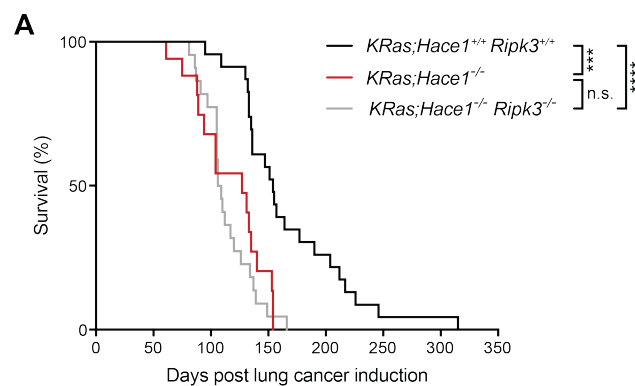


## Supplementary data

### Supplementary Table S1. *HACE1* mutational landscape in human cancer.

*HACE1* mutations, including missense, nonsense, frameshift mutations, splice site mutations that occur in an intron (in a splice acceptor or donor site), splice region mutations that occur near the intron/exon junction, and protein-protein fusions, in individual cancer types as available from the cBioPortal and TGen datasets.

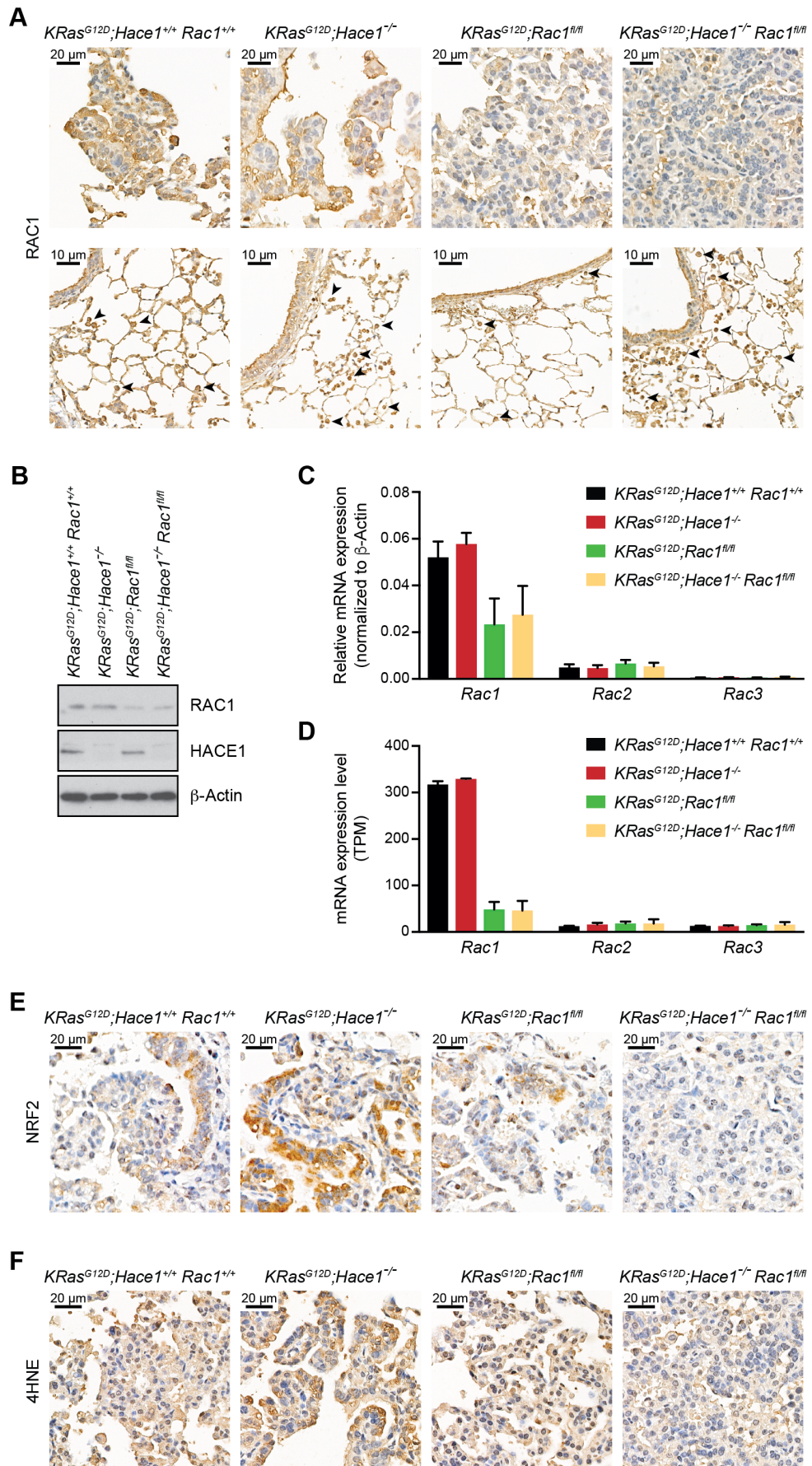
### Supplementary Figure S1



### Supplementary Figure S1. Loss of *Hace1* results in increased lung tumorigenesis independent of RIPK3.

(A) Kaplan-Meier survival curves of  $KRas^{G12D};Hace1^{+/+}Ripk3^{+/+}$  (n=23),  $KRas^{G12D};Hace1^{-/-}$  (n=15) and  $KRas^{G12D};Hace1^{-/-}Ripk3^{-/-}$  (n=22) mice. Upon intratracheal instillation of Adeno-Cre on day 0, mice carrying the conditional *Lox-Stop-Lox (LSL)-KRas<sup>G12D</sup>* allele develop lung adenocarcinomas due to the removal of the Stop cassette and the induction of oncogenic *KRas<sup>G12D</sup>*. \*\*\*  $P < 0.001$ , \*\*\*\*  $P < 0.0001$ , ns (not significant) (log-rank test).

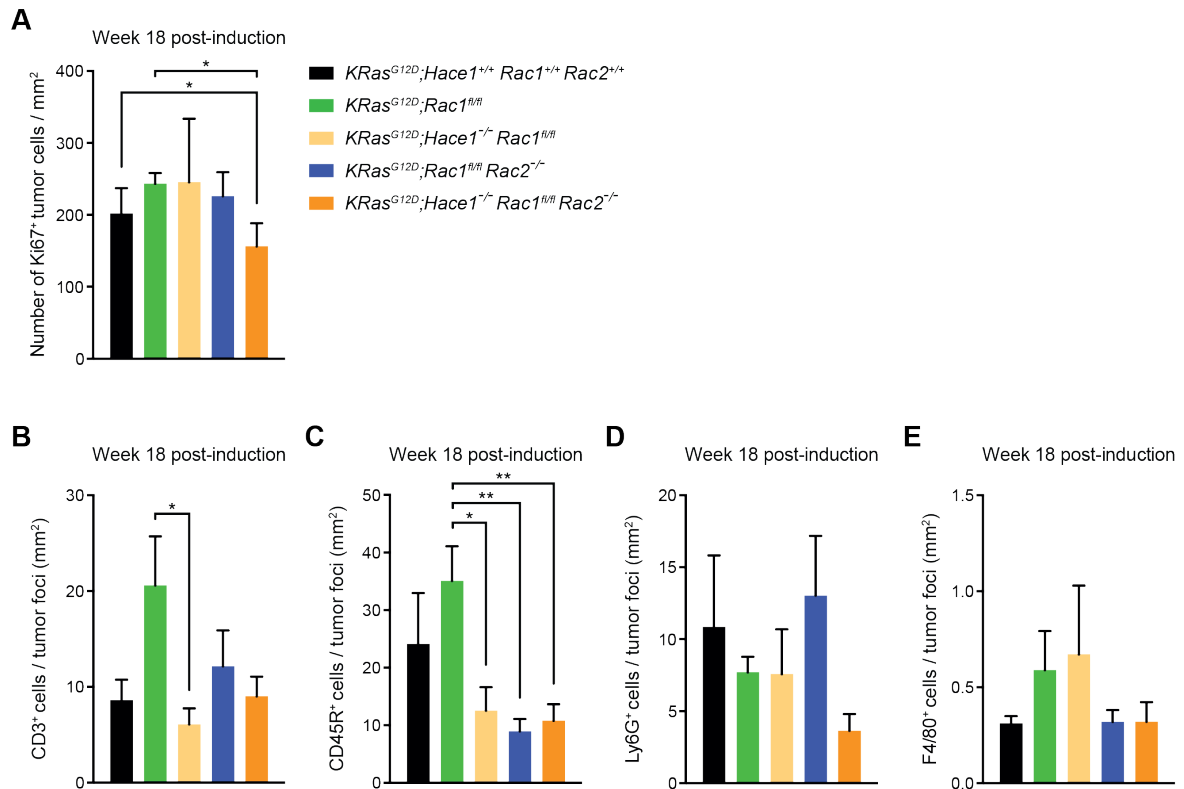
## Supplementary Figure S2



**Supplementary Figure S2. Analysis of RAC, NRF2 and 4HNE expression.**

**(A)** Representative pictures of RAC1 immunostaining of lungs at week 14 post lung cancer induction for *KRas*<sup>G12D</sup>;*Hace1*<sup>+/+</sup>*Rac1*<sup>+/+</sup>, *KRas*<sup>G12D</sup>;*Hace1*<sup>-/-</sup>, *KRas*<sup>G12D</sup>;*Rac1*<sup>fl/fl</sup> and *KRas*<sup>G12D</sup>;*Hace1*<sup>-/-</sup>*Rac1*<sup>fl/fl</sup> mice. The upper panels show RAC1 expression in tumor tissue, the lower panels show RAC1 expression in adjacent tissue. Macrophages are indicated (black arrows). Scale bars, 20µm or 10µm. **(B-C)** Lung tumor cells were isolated from *KRas*<sup>G12D</sup>;*Hace1*<sup>+/+</sup>*Rac1*<sup>+/+</sup>, *KRas*<sup>G12D</sup>;*Hace1*<sup>-/-</sup>, *KRas*<sup>G12D</sup>;*Rac1*<sup>fl/fl</sup> and *KRas*<sup>G12D</sup>;*Hace1*<sup>-/-</sup>*Rac1*<sup>fl/fl</sup> mice at week 12 post lung cancer induction. **(B)** Immunoblotting for RAC1, HACE1, and β-Actin as loading control. Representative Western blots are shown. **(C)** qRT-PCR analysis of *Rac1*, *Rac2* and *Rac3* mRNA expression (n≥4). **(D)** Relative *Rac1*, *Rac2* and *Rac3* mRNA expression (TPM) in primary pneumocytes isolated from *KRas*<sup>G12D</sup>;*Hace1*<sup>+/+</sup>*Rac1*<sup>+/+</sup>, *KRas*<sup>G12D</sup>;*Hace1*<sup>-/-</sup>, *KRas*<sup>G12D</sup>;*Rac1*<sup>fl/fl</sup> and *KRas*<sup>G12D</sup>;*Hace1*<sup>-/-</sup>*Rac1*<sup>fl/fl</sup> mice. Purified pneumocytes were infected with Adeno-Cre for 4 days to delete *Rac1*. Relative expression levels were determined in triplicate (except for *KRas*<sup>G12D</sup>;*Hace1*<sup>-/-</sup>*Rac1*<sup>fl/fl</sup> mice: n=2) and are shown compared to *KRas*<sup>G12D</sup>;*Hace1*<sup>+/+</sup>*Rac1*<sup>+/+</sup> control cells (values set to 1). Representative pictures of **(E)** NRF2 and **(F)** 4HNE immunostaining of lungs at week 16 post lung cancer induction for *KRas*<sup>G12D</sup>;*Hace1*<sup>+/+</sup>*Rac1*<sup>+/+</sup>, *KRas*<sup>G12D</sup>;*Hace1*<sup>-/-</sup>, *KRas*<sup>G12D</sup>;*Rac1*<sup>fl/fl</sup> and *KRas*<sup>G12D</sup>;*Hace1*<sup>-/-</sup>*Rac1*<sup>fl/fl</sup> mice. Scale bars, 20µm. Data in (B) are presented as mean values ± SEM.

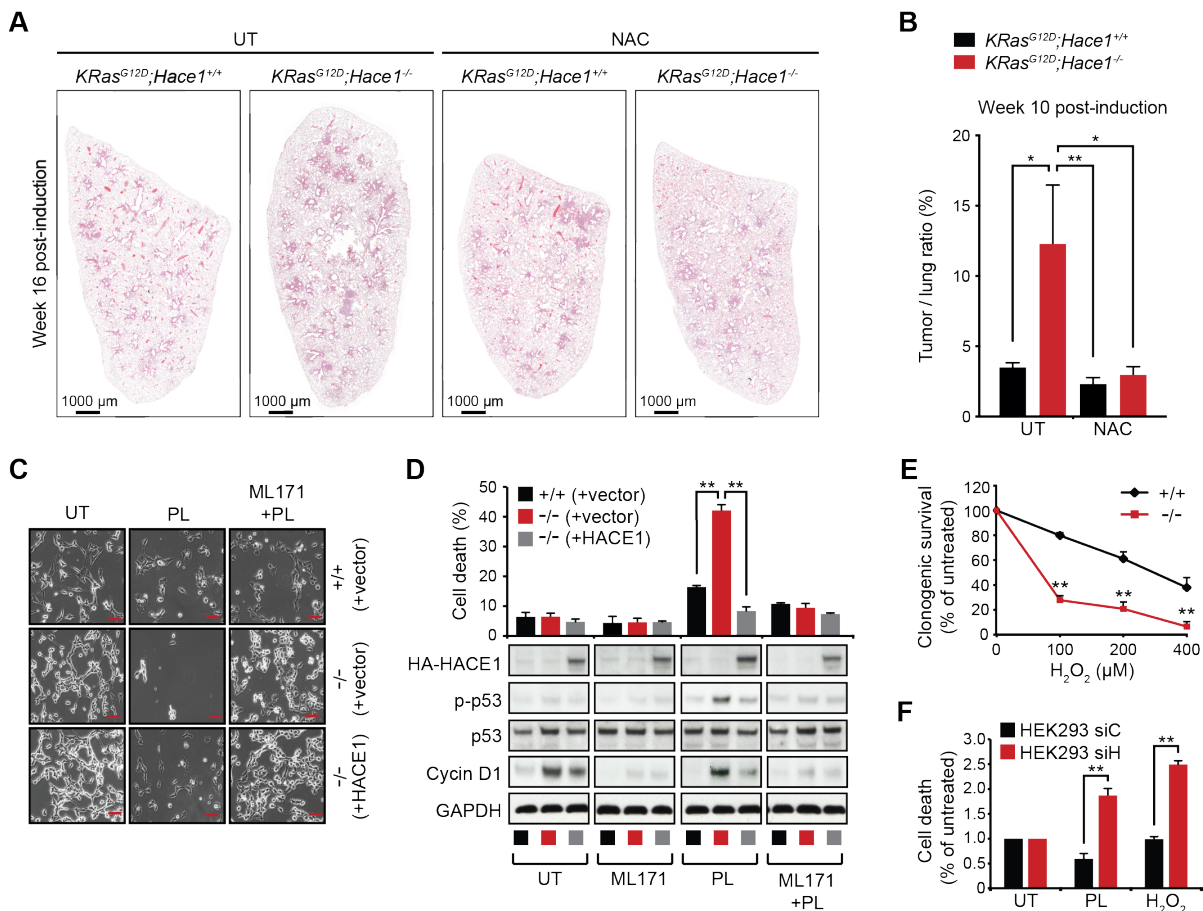
## Supplementary Figure S3



### Supplementary Figure S3. Analysis of tumor microenvironment.

Immunohistochemical analysis at week 18 post lung cancer induction for  $KRas^{G12D};Hace1^{+/+}Rac1^{+/+}Rac2^{+/+}$ ,  $KRas^{G12D};Rac1^{fl/fl}$ ,  $KRas^{G12D};Hace1^{-/-}Rac1^{fl/fl}$ ,  $KRas^{G12D};Rac1^{fl/fl}Rac2^{-/-}$  and  $KRas^{G12D};Hace1^{-/-}Rac1^{fl/fl}Rac2^{-/-}$  mice. Slides are derived from the same experiment shown in Fig. 5E,F. **(A)** Quantification of Ki67<sup>+</sup> tumor cells. **(B-E)** Quantification of CD3<sup>+</sup> T cells (B), CD45R<sup>+</sup> B cells (C), Ly6G<sup>+</sup> neutrophils (D) and F4/80<sup>+</sup> macrophages (E) within the tumors of  $KRas^{G12D};Hace1^{+/+}Rac1^{+/+}Rac2^{+/+}$ ,  $KRas^{G12D};Rac1^{fl/fl}$ ,  $KRas^{G12D};Hace1^{-/-}Rac1^{fl/fl}$ ,  $KRas^{G12D};Rac1^{fl/fl}Rac2^{-/-}$  and  $KRas^{G12D};Hace1^{-/-}Rac1^{fl/fl}Rac2^{-/-}$  mice. \* P<0.05, \*\* P<0.01 (One-way ANOVA, Tukey's post-hoc test, n≥5 mice per cohort). Data are presented as mean values ± SEM.

## Supplementary Figure S4



**Supplementary Figure S4. Treatment of  $KRas^{G12D};Hace1^{-/-}$  mice with a ROS scavenger diminishes lung tumorigenesis and  $Hace1$ -deficient cells are sensitive to exogenous induction of oxidative stress.**

**(A-B)**  $KRas^{G12D};Hace1^{+/+}$  and  $KRas^{G12D};Hace1^{-/-}$  were treated with NAC or left untreated (UT) starting 9 days post lung cancer induction with Adeno-Cre ( $4 \times 10^{10}$  pfu/ml). **(A)** Representative pictures of haematoxylin and eosin (H&E) stained-lung sections and **(B)** tumor-to-lung ratios at week 10 post lung cancer induction for untreated and NAC-treated  $KRas^{G12D};Hace1^{+/+}$  and  $KRas^{G12D};Hace1^{-/-}$  mice. Scale bars, 1 mm for 10x images and 50 $\mu m$  for 40x images of lung sections. \*  $P < 0.05$ , \*\*  $P < 0.01$  (One-way ANOVA, Tukey's post-hoc test,  $n \geq 5$  mice per cohort). **(C)** Phase contrast images of  $Hace1$  wildtype (+/+) and KO (-/-) MEFs reconstituted with empty vector or wildtype  $Hace1$ , 72 h post treatment with the ROS-inducer piperlongumine (PL - 1  $\mu M$ ) and the NOX1 inhibitor ML171 [10  $\mu M$ ] as indicated. Scale bars, 10 $\mu m$ . **(D)** Percent cell death (top) and expression of indicated proteins (bottom, determined by Western blotting) of  $Hace1$  wildtype (+/+) and KO (-/-) MEFs reconstituted with empty vector or wildtype  $Hace1$ , left untreated (UT) or 49 h post-treatment with PL [1

$\mu\text{M}$ ] and/or ML171 [10  $\mu\text{M}$ ] as indicated. \*\*  $P < 0.001$  (Student's two-tailed  $t$ -test,  $n=3$ ). **(E)** Clonogenic survival of *Hace1* wildtype (+/+) and KO (-/-) MEFs treated with indicated concentrations of  $\text{H}_2\text{O}_2$  relative to untreated cells. Clonogenic survival was determined on day 7 after  $\text{H}_2\text{O}_2$  treatment in triplicate cultures. \*\*  $P < 0.001$  (Student's two-tailed  $t$ -test,  $n=3$ ). **(F)** Cell death of HEK293 cells 72 h after transfection with control (siC) or *HACE1* (siH) siRNAs, left untreated (UT) or 48 h post-treatment PL [1  $\mu\text{M}$ ] or  $\text{H}_2\text{O}_2$  [50  $\mu\text{M}$ ]. Cell death was determined on day 2 after PL or  $\text{H}_2\text{O}_2$  treatment in triplicate cultures. \*\*  $P < 0.001$  (Student's two-tailed  $t$ -test,  $n=3$ ). Data in (B), (C) and (D) are presented as mean values  $\pm$  SEM.

## Supplementary methods

**Immunohistochemistry.** The following primary antibodies were also used: rabbit polyclonal anti-CD3 (Abcam, ab49943, 1:3000 dilution), rat monoclonal anti-CD45R (BD Pharmingen, 550286, 1:50 dilution), rat monoclonal anti-Ly6G (BioLegend, 127601, 1:500 dilution), rat monoclonal anti-F4/80 (Bio-Rad, MCA497G, 1:100 dilution), rabbit polyclonal anti-RAC1 (Invitrogen, PA1-091, 1:50 dilution), rabbit polyclonal anti-4HNE (Abcam, ab46545, 1:200) and rabbit polyclonal anti-NRF2 (Abcam, ab31163, 1:100). CD3, CD45R, Ly6G, F4/80 were automatically evaluated by an algorithm programmed and executed using the Definiens Developer software suite. Representative IHC images were selected from scans of the 3D Histech Panoramic Flash II.

**Isolation and culture of primary pneumocytes.** Primary pneumocytes were purified as described (1,2). In brief, lungs were dissected from 8–12-week-old mice, infused with IMDM containing 600 U/mL collagenase IV (Worthington) and 200 U/mL DNase (Worthington) through the trachea, and incubated for 1 h at 37°C. After the isolation, cells were maintained in Ham's F-12 media supplemented with 15 mM HEPES, 0.8 mM CaCl<sub>2</sub>, 0.25% BSA, ITS (Sigma) and 2% FCS, at 37°C and 5% CO<sub>2</sub> conditions. Cells were infected with Adeno-Cre (MOI = 100) *in vitro* for 2 h at 37°C and harvested after 4 days of culture.

**RAC1 activation assay.** Primary lung tumor cells were serum starved for 6 h and then stimulated with 50 ng/ml EGF for 5 min. Clarified cell lysates with equal protein concentrations were affinity precipitated for 1 h at 4°C using GST-PBD-containing glutathione agarose resin. The resin was washed and boiled in Laemmli buffer to remove bound proteins. Active GTP-RAC1 was detected by immunoblotting with mouse anti-RAC1 antibody (Cytoskeleton). For positive and negative controls for active and inactive RAC1, the non-hydrolysable GTP analog GTP $\gamma$ S and GDP were used, respectively. Cell lysates were loaded with 100  $\mu$ M GTP $\gamma$ S or 1 mM GDP in the presence of 10 mM EDTA for 15 min at 30°C. To terminate the reaction, the lysates were placed on ice and supplemented with 60 mM MgCl<sub>2</sub>. These control samples were then incubated with the GST-PBD-containing resin and further processed in the same manner as the other samples.

***In vitro* clonogenic survival and cell death assays.** For clonogenic survival assays (3), MEFs were seeded in 6 cm dishes (5,000 cells/dish) and treated with H<sub>2</sub>O<sub>2</sub> as indicated. After visualization with crystal violet, live cells were counted on the NC-3000 nucleocounter (ChemoMetec). To assess cell death after treatment with PL and ML171, cells were stained with 2.5 µg/mL Hoechst 33342 (Molecular Probes, Invitrogen) and cells containing condensed nuclei were counted using an inverted Olympus (Center Valley, PA) IX-70 fluorescent microscope (Filter U-MWU, 330–385 nm) connected to an Olympus C-3030 digital camera. For each experiment, a minimum of six areas with at least 30 cells each were randomly chosen and counted. The same microscope settings were used to take representative phase-contrast images of the cells.

**Quantitative RT–PCR.** Total RNA from the primary pneumocytes and lung tumor cells was extracted using Trizol (Invitrogen). cDNA was synthesized using iScript™ cDNA Synthesis Kit (BioRad). qRT-PCR was performed with iQ™ SYBR® Green Supermix (BioRad) and gene-specific primers using CFX Real-Time PCR Detection Systems (BioRad). The following primers were used: *Rac1* fwd: ACA CCA CTG TCC CAA TA CTC C, rev: GCA CTC CAG GTA TTT GAC AGC; *Rac2* fwd: GGA CAC CAT CGA GAA GCT GA, rev: GGT CTT CAG GCC TCG CTG; *Rac3* fwd: GAC AAG AAG CTG GCA CCC A, rev: GCC TCG TCG AAC ACT GTC TT. The data were analyzed by relative  $\Delta\Delta$ CT quantification method using *Gapdh* CT values as internal reference in each sample.

## References

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