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Gli transcriptional activity is essential for Kras-induced pancreatic tumorigenesis and regulates IKBKE/ NF-κB activity in the tumor epithelium

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Running title: Gli activity in pancreatic tumorigenesis
**ABSTRACT**

Pancreatic ductal adenocarcinoma (PDAC), one of the most aggressive human malignances, is thought to be initiated by KRAS activation. Here we find that transcriptional activation mediated by the Gli family of transcription factors, although dispensable for pancreatic development, is required for Kras-induced proliferation and survival in primary pancreatic epithelial cells in culture, and Kras-driven pancreatic intraepithelial neoplasia and PDAC formation *in vivo*. Further, ectopic Gli1 activation in the mouse pancreas accelerates Kras-driven tumor formation, underscoring the importance of Gli transcription factors in pancreatic tumorigenesis. Interestingly, we demonstrate Gli-stimulated IKBKE (IKKe)/nuclear factor-kappaB (NF-κB) activity in pancreatic cancer cells in culture and *in vivo*, and show that this activity is a critical downstream mediator for Gli-dependent PDAC cell transformation and survival. Together, these studies demonstrate for the first time the requirement for Gli in Kras-dependent pancreatic epithelial transformation, implicate a novel mechanism of Gli-NF-κB oncogenic activation, and provide genetic evidence supporting the therapeutic targeting of Gli activity in pancreatic cancer.
INTRODUCTION

Pancreatic ductal adenocarcinoma (PDAC) is the fourth leading cause of cancer mortality in the United States, with a 5-year survival rate of less than 5% (1, 2). PDAC is thought to arise from precursor lesions termed pancreatic intraepithelial neoplasias (PanINs), which are characterized by mutations in KRAS and are believed to be initiating events in this cancer (3, 4). The importance of activating KRAS mutations in PDAC development is further underscored by studies of mouse models of the disease (5-7). Thus, understanding of the molecular and genetic mechanisms in Kras-dependent pancreatic tumorigenesis is essential for the development of early diagnostic and treatment tools.

The Gli transcription factors - Gli1, Gli2, and Gli3 - are effectors of the Hedgehog (Hh) signaling pathway. In mammalian cells, the Hh ligands bind to the 12-pass transmembrane receptor, Patched1 (Ptch1), leading to activation of the seven-pass membrane protein, Smoothened (Smo). Smo-mediated intracellular signal transduction controls the activity of the Gli proteins, resulting in transcriptional responses in target tissues (8-10). Dysregulation of Hh-Gli signaling is likely involved in multiple aspects of PDAC formation (11-18); yet its exact roles remain poorly characterized. Unlike Hh-related tumors associated with Gorlin syndrome, mutations in cell surface molecules such as Ptch and Smo have not been identified in human pancreatic cancers (11, 19-21). However, Hh ligands are highly expressed in human and mouse PDAC (12, 13, 15, 18), and emerging evidence suggests that the ligands regulate pancreatic tumor development through a paracrine mechanism. In this model, Hh ligands produced by epithelial tumor cells signal to the adjacent stroma, thereby altering the tumor
microenvironment and regulating tumor growth (16, 17, 22, 23). This model is further supported by recent studies demonstrating that neither genetic removal nor activation of \textit{Smo} in the pancreatic epithelium affects Kras-induced pancreatic tumor formation (18, 23). Consistent with this, treatment of a PDAC mouse model with a Smo antagonist led to alterations in the tumor stroma and enhanced tumor response in combination with gemcitabine (17).

Surprisingly, Gli expression within the pancreatic tumor epithelium is maintained despite Smo deletion and does not correlate with Hh ligand levels (18), suggesting a more complex regulation of the pathway. Several recent studies have also shown that Gli1 gene expression in PDAC cells is regulated by oncogenic pathways such as Kras and transforming growth factor beta (TGF-\(\beta\)), independently of Hh ligand input and the canonical intracellular pathway through Ptch and Smo (18, 24). Gli1 is also required for PDAC cell survival and transformation in culture (18), and ectopic activation of Gli2 in the mouse pancreas induces the formation of undifferentiated tumors (14). Interestingly, sequencing of human PDAC specimens identified mutations in genes encoding Gli transcription factors, including \textit{GLI1} and \textit{GLI3} (3). Together, these data suggest a cell-autonomous regulation of Gli activity in pancreatic tumor epithelial cells, independent of Hh ligands. However, the requirement for Gli activation within the tumor epithelium has not been established in vivo, and the underlying molecular consequences of Gli-mediated transcription during pancreatic tumorigenesis remain unexplored.

In this study, we describe the generation of a novel mouse model of epithelium-specific inhibition of Gli transcriptional activity in Kras-induced pancreatic cancer. We find that although blocking Gli-induced transcription does not affect pancreatic development, it
potently inhibits Kras-driven PanIN and PDAC formation. Conversely, ectopic Gli1 expression accelerates Kras-mediated pancreatic tumorigenesis. Using gene expression profiling and functional assays, we identify downstream regulation of the IKBKE/NF-κB pathway as a novel mechanistic link between Gli transcriptional activation and PDAC cell transformation.

RESULTS

Gli activity is not required for pancreatic development

To investigate the role of Gli transcriptional activity in pancreatic development, we used a conditional Rosa26 knock-in allele of Gli3T (R26-Gli3T), which allows ectopic expression of Gli3T protein from the ubiquitously expressed Rosa26 locus following Cre-mediated recombination (25). Gli3T is a C-terminally truncated form of Gli3 that acts as a dominant repressor of Gli transcription. Over-expression of Gli3T specifically inhibits Gli1- and Gli2-dependent gene transcription, but not lymphoid enhancer-binding factor-1 (LEF1) or serum-response-factor (SRF)-mediated gene transcription in cultured NIH3T3 cells (Fig. 1A-C). These results show the specificity and effectiveness of the Gli3T allele in blocking Hh/Gli transcriptional activation.

We crossed R26-Gli3T mice to Ptf1a-Cre transgenic mice that direct Cre recombinase expression to the epithelial lineages of the mouse pancreas (26). Ptf1a-Cre;R26-Gli3T mice were born at the expected frequency, and their pancreata showed normal parenchymal architecture and cytodifferentiation up to the age of 12 months, the longest time examined (n = 10) (Fig. 1E and J). In the R26-Gli3T allele, a 3XFlag tag and IRES-
Venus unit are also inserted at the C-terminus of Gli3T to facilitate identification of transgene expression (25). Therefore, we used detection of the Flag tag with immunoblotting (Fig. 1D) and Venus fluorescence on cyrosections (Fig. 1N) to confirm Cre-mediated expression of Gli3T in pancreatic tissue from Ptf1a-Cre;R26-Gli3T mice. We analyzed the expression of the endocrine markers insulin and glucagon and the acinar cell marker amylase, and found no significant differences between Gli3T-expressing and control pancreata (Fig. 1F, G, H, K, L and M). These data show that Gli3T inhibition does not affect differentiation of the pancreatic epithelial lineages, and suggest that cell-autonomous Hh-Gli activity is largely dispensable for the proper development of mouse pancreas.

**Gli activation is required for Kras-induced PanIN lesion formation**

We next investigated the specific role for Gli transcription in regulating Kras-initiated tumor development in vivo. We generated a mouse model in which simultaneous activation of Kras and inhibition of Gli transcription was achieved by breeding mice harboring a conditionally activated Kras allele (LSL-KrasG12D) (27) with Ptf1a-Cre;R26-Gli3T mice. As reported previously, Cre-mediated activation of the LSL-KrasG12D allele in the mouse pancreas results in the development of slowly progressive PanINs (5). At 6 months of age, Ptf1a-Cre;LSL-KRASG12D mice developed early PanIN lesions, most of which were classified histologically as PanIN1A and PanIN1B (Fig. 2A). These lesions showed a high proliferation index, demonstrated by Ki67 immunohistochemistry (IHC), and evidence of epithelial transformation with associated mucin accumulation as detected by Alcian blue staining (Fig. 2C and E). By 12 months of age, the pancreata of
the Ptf1a-Cre;LSL-Kras\textsuperscript{G12D} mice displayed evidence of more advanced lesions, including PanIN2 and PanIN3 lesions (Fig. 2G).

In contrast, inhibition of Gli activity resulted in a dramatic reduction in Kras-driven tumorigenesis. Ptf1a-Cre;LSL-Kras\textsuperscript{G12D};R26-Gli3T mice (n=15) examined at 6 months and 12 months of age showed a largely normal parenchymal architecture in the pancreas with little evidence of epithelial transformation (Fig. 2B and 2H). Most of the cells in the pancreas were nonproliferating as determined by Ki67 staining, and there was no reactive stroma (Fig. 2D and 2F), suggesting a critical requirement for Gli transcriptional activation in Kras-induced PanIN lesion formation in vivo.

Pancreatic ductal epithelial transformation is a critical step in the development of Kras-initiated PanIN lesions. Thus, we examined the effect of Gli3T expression on Kras-induced phenotypes in primary pancreatic duct epithelial cells (PDECs) in culture. Consistent with our previous work (15), we found that Kras activation induced the proliferation of PDECs and enhanced their survival in response to challenge by apoptotic stimuli (Fig. S1). However, Gli3T expression abrogated Kras-induced PDEC survival after exposure to cycloheximide (Fig. S1A), and also impaired Kras-induced proliferation in PDECs (Fig. S1B). Together, our in vivo and in vitro data suggest that Gli activation is critical for Kras-initiated pancreatic tumorigenesis, potentially by mediating Kras-induced epithelial cell proliferation and survival.

Interestingly, we did detect a few rare PanIN1 lesions in three Ptf1a-Cre;LSL-Kras\textsuperscript{G12D};R26-Gli3T mice (Fig. 2H and I). This observation suggests the possibility that the Gli requirement could eventually be overcome, or that the lesions that developed
failed to express Gli3T. To differentiate between these possibilities, we assayed for transgene expression in these lesions. Because of the high background in detecting the Gli3T C-terminal Flag tag with immunofluorescence staining or IHC, we took advantage of the IRES-Venus unit inserted in the R26-Gli3T allele that allows detection of transgene expression by Venus fluorescence on cryosections. We found that the lesions from Ptf1a-Cre;LSL-Kras^{G12D};R26-Gli3T mice were Venus negative compared to the adjacent normal-appearing islet and acinar tissues (Fig. 2I and J), indicating that the Gli3T transgene was not expressed in these lesions. These results suggest that the development of rare lesions in animals bearing the R26-Gli3T allele is probably due to inefficient Cre recombination and the failure to express Gli3T.

**Gli activation is required for Kras-dependent PDAC formation**

Our data suggest that Gli transcriptional activity is required for Kras-initiated formation of precursor PanIN lesions. To test whether Gli activity is required for progression to adenocarcinoma, we generated compound mice bearing a single floxed Trp53 allele (28) in addition to the LSL-Kras^{G12D}, R26-Gli3T, and Ptf1a-Cre alleles. Mice negative for the R26-Gli3T allele rapidly developed pancreatic carcinomas with a median latency of 111 days (range 85-164 days) (Fig. 3A). These tumors were predominantly moderately- to poorly-differentiated ductal adenocarcinomas that were frequently invasive and metastatic, with dissemination to lymph nodes, the adjacent intestine, liver, peritoneal cavity and lungs (Fig. 3B, panels i-v). Non-tumor-bearing pancreatic tissue displayed acinar atrophy and contained numerous PanINs from PanIN1 to PanIN3 (Fig. 3B, panel I). By contrast, mice bearing the R26-Gli3T allele developed carcinomas with a
significantly longer latency, with a median age of 193 days (range 115-270 days), p <0.001 by Log-rank test (Fig. 3A). Histologically, the tumors that developed in the R26-Gli3T-positive animals were indistinguishable from those in R26-Gli3T-negative mice, and were also commonly metastatic (Fig. 3B, panels vi-ix). Characterization of tumors by immunostaining for Ki67 or the pancreas progenitor marker PDX1, and immunoblotting for AKT and ERK phosphorylation, showed no differences between tumors induced in R26-Gli3T-positive and -negative animals (Fig. S2).

Despite the delayed kinetics, the eventual formation of pancreatic tumors in animals bearing the R26-Gli3T allele again raises the question whether the tumors that developed failed to express Gli3T, or whether Trp53 deletion obviates the need for Gli activity, as suggested by a previous study (29). Thus, we assayed for the presence of Gli3T protein in lysates from tumors, and cell lines derived from these tumors, by immunoblotting with an anti-Flag antibody. While Gli3T protein could be readily detected in 293T cells transfected with a Gli3T expression construct (and pancreas tissue from Ptf1a-Cre;R26-Gli3T mice, see Fig. 1), Gli3T could not be detected in any of the tumor (Fig. 3C, top panel) or cell line (Fig. 3C, lower panel) lysates. To determine whether these tumors were derived from cells that failed to undergo recombination, we analyzed DNA extracted from tumors and cell lines with PCR primers that differentiate between unrecombined and recombinant R26-Gli3T alleles. The unrecombined allele was readily detected in all samples isolated from mice carrying the R26-Gli3T allele, whereas only one tumor sample tested positive for the presence of the recombinant allele (Fig. 3D). Interestingly, a cell line derived from the tumor that tested positive for recombination was negative for the presence of the recombinant R26-Gli3T allele, suggesting that the
cells in the tumor carrying the recombined allele represented a minority of the sample, or were normal epithelial cells entrapped within the mass of the tumor. Collectively, our data demonstrate that Gli transcriptional activity is required for pancreatic carcinoma development in vivo.

**Gli1 accelerates Kras-initiated pancreatic tumorigenesis**

Prior work suggested that Kras regulates Gli1 expression in PDAC cells, and Gli1 activity is critical for PDAC cell survival and transformation in vitro (18). However, the tumorigenic activity of Gli1 has not been examined in the pancreas in vivo. Therefore, we used a recently established conditional Rosa26 knock-in allele of Gli1, R26-Gli1 (30, 31), to ectopically express Gli1 in the mouse pancreas.

*Ptf1a-Cre;R26-Gli1* mice were generated and monitored for over 12 months. Gli1 activation alone did not initiate pancreatic tumors, and the pancreatic development and cytodifferentiation appeared normal in *Ptf1a-Cre;R26-Gli1* mice compared to control R26-Gli1 mice (Fig. S3). However, activation of both Kras and Gli1 within the pancreas dramatically accelerated tumorigenesis. Although the pancreas appeared normal at birth, the health of the triple-transgenic *Ptf1a-Cre;LSL-Kras<sup>G12D</sup>;R26-Gli1* mice deteriorated rapidly, and the majority of the animals were sacrificed between 6 and 12 weeks of age, although few survived to the age of 10 months (Fig. 4A). At 2 months of age, the *Ptf1a-Cre;LSL-Kras<sup>G12D</sup>* mice demonstrated only few early PanIN1 lesions as reported previously (5), while the vast majority of the pancreas contained well-organized acinar, islet and ductal tissue (Fig. 4C). In contrast, the *Ptf1a-Cre;LSL-Kras<sup>G12D</sup>;R26-Gli1* mice had wide-spread formation of PanIN lesions resulting in almost complete
disruption of normal pancreatic architecture. These lesions showed a variety of nuclear atypia in the ductal epithelium; some corresponding to human PanIN3 lesions (Fig. 4D). Cytokeratin 8 (CK8) staining confirmed the epithelial phenotype (Fig. 4E). A prominent desmoplastic stromal response, confirmed by smooth muscle actin (SMA) staining, was also present (Fig. 4E).

Molecular analysis of the Kras/Gli1 advanced lesions revealed that cell proliferation as measured by Ki67 staining was significantly increased compared to the lesions with Kras activation alone (Fig. 4F and G, and Fig. S4A). Consistent with a previous report (32), we also detected senescence-associated β-galactosidase expression in early PanIN lesions from two-month-old Ptf1a-Cre;LSL-KrasG12D mice (Fig. 4H), while high-grade PanIN lesions from age-matched Ptf1a-Cre;LSL-KrasG12D;R26-Gli1 mice did not exhibit detectable senescence-associated β-galactosidase staining (Fig. 4I and Fig. S4B), suggesting escape from KrasG12D-induced growth arrest/senescence. However, we did not detect invasive PDAC in the Ptf1a-Cre;LSL-KrasG12D;R26-Gli1 mice, and metastasis was not observed in any of the mice we examined. Interestingly, we detected large multilocular cystic lesions resembling mucinous cystic neoplasms (Fig. 4J) in two of the Ptf1a-Cre;LSL-KRASG12D;R26-Gli1 mice, one at 6 weeks of age and the other at 8 months of age, in addition to the PanIN lesions we described above. The cysts from the Ptf1a-Cre;LSL-KrasG12D;R26-Gli1 mice were as large as 2 cm in diameter and lined by columnar epithelial cells, where abundant mucin production was demonstrated by reaction with Alcian blue (Fig. 4K). Immunohistochemistry for estrogen receptor (ER) and progesterone receptor (PR) in these cystic lesions showed the presence of ER or PR positive cells in the stroma (Fig. S4C and D), a key feature of
human mucinous cystic neoplasms. Taken together, these results suggest that Gli1 activation is not sufficient to initiate PDAC, but synergizes with Kras to promote pancreatic tumor formation in vivo.

A Gli-dependent transcriptional program in PDAC cells

The results from our loss-of-function and gain-of-function genetic analyses underscore the functional importance of Gli activation in pancreatic ductal epithelial transformation. However, the Gli-mediated transcriptional program in pancreatic cancer remains largely unexplored.

Panc1 and MiaPaCa2 are human PDAC cell lines that contain activating mutations in Kras and require Gli1 activity for survival and maintenance of their oncogenic properties (18). To further examine Gli-mediated transcriptional regulation in these cells, Panc1 or MiaPaCa2 cells were transfected with a Gli3T expression vector, infected with shRNA constructs against Gli1, or treated with a small molecule Gli inhibitor, GANT61. We found that Gli3T effectively blocked Gli-dependent transcriptional activation in the Panc1 or MiaPaCa2 cells (Fig. 5A), consistent with the result that expression of the Gli target genes, Ptch1 and Gli1, was down-regulated in Ptf1a-Cre;LSL-KrasG12D;R26-Gli3T mouse mutant pancreas (Fig. S5A). In agreement with previous studies (18), we found that inhibition of Gli-mediated transcription by expression of Gli3T, shRNAs against Gli1, or treatment of GANT61, inhibited cell proliferation, increased apoptosis, and impaired anchorage independent growth in these cell lines (Fig. 5B-D, and Fig. S5F-K). Together, these data demonstrated the importance of Gli transcriptional activation in human PDAC cells.
To identify Gli-dependent downstream target genes, we performed gene expression profiling on Gli3T-expressing Panc1 cells and vector controls. We transfected Panc1 cells with a Gli3T-IRES-nuclear GFP expression construct, and 24 hours post-transfection we isolated GFP-positive cells by FACS and performed expression profiling using Affymetrix chips. As expected, we detected upregulation of Gli3 that likely reflects the expression of the ectopic Gli3T transgene. We identified 265 genes that were significantly downregulated by Gli3T (Table S1); among them, *Ptch1* and *FoxA2* are known transcriptional targets of the Hh-Gli pathway (Fig. 5E). Interestingly, we also identified several genes involved in regulating Ras intracellular signal transduction, including *SOS2* (RasGEF), *RASA1* (RasGAP), *RIN2* and *RASSF4/5* (Fig. 5E), suggesting possible feedback regulation of Kras signaling in cancer cells influenced by Gli activity.

The PI3K/AKT and MEK/ERK pathways are Kras-stimulated signaling pathways that have been implicated in tumorigenesis (33). In our transcriptional profiling, we found that two subunits of *PI3K*, *PIK3R1* and *PIK3C2B*, were among the genes whose expression was significantly downregulated by Gli3T (Fig. 5E), indicating a possible interaction between Gli and PI3K/AKT signaling. Thus, we further examined the status of these two critical Kras downstream pathways in PDAC cells. We found that Akt phosphorylation was markedly downregulated in Gli3T-expressing Panc1 cells (Fig. 5F), but was elevated in mouse pancreatic tumors with both Kras and Gli1 activation (Fig. 5G and H). In contrast, ERK phosphorylation was not significantly changed in mouse PanIN lesions and human cancer cells upon Gli regulation (Fig. 5F, I and J). These
results are in agreement with a previous report that showed activation of AKT, but not ERK, when an active form of Gli2 was expressed in mouse pancreas (14).

Hh-Gli regulates Wnt signaling in several developmental, tissue regeneration and tumorigenic contexts (16, 34-37). Interestingly, a recent study suggested that Wnt signaling may also be regulated by Hh signaling in pancreatic tumors (38). Thus, we examined the canonical Wnt activity in Panc1 cells where Gli transcription activity was inhibited by Gli3T. Quantitative RT-PCR (qPCR) analysis showed that the expression of a well-established Wnt target gene AXIN2 was not inhibited by Gli3T expression in Panc1 and MiaPaCa2 cells (Fig. S6). This result is consistent with the absence of Wnt pathway target genes from the list of differentially expressed genes identified by our microarray experiments (Table S1), and the absence of β-catenin nuclear accumulation in the PanIN lesions with both Kras and Gli1 activation (Fig. S6). These data are also consistent with our genetic result that Gli3T expresion did not affect embryonic pancreatic development (Fig. 1), where canonical Wnt signaling plays a prominent role (39, 40). Together, these data suggest that regulation of canonical Wnt signaling may not play a major role in our Gli-dependent pancreatic tumor models.

**Gli-mediated regulation of IKBKE and NF-κB activation in pancreatic tumors.**

Our gene expression profile analysis detected an enrichment of genes associated with the NF-κB pathway, including IKBKE (IKKε), TRAF1, TRAF3IP2 and NFKBIE (Fig. 5E). IKBKE (IKKε) is a IκB Kinase (IKK)-related kinase involved in the activation of the NF-κB pathway (41, 42), and was recently identified as a breast cancer oncogene (43).
Importantly, elevated IKBKE expression was recently shown to be a common feature of PDAC(44). Thus, we examined whether IKBKE/NF-κB activation constituted a novel downstream mechanism of Gli transcription in pancreatic cancer.

We first examined whether NF-κB transcriptional activity is regulated by Gli-mediated transcription. Panc1 cells expressing Glil3T, shRNAs against Glil1, or treated with GANT61, exhibited a significantly lower level of NF-κB activity compared to cells expressing a control plasmid as assayed by measuring the activity of a synthetic NF-κB reporter gene (Fig. 6A). Inhibition of Gli transcriptional activation in Panc1 cells also resulted in marked downregulation of IKBKE gene expression as measured by qPCR or immunoblot analysis (Fig. 6B and C). To determine the functional importance of IKBKE in PDAC cells, we used two shRNA constructs against human IKBKE to silence IKBKE expression in Panc1 or MiaPaCa2 cells, and confirmed knockdown efficiency by qPCR (Fig. 6D and Fig. S7A). We found that inhibition of IKBKE expression reduced cell numbers, relative to a non-silencing shRNA control, as measured by an MTT assay (Fig. 6F and Fig. S7C). Further, IKBKE knockdown increased apoptosis, as illustrated by caspase 3 cleavage (Fig. 6G and Fig. S7D), and impaired the ability of PDAC cells to form colonies in soft-agar (Fig. 6H and Fig. S7E). Importantly, these phenotypes were rescued by co-expression of a mouse IKBKE expression vector that is resistant to the two shRNAs targeting human IKBKE (Fig. 6E-H and Fig. S7B-E). Together, these data indicate that IKBKE is required for the survival and transformation phenotypes of human PDAC cells.
Next, we determined whether IKBKE and NF-κB activity are regulated by Gli-mediated transcription in vivo. RelA is a member of the NF-κB family, and nuclear accumulation of RelA indicates activation of the classical NF-κB pathway. We therefore performed IHC for IKBKE and RelA in tissue samples from *Ptf1a-Cre;LSL-Kras*<sup>G12D</sup> and *Ptf1a-Cre;LSL-Kras*<sup>G12D,R26-Gli1</sup> mice at the age of 2 months. We found that, compared to those in *Ptf1a-Cre;LSL-Kras*<sup>G12D</sup> mice, epithelial cells in *Ptf1a-Cre;LSL-Kras*<sup>G12D,R26-Gli1</sup> mice exhibited significantly increased IKBKE expression and nuclear RelA staining (Fig. 6I-L).

In summary, these observations demonstrate activation of IKBKE/NF-κB signaling by Gli proteins in PDAC cells, and highlight a potential mechanism for the observed requirement for Gli transcription for PDAC development in vivo.

**DISCUSSION**

**Non-canonical Gli function in pancreatic tumor cells**

Non-canonical Gli regulation has been reported and implicated in several oncogenic settings (29, 45-48). A growing body of evidence also suggests a cell-autonomous non-canonical Gli regulation in pancreatic cancer that is distinct from the the Hh ligand-dependent paracrine effect on the tumor stroma (3, 11, 18, 24, 49). Our results here, together with a previous report (14), show that, unlike Smo activation (23), Gli1 or Gli2 activation is able to cooperate with Kras to promote pancreatic tumorigenesis. Moreover, *GLI1* and *GLI3* were recently reported to be mutated in human PDAC-derived cells (3), and the expression of Gli1 and Gli3 can be regulated in Smo-null
mouse pancreatic tumor cells (18). Together, these studies support the non-canonical model, and indicate a broad involvement of Gli mis-regulation in pancreatic cancer.

Using a dominant repressor Gli3T allele that inhibits all Gli-mediated transcriptional activation, we demonstrate for the first time that Gli transcriptional activity is specifically required for pancreatic tumor formation in vivo, although it is dispensable for normal pancreatic development. Importantly, our data show that Gli activity is required not only for pancreatic tumor initiation, but also for the maintenance of established PDAC cells. Given the demonstrated importance of Hh ligands on the desmoplastic stroma, our results suggest that Gli proteins are attractive therapeutic targets (45, 50) in PDAC, as their inhibition would affect both the tumor epithelium and the reactive stroma.

It is currently not well understood why the pancreatic epithelium is refractory to Ptch/Smo-mediated canonical signaling or how Kras potentially regulates Gli expression levels (18, 49, 51); however, recent work points to an interesting potential connection with the primary cilium (52). Significant Gli signal up-regulation was observed within the pancreatic epithelium after disruption of primary cilium (52), a cellular organelle that is intimately associated with Hh-Gli signal transduction (53). Interestingly, another recent study showed that Kras-mediated transformation of the pancreatic duct epithelium correlates the loss of this organelle in PanIN and PDAC cells in vivo (54). Thus, Kras activation may lead to loss of the primary cilium, which could potentially facilitate the Hh ligand-independent activation of Gli activity in tumor epithelium.

**Gli1 activation in pancreatic cancer**
Our results on the cooperation of Gli1 with Kras provided the first evidence for the in vivo tumorigenic potential of Gli1 in the pancreas. However, it is interesting to note the phenotypic differences between Gli1 and Gli2 activation in pancreatic tumor initiation. Whereas Gli1 is unable to initiate pancreatic tumorigenesis on its own, activation of Gli2 by the CLEG2 allele drives pancreatic neoplasia, albeit the development of undifferentiated tumors that do not progress via PanINs (14). Several possibilities may account for the difference. First, there are differences in the design of the transgenes. The R26-Gli1 allele (30) allows Cre-dependent expression of the full-length Gli1 protein from the ubiquitously expressed Rosa26 locus, whereas in the CLEG2 allele (14), a dominant active version of Gli2, Gli2ΔN, is expressed via control of the CAGGS promoter, a highly active hybrid CMV/β-actin promoter. Furthermore, Gli2ΔN consists of an N-terminally truncated form of the protein that lacks an N-terminal repressor domain, which may result in resistance to posttranslational regulation (55). Second, different Cre drivers were used in these two studies. Compared to Ptf1a-Cre (26), the Pdx1-Cre transgene (56) used in the Gli2ΔN study directs Cre expression in earlier embryonic pancreatic progenitor cells. However, it is possible that the phenotypic difference may indeed reflect distinct properties of these two Gli proteins; indeed, differential transcriptional outputs mediated by Gli1 and Gli2 have been reported (57).

However, in the context of Kras-initiated pancreatic tumorigenesis, both Gli1 and Gli2 showed remarkable capacity to accelerate tumor development. Ectopic expression of either Gli1 or Gli2ΔN, together with Kras activation, resulted in the formation of advanced PanIN lesions by 2 months of age. Only minimal early PanIN1A lesions are detected at this age in mice with Kras activation alone. Extensive fibrosis was also
evident in both Gli1/Kras and Gli2ΔN/Kras tumors, a feature similar to desmoplasia observed in human PDAC. Despite the frequent formation of advanced lesions at an early age, we did not observe invasive or metastatic PDAC in the Ptf1a-Cre;LSL-KrasG12D,R26-Gli1 mice that survived to 10 months of age, suggesting the requirement for additional oncogenic alterations, possibly loss of p53 or p16 function (6, 7). Another intriguing possibility is that paracrine signaling of Hh ligands to the reactive stroma is involved in the stimulation of metastasis. It would be interesting to test whether Gli activation, together with Hh ligand up-regulation in postnatal mouse pancreas, may lead to the development of metastatic PDAC.

A unique Gli transcriptional program in PDAC

Despite the importance of Kras in PDAC, the transcriptional output regulated by this signaling in pancreatic cancer cells remains poorly characterized. Our data here, in agreement with prior studies, place Gli transcription factors downstream of Kras in pancreatic cancer, and our gene expression profiling studies potentially describe a non-canonical transcriptional regulation controlled by Gli proteins in PDAC cells. Interestingly, we did not detect down-regulation of typical Hh-Gli mitogenic targets, such as cyclin D1 and MYC that are commonly found in Hh-related tumors (58-60). Although we can not rule out the possibility that Gli3T inhibition may not fully recapitulate the Gli1/2 null phenotypes in PDAC cells, our data support the idea that Gli proteins may exert a unique transcriptional program in pancreatic cancer cells, a notion that is consistent with recent studies that Gli-mediated transcriptional output is highly context dependent (25, 31, 61). Our data also suggest that canonical Wnt signaling is unlikely to
play a major role in Gli-dependent pancreatic epithelial transformation. Instead, we identified a cluster of Gli-dependent genes that are possibly involved in selective feedback regulation of Kras-stimulated signal transduction in PDAC cells. Further, our finding that Gli3T expression in Panc1 cells suppresses Akt phosphorylation, and that Gli activity is required for the elevated expression of the PI3K subunits \textit{PIK3R1} and \textit{PIK3C2B} in these cells, supports the intriguing possibility that Gli proteins may directly, or indirectly, contribute to the selective activation of the PI3K/AKT pathway.

\textbf{IKBKE and NF-κB activation in pancreatic cancer}

NF-κB activity has long been linked to inflammation-related tumorigenesis (62-64). There is also increasing recognition of intrinsic dysregulation of the pathway in solid tumors. Alteration of NF-κB pathway components was a common finding in a recent comprehensive genomic screen of somatic copy-number alterations across human cancers (65). Further, activation of the NF-κB pathway, possibly via non-canonical IKK kinases such as IKBKE and TBK1, has recently been shown to be critical for several epithelial tumors, including breast and lung carcinomas that harbor \textit{KRAS} mutations (42, 43, 66, 67). Our results in human PDAC cells and mouse tumors indicate enhanced NF-κB activity in the tumor epithelium, a finding that is consistent with previous studies on NF-κB activation in human PDAC cells (68, 69). Our data further suggest that the IKK-related kinase, IKBKE, may play an important functional role in PDAC downstream of Gli proteins. IKBKE levels are elevated in pancreatic tumors with concomitant expression of activated Kras and Gli1, and IKBKE knockdown impairs the survival and transformation of PDAC cells. \textit{IKBKE} was recently identified as a breast cancer
oncogene (43), and recent work demonstrated elevated levels in PDAC samples (44). Therefore, it will be interesting to test whether IKBKE functions as an oncogene in PDAC as well. Our finding that multiple components of the NF-κB pathway are regulated downstream of Gli3T also suggest a potential link between Kras activation and NF-κB mediated, in part, by Gli transcription factors. Interestingly, while our data show a novel cell-autonomous regulation of IKBKE/NF-κB by Gli, a recent report suggested that Shh ligand production may be regulated by NF-κB activity in PDAC cells (70). Clearly, further in vivo studies are warranted to elucidate the mechanism of, and requirement for, the interplay among these critical pathways in the pathogenesis of pancreatic cancer.

MATERIALS AND METHODS

**Mouse strains:** Ptf1a-Cre, LSL-Kras<sup>G12D</sup>, Trp53<sup>lox</sup>, R26-Gli3T and R26-Gli1 mice have been described before (25-28, 31). Ptf1a-Cre;LSL-Kras<sup>G12D</sup>, Ptf1a-Cre;LSL-Kras<sup>G12D</sup>;R26-Gli3T, and Ptf1a-Cre;LSL-Kras<sup>G12D</sup>;R26-Gli1 mice were obtained by crossing LSL-Kras<sup>G12D</sup> to Ptf1a-Cre;R26-Gli3T or Ptf1a-Cre;R26-Gli1 mice. Offspring from the cross of LSL-Kras<sup>G12D</sup>;R26-Gli3T to Ptf1a-Cre;Trp53<sup>lox</sup>/Trp53<sup>lox</sup> mice were followed longitudinally for tumor development for 270 days. All mouse experiments were performed according to the guidelines of IACUC at University of Massachusetts Medical School.

**Tissue collection and histology:** Upon euthanasia, primary pancreatic tissues and metastatic lesions were separated in pieces and fixed in 4% paraformaldehyde. For
paraffin sections, tissues were dehydrated, and embedded in paraffin blocks, and cut at
a thickness of 6 μm. For frozen sections, tissues were dehydrated in 30% sucrose, and
embedded in OCT, and sections were cut at a thickness of 12 μm. For RNA and protein
analysis, tissues were flash frozen in liquid nitrogen. Tissue sections (6 μm) were
stained with hematoxylin and eosin (H&E) using standard reagents and protocols.

**Generation of cell lines from tumor tissue:** Pancreatic tumors were dissected,
minced, and digested at 37°C in a Hank’s balanced salt solution (HBSS) containing 2
mg/mL type V collagenase (Sigma) with agitation. After 20 minutes, the digested
material was filtered through a 105-μm nylon mesh, and proteases were inactivated by
the addition of DMEM/F12 (Invitrogen) supplemented with 10% fetal bovine serum. The
tissue was then washed 3 times in HBSS to remove collagenase. The ductal fragments
were plated on plastic dishes precoated with rat tail collagen type 1 (BD Bioscience) for
further growth in monolayer.

**Immunohistochemistry, immune fluorescence and immunoblotting:** For
immunohistochemistry, high-temperature antigen retrieval was conducted in Sodium
Citrate solution (pH 6.0) on paraffin sections for 30 minutes. Sections were blocked in a
buffer containing 5% BSA and 0.1% Triton X-100 in PBS and then incubated overnight
at 4°C in primary antibodies diluted in blocking buffer. Primary antibodies used were:
Ki67 (1:500, Abcam), phospho-AKT (1:50, Cell Signaling), phospho-ERK (1:500, Cell
Signaling), IKBKE (1:50, Santa Cruz), RelA (1:50, Santa Cruz), β-Catenin (1:400, BD
Transduction), Estrogen receptor (1:1000, Santa Cruz), Progesterone receptor (1:1000,
Santa Cruz) and PDX1 (1:5000, gift of Dr. Chris Wright, Vanderbilt University). Signal
detection was accomplished with biotinylated secondary antibodies in the Vectastain ABC kit (Vector Labs).

For immunofluorescence, OCT sections were washed with PBS and incubated in blocking buffer containing 5% sheep serum, 1% FBS and 0.1% Triton X-100 in PBS. Sections were then incubated overnight at 4°C in primary antibodies diluted in blocking buffer. Primary antibodies used were: Glucagon (1:3000, gift of Dr. Andrew Leiter, UMMS), Amylase (1:800, Sigma), Insulin (1:100, Abcam), Smooth muscle actin (1:500, Sigma), Cytokeratin-8 (1:100, DSHB). Alexa-Fluor fluorescent conjugated secondary antibodies (Invitrogen) were used for detection at a concentration of 1:500 diluted in blocking buffer. Slides were then mounted in mounting media containing DAPI.

For immunoblotting, primary antibodies used were: FlagM2-HRP (1:1000, Sigma), β-Actin (1:1000, Sigma), phospho-AKT (1:1000, Cell Signalling), phospho-ERK (1:1000, Cell Signaling), AKT (1:1000, Cell Signaling), ERK (1:1000, Cell Signaling), IKBKE (1:1000, Sigma), and Myc (1:1000, DSHB). HRP conjugated secondary antibodies used for detection were obtained from Jackson Laboratories.

**Alcian blue staining and senescence-associated β-galactosidase staining:** For Alcian blue staining, paraffin sections were hydrated and stained for 30 minutes at room temperature using Alcian blue reagent (IHC World). Sections were counterstained with Nuclear Fast Red. For senescence associated β-galactosidase staining, frozen sections were washed in PBS and stained overnight using Senescence β-galactosidase staining solution (Cell Signaling Technology). Sections were counterstained using eosin.
**Cell proliferation, apoptosis and soft-agar assays:** Gli3T-expressing GFP positive Panc1 or MiaPaCa2 cells were isolated 24 hours after transfection using flow cytometry. For shRNA knockdown, Panc-1 or MiaPaca2 cells were infected with pLKO based lentiviruses expressing shRNAs, and selected for 4 days using puromycin. For GANT61 inhibition, Panc-1 or MiaPaca2 cells were treated with 5 µM or 10 µM GANT61 dissolved in DMSO.

For MTT-based cell proliferation assay, the cells were seeded at a density of 3000 per well in a 96-well plate, treated with 5 mg/ml MTT 5 days after seeding, and lysed in DMSO 4 hours later. Absorbance was measured at 595 nm. Assay was performed in triplicates, and standard deviation was used to calculate error bars.

For apoptosis assay, cells were plated in chamber slides after cell sorting, drug selection, or GANT61 treatment. Cells were fixed in 4% PFA. Immunostaining with a polyclonal antibody against cleaved caspase 3 (1:400, Cell Signaling) was used as a marker for apoptosis. Apoptotic cells were counted in three wells, and relative apoptosis was measured by comparing number of apoptotic cells with control sample. Standard deviation was used to calculate error bars.

For anchorage-independent growth assay using soft-agar, cells were seeded at a density of 6000 cells/well in a 6-well plate of 0.3% agarose in DMEM media containing 10% FBS. Colonies from 12 fields of view were counted 14 days later. Assays were performed in triplicate. Error bars were calculated using standard deviation between triplicates.
**Luciferase reporter analysis:** NIH3T3 or Panc1 cells were co-transfected with luciferase reporter constructs, GliBS-Luc (gift of Dr. H. Kondoh, Osaka University), TOPflash (Addgene), SRE-luc (gift of Dr. D. Wu, Yale University), NF-κB-Luc (gift of Dr. F. Chan, UMMS), and expression vectors for Renila luciferase, Gli3T, Gli1, Gli2, Lef1 and CDC42. For Gli1 knockdown, the cells were co-transfected with shRNAs targeting Gli1 along with NF-κB luciferase, and Renila expression plasmids. For GANT61 treatment, the Panc-1 cells were co-transfected with NF-κB reporter, and Renila Luciferase, and then treated with 5 µM or 10 µM GANT61 6 hours post transfection. Luciferase assays were conducted 48 hours after transfection using the dual-luciferase reporter kit (Promega). Assays were conducted in triplicates, and standard deviation was used to calculate error bars.

**Detection of recombination at the R26-Gli3T locus:** Polymerase chain reaction was performed on isolated genomic DNA using the primer pair (Forward: 5’-GTAGTCCAGGGTTTCTTGTATG-3’, Reverse: 5’-TGCTACTTCCATTGTGCACGTC-3’) for detection of the unrecombined R26-Gli3T allele, and (Forward: 5’-GTAGTCCAGGGTTTCTTGTATG-3’, Reverse: 5’-GGACTTTCATCCTCATTGGAAG-3’) for detection of the recombined allele. Primers to the native R26 locus were used as a control (Forward: 5’-GGAGCGGGAGAAATGGATATG-3’, Reverse: 5’-AAAGTCGCTCTGAGTTGTAT-3’)

**Quantitative RT-PCR:** cDNA synthesis was conducted using Invitrogen Superscript II kit. Primers used for quantitative RT-PCR were: human IKBKE (Forward: 5’-TGCCTGCAAGAATCAAGC-3’; Reverse: 5’-TACAGCAGGCAGCCACAGAACG-3’), mouse IKBKE (Forward: 5’-GGAGGGAGGCTGATCAGG-3’; Reverse: 5’-
GAAAGCCCGAACGTGTTCTCA-3'), Axin2 (Forward: 5'-AGTGTAGGGTGCTCCACCGAAAAC-3'; Reverse: 5'-CTTCACACTGCAGGATTCATTT-3'), human GAPDH (Forward: 5'-ATGGGGAGGGTGAAGGTCA-3'; Reverse: 5'-GGGTCATTGATGGCAACAATA-3'), mouse GAPDH (Forward: 5'-AGGCCGCTGCTGATGATGCT-3'; Reverse: 5'-TGCCCCTTCACCACCCCTC-3'), β-actin (Forward: 5'-TGACAGGAGTCGAGGAGA-3'; Reverse: 5'-CTGGAAGGTGGACAGTGGG-3'), human Gli1 (Forward: 5'-CCAGCGCCCCACCGAGTCTTCACGC-3'; Reverse: 5'-CTGTAATTTCGCCCCTTCC-3') and mouse Gli1 (Forward: 5'-GTGGAGATGCAGAAGGAGA-3'; Reverse: 5'-CTGGAAGGTGGACAGTGGG-3'). All qPCR assays were conducted in triplicates, and standard deviation was used to calculate error bars.

**Gli1 and IKBKE knockdown:** Panc1 or MiaPaCa2 cells were infected with pLKO-based lentiviruses encoding shRNAs targeting human Gli1 (shGli1#1: CATCCATCACAGATGCTTATT; shGli1#2: GCTCCTTGCTGATGCTTATTAT), and human IKBKE (shIKBKE#1: TGGCAGGAGCTAATGTTTG; shIKBKE#2: GAGCATTGGAGCTGACCTTGA). Infected cells were selected in 5 μg/ml puromycin for 4 days. MTT assay, soft agar assay, and Caspase staining for apoptosis were conducted as described previously.
**PDEC proliferation and survival:** PDECs from *Keratin19-tv-a;R26-Gli3T* double transgenic mice were isolated and cultured as previously described (15). The retroviral constructs *RCAS-GFP* and *RCAS-KrasG12D-IRES-GFP* (15) have been previously described. *RCAS-Cre* was a gift from Eric Holland (Memorial Sloan-Kettering Cancer Center). Isolated PDECs were infected with either *RCAS-KrasG12D-IRES-GFP* or *RCAS-GFP*, and subsequently infected with *RCAS-Cre* to induce Gli3T expression, or with *RCAS-GFP* as a control. Cell proliferation and survival assays were performed as previously described (15).

**Affymetrix gene chip analysis:** Panc-1 cells were transfected with a GFP expressing vector carrying Gli3T (pCIG-Gli3T) or a GFP expressing empty vector (pCIG). GFP positive cells were isolated 24 hours post transfection using flow cytometry. RNA was isolated, labeled and hybridized to mouse GeneST1.0 chips (Affymetrix) according to Affymetrix protocols. Three independent biological samples were used for chip analysis. Statistical analyses were performed using R, a system for statistical computation and graphics (http://www.r-project.org). Genes with adjusted p-value <0.05 and absolute fold change ≥1.5 were considered potential targets for further investigation.

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FIGURE LEGENDS

Figure 1. Gli-induced transcriptional activation is dispensable for pancreatic development. (A-C) Gli3T blocks Gli-dependent transcriptional activity. Gli3T inhibits Gli-mediated luciferase reporter activity induced by Gli1 and Gli2 in transfected NIH3T3 cells (A). Gli3T does not inhibit TCF4-induced TopFlash reporter activity (B), or serum response factor-dependent SRE-luciferase reporter activity induced by the CDC42 GTPase (C). Open bars: control cells; black bars: Gli3T-expressing cells. (D) Immunoblot detection of Gli3T expression in pancreatic lysates from 6-month-old R26-Gli3T and Ptf1a-Cre;R26-Gli3T mice using an antibody against the Flag epitope tag. (E-N) H&E staining (E and J), immunofluorescence staining of amylase (F and K), glucagon (G and L) and insulin (H and M), and Venus fluorescence (I and N) in pancreata derived from R26-Gli3T (E-I) and Ptf1a-Cre;R26-Gli3T (J-N) mice.

Figure 2. Gli-mediated transcription is required for Kras-initiated PanIN formation. (A-F) Representative histological sections from Ptf1a-Cre;LSL-KrasG12D (A, C and E) and Ptf1a-Cre;LSL-KrasG12D;R26-Gli3T (B, D and F) mice stained with H&E (A and B), Alcian blue (C and D) and an antibody against Ki67 (E and F). (G-J) PanIN lesions detected in Ptf1a-Cre;LSL-KrasG12D;R26-Gli3T mice. H&E staining shows wide-spread advanced PanIN formation in Ptf1a-Cre;LSL-KrasG12D pancreata (G), while only rare PanIN1 lesions were detected in a 12-month-old Ptf1a-Cre;LSL-KRASG12D;R26-Gli3T mouse (H, I). Note robust Venus fluorescence in adjacent acinar and endocrine cells.
indicating expression of Gli3T. The boundary of the lesions from the adjacent slides is delineated by dashed black (I) and white (J) lines.

**Figure 3. Gli transcriptional activation is required for PDAC formation.** (A) Kaplan-Meier survival curve for *Ptf1a-Cre;LSL-KrasG12D;Trp53^flox/wt* mice, *Ptf1a-Cre;LSL-KrasG12D;Trp53^flox/wt;R26-Gli3T* mice, and *Ptf1a-Cre* and *LSL-KrasG12D*-negative littermate controls. p < 0.001 for comparison between *R26-Gli3T*-positive and –negative animals. (B) Representative H&E stained histological sections from lesions arising in *Ptf1a-Cre;LSL-KrasG12D;Trp53^flox/wt* (i-v) and *Ptf1a-Cre;LSL-KrasG12D;Trp53^flox/wt;R26-Gli3T* mice (vi-ix). PanIN lesions (i), glandular PDAC (ii), undifferentiated carcinoma (iii), lymph node metastasis (iv), and liver metastasis identified in *Ptf1a-Cre;LSL-KrasG12D;Trp53^flox/wt* mice. Glandular PDAC (vi), undifferentiated carcinoma (vii), liver metastasis (viii) and intestinal invasion (ix) observed in *Ptf1a-Cre;LSL-KrasG12D;Trp53^flox/wt;R26-Gli3T* mice. (C) Immunoblotting for Gli3T protein (using an anti-Flag antibody) in lysates from *R26-Gli3T*-positive and -negative tumors (top panel) and cell lines derived from these tumors (bottom panel). (D) PCR of genomic DNA to detect the recombination status of the *R26-Gli3T* allele in *R26-Gli3T*-positive tumor samples. Amplification of the native Rosa26 locus was used as a control.

**Figure 4. Gli1 promotes Kras-initiated pancreatic tumorigenesis.** (A) Survival of *Ptf1a-Cre;LSL-KrasG12D;R26-Gli1* mice is significantly less than that of *Ptf1a-Cre;LSL-KrasG12D* and *Ptf1a-Cre;R26-Gli* mice. (B-D) H&E staining of panceata derived from 2-
month-old Ptf1a-Cre;R26-Gli1 (B), Ptf1a-Cre;LSL-Kras<sup>G12D</sup> (C) and Ptf1a-Cre;LSL-Kras<sup>G12D</sup>,R26-Gli1 (D) mice. (E) Immunostaining for cytokeratin 8 (red) and α-smooth muscle actin (green) in a Ptf1a-Cre;LSL-Kras<sup>G12D</sup>,R26-Gli1 derived pancreatic lesion. (F and G) IHC for Ki67 in Ptf1a-Cre;LSL-Kras<sup>G12D</sup> (F) and Ptf1a-Cre;LSL-Kras<sup>G12D</sup>,R26-Gli1 (G) pancreata. (H and I) Senescence-associated β-galactosidase staining of pancreatic lesions from Ptf1a-Cre;LSL-Kras<sup>G12D</sup> (H) and Ptf1a-Cre;LSL-Kras<sup>G12D</sup>,R26-Gli1 (I) mice. (J) H&E staining of pancreatic cystic lesions from a 1-month-old Ptf1a-Cre;LSL-Kras<sup>G12D</sup>,R26-Gli1 mouse. (K) Alcian blue staining revealing abundant mucin production in epithelial cells in the cysts.

**Figure 5. Gli-mediated transcriptional program in pancreatic cancer cells.** (A) Changes in Gli-luciferase reporter activity in Gli3T-expressing and control Panc1 (black bars) and MiaPaCa2 (gray bars) cells. (B) Cell proliferation, measured by MTT assay, (C) apoptosis, and (D) anchorage-independent soft agar colony formation by FACS-isolated Gli3T-expressing and control Panc1 (black bars) and MiaPaCa2 (gray bars) cells. (E) Heat map illustrating mRNA expression of selected genes in Gli3T-expressing and control Panc1 cells. Red, high expression; green, low expression. (F) Immunoblot analysis of the levels of AKT phosphorylation (p-AKT), total AKT, ERK phosphorylation (p-ERK), and total ERK, in isolated Gli3T-expressing and control Panc1 cells. (G-J) IHC for p-AKT (G and H) and p-ERK (I and J) in pancreatic lesions from Ptf1a-Cre;LSL-Kras<sup>G12D</sup> (G and I) and Ptf1a-Cre;LSL-Kras<sup>G12D</sup>,R26-Gli1 (H and J) mice at 2 months of age.
Figure 6. Gli regulates IKBKE and NF-κB activity in pancreatic cancer cells. (A) Inhibition of NF-κB reporter activity by Gli3T, shRNAs against Gli1, and GANT61 in Panc1 cells 48 hours after transfection. (B) qPCR analysis of IKBKE mRNA expression in response to Gli3T expression, Gli1 knockdown, and GANT61 treatment. (C) Immunoblot analysis of IKBKE expression in control and Gli3T-expressing Panc1 cells. (D) qPCR analysis of IKBKE mRNA level in Panc1 cells expressing shRNA constructs against GFP (control) or IKBKE (shIKBKE #1 and shIKBKE #2). (E) Immunoblot analysis for expression of myc-tagged mouse IKBKE (mIKBKE) in Panc1 cells expressing shRNA constructs against human IKBKE. Cell proliferation (F), apoptosis (G) and soft agar colony formation (H) in Panc1 cells expressing shRNA constructs against GFP or IKBKE with or without mouse IKBKE expression. IHC staining of IKBKE (I, J) and RelA (K,L) in pancreatic lesions from Ptf1a-Cre;LSL-Kras<sup>G12D</sup> (I,K) and Ptf1a-Cre;LSL-Kras<sup>G12D</sup>;R26-Gli1 (J, L) mice. Note the predominantly cytoplasmic staining of RelA in panel J, and increased nuclear staining in panel K.
Figure 2
Figure 3. Gli transcriptional activation is required for PDAC formation. (A) Kaplan-Meier survival curve for Ptf1a-Cre;LSL-KrasG12D;Trp53flox/wt, Ptf1a-Cre;LSL-KrasG12D;Trp53flox/wt;R26-Gli3T, and Ptf1a-Cre- and LSL-KrasG12D-negative littermate control mice. p < 0.001 for comparison between R26-Gli3T-positive and -negative animals. (B) Representative histological sections from lesions arising in Ptf1a-Cre;LSL-KrasG12D;Trp53flox/wt (i-v) and Ptf1a-Cre;LSL-KrasG12D;Trp53flox/wt;R26-Gli3T mice (vi-ix). PanIN lesions (i), glandular PDAC (ii), undifferentiated carcinoma (iii), lymph node metastasis (iv), and liver metastasis (v) identified in Ptf1a-Cre;LSL-KrasG12D;Trp53flox/wt mice. Glandular PDAC (vi), undifferentiated carcinoma (vii), liver metastasis (viii) and intestinal invasion (ix) observed in Ptf1a-Cre;LSL-KrasG12D;Trp53flox/wt;R26-Gli3T mice. (C) H&E stained histological sections from the pancreas of a 4-month old Ptf1a-Cre;LSL-KrasG12D;Trp53flox/wt;R26-Gli3T mouse, a time at which PDAC is commonly observed in Ptf1a-Cre;LSL-KrasG12D;Trp53flox/wt littermates. (D) Immunoblotting for Gli3T protein (using an anti-Flag antibody) in lysates from R26-Gli3T-positive and -negative tumors (top panel) and cell lines derived from these tumors (bottom panel). (E) PCR of genomic DNA to detect the recombination status of the R26-Gli3T allele in R26-Gli3T-positive tumor samples. Amplification of the native Rosa26 locus was used as a control.
Figure 4

- $Ptf1a$-Cre;R26-Gli1 (n=10)
- $Ptf1a$-Cre;Kras$^{G12D}$ (n=10)
- $Ptf1a$-Cre;Kras$^{G12D}$;R26-Gli1 (n=19)

Figure 4
Figure 5
Figure S1
Figure S3
Figure S4
Figure S6
Figure S7