Inactivation of SAG/RBX2
E3 ubiquitin ligase suppresses
KrasG12D-driven lung tumorigenesis
Hua Li,1 Mingjia Tan,1 Lijun Jia,1 Dongping Wei,1 Yongchao Zhao,1 Guoan Chen,2 Jie Xu,1 Lili Zhao,3 Dafydd Thomas,4 David G. Beer,2 and Yi Sun1

1Division of Radiation and Cancer Biology, Department of Radiation Oncology, 2Thoracic Surgery, Department of Surgery, 3Department of Biostatistics, and 4Department of Pathology and Internal Medicine, University of Michigan, Ann Arbor, Michigan, USA.

Cullin-RING ligases (CRLs) are a family of E3 ubiquitin ligase complexes that rely on either RING-box 1 (RBX1) or sensitive to apoptosis gene (SAG), also known as RBX2, for activity. RBX1 and SAG are both overexpressed in human lung cancer; however, their contribution to patient survival and lung tumorigenesis is unknown. Here, we report that overexpression of SAG, but not RBX1, correlates with poor patient prognosis and more advanced disease. We found that SAG is overexpressed in murine KrasG12D-driven lung tumors and that Sag deletion suppressed lung tumorigenesis and extended murine life span. Using cultured lung cancer cells, we showed that SAG knockdown suppressed growth and survival, inactivated both NF-κB and mTOR pathways, and resulted in accumulation of tumor suppressor substrates, including p21, p27, NOXA, and BIM. Importantly, growth suppression by SAG knockdown was partially rescued by simultaneous knockdown of p21 or the mTOR inhibitor DEPTOR. Treatment with MLN4924, a small molecule inhibitor of CRL E3s, also inhibited the formation of KrasG12D-induced lung tumors through a similar mechanism involving inactivation of NF-κB and mTOR and accumulation of tumor suppressor substrates. Together, our results demonstrate that Sag is a Kras-cooperating oncogene that promotes lung tumorigenesis and suggest that targeting SAG-CRL E3 ligases may be an effective therapeutic approach for Kras-driven lung cancers.

Introduction
CRL (Cullin-RING ligase) complexes consist of a scaffold protein cullin (8 family members), an adaptor protein (few family members), a substrate-recognition protein (many family members), and a RING component (2 family members) (1). Various combinations of these components constitute the largest family of E3 ubiquitin ligases, which are responsible for the ubiquitylation of about 20% of all ubiquitylated proteins for targeted degradation by the 26S proteasome (1, 2). By promoting ubiquitylation and degradation of various substrates, CRLs regulate numerous biological processes, including cell-cycle progression, DNA damage response, signal transduction, and tumorigenesis (3, 4). The activity of CRL E3s requires (a) 1 of 2 RING components, RING-box 1 (RBX1), also known as regulator of cullins 1 (ROC1) or RBX2/Roc2/SAG (where SAG indicates sensitive to apoptosis gene), also known as RNF7 (RING finger protein 7) (5, 6) and (b) cullin neddylation (7, 8), a process catalyzed by NEDD8-activating enzyme (NAE) (E1), NEDD8-conjugating enzyme (E2), and NEDD8 ligase (E3) (9).

RBX1 was initially identified as an essential protein for the full activity of SKP1–Cul1–F-Box protein (SCF) E3 ligase, also known as CRL-1, the founding member of CRL (10–13). SAG, originally cloned in our laboratory, is a redox-inducible antioxidant protein (14), that was later characterized as the second member of the RBX/ROC RING component in SCF/CRL E3s (15). Although RBX1 and SAG are biochemically interchangeable in carrying out E3 ligase activity (15, 16), the in vivo physiological functions of both family members was found to be non-redundant. Our knockout studies revealed that disruption of either Rbx1 or Sag in mice caused embryonic lethality, although at different developmental stages (17, 18), suggesting that in vivo, the 2 family members potentially target different sets of nonoverlapping substrates.

As a redox-inducible antioxidant protein (14, 19), SAG protects cells from apoptosis induced by a variety of stimuli (for review see ref. 20). When forming a complex with other components of SCF/CRL E3 ubiquitin ligases, SAG has E3 ubiquitin ligase activity (15, 16, 21) and promotes the ubiquitylation and subsequent degradation of various cellular proteins, including p27 (22, 23), c-Jun (24), pro-caspase-3 (25), IkBα (16, 26), HIF-1α (27), NOXA (28), and NF1 (18) in a cell context–dependent manner. Whole animal studies revealed that SAG overexpression protects mouse brain tissues from ischemia/hypoxia-induced damage (29, 30). SAG transgenic expression in mouse skin inhibited tumor formation at the early stage by targeting c-Jun/AP1, but enhanced tumor growth at later stages in a DMBA-TPA carcinogenesis model by targeting IkBα to activate NF-κB (26) and promoted UVB-induced skin hyperplasia by targeting p27 (23). Finally, targeted disruption of Sag in the mouse caused embryonic lethality at E11.5–E12.5, which was associated with overall growth retardation, massive apoptosis, and reduced vasculogenesis (18). However, despite all this progress in our understanding of this RING protein, it has not been systematically shown whether Sag is an oncogenic-cooperating gene required for tumorigenesis, induced by a dominant oncogene. Furthermore, although SCF/CRL1 E3 ligase has been suggested as a valid cancer target (31, 32), no study has been conducted to elucidate its role in the development of lung cancer, in which SAG is often overexpressed and correlated with poor patient survival (28, 33).
Lung cancer is the leading cause of cancer-related death both in the USA and world wide, with non–small cell lung cancer (NSCLC) being the most common type and representing nearly 80% of all cases (34). Among the molecular changes found in NSCLC, mutational activation of Kras is one of the most common genetic alterations (35). We recently found that SAG is overexpressed in human NSCLC (28), and it was also previously reported in a study with limited samples (33). However, it is unknown whether SAG overexpression plays a causal role or is merely a consequence of lung tumorigenesis.

In this study, we used a Sag conditional KO mouse model in combination with the KrasG12D, lung cancer model (36) to determine the in vivo role of SAG in lung tumorigenesis, and found that Sag inactivation substantially suppressed KrasG12D-induced lung tumor formation by inactivation of NF-κB (via IκB), mTOR (via DEPTOR), and CDKs (via p21 and p27). Consistently, Sag knockout suppressed, whereas SAG overexpression promoted (in a cell line-dependent manner), the growth and survival of lung cancer cells harboring the same Kras mutation at codon 12. Importantly, pharmaceutical inactivation of CRL E3 ligases by the small molecule MLN4924 also markedly inhibited lung tumor formation triggered by KrasG12D, again through inactivation of NF-κB, mTOR, and CDKs. Our study provides what we believe is the first in vivo demonstration that (a) Sag is a Kras-cooperative oncogene that is overexpressed in human lung cancer and (b) the CRL ligase inhibitor MLN4924, which inhibits both SAG- and RBX1-associated CRLs, has potential for future development as a class of anticancer drugs for the treatment of Kras-driven lung cancer patients where effective treatments are greatly needed.

Results

SAG overexpression in lung cancer tissues correlates with poor patient survival. Our recent work showed that both RBX1/ROC1 and SAG/RBX2/ROC2 are overexpressed in human NSCLC, including adenocarcinomas and squamous cell carcinomas (28, 37). A previous study with limited sample size suggested that SAG overexpression in NSCLC correlated with worse prognosis (33). To confirm and extend this work, we performed a large-scale analysis of SAG mRNA expression and prognosis using data from 442 lung adenocarcinoma patients (38). As shown in Figure 1 and Table 1, patients with high SAG mRNA levels had a statistically significant lower survival probability, whereas those with low SAG levels had better survival (P = 0.001) (Figure 1A). Consistent with this, high SAG expression was significantly correlated with larger tumor size (Figure 1B) and with poor tumor differentiation (Figure 1C).

Furthermore, SAG remained a significant independent prognostic factor after adjusting for stage, age, sex, and grade (HR = 1.41; 95% CI: 1.05-1.89; P = 0.023) (Table 1). In contrast, RBX1 expression was not associated with patient survival or disease progression (Figure 1D and Supplemental Table 1; supplemental material available online with this article; doi:10.1172/JCI70297DS1). Taken together, these results show that overexpression of SAG, but not RBX1, is directly associated with and may potentially be causally related to lung cancer development and that SAG overexpression may serve as a biomarker for prognosis of lung cancer patients. We, therefore, focused our remaining studies on SAG.

Sag deletion inhibits KrasG12D-induced lung tumorigenesis and extends life-span in the mouse. We next determined whether SAG overexpression seen in human lung cancer patients is causally related to, or merely the consequence of lung tumorigenesis, using a well-established LSL-KrasG12D (Lox-STOP-Lox KrasG12D) conditional mouse lung tumor model, in which KrasG12D is activated by Cre-recombinase via the removal of the STOP element to induce epithelial hyperplasia, adenomas, and adenocarcinomas in the lung (36). We first confirmed that SAG is indeed overexpressed in lung tumors induced by KrasG12D in 3 individual mice (Supplemental Figure 1). We then generated a Sag conditional KO mouse model (Saggt/fl, Supplemental Figure 2) and crossed it with Saggt/+ gene-trap mice (18) to generate Saggt/fl mice (1 gene-trap Sag-null allele, gt and 1 Sag-floxed allele, fl). Two-step crossing with LSL-KrasG12D mice generated compound mice with the following 4 genotypes: (a) KrasG12D;Saggt/+ (positive control), (b) LSL-KrasG12D;Saggt/fl, (c) LSL-KrasG12D;Saggt/fl, and (d) Saggt/fl (negative and toxicity control). The mice were intratracheally administrated with Ad-Cre to activate KrasG12D and simultaneously inactivate Sag in group c mice. Mice were euthanized 12 weeks after infection. As expected, both LSL-KrasG12D;Saggt/fl and LSL-KrasG12D;Saggt/fl mice developed substantial numbers of adenomas with few adenocarcinoma (classified as tumors), consistent with our previous observation that heterozygous Sag deletion had no phenotype compared with WT mice (18). Remarkably, Sag inactivation in group c mice significantly reduced lung tumor burden induced by KrasG12D, although the number of hyperplastic loci was not affected by Sag inactivation (Figure 2, A and B, and Supplemental Figure 3, A and B). It is worth noting that Sag inactivation in adult mice (group d) had no toxic effects on normal lung tissues (Figure 2A). The results clearly suggest that Sag inactivation may not affect tumor initiation but markedly inhibits the progression from hyperplasia to adenomas. Thus, Sag is required for the progression of lung tumor development triggered by KrasG12D activation.

We noticed that adenomas did develop in some LSL-KrasG12D;Saggt/fl mice (Supplemental Figure 3C). We reasoned that this could be due to incomplete deletion of the floxed Sag allele, a phenomenon often seen in compound KrasG12D mouse models (39, 40). To test this, we microdissected 2 tumors via laser capture and performed PCR-based genotyping. As shown in Supplemental Figure 3D, in both tumor cases, we detected floxed Sag allele, indicating incomplete excision. Activation of KrasG12D was also confirmed in these tumors (Supplemental Figure 3E). We further dissected

<table>
<thead>
<tr>
<th>Predictor</th>
<th>HR (95% CI)</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>SAG/RNF7</td>
<td>1.64 (1.22, 2.19)</td>
<td>0.001</td>
</tr>
<tr>
<td>Multivariate analysis (n = 434)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Predictor</td>
<td>HR (95% CI)</td>
<td>P value</td>
</tr>
<tr>
<td>SAG/RNF7</td>
<td>1.41 (1.05, 1.89)</td>
<td>0.023</td>
</tr>
<tr>
<td>Stage</td>
<td></td>
<td></td>
</tr>
<tr>
<td>II vs. I</td>
<td>2.75 (1.95, 3.87)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>III vs. I</td>
<td>1.67 (2.20, 6.80)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Age (yr, continuous)</td>
<td>1.03 (1.01, 1.04)</td>
<td>0.001</td>
</tr>
<tr>
<td>Sex (female vs. male)</td>
<td>0.83 (0.62, 1.11)</td>
<td>0.208</td>
</tr>
<tr>
<td>Grade</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2 vs. 1</td>
<td>0.86 (0.52, 1.41)</td>
<td>0.545</td>
</tr>
<tr>
<td>3 vs. 1</td>
<td>1.06 (0.64, 1.77)</td>
<td>0.824</td>
</tr>
</tbody>
</table>

Univariate analysis (n = 442)

<table>
<thead>
<tr>
<th>Predictor</th>
<th>HR (95% CI)</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>SAG/RNF7</td>
<td>1.41 (1.05, 1.89)</td>
<td>0.023</td>
</tr>
<tr>
<td>Multivariate analysis (n = 434)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Univariate analysis (n = 442)
Overexpression of SAG, but not RBX1, correlates with poor survival of lung cancer patients, increased tumor size, and poor differentiation. (A) SAG mRNA expression versus the survival of lung cancer patients: Affymetrix U133A microarray data including 442 lung adenocarcinomas was downloaded from Shedden et al. (38). Robust multi-array average (RMA) normalized (62) and log2 transformed data were used in this study. Survival functions were estimated by the Kaplan-Meier method for patients with low and high expressions SAG (A) and RBX1 (D). Continuous expression levels were dichotomized using median splits (n = 220 and n = 222 in low and high groups in SAG [A]; n = 222 and n = 220 in Low and High groups in RBX1 [D], respectively). Patients with higher SAG levels had a worse overall survival (HR = 1.64; 95% CI: 1.22–2.19; P = 0.001, log-rank test). (B) SAG mRNA was higher in T3–T4 tumors as compared with T1 tumors (P < 0.001, t test). (C) SAG mRNA was higher in poorly differentiated tumors as compared with well-differentiated tumors (P < 0.001, t test). Definition of boxplot: the bounds of the box represent the middle 50% of all value, the line within the box is the median value, the upper line of the box is the value at 25%, the lower line of the box is the value at 75%. The upper and lower whiskers represent the maximum and minimum values. Few outlying values are located outside of whiskers. (D) RBX1 mRNA expression was not related to the survival of lung cancer patients (P = 0.53, log-rank test).

Figure 1

10 individual larger tumors that were developed 16 weeks after Ad-Cre administration in 10 individual LSL-KrasG12D;Saggt/− mice and found the floxed Sag allele remained in every single case (Supplemental Figure 3F). Thus, development of the lung tumors in some LSL-KrasG12D;Saggt/− mice is due to incomplete Sag deletion.

We next determined the effect of Sag inactivation on overall mouse survival upon KrasG12D activation by comparison of the survival probability between LSL-KrasG12D;Saggt/+ and LSL-KrasG12D;Saggt/− mice. Consistent with published reports (40, 41), while LSL-KrasG12D;Saggt/+ mice had a median time to death of 27.6 weeks, with all mice dying by 33 weeks after KrasG12D activation, the LSL-KrasG12D;Saggt/− mice had a median time to death of 37.9 weeks, with 4 mice remaining alive after 60 weeks. This difference is statistically significant, with a log-rank P value of less than 0.0001 (Figure 2C). Taken together, our results clearly demonstrate the requirement of Sag for lung tumor development in this KrasG12D model, suggesting that targeting SAG E3 ligase could be an effective approach for the treatment of lung cancer associated with Kras mutation.

Sag deletion suppresses proliferation and causes accumulation of tumor suppressor substrates. We then determined the rate of proliferation and apoptosis in hyperplasia or adenomas derived from KrasG12D;Saggt/− mice as compared with those from KrasG12D;Saggt/+ and found a reduced proliferation, as reflected by Ki67 staining (Figure 3), but not apoptosis, as indicated by lack of cleaved caspase-3 staining (not shown). Immunohistochemistry staining also showed in KrasG12D;Saggt/+ hyperplasia/adenomas the increased levels of several tumor suppressor proteins known to be SAG substrates, including iKB (with corresponding inhibition of p65 nuclear translocation), p21, and p27. Reduction of mTOR1 pathway, as reflected by a reduced pS6K staining, was also observed (Figure 3). Thus, inhibition of tumor progression by Sag deletion is attributable to reduced proliferation as a result of accumulation of tumor suppressor substrates.

SAG knockdown inhibits the growth and survival of human lung cancer cells via inactivation of NF-kB and mTOR and accumulation of p21, p27, NOXA, and BIM. We further used in vitro cell culture models to elucidate the role of SAG in the growth and survival of lung cancer cells. We first used the human lung cancer line A549, which harbors a Kras mutation at the 12th codon position (G12S), identical to that in our mice model (41, 42). Indeed, SAG knockdown via lentivirus-based siRNA caused significant reduction in (a) monolayer growth, (b) clonogenic survival, and (c) anchorage-independent soft-agar growth (Figure 4, A–C). Similar growth suppression was also observed when an independent SAG-targeting siRNA oligonucleotide was used to knock down Sag in A549 cells (Supplemental Figure 4, A–C). We further knocked down Sag in 2 additional lung cancer lines, A427 and H358, which harbor the same Kras mutation at codon 12 (G12D for A427 and G12C for H358; ATCC), and found a similar level of growth suppression (Supplemental Figure 5, A and B, and Supplemental Figure 6A). Note that H358 cells are unable to form colonies in both monolayer culture and in soft agar, whereas A427 cells are unable to form colonies in soft agar in our experimental conditions. Taken together, our results clearly showed that SAG is required for the growth and survival of lung cancer cells as well as for the maintenance of the tumor cell phenotype in A549 cells.

To explore the potential mechanisms by which SAG knockdown suppresses the growth of lung cancer cells, we first focused on Kras itself, since Kras activity is subjected to ubiquitlization regulation (43), whereas Ras proteins are subjected to degradation by SCF-TCP (44). Compared with control human bronchial epithelial BEAS-2B cells, in which no active Kras activity was detected, Kras activity was very high in all 3 lung cancer cell lines, A549, H358,
and A427 (Supplemental Figure 4D). However, SAG knockdown affected neither the activity nor the protein levels of Kras (Supplementary Figure 4D), indicating that growth suppression by SAG knockdown is not mediated via modulation of Kras itself.

We next determined the potential accumulation of known substrates of SAG E3 ligase (20). SAG knockdown caused accumulation of phosphor-IκBα, an indicator of the lack of IκBα degradation (Figure 4D and Supplemental Figure 4E). Follow-up studies revealed that upon SAG knockdown, TNF-α-induced p65 nuclear localization, p65 DNA binding, and NF-κB transactivation were all significantly reduced (Figure 4, E–G), indicating blockage of NF-κB activation. We also found that SAG knockdown caused accumulation of DEPTOR, a naturally occurring inhibitor of mTOR (45) and a physiological substrate of SCFβTrCP (46), with the associated inactivation of mTOR signals, as reflected by reduced phosphorylation of S6K1 and 4E-BP1 (Figure 4D). Finally, SAG knockdown caused the accumulation of several tumor suppressor substrates, including p21, p27, NOXA, and BIM, but not oncogenic substrates, such as c-Myc, cyclin D1, and NOTCH-1 (Figure 4D and Supplemental Figure 4E). Similar results were seen when SAG was knocked down in A549 cells (Figure 5A) partially reversed the growth suppression in monolayer proliferation (Figure 5B), clonal survival (Figure 5C), and soft agar-independent growth (Figure 5D). Complete rescue by DEPTOR knockdown is likely attributable to a growth-stimulating effect upon DEPTOR knockdown alone. Similar partial rescue effects were also observed in H358 cells (Supplemental Figure 7). Thus, accumulation of p21 or DEPTOR upon SAG knockdown plays at least in part a causal role in growth suppression.

SAG ectopic expression reduces the levels of tumor suppressor substrates and promotes cell growth in a cell line–dependent manner. Given that SAG is overexpressed in both human and mouse lung cancer tissues, we next investigated potential growth stimulating effect of SAG overexpression. We ectopically expressed SAG at a level comparable to that of endogenous SAG in all 3 lung cancer cell lines and found that SAG overexpression had a cell line–dependent effect on the substrate levels and cell growth. In A427 cells, SAG ectopic expression reduced the levels of tumor suppressor sub-
strates, including pIkB, Deptor, p21 and p27 (Figure 6A), and consistently promoted cell growth in monolayer culture and increased clonogenic survival (Figure 6, B and C). In A549 and H358 cells, however, SAG ectopic expression had no effect on its substrate levels or cell growth (Supplemental Figure 8). Thus, SAG overexpression promotes the degradation of tumor suppressor substrates and cell growth in a cell line–dependent manner.

MLN4924, a small molecule inhibitor of CRL ligase, inhibits lung tumor formation in vivo and lung cancer cell growth in vitro by blockade of NF-κB and mTOR and accumulation of p21 and p27. SAG is the RING component of SCF-CRL E3 ligases, required for its enzymatic activity. Activity of CRLs also requires cullin neddylation (3, 49). MLN4924 is a recently discovered small molecule inhibitor of NAE, whose inhibition blocks cullin neddylation, thus having a broader effect by inactivating both SAG-associated and RBX1-associated CRL E3s (2, 50). We used MLN4924 as a pharmaceutical approach of SAG (as well as RBX1) targeting and examined its anti–lung cancer activity. To this end, LSL-KrasG12D mice were treated with MLN4924 for 4 weeks using a nontoxic dose regimen (60 mg/kg, once a day, 5 days per week) (2, 51) beginning at 13 weeks after Ad-Cre administration and when tumors had already formed (Figure 2A and Supplemental Figure 3A). Lung tissues were harvested after 16 weeks, sectioned, and examined for tumors. We found that MLN4924 treatment significantly reduced the tumor burden, with a remarkable reduction in both number of hyperplastic areas and adenomas as well as the size of the tumors (Figure 7, A and B, and Supplemental Figure 9, A and B), indicating potential anti–lung cancer activity of MLN4924. Using immunohistochemistry analysis, we found that, compared with vehicle controls, lung tumor tissues from MLN4924-treated mice had (a) decreased proliferation, reflected by reduced Ki67 staining (Figure 7C), but not apoptosis (not shown); (b) increased staining of pIkBα; (c) reduced number of cells with p65 nuclear staining; (d) increased staining of p21 and p27; and (e) reduced staining of pS6K1 (Figure 7, C and D). We further found that only 1 week of MLN4924 treatment is sufficient to reduce proliferation, as evidenced by decreased BrdU incorporation and Ki67 staining (Supplemental Figure 9C), but had no effect on apoptosis (not shown). Taken together, these results further support the notion that inactivation of both SAG- and RBX1-associated CRL E3s inhibits the growth of Kras-induced lung tumors by inhibiting, at least in part, NF-κB and mTOR signaling pathways.

We next determined the effect of MLN4924 on the growth of 3 human lung cancer cell lines and found that MLN4924 effective-
SAG siRNA knockdown inhibits growth and survival of human lung cancer cells via inactivation of NF-κB and mTOR. (A–C). Growth of A549 human lung tumor cells upon SAG siRNA knockdown. Human lung cancer A549 cells were subjected to lentivirus-based siRNA silencing of SAG (Lt-SAG) along with scramble siRNA control (Lt-Con). Cells were tested by ATP-lite based proliferation assay (n = 3) (A); clonogenic survival assay (n = 3) (B); and soft agar assay (n = 3) (C). (D) Accumulation of tumor-suppressive proteins upon SAG knockdown: A549 cells were infected with Lt-SAG or Lt-Con, followed by immunoblotting using indicated Abs. (E) SAG knockdown blocks p65 nuclear translocation. Cells upon SAG knockdown were treated with or without TNF-α (100 ng/ml) for 1 hour, followed by nuclear fractionation and immunoblotting. Caspase-3 and PARP were subjected to DNA-binding assay using TransAM NF-κB assay kit. (G). Luciferase reporter–based NF-κB activity assay. Lentiviral infected cells were transiently transfected with pNifty plasmid, along with renilla for transfection efficiency control. Cells were untreated or treated with TNF-α (10 ng/ml) and assayed for luciferase activity (n = 3). *P < 0.05; **P < 0.01.

Discussion

Lung cancer, primarily NSCLC, is the leading cause of cancer-related deaths (34), with Kras mutations being one of the most common genetic alterations (35). Our recent studies revealed that both RBX1 and SAG are overexpressed in non–small cell lung carcinomas (28, 37) and SAG overexpression is likely mediated through CRL E3 ligases suppression lung cancer growth in both in vivo animal and in vitro cell culture models with mechanism(s) involving blockage of NF-κB/mTOR signals and accumulation of p21 and p27. Furthermore, in all 3 lines tested, MLN4924 treatment caused remarkable accumulation of tumor suppressors p21 and p27, with accumulation of NOXA and BIM varying among the lines (Figure 8D and Supplemental Figure 10C). Accumulation of oncogenic substrates by MLN4924 varied among 3 lines as well, with no accumulation of c-Jun and cyclin D in A549, but they did accumulate in 2 other lines (Figure 8D and Supplemental Figure 10C). Taken together, our results demonstrate that inactivation of CRL E3 ligases suppresses lung cancer growth in both in vivo animal and in vitro cell culture models with mechanism(s) involving blockage of NF-κB/mTOR signals and accumulation of p21 and p27.
provides supporting evidence that SAG overexpression has biological consequences and could serve as a prognostic biomarker as well as the biomarker of patient selection for MLN4924 treatment. Overexpression of a specific gene in human cancers does not predict whether the overexpression is causally related to, or just the consequence of, tumorigenesis. In the case of SAG, it has never been mechanistically pursued whether SAG is required for lung cancer initiation and progression or for the maintenance of lung cancer cell phenotypes or simply as the consequence of tumorigenesis. Here, we addressed this important issue using a loss-of-function approach in 3 lung cancer cell lines harboring the same codon 12 \( \text{KrasG12D} \), as evidenced by reducing tumor burden both in tumor size and number and significantly extending the life span of the mice (Figure 2). The suppressive effect of \( \text{Sag} \) deletion is likely attributable to inactivation of the NF-\( \kappa \)B and mTOR pathways and accumulation of p21 and p27 tumor suppressors (Figure 3). Furthermore, the suppression occurred mainly during hyperplasia-to-adenoma progression under our experimental conditions for a period of 12 weeks after \( \text{KrasG12D} \) activation, which is consistent with the observation that SAG overexpression is associated with later, but not early, stages of human lung cancer (Figure 1). It is worth noting that the in vivo anti-Kras activity of \( \text{Sag} \) inactivation/deletion was observed in the presence of WT \( \text{Rbx1/Roc1} \), the only other member of the RBX/ROC family, indicating that RBX1/ROC1 cannot compensate for the loss of SAG/RBX2/ROC2. These results are consistent with our recent observation using genetic knockout approaches that there is no in vivo redundancy during embryogenesis between these 2 family members of the RING component of CRL E3 ubiquitin ligases (5, 17, 18). Thus, SAG and RBX1 play the nonredundant roles at least during mouse embryogenesis and in \( \text{KrasG12D} \)-induced lung tumorigenesis.

To gain mechanistic insight into SAG action, we used the loss-of-function approach in 3 lung cancer cell lines harboring the same codon 12 \( \text{Kras} \) mutation and found that siRNA-based \( \text{Sag} \) knockdown caused in general accumulation of (a) pIkB\( \alpha \), which is required for \( \text{Kras} \)-mediated lung tumorigenesis (47, 48), (b) DEPTOR, a naturally occurring inhibitor of mTOR to block the mTOR signaling pathway, and (c) tumor suppressors p21 and p27 to block cell-cycle progression. Interestingly, although oncogenes such as cyclin D1, c-Myc, and Notch-1 are known substrates of SCF/CRL-1 E3 ligase (4, 5, 53), none of these oncogenic proteins were found to accumulate upon \( \text{Sag} \) knockdown (Figure 4D, Supplemental Figure 4E, and Supplemental Figure 5, B and C). Thus, it appears that \( \text{Sag} \) inactivation selectively accumulates tumor-suppressive substrates to block \( \text{KrasG12D} \)-induced lung tumorigenesis. This notion was further supported by our rescue experiment in which knockdown of either p21 or DEPTOR abrogated the growth suppression triggered by \( \text{Sag} \) knockdown in both A549 and H358 lung cancer cells (Figure 5 and Supplemental Figure 7). Thus, SAG and RBX1 play the nonredundant roles at least during mouse embryogenesis and in \( \text{KrasG12D} \)-induced lung tumorigenesis.
level in H358 cells. Rather it might be explained by the likelihood that SAG is not limited in these lines or unavailability of associated kinase/F-box proteins, since SAG-mediated degradation of a given substrate depends upon the accessibility of a kinase to phosphorylate the substrate and availability of an F-box protein to bind to phosphorylated substrate.

To explore the therapeutic application of our finding in a Sag conditional knockout mouse model, we used the same KrasG12D lung cancer model and tested anti–lung cancer efficacy of MLN4924, an investigational small molecule inhibitor of both SAG-associated and RBX1-associated CRL E3 ligases via cullin deneddylation (2), which is currently in several phase 1 clinical trials directed against several human malignancies (54–56). Our results clearly demonstrate a therapeutic value of the compound administrated when tumors had been formed following Kras activation for 12 weeks (Figure 7 and Supplemental Figure 9). It is anticipated that compared with permanent Sag deletion (even though some incomplete Sag deletion can be seen), the anti–lung cancer effect of MLN4924 is less, since the compound was only given for the last 4 weeks and the drug effect is temporary. Mechanistically, and similar to Sag KO or knockdown, MLN4924 treatment also blocks NF-kB and mTOR pathways and activates tumor suppressive p21, p27, NOXA, and BIM (Figures 7 and 8, and Supplemental Figures 9 and 10). Apparently, the effect of Sag knockdown or MLN4924 treatment on known substrates of SAG-SCF E3 ligase occurs in a cell context, temporal, and spatially dependent manner (5, 31). Selective accumulation of tumor suppressor proteins that target multiple oncogenic pathways in lung cancer cells makes MLN4924 an appealing anti–lung cancer agent. It should be noted that MLN4924 is an NAE inhibitor and would probably inhibit other cellular neddylation reactions (49, 57), although cullins are the only known physiological substrates (49, 58). Nevertheless, given the fact that MLN4924 phenocopies Sag deletion biologically and mechanistically, the major effect of MLN4924 against lung cancer is through the inhibition of CRL E3s. Furthermore, MLN4924 is the first-in-class and only CRL E3 ligase inhibitor currently in phase I clinical trials for anticancer therapy (54, 56). Our study using both genetic and pharmaceutical approaches provides sound rationale for future development of MLN4924 as a class of drug against deadly lung cancer, particularly those resulting from Kras mutation and SAG overexpression.

In summary, our study supports the following model. During lung tumorigenesis, SAG is induced in response to various stresses, such as ROS, hypoxia, and likely KrasG12D activation through transcription activation by AP1 and HIF1 (20). Increased SAG then recruits other components of SCF/CRL E3s (e.g., SCFβTrCP) to promote the degradation of tumor suppressor proteins, such as IκBα, DEPTOR, p21, p27, NOXA, and BIM, leading to activation of the NF-kB and mTOR pathways, cell-cycle progression, and apoptosis inhibition, respectively, which then cooperates with KrasG12D to induce lung tumorigenesis. Sag inactivation by genetic deletion or Sag-CRL inhibition by small molecule MLN4924 abrogates these oncogenic processes by inducing the accumulation of tumor suppressive proteins to antagonize Kras effects, eventually leading to the suppression of lung tumor development (Figure 9). Our study, therefore, provides (a) convincing evidence of SAG-SCF/CRL-1 E3 as a valid anti–lung cancer target and (b) sound rationale for future clinical trials of MLN4924 as a class of anti–lung cancer agent that abrogates multiple oncogenic pathways.
Methods

PCR-based genotyping. Genomic DNA was isolated from the tips of mouse tails and genotyped using the primer set of Baygen 08: 5′-CATCCGGCTACCG-GCTAAAACCTT-3′ and SAGsi09: 5′-CAGAAGGCTCATGGTAAAACATC-3′ for "Sag" gene-trapped allele (477 bp) and SAGsi09 and SAGsi14: 5′-CATGGTAATCACCCTGCCTG-3′ for "Sag" WT allele (585 bp). The primer set for "Sag" floxed allele is PSAG-KO-F: 5′-TTCTGGCCAGGTGTGGTGATATC-3′ and PSAG-KO-G: 5′-CTTAGCCTTGGTTGTGTAGAC-3′ to detect floxed allele (140 bp) and WT allele (105 bp). The primer set for removing the "Sag" targeting fragment (1.3 kb, Supplemental Figure 2) is PSAG-KO-Seq-B: 5′-TCTTCCTCGAGTTGTGTTGATATC-3′ and PSAG-KO-Seq-R: 5′-TTGGCCAGGTGTGGTGATATC-3′ and PSAG-KO-G: 5′-CTTAGCCTTGGTTGTGTAGAC-3′ to detect floxed allele (140 bp) and WT allele (105 bp). The primer set for detecting the removal of the "Sag" targeting fragment (1.3 kb, Supplemental Figure 2) is PSAG-KO-Seq-B: 5′-TCTTCCTCGAGTTGTGTTGATATC-3′ and PSAG-KO-Seq-R: 5′-TTGGCCAGGTGTGGTGATATC-3′ and PSAG-KO-G: 5′-CTTAGCCTTGGTTGTGTAGAC-3′ to detect floxed allele (140 bp) and WT allele (105 bp). The primer set for removing the "Sag" targeting fragment (1.3 kb, Supplemental Figure 2) is PSAG-KO-Seq-B: 5′-TCTTCCTCGAGTTGTGTTGATATC-3′ and PSAG-KO-Seq-R: 5′-TTGGCCAGGTGTGGTGATATC-3′ and PSAG-KO-G: 5′-CTTAGCCTTGGTTGTGTAGAC-3′ to detect floxed allele (140 bp) and WT allele (105 bp). The primer set for removing the "Sag" targeting fragment (1.3 kb, Supplemental Figure 2) is PSAG-KO-Seq-B: 5′-TCTTCCTCGAGTTGTGTTGATATC-3′ and PSAG-KO-Seq-R: 5′-TTGGCCAGGTGTGGTGATATC-3′ and PSAG-KO-G: 5′-CTTAGCCTTGGTTGTGTAGAC-3′ to detect floxed allele (140 bp) and WT allele (105 bp). The primer set for removing the "Sag" targeting fragment (1.3 kb, Supplemental Figure 2) is PSAG-KO-Seq-B: 5′-TCTTCCTCGAGTTGTGTTGATATC-3′ and PSAG-KO-Seq-R: 5′-TTGGCCAGGTGTGGTGATATC-3′ and PSAG-KO-G: 5′-CTTAGCCTTGGTTGTGTAGAC-3′ to detect floxed allele (140 bp) and WT allele (105 bp). The primer set for removing the "Sag" targeting fragment (1.3 kb, Supplemental Figure 2) is PSAG-KO-Seq-B: 5′-TCTTCCTCGAGTTGTGTTGATATC-3′ and PSAG-KO-Seq-R: 5′-TTGGCCAGGTGTGGTGATATC-3′ and PSAG-KO-G: 5′-CTTAGCCTTGGTTGTGTAGAC-3′ to detect floxed allele (140 bp) and WT allele (105 bp). The primer set for removing the "Sag" targeting fragment (1.3 kb, Supplemental Figure 2) is PSAG-KO-Seq-B: 5′-TCTTCCTCGAGTTGTGTTGATATC-3′ and PSAG-KO-Seq-R: 5′-TTGGCCAGGTGTGGTGATATC-3′ and PSAG-KO-G: 5′-CTTAGCCTTGGTTGTGTAGAC-3′ to detect floxed allele (140 bp) and WT allele (105 bp). The primer set for removing the "Sag" targeting fragment (1.3 kb, Supplemental Figure 2) is PSAG-KO-Seq-B: 5′-TCTTCCTCGAGTTGTGTTGATATC-3′ and PSAG-KO-Seq-R: 5′-TTGGCCAGGTGTGGTGATATC-3′ and PSAG-KO-G: 5′-CTTAGCCTTGGTTGTGTAGAC-3′ to detect floxed allele (140 bp) and WT allele (105 bp).

Ad-Cre infection of mouse lung. To activate Kras\(^{G12D}\) in mouse lung, intranasal administration of Ad-Cre was performed as described (36, 59). Briefly, 6- to 8-week-old mice were anesthetized with isoflurane via a gas chamber. Ad-Cre (purchased from University of Iowa Vector Delivery Core) at the dose of 3 \times 10^7 pfu in a total volume of 125 μl as CaPi coprecipitates were loaded in a gel-loading tip and administered nasally using two 62.5-μl instillations with a 5-minute interval.

Immunohistochemical staining. Mouse lung organs were isolated after 10% formalin perfusion, fixed in 10% formalin, and embedded in paraffin (26). Sections that were 5-μm thick were cut for H&E staining and examined under a microscope. Immunohistochemistry was performed using the ABC Vectastain Kit (Vector Laboratories) with Abs against SAG (28), pIκBα, pErK, pS6K (Cell Signaling Technology Inc.), p27, p21 (BD Biosciences), Ki67 (Millipore), and p65 (Santa Cruz Biotechnology). Sections were developed with DAB and counterstained with hematoxylin.

Lung tissue scanning and lung lesion counting. The lung tissue slides were scanned by an Aperio Whole Slide Scanner (ScanScope XT; Aperio Tech-
The IC_{50} value of MLN4924 against human lung cancer cells, cells were seeded in 96-well plates in triplicate and treated with MLN4924 at the indicated concentrations. Growth suppression effect was tested by monolayer growth (n = 3) (A), clonogenic survival (n = 4) (B), and soft agar (C, n = 2). **P < 0.01. (D). Accumulation of tumor-suppressive proteins: A549 cells were treated with indicated concentrations of MLN4924 for 24 hours, followed by immunoblotting using indicated Abs. (E). MLN4924 treatment blocks p65 nuclear translocation. Cells after 24-hour treatment of MLN4924 (1 μM) were exposed to TNF-α (100 ng/ml) or control vehicle for 1 hour, followed by nuclear fractionation and immunoblotting. Caspase-3 and PARP were used to demonstrate the purity of cytoplasm and nuclear fractions. (F) Time-dependent induction of DEPTOR and inactivation of mTORC1: cells were treated with 1 μM MLN4924 as well as DMSO for indicated periods and subjected to immunoblotting.

Figure 8
MLN4924 suppresses growth of lung cancer cells by targeting NF-κB and mTOR pathways and by accumulating tumor suppressor substrates. (A–C) A549 cells were treated with MLN4924 at the indicated concentrations. (D) Accumulation of tumor-suppressive proteins: A549 cells were treated with indicated concentrations of MLN4924 for 24 hours, followed by immunoblotting using indicated Abs. (E). MLN4924 treatment blocks p65 nuclear translocation. Cells after 24-hour treatment of MLN4924 (1 μM) were exposed to TNF-α (100 ng/ml) or control vehicle for 1 hour, followed by nuclear fractionation and immunoblotting. Caspase-3 and PARP were used to demonstrate the purity of cytoplasm and nuclear fractions. (F) Time-dependent induction of DEPTOR and inactivation of mTORC1: cells were treated with 1 μM MLN4924 as well as DMSO for indicated periods and subjected to immunoblotting.

Figure 9
A model for SAG cooperation with Kras for driving lung tumorigenesis. During lung tumorigenesis, triggered by mutant Kras, SAG is induced and recruits other components of SCF/CRL E3s to promote the ubiquitylation and degradation of tumor suppressor substrates. SAG inactivation by genetic deletion or small molecule inhibitor MLN4924 causes the accumulation of these tumor suppressor substrates to antagonize Kras effects, leading to suppression of lung tumor development.
or Lt-Con for 48 to 72 hours in 60-mm dishes. Cells were then split into three 60-mm dishes and transiently transfected with si-Con, si-p21, or si-DEPTOR, respectively, using Lipofectamine 2000. Forty-eight hours later, cells were harvested for proliferation, clonal survival, and soft agar assays as described (24, 61). The sequences for these siRNA oligonucleotides were as follows: Si-Con: 5′-AUUAGUAUCGCGACGACG-3′; Si-SAG: 5′-GAGGACUGCGUGUUGUGGCUCU-3′; Si-p21: 5′-GUGGACGCGACGCCGCAUG-3′; and Si-DEPTOR 5′-GCCAUAACUAGGGAAACUCA-3′. 

**SAG ectopic expression.** A549, A427, and H358 cells were transfected with FLAG-tagged SAG construct, along with pcDNA3 control. Cells were G418 selected for 2 weeks and all G418-resistant stable clones were pooled and subjected to immunoblotting and cell growth assays.

**Immunoblotting analysis.** Lung cancer cells with or without MLN4924 treatment were harvested, lysed in a Tritton X-100 lysis buffer and subjected to immunoblotting analysis (60). SAG monoclonal Ab was raised against the RING domain (AA44-113) (28). Other Abs were purchased commercially as follows: S6K1, cyclin D1, and c-Jun (Santa Cruz Biotechnology Inc.), human NOXA (Calbiochem), p21 (BD Transduction Labs), β-actin (Sigma-Aldrich), DEPTOR (Millipore and Cell Signaling Technology), phospho-4E-BP1, 4E-BP1, phospho-S6K1 (Thr389), p53, BIM, Notch-1, and phospho-β-tubulin (Cell Signaling Technology), and p27 (BD Biosciences — Pharmingen) and c-Myc (Epitomics). 

**Nuclear and cytoplasmic fractionation.** Cells after siRNA knockdown or MLN4924 treatment were washed with cold PBS and collected by scraping after addition of lysis buffer A (20 mM HEPES, pH 8.0, 20% glycerol, 10 mM NaCl, 1.5 mM MgCl2, 0.2 mM EDTA, pH 8.0, 1 mM DTT, 0.1% NP-40 and a proteasine inhibitor cocktail; Roche). Cell lysates were incubated on ice for 10 minutes, followed by centrifugation at 400 g for 5 minutes at 4°C. The supernatants were collected as the cytoplasmic fractions. The pellets were washed 3 times with lysis buffer A and then lysed in buffer B (20 mM HEPES, pH 8.0, 20% glycerol, 500 mM NaCl, 1.5 mM MgCl2, 0.2 mM EDTA, pH 8.0, 1 mM DTT, 0.1% NP-40 and a proteasine inhibitor cocktail) for 30 minutes on ice, followed by centrifugation at 15,000 g at 4°C for 15 minutes. The supernatants were collected as the nuclear fractions.

**p65 DNA binding and NF-κB reporter activity assay.** Five micrograms of nuclear extracts was used to determine p65 DNA-binding activity by an ELISA-base assay kit, according to the manufacturer's protocols (TransAM NF-κB, Active Motif). Briefly, the κB oligonucleotide–coated plates in a 96-well plate were incubated for 1 hour with the nuclear extract. Specificity was achieved by incubation with anti-p65 primary Abs for 1 hour. HRP-conjugated secondary Abs were used for the detection of p65 bound to the κB sequences (48). Luciferase-based reporter assay for NF-κB transcription activity was performed as described previously (16). 

**MLN4924 in vivo antitumor study.** Mice with the genotype LSL-KrasG12D in combination with WT or heterozygous Sarg at the age of 6 to 8 weeks were administered with Ad-Cre as described above. MLN4924 (60 mg/kg, s.c.) was given once a day, 5 days a week, for 4 weeks, beginning at the 13th week, following Ad-Cre installation. Mice in the drug control group received 10% 2-hydroxypropyl-β-cyclodextrin (HPBCD) as the vehicle control (2, 51). Mice were euthanized at the end of the 16th week, and their lungs were harvested after 10% formalin perfusion, fixed, sectioned, and stained with H&E. The slides were scanned, and lung lesions were counted.

**Statistics.** Overall survival was defined from the date of diagnosis to death. The maximum follow-up time for each patient was 5 years, and patients who were alive were censored at the last follow-up time. Survival functions were plotted using the Kaplan-Meier method, and comparison of survival functions was performed by the log-rank test. In patient survival, Cox proportion-hazard models were used to compare the overall survival after controlling for important prognostic factors including age, sex, stage, and grade. Two-sided Student's t test was used for tumor cell growth and tumor lesion comparison, as well as for comparing marker expression between different stages and grades. Data represent mean ± SEM. P < 0.05 was considered significant.

**Study approval.** All procedures were approved by the University of Michigan Committee for the Use and Care of Animals. Animal care was provided in accordance with the principles and procedures outlined in the National Research Council Guide for the Care and Use of Laboratory Animals.

**Acknowledgments.** We thank Millennium Pharmaceuticals Inc. for providing MLN4924. We also thank Ronald Craig at the Department of Pathology, University of Michigan, for scanning the lung tissue slides. This work is supported by NCI grants CA118762, CA170995, and CA171277 (to Y. Sun).

Received for publication April 4, 2013, and accepted in revised form November 7, 2013.

Address correspondence to: Yi Sun, 4424B, MS-1, 1301 Catherine Street, Ann Arbor, Michigan 48109, USA. Phone: 734.615.1989; Fax: 734.763.1581; E-mail: sunyi@umich.edu.

---

8. Wu K, Chen A, Pan ZQ. Conjugation of Nedd8 to CUL1 enhances the ability of the ROC1-CUL1 complex to promote ubiquitination polymerization. J Biol Chem. 2000;275(41):32317–32324. 
The Journal of Clinical Investigation


