



Suppression of non-small cell lung tumor development by the *let-7* microRNA family

Madhu S. Kumar*, Stefan J. Erkeland†, Ryan E. Pester*, Cindy Y. Chen*, Margaret S. Ebert*, Phillip A. Sharp**‡, and Tyler Jacks**§

*Center for Cancer Research and †Department of Biology, Howard Hughes Medical Institute, Massachusetts Institute of Technology, Cambridge, MA 02139; and ‡Department of Hematology, Erasmus University Medical Center, 3015 GE, Rotterdam, The Netherlands

Contributed by Phillip A. Sharp, December 31, 2007 (sent for review December 4, 2007)

Many microRNAs (miRNAs) target mRNAs involved in processes aberrant in tumorigenesis, such as proliferation, survival, and differentiation. In particular, the *let-7* miRNA family has been proposed to function in tumor suppression, because reduced expression of *let-7* family members is common in non-small cell lung cancer (NSCLC). Here, we show that *let-7* functionally inhibits non-small cell tumor development. Ectopic expression of *let-7g* in K-Ras^{G12D}-expressing murine lung cancer cells induced both cell cycle arrest and cell death. In tumor xenografts, we observed significant growth reduction of both murine and human non-small cell lung tumors when overexpression of *let-7g* was induced from lentiviral vectors. In *let-7g* expressing tumors, reductions in Ras family and HMGA2 protein levels were detected. Importantly, *let-7g*-mediated tumor suppression was more potent in lung cancer cell lines harboring oncogenic K-Ras mutations than in lines with other mutations. Ectopic expression of K-Ras^{G12D} largely rescued *let-7g* mediated tumor suppression, whereas ectopic expression of HMGA2 was less effective. Finally, in an autochthonous model of NSCLC in the mouse, *let-7g* expression substantially reduced lung tumor burden.

K-Ras | lung cancer

MicroRNAs (miRNAs) are a class of short highly conserved noncoding RNAs known to play important roles in numerous developmental processes. MiRNAs are initially transcribed as longer primary transcripts that undergo sequential processing by the RNase III-like enzymes Droscha and Dicer (1). After maturation, miRNAs regulate gene expression through incomplete basepairing to a complementary sequence in the 3' untranslated region (UTR) of a target mRNA. The miRNA-mRNA interaction results in translational repression and, to a lesser extent, accelerated turnover of the target transcript (2). Computational analyses predict that mammalian miRNAs regulate ~30% of all protein-coding genes, because an individual miRNA can target many different mRNAs and an individual mRNA can be regulated by several different miRNAs (3, 4).

Numerous findings suggest that miRNAs undergo aberrant regulation during tumorigenesis. MicroRNA genes are frequently located in genomic regions gained and lost in mammalian cancers (5, 6). Functionally, several miRNAs have been described as oncogenes. For example, the miRNA cluster miR-17-92 is amplified in human B-cell lymphomas and was found to cooperate with c-Myc to accelerate lymphomagenesis in the mouse (7). The *BIC* transcript, which was isolated from a common retroviral insertion site that cooperates with c-Myc in lymphomagenesis and is highly up-regulated in Burkitt's lymphoma, encodes a primary miRNA transcript for miR-155 (8). Moreover, miR-372 and miR-373 were shown to be oncogenic in an expression screen and were implicated in testicular cancer through inactivation of the p53 pathway (9). Other miRNAs have been described as tumor suppressors. Intriguingly, miRNA expression profiling has shown that miRNAs are globally down-regulated in tumors relative to normal tissue (10). Recent work from our group demonstrated that global down-regulation can

promote tumorigenesis (11). MiR-15 and miR-16 are located in chromosome 13q14, a region frequently deleted in chronic lymphocytic leukemia (CLL) (12). Furthermore, recent studies have shown that p53 transcriptional activation targets the miR-34 family in a step important for cell cycle control (13–15). In total, these findings provide several lines of evidence for the importance of miRNA in tumorigenesis.

Let-7 was originally identified in *Caenorhabditis elegans* as a regulator of developmental timing and cellular proliferation (16). The discovery of mammalian *let-7* family members prompted speculation that these miRNAs might be tumor suppressors (17). There are at least nine individual members of the *let-7* family in mammals, and several *let-7* genes are located in regions frequently deleted in human cancer (5). Moreover, *let-7* expression is reduced in a subset of non-small cell lung cancer (NSCLC) patients, and this reduction is correlated with poor prognosis (18, 19). When ectopically expressed in cancer cell lines, *let-7* miRNA can repress cellular proliferation (20, 21). Finally, *let-7* family members functionally inhibit the mRNAs of well characterized oncogenes, such as the Ras family (22), HMGA2 (21, 23, 24), c-Myc (11, 25), and cell cycle regulators like CDC25A, CDK6, and Cyclin D2 (20).

The two best characterized *let-7* targets are the Ras family and HMGA2. Activating mutations in Ras family members (H-ras, K-ras, and N-ras) are found in many human tumors including ~30% of NSCLCs (26). The *let-7* family has been shown to regulate both N-Ras and K-Ras mRNAs via *let-7* binding sites in the 3' UTRs (22). Notably, all previous studies reporting *let-7*-mediated repression of proliferation have been performed in cells expressing mutant forms of N- and K-Ras (20, 21). The high mobility group A (HMGA) proteins are major nonhistone chromosomal proteins involved in transcriptional regulation controlling proliferation and differentiation. HMGA2 is implicated in tumorigenesis via chromosomal translocations and transcriptional up-regulation in several tumor types, although the function of this up-regulation in tumorigenesis is unclear (27–29). The HMGA2 3'UTR contains seven *let-7* target sites and disruption of these sites enhances oncogenic transformation (30). Finally, *let-7* expression is inversely correlated with expression of HMGA2 in NSCLC and ectopic overexpression of HMGA2 promotes cellular proliferation in the presence of *let-7* (21).

The above findings suggest that the *let-7* miRNA family functions in tumor suppression. However, studies to date have not demonstrated that *let-7* miRNA can suppress tumorigenesis *in vivo*. Moreover, there is a lack of functional data related to the

Author contributions: M.S.K. and S.J.E. contributed equally to this work; M.S.K., S.J.E., P.A.S., and T.J. designed research; M.S.K., S.J.E., R.E.P., C.Y.C., and M.S.E. performed research; M.S.K. and S.J.E. analyzed data; and M.S.K., S.J.E., P.A.S., and T.J. wrote the paper.

The authors declare no conflict of interest.

†To whom correspondence may be addressed. E-mail: sharp@mit.edu or tjacks@mit.edu.

This article contains supporting information online at www.pnas.org/cgi/content/full/0712321105/DC1.

© 2008 by The National Academy of Sciences of the USA

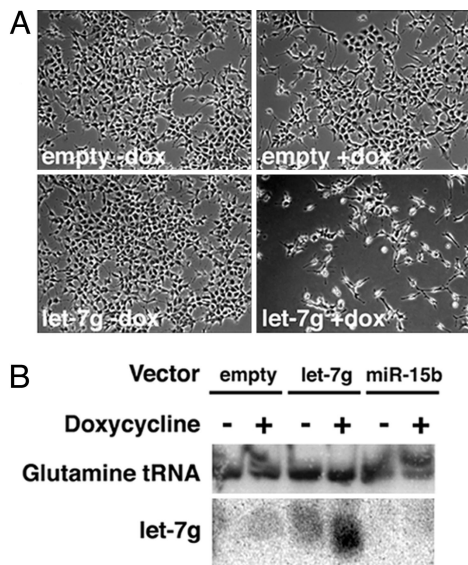


Fig. 1. Let-7g impairs proliferation and enhances cell death. (A) LKR13-Tet-On-KRAB-TE-empty and -let-7g cells were plated (5×10^5 cells per plate). Twelve hours later, cells were placed in the presence/absence of $5 \mu\text{g/ml}$ doxycycline. Forty-eight hours later, images were taken by phase contrast microscopy. (B) Small RNA Northern blot analysis was performed against let-7g and Glutamine tRNA in LKR13-Tet-On-KRAB-TE-empty, -miR-15b, and -let-7g (see *SI Text* for details) cells in the presence or absence of $5 \mu\text{g/ml}$ doxycycline.

regulation of individual let-7 targets on tumorigenesis *in vivo*. Finally, no studies to date have examined let-7 function in autochthonous tumors, which allows the evaluation of the roles of let-7 in tumor initiation and progression. Here, we have used

constitutive and inducible expression of let-7 to examine its effect on tumor development.

Results

Let-7g Impairs Tumor Cell Proliferation and Promotes Tumor Cell Death *in Vitro*. To assess the roles of the let-7 miRNA on cell cycle control and cell death, we transfected a let-7g miRNA duplex into murine K-Ras^{G12D}-expressing lung adenocarcinoma cells (LKR13). Consistent with the studies in refs. 20 and 21, transfected let-7g triggered a significant shift in the cell cycle distribution, with an accumulation of G₀/G₁- and G₂/M-phase cells and a corresponding reduction of S-phase cells [supporting information (SI) Fig. 6A]. In addition, transfection of let-7g caused significant cell death in LKR13 cells (Fig. 6B). To extend these findings, we developed a doxycycline (dox)-regulated expression system to induce miRNA expression in cell lines. Using the inducible vector system, we observed a substantial (≈ 5 -fold) induction of let-7g in the presence of dox (Fig. 1B). Furthermore, induction of let-7g in LKR13 cells caused a robust decrease in cell density (Fig. 1A). Overall, these results indicate that let-7g can restrict cellular proliferation and induce cell death.

Let-7g Suppresses Tumorigenesis *in Vivo*. The LKR13 cells with inducible let-7g were transplanted into immune compromised mice to which dox was administered in the drinking water. Using this system, we observed a substantial reduction in tumor growth in mice after induction of let-7g compared with controls; induction of miR-15b, although putatively described as a tumor suppressor in CLL (12), did not alter tumor growth in this system (Fig. 2A). However, this does not exclude the possibility of miR-15b suppressing tumor growth in other contexts. Importantly, this reduction in tumor growth depended on induction of let-7g, because transplantation of the same cells into animals without dox treatment led to rapid tumor development (Fig. 2B). Interestingly, tumors with ectopic let-7g expression, although

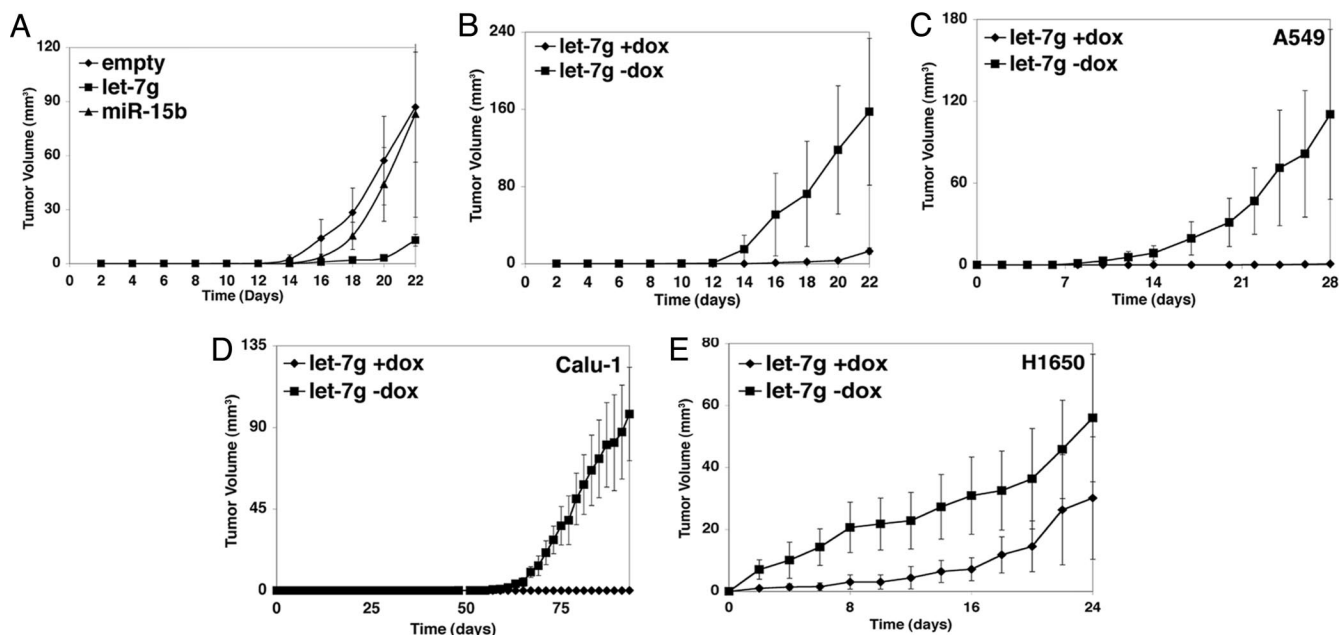


Fig. 2. Let-7g suppresses tumorigenesis *in vivo*. (A) LKR13-Tet-On-KRAB-TE-empty, -miR-15b, and -let-7g cells were plated in the presence of $5 \mu\text{g/ml}$ doxycycline. Twenty-four hours later, cells were sorted and injected s.c. into immune-compromised mice (2.5×10^4 cells per injection). Two days later, mice were treated with drinking water containing doxycycline (2 mg/ml) and sucrose ($4\% \text{ wt/vol}$), and tumor values were measured over time. Values are mean \pm SEM ($n = 6$). (B) LKR13-Tet-On-KRAB-TE-let-7g cells were treated with doxycycline, sorted, and injected as described above. Two days later, mice were treated with either drinking water containing doxycycline (2 mg/ml) and sucrose ($4\% \text{ wt/vol}$) or drinking water containing sucrose alone. Tumor values were measured over time. Values are mean \pm SEM ($n = 6$). (C–E) Tet-On-KRAB-TE-let-7g cells were generated in A549 (C), Calu-1 (D), and H1650 (E) cells. Cells were prepared and injected (10^6 cells per injection) into immune-compromised mice. Mice were treated and tumors were measured as above. Values are mean \pm SEM ($n = 6$).

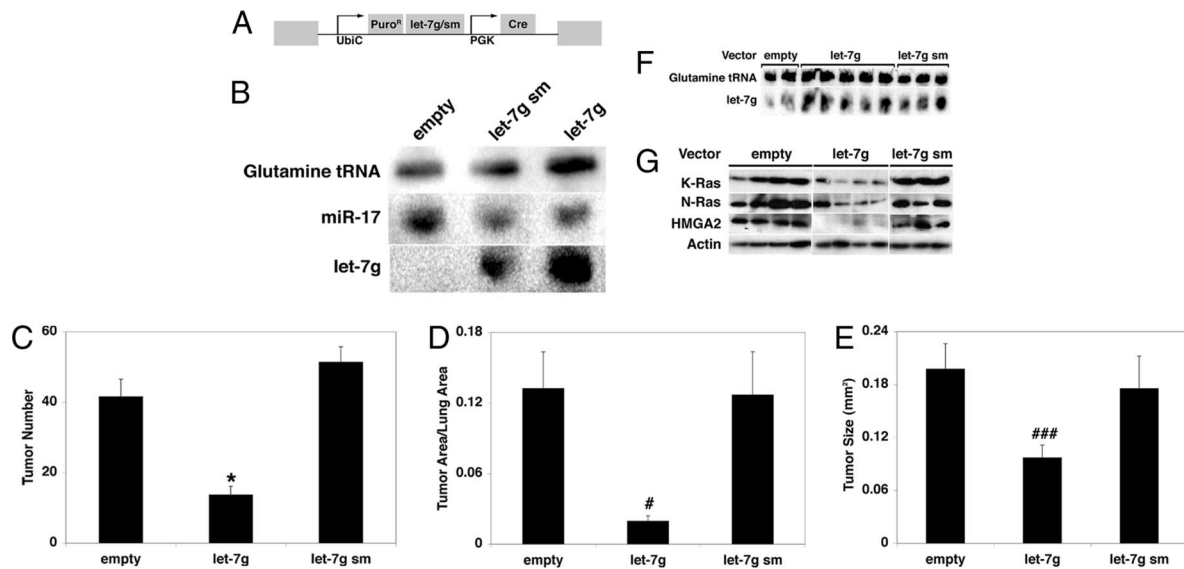


Fig. 5. Let-7g suppresses empty tumor initiation in an autochthonous NSCLC model. (A) Diagram of the Puro.Cre lentiviral vector for coexpression of let-7g/let-7g sm with Cre recombinase. (B) Small RNA Northern blot analysis was performed against let-7g (both wild type and seed mutant), miR-17 and Glutamine tRNA in HEK293 cells infected with Puro.Cre (empty), Puro.let7gsm.Cre (let-7g sm), and Puro.let7g.Cre (let-7g). (C–E) *Kras^{LSL-G12D};Trp-53^{flx/flx}* mice were intratracheally infected with the Puro.Cre lentiviral vectors described above. Twelve weeks after infection, animals were killed, and tumor number (C), tumor and lung area (D), and tumor size (E) were quantified with Bioquant software. Values are mean ± SEM ($n = 9$ for empty, $n = 11$ for let-7g, and $n = 11$ for let-7g sm). *, $P < 0.0005$, #, $P < 0.01$; ###, $P < 0.1$. (F) Small RNA Northern blotting was performed against let-7g (both wild type and seed mutant), and Glutamine tRNA on lung tumors generated from *Kras^{LSL-G12D};Trp-53^{flx/flx}* mice infected with Puro.Cre (empty), Puro.let7g.Cre (let-7g), and Puro.let7gsm.Cre (let-7g sm). (G) Western blot analysis was performed on lung tumors generated from *Kras^{LSL-G12D};Trp-53^{flx/flx}* mice infected with Puro.Cre (empty), Puro.let7g.Cre (let-7g), and Puro.let7gsm.Cre (let-7g sm). All samples were probed on the same blot.

likely including HMGA2, are also relevant for let-7g-mediated tumor suppression.

Let-7g Suppresses Tumor Initiation in an Autochthonous NSCLC Model.

We next examined the tumor suppressive effect of let-7g in naturally arising lung tumors in the mouse. When infected with Cre-expressing virus in the lung epithelium, *Kras^{LSL-G12D};Trp-53^{flx/flx}* mice develop highly aggressive NSCLC following a well defined time course (31). These lesions recapitulate advanced human lung adenocarcinoma in many ways, including stromal desmoplasia. To deliver let-7g to the lung epithelium, we generated a lentiviral vector coexpressing let-7g or a seed-mutant version of let-7g (let-7g sm) with Cre, using a dual-expression system (Fig. 5A). This vector generated substantial expression of let-7g and let-7g sm relative to controls in cultured cells (Fig. 5B). In addition, let-7g expressed from this vector caused robust repression of a reporter through the K-Ras 3' UTR, which was not observed with the seed mutant of let-7g (SI Fig. 13).

Kras^{LSL-G12D};Trp-53^{flx/flx} mice were infected with let-7g- and let-7g sm-containing lentiviruses, and effects on tumor development were determined by visual inspection and histological analysis. We observed a significant reduction in both lung tumor number and tumor area after infection with the vector expressing let-7g versus controls (Fig. 5 C and D). In addition, there was a slight decrease in average tumor size in let-7g expressing mice (Fig. 5E). The levels of let-7g and let-7g sm expression in these tumors were determined by Northern blot analysis. Consistent with findings in xenograft tumors, there was sustained overexpression of let-7g and let-7g sm in tumors from mice infected with the corresponding lentiviruses (Fig. 5F). Moreover, these let-7g overexpressing tumors have reduced protein levels of N-Ras, K-Ras, and HMGA2, indicating functional repression of known let-7 targets (Fig. 5G). In total, these findings suggest that let-7g effectively suppresses tumor initiation in an autochthonous mouse model of mutant K-Ras-driven NSCLC. However, the tumors that do form continue to express let-7g and suppress

known targets, supporting the conclusion that naturally arising tumors may gain resistance to let-7g.

Discussion

In this study, we investigated the functional consequence of let-7g expression on non-small cell lung tumorigenesis. Using both inducible and constitutive expression systems, we observed substantial tumor suppression by let-7g both in xenografts and in a mouse lung tumor model. Two lines of evidence suggest that let-7g-mediated tumor suppression is representative of the let-7 family. First, transfection of other let-7 family members caused comparable induction of cell death to let-7g (data not shown). Second, transfection of a miRNA sponge (32) targeting the entire let-7 family shifted the cell cycle distribution opposite to let-7g overexpression with a significant reduction of G₀/G₁-phase cells and a corresponding increase in S- and G₂/M-phase cells (SI Fig. 6C).

Studies of the effect of let-7 on cellular proliferation have used cells containing activating mutations in K-Ras (A549) and N-Ras (H1299 and HepG2) (20, 21). Because both K-Ras and N-Ras are previously characterized targets of the let-7 family, it was possible that the effects of let-7 on proliferation in these cell lines were largely due to down-regulation of the Ras family. In the present study, we determined that K-Ras^{G12D}-mediated rescue of tumor growth was not complete, suggesting that other let-7 targets are also relevant to tumor suppression. In sum, these findings suggest that let-7-mediated tumor suppression occurs largely, although not completely, through regulation of the Ras family.

Although let-7g expression potently suppressed non-small cell lung tumorigenesis, tumors inevitably formed in the presence of sustained let-7g induction. Notably, these tumors continued to express let-7g and actively repressed let-7 targets, suggesting the tumors that form do not propagate because of silencing of the let-7g vector. Moreover, this continued let-7g expression occurred both in xenograft models and autochthonous lung tumors

expressing let-7g. This apparent resistance to let-7 was not observed in the studies in refs. 20 and 21, because they relied on transient delivery of let-7 family members. This distinction highlights the importance of stable induction of let-7 when analyzing its role in tumorigenesis, because transient expression of let-7 does not recapitulate the long-term effects of let-7 on tumorigenesis *in vivo*.

Although we cannot exclude the possibility that the let-7g target repression observed here was insufficient to suppress tumorigenesis, the data suggest that let-7g is present and active in escaping tumors. It is possible that escaping tumors have activated pathways downstream of targets in the presence of let-7; escape could also occur through activation of a distinct set of oncogenes not targeted by the let-7 family. Overall, the apparent resistance to let-7g expression has significant implications for the use of let-7 miRNAs as a therapeutic agent. Our data indicate that sustained let-7 delivery might lead to initial suppression of tumor growth but that let-7 resistant tumors might eventually emerge. Using the systems described here, one could probe downstream pathways from let-7 targets, including Ras, HMGA2, and others, to assess their roles in let-7 resistant tumors. Additionally, expression analysis of sensitive and resistant tumors might reveal novel pathways functionally related to let-7 resistance.

Here, we describe one of the first cases of a miRNA family functioning as a tumor suppressor *in vivo*. Our findings make clinically relevant predictions related to the use of let-7-based therapeutic agents in NSCLC. The systems outlined in this study provide insight into let-7-mediated tumor suppression and also establish unique tools for understanding the basis for resistance of cancer cells to miRNA-mediated control of tumorigenesis. Moreover, the doxycycline-based and lentiviral systems described could be applied to examine other small RNAs suggested to function in tumorigenesis.

Materials and Methods

Cell Culture. Human cell lines (HEK293, A549, Calu-1, and H1650) were originally obtained from ATCC. 3T3 cells are described in ref. 33. LKR13 cells are described in ref. 34. Cells were grown under standard conditions. After introduction of pTE vectors, cells were maintained under standard conditions in Tet-Free Serum per the manufacturer's instructions (Clontech).

Cell Cycle and Cell Death Analysis. MicroRNA duplex sequences were transfected in triplicate into LKR13 cells with DharmaFECT-1 (Dharmacon) according to manufacturer's protocol. Cells were harvested after 48 and 72 h and either fixed in methanol and stained with 7-AAD (Stem-Kit reagent, Beckman Coulter) or stained with the Apoptest-FITC kit (Nexins Research) and analyzed by flow cytometry.

Lentivirus Production and Infection. Lentivirus production was performed as described in ref. 35.

Allograft/Xenograft Studies. Tet-On-KRAB-TE cells were treated for 24 h with doxycycline (5 μ g/ml) and sorted by flow cytometry. Balb/C/Nu males (Taconic)

were injected with cells as described in ref. 36. Two days after injection, mice were treated with drinking water containing doxycycline (2 mg/ml) and sucrose (4% wt/vol). Tumor sizes were measured every two days. After indicated days, mice were killed and tumors were isolated for histology and Western and Northern blot analyses.

Intervention Studies. Mice were injected with LKR13-Tet-On-KRAB-TE cells and monitored for tumors. Once tumors were greater than 2 mm in diameter, mice were i.p. injected with doxycycline (40 mg/kg) and tumors were measured as above.

Secondary Transplant Studies. Mice were injected with LKR13-Tet-On-KRAB-TE cells and treated with doxycycline in the drinking water as above. Tumors were then explanted, retreated for 24 h with doxycycline (5 μ g/ml) and sorted by flow cytometry. Cells were then injected and mice were treated with doxycycline in the drinking water as above. Tumor sizes were measured every 2 days. After indicated days, mice were killed and tumors were isolated for Northern blot analysis.

Genetically Engineered Mice. *Kras^{LSL-G12D}; Trp-53^{flx/flx}* mice were generated as described in ref. 31.

Intratracheal Infection and Tumor Analysis. *Kras^{LSL-G12D}; Trp-53^{flx/flx}* mice were infected intratracheally with Puro.Cre lentivirus essentially as described in ref. 37. Tumor analysis was performed as described in ref. 11.

Animal Care and Use. Research was approved by the Committee for Animal Care, and conducted in compliance with the Animal Welfare Act Regulations and other Federal statutes relating to animals and experiments involving animals and adheres to the principles set forth in the Guide for Care and Use of Laboratory Animals, National Research Council, 1996 (institutional animal welfare assurance no. A-3125-01).

Further Details. For more information on the materials and methods, see [SI Text](#).

Note Added in Proof. A recent study described in ref. 38 suggested that let-7 suppresses tumorigenesis via alteration of self-renewal and differentiation of breast cancer stem cells. Studies should look to characterize these effects in the described lung cancer models.

ACKNOWLEDGEMENTS. We thank P. Stern (Massachusetts Institute of Technology Center for Cancer Research) for the PUV1 lentiviral vector, P. Sandy (Massachusetts Institute of Technology Center for Cancer Research, Cambridge, MA) for the K-Ras4B^{G12D} luciferase fusion expression vector, M. Dupage (Massachusetts Institute of Technology Center for Cancer Research) for the UbC.Luciferase.PGK.Cre lentiviral vector, and C. Mayr and D. Bartel (Whitehead Institute of Biomedical Research, Cambridge, MA) for the human HMGA2 cDNA expression vector, M. Narita (Cambridge Research Institute, Cambridge, U.K.) for the HMGA2 antibody. We thank members of the P.A.S. and T.J. laboratories for experimental advice and M. Calabrese, C. Reinhardt, and D. McFadden for critical review of the manuscript. This work was supported by National Cancer Institute Grant 2-PO1-CA42063-21, United States Public Health Service Grant RO1-GM34277, National Institutes of Health Integrative Cancer Biology Program Grant U54 CA112967 (to P.A.S.), and National Cancer Institute Cancer Center Support Grant P30-CA14051. M.S.K. is a National Science Foundation Graduate Research Fellow. S.J.E. is supported by KWF kankerbestrijding (the Dutch Cancer Society). M.S.E. is supported by a Howard Hughes Medical Institute Predoctoral Fellowship and a Paul and Cleo Schimmel Scholarship. T.J. is an investigator of the Howard Hughes Medical Institute and a Ludwig Scholar.

- Bartel DP (2004) MicroRNAs: genomics, biogenesis, mechanism, and function. *Cell* 116:281–297.
- Valencia-Sanchez MA, Liu J, Hannon GJ, Parker R (2006) Control of translation and mRNA degradation by miRNAs and siRNAs. *Genes Dev* 20:515–524.
- Lewis BP, Burge CB, Bartel DP (2005) Conserved seed pairing, often flanked by adenosines, indicates that thousands of human genes are microRNA targets. *Cell* 120:15–20.
- Lewis BP, Shih IH, Jones-Rhoades MW, Bartel DP, Burge CB (2003) Prediction of mammalian microRNA targets. *Cell* 115:787–798.
- Calin GA, et al. (2004) Human microRNA genes are frequently located at fragile sites and genomic regions involved in cancers. *Proc Natl Acad Sci USA* 101:2999–3004.
- Sevignani C, et al. (2007) MicroRNA genes are frequently located near mouse cancer susceptibility loci. *Proc Natl Acad Sci USA* 104:8017–8022.
- He L, et al. (2005) A microRNA polycistron as a potential human oncogene. *Nature* 435:828–833.
- Metzler M, Wilda M, Busch K, Viehmann S, Borkhardt A (2004) High expression of precursor microRNA-155/BIC RNA in children with Burkitt lymphoma. *Genes Chromosomes Cancer* 39:167–169.
- Voorhoeve PM, et al. (2006) A genetic screen implicates miRNA-372 and miRNA-373 as oncogenes in testicular germ cell tumors. *Cell* 124:1169–1181.
- Lu J, et al. (2005) MicroRNA expression profiles classify human cancers. *Nature* 435:834–838.
- Kumar MS, Lu J, Mercer KL, Golub TR, Jacks T (2007) Impaired microRNA processing enhances cellular transformation and tumorigenesis. *Nat Genet* 39:673–677.
- Cimmino A, et al. (2005) miR-15 and miR-16 induce apoptosis by targeting BCL2. *Proc Natl Acad Sci USA* 102:13944–13949.
- Chang TC, et al. (2007) Transactivation of miR-34a by p53 broadly influences gene expression and promotes apoptosis. *Mol Cell* 26:745–752.
- He L, et al. (2007) A microRNA component of the p53 tumour suppressor network. *Nature* 447:1130–1134.
- Raver-Shapira N, et al. (2007) Transcriptional activation of miR-34a contributes to p53-mediated apoptosis. *Mol Cell* 26:731–743.
- Reinhart BJ, et al. (2000) The 21-nucleotide let-7 RNA regulates developmental timing in *Caenorhabditis elegans*. *Nature* 403:901–906.

17. Pasquinelli AE, et al. (2000) Conservation of the sequence and temporal expression of let-7 heterochronic regulatory RNA *Nature* 408:86–89.
18. Takamizawa J, et al. (2004) Reduced expression of the let-7 microRNAs in human lung cancers in association with shortened postoperative survival. *Cancer Res* 64:3753–3756.
19. Yanaihara N, et al. (2006) Unique microRNA molecular profiles in lung cancer diagnosis and prognosis. *Cancer Cell* 9:189–198.
20. Johnson CD, et al. (2007) The let-7 microRNA represses cell proliferation pathways in human cells. *Cancer Res* 67:7713–7722.
21. Lee YS, Dutta A (2007) The tumor suppressor microRNA let-7 represses the HMGA2 oncogene. *Genes Dev* 21:1025–1030.
22. Johnson SM, et al. (2005) RAS is regulated by the let-7 microRNA family. *Cell* 120:635–647.
23. Hebert C, Norris K, Scheper MA, Nikitakis N, Sauk JJ (2007) High mobility group A2 is a target for miRNA-98 in head and neck squamous cell carcinoma. *Mol Cancer* 6:5.
24. Wang T, et al. (2007) A micro-RNA signature associated with race, tumor size, and target gene activity in human uterine leiomyomas. *Genes Chromosomes Cancer* 46:336–347.
25. Koscianska E, et al. (2007) Prediction and preliminary validation of oncogene regulation by miRNAs. *BMC Mol Biol* 8:79.
26. Bos JL (1989) ras oncogenes in human cancer: A review. *Cancer Res* 49:4682–4689.
27. Meyer B, et al. (2007) HMGA2 overexpression in non-small cell lung cancer. *Mol Carcinog* 46:503–511.
28. Sarhadi VK, et al. (2006) Increased expression of high mobility group A proteins in lung cancer. *J Pathol* 209:206–212.
29. Young AR, Narita M (2007) Oncogenic HMGA2: Short or small? *Genes Dev* 21:1005–1009.
30. Mayr C, Hemann MT, Bartel DP (2007) Disrupting the pairing between let-7 and Hmga2 enhances oncogenic transformation. *Science* 315:1576–1579.
31. Jackson EL, et al. (2005) The differential effects of mutant p53 alleles on advanced murine lung cancer. *Cancer Res* 65:10280–10288.
32. Ebert MS, Neilson JR, Sharp PA (2007) MicroRNA sponges: competitive inhibitors of small RNAs in mammalian cells. *Nat Methods* 4:721–726.
33. Psarras S, et al. (2004) Gene transfer and genetic modification of embryonic stem cells by Cre- and Cre-PR-expressing MESV-based retroviral vectors. *J Gene Med* 6:32–42.
34. Wislez M, et al. (2006) High expression of ligands for chemokine receptor CXCR2 in alveolar epithelial neoplasia induced by oncogenic kras. *Cancer Res* 66:4198–4207.
35. Rubinson DA, et al. (2003) A lentivirus-based system to functionally silence genes in primary mammalian cells, stem cells and transgenic mice by RNA interference. *Nat Genet* 33:401–406.
36. Sage J, et al. (2000) Targeted disruption of the three Rb-related genes leads to loss of G (1) control and immortalization. *Genes Dev* 14:3037–3050.
37. Murphy GJ, Mostoslavsky G, Kotton DN, Mulligan RC (2006) Exogenous control of mammalian gene expression via modulation of translational termination. *Nat Med* 12:1093–1099.
38. Yu F, et al. (2007) let-7 regulates self-renewal and tumorigenicity of breast cancer cells. *Cell* 131:1109–1123.