Mammalian target of rapamycin regulates murine and human cell differentiation through STAT3/p63/Jagged/Notch cascade

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The receptor tyrosine kinase/PI3K/AKT/mammalian target of rapamycin (RTK/PI3K/AKT/mTOR) pathway is frequently altered in cancer, but the underlying mechanism leading to tumorigenesis by activated mTOR remains less clear. Here we show that mTOR is a positive regulator of Notch signaling in mouse and human cells, acting through induction of the STAT3/p63/Jagged signaling cascade. Furthermore, in response to differential cues from mTOR, we found that Notch served as a molecular switch to shift the balance between cell proliferation and differentiation. We determined that hyperactive mTOR signaling impaired cell differentiation of murine embryonic fibroblasts via potentiation of Notch signaling. Elevated mTOR signaling strongly correlated with enhanced Notch signaling in poorly differentiated but not in well-differentiated human breast cancers. Both human lung lymphangioleiomyomatosis (LAM) and mouse kidney tumors with hyperactive mTOR due to tumor suppressor TSC1 or TSC2 deficiency exhibited enhanced STAT3/p63/Notch signaling. Furthermore, tumorigenic potential of cells with uncontrolled mTOR signaling was suppressed by Notch inhibition. Our data therefore suggest that perturbation of cell differentiation by augmented Notch signaling might be responsible for the underdifferentiated phenotype displayed by certain tumors with an aberrantly activated RTK/PI3K/AKT/mTOR pathway. Additionally, the STAT3/p63/Notch axis may be a useful target for the treatment of cancers exhibiting hyperactive mTOR signaling.

Introduction

The receptor tyrosine kinase/PI3K/AKT/mammalian target of rapamycin (RTK/PI3K/AKT/mTOR) pathway, which plays multiple roles in cell growth, proliferation, and survival, is frequently deregulated in cancer (1, 2). mTOR, a serine/threonine protein kinase which exists as both rapamycin-sensitive (mTOR complex 1 [mTORC1]) and rapamycin-insensitive multimeric protein complexes (mTORC2) (3, 4), functions as a nutrient and energy sensor and regulates protein synthesis and autophagy to modulate cell growth and survival (1, 2, 5–9). It is frequently activated in human cancers by gain-of-function mutations in its activators, such as those encoding epidermal growth factor receptor, PI3K, or AKT, and by loss-of-function mutations in its suppressors, such as PTEN, LKB1, or the tuberous sclerosis complex (TSC) genes TSC1 and TSC2 (1, 2). However, the precise mechanisms of activation of the mTOR signaling pathway to enhance cancer development are less clear (1, 2, 10–12).

Aberrant cell differentiation occurs in nearly all cancers, and there is an association between poor differentiation and worsening clinical prognosis. Inactivating mutations of either TSC1 or TSC2, major negative regulators of mTOR (10, 11, 13), cause TSC and LAM (12, 14) with tumor lesions featuring aberrant cellular differentiation and proliferation (15–17). Because physiological mTOR is required for cell differentiation...
(18–21), hyperactivation of mTOR may play a role in abnormal cell differentiation. We thus reasoned that malfunctioning of cell differentiation regulators might contribute to the pathology of TSC and LAM. Among them, Notch is a major regulator of cell differentiation (22, 23). Ligand engagement causes the intracellular domain of transmembrane receptor Notch (NICD) to be cleaved from the membrane and translocated to the nucleus, where it associates with the CSL family of DNA binding proteins to form a transcriptional active complex to activate transcription of Notch target genes such as hairy and enhancer-of-split 1 (Hes1) (22). All of these processes are subject to multilevel regulation (24). Furthermore, Notch signaling regulates cell differentiation, proliferation, and survival as well as oncogenic transformation in a dose- and context-dependent manner (22, 25–30). Therefore, the potential functional interaction of mTOR and Notch might contribute greatly to tumor development.

To elucidate the putative relationship between mTOR and Notch signaling pathways, we analyzed various genetically defined mouse embryonic fibroblasts (MEFs) and kidney tumors, human cancer cell lines, and breast cancers and lung LAM tissues. We report here that the RTK/PI3K/AKT pathway activates the STAT3/p63/Jagged/Notch signaling cascade via mTORC1 and that mouse kidney tumors and human LAM resulting from TSC1 or TSC2 deficiency exhibited hyperactive mTOR/STAT3/p63/Notch signaling. Oncogenically activated mTOR impaired cell differentiation via this potentiated pathway. Uncontrolled mTOR signaling was strongly correlated with the enhanced Notch signaling in poorly differentiated but not in well-differentiated human breast cancers. Inhibition of Notch signaling blocked tumorigenesis of cells with activated mTOR signaling. We suggest that the newly identified mTOR effectors p63, Jagged1, Notch, and Hes1 are novel candidates for targeted therapy in diseases associated with deregulated RTK/PI3K/AKT/mTOR signaling.
Results

Hyperactive mTOR blocks cell differentiation. Uncontrolled cell proliferation is usually coupled with blockade of cell differentiation, and we therefore postulated that hyperactive mTOR signaling might hinder cell differentiation, even though normal functioning of AKT-mTOR is required for cell differentiation (18–21). To test this idea, we utilized MEFs that were deficient in the mTOR suppressor genes Tsc1 and Tsc2 and consequently demonstrated hyperactive mTOR signaling (10, 31). MEFs have the ability to differentiate into various cell lineages, including myocytes and adipocytes (32, 33), and we therefore examined the effects of mTOR activation on this differentiation process (Figure 1). To induce myogenic differentiation, WT MEFs were transduced with retroviruses expressing MyoD, a master myogenic regulator (Figure 1A). The MEFs underwent myogenic differentiation, as demonstrated by the formation of myotubes and the expression of myosin, a muscle marker (Figure 1B). This differentiation was blocked by the mTOR inhibitor rapamycin (Figure 1B), indicating that normal mTOR signaling was required for myogenic differentiation. In contrast, Tsc2–/– MEFs with exogenous MyoD expression were unable to differentiate into myocytes until they were treated with rapamycin, at which point they differentiated in a dose-dependent manner (Figure 1B), suggesting that hyperactive mTOR signaling due to Tsc2 deficiency inhibits myogenic differentiation.

mTOR is a positive regulator of Notch signaling. We next investigated any potential role of the Notch pathway in the mechanism underlying the impaired differentiation potential of mTOR-activated cells. We first investigated whether hyperactive mTOR could cause abnormal Notch signaling by monitoring the levels of Hes1, a direct target of Notch. We found that Hes1 protein expression was dramatically elevated in cells with constitutively active mTOR caused by loss of the Tsc2 or Pten tumor suppressor gene or oncogenic myristoylation of AKT1 (myrAKT1) (34) (Figure 2A). The expression of Hes1 in all cell lines examined was reduced by rapamycin treatment, indicating that it was mTOR dependent (Figure 2A). Similarly, WT MEFs transduced with retroviruses expressing PPARY (Figure 1A), a master adipogenic regulator, underwent adipogenic differentiation, as shown by the formation of lipid droplets and the expression of aP2 and c/EBPα, two adipocyte markers (Figure 1C). However, in parallel with the results of myogenic differentiation, both Tsc1–/– and Tsc2–/– MEFs expressing PPARγ failed to produce lipid droplets or express aP2 or c/EBPα (Figure 1C). In addition, adipogenic differentiation of the WT MEFs was inhibited by treatment with rapamycin, while conversely, it was restored by rapamycin in Tsc1–/– and Tsc2–/– MEFs. Thus, these data on myogenic and adipogenic differentiation of MEFs suggest that a normal range of mTOR activity is critical for cell differentiation, but that cells with either too much or too little mTOR activity fail to differentiate normally.
The upregulation of Hes1 by mTOR was also observed in vivo, as mouse kidney tumors with hyperactive mTOR due to Tsc2 exon 3 deletion (35) exhibited enhanced Hes1 expression (Figure 2B). Promoter reporter assays and quantitative real-time PCR analysis showed increased Hes1 promoter activity and transcript levels, indicating that the upregulation of Hes1 expression likely occurs at the transcriptional level in an mTOR-dependent manner (Figure 2C). In addition, the Notch transactivator NICD domain was also elevated in cells devoid of either Tsc2 or Pten or expressing oncogenic AKT1 E17K (AKT1-E17K) (36), and this elevation was attenuated by rapamycin treatment (Figure 2D). To provide further evidence for activated Notch signaling in cells with hyperactive mTOR, we examined the effects of ectopic expression of NICD on Hes1 expression and found that it was resistant to rapamycin treatment (Figure 3A), which suggests that Jagged1 expression is influenced by both upstream and downstream signaling events.

**mTOR regulates cell differentiation through the Notch pathway.** As mTOR is a positive regulator of the Jagged1/Notch/Hes1 pathway, we then investigated the effects of activated Notch signaling on the ability of cells with activated mTOR to differentiate. Inhibition of Notch signaling either by a dominant-negative form of the Notch transcriptional coactivator MAML1 (DN-MAML1) (32) (Figure 4A) or compound E, a γ-secretase inhibitor known to block Notch cleavage (Figure 4B), suppressed the adipogenic differentiation of WT MEFs expressing PPARY. In contrast, treatment of Tsc2−/− or Tsc2+/− MEFs expressing PPARY with either DN-MAML1 (Figure 4A) or compound E (Figure 4B) markedly restored their adipogenic differentiation capacity (Figure 4B). Moreover, reduction of Notch by siRNA potentiated the adipogenic differentiation of Tsc2−/− MEFs expressing PPARY (Figure 4C). In addition, activation of Notch-Hes1 by overexpression of Jagged1 reduced the conversion of WT MEFs with PPARY into adipocytes (Figure 4D). Therefore, Notch acts as an effector of mTOR signaling, while the deregulated mTOR activation inhibits cell differentiation through upregulation of Notch signaling. It is possible that mTOR exerts its dual effects on cell differentiation via the binary roles of Notch in cell differentiation.

**Inhibition of Notch suppresses the tumorigenesis of cells with activated mTOR.** Since the role of Notch in tumorigenesis is context dependent and Notch signaling was potentiated in cells with an oncogenically activated AKT/mTOR pathway, we reasoned that activation of Notch signaling might be critical for AKT/mTOR-mediated tumorigenesis and could therefore be targeted for the treatment of cancers with active mTOR signaling. We indeed found that suppression of the Notch pathway by the Notch inhibitor N-[N-(3,5-difluorophenacetyl-L-alanyl)]S-phenylglycine t-butyl ester (DAPT) compromised the proliferation of both MEFs and human cancer cells with activated mTOR signaling caused either by lack of the Tsc2 or PTEN (PC3 cells) tumor suppressors or by expression of AKT1-E17K (Figure 5A). Furthermore,
the tumorigenicity of Pten−/− MEFs in nude mice was attenuated by inhibition of Notch signaling with dominant-negative Notch, DNL1 (DN-MAML1) (Figure 5B).

mTOR activation of Notch pathway through upregulation of p63. To explore the mechanism by which mTOR activation leads to the upregulation of Jagged1/Notch/Hes1 signaling, we examined the expression of p63, a TP53 family member, since p63 is a positive regulator of Jagged1 or Jagged2 expression and Notch activity (40–42) and PI3K is an inducer of p63 expression (43). The p63 gene has 2 promoter regions generating TA-p63 and ΔN-p63 isoforms, each of which has 3 splicing variants on its C terminus as α/β/γ of TA-p63 and ΔN-p63 isoforms (41). The TA-p63 isoform has been observed to activate the expression of ΔN-p63 isoform (44). Both TA-p63 and ΔN-p63 were overexpressed in cells with mTOR activation because of either a lack of Tsc2 or Pten or expression of AKT1-E17K, and were repressed by rapamycin (Figure 4).
κ plays an important role in cell differentiation. Moreover, the mTOR/p63/Notch signaling cascade knockdown by siRNA (Figure 7C) led to reductions in p63, Jagged1, pancreatic (PANC-1), and liver (HepG2) cancer cell lines treated with rapamycin (Figure 8A). In addition, restoration of PTEN in the PTEN-deficient prostate cancer cell line PC3 normalized AKT/mTOR/STAT3/p63/Notch signaling (Figure 8B). Therefore, the mTOR/STAT3/p63/Jagged1/Notch/Hes1 signaling cascade also presents in human cancer cell lines.

Since mTOR regulates STAT3/p63/Notch signaling network in human cancer cell lines in vitro, we predicted that this signaling regulation should also exist in human tumors in vivo. We first tested this hypothesis by analyzing mRNA microarray data of lung LAM tissues, which are known for mTOR hyperactivation due to inactivative mutations of either the TSC1 or the TSC2 gene, in comparison with normal pulmonary artery smooth muscle cells from the Gene Expression Omnibus database (GEO accession number GSE12027, mRNA microarray data deposited by Y. Zhang and G. Pacheco-Rodriguez) (Supplemental Tables 1–3; supplemental material available online with this article; doi:10.1172/JCI37964DS1). As expected, VEGF-D (activated by mTOR) and considered to be a diagnostic marker for LAM) (50), Jagged2, and Hes1 were significantly increased in LAM tissues (Table 1), suggesting that mTOR regulates Notch in human LAM. This finding is also consistent with our in vitro observation that mTOR-regulated expression of either Jagged1 or Jagged2 was cell type specific, but in a mutually exclusive manner (our unpublished observations).

We then examined the correlation between p-S6 levels and Notch markers in breast cancer. Using regression analysis of immunoblots for breast cancer tissues, we found that p-S6 levels correlated well with Hes1 expression in poorly differentiated but not in well-differentiated human breast ductal carcinoma samples (Figure 8C, Supplemental Table 4, and Table 2). In addition, p-S6, p-STAT3, p63, and Jagged1 were all correlated with each of their downstream targets and the proteins further downstream in the mTOR/STAT3/p63/Jagged1/Notch signaling cascade, with the single exception of p63: Hes1 (Figure 8C and Supplemental Table 5). Taken together, these results suggest that mTOR activates STAT3/p63/Notch and inhibits cell differentiation in these human tumors.

STAT3/p63/Notch signaling is controlled under mTOR complex 1. All of the observations presented thus far indicate that the effects of mTOR on STAT3/p63/Notch signaling is rapamycin sensitive, suggesting that STAT3/p63/Notch is under the control of mTORC1. To confirm this model, mTOR or rictor (an important component in mTORC2) (3, 4) was knocked down in Tsc2−/−MEFs (Figure 9). While the reduction of mTOR markedly abolished STAT3, p63, and Notch signaling (Figure 9A), decreased expression of rictor did not affect the STAT3/p63/Notch signaling cascade (Figure 9B). These data thus confirm that mTORC1 regulates STAT3/p63/Notch signaling, and this effect is independent of mTORC2 (Figure 9C).

NF-κB and STAT3/p63 control Notch signaling downstream of mTORC1 in parallel. During the preparation of this manuscript, Bedogni et al. reported that hyperactivated AKT signaling led
to upregulation of Notch1 through NF-κB activity in melanoma (51). NF-κB is a key transcriptional factor family that plays important roles in multiple physiological and pathological processes, including cell proliferation/differentiation and tumorigenesis (51). Therefore, we examined the relationship of this newly identified AKT/NF-κB/Notch signaling cascade and the RTK/PI3K/PTEN/AKT/TSC1/2/mTORC1/STAT3/p63/Notch signaling pathway defined above. Because the enhanced NF-κB signaling in Tsc2−/− MEFs was abolished by rapamycin treatment, NF-κB signaling appeared to be downstream of mTORC1 (Figure 10A). However, knockdown of NfkB did not change the state of STAT3 and p63, and knockdown of STAT3 was unable to influence NF-κB, suggesting that NF-κB has no functional interaction with STAT3/p63 (Figure 10B). Since both NF-κB and p63 are inducers of Jagged1 expression (40, 52), NF-κB therefore, in parallel with STAT3/p63, modulates Notch signaling downstream of mTORC1 (Figure 10C).

**Discussion**

We provide evidence that mTORC1 positively regulates Notch signaling through upregulation of the STAT3/p63/Jagged cascade, and that Notch cascade activation impedes cell differentiation, in cells in which mTORC1 is activated due to loss of Pten, Tsc1, and Tsc2 or acquisition of oncogenic AKT1 mutants. In addition, mouse and human tumors caused by hyperactive mTOR signaling present aberrant high STAT3/p63/Notch activity, while inhibition of Notch signaling extends survival in a Pten-null nude mouse tumor model.

Although the RTK/PI3K/AKT/mTOR pathway is one of the most frequently altered signaling networks in cancer, the mechanism by which it contributes to tumorigenesis remains uncertain. By studying various cell lines with activated mTOR signaling, we observed hyperactivation of STAT3/p63/Jagged1/Notch/Hes1 signaling in those cells and showed that these events were sensitive to rapamycin treatment and independent of mTORC2. We have therefore identified mTORC1 as a positive regulator of Notch signaling (Figure 9C). In support of this mTORC1-Notch connection, mouse kidney tumors and human LAM tissues driven by upregulated mTOR due to TSC2 deficiency, as well as poorly differentiated breast cancers, exhibited hyperactive STAT3/p63/Notch signaling (Figure 2B, Figure 7D, Figure 8C, Tables 1 and 2, and Supplemental Table 5). Therefore, Notch effectors such as Hes1 may serve as surrogate markers for mTOR activation.

The p53 family consists of 3 transcription factors, p53, p63, and p73, which share overlapping and distinct functions as key regulators of cell cycle and cell death in the regulation of development, proliferation/differentiation, and response to cellular...
stress (53, 54). Dysfunction of this family has been implicated in the majority of human cancers (55). mTOR has been reported to be a positive modulator of p53 (31, 56) and a negative regulator of p73 (57). To our knowledge, we have now identified p63 as a novel effector of mTOR signaling downstream of the transcriptional activator STAT3. p63 in turn activates Notch signaling through stimulation of Jagged1 gene expression, although we were unable to determine which of the 6 isoforms were responsible for Jagged1 activation at this time. Even if members of the p53 family are generally considered to be tumor suppressors, the function of p63 in tumorigenesis remains uncertain (55, 58). The mTOR/p63/Notch connection should cast some insights on the role of p63 and its regulation in tumor development. As another effector of mTOR (31, 56), p53 appears to play no role in mTOR-

Figure 7
STAT3 transduces mTOR signaling to the p63/Notch axis. (A) WT and Pten−/− MEFs and WT MEFs transduced with the retroviruses for AKT1E17K in pLXIN-hyg or the control vector pLXIN-hyg (V) were treated with or without 10 nM rapamycin for 24 hours and then subjected to immunoblotting for p-S6 (Ser235/236) and p-STAT3 (Ser705). (B) Tsc1−/−, Tsc2−/−, and Pten−/− MEFs and WT MEFs transduced with the retroviruses for myristoylated AKT1 in pLXIN-hyg or the control vector pLXIN-hyg (V) were treated with or without 50 nM AG490 for 24 hours and then subjected to immunoblotting. (C) Tsc1−/− or Tsc2−/− MEFs were transfected with STAT3 siRNA to knock down STAT3 expression for 48 hours and then subjected to immunoblotting. Non–target-directed random siRNA served as a control. (D) Expression of STAT3, p63, NICD, and p-S6 were assessed in age-matched kidneys from 2 normal mice and kidney tumors from 2 Tsc2−/− mice by immunoblotting.

Figure 8
mTOR regulates STAT3/p63/Notch signaling in human cancers. (A) Human breast (MCF7 and MDA-MB-468), prostate (PC3), lung (A549), pancreatic (PANC-1), and liver (HepG2) cancer cell lines were treated with 10 nM rapamycin for 24 hours and then subjected to immunoblotting for components of the mTOR/STAT3/p63/Notch signaling pathway. (B) PC3 cells were transduced with either pLXIN-hyg retroviruses (V) or pLXIN-hyg-PTEN retroviruses (PTEN) and then subjected to immunoblotting for PTEN and mTOR/STAT3/p63/Notch signaling pathway components. (C) Human breast cancer tissues were immunoblotted for components of the mTOR/STAT3/p63/Notch signaling cascade. A representative blot is shown. The differentiation states (Diff.) of cancer cells were as indicated.
mediated Notch activation (our unpublished observations). It would be of interest to determine whether p73 participates in the regulation by mTOR on Notch.

The serine/threonine kinase AKT is a central regulator of cell proliferation, survival, and metabolism by phosphorylating multiple protein substrates including TSC2 and IκB kinase (IKK). AKT activates NF-κB via IKK and mTOR through TSC2 (1). Bedogni et al. recently reported that hyperactivated AKT signaling led to upregulation of Notch1 through NF-κB activity in melanoma (51). We have confirmed their findings here and further defined NF-κB, in parallel with the STAT3/p63 cascade, as a regulator of Notch signaling downstream of mTOR (Figure 10).

Furthermore, we found that this mTOR/STAT3/p63/Jagged1/Notch/Hes1 cascade plays an important role in the regulation of cell differentiation. Interestingly, while inhibition of mTOR/p63/Notch inhibits the differentiation of normal cells, sustained activation of mTOR impairs cell differentiation through overactivation of the p63/Jagged/Notch cascade. This observation is consistent with a recent report showing that differentiation of HepaRG cells into hepatocyte-like cells is attenuated by expression of an activated mutant mTOR (59). Given the dose-dependent binary effects of both mTOR and Notch on cell differentiation, the functioning of Notch appears to depend on the status of mTOR activity. This mechanism may be the molecular basis of the dose-dependent role of Notch in hematopoiesis and leukemogenesis (60). These observations are in accordance with the multifaceted roles of Notch signaling as both a repressor and an inducer of terminal differentiation in different settings, possessing both growth-promoting and tumor-suppressor functions in different contexts (26, 61).

The results of this study suggest that, in response to differential cues from mTOR, Notch serves as a molecular switch to couple 2 seemingly unrelated cellular processes: proliferation and differentiation. If the activity of RTK/P13K/AKT/mTOR/p63/Notch deviates from the normal physiological range, cells may fail to differentiate or proliferate normally and may cause developmental defects or tumors. The inhibition of cell differentiation due to aberrant Notch signaling might be one of the underlying mechanisms responsible for tumorigenesis associated with aberrant RTK/P13K/AKT/mTOR pathway activation, which is supported by the correlation between activation of mTOR and Notch signaling in poorly differentiated breast cancers (Figure 8C and Table 2). Moreover, uncontrolled RTK/P13K/AKT/mTOR activation may underlie the ligand-mediated activation of Notch in tumors with overexpressed Jagged and unopposed Notch signaling. The Notch signaling pathway indeed appears to be critical for active mTOR-mediated tumorigenesis, since blunted Notch signaling compromised the proliferation and tumorigenic potential of cells with an activated mTOR pathway (Figure 5).

Even though the possibility of cancer treatment using Notch inhibitors is controversial due to the complex role of Notch in both embryonic and cancer development (26, 29, 62), our data suggest that components of the STAT3/p63/Jagged1/Notch axis may become novel targets for the treatment of cancers caused by deregulation of RTK/P13K/AKT/mTOR signaling. Conversely, intervention in the P13K/mTOR signaling pathway might be an option for cancers with activated Notch signaling. Furthermore, RTK/P13K/AKT/mTOR/STAT3/p63/Jagged1/Notch/Hes1 networks are likely the candidates for targeted combination cancer therapy. Because the Notch pathway has also been reported to be a positive regulator of the P13K/AKT/mTOR pathway (63, 64), our current findings indicate that mTOR and Notch interact in a reciprocal regulatory loop. The interplay between mTOR and Notch may be of wider significance in development, physiology, and pathophysiology beyond its potential cancer connection.

### Methods

**Reagents and antibodies.** Reagents were obtained from the following sources: rapamycin, AG490, DAPT, hygromycin B, and puromycin from Sigma-Aldrich; compound E from Axonova; DMEM, FBS, 4%–12% Bis-Tris Nu-PAGE gels, and Lipofectamine 2000 from Invitrogen.

Anti-p-S6 (Ser235/236) and anti-S6 antibodies have been described previously (34). The myosin antibody MF20 developed by Donald A. Fischman was obtained from the Developmental Studies Hybridoma Bank. TSC2, AKT, PPARγ, c/EBPα, MyoD, p63, and Jagged1 antibodies and all HRP-labeled secondary antibodies were from Santa Cruz Biotechnology Inc. aP2 and Hes1 antibodies were from CHEMICON. STAT3, p-STAT3 (Ser705), p65, p-p65 (Ser536), p-IκBα (Ser32), p-AKT (Ser473), and PTEN antibodies were from Cell Signaling Technology. Notch1 (NICD) antibody was from Epitomics, and β-actin antibody was from Sigma-Aldrich.

Plasmids pMSCV, pMSCV-MyoD, pMSCV-PPARγ, pMIG (pMSCV-IRES-GFP), pMIG-DNL1 (pMSCV plasmids expressing MAML13-74-GFP fusion protein as a dominant-negative mutant for blocking Notch signaling), the Hes1-luc reporter plasmid encoding firefly luciferase, and

### Table 1

**Human lung LAM with hyperactive mTOR/Notch signaling**

| Probe | Fold change<sup>a</sup> | t   | P    | Fold change | t   | P    | Fold change | t   | P    | Fold change | t   | P    |
|-------|------------------------|-----|------|------------|-----|------|------------|-----|------|------------|-----|------|------------|-----|------|
| 1     | 30.2                   | 2.8 | <0.001 | 2.8         | 5.64| <0.001 | 2.2         | 3.36| <0.001 |
| 2     | 1.8                    | 4.18| <0.001 | 3.4         | 5.97| <0.001 | 0.0034     |

mRNA microarray data of 14 lung LAM nodules and 7 pulmonary artery smooth muscle cell lines were derived from the Gene Expression Omnibus database. <sup>a</sup>Fold change is LAM versus pulmonary artery smooth muscle cells. <sup>b</sup>t statistic. <sup>c</sup>Significance at 1%.
the internal nonspecific control pRL-TK plasmid, pMIG-ICN1 plasmid expressing human NICD, and pLXIN-hyg-myrAKT1 have been reported previously (32, 34, 65, 66). pLNCX-HA-AKT1 was from Addgene. Generation of pLXIN-hyg-Jagged1, pLXIN-hyg-PTEN, and pLXIN-hyg-AKT1(E17K) is described in Supplemental Methods.

**Cell culture.** All MEFs were described previously (10, 31, 34). Pten–/– MEFs were provided by Ronald A. DePinho (Dana-Farber Cancer Institute). PT67 was from Clontech. MCF7, MDA-MB-468, PANC-1, A549, PC3, and HepG2 were from ATCC. Cells were cultured in DMEM with 10% FBS in 5% CO₂ at 37°C. Production of retroviruses and subsequent generation of stable gene expression cell lines have been described (34) and detailed in Supplemental Methods.

**Quantitative real-time RT-PCR.** Total RNA was extracted from cells using Trizol (Invitrogen) and reversely transcribed using the iScript cDNA Synthesis Kit (Bio-Rad). cDNA was used as a template in a quantitative PCR reaction (Supplemental Methods).

**siRNA knockdown.** siRNAs were synthesized and transfected into cells for mRNA knockdown (Supplemental Methods).

**Notch luciferase reporter assay.** Hes1-luc reporter plasmid encoding firefly luciferase and an internal nonspecific control pRL-TK plasmid encoding renilla luciferase were used for the assay (Supplemental Methods).

**Muscle differentiation.** MEF cells were transduced with pMSCV-MyoD retroviruses or pMSCV control viruses for differentiation (Supplemental Methods).

**Adipocyte differentiation.** MEF cells were transduced with pMSCV-PPARγ retroviruses or pMSCV control viruses for differentiation into adipocytes (Supplemental Methods).

**Mouse kidney tumor assessment.** For Figure 2B, the kidney tumors were from 2 heterozygous Tsc2 exon 3 deletion (Tsc2 del3/+ ) mice (19 and 22 months old), and the kidneys were from 2 WT mice (22 and 23 months old) (35). For Figure 7D, the tumors from Tsc2–/– mice and kidneys from WT mice were previously described (31). Samples were sonicated and extracted for immunoblotting (10, 31). Animal protocols were approved by the Center for Animal Resources and Comparative Medicine of the Harvard Medical School and were compliant with federal, local, and institutional guidelines on the care of experimental animals.

**Human breast cancer analysis.** Invasive ductal carcinoma samples were freshly obtained from the patients undergoing surgery at the Peking Union Medical College Hospital. The institutional review board at Peking Union Medical College Hospital approved the study protocol, and all patients provided written informed consent. Detailed information for tumor samples is listed in Supplemental Table 4. A portion of the tissue specimens was assessed for differentiation stages by histology.
were normalized with the AlphaEaseFC Imaging Software (Alpha Innotech), and expression levels were normalized with β-actin.

Bioinformatic analysis of human tumor microarray data for mTOR regulation on Notch signaling. mRNA microarray data of 14 lung LAM nodules versus 7 pulmonary artery smooth muscle cell lines were derived from the Gene Expression Omnibus database (http://www.ncbi.nlm.nih.gov/projects/geo/query/acc.cgi?acc=GSE12027). Data analysis is described in the Supplemental Methods.

Cell proliferation assay. Cell proliferation was measured using an MTT Assay (Supplemental Methods).

Induction of subcutaneous tumors in nude mice. Subcutaneous tumors were established as described previously (34). Immunodeficient nude mice (BALB/c, 6–8 weeks old) were obtained from the Institute of Laboratory Animal Sciences, Chinese Academy of Medical Sciences and Peking Union Medical College (CAMS/PUMC). Six male mice were used in each cohort. Animal protocol was approved by the Animal Center of the Institute of Basic Medical Sciences of the CAMS/PUMC and was compliant with the regulations of the Beijing Administration Office of Laboratory Animals on the care of experimental animals.

Statistics. The Kaplan-Meier log-rank test was used to analyze mouse tumor development and survival data using GraphPad Prism software. Cell proliferation and quantitative real-time RT-PCR were analyzed using the 2-tailed Student's t test with Excel software. Quantified protein expressions of mTOR/STAT3/p63/Notch components in human breast cancer tissues were subjected to OLS regression analysis using the Stata 9.0 software (StataCorp). A P value less than 0.05 was considered significant.

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