Hippo signaling differentially regulates distal progenitor subpopulations and their transitional states to construct the mammalian lungs

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Abstract

Lung size control and cell type specification are key unresolved issues. In this study, we have engineered mosaic patterns of Hippo signaling to reveal the developmental potential of SOX9$^+$ progenitors at the distal lung buds. Our results show that the distal SOX9$^+$ subdomain is sufficient to direct lung outgrowth through bifurcation, providing a mechanism for lung size control. Through single-cell analyses, we identify transitional cell states and candidates for promoting cell fates. Moreover, genetic analysis reveals that Hippo signaling induces distinct cell fates at different SOX9$^+$ subdomains to produce the conducting airways and the alveolar epithelium. These results provide the first map of the developmental paths of lung cells. Some of the developmental paths of transitional cell states in mice correspond to those in human lungs. Together, these studies provide mechanistic insight into how Hippo signaling controls the sequential expansion and differentiation of SOX9$^+$ progenitors to construct the mammalian lungs.

Introduction

Execution of a stereotypical branching program during lung development generates an elaborate respiratory tree. Following branching, the distal ends of lung branches enlarge to form saccules, the precursor of alveoli. During these developmental processes, distinct lung cell types that carry out requisite physiological functions are produced at designated locations. This design enables mucociliary clearance in the airways and gas exchange in the alveoli. The time sequence of morphological changes of the developing lung has been characterized[1, 2, 3, 4]. However, a mechanistic understanding of lung development and cell differentiation remains incomplete[4, 5, 6].

Lineage tracing, transcriptome analysis, and phenotypic study have led to a model in which a SOX9$^+$ progenitor pool located at the distal tip of lung branches gives rise to all lineages in the lung except for the trachea and main-stem bronchi[2, 7]. In this model, distal SOX9$^+$ progenitors first produce SOX2$^+$ cells, which subsequently give rise to lung cells in the conducting airways. Later in lung development, distal SOX9$^+$ progenitors produce alveolar type 1 (AT1) and alveolar type 2 (AT2) cells, essential components of the alveoli[7]. A main deficiency of this model is the lack of functional data on SOX9$^+$ progenitors at different subdomains. It also does not provide a mechanistic description of how to maintain a SOX9$^+$ progenitor pool of proper size and how to induce differentiation of SOX9$^+$ cells into either the conducting or alveolar cell fates along the proximo-distal axis of lung branches. In this study, we employed the Hippo signaling pathway as a tool to gain molecular insight into these key issues.

The Hippo pathway was discovered for its role in controlling organ size[8]. Hippo signaling regulates fundamental cellular processes critical to tissue growth and regeneration. The basic framework of Hippo signal transduction has been elucidated[9, 10, 11, 12, 13, 14]. In response to

external cues or high cell density, a kinase cascade leads to the phosphorylation of the transcription coactivators, YAP (Yes-associated protein) and TAZ (transcriptional coactivator with PDZ-binding motif), which are sequestered in the cytoplasm and degraded. In this process, STK3/4 (*i.e.*, MST1/2 [mammalian sterile 20-related 1 and 2 kinases]) phosphorylate LATS1/2 (large tumor suppressor kinase 1 and 2), which in turn phosphorylate YAP (denoted as phospho-YAP or pYAP) and TAZ. When cell density is low, STK3/4 and LATS1/2 kinases are inactive. Unphosphorylated YAP and TAZ enter the nucleus and bind to the TEAD transcription factor to activate target gene expression and influence many cellular functions. Among them are cell proliferation, cell migration, cell differentiation, and cell apoptosis.

Analysis of mouse lungs deficient in *Stk3/4* (*Mst1/2*), *Lats1/2,* and *Yap/Taz* has been reported[15, 16, 17, 18, 19]. These studies established an essential role of Hippo signaling in lung development. Nevertheless, the molecular mechanisms by which Hippo signaling controls the distinct steps of expansion and differentiation of SOX9$^+$ progenitors remain unclear. A main hurdle is the inability to manipulate Hippo signaling in a subset of SOX9$^+$ progenitors at different locations for phenotypic and molecular analysis. In this study, we have utilized mosaic or regional inactivation of *Yap/Taz* and *Lats1/2* by Cre/CreER lines in different subdomains of SOX9$^+$ progenitors to reveal the role of Hippo signaling. The phenotypic analysis is coupled with transcriptome and chromatin accessibility assays, which identify distinct transitional states and their regulators. Together, our findings provide mechanistic insight into how the SOX9$^+$ progenitor pool enables the construction of the respiratory tree and the production of its relevant cell types.

Results

Hippo signaling regulates the size of the distal SOX9$^+$ domain of lung branches in mice

Branching defects in *Yap*- and *Lats1/2*-deficient lungs have been reported[15, 17, 18, 19]. Although these studies suggest that the distal SOX9$^+$ domain is regulated by Hippo signaling, they failed to reveal how YAP/TAZ levels affect the SOX9$^+$ progenitor pool at the molecular level.

Yap$^{f/f}$; Shh$^{Cre/+}$ and *Yap$^{f/f}$; Sox9$^{Cre/+}$* lungs, in which *Shh^{Cre}* [20] or *Sox9^{Cre}* [21] converted a floxed allele of *Yap* (*Yap^f*)[22] into a null allele, are characterized by distal lung cysts. While *Shh^{Cre}* is broadly expressed in lung epithelial cells, *Sox9^{Cre}* is mainly restricted to the distal SOX9$^+$ cells. We found that lung cysts were lined by SOX9$^+$ cells and lacked SOX2$^+$ cells. SOX2$^+$ cells are derived from SOX9$^+$ cells, located proximal to SOX9$^+$ cells, and will produce the conducting airways. This suggests that SOX2$^+$ cells failed to be produced in *Yap*-deficient lung epithelium (Supplementary Fig. 1). Moreover, the number of SOX9$^+$ cells appeared to be reduced in the mutant lung (Supplementary Fig. 1a-1d).

Unexpectedly, activation of YAP/TAZ through the removal of *Lats1/2* also resulted in a smaller SOX9$^+$ domain (Supplementary Fig. 1e-1h). The LATS1/2 kinases phosphorylate YAP, leading to the sequestration and degradation of pYAP in the cytoplasm. Thus, loss of *Lats1/2* would block YAP degradation and activate YAP targets. *Lats1$^{f/f}$; Lats2$^{f/f}$*; *Shh$^{Cre/+}$* mice have been reported[18], in which the epithelial *Shh^{Cre}* converted floxed alleles of *Lats1* (*Lats1^f*) and *Lats2* (*Lats2^f*)[23, 24] into null alleles.

Together, these studies support a model in which Hippo signaling regulates the balance between the proliferation and differentiation of SOX9$^+$ progenitors. We propose that YAP/TAZ levels need to be tightly regulated to prevent depletion of the SOX9$^+$ progenitor pool due to either an undersized pool (low YAP/TAZ) or precocious differentiation (high YAP/TAZ), respectively. We will further test this model in this study.

YAP/TAZ levels regulate lung cell differentiation in mice

To test whether a SOX9^{+} progenitor pool provides the source for lung growth and cell differentiation, we activated YAP/TAZ in the lung epithelium through *Lats1/2* removal. The removal of *Lats1/2* by *Shh*^{Cre} failed to reveal the direct effects of YAP/TAZ on SOX9^{+} progenitors due to the early and broad expression of *Shh*^{Cre}. Moreover, we found that mouse embryos in which *Lats1/2* were inactivated by *Sox9*^{Cre}, another mouse epithelial Cre line, died prior to the initiation of lung development and were uninformative. To overcome a lack of precise spatial Cre activity in the lung epithelium, we took advantage of *SPC*^{Cre} (*i.e.*, *Sftpc*^{Cre}), in which Cre expression under the *surfactant protein C* (SPC or SFTPC) promoter exhibited non-uniform conversion of floxed alleles to null alleles in the lung epithelium, as we previously reported[17].

Lats1$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ mice (denoted as *Lats1/2*-mosaic mice in this study) were born alive but died soon after birth. The lungs of most mutants were devoid of air (Fig. 1a, 1b). The lung size of *Lats1/2* mosaic mice was similar to or slightly less than that of their littermate controls (Fig. 1c).

Lung branching was disrupted (Fig. 1d, 1e) and marker expression for cells in the conducting airways was diminished in *Lats1/2*-mosaic lungs (Fig. 1f, 1g). For instance, the number of secretory club (Clara) cells (SCGB1A1^{+} [CC10^{+}]) and ciliated cells (Ac-tub^{+}) was greatly decreased in *Lats1/2*-mosaic lungs compared to controls (Fig. 1f, 1g). This indicates that not only did proper branching fail to occur in *Lats1/2*-deficient descendants, but elevated YAP/TAZ levels also disrupted the production of cell types in the conducting airways. This is consistent

with a model in which the immediate progeny (the transition progenitors) of the SOX9^{+} tip progenitors[7] are the source for constructing the conducting airways (Fig. 1p).

Saccules, which are enlargements of the terminal ends of lung branches, failed to form in the mutant lungs (Fig. 1h, 1i). *Lats1/2*-deficient cells (SOX9^{-}SOX2^{-}) (details below) that occupied the disorganized airways in *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ (*Lats1/2*-mosaic) lungs expressed AT1 markers (*e.g.*, HOPX) (Fig. 1j-1m). Fibroblasts/myofibroblasts (PDGFRA^{+}) and vascular smooth muscle cells (PDGFRB^{+}) were interspersed with AT1 cells (HOPX^{+}) (Fig. 1n, 1o), mimicking the interactions between these cell types in the developing saccules/alveoli. By contrast, few, if any, cells expressed AT2 markers (*e.g.*, SFTPC) in *Lats1/2*-mosaic lungs (Fig. 1j-1m). These results suggest that high YAP/TAZ activity converts SOX9^{+} or SOX2^{+} cells into the SOX9^{-} SOX2^{-} state, which then turns on the AT1 fate (Fig. 1p)**.**

***Yap*/*Taz* mediate *Lats1/2* function in regulating murine lung development**

The Hippo pathway is known for its context-dependent signaling. The signaling network that involves Hippo signaling may differ in various tissues and organs. Moreover, kinases other than STK3/4 and LATS1/2 can participate in the network, leading to YAP/TAZ phosphorylation. It was thus uncertain if the lung phenotypes in *Lats1/2*-deficient mice were due to increased YAP/TAZ levels. To resolve this issue, we generated *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Yap*$^{f/+}$; *Taz*$^{f/+}$; *Shh*$^{Cre/+}$ mice, in which one copy of *Yap* and *Taz* was removed in *Lats1/2*-deficient lungs by *Shh*^{Cre}. Namely, a floxed allele of *Yap* (*Yap*^{f}) or *Taz* (*Taz*^{f})[25] was converted into a null allele. Analysis of lungs from *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Yap*$^{f/+}$; *Taz*$^{f/+}$; *Shh*$^{Cre/+}$ mice revealed normal branching and proper production of lung cell types at the correct positions, in a pattern similar to that of control lungs (Supplementary Fig. 2). These results suggest that *Lats1/2* function through *Yap/Taz* in

controlling the SOX9^{+} progenitors. Surprisingly, *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Yap*$^{f/+}$; *Taz*$^{f/+}$; *Shh*$^{Cre/+}$ mice did not survive after birth, suggesting that the rescue was partial. It is unclear if some aspects of pulmonary and/or extrapulmonary function were not fully restored.

We also produced control and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Yap*$^{f/+}$; *Taz*$^{f/+}$; *Sftpc*$^{Cre/+}$ mice. Analysis of lungs from *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Yap*$^{f/+}$; *Taz*$^{f/+}$; *Sftpc*$^{Cre/+}$ mice disclosed partial rescue of the branching defects (Fig. 2a-2c) and cell type specification (Fig. 2d-2j). This reinforced the notion that *Sftpc*^{Cre} has a lower efficiency in eliminating *Yap* and *Taz* compared to *Shh*^{Cre}. *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Yap*$^{f/+}$; *Taz*$^{f/+}$; *Sftpc*$^{Cre/+}$ mice also failed to survive after birth.

Together, these results support the idea that *Lats1/2* function through *Yap/Taz* in controlling the number and differentiation of SOX9^{+} progenitors (Fig. 2k). This information is critical for modeling lung development based on a *Lats1/2–Yap/Taz* axis.

A fraction of SOX9^{+} tip progenitors at the distal subdomain of lung branches is sufficient to drive lung outgrowth through bifurcation

The seemingly preserved lung size in *Lats1/2* mosaic mice prompted us to investigate if it was associated with the size of the SOX9^{+} domain. *Sftpc*^{Cre} inactivated *Lats1* and *Lats2* only in a subdomain of SOX9^{+} cells, as indicated by pYAP loss (Fig. 3a-3f). In regions where *Lats1/2* was removed by *Sftpc*^{Cre}, a corresponding reduction in pYAP levels was observed, suggesting YAP/TAZ activation (Fig. 3a-3f). Specifically, pYAP (and thus *Lats1/2*) expression was preserved in 15–50% of the distal SOX9^{+} subdomain where the relative pYAP intensity was also maintained (Fig. 3i). By contrast, pYAP expression disappeared in a majority of the more proximal SOX9^{+} subdomain and a fraction of the SOX2^{+} domain (Fig. 3i), which is proximal to the SOX9^{+} domain and forms the future conducting airways. Thus, *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$

mice produced a mosaic pattern of YAP/TAZ activation in the developing lungs (Fig. 3g, 3h). This unique property allowed us to evaluate how regulating SOX9$^+$ progenitors in a subdomain of the lung epithelium affects lung growth and development.

Selective YAP/TAZ activation in *Lats1/2*-mosaic lungs was correlated with the loss of SOX9$^+$ cells in the proximal subdomain with higher YAP/TAZ activity (Fig. 3j-3o). In particular, 15–50% of the distal SOX9$^+$ subdomain was retained in the mutant branches (Fig. 3p). Dichotomous branching (bifurcation) was unperturbed at the distal tips of *Lats1/2*-mosaic lungs, where *Lats1/2* expression was preserved. Moreover, the rate of EdU incorporation in the most distal SOX9$^+$ regions where *Lats1/2* were intact was similar to that in control lungs (Supplementary Fig. 3). The apparent preservation of the mutant lung size suggests that only a fraction of the distal SOX9$^+$ cells is required for lung outgrowth. In control lungs, new buds were generated through domain branching from the stalk (Fig. 3q, 3r). By contrast, in regions proximal to the distal tips where *Lats1/2* were eliminated in *Lats1/2*-mosaic lungs, lung branching through domain branching (lateral sprouting) was significantly reduced (Fig. 3s-3u). These regions were instead lined by an unbranched multilayered epithelium (Fig. 3v, 3w). These observations suggest that lungs produced by only a fraction of the bifurcation events that are distributed throughout different branches can reach the size of control lungs. The branching defects in the mutant lungs were discernible at 13.5 *dpc* and became more pronounced at 14.5 *dpc*. The trachea and main stem bronchi were unaffected in the mutant lungs. Despite the apparent preservation of the lung size, the branches located more proximally within *Lats1/2*-mosaic lungs became disorganized as development proceeded.

Together, when the non-distal SOX9$^+$ pool was removed by *Sftpc*^{Cre}, lung outgrowth was largely preserved. By contrast, when the entire SOX9$^+$ pool was removed by *Shh*^{Cre}, lung

outgrowth was blocked. These results suggest that a SOX9^{+} progenitor pool at the most distal subdomain is sufficient to direct overall lung outgrowth through bifurcation (Fig. 3x).

YAP/TAZ levels regulate cell differentiation in the transition zone (proximal to the distal tips) to produce the conducting airways in mice

The branching patterns in *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ (*Lats1/2*-mosaic) lungs appeared similar to those in control lungs up to 12.5 *dpc* (Supplementary Fig. 4). We noticed that the SOX2^{+} domain in *Lats1/2* mosaic lungs gradually shrank from 13.5 to 16.5 *dpc* (Fig. 4a-4d). This reduction was associated with a failure to form the conducting airways in *Lats1/2* mosaic lungs (Fig. 4e, 4f). These results suggest that the loss of *Lats1/2* in the SOX2^{+} domain abolished SOX2 expression (Fig. 4g, 4h). SOX9^{-}SOX2^{-} cells in the conducting airways of the mutant lungs then turned on markers of AT1 cells as described below.

In regions that correspond to the more proximal SOX9^{+} subdomain, *Lats1*/*2* were eliminated by *Sftpc*^{Cre} in the majority of this subdomain. These *Lats1/2*-deficient cells not only ceased to express SOX9 but also failed to express SOX2 (Fig. 4i), which is associated with cell-type formation in the conducting airways. Loss of SOX9 expression could be detected at 13.5 *dpc* in *Lats1/2* mosaic lungs, and the number of SOX9^{-}SOX2^{-} cells, which occupied the intermediate domain between the SOX9^{+} and SOX2^{+} domains, significantly increased from 13.5 to 16.5 *dpc* (Fig. 4i, 4j). At 16.5 *dpc*, SOX9^{-}SOX2^{-} cells were distributed in a mosaic pattern in the entire lung except the most distal part, where *Sftpc*^{Cre} failed to eliminate *Lats1/2* (Fig. 4g, 4h). This suggests that *Lats1* and *Lats2* were inactivated in the progeny produced from the distal SOX9^{+} progenitors as the descendants took up a more proximal location. SOX9^{-}SOX2^{-} cells can originate from (1) SOX9^{+} cells that lost SOX9 and failed to turn on SOX2; and (2) SOX2^{+} cells

that turned off SOX2 in *Lats1/2*-deficient epithelium. The size of residual SOX9$^+$ cells in *Lats1/2* mosaic lungs ranged from 15–50% of that in control lungs, as described above.

To gain molecular insight into how *Lats1/2* regulate lung branching, we collected lungs from control and *Lats1/2*-mosaic mice at 13.5 *dpc* and performed bulk RNA-seq analysis to probe the changes in transcriptomes in the absence of *Lats1/2*. The expression levels of canonical YAP targets, such as *Ctgf* (connective tissue growth factor, Ccn2), *Cyr61* (cysteine-rich protein 61, CCN1), and *Ajuba* (ajuba LIM protein), were increased in *Lats1/2* mosaic lungs compared to controls (Fig. 4k). This was confirmed by qPCR analysis (Fig. 4l). These results indicate that YAP targets in the lung epithelium are activated in the absence of *Lats1/2*. Consistent with a reduced SOX9$^+$ domain at the distal tip of *Lats1/2* mosaic lungs, bulk RNA-seq data revealed reduced expression of markers of the distal domain, such as *Sox9*, *Id2*, *Etv5*, and *Wnt7b* (Fig. 4k). Several regulators of the cell cycle (*e.g.*, *Cdkn2b*) or growth-promoting pathways (*e.g.*, *Wnt*) were upregulated in the mutant lungs (Fig. 4m).

The stalks populated by SOX9$^-$SOX2$^-$ cells in *Lats1/2*-mosaic lungs failed to undergo domain branching and presented as thickened multilayers of epithelial cells (Fig. 4f). Consistent with this phenotype, pathway analysis of bulk RNA-seq revealed upregulation of pathways that regulate cell proliferation, focal adhesion, the actin cytoskeleton, cell migration, cell motility, and ECM-receptor interaction in the mutant lungs (Fig. 4k, 4m, Supplementary Fig. 5). Disruption of these pathways is expected to perturb proper cell-cell interactions required for branching.

The rate of EdU incorporation in SOX9$^-$SOX2$^-$ cells in *Lats1/2*-mosaic lungs was similar to or slightly higher than that in control lungs (Supplementary Fig. 3). This result suggests that the failure of domain branching caused by YAP/TAZ activation was not due to reduced cell

proliferation. Together, these results reveal the fate of SOX9$^+$ cells in response to different levels of YAP/TAZ activity (Fig. 4n).

YAP/TAZ activation in SOX9$^+$ progenitors promotes the AT1 fate, while YAP/TAZ inactivation in SOX9$^+$ progenitors increases the AT2–to–AT1 ratio in the mouse lungs

Sftpc^{Cre} is active prior to the differentiation of SOX9$^+$ progenitors to produce alveolar epithelial cells and does not provide the genetic setting to assess the developmental potential of SOX9$^+$ progenitors during sacculation. To address this issue, we deployed *Sox9^{CreER}* [26] to remove *Lats1/2* in SOX9$^+$ progenitors at the distal lung epithelium. We generated control and *Lats1$^{f/f}$; Lats2$^{f/f}$*; *Sox9$^{CreER/+}$* mice and administered tamoxifen to pregnant females at 14.5 *dpc* (Fig. 5a). Analysis of mouse lungs from *Lats1$^{f/f}$; Lats2$^{f/f}$*; *Sox9$^{CreER/+}$* mice collected at 18.5 *dpc* revealed an increased ratio of AT1–to–AT2 compared to control lungs (Fig. 5b-5d). In fact, very few AT2 (SFTPC$^+$) cells were detected in the mutant lungs (Fig. 5c). Thus, higher YAP/TAZ levels in SOX9$^+$ progenitors drive the transition to the AT1 fate.

To further test our model, we used *Sox9^{CreER}* to remove *Yap/Taz* in SOX9$^+$ progenitors at the distal lung epithelium. We generated control and *Yap$^{f/f}$; Taz$^{f/f}$*; *Sox9$^{CreER/+}$* mice and administered tamoxifen to pregnant females at 13.5 *dpc* (Fig. 5e). Analysis of mouse lungs from *Yap$^{f/f}$; Taz$^{f/f}$*; *Sox9$^{CreER/+}$* mice collected at 18.5 *dpc* revealed an increased ratio of AT2–to–AT1 compared to control lungs (Fig. 5f-5h). Moreover, aggregates of AT2 cells were observed in the mutant lungs (Fig. 5g). These findings are consistent with our model in which lower YAP/TAZ levels maintain the progenitor pool.

To perturb Hippo signaling in a subset of SOX9$^+$ progenitors, we generated control and *Yap$^{f/f}$; Taz$^{f/f}$*; *Sftpc$^{CreER/+}$* lungs and administered tamoxifen to these animals at 13.5 *dpc* (Fig.

5i). This setup enabled the manipulation of Hippo signaling by *Sftpc*^{CreER} [27] in SFTPC^{+} cells. Likewise, *Yap*$^{f/f}$; *Taz*$^{f/f}$; *Sftpc*$^{CreER/+}$ lungs collected at 18.5 *dpc* exhibited an increased ratio of AT2–to–AT1 compared to control lungs, as well as AT2 aggregation (Fig. 5j-5l). Together, these studies support the role of YAP/TAZ levels in controlling the AT1/AT2 fate (Fig. 5m).

scRNA-seq and multiomics analysis of control and *Lats1/2*-mosaic lungs reveals different transitional states and candidate regulators during branching

To uncover the molecular mechanisms by which YAP/TAZ control the SOX9^{+} progenitor pool, we performed scRNA-seq analysis on cells isolated from control (n=13) and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ (*Lats1/2*-mosaic) (n=13) mouse lungs at 14.5 *dpc*. Lung cells were dissociated through enzymatic digestion and purified against immune cells (CD45) and hematopoietic cells (TER119) by fluorescence-activated cell sorting (FACS). We performed scRNA-seq analysis using the 10x Genomics platform. Analysis of scRNA-seq data was conducted using Seurat, Monocle, and other bioinformatics programs. A total of 13,985 control and 13,275 mutant lung cells were analyzed. We also re-analyzed published scRNA-seq of control lungs at 12.5 and 14.5 *dpc*[28, 29, 30], which showed similar patterns of gene expression to our control lungs (Supplementary Fig. 6).

In control lungs at 14.5 *dpc*, several clusters were discerned among *Epcam*$^{+}$ epithelial cells (Fig. 6a, 6b, Supplementary Fig. 7a). We computationally removed non-epithelial cells for cluster analysis. Based on gene expression, we inferred that cells in cluster 0 (*Sox9*$^{+}$) went through clusters 1 and 2 (transitional states) to reach cluster 3 (*Sox2*$^{+}$) (Fig. 6c). This trajectory could be in parallel (0–1–3 or 0–2–3) or in sequence (0–1–2–3). In this trajectory, the number of *Sox9*$^{+}$ cells decreased while the number of *Sox2*$^{+}$ cells increased. Cluster 4 is a distinct cluster of

Sox2^{+} cells, which express neuroendocrine markers (see below). Expression of *Lgals3* (a marker for the reported pre-AT1 transitional state, PATS, following lung injury) and *F3* was low in control lungs at 14.5 *dpc* and in multiple published datasets[29, 31].

In *Lats1/2*-mosaic mice lungs at 14.5 *dpc*, scRNA-seq analysis revealed a reduction in *Sox9*$^{+}$ and *Sox2*$^{+}$ cells, while the number of *Sox9*$^{-}$*Sox2*$^{-}$ cells increased (Fig. 6e, 6f), consistent with our phenotypic analysis. This observation suggests that the *Sox9*$^{+}$ pool was downsized, while its progeny failed to turn on *Sox2* in the absence of *Lats1/2*. Compared to the control lungs, the trajectory of cell clusters in *Lats1/2*-deficient lungs was altered (Fig. 6g). A trajectory of 0–1–3 was still present in the mutant lungs, in which cells in cluster 0 (*Sox9*$^{+}$) went through cluster 1 (a transitional state) to reach cluster 3 (*Sox2*$^{+}$). However, a new trajectory of 0–2–5 in the mutant lungs led to the expression of AT1 markers, such as *Hopx* and *Ager,* in clusters 2 and 5, which were also *Sox9*$^{-}$*Sox2*$^{-}$. This suggests that increased YAP/TAZ activity promotes the expression of AT1 markers. *Lgals3* was expressed in clusters 2 and 5, supporting the notion that clusters 2 and 5 could represent the pre-AT1 state. We noticed that cluster 2 in the mutant lungs shared certain patterns of gene expression (heatmap) to cluster 2 in the control lungs but has lost *Sox2* expression (Supplementary Fig. 7b). Cluster 2 in the control and mutant lungs can also be distinguished by unique sets of gene expression (Supplementary Fig. 7b). Cluster 5 can be subclustered; each subcluster requires additional analysis. These studies provide key insight into how YAP/TAZ activity levels direct the fate of *Sox9*$^{+}$ cells through different paths of transitional states.

We also computationally distinguished between control and mutant cells in scRNA-seq data from *Lats1/2*-mosaic lungs (Supplementary Fig. 8). Consistent with this finding, mutant cells expressed high levels of YAP targets (such as *Ctgf*, *Ajuba*, and *Amotl2*) (Supplementary Fig. 8).

Mutant cells constituted the new clusters and transitional states that are only present in the mutant lungs (Supplementary Fig. 8). This observation also suggests that the phenotypic consequences are due to the behavior of mutant cells.

scRNA-seq analysis revealed differentially expressed genes (DEGs) in each cluster of control and mutant lungs at 14.5 *dpc* (Fig. 6d, 6h). These DEGs not only define the cell clusters but also can be used to validate the path from the *Sox9*$^{+}$ to the *Sox2*$^{+}$ state. DEGs associated with the transition between cell clusters are also candidates for fate change. In particular, we identified transcription factors among DEGs (Supplementary Fig. 9), and a transcription factor network can be constructed (Supplementary Fig. 10). Several of these transcription factors have been previously reported to regulate lung branching and/or cell differentiation. For instance, retinoic acid receptor β (RARB), a nuclear receptor and ligand-activated transcription factor, was enriched when cluster 0 transitions to 1 or 2 at 14.5 *dpc*. Retinoic signaling has been implicated in lung branching[32]. Our scRNA-seq analysis has identified a cell population in which RA signaling controls early lung development. The transition of cluster 0 to 1 or 2 was also associated with the downregulation of *Lef1*, a transducer of Wnt signaling, and *Rbpjl*, an antagonist of Notch signaling. Genetic loss of *Lef1* and its paralogs in mice accelerated differentiation into SOX2 progeny[31]. Thus, our scRNA-seq has identified a potential target population of Wnt and Notch signaling, the downregulation of which is required for state transition. Several other DEGs have been implicated in lung development or cell fate specification (*e.g.*, *Etv5*, *Sp5*, *Six1*)[33, 34, 35]. Our analysis thus has provided a cellular framework in which these regulators function. Moreover, several other regulators and transcription factors are not known to control lung branching and/or cell differentiation (*e.g.*, *Npas2*, which regulates

circadian rhythm). Our scRNA-seq analysis could reveal their new functions in the developing lung.

To reveal the signaling network that controls the SOX9$^+$ progenitors, we performed multiomics analysis on cells isolated from control (n=12) and *Lats1$^{f/f}$; Lats2$^{f/f}$*; *Sftpc$^{Cre/+}$* (*Lats1/2*-mosaic) (n=11) lungs at 14.5 *dpc*. We isolated nuclei from control and *Lats1/2*-mosaic lung cells at 14.5 *dpc* and performed multiomics analysis using the 10x Genomics platform. snRNA-seq and snATAC-seq data from 2339 control and 3292 mutant lung nuclei were analyzed.

We identified differentially accessible regions (DARs) between SOX9$^+$ and SOX2$^+$ cells in control lungs at 14.5 *dpc* (Supplementary Fig. 11). Multiple motifs within DARs were revealed. The motifs enriched in either SOX9$^+$ or SOX2$^+$ cells provide insight into potential regulators for differentiating SOX9$^+$ cells into SOX2$^+$ cells in the conducting airways. Several DEGs associated with the transition between the SOX9$^+$ and SOX2$^+$ states contain the TEAD motif in their regulatory regions (Supplementary Fig. 11). This suggests that YAP/TAZ utilizes a regulatory network to control the transition of SOX9$^+$ to SOX2$^+$ cells.

Together, we have identified the developmental path of SOX9$^+$ cells to produce SOX2$^+$ cells and how their transitional states are affected by YAP/TAZ levels and regulators.

scRNA-seq and multiomics analysis of control and *Lats1/2*–mosaic lungs uncovers different transitional states associated with the progression of the AT1 fate and candidate regulators during sacculation

To unveil the molecular mechanisms by which YAP/TAZ controls the SOX9$^+$ progenitor pool during sacculation, we performed scRNA-seq on cells isolated from control (n=4) and *Lats1$^{f/f}$;*

Lats2$^{f/f}$*; Sftpc*$^{Cre/+}$ (*Lats1/2*-mosaic) (n=4) mouse lungs at 17.5 *dpc*. Lung cell isolation and scRNA-seq were performed as described above. A total of 8,979 control and 31,392 mutant lung cells were analyzed. Likewise, we re-analyzed published scRNA-seq of control lungs at 15.0, 15.5, 16.5, 17.5, and 18.5 *dpc*[28, 31, 36, 37], which showed similar patterns of gene expression to our control lungs (Supplementary Fig. 12).

In control lungs at 17.5 *dpc*, several cell clusters were discerned among *Epcam*$^{+}$ epithelial cells (Fig. 7a, 7b, Supplementary Fig. 13). Based on gene expression, we inferred that cells in cluster 0 (*Sox9*$^{+}$*Sftpc*$^{+}$) went through cluster 1 (*Sftpc*$^{+}$*Hopx*$^{+}$*Ager*$^{+}$) to reach clusters 2 and 3 (*Hopx*$^{+}$*Ager*$^{+}$) (Fig. 7c). In this trajectory, *Sox9*$^{+}$ cells produced AT1/AT2 cells and then AT1 cells. *Sox9*$^{-}$*Sftpc*$^{+}$ cells in cluster 0 lost *Sox9* expression and likely generated AT2 cells. *Hopx*$^{+}$*Ager*$^{+}$ cells in clusters 2 and 3 expressed *Lgals3*, suggesting a more mature state compared to 14.5 *dpc*.

We found that the cluster of *Hopx*$^{+}$*Ager*$^{+}$ (AT1) cells was significantly larger in the mutant lungs (Fig. 7e, 7f). By contrast, the cell cluster that expresses AT2 markers was greatly diminished in *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Sftpc*$^{Cre/+}$ mouse lungs (Fig. 7e). This supports our model in which activation of YAP/TAZ depletes the AT2 pool and promotes the AT1 fate. The mutant *Hopx*$^{+}$*Ager*$^{+}$ cluster contained several subclusters, among which cluster 5 expressed *Krt8*, *Cldn4*, *Sfn,* and *Lgals3* (Fig. 7g, 7h).

Moreover, we performed a comparative analysis between (1) *Lats1/2*-deficient *Hopx*$^{+}$*Ager*$^{+}$ cells at 14.5 *dpc* [designated as state 1], (2) control *Hopx*$^{+}$*Ager*$^{+}$ cells at 17.5 *dpc* [state 2], (3) *Lats1/2*-deficient *Hopx*$^{+}$*Ager*$^{+}$ cells at 17.5 *dpc* [state 3], and (4) control *Hopx*$^{+}$*Ager*$^{+}$ cells at neonatal and adult lungs [state 4]. We found that they represent different stages of AT1 maturation (Fig. 7i, 7j). For instance, only states 2 and 3 (not 1) expressed *Lgals3* (which is also

expressed in adult AT1), *Emp2,* and *Clic5*. Only state 3 (not 1 or 2) expressed *S100a6*, *Krt7*, and *Cryab* (which are all expressed in neonatal or adult AT1 [state 4]). These states (1–2–3) thus represent the sequential maturation of AT1 cells during development.

We also computationally distinguished between control and mutant cells in scRNA-seq data from *Lats1/2*-mosaic lungs (Supplementary Fig. 8). Consistent with this finding, mutant cells also expressed high levels of YAP targets (such as *Ctgf*, *Ajuba*, and *Amotl2*) (Supplementary Fig. 8). Mutant cells constituted the new clusters that are only present in the mutant lungs (Supplementary Fig. 8).

scRNA-seq analysis revealed differentially expressed genes (DEGs), including transcription factors among DEGs (Supplementary Fig. 14) in each cluster of control and mutant lungs (Fig. 7d, 7h, 7j), and a transcription factor network can be constructed (Supplementary Fig. 15). Likewise, they will define the cell clusters and provide candidates that control fate change. For example, the expression of *Rarb* and *Sox5* was increased when cluster 0 transitioned to 1 at 17.5 *dpc*. Lung development failed to progress to the saccular stage in *Sox5* knockout mice[38], although the molecular basis of the phenotype is unknown. Our scRNA-seq analysis revealed where and when *Rarb* and *Sox5* may act. The transition from cluster 0 to 1 was associated with reduced expression of several regulators, including *Cebpa*, *Elf5* (a *Fgf*-sensitive transcription factor), *Etv5*, *Sp5*, and *Tfcp2l1* (a grainyhead transcription factor), which have been reported to regulate lung development. For instance, loss of *Cebpa* is associated with dysfunction of AT2 cells[39]. *Etv5* is required for the maintenance of AT2 cells[40]. *Sp5* drives primary cilia formation[34]. Misexpression of *Elf5* was known to disrupt lung branching and differentiation[41]. Loss of *Tfcp2l1* enhanced AT2-AT1 differentiation in a mouse model of alveolar regeneration induced by influenza[42]. These examples illustrate that our scRNA-seq has identified a target cell

population and their cellular trajectory for these regulators during alveolar fate determination. As described above, further analysis of other regulators and transcription factors identified in this study could reveal their new functions in lung development and cell fate determination.

To identify the YAP/TAZ targets and their regulators that control the AT1/2 fate in the alveolar epithelium, we performed multiomics analysis on isolated nuclei from control (n=7) and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ (*Lats1/2*-mosaic) (n=7) lungs at 17.5 *dpc*. snRNA-seq and snATAC-seq data from 2526 control and 3210 mutant lung nuclei were analyzed.

We identified differentially accessible regions (DARs) between AT1 and AT2 cells in control lungs at 17.5 *dpc* (Supplementary Fig. 16). Multiple motifs within DARs were revealed. The TEAD motifs were enriched in AT1 cells as expected. The other motifs enriched in either AT1 or AT2 cells provide insight into potential regulators for differentiating SOX9$^+$ cells into AT1/2 cells in the alveolar epithelium. DEGs associated with AT1 cells contain multiple motifs (DARs) in their regulatory regions (Supplementary Fig. 16). Several DEGs associated with the transition between SOX9$^+$ and AT1$^+$ states contain the TEAD motif in their regulatory regions (Supplementary Fig. 16). This suggests that YAP/TAZ utilizes a regulatory network to control the transition of SOX9$^+$ to AT1$^+$ cells.

The developmental path of SOX9$^+$ cells in mouse lungs can be mapped onto human lungs

Our molecular analysis of mouse lungs has produced the developmental paths and fate determination of SOX9$^+$ cells (Fig. 6c, 7c). Taking advantage of the available scRNA-seq data on human fetal lungs[43], we asked if these paths could be mapped onto human lungs. We found that cluster 0 of control mouse lungs at 14.5 *dpc* expressed several markers that correspond to the early tip of human lungs, while cluster 2 can be identified with markers of the early stalk of

human lungs (Supplementary Fig. 17a). Such correspondence was preserved in clusters 0 and 2 of *Lats1*$^{f/f}$, *Lats2*$^{f/f}$, *Sftpc*$^{Cre/+}$ (*Lats1/2*-mosaic) mouse lungs at 14.5 *dpc* (Supplementary Fig. 17b). For control and mutant mouse lungs at 17.5 *dpc*, cluster 0 corresponds to the late stalk of human lungs (Supplementary Fig. 17c, 17d). Interestingly, cluster 4 in control and mutant mouse lungs contains neuroendocrine cells, similar to those found in human lungs (Supplementary Fig. 17e, 17f). These results reveal parallel developmental paths of lung cells in mice and humans. It also highlights the importance of molecular analysis of mouse lungs to complement studies of human lungs.

Discussion

Our study has advanced the mechanistic understanding of lung size control and cell fate specification (Fig. 8). Hippo signaling shapes lung development through its effects on SOX9^{+} progenitors. By controlling the expansion of a SOX9^{+} progenitor pool at the tip of lung branches, Hippo signaling regulates tip bifurcation and lung outgrowth, a key element in controlling lung size. Moreover, Hippo signaling is modulated in subpopulations of SOX9^{+} progenitors, regulating their differentiation through distinct sequences of transitional states toward cell fates in the conducting airways or the alveolar epithelium. These advances rely on the ability to generate a mosaic pattern of Hippo activity, coupled with transcriptome and chromatin accessibility analysis.

Our results suggest that Hippo signaling is tuned to a lower level in the distal SOX9^{+} subdomain. However, YAP/TAZ levels at the distal domain can display wave-like fluctuations. The molecular basis of Hippo signal modulation in different subdomains is unclear. This process likely involves additional signaling pathways and feedback controls. Cells in different

subdomains may regulate YAP/TAZ levels in response to mechanical stress. In support of this notion, the stiffness of the extracellular matrix varies along the proximo-distal axis of lung branches. Analysis of chromatin accessibility and regulation of YAP/TAZ targets in subpopulations of SOX9^{+} progenitors could provide candidates for modulating the spatial activity of the Hippo pathway.

Despite a significant reduction in the number of SOX9^{+} cells at the tip, dichotomous branching and lung size are largely preserved in *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ (*Lats1/2*-mosaic) lungs. It is possible that only a fraction of SOX9^{+} cells are utilized for dichotomous branching. Alternatively, a lower number of SOX9^{+} cells triggers a regulatory mechanism for size control of distal branches. This process may involve changes in cell proliferation rates and the recruitment of additional signaling pathways. The molecular machinery downstream of Hippo signaling to execute lung size control is unknown. Likewise, identifying YAP/TAZ targets and their regulators could be informative. The discovery that dichotomous branching is controlled through Hippo signaling in the distal SOX9^{+} progenitors sheds light on the mechanism of lung size control.

In regions populated by SOX9^{-}SOX2^{-} cells in *Lats1/2*-mosaic lungs, domain branching fails to occur. SOX9^{-}SOX2^{-} cells display elevated YAP/TAZ activities. We surmise that the downstream events of YAP/TAZ activation, such as aberrant cell junctions and cell migration, disrupt the cell-cell interactions necessary for domain branching.

While the size of *Lats1/2*-mosaic lungs was mostly preserved, and dichotomous branching at the tips proceeded, saccules failed to be produced. We speculate that the number of SOX9^{+} cells at the tip, while adequate for bifurcation, is insufficient to generate saccules. Alternatively, a reduction in AT2 cells in *Lats1/2*-mosaic lungs contributes to defective sacculation. This is

consistent with the observation that the appearance of AT2 cells is associated with the formation of the saccules and alveoli.

Our transcriptome and chromatin accessibility studies provide molecular insight into how subpopulations of SOX9$^+$ progenitors undergo different sequences of transitional states to generate cell types in either the conducting airways or the respiratory epithelium. We have not only revealed how YAP/TAZ levels control this process but also identified candidate regulators of the transitional states. The function and transition of some of these cell states are supported by genetic analysis. Despite the new insight, our conclusions require experimental validations. For instance, these results form the basis of future investigations to reveal the spatial and temporal distribution of cell populations in a particular transitional state and understand how the transition of cell fates is regulated at the molecular level. Additional experiments are also required to probe the path, plasticity, and reversibility between cell states. In this regard, it is crucial to identify and test key transcription factors associated with different cell fates.

Our findings represent the first report of transitional states from SOX9$^+$ to SOX2$^+$ cells to construct the conducting airway. The trajectory of at least two paths to reach the SOX2$^+$ state may reflect the plasticity of SOX9$^+$ to SOX2$^+$ transition for a given SOX9$^+$ cell. Another possibility is that SOX9$^+$ cells at different locations along the proximo-distal axis of lung branches follow different paths to become SOX2$^+$ cells.

Our results also depict the first characterization of the transitional states from SOX9$^+$ to AT2$^+$ or AT1$^+$ to generate alveoli. In this setting, only one trajectory was revealed. Analysis of cells expressing AT1 markers in control and *Lats1/2*-mosaic lungs at 14.5 and 17.5 *dpc* reveals a path of AT1 maturation associated with transcriptome changes. We envision that additional scRNA-seq analysis will uncover intermediate steps between the transitional states we have

identified for AT1 maturation. AT1 cells are produced from AT2 cells following lung injury. During the repair process, the transitional states that connect AT2 to AT1 cells have been reported[44, 45]. A fundamental question is whether the production of AT1 cells charts a common path during development and following lung injury. Our analysis delineates several maturation states of AT1 cells during development, which enables comparative studies on the production of AT1 cells following lung injury. Even if the production of AT1 cells adopts different paths during development and following lung injury, both paths can be exploited to stimulate AT1 cell generation in adult lungs.

Loss of *Lats1/2* in the progeny of SOX9^{+} cells results in a failure to produce SOX2^{+} cells to form the conducting airways. In fact, these cells also lose *Sox9* expression. Inactivation of *Lats1/2* in SOX2^{+} cells results in the termination of *Sox2* expression. Despite multiple differentiation trajectories to reach the SOX9^{-}SOX2^{-} state, SOX9^{-}SOX2^{-} cells turn on the fate of AT1 cells once Hippo signaling is active. The molecular mechanisms that underlie the changes in cellular properties are unclear. Addressing this issue would require scRNA-seq and multiomics analyses at additional time points of lung development.

SOX9^{+} cells are present in human lungs[43]. Organoids derived from human fetal lungs display progenitor properties. Our analysis of mouse and human scRNA-seq data suggests that at least one common path can be identified in both species. The path of cluster 0 to 2 in mice is associated with the production of AT1 cells. This raised the possibility that the path from cluster 0 to 1 in mice leads to cell fates of the conducting airways. In this model, the paths that lead to segregation of the fates for conducting airways and alveolar epithelium can be discerned at 14.5 *dpc*[46, 47, 48]. Differences likely exist in the stepwise differentiation program between mouse and human lungs. In both systems, the signaling pathways and transcription factors used to specify

cell types are not fully understood. The eventual validation of fate determination models inferred from human lung organoids would need to await genetic and molecular studies in non-human primates. In this regard, our mouse studies provide key experimental settings that are not available in human lungs.

Together, our work has provided a new conceptual framework for understanding how Hippo signaling controls the distinct steps of SOX9^{+} cell proliferation and differentiation. This information lays the groundwork for further functional studies. It also provides a platform to investigate how other signaling pathways interact with Hippo signaling during lung growth and fate specification in mammals.

Methods

Animal husbandry

All mouse experiments in this study were performed in accordance with protocols approved by the Institutional Animal Care and Use Committee (IACUC) of the University of California, San Francisco (UCSF). Mouse matings were set up to obtain animals with the genotypes described in this study. Information on mouse ages, numbers, and genotypes was included in the text and figures. N pairs in the figure legends denote n controls and n mutants, which were collected from as many litters as needed to reach that number. All the controls used in this study are littermate controls. Their genotypes vary depending on the crosses used in a given experiment.

The mouse strains used in this study and their sources are listed below. *Yap* floxed allele (*Yap*^{f}) [*Yap1*$^{tm1.1Eno}$; MGI: 5446483; Dr. Eric Olson], *Taz* floxed allele (*Taz*^{f}) [*Wwtr1*$^{tm1.1Eno}$; MGI: 5544289; Dr. Eric Olson], *Lats1* floxed allele (*Lats1*^{f}) [RRID: IMSR_JAX:024941], *Lats2* floxed allele (*Lats2*^{f}) [RRID: IMSR_JAX:025428], *ROSA26*^{mTmG} [RRID: IMSR_JAX:007676], *Shh*^{Cre} [RRID: IMSR_JAX:005622], *Spc*^{Cre} (*Sftpc*^{Cre}) [*Tg(Sftpc-cre)1Blh*; MGI:3574949; Dr. Brigid Hogan], *Sox9*^{Cre} [*Sox9t*$^{m3(Cre)Crm}$; MGI: 3608931; Dr. Benoit de Crombrugghe], *Sox9*^{CreER} [RRID: IMSR_JAX:035092], *Sftpc*^{CreER} [our laboratory].

Tamoxifen administration

The stock solution of tamoxifen (50 mg/ml) was prepared by dissolving tamoxifen in corn oil. To prepare a working solution of tamoxifen (10 mg/ml), the stock solution was diluted 1:5 in corn oil. In general, 75-100 μl of the working solution was delivered to pregnant female mice through intraperitoneal injection. However, different mouse CreER lines may require varying amounts of

tamoxifen to achieve efficient recombination. Detailed information on the stages of tamoxifen injection and lung collection was provided in the figures or figure legends.

Whole-mount immunofluorescence

Embryonic mouse lungs were harvested at the indicated time points and fixed in 4% PFA/PBS on ice for 1 h. The lungs were washed with 0.1% Tween-20/PBS for 30 min. Samples were then treated with graded methanol solutions (25%, 50%, 75%, 100%) and then incubated in 5% H_2O_2/methanol overnight. The next day, the samples were rehydrated through a series of graded methanol solutions (100%, 75%, 50%, 25%, and 0%), which were diluted in 0.1% Tween-20/PBS. After incubation in blocking buffer (1.5% BSA/0.5% Triton X-100/PBS) for 6 h, the samples were then incubated with primary antibodies at 4°C overnight. The next day, samples were washed with blocking buffer for 5 h and then incubated with secondary antibodies at 4°C overnight. A Nikon Eclipse E1000 microscope with a SPOT 2.3 CCD camera was used to capture the images.

The primary antibodies for whole-mount immunostaining were rat anti-E Cadherin (1:200, Life Technologies, Cat# 13-1900; RRID:AB_2533005), rabbit anti-phospho-YAP (Ser127) (1:100, Cell Signaling, Cat#4911S; RRID:AB_2218913), rabbit anti-SOX2 (D9B8N) (1:200, Cell Signaling Technology, Cat# 23064S; RRID:AB_2714146), goat anti-SOX9 (1:200, R&D Systems, Cat# AF3075; RRID:AB_2194160).

Immunofluorescence and Immunohistochemistry

Dissected mouse lungs were fixed in 4% paraformaldehyde (PFA) in PBS for 1-2 h at 4°C. Lungs were embedded in paraffin wax and sectioned at 6 μm or embedded in OCT and sectioned at 6 μm. Histological analysis was performed as previously reported[49, 50, 51].

Immunofluorescence was performed as previously described[49, 50, 51]. The primary antibodies used include: rabbit anti-NKX2.1 (1:100, Epitomics, Cat# 2044-1; RRID:AB_1310784), chicken anti-GFP (1:200, Aves Labs, Cat# GFP-1010; RRID:AB_2307313), rabbit anti-prosurfactant protein C (proSP-C) (1:200, Seven Hills Bioreagents, Cat# WRAB-9337; RRID:AB_2335890), Syrian hamster anti-T1a (1:200, Developmental Studies Hybridoma Bank, Cat# 8.1.1; RRID:AB_531893), mouse anti-HOPX (E-1) (1:100, Santa Cruz Biotechnology, Cat# sc-398703; RRID:AB_2687966), goat anti-CC10 (1:200, Santa Cruz Biotechnology, Cat# sc-9773; RRID:AB_2183391), mouse anti-acetylated tubulin (1:200, Santa Cruz Biotechnology, Cat# sc-23950; RRID:AB_628409), mouse anti-ACTA2, clone 1A4 (1:200, Thermo Scientific Lab Vision, Cat# MS-113-P0; RRID:AB_64001), rat anti-PECAM-1 (CD31) (1:150, Santa Cruz Biotechnology, Cat# sc-18916; RRID:AB_627028), rabbit anti-PDGFRA (1:150, Cell Signaling Technology, Cat# 3164S; RRID:AB_2162351), rabbit anti-phospho- PDGFRA (Tyr754) (23B2) (1:100, Cell Signaling Technology, Cat# 2992S; RRID:AB_390728), and goat anti-PDGFRB (1:200, R&D Systems, Cat# AF1042; RRID:AB_2162633).

Secondary antibodies and conjugates used were donkey anti-rabbit Alexa Fluor 488 (1:1000, Life Technologies, Cat# A-21206; RRID:AB_2535792) or 594 (1:1000, Life Technologies, Cat# A-21207; RRID:AB_141637), donkey anti-chicken Alexa Fluor 488 (1:1000, Jackson ImmunoResearch, Cat# 703-546-155; RRID:AB_2340376) or 647 (1:1000, Jackson ImmunoResearch, Cat# 703-606-155; RRID:AB_2340380), donkey anti-mouse Alexa Fluor 488 (1:1000, Life Technologies, Cat# A-21202; RRID:AB_141607) or 594 (1:1000, Life

Technologies, Cat# A-21207; RRID:AB_141637), and donkey anti-rat Alexa Fluor 594 (1:1000, Life Technologies, Cat# A-21209; RRID:AB_2535795). The biotinylated secondary antibodies used were goat anti-hamster (1:1000, Vector Laboratories, Cat# BA-9100; RRID:AB_2336137), donkey anti-rabbit (1:1000, Jackson ImmunoResearch, Cat# 703-066-155; RRID:AB_2340355), donkey anti-rat (1:1000, Jackson ImmunoResearch, Cat# 712-065-150; RRID:AB_2340646), and horse anti-mouse (1:1000, Vector Laboratories, Cat# BA-2000; RRID:AB_2313581). The signal was detected using streptavidin-conjugated Alexa Fluor 488 (1:1000, Jackson ImmunoResearch, Cat# 016-540-084; RRID:AB_2337249), 594 (1:1000, Jackson ImmunoResearch, Cat# 016-580-084; RRID:AB_2337250), or 647 (1:1000, Jackson ImmunoResearch, Cat# 016-600-084; RRID:AB_2341101) or HRP-conjugated streptavidin (1:1000, Jackson ImmunoResearch, Cat# 016-030-084; RRID:AB_2337238) coupled with fluorogenic substrate Alexa Fluor 594 tyramide for 30 s (1:200, TSA kit; Akoya Biosciences, Cat# NEL753001KT).

Confocal images were captured on a Leica SPE laser-scanning confocal microscope. Adjustments to the red/green/blue/grey histograms and channel merges were performed using LAS AF Lite (Leica Microsystems).

Cell proliferation assays

Cell proliferation in embryonic lungs was assessed by EdU incorporation. Briefly, 1 h prior to lung collection, 300 μl of EdU (Research Products International, Cat# B71800-1.0)/PBS solution (5 mg/ml) was injected intraperitoneally into pregnant female mice at the indicated time points. EdU incorporation was evaluated by the Click-iT EdU Alexa Fluor 488 Imaging Kit (Thermo Fisher, Cat# C10337). To measure the proliferation rate of $SOX9^{+}$, $SOX2^{+}$, $SOX9^{-}SOX2^{-}$ cells,

EdU spots were co-stained with SOX2 or SOX9 on adjacent sections, where DAPI was used to identify individual lung cells. The signals of EdU, SOX2, and SOX9 all reside in the nucleus and also co-localize with the DAPI signal. The number of proliferating $SOX2^+$ cells ($EdU^+SOX2^+DAPI^+$), proliferating $SOX9^+$ cells ($EdU^+SOX9^+DAPI^+$), proliferating $SOX9^-$ $SOX2^-$ cells ($EdU^+SOX9^-SOX2^-DAPI^+$), the total number of $SOX2^+$ cells ($SOX2^+DAPI^+$), the total number of $SOX9^+$ cells ($SOX9^+DAPI^+$), and the total number of $SOX9^-SOX2^-$ cells ($SOX9^-SOX2^-DAPI^+$) were manually counted using ImageJ. The proliferation rates of $SOX2^+$ cell, $SOX9^+$ cell, and $SOX9^-SOX2^-$ cell were calculated as the ratios of (EdU^+SOX2^+)/($SOX2^+$), (EdU^+SOX9^+)/($SOX9^+$), and (EdU^+ $SOX9^-SOX2^-$)/($SOX9^-SOX2^-$). For each biological replicate, at least 5 sections were used for quantification.

Quantification assays

The branching pattern was traced on *Sftpc*$^{Cre/+}$*; ROSA26*$^{mTmG/+}$ (control) and *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Sftpc*$^{Cre/+}$*; ROSA26*$^{mTmG/+}$ (mutant) lungs following the published method[1]. All the lineages, including domain branching and bifurcation from branch L.L1 until 14.5 *dpc*, were quantified. Epithelial counting relied on both the *ROSA26*^{mTmG} reporter line and SOX2/SOX9 whole-mount immunostaining.

Quantification of immunostaining signals was performed on images of control and *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Sftpc*$^{Cre/+}$*; ROSA26*$^{mTmG/+}$ (mutant) lungs at 14.5 *dpc* under the same exposure. A square box of the same size was placed on the distal and proximal lung epithelium stained with anti-pYAP. Image J was used to measure and calculate the relative signal intensity of pYAP staining.

Bulk RNA-Seq analysis

Bulk RNA-seq was performed as previously described[49]. Briefly, the embryonic lungs were dissected from control and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ mice at 13.5 *dpc* and lysed in 0.5 ml TRIzol (Life Technologies). 100 µl chloroform was then added to the lysates. The samples were then centrifuged at 4˚C for 15 min. The upper aqueous layer was collected and mixed with an equal volume of 70% ethanol. RNAs were extracted with the RNeasy Mini Kit (Qiagen) following the manufacturer's instructions. RNA quality was evaluated using an Agilent 2100 Bioanalyzer. Samples were sequenced on an Illumina HiSeq. Differential gene expression, gene ontology (GO) enrichment analyses, and the barplot of gene ontology enrichments were performed using RStudio. Datasets have been deposited in NCBI's Gene Expression Omnibus database and are accessible through the GEO Series accession number (GSE269537).

qPCR analysis

qPCR analysis was performed as previously described. The following primers for mouse genes were used: *Gapdh* (forward, 5'-AGGTTGTCTCCTGCGACTTCA-3'; reverse, 5'-CCAG GAAATGAGCTTGACAAAGTT-3'), *Ctgf* (forward, 5'-CTCCACCCGAGTTACCAATG-3'; reverse, 5'-TGGCGATTTTAGGTGTCCG-3'), *Ajuba* (forward, 5'-GGTATCTATGGGCAGAGCAATG-3'; reverse, 5'- CAGTAGACAGAGCCATTGACG-3'), *Cyr61* (forward, 5'-GTGAAGTGCGTCCTTGTGGACA-3'; reverse, 5'-CTTGACACTGGAGCATCCTGCA-3'),

Lung cell dissociation

Lungs were harvested and dissociated as previously described[52]. Briefly, mouse lungs were dissected from embryos and rinsed in DPBS (Gibco 14190-144). Tissues were minced into small pieces using scissors or razor blades and then transferred to 1.5 ml tubes containing 0.5 mL Dissociation Buffer (0.05% Collagenase B (Roche 11088835001), 1.2 U/mL Dispase II (Gibco 17105-041), 80 Kunitz units/mL DNase I (MilliporeSigma DN25)). The samples were incubated at 37°C for 30-50 minutes and triturated every 10 minutes using a P-1000 pipette. Cells were washed with 1 mL PBS and then resuspended in 90% fetal bovine serum (FBS; Phoenix Scientific PS-100) + 10% DMSO (MilliporeSigma D2650). Cells were stored at -80°C overnight and then transferred to liquid nitrogen for long-term storage.

Cells were thawed in a 37°C water bath for 2 minutes and then washed with 1 mL 10% FBS/Leibovitz L-15 media (Gibco 21083-027). The cells were resuspended in 100 µL DNase I (1600 Kunitz units/mL) and then washed with 1 mL DPBS. The cells were passed through a 70 µm strainer (Bel-Art Products H13680-0070) and resuspended in 200 µL 0.5% bovine serum albumin (BSA; Miltenyi Biotec 130-091-376).

Sample preparation for scRNA-seq and multiomics analysis

For scRNA-seq and multiome (snRNA-seq/snATAC-seq) experiments, mouse lung cells were incubated with eFluor 450 anti-CD45 (eBioscience 48-0451-80) and eFluor 450 rat anti-TER-119 (eBioscience 48-5921-80) for 30 minutes at 4°C. Cells were washed with 1 mL 0.5% BSA, then passed through a 40 µm strainer (Bel-Art Products H13680-0040) and resuspended in 0.5% BSA + 0.5 µg/mL DAPI (MilliporeSigma D9542) before sorting on a BD FACSAria Fusion flow cytometer.

Multiome samples were prepared following the 10x Genomics protocol. Briefly, 50,000-100,000 sorted cells were incubated in 0.1X Lysis Buffer (10 mM Tris-HCl (pH 7.4), 10 mM NaCl, 3 mM MgCl2, 0.1% Tween-20, 0.1% Nonidet P40 Substitute, 0.001% Digitionin, 1% BSA, 1 mM DTT, 1 U/µL RNase inhibitor in nuclease-free water) on ice for 3 min. The samples were washed three times with Wash Buffer (10 mM Tris-HCl (pH 7.4), 10 mM NaCl, 3 mM MgCl2, 0.1% Tween-20, 1 mM DTT, 1 U/µL RNase inhibitor in nuclease-free water), then resuspended in Diluted Nuclei Buffer prior to library preparation.

scRNA-seq analysis

scRNA-seq was performed using the GEM-X Universal 3' Gene Expression kit (10x Genomics) following the manufacturer's instructions.

Sequencing reads from each single-cell RNA-seq (scRNA-seq) sample were preprocessed, aligned, and quantified using the CellRanger pipeline (version 8.0.1, 10x Genomics) with the mm10 mouse reference genome (refdata-gex-mm10-2020-A, 10x Genomics).

Seurat R package (version 5.2.1) was used for quality control (QC), normalization, scaling, and identification of variable features for each sample. Cells with 200-7500 Unique Molecular Identifiers (UMIs) mapped to unique genes, and with less than 5% of UMIs mapped to mitochondrial genes, were retained. EmptyDrops was used to generate a barcode rank plot of UMI count and a fitted spline, which was used for detecting the knee point. Barcodes detected as putative cell-containing droplets at a false discovery rate (FDR) of 0.1% or less were kept. Clusters that expressed lineage markers for hematopoietic, endothelial, mesenchymal, and mesothelial cells were removed. Highly variable genes for dimensionality reduction were selected using the Seurat::FindVariableGenes function (nfeatures = 2000). Principal components

(PCs) were identified using the Seurat::RunPCA function. The number of PCs accounting for more than 90% of the cumulative variation in each sample was identified for downstream analysis. A K-nearest neighbor (KNN) graph was built using the Seurat::FindNeighbors function. Graph-based clustering of the PC analysis was done using the Seurat::FindClusters function (Louvain algorithm). Projection of the cells on a 2D map was performed with uniform manifold approximation and projection (UMAP) using the Seurat::RunUMAP function. UMAP plots overlaid with gene expression levels were generated using the Seurat::FeaturePlot function. Dot charts for gene expression were generated using the Seurat::DotPlot function.

Differentially expressed genes (DEGs) were identified using the Seurat::FindMarkers function (test.use = "wilcox"). Markers with a false discovery rate (FDR) less than 0.05 were kept. Volcano plots for DEGs between clusters/samples were generated using ggplot2 (v3.5.1) and ggrepel (v0.9.6). The x-axis represents the difference in the percentage of cells expressing the gene of interest between the two clusters/samples; the y-axis shows the average fold change in gene expression between the two clusters/samples.

Pseudotemporal analysis was done using the Monocle3 R package (v1.3.7). Monocle3 was used to learn the sequence of gene expression changes using the monocle3::learn_graph function. Cells were then ordered according to their progression through the developmental program using the monocle3::order_cells function. Predicted pseudotime values for each cell were overlaid onto the previously generated UMAP projection.

The SCENIC (v0.12.1) pipeline was used to infer co-expression modules from single-cell expression matrices of $EPCAM^+$ cell clusters. The cisTarget database (mc_v10_clust) and Motif2TF annotations database (v10) (Aerts lab) were used for motif enrichment in gene sets. Transcription factor (TF)–target gene adjacency lists were pruned to retain transcription factors

with highly enriched motifs (within the top 300 ranked motifs) around the predicted transcription start site (TSS) of their target genes. The search space is within 500 base pairs upstream and 100 base pairs downstream of the TSS of the target gene. Gene regulatory networks (GRNs) were constructed using previously predicted TF–target connections within the differentially expressed genes (DEGs) between two cell clusters, based on pruned TF–target gene lists. Pearson correlation coefficients were used to assess the direction of the relationship between TFs and their target genes. GRN plots were generated using the RStudio package igraph (v2.1.4) and ggplot2 (v3.5.1).

Merging and integration of scRNA-seq data of multiple samples were performed as follows. For publicly available data, EPCAM^{+} cells were aggregated, and clusters that expressed lineage markers for hematopoietic, endothelial, mesenchymal, and mesothelial cells were removed. Highly variable genes for dimensionality reduction were selected using the Seurat::FindVariableGenes function (nfeatures = 2000). The batch effect was corrected using the Fast Mutual Nearest Neighbors Integration (Fast MNN Integration) method in the Batchelor (v1.24.0) package. A K-nearest neighbor (KNN) graph was built using the Seurat::FindNeighbors function. Graph-based clustering of the Fast MNN-reduced data was performed using the Seurat::FindClusters function (Louvain algorithm). Projection of the cells on a 2D map was performed with uniform manifold approximation and projection (UMAP) using the Seurat::RunUMAP function. Cell annotation was performed using LungMAP mouse lung Cellref as the reference (LungMAP_MouseLung_CellRef.v1.1). Anchors were identified using Seurat::FindTransferAnchors. Labels were transferred from reference and added to query object metadata using Seurat::TransferData and Seurat::AddMetaData, respectively. Similarly, label transfer was performed from the control to the *Lats1/2*-Mosaic mutant data. Cells with a

predicted score (predicted.score.max) of more than 0.8 in *Lats1/2*-mosiac mutants were identified as highly similar to control cells.

Multiomics analysis

Multiomics was performed using the Chromium Next GEM Single Cell Multiome ATAC + Gene Expression (10x Genomics) following the manufacturer's instructions.

Raw sequencing reads were processed using the 10x Genomics Cell Ranger Arc (v2.0.2) pipeline. Reads were aligned with cellranger-arc count to the mm10 mouse reference genome. For downstream analysis, both the Signac R package (v1.14.0) and the Seurat R package (v5.2.1) were used. For snATAC-seq, nuclei with a read count more than 100000, or less than 1800, or nucleosome signals more than 2, and with transcription factor enrichment scores less than 1 were excluded. For snRNA-seq, nuclei with a read count of more than 25000 or less than 1000 were excluded. For epithelial cell analysis, we aggregated $EPCAM^{+}$ nuclei, and clusters that expressed lineage markers for hematopoietic, endothelial, mesenchymal, and mesothelial nuclei were removed. Variable genes for dimensionality reduction were selected using Seurat::FindVariableGenes (nfeatures = 2000) for the snRNA-seq assay. Variable peaks for dimensionality reduction were selected using Signac::FindTopFeatures (with a minimum cut-off of 5) of the snATAC-seq assay. Dimensionality reduction of snATAC-seq was done with the Latent Semantic Indexing (LSI) method. Multimodal data from snATAC-seq and snRNA-seq were integrated using the Signac::FindMultiModalNeighbors function to construct a joint nearest-neighbor (JNN) graph using information from both assay modalities for clustering and visualization. Visualization of the clusters on a 2D map was performed with uniform manifold approximation and projection (UMAP) using the Seurat::RunUMAP function. Differentially

expressed genes of each cluster were identified using the Seurat::FindAllMarkers function. Differentially accessible peaks for the desired group of nuclei were identified using the Seurat::FindMarkers function with the Likelihood Ratio Test (LR test), requiring a minimum presence in the tested group of nuclei of at least 5%. The peaks were considered significantly different if they had a p-value of less than 0.005 and were present in at least 20% of the tested group of nuclei. Visualization of the peaks was done using the Signac::CoveragePlot function.

Enriched motifs within the test group of cells were identified using the Signac::FindMotifs function. Specific peaks within the differentially accessible regions (DARs) where each motif is enriched were identified, separated, and annotated to the nearest transcription start site (TSS) using the annotatePeak function from the ChIPseeker package. Peak annotations were then matched to the top 10% (fold change) of differentially expressed genes (DEGs) or transcription factors (TFs) within the DEGs between the test groups.

Acknowledgments

We thank Tatsuya Tsukui for invaluable suggestions on experimental procedures; Jianying Li for technical assistance; Kaveh Ashrafi, Andy Chang, Peng He, and Tatsuya Tsukui for their insightful comments on the manuscript. Some data for this study were acquired at the Nikon Imaging Center at CVRI. This work was supported by grants (R01 HL157446) from the National Institutes of Health to P.T.C.

Author contributions

K.Z., M.B., Y.Z., E.Y., and P.T.C designed the study. K.Z., M.B., Y.Z., E.Y., S.A.W., and T.A. performed the experiments. K.Z., M.B., Y.Z., E.Y., S.A.W., and T.A. analyzed the data. K.Z., Y.Z., and P.T.C. wrote the manuscript. P.T.C. supervised the research.

Declaration of interests

The authors declare that they have no conflict of interest.

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Figure Legends

Fig. 1 The distal SOX9^{+} progenitors control lung size

(a, b) Whole-mount imaging of lungs (ventral view) from *Sftpc*$^{Cre/+}$*; ROSA26*$^{mTmG/+}$ (control) and *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Sftpc*$^{Cre/+}$*; ROSA26*$^{mTmG/+}$ (mutant) mice at postnatal (P) day 0. The GFP signal from the *ROSA26* locus was induced by *Sftpc*^{Cre}. It has been noted that GFP expression from the *ROSA26*^{mTmG} reporter mice can be induced by low levels of Cre, at which conversion of floxed alleles into null alleles may not occur. While all epithelial cells in *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Sftpc*$^{Cre/+}$*; ROSA26*$^{mTmG/+}$ lungs were labeled by GFP, removal of epithelial *Lats1/2* was mosaic. (c) Measurement of the wet weight of lungs from control, *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Sftpc*$^{Cre/+}$ and *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Shh*$^{Cre/+}$mice at 14.5 and 18.5 *days post-coitus* (*dpc*). The wet weight of *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Sftpc*$^{Cre/+}$ lungs was only slightly less than that of control lungs at 18.5 *dpc*. By contrast, the wet weight of *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Shh*$^{Cre/+}$ lungs was a small fraction of that of control lungs. Of note, loss of one, two, or three alleles of *Lats1/2* by *Sftpc*^{Cre} or *Shh*^{Cre} did not result in any apparent lung defects, consistent with a functional redundancy between *Lats1* and *Lats2*. (d, e) Whole-mount imaging of dissected lungs from *Sftpc*$^{Cre/+}$*; ROSA26*$^{mTmG/+}$ (control), *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Sftpc*$^{Cre/+}$*; ROSA26*$^{mTmG/+}$ (mutant) mice at 16.5 *dpc*. The images showed a surface view of the distal part of the lung, where the edge of the lung was visible. EGFP was activated from the *ROSA26*$^{mTmG/+}$ allele in almost all lung epithelial cells except those in the trachea; tdTomato marked all non-epithelial cells. (f, g) Immunostaining of lung sections collected from control and mutant mice at 18.5 *dpc*. SCGB1A1 (CC10) marked club (Clara) cells; acetylated tubulin (Ac-tub) marked ciliated cells in the airways. (h, i) Whole-mount immunostaining of lungs from control and mutant lungs at P0. The branching pattern was disrupted, and saccules failed to form in the mutant lungs. (j-o) Immunostaining of lung sections collected from control

and mutant mice at 16.5 *dpc* and P0. SFTPC labeled alveolar epithelial type 2 (AT2) cells, and HOPX detected alveolar epithelial type 1 (AT1) cells. PDGFRA marked fibroblasts and PDGFRB characterized pericytes. The mutant lungs were distinguished by a stratified airway epithelium that was dispersed and occupied by AT1 cells. (p) Schematic diagram of the production of the conducting airways and the alveoli from the distal SOX9^{+} progenitors through Hippo signaling.

All values are mean ± SEM. (*) $p < 0.05$; (***) $p < 0.001$; ns, not significant (unpaired Student's *t*-test).

Scale bars, 1 mm (a, b), 100 μm (d, e), 50 μm (f, g), 100 μm (h-m), 25 μm (n, o).

Fig. 2 A Lats1/2–YAP/TAZ axis regulates lung development

(a-c) Whole-mount imaging of dissected lungs from *Sftpc*$^{Cre/+}$*; ROSA26*$^{mTmG/+}$ (control), *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Sftpc*$^{Cre/+}$*; ROSA26*$^{mTmG/+}$ (mutant), and *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Yap*$^{f/+}$*; Taz*$^{f/+}$*; Sftpc*$^{Cre/+}$*; ROSA26*$^{mTmG/+}$ (rescued) mice at 18.5 *days post-coitus* (*dpc*). The images showed a surface view of the distal part of the lung, where the edge of the lung was visible. EGFP was activated from the *ROSA26*$^{mTmG/+}$ allele in almost all lung epithelial cells except those in the trachea; tdTomato marked all non-epithelial cells. Removal of one allele of *Yap* and *Taz* partially rescued the lung defects in the mutant lungs. (d-i) Immunostaining of lung sections collected from control, mutant, and rescued mice at 18.5 *dpc*. SCGB1A1 (CC10) marked club (Clara) cells; acetylated tubulin (Ac-tub) marked ciliated cells in the airways, SFTPC labeled alveolar epithelial type 2 (AT2) cells, and HOPX detected alveolar epithelial type 1 (AT1) cells. Rescue of the lung phenotypes was associated with the appearance of cell types in the conducting airways and the saccules. (j) Quantification of the percentage of SOX2^{+}, SCGB1A1^{+}, and Ac-

tub^{+} cells in the airways and SFTPC^{+}, HOPX^{+}, and SFTPC^{+}HOPX^{+} cells in the saccules of control, mutant, and rescued mice at 18.5 *dpc*. (k) Schematic diagram of a genetic pathway of Hippo signaling that controls lung development.

All values are mean ± SEM. (*) $p < 0.05$; (***) $p < 0.001$; ns not significant (Two way ANOVA).

Scale bars, 100 μm (a-c), 25 μm (d-i).

Fig. 3 YAP/TAZ activity determines the cell fates of the conducting airways

(a-d) Immunofluorescence of lung sections from control and *Lats1$^{f/f}$; Lats2$^{f/f}$; Sftpc$^{Cre/+}$; ROSA26$^{mTmG/+}$* (mutant) mice at 14.5 *days post-coitus* (*dpc*). *Lats1/2* removal activated YAP/TAZ, leading to the degradation of phospho-YAP (pYAP). Loss of pYAP is thus indicative of YAP/TAZ activation. pYAP was detected along the proximo-distal axis of lung branches in controls. By contrast, in the mutant lungs, pYAP was retained at the distal tips of lung branches (white arrowheads in c), but it was absent from the proximal part of the lung branches. CATNB (β-catenin) labeled adherens junctions. (e, f) Whole-mount immunostaining of lungs from control and *Lats1$^{f/f}$; Lats2$^{f/f}$; Sftpc$^{Cre/+}$; ROSA26$^{mTmG/+}$* mice at 14.5 *dpc*. White arrowheads in (f) pointed to residual pYAP signals at the distal tips. The boxed areas were enlarged to visualize Ecad (epithelial) and pYAP. (*) marked epithelial pYAP in control lungs or residual epithelial pYAP in the mutant lungs, while (+) depicted regions with reduced epithelial pYAP in the mutant lungs. Note that reduced epithelial pYAP in the mutant lungs was apparent in comparison to mesenchymal pYAP. Ecad (E-cadherin) labeled adherens junctions. (g, h) Schematic diagrams of pYAP distribution along the lung branches in control and mutant lungs. (i) Quantification of the relative pYAP intensity in the proximal and distal domains of lung branches in control (CL)

and mutant (MT) lungs at 14.5 *dpc*. (j, k) Whole-mount immunostaining of representative lungs (ventral view) from control and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$; *ROSA26*$^{mTmG/+}$ (mutant) mice at 14.5 *dpc*. SOX9 labeled the distal airway epithelium, while SOX2 labeled the proximal airway epithelium. The mutant lungs appeared slightly smaller but denser. No difference in proliferation was noted at 14.5 *dpc*. Together, the wet weights were similar between the control and mutant lungs. (l, m) Immunostaining of lung sections from control and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$; *ROSA26*$^{mTmG/+}$ (mutant) mice at 14.5 *dpc*. SOX9^{+} signal was retained in the distal lung buds but reduced in the proximal part of lung branches (white arrowheads in (m)) in the mutants. (n, o) Schematic diagrams of SOX9 and SOX2 distribution in control and mutant lungs. Note that one SOX9^{+} distal domain contains multiple distal buds. (p) Quantification of the relative SOX9^{+} area in each distal domain or distal bud. (q-t) Whole-mount immunostaining of lungs (ventral view for (q) and (s)) from control and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$; *ROSA26*$^{mTmG/+}$ (mutant) mice at 14.5 *dpc*. Bifurcation in the mutant lungs (white arrows in u) was preserved while domain branching was disrupted. (u) Quantification of the number of branches through domain branching or bifurcation in the LL1 branch of control (CL) and mutant (MT) lungs at 14.5 *dpc*. (v, w) Immunofluorescence of lung sections from control and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ (mutant) mice at 16.5 *dpc*. NKX2.1 marked lung epithelial cells, while SMA labeled mesenchymal myofibroblasts. The multilayer epithelium (asterisks) was observed in the mutant lungs, which was also revealed in Fig. 1k and Fig. 2h. (x) Schematic diagram of lung size control through bifurcation regulated by Hippo signaling.

All values are mean ± SEM. (*) $p < 0.05$; (**) $p < 0.01$; (***) $p < 0.001$; ns, not significant (unpaired Student's *t*-test).

Scale bars, 50 μm (a-d), 25 μm (e, f), 0.5 mm (j, k, q, s), 50 μm (l, m), 100 μm (r, t), 50 μm (v, w)

Fig. 4 YAP/TAZ activity regulates the SOX9–SOX2 transition

(a-d) Whole-mount immunostaining of dissected lungs (ventral view for (a) and (b)) from control and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$; *ROSA26*$^{mTmG/+}$ (mutant) mice at 16.5 *days post-coitus* (*dpc*). SOX9 and SOX2 marked the distal and proximal airway epithelium, respectively. A reduction in SOX9 and SOX2 signals was discerned in the more proximal regions, while the SOX9 signal was preserved in the distal tips of the mutant lungs. (e, f) Immunostaining of lung sections from control and mutant mice at 16.5 *dpc*. In control lungs, the SOX9^{-}SOX2^{-} region sandwiched between the SOX9^{+} and SOX2^{+} domains became more noticeable than in earlier stages. In the absence of *Lats1/2*, the SOX9^{-}SOX2^{-} region was significantly expanded. White arrowheads in (f) pointed to residual distal SOX9^{+} cells. (g, h) Schematic diagrams depicting the distribution of the SOX9^{+}, SOX9^{-}SOX2^{-}, and SOX2^{+} domains in control and mutant lungs. (i) Quantification of the SOX2^{+} area within the domain that contains both SOX2^{+} and SOX9^{-}SOX2^{-} cells in control and mutant lungs at 14.5 and 16.5 *dpc*. (j) Quantification of the SOX9^{-}SOX2^{-} domain in control and mutant lungs at 14.5 and 16.5 *dpc*. The relative length refers to the relative length between control and mutant lungs measured in Image J. (k) Heatmap of gene expression by bulk RNA-seq analysis from control (CT) and mutant (MT) lungs at 13.5 *dpc*. Out of the 919 genes with differential expression, 308 genes were downregulated and 611 genes were upregulated in the mutant lungs. The number next to the gene indicates its position in the heatmap. 1-308 are genes downregulated, and 309-919 are genes upregulated in the mutant lungs. Canonical YAP targets, such as *Ctgf*, *Ajuba*, and *Cyr61*, were upregulated in the mutant lungs. (l) qPCR analysis

of control and mutant lungs at 13.5 *dpc*. The transcript levels of canonical YAP targets, such as *Ctgf*, *Ajuba*, and *Cyr61*, were upregulated in the mutant lungs. (m) Volcano plots of up-regulated and down-regulated genes in the mutant lungs at 13.5 *dpc*. Several regulators of the cell cycle (*e.g.*, *Cdkn2b*) or growth-promoting pathways (*e.g.*, *Wnt*) were upregulated in the mutant lungs. Blue dots represent the most down-regulated genes with expression levels less than 3.5 fold, while red dots represent the most up-regulated genes with expression levels greater than 3.5 fold. (n) Schematic diagram of the production of $SOX2^+$ cells from the distal $SOX9^+$ progenitors through regulating YAP/TAZ levels.

All values are mean ± SEM. (*) $p < 0.05$; (***) $p < 0.001$ (unpaired Student's *t*-test).

Scale bars, 1 mm (a, b), 100 μm (c, d), 100 μm (e, f).

Fig. 5 YAP/TAZ activity controls the AT1–AT2 fate

(a) Schematic diagram of the time course of tamoxifen (TAM) administration and lung collection for control and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sox9*$^{CreER/+}$ lungs. *dpc*, *days post-coitus*. (b, c) Immunofluorescence of representative areas in control and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sox9*$^{CreER/+}$ lungs. AT1 ($HOPX^+$) cells were prevalent in the mutant lungs, whereas AT2 ($SFTPC^+$) cells were scant. (d) Quantification of the number of $SFTPC^+$ (AT2) cells, $HOPX1^+$ (AT1) cells, and $SFTPC^+HOPX^+$ cells in control and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sox9*$^{CreER/+}$ lungs collected at 18.5 *dpc*. Loss of *Lats1/2* led to an increased ratio of AT1 to AT2 cells. (e) Schematic diagram of the time course of tamoxifen administration and lung collection for control and *Yap*$^{f/f}$; *Taz*$^{f/f}$; *Sox9*$^{CreER/+}$ lungs. (f, g) Immunofluorescence of representative areas in control and *Yap*$^{f/f}$; *Taz*$^{f/f}$; *Sox9*$^{CreER/+}$ lungs. AT2 cells were prevalent in the non-cystic region. The cystic wall was lined primarily by AT1 cells (not shown). (h) Quantification of the number of $SFTPC^+$ (AT2) cells, $HOPX^+$ (AT1)

cells, and SFTPC$^+$HOPX$^+$ cells in control and *Yap$^{f/f}$; Taz$^{f/f}$; Sox9$^{CreER/+}$* lungs collected at 18.5 *dpc*. Loss of *Yap/Taz* led to an increased ratio of AT2 to AT1 cells. (i) Schematic diagram of the time course of tamoxifen administration and lung collection for control and *Yap$^{f/f}$; Taz$^{f/f}$; Sftpc$^{CreER/+}$* lungs. (j, k) Immunofluorescence of representative areas in control and *Yap$^{f/f}$; Taz$^{f/f}$; Sftpc$^{CreER/+}$* lungs. (l) Quantification of the number of SFTPC$^+$ (AT2) cells, HOPX1$^+$ (AT1) cells, and SFTPC$^+$HOPX$^+$ cells in control and *Yap$^{f/f}$; Taz$^{f/f}$; Sftpc$^{CreER/+}$* lungs collected at 18.5 *dpc*. Likewise, the loss of *Yap/Taz* led to an increased ratio of AT2 to AT1 cells. (m) Schematic diagram of differentiating the distal SOX9$^+$ progenitors toward the AT1 and AT2 fate by YAP/TAZ levels.

All values are mean ± SEM. (**) $p < 0.01$; (***) $p < 0.001$; ns, not significant (unpaired Student's *t*-test).

Scale bars, 25 μm (b, c, j, k), 25 μm (f, g).

Fig. 6 Multiple transitional states mediate the SOX9–SOX2 transition to generate the conducting airways

(a) UMAP (uniform manifold approximation and projection) visualization of major cell clusters from control lungs at 14.5 *days post-coitus* (*dpc*) profiled by scRNA-seq. Only lung epithelial cells (*Epcam*$^+$) were shown. Cells that expressed the featured genes were indicated. Pseudotime analysis was used to map the trajectories of cell clusters. The color gradient, ranging from dark blue to light yellow, indicates the progression of cell states over pseudotime. (b) Dot plot of a partial list of markers that were used to identify cell clusters in this study. (c) Schematic diagrams of the trajectories of cell clusters from the SOX9$^+$ to SOX2$^+$ states in control lungs at 14.5 *dpc*. Blue genes are those that are upregulated as cells transition from the left cluster to the

right. Red genes are those that are downregulated as cells transition from the left cluster to the right. Additional differentially expressed genes (DEGs) between different cell clusters at 14.5 *dpc* are listed in Supplementary Fig. 9. (d) Volcano plots of DEGs between different cell clusters in control lungs at 14.5 *dpc*. DEGs in a given cluster carry the same color as shown in (a). The y-axis represents the average change in gene expression for a given gene between the two designated clusters. The x-axis represents the difference in the percentage of cells expressing the given gene between the two clusters shown. Changes in gene expression are statistically significant ($p < 0.05$) for all depicted DEGs. (e) UMAP visualization of major cell clusters from the lungs of *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ (mutant) mice at 14.5 *dpc* profiled by scRNA-seq. Only lung epithelial cells (*Epcam*$^{+}$) were shown. Cells that expressed the featured genes were indicated. Pseudotime analysis was included to map the trajectories of cell clusters. The color gradient, ranging from dark blue to light yellow, indicates the progression of cell states over pseudotime. (f) Dot plot of a partial list of markers that were used to identify cell clusters in this study. (g) Schematic diagrams of the trajectories of cell clusters in the mutant lungs at 14.5 *dpc*. The trajectory of SOX9^{+} to SOX2^{+} transition was present in the mutant lungs. A new trajectory of SOX9^{+} to HOPX^{+}AGER^{+} transition was found in the mutant lungs. (h) Volcano plots of DEGs between different cell clusters in the mutant lungs at 14.5 *dpc*. DEGs in a given cluster carry the same color as shown in (e). The y-axis represents the average change in gene expression for a given gene between the two designated clusters. The x-axis represents the difference in the percentage of cells expressing the given gene between the two clusters shown. Changes in gene expression are statistically significant ($p < 0.05$) for all depicted DEGs.

Fig. 7 Multiple transitional states mediate the fate transition from SOX9$^+$ progenitors to the alveolar epithelial cells

(a) UMAP (uniform manifold approximation and projection) visualization of major cell clusters from control lungs at 17.5 *days post-coitus* (*dpc*) profiled by scRNA-seq. Only lung epithelial cells (*Epcam*$^+$) were shown. Cells that expressed the featured genes were indicated. Pseudotime analysis was used to map the trajectories of cell clusters. The color gradient, ranging from dark blue to light yellow, indicates the progression of cell states over pseudotime. (b) Dot plot of a partial list of markers that were used to identify cell clusters in this study. (c) Schematic diagrams of the trajectories of cell clusters from the SOX9$^+$ to HOPX$^+$AGER$^+$ (AT1) transition in control lungs at 17.5 *dpc*. Blue genes are those that are upregulated as cells transition from the left cluster to the right. Red genes are those downregulated as cells transition from the left cluster to the right. Additional differentially expressed genes (DEGs) between different cell clusters at 17.5 *dpc* are listed in Supplementary Fig. 13. (d) Volcano plots of DEGs between different cell clusters in control lungs at 17.5 *dpc*. DEGs in a given cluster carry the same color as shown in (a). The y-axis represents the average change in gene expression for a given gene between the two designated clusters. The x-axis represents the difference in the percentage of cells expressing the given gene between the two clusters shown. Changes in gene expression are statistically significant ($p < 0.05$) for all depicted DEGs. (e) UMAP visualization of major cell clusters from lungs from *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ (mutant) mice at 17.5 *dpc* profiled by scRNA-seq. Only lung epithelial cells (*Epcam*$^+$) were shown. Cells that expressed the featured genes were indicated. Pseudotime analysis was included to map the trajectories of cell clusters. The color gradient, ranging from dark blue to light yellow, indicates the progression of cell states over pseudotime. (f) Dot plot of a partial list of markers that were used to identify cell clusters in this

study. (g) Schematic diagrams of the trajectories of cell clusters from the SOX9$^+$ to HOPX$^+$AGER$^+$ (AT1) transition in the mutant lungs at 17.5 *dpc*. Additional clusters in the AT1 states were uncovered in the mutant lungs compared to the control lungs. (h) Volcano plots of DEGs between different cell clusters in the mutant lungs at 17.5 *dpc*. DEGs in a given cluster carry the same color as shown in (e). The y-axis represents the average change in gene expression for a given gene between the two designated clusters. The x-axis represents the difference in the percentage of cells expressing the given gene between the two clusters in question. Changes in gene expression are statistically significant ($p < 0.05$) for all depicted DEGs. (i) A partial list of representative genes that were used to identify AT1 cells at four differentiation states. State 1: cells from *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ lungs at 14.5 *dpc*. State 2: cells from control lungs at 17.5 *dpc*. State 3: cells from *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ lungs at 17.5 *dpc*. State 4: cells from the control lungs of neonatal or adult mice. (j) Volcano plots of DEGs between two different AT1 states at the stages as indicated. DEGs in a given cluster carry the same color. The y-axis represents the average change in gene expression for a given gene between the two designated clusters. The x-axis represents the difference in the percentage of cells expressing the given gene between the two clusters in question. Changes in gene expression are statistically significant ($p < 0.05$) for all depicted DEGs.

Fig. 8 A model of mouse lung development that is regulated by YAP/TAZ activity

(a) Schematic diagram of the main findings of this study. Hippo signaling (YAP/TAZ levels) regulates the size and differentiation of the distal SOX9$^+$ progenitors. Bifurcation at the distal tip forms the basis of lung size control. YAP/TAZ levels also control the differentiation of SOX9$^+$ progenitors through transcriptional states to generate SOX2$^+$ cells that form the conducting

airways, or later to generate AT1/AT2 cells that produce alveoli. (b) A model illustrating how YAP/TAZ activity controls lung development, in particular, the SOX9 to SOX2 transition to produce the conducting airways. Lower YAP/TAZ activity (as in *Yap*$^{f/f}$; *Shh*$^{Cre/+}$ lungs) fails to maintain SOX9^{+} progenitors and blocks bifurcation and domain branching. Higher YAP/TAZ activity (*e.g.*, loss of *Lats1/2*) promotes precocious differentiation of SOX9^{+} progenitors and blocks bifurcation and domain branching. The removal of *Lats1/2* by *Sftpc*^{Cre} is mosaic (as in *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ lungs). Since the distal SOX9^{+} domain is spared, bifurcation is unaffected. In contrast, removal of *Lats1/2* by *Shh*^{Cre} (as in *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Shh*$^{Cre/+}$ lungs) affects both domain branching and bifurcation. As a result, YAP/TAZ is depicted to affect both domain branching and bifurcation. (c) A model of how YAP/TAZ activity controls lung development, in particular, the production of AT1 and AT2 cells to produce the alveoli. Lower YAP/TAZ activity (*e.g.*, loss of *Yap/Taz* induced by tamoxifen as in *Yap*$^{f/f}$; *Taz*$^{f/f}$; *Sox9*$^{CreER/+}$ and *Yap*$^{f/f}$; *Taz*$^{f/f}$; *Sftpc*$^{CreER/+}$ lungs) increases the AT2 to AT1 ratio. Higher YAP/TAZ activity (*e.g.*, loss of *Lats1/2* induced by tamoxifen as in *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sox9*$^{CreER/+}$ lungs) promotes the differentiation of AT1 cells.

Supplementary Figure Legends

Supplementary Fig. 1 The SOX9$^+$ domain is reduced when the Hippo pathway is perturbed

(a, b) Whole-mount immunostaining of dissected lungs (ventral view) from control and *Yap$^{f/f}$; Shh$^{Cre/+}$* mice at 13.5 *days post-coitus* (*dpc*). SOX9 and SOX2 marked the distal and proximal airway epithelium, respectively. A reduction in SOX9 and SOX2 signals was discerned when *Yap* was eliminated. (c, d) Whole-mount immunostaining of dissected lungs from control and *Yap$^{f/f}$; Taz$^{f/f}$; Sox9$^{Cre/+}$* (mutant) mice at 14.5 *dpc*. *Sox9^{Cre}* converted a floxed allele of *Yap* (*Yap^f*) or *Taz* (*Taz^f*) into a null allele. *Taz* is a minor player in lung branching, and the removal of *Taz* did not exacerbate the lung defects resulting from *Yap* loss. Distal lung cysts were present in the mutant lungs, resulting in a reduced size of the SOX9$^+$ pool. (e, f) Whole-mount immunostaining of dissected lungs from control and *Lats1$^{f/f}$; Lats2$^{f/f}$; Shh$^{Cre/+}$* mice at 12.5 *dpc*. Both the SOX2$^+$ and SOX9$^+$ domains were severely diminished. (g, h) Whole-mount immunostaining of dissected lungs from control and *Lats1$^{f/f}$; Lats2$^{f/f}$; Shh$^{Cre/+}$* mice at 15.5 *dpc*. The size reduction of both the SOX2$^+$ and SOX9$^+$ domains persisted as lung development proceeded.

Scale bars, 0.5 mm (a-f), 1 mm (g, h).

Supplementary Fig. 2 Loss of one copy of *Yap* and *Taz* partially rescues the lung defects in *Lats1$^{f/f}$; Lats2$^{f/f}$; Shh$^{Cre/+}$* mice

(a-c) Whole-mount imaging of lungs (ventral view) from control, *Lats1$^{f/f}$; Lats2$^{f/f}$; Shh$^{Cre/+}$; ROSA26$^{mTmG/+}$* (mutant) and *Lats1$^{f/f}$; Lats2$^{f/f}$; Yap$^{f/+}$; Taz$^{f/+}$; Shh$^{Cre/+}$; ROSA26$^{mTmG/+}$* (rescued) mice at 18.5 *days post-coitus* (*dpc*). The GFP signal from the *ROSA26* locus was induced by *Shh^{Cre}*. (d-i) Immunostaining of lung sections from control, mutant, and rescued

mice. SCGB1A1 marked club cells, ac-tubulin (ac-tub) labeled ciliated cells, SFTPC identified alveolar type 2 (AT2) cells, and T1α characterized alveolar type 1 (AT1) cells. (j, k) Quantification of cell types in the airways and saccules of control, mutant, and rescued mice.

All values are mean ± SEM. (***) $p < 0.001$; ns not significant (two-way ANOVA).

Scale bars, 1 mm (a-c), 25 μm (d-f), 100 μm (g-i).

Supplementary Fig. 3 The proliferation rate is not reduced in the SOX9⁻SOX2⁻ domain of *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Sftpc*$^{Cre/+}$ lungs

(a-l) Immunostaining of lung sections from control and *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Sftpc*$^{Cre/+}$ mice at 14.5 *days post-coitus* (*dpc*). SOX9 and SOX2 marked the distal and proximal airway epithelium, respectively. EdU labeled proliferating cells. (m) Quantification of the relative cell proliferation in different domains of the lung branches, as indicated.

All values are mean ± SEM. (*) $p < 0.05$; ns not significant (unpaired Student's *t*-test).

Scale bars, 50 μm (a-l).

Supplementary Fig. 4 Early lung branching is not disrupted in *Lats1/2*-mosaic lungs

(a-f) Whole-mount immunostaining of representative lungs (ventral view) from control and *Lats1*$^{f/f}$*; Lats2*$^{f/f}$*; Sftpc*$^{Cre/+}$*; ROSA26*$^{mTmG/+}$ (*Lats1/2*-mosaic) mice at 12.5 *days post-coitus* (*dpc*). SOX9 labeled the distal airway epithelium, while SOX2 labeled the proximal airway epithelium. No apparent difference in the branching pattern was noted between control and mutant lungs at 12.5 *dpc*.

Scale bars, 0.5 mm (a-f).

Supplementary Fig. 5 Pathway analysis of bulk RNA-seq data reveals changes in cellular properties in the absence of *Lats1/2*

Pathway analysis of bulk RNA-seq data from control and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ mice at 13.5 *days post-coitus* (*dpc*). Pathways regulating focal adhesion, cytoskeleton, cell motility, and cell migration were upregulated in the absence of *Lats1/2*. Each graph shows the top 15 pathways that are enriched. The bold text and asterisk mark pathways with a p-value less than 0.05.

Supplementary Fig. 6 Re-analysis of published scRNA-seq data at different stages of mouse lung development

UMAP (uniform manifold approximation and projection) visualization of major cell clusters from analysis of scRNA data in this study and those previously published. Cells that expressed the featured genes were indicated.

Supplementary Fig. 7 Cell clusters in control and *Lats1/2*-deficient lungs during branching are distinguished by sets of markers

(a) A combined scRNA-seq analysis of control (CT) and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ (mutant, MT) lungs at 14.5 *days post-coitus* (*dpc*). The left panel showed the composite of cell clusters, while the right panel showed the respective cell clusters for control or mutant lungs. (b) Heatmap of cell clusters in control and *Lats1/2*-deficient lungs. Cluster 2 in control and mutant lungs shares specific patterns of gene expression (heatmap), but could also be distinguished by other unique sets of gene expression. For instance, clusters 2 and 5 in the mutant lungs share specific patterns of gene expression that are not present in cluster 2 of the control lungs.

Supplementary Fig. 8 scRNA-seq analysis of control and *Lats1/2*-mosaic lungs reveals the distribution and trajectory of mutant cells

(a) UMAP (uniform manifold approximation and projection) visualization of the major cell clusters from lungs of control (CT) and *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ (mutant, MT) mice at 14.5 *days post-coitus* (*dpc*) profiled by scRNA-seq. Cells in the mutant lungs with a transcriptome similar to that in the control lungs were labeled, representing wild-type cells in the mutant lungs at 14.5 *dpc*. Note that the cell clusters depicted here correspond to those in Fig. 6. (b) UMAP visualization of representative YAP targets (*e.g.*, *Ctgf*, *Ajuba*, and *Amotl2*) in control and mutant lungs at 14.5 *dpc*. (c) UMAP visualization of the major cell clusters from control and mutant lungs at 17.5 *dpc*. Cells in the mutant lungs with a transcriptome similar to that in the control lungs were labeled, representing wild-type cells in the mutant lungs at 17.5 *dpc*. Note that the cell clusters depicted here correspond to those in Fig. 7. (d) UMAP visualization of representative YAP targets (*e.g.*, *Ctgf*, *Ajuba*, and *Amotl2*) in control and mutant lungs at 17.5 *dpc*.

Supplementary Fig. 9 Transitional cell states from the SOX9^{+} to SOX2^{+} state are associated with changes in the expression of transcription factors

(a) A partial list of transcription factors, the expression of which was either upregulated (blue) or downregulated (red) between two transitional cell states in control lungs at 14.5 *days post-coitus* (*dpc*) as indicated. For instance, genes colored in blue were upregulated while genes colored in red were downregulated when cells transitioned from cluster 0 to 1. (b) UMAP (uniform manifold approximation and projection) visualization of a select group of transcription factors

from the partial list for the control lungs. (c) A partial list of transcription factors, the expression of which was either upregulated (blue) or downregulated (red) between two transitional cell states in *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ (mutant) lungs at 14.5 *dpc,* as indicated. (d) UMAP visualization of a select group of transcription factors from the partial list for the mutant lungs.

Supplementary Fig. 10 Transcription factor network for cell state transition during SOX9 to SOX2 transition

A transcription factor network that centers on transcription factors, *Rarb*, *Meis2*, *Mxd4, Etv5, E2f7, Sp5,* and *Sox2*, which are differentially expressed between cluster 0 and cluster 1 (Fig. 6a, Supplementary Fig. 9a). The potential targets of these transcription factors shown are differentially expressed genes (DEGs) between cluster 0 and cluster 1 (Fig. 6a, Supplementary Fig. 9a). The blue lines indicate positive regulation, while the red lines indicate negative regulation.

Supplementary Fig. 11 Transitional cell states from the SOX9$^+$ to SOX2$^+$ state are associated with changes in open chromatin

(a) A partial list of motifs identified from multiomics analysis of control lungs at 14.5 *days post-coitus* (*dpc*). These motifs were enriched in SOX9$^+$ cells (relative to SOX2$^+$ cells) within differentially accessible regions (DARs). (b) A partial list of motifs enriched in SOX2$^+$ cells (relative to SOX9$^+$ cells) within DARs. (c) A partial list of differentially expressed genes (DEGs) between the SOX9$^+$ and SOX2$^+$ states that contain the TEAD motif in their regulatory regions.

Supplementary Fig. 12 Re-analysis of published scRNA-seq data at different stages of mouse lung development

UMAP (uniform manifold approximation and projection) visualization of major cell clusters from analysis of scRNA data in this study and those previously published. Cells that expressed the featured genes were indicated.

Supplementary Fig. 13 Cell clusters in control and *Lats1/2*-deficient lungs during sacculation are distinguished by select sets of markers

(a) Heatmap of cell clusters in control lungs at 17.5 *days post-coitus* (*dpc*). (b) Heatmap of cell clusters in *Lats1/2*-deficient lungs at 17.5 *dpc*. While cell clusters can be identified with select sets of markers, whether cell clusters represent functional cell states requires further investigation.

Supplementary Fig. 14 Transitional cell states from the SOX9^{+} state to the alveolar fate are associated with changes in the expression of transcription factors

(a) A partial list of transcription factors, the expression of which was either upregulated (blue) or downregulated (red) between two transitional cell states in control lungs at 17.5 *days post-coitus* (*dpc*) as indicated. For instance, genes colored in blue were upregulated while genes colored in red were downregulated when cells transitioned from cluster 0 to 1. (b) UMAP (uniform manifold approximation and projection) visualization of a select group of transcription factors from the partial list for the control lungs. (c) A partial list of transcription factors, the expression of which was either upregulated (blue) or downregulated (red) between two transitional cell

states in *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ (mutant) lungs at 17.5 *dpc,* as indicated. (d) UMAP visualization of a select group of transcription factors from the partial list for the mutant lungs.

Supplementary Fig. 15 Transcription factor network for cell state transition during AT2 to AT1 transition

A transcription factor network that centers on transcription factors, *Tead4*, *Rarb*, *Cebpa, Etv5,* and *Elf5*, which are differentially expressed between cluster 0 and cluster 1 (Fig. 7a, Supplementary Fig. 14a). The potential targets of these transcription factors shown are differentially expressed genes (DEGs) between cluster 0 and cluster 1 (Fig. 7a, Supplementary Fig. 14a). The blue lines indicate positive regulation, while the red lines indicate negative regulation.

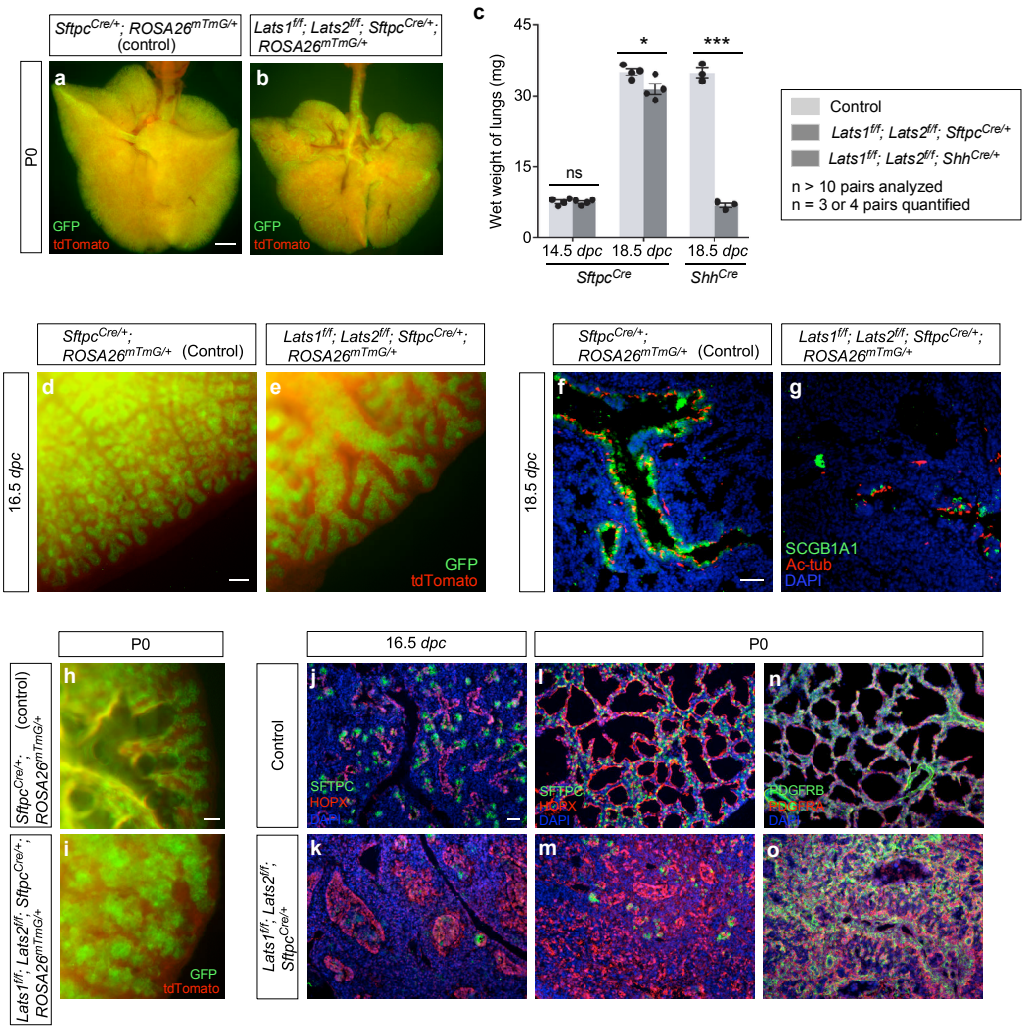
Supplementary Fig. 16 Transitional cell states from the SOX9^{+} state to the alveolar fate are associated with changes in open chromatin

(a) A partial list of motifs identified from multiomics analysis of control lungs at 17.5 *days post-coitus* (*dpc*). These motifs were enriched in AT1^{+} cells (relative to AT2^{+} cells) within differentially accessible regions (DARs). (b) A partial list of motifs enriched in AT2^{+} cells (relative to AT1^{+} cells) within DARs. (c) A partial list of motifs identified in the regulatory regions of differentially expressed genes (DEGs) in AT1^{+} cells (relative to AT2^{+} cells). A partial list of differentially expressed genes (DEGs) between the SOX9^{+} and AT1^{+} states that contain the TEAD motif in their regulatory regions.

Supplementary Fig. 17 Cell clusters in the developing mouse lung are connected to distinct regions of the developing human lung

(a) UMAP (uniform manifold approximation and projection) visualization of representative markers as cells transition from cluster 0 to cluster 2 in control mouse lungs at 14.5 *days post-coitus* (*dpc*) profiled by scRNA-seq. This pattern of gene expression corresponds to the early tip and early stalk in human lungs, respectively. (b) UMAPs of representative markers as cells transition from cluster 0 to cluster 2 in *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ mouse lungs at 14.5 *dpc*. This pattern of gene expression corresponds to the early tip and early stalk in human lungs, respectively. (c) UMAPs of representative markers of cluster 0 in control mouse lungs at 17.5 *dpc*. This pattern of gene expression corresponds to the late tip in human lungs. (d) UMAPs of representative markers of cluster 0 in *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ mouse lungs at 17.5 *dpc*. This pattern of gene expression corresponds to the late tip in human lungs. (e) UMAPs of representative markers of cluster 4 in control mouse lungs at 14.5 *dpc*. This pattern of gene expression corresponds to neuroendocrine cells in human lungs. (f) UMAPs of representative markers of cluster 4 in *Lats1*$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ mouse lungs at 14.5 *dpc*. This pattern of gene expression corresponds to neuroendocrine cells in human lungs.

Zhang et al. Figure 1



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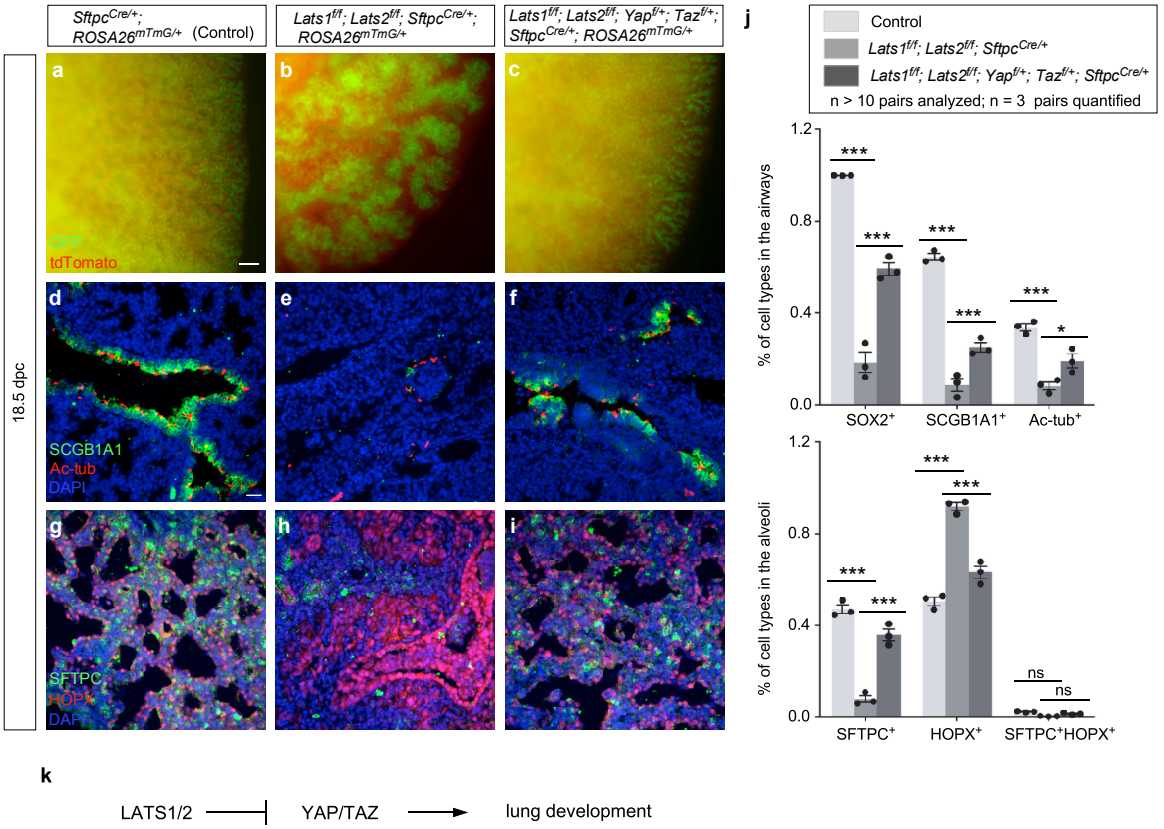

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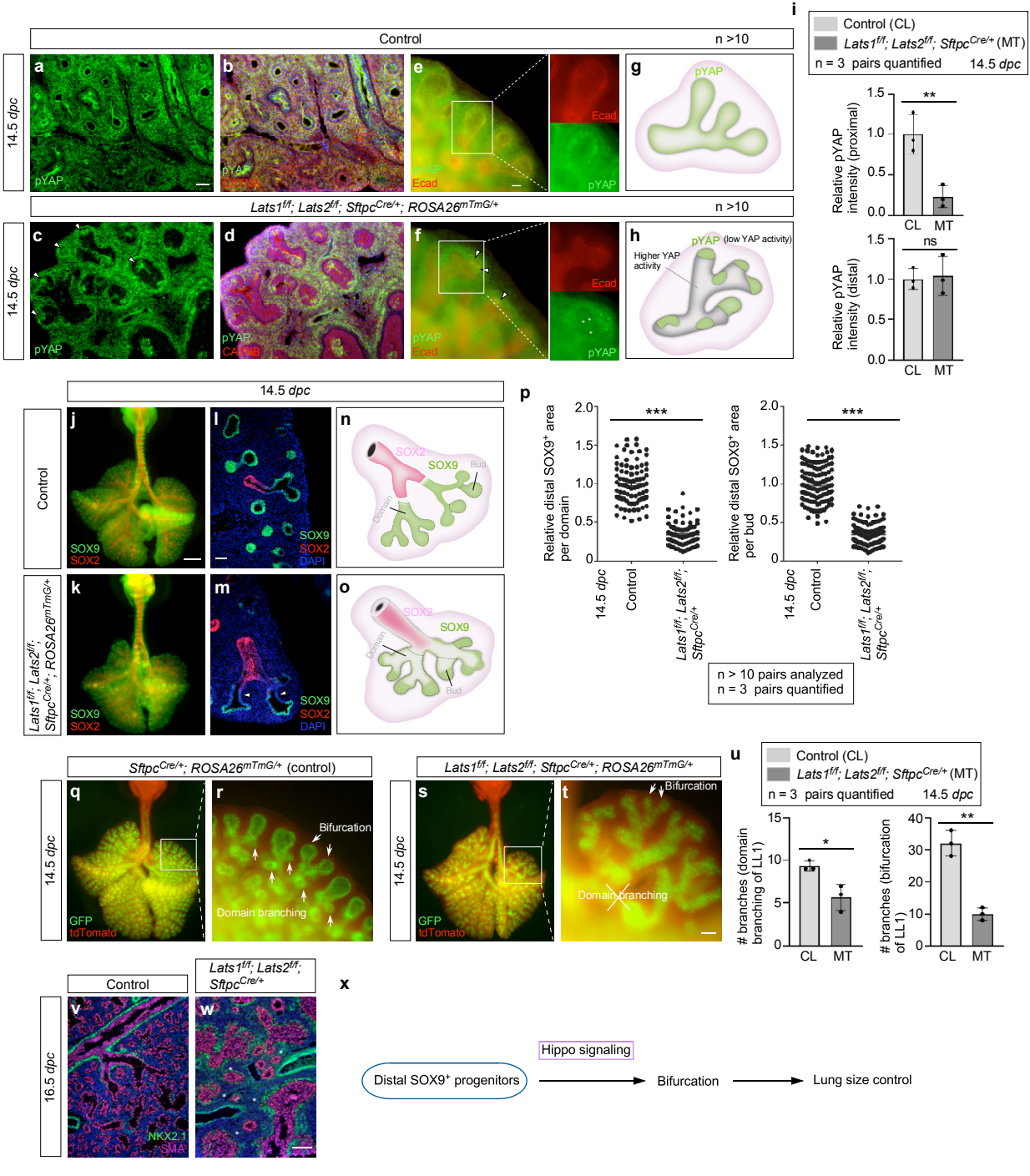

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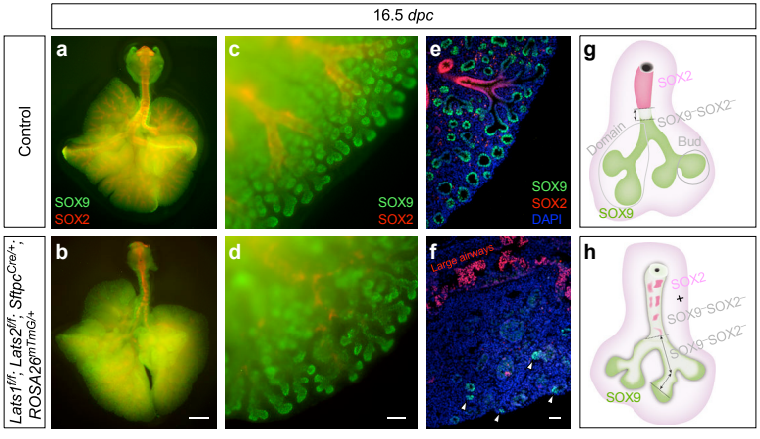
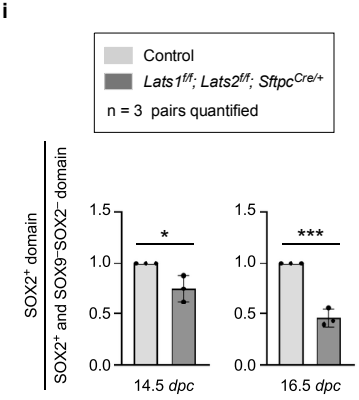
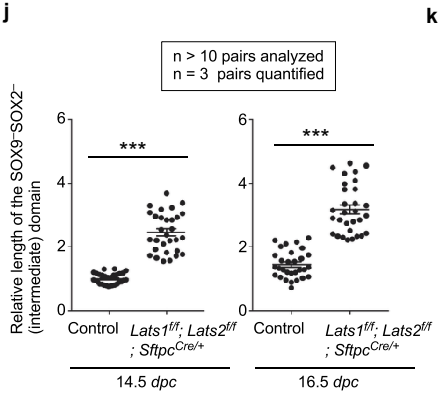
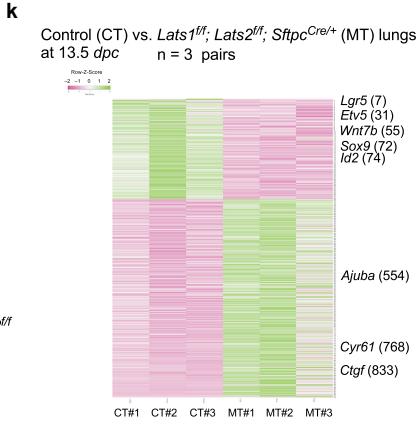
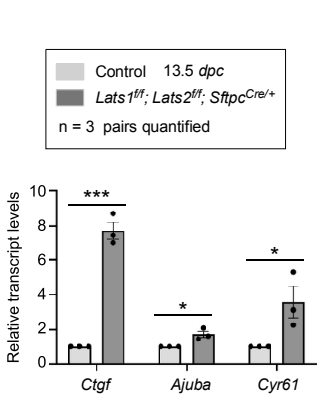
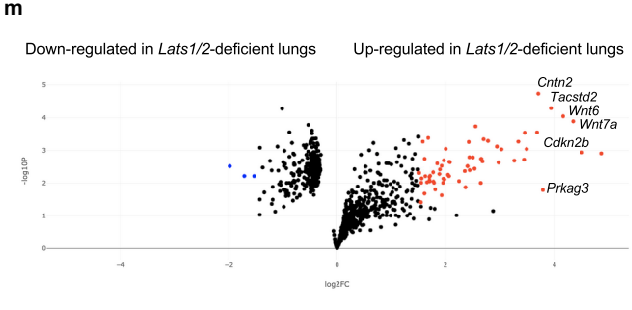


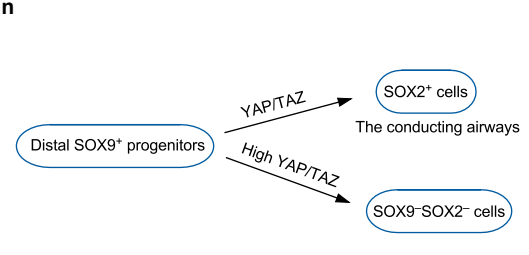




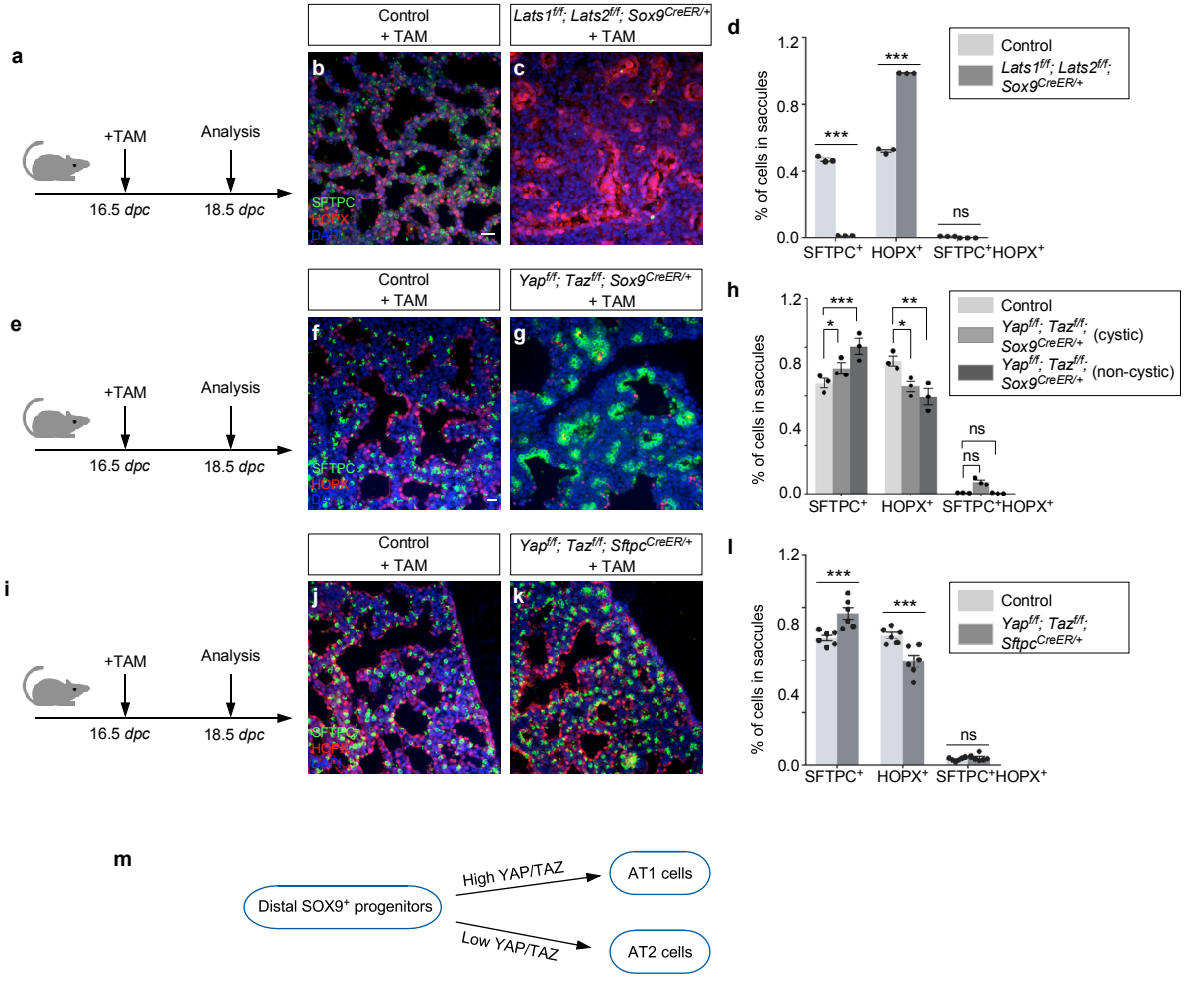








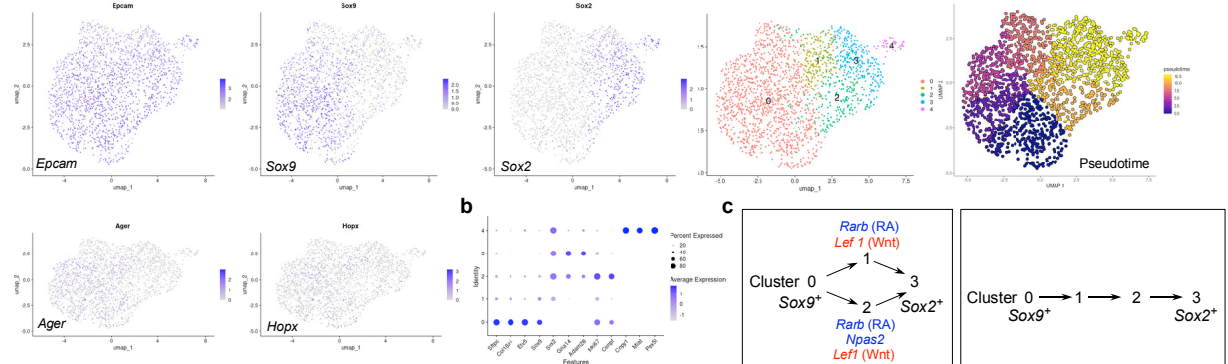
Zhang et al. Figure 5



Zhang et al. Figure 6

a

Control lungs 14.5 *dpc*

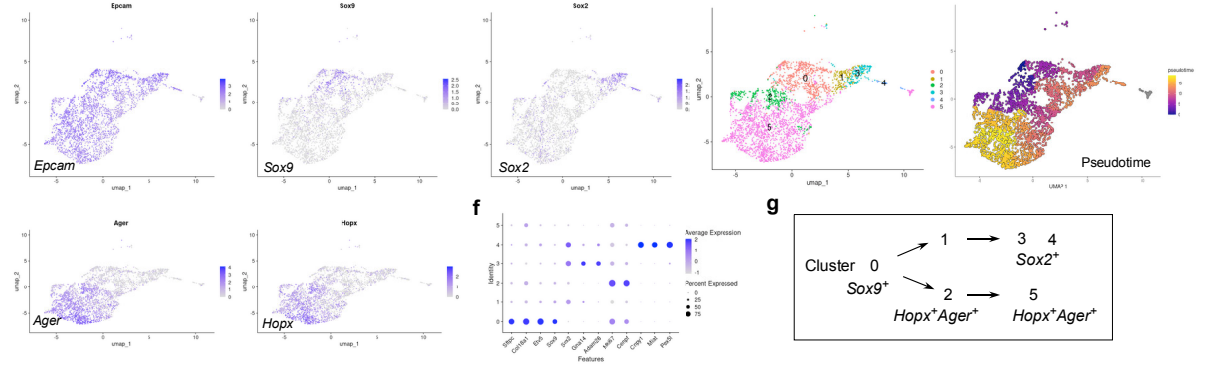


d

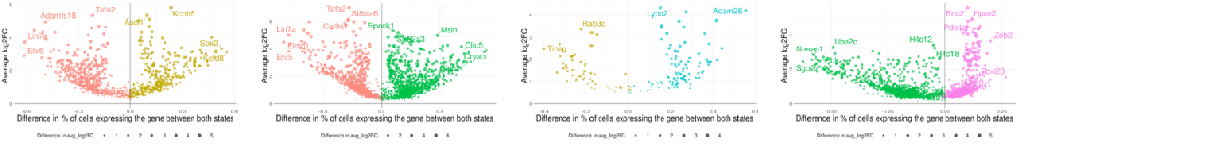
Cluster 0 —— 1 Cluster 0 —— 2 Cluster 1 —— 2 Cluster 1 —— 3 Cluster 2 —— 3

e

Lats1$^{f/f}$; *Lats2*$^{f/f}$; *Sftpc*$^{Cre/+}$ lungs 14.5 *dpc*

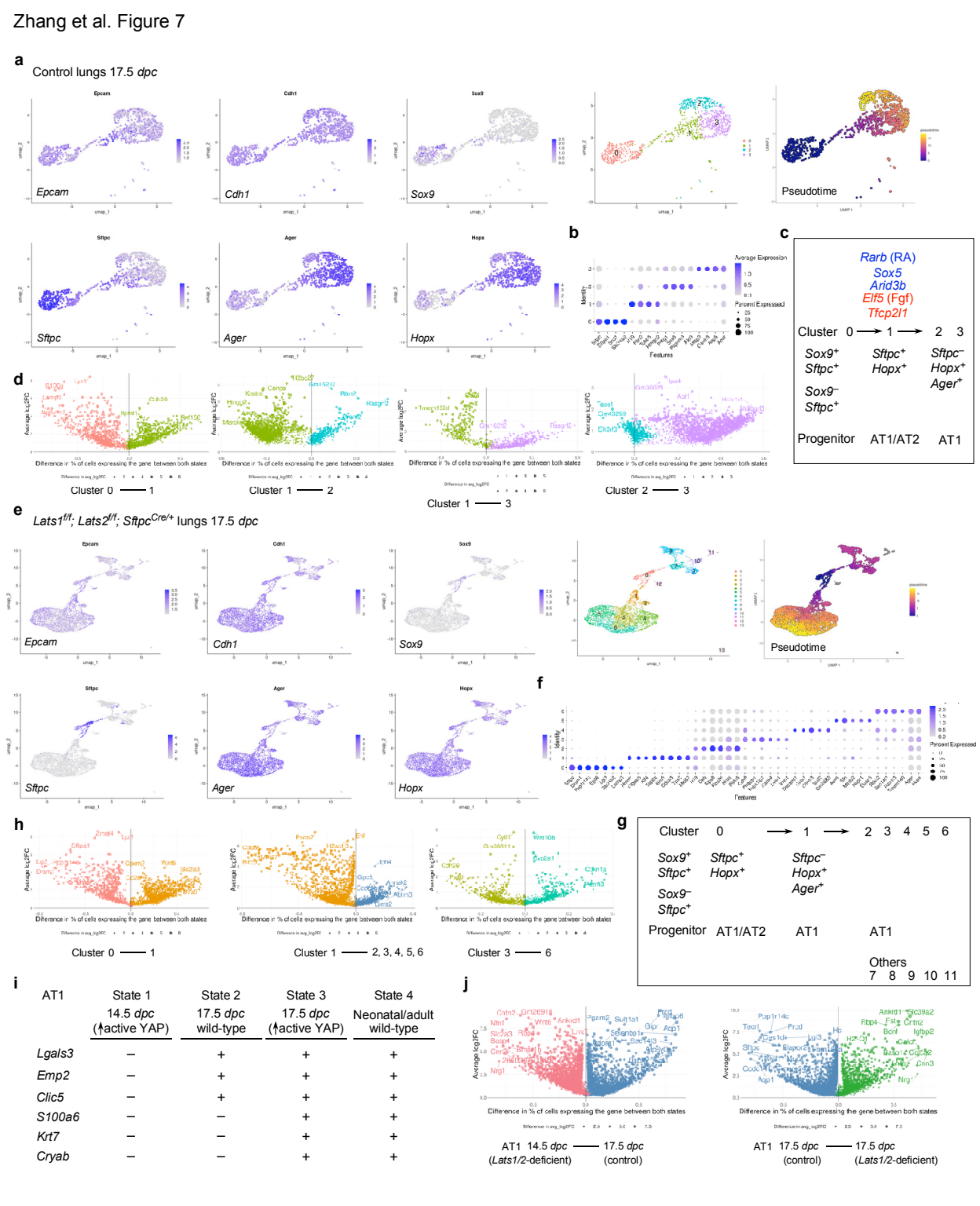


h

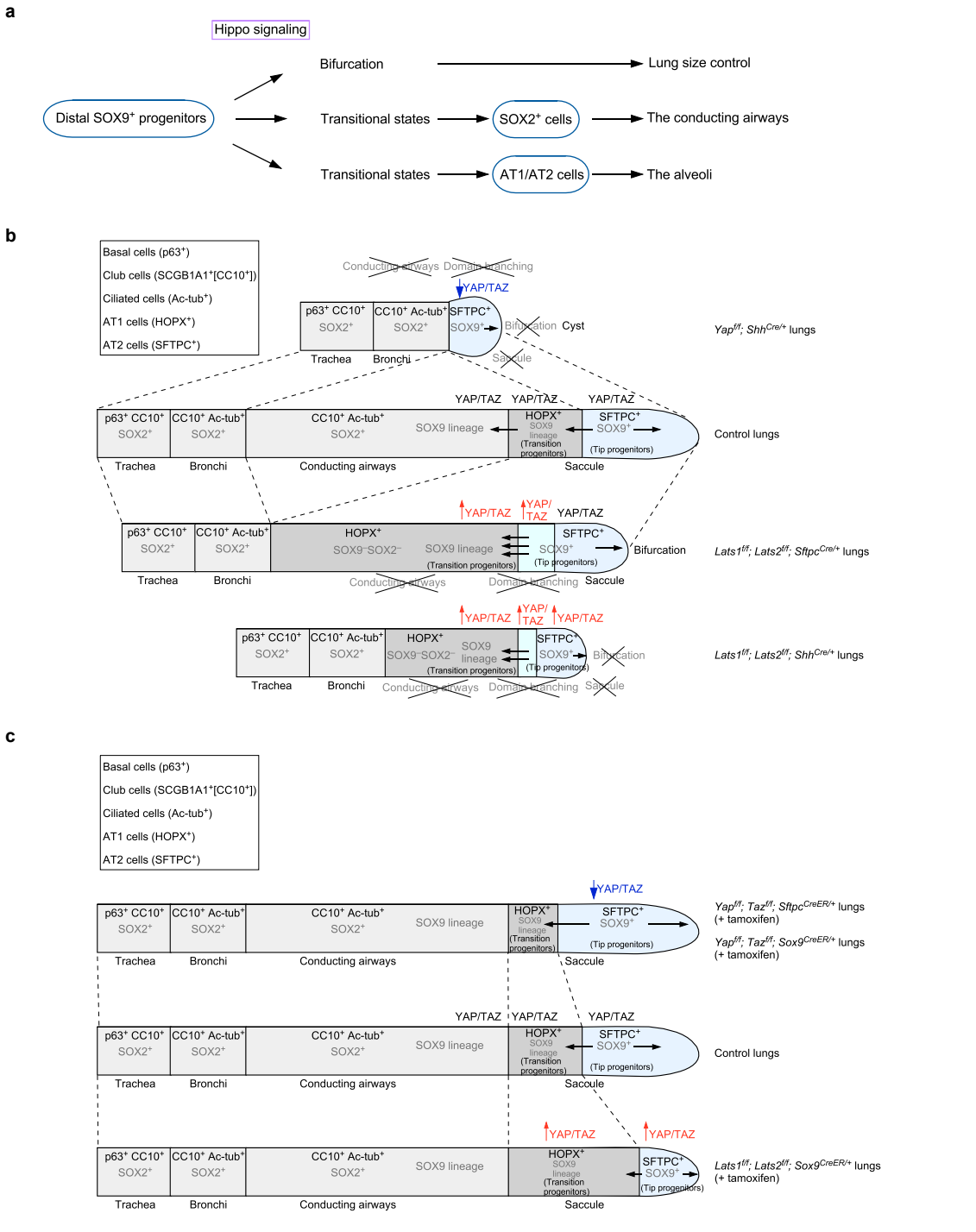


Cluster 0 —— 1 Cluster 0 —— 2 Cluster 1 —— 3 Cluster 2 —— 5

Zhang et al. Figure 7



i

AT1	State 1 14.5 *dpc* (↑active YAP)	State 2 17.5 *dpc* wild-type	State 3 17.5 *dpc* (↑active YAP)	State 4 Neonatal/adult wild-type
Lgals3	–	+	+	+
Emp2	–	+	+	+
Clic5	–	+	+	+
S100a6	–	–	+	+
Krt7	–	–	+	+
Cryab	–	–	+	+

Zhang et al. Figure 8