n=8) groups compared by *t*-test. (C) Mean number of tumors per mouse in *K181*^{+/+} (n=9) and *K181*^{-/-} (n=8) mice compared by *t*-test. (D) Average tumor size in *K181*^{+/+} (n=632) and *K181*^{-/-} (n=222) groups compared by Mann-Whitney U test. (E). *Left.* Average percentage of Ki67+ cells in tumors from *K181*^{+/+} (n=9) and *K181*^{-/-} (n=8) mice compared by *t*-test. *Right.* Immunohistochemistry for Ki67 expression in representative sections. Scale bars 200 μ m (inset: 50 μ m). (F). Kaplan-Meier plot of *K181*^{+/+} (n=23, median survival=151.5) and *K181*^{-/-} (n=19, median survival=217) mice (log-rank test).

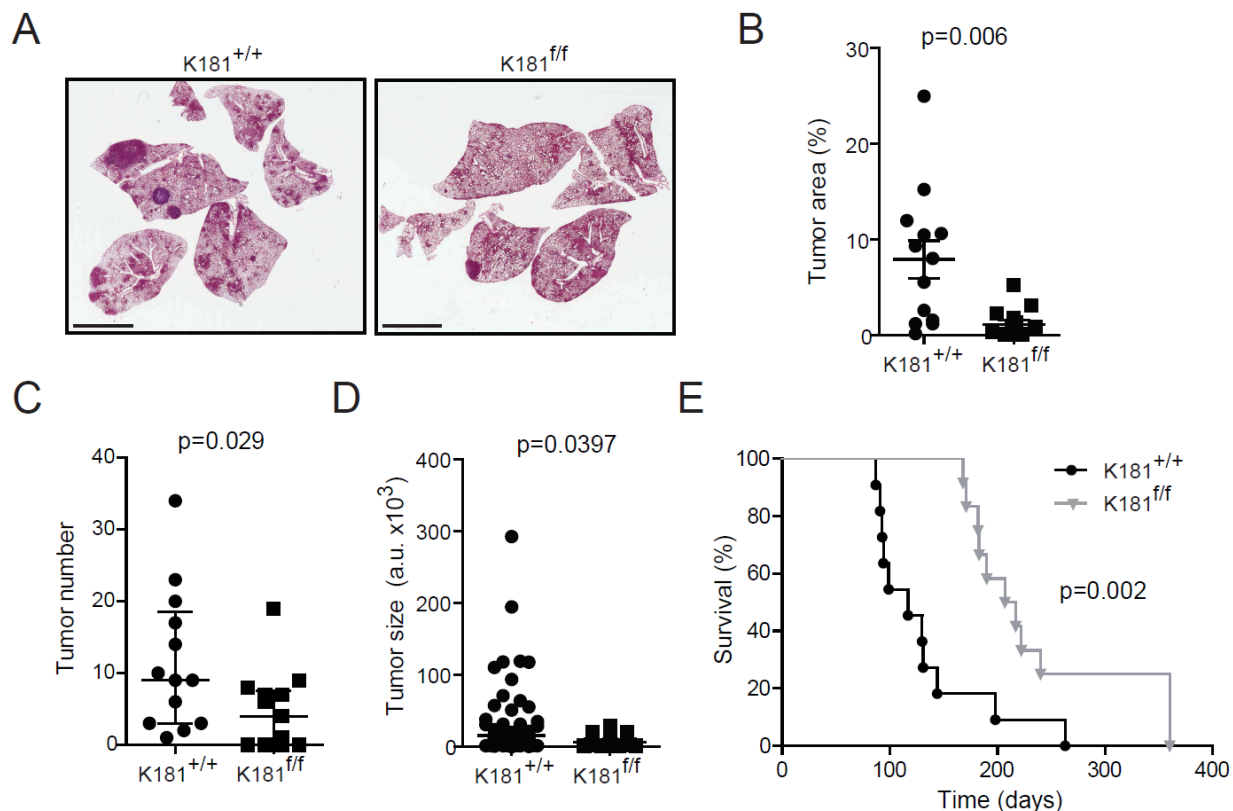


Figure 2. Conditional *Mir181ab1* knockout negatively impacts lung cancer formation. (A) Representative H-E stained sections of $K181^{+/+}$ and $K181^{ff}$ lungs 20 weeks post-adCre infection. Scale bar is 5 mm. (B) Quantification of tumor area in $K181^{+/+}$ (n=13) and $K181^{ff}$ (n=14) mice compared by *t*-test. (C) Mean number of tumors per mouse in $K181^{+/+}$ (n=13) and $K181^{ff}$ (n=14) mice compared by Mann-Whitney U test. (D) Average tumor size of $K181^{+/+}$ (n=151) and $K181^{ff}$ (n=61) mice compared by *t*-test. Error bars correspond to SEM. (E) Kaplan-Meier plot of $K181^{+/+}$ (n=10, median survival=117) and $K181^{ff}$ (n=13, median survival=212) mice (log-rank test).

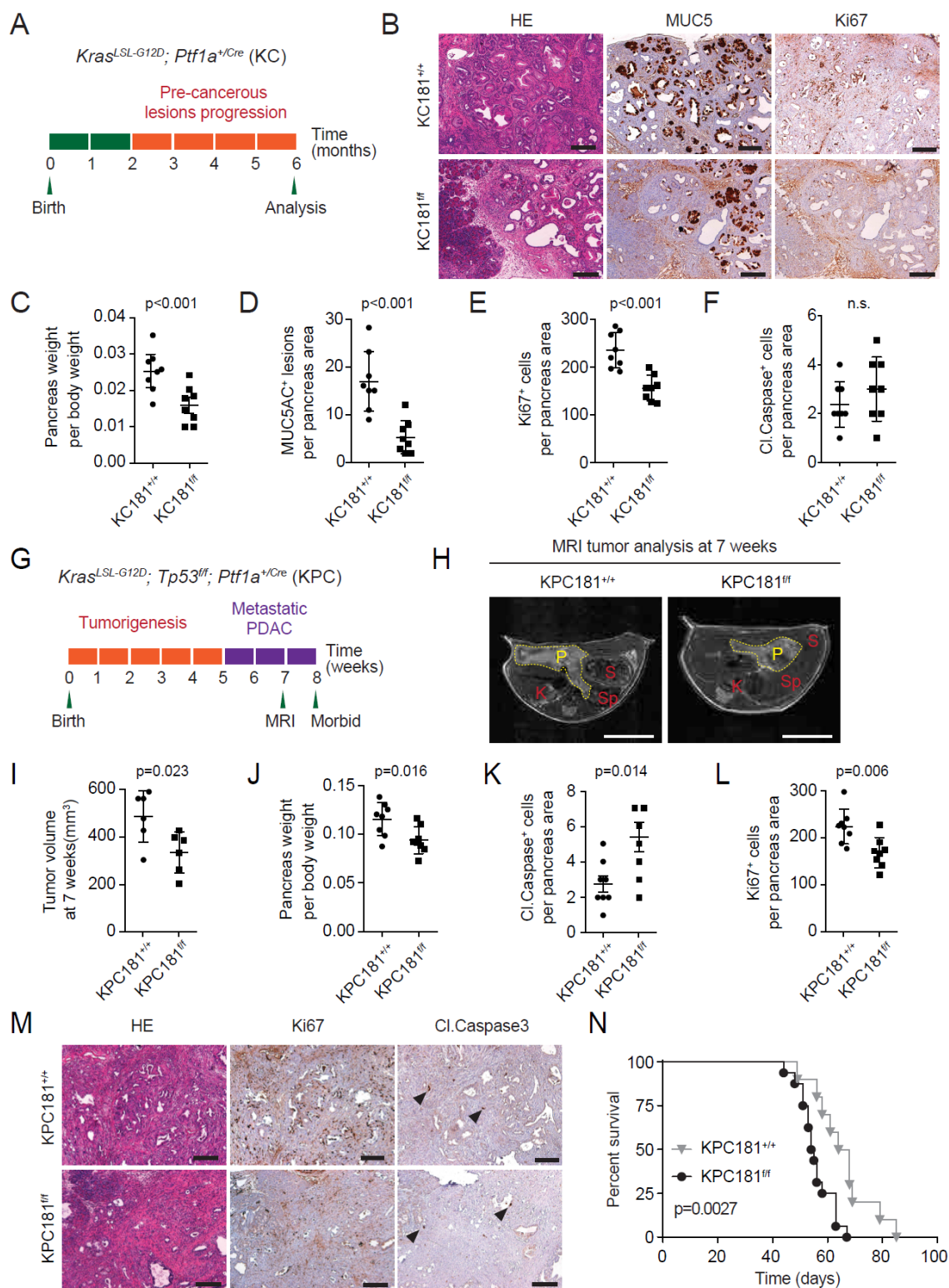


Figure 3. *Mir181ab1* deletion represses *Kras*-driven pancreatic tumorigenesis *in vivo*.

(A) Schematic representation of the tumor initiation experiment used to measure

precancerous (PanINs) lesion formation. (B) Representative H-E staining sections and IHC for MUC5AC, a marker of PanIN lesions, and Ki67, a marker of cell proliferation (n=8). Scale bars, 100 μ m. (C) Quantification of pancreas weight at 6 months in KC181^{ff} (n=8) and control KC181^{+/+} (n=8) mice compared by *t*-test. (D-F) Quantification of MUC5AC-positive lesions, Ki67-positive proliferating cell and cleaved caspase 3 (CC3)-positive apoptotic cells in KC181^{ff} (n=8) and control KC181^{+/+} (n=8) mice. Data are compared by *t*-test. (G) Schematic representation of the tumor progression experiment used to measure PDAC development. (H) Representative MRI scan in 7th week in KPC181^{ff} and KPC181^{+/+} mutant mice. Yellow dotted lines indicate pancreas area; abbreviations used: P=pancreas, S=stomach, K=kidney, Sp=spleen. Scale bars, 1cm. (I) Tumor volume quantification in KPC181^{ff} and KPC181^{+/+} mutant mice at 7 weeks of age based on MRI scan (n=6 per group). Data are compared by *t*-test and represented as mean \pm SEM. (J) Quantification of pancreas weight to body weight in KPC181^{ff} and KPC181^{+/+} (n=8 mice/group) compared by *t*-test. (K-L) Quantification of Ki67-positive proliferating cell and CC3 apoptotic cells in pancreas tumors of KPC181^{ff} and KPC181^{+/+} mutant mice (n=8 mice/group) compared by *t*-test. (M) Representative H-E and IHC for Ki67 and CC3 in pancreas tumors of KPC181^{ff} and KPC181^{+/+} mice. Scale bars, 100 μ m. (N) Kaplan-Meier survival curves of KPC181^{+/+} mice (n=16; median survival=54.5 days) and KPC181^{ff} mice (n=10; median survival=66 days) (log-rank test).

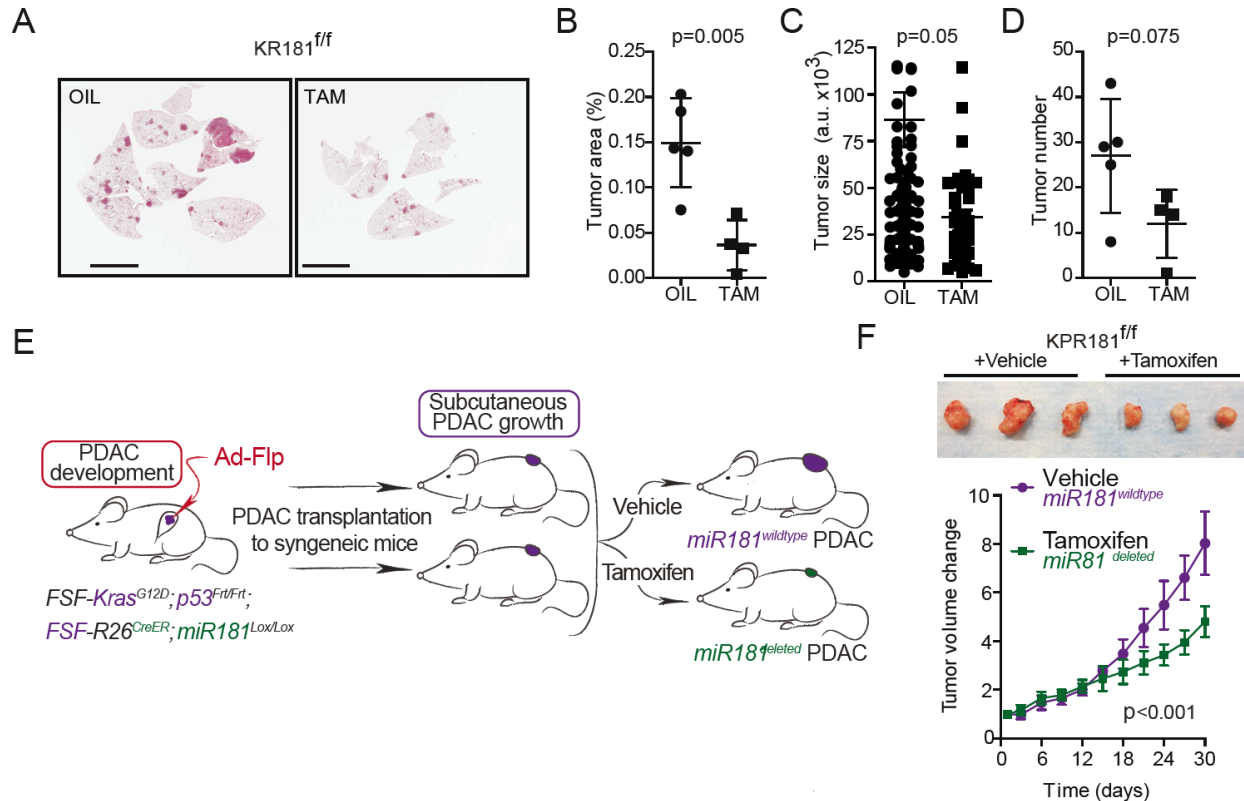


Figure 4. Mutant *Kras* lung and pancreatic cancer progression is dependent on miR181ab1 expression. (A) Representative H-E stained sections of KR181^{ff/ff} vehicle and tamoxifen treated lungs. Scale bar is 5 mm. (B) Tumor area in KR181^{ff/ff} mice treated with vehicle (oil, n=5) or tamoxifen (n=4) compared by *t*-test. (C) Average of tumor size in KR181^{ff/ff} vehicle- (n=135) and tamoxifen-treated (n=48) groups compared by median test. (D) Mean number of tumors per mouse in KR181^{ff/ff} vehicle- and tamoxifen-treated mice compared by *t*-test. (E) Schematic representation of experiment. Ad-Flp: adenoviral FLP recombinase. (F). Representative images of xenografted *Kras* mutated PanIN from KPR181^{ff/ff} mice treated with vehicle (n=8) or tamoxifen (n=8) (upper panel) and bar graph of the average of tumor size in each group (lower panel) compared by *t*-test.

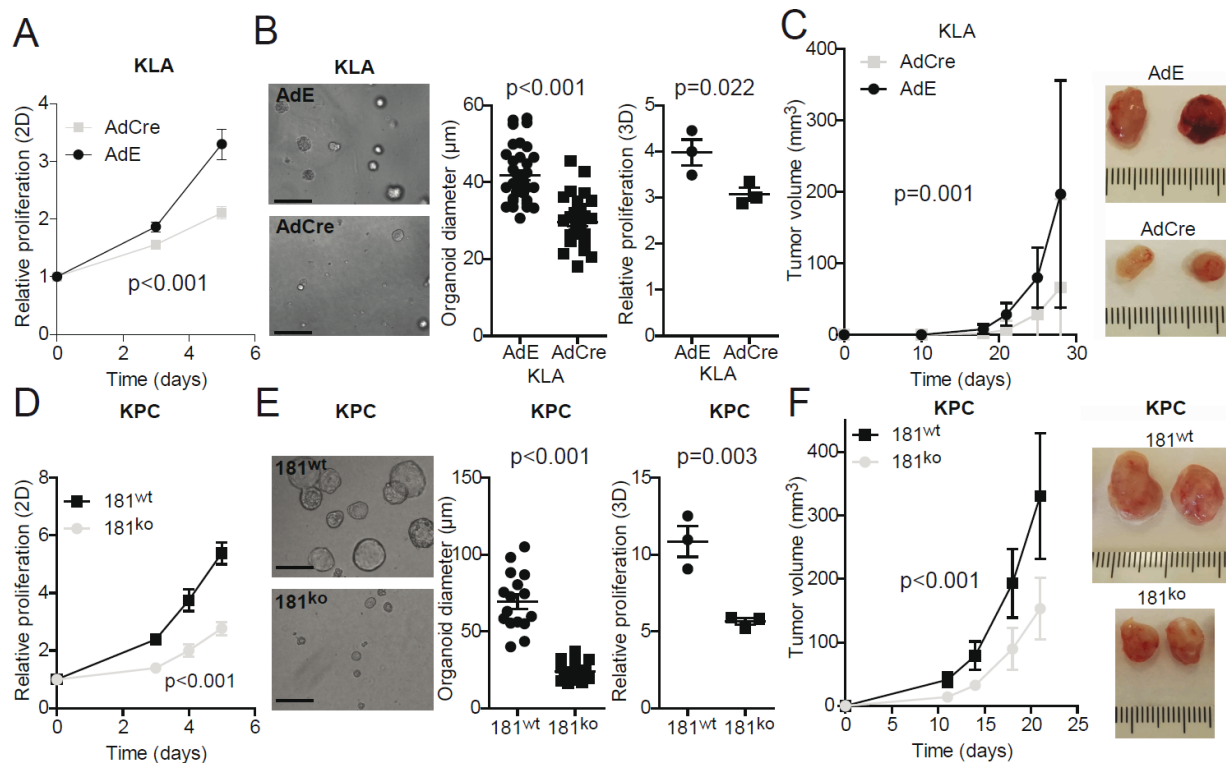


Figure 5. Effect of *Mir181ab1*-loss in mutant *Kras*-driven cancer cells. (A) Cell proliferation of KLA cells, plated after 48 h adCre or adEmpty (adE) treatment, assessed by MTS (n=5) and compared by *t*-test. (B) 3D culture of KLA cells previously treated with adCre or adE for 48 h. *Left*. Representative KLA organoids images at day 4 after seeding. Scale bars: 100 μm. *Middle*. KLA organoids size quantification at day 4 post-seeding (n=29-45) compared by *t*-test. *Right*. Proliferation of KLA organoids measured by CellTiterGLO (n=3) and compared by Mann-Whitney U test. (C) *Left*. Average tumor volume of allografts from mouse KLA cells previously treated with adE or adCre for 48 h (n=6 per group) and compared by *t*-test. *Right*. Representative images of KLA tumors in the presence and absence of *Mir181ab1*. (D) Cell proliferation of KPC miR181^{wt} and miR181^{ko} cells assessed by MTS (n=6) and compared by *t*-test. (E) *Left*. Representative images of KPC miR181^{wt} and miR181^{ko} organoids at day 4. Scale bars: 100μm. *Middle*. Organoids size quantification at day 4 post-seeding (n=16) and compared by *t*-test.

Right. Proliferation of KPC miR181^{wt} and miR181^{ko} organoids measured by CellTiterGLO (n=3) and compared by Mann-Whitney U test. (F) *Left.* Average tumor volume of allografts from mouse KPC miR181^{wt} and miR181^{ko} cells (n=8 per group) and compared by *t*-test. *Right.* Representative images of KPC miR181^{wt} and miR181^{ko} tumors. Proliferation assays (A, B, D and E) are representative of three independent experiments.

Left. Representative images of KLA miR181 organoids at day 4 after 48 h treatment with adE or adCre. Scale bars: 100µm. *Right.* KLA miR181 organoids size quantification at day 3 post-seeding (n=14-20) and compared using ANOVA. (C) Average tumor volume of allografts from mouse KLA cells transduced with the different *Mir181a1* and *Mir181b1* constructs, previously treated with adE or adCre (n=6 per group), assessed by ANOVA. (D) 3D culture of KPC miR181^{ko} cells transduced with the *Mir181a1* and *Mir181b1* constructs. *Left.* KPC miR181^{ko} organoids at day 4 after seeding. Scale bars: 100 µm. *Right.* Organoids size quantification at day 4 post-seeding (n=8-18) and compared by ANOVA. (E) Average tumor volume of allografts from mouse KPC miR181^{wt} and miR181^{ko} cells (n=6 per group) and compared using ANOVA. (F and G) Phospho-histone H3 immunofluorescence images and analyses of wt/wt and mut/mut adCre-treated KLA cells (F), and in KPC181^{ko} wt/wt and mut/mut cells (G) 72 h after seeding. Inset is 50 µm. (n=6-8). Results were compared by Kruskal-Wallis test.

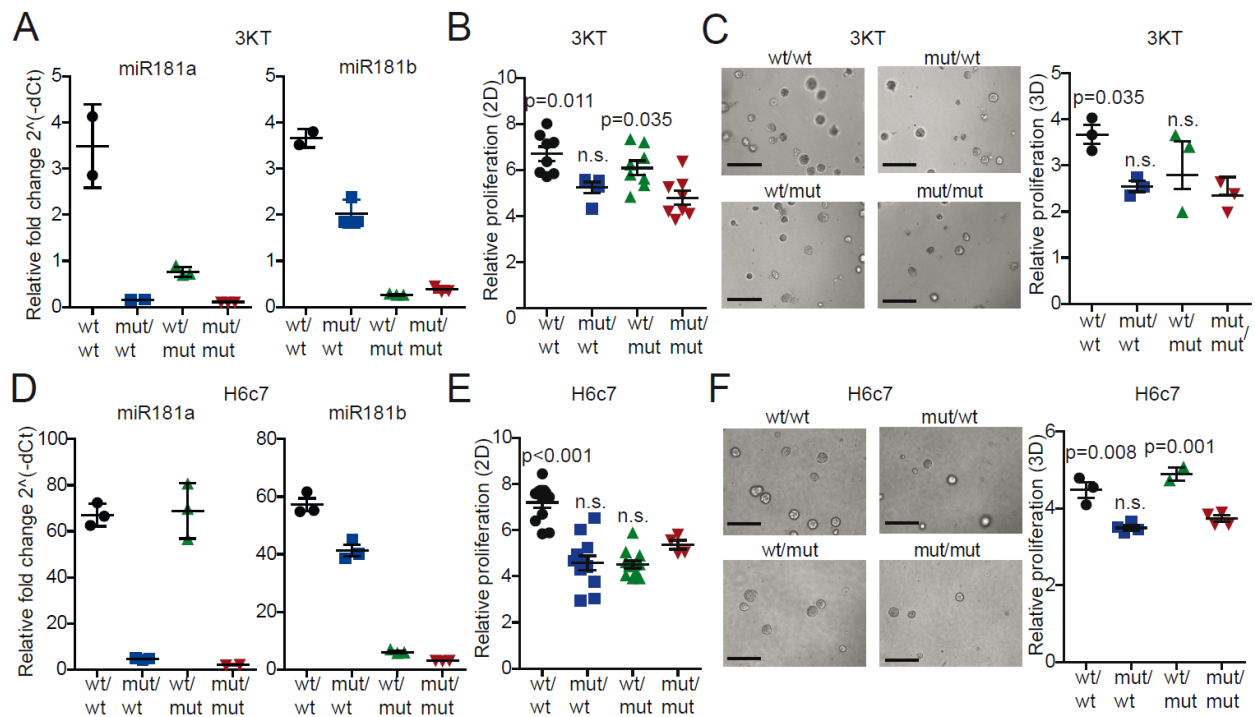


Figure 7. MiR181ab1 promotes 2D and 3D proliferation in lung and pancreas epithelial cells. (A) miR181a and miR181b expression by quantitative PCR in 3KT cells transduced with the different *Mir181a1* and *Mir181b1* constructs (n=3). (B) Cell proliferation of the same cells as in A assessed by MTS (n=5-8) and compared using ANOVA. (C) 3D culture of the same cells as in A. *Left.* Representative images of organoids at day 4. Scale bars: 100 μ m. *Right.* Proliferation of organoids measured at day 4 relative to day 1 after seeding by CellTiterGLO (n=3) and compared by ANOVA. (D) miR181a and miR181b expression in human pancreatic ductal cells (H6c7) transduced with the different *Mir181a1* and *Mir181b1* constructs (n=3). (E) Cell proliferation of the same H6c7 cells as in D assessed by MTS (n=4-12) and compared by ANOVA. (F) 3D culture of the same H6c7 cells as in D. *Left.* Representative images of organoids at day 3. Scale bars: 100 μ m. *Right.* Proliferation of organoids measured at day 4 relative to day 1 after seeding by CellTiterGLO (n=3) and compared by ANOVA and Dunnett multiple comparison test.

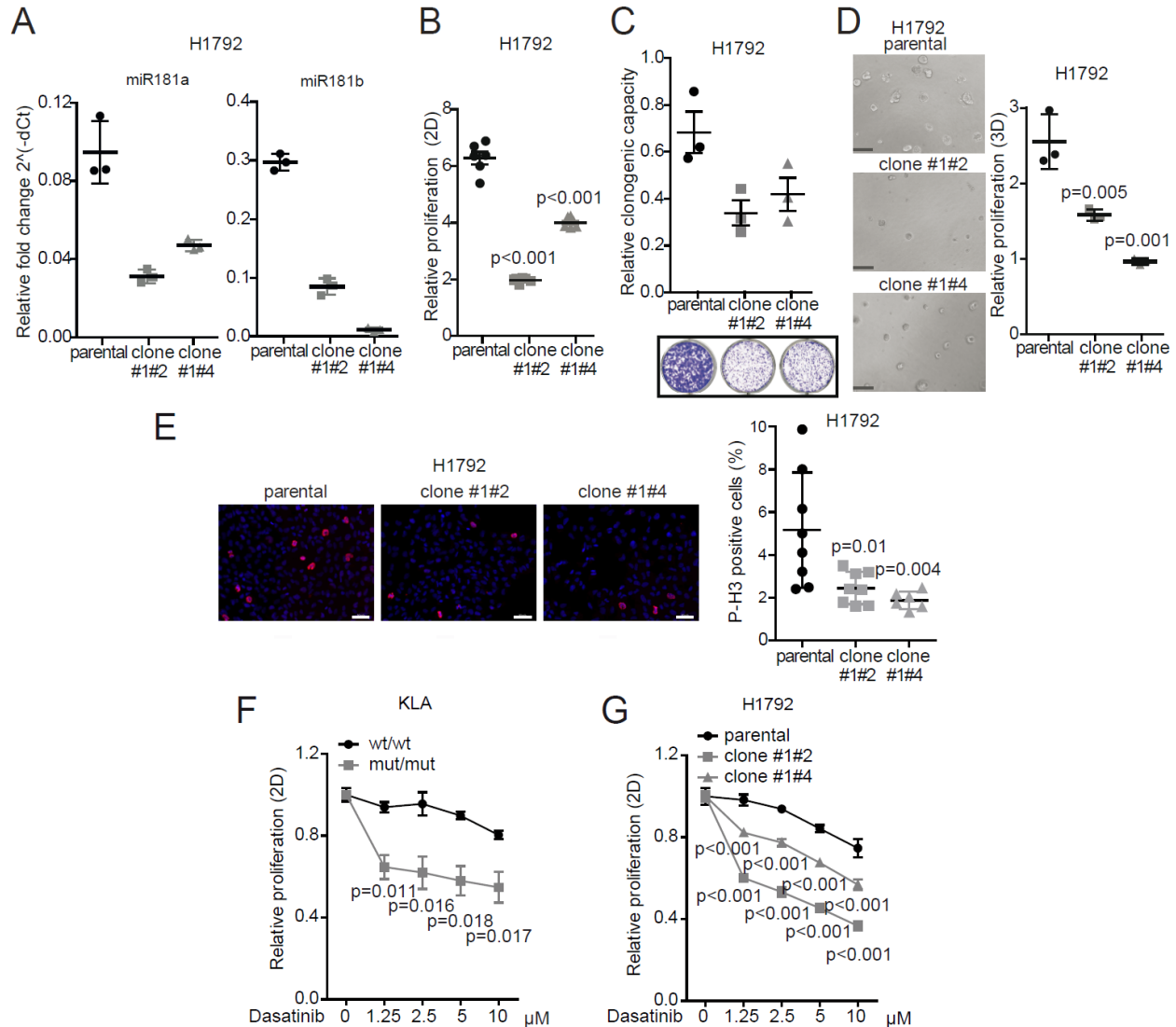


Figure 8. A functional role for miR181ab1 in human cancer. (A) miR181a and miR181b expression assessed by quantitative PCR of control and partially-CRISPR'ed knockout clones for mir181ab1 (clones #1#2 and #1#4) of human lung cancer cells (H1792) (n=3). (B) Cell proliferation of H1792 control and mir181ab1-CRISPR'ed clones assessed by MTS 3 days after seeding (n=6) and compared by ANOVA. (C) Clonogenic ability of H1792 control and mir181ab1-CRISPR'ed clones. *Up*. Relative absorbance of dissolved crystal violet at day 10 (n=3) was compared by ANOVA. *Down*. Representative images of H1792 parental and mir181ab1-CRISPR'ed clones at day 10.

(D) 3D culture of parental and mir181ab1-CRISPR'ed H1792 clones. *Left.* Representative images of organoids at day 4. Scale bars: 100µm. *Right.* Proliferation of organoids measured at day 4 relative to day 1 post-seeding by CellTiterGLO (n=3) was compared by ANOVA. (E) Phospho-histone H3 immunofluorescence images and analyses of H1792 control and mir181ab1-CRISPR'ed clones (n=7-8). Results were compared by Brown-Forsythe test. Inset is 50 µm. (F) Wt/wt and mut/mut adCre-administered KLA cells treated with dasatinib for 72h at indicated doses (n=4). Results are relative to non-treated control cells and compared by *t*-test. (G) H1792 control and mir181ab1-CRISPR'ed clones (clones #1#2 and #1#4) treated with dasatinib for 72h at indicated doses (n=4) and compared by ANOVA.

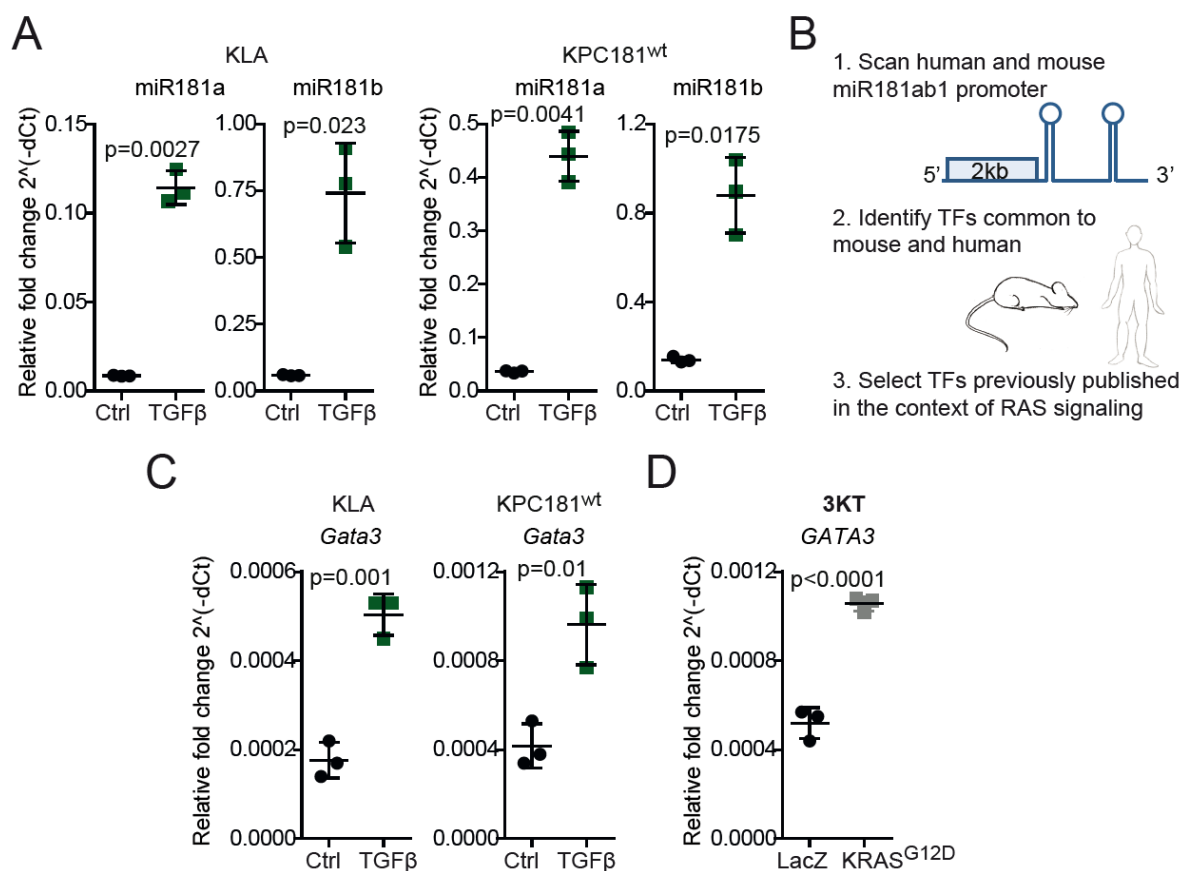


Figure 9. Regulation of the *Mir181ab1* cluster. (A) miR181a and miR181b expression assessed by quantitative PCR in mouse lung cancer (KLA) and pancreatic cancer (KPC) cells treated with 10 ng/mL TGF β for 3 h (n=3) and compared by *t*-test. (B) Schematic representation of the strategy to unveil transcription factors potentially regulating miR181ab1 expression. (C) *Gata3* expression assessed by quantitative PCR in the same cell lines as in A (n=3) compared by *t*-test. Error bars correspond to SD. (D) *GATA3* expression assessed by quantitative PCR in 3KT cells expressing a control gene (LacZ) or a mutated version of *KRAS* (G12D) (n=3) compared by *t*-test.

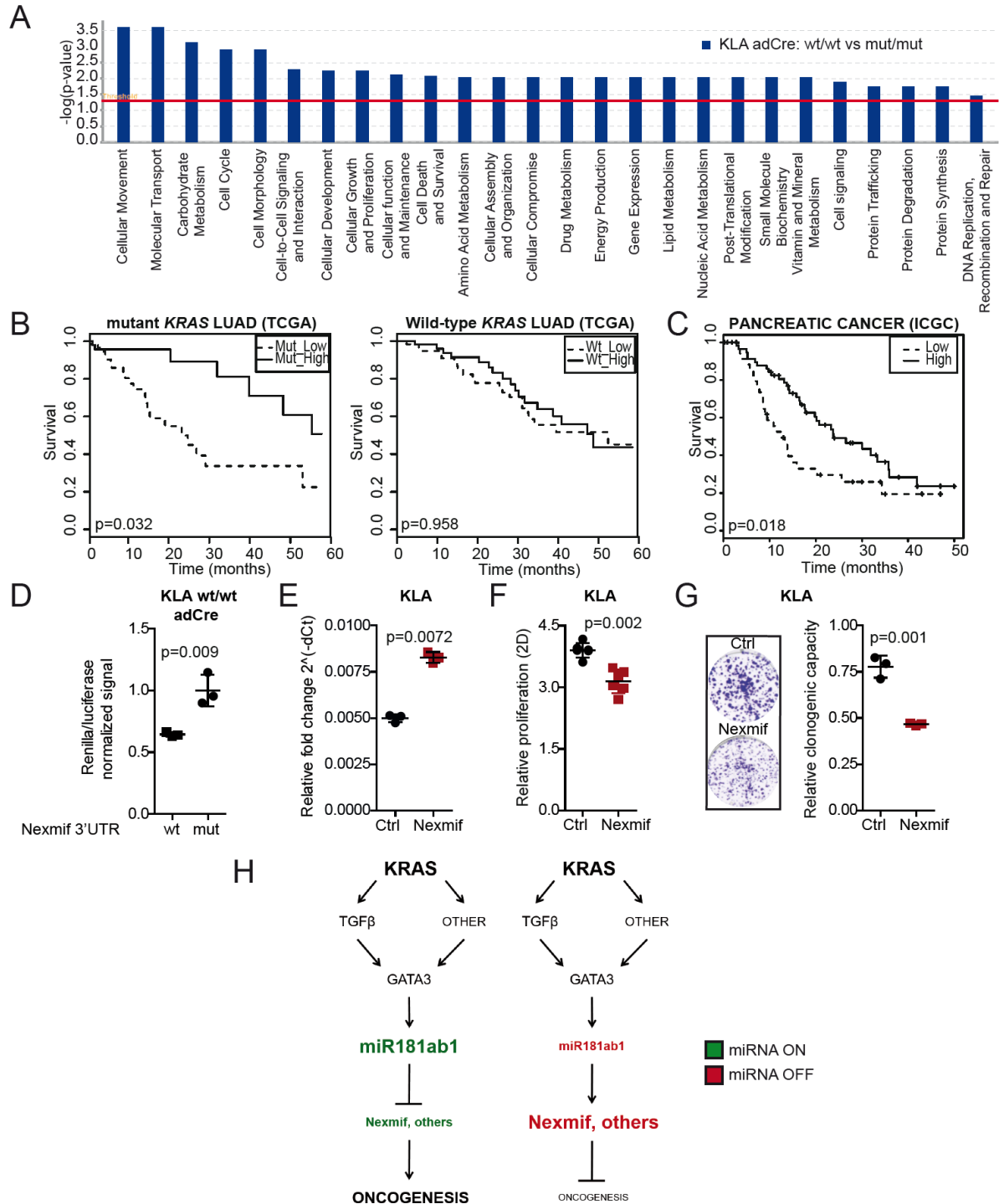


Figure 10. MiR181ab1 targets involved in human KRAS-driven cancer. (A) Graph representing biological processes enriched in KLA wt/wt with regard to KLA mut/mut adCre-treated cells by Ingenuity Pathways Analysis (IPA). (B) Kaplan-Meier plot of lung

adenocarcinoma (LUAD) patients from TCGA stratified based on median expression of the 10-gene miR181ab1-signature (log-rank test). (Left) Mutant *KRAS* LUAD patients. (Right) Wild-type *KRAS* LUAD patients. Putative miR181ab1 targets in human cancer were selected if a seed sequence was predicted to exist in the 3'UTR by at least 3 prediction algorithms. (C) Kaplan–Meier plot of pancreatic ductal adenocarcinoma (PDAC) patients from ICGC based on the 10-gene miR181ab1-target signature (log-rank test). (D) Luciferase assay of KLA wt/wt adCre-treated cells and transfected with a psiCheck vector encoding the wild-type functional 3'UTR of *Nexmif* or a seed-mutated (mut) version that impedes miR181ab1 binding (n=3). Renilla results are normalized to luciferase signal and compared by *t*-test. (E) *Nexmif* expression assessed by quantitative PCR in control- (GFP) and *Nexmif*-overexpressing KLA cells (n=3) compared by *t*-test. (F) Cell proliferation analysis by MTS of control- (GFP) and *Nexmif*-overexpressing KLA cells (n=6) compared by *t*-test. (G) Clonogenic analysis of the same cells as in F (n=3) compared by *t*-test. (H) Proposed model of miR181ab1 regulation and function in the context of mutant *KRAS* oncogenesis.