

Supplemental Information Inventory

1. Supplemental Figures and Legends

- Figure S1 (Related to Figure 1). Expression pattern of Hdac3 during lung development and assessment of cell proliferation and survival in the *Shh^{cre}:Hdac3^{ff}* mutant lungs.
- Figure S2 (Related to Figure 2). Examination of cell differentiation marker gene expression in *Shh^{cre}:Hdac3^{ff}* mutant lungs.
- Figure S3 (Related to Figure 3). qPCR analysis on isolated primary epithelial cells and the miRNA expression in the mesenchymal cells of *Shh^{cre}:Hdac3^{ff}* mutant lungs.
- Figure S4 (Related to Figure 4). qPCR analysis on the Tgf- β pathway in the mesenchyme of *Shh^{cre}:Hdac3^{ff}* mutant lungs and the effect of SB431542 and Tgf- β on p-Smad2 expression.
- Figure S5 (Related to Figure 5). Over-expression of miR-17-92 by the *R26^{MIR17-92}* allele does not affect epithelial progenitor marker expression.
- Figure S6 (Related to Figure 6). Loss of epithelial miR-17-92 alleviates the defects of lung sacculation in the *Shh^{cre}:Hdac3^{ff}* mutant lungs.

2. Supplemental Movies

- Movie S1 (Related to Figure 1). 3D reconstruction of Aqp5 whole mount staining showing the distal saccular region of an E18.5 control lung.
- Movie S2 (Related to Figure 1). 3D reconstruction of Aqp5 whole mount staining showing the distal saccular region of an E18.5 *Shh^{cre}:Hdac3^{ff}* mutant lung.

3. Supplemental Tables

- Table S1 (Related to Figure 3). A list of all the differentially expressed genes in the microarray comparing control lungs and *Shh^{cre}:Hdac3^{ff}* mutant lungs at E18.5.
- Table S2 (Related to Figure 3). Result of SPIA pathway analysis on the common predicated targets of miR-17-92 and Dlk1-Dio3 miRNAs that were differentially expressed in the microarray data.
- Table S3 (Related to Figure 3). Result of SPIA pathway analysis on the predicated targets of all the differentially up-regulated miRNAs in the microarray data.
- Table S4 (Related to Figure 4) Result of SPIA pathway analysis on all the differentially down-regulated genes in the microarray data.

4. Supplemental Experimental Procedure