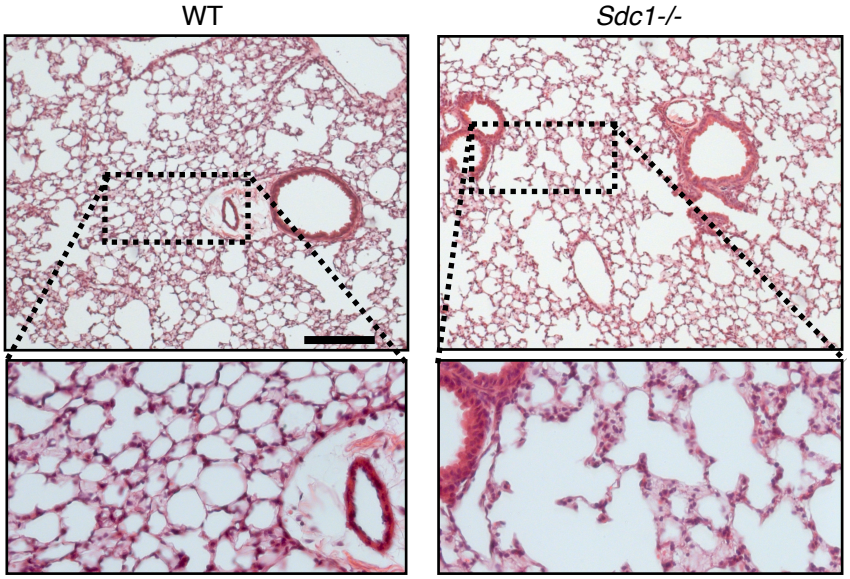
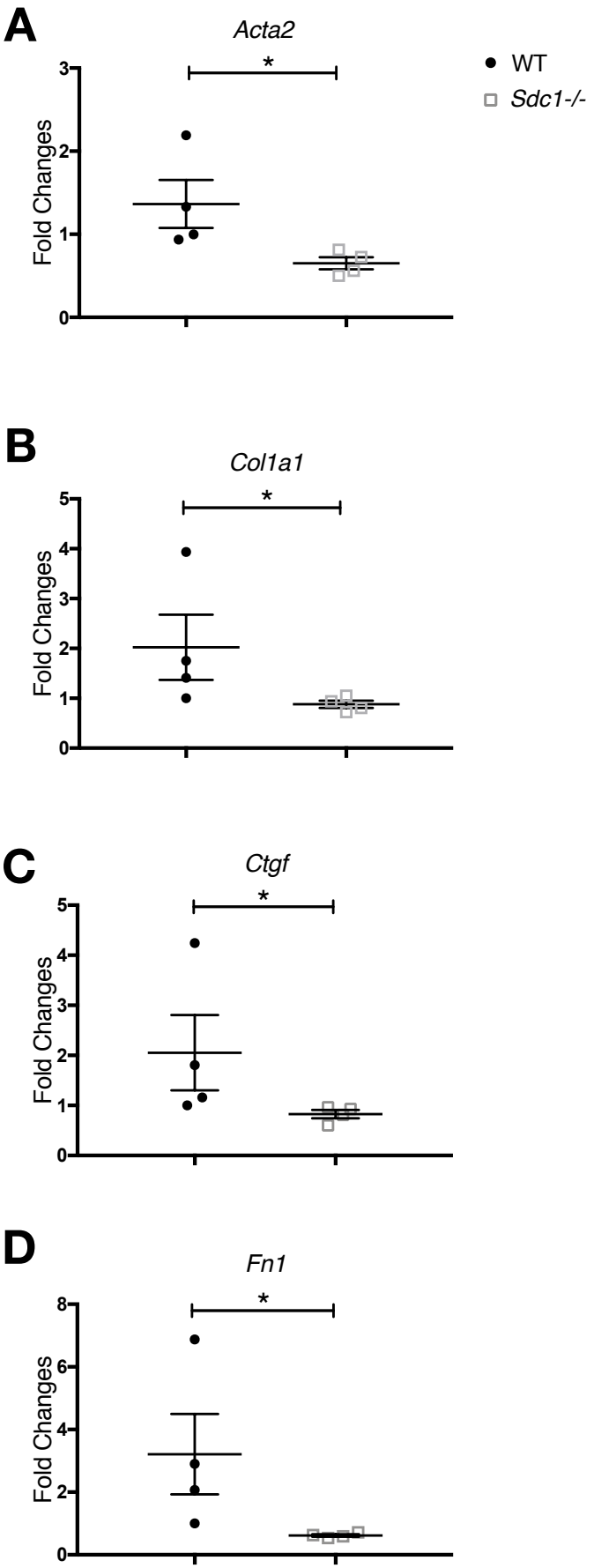


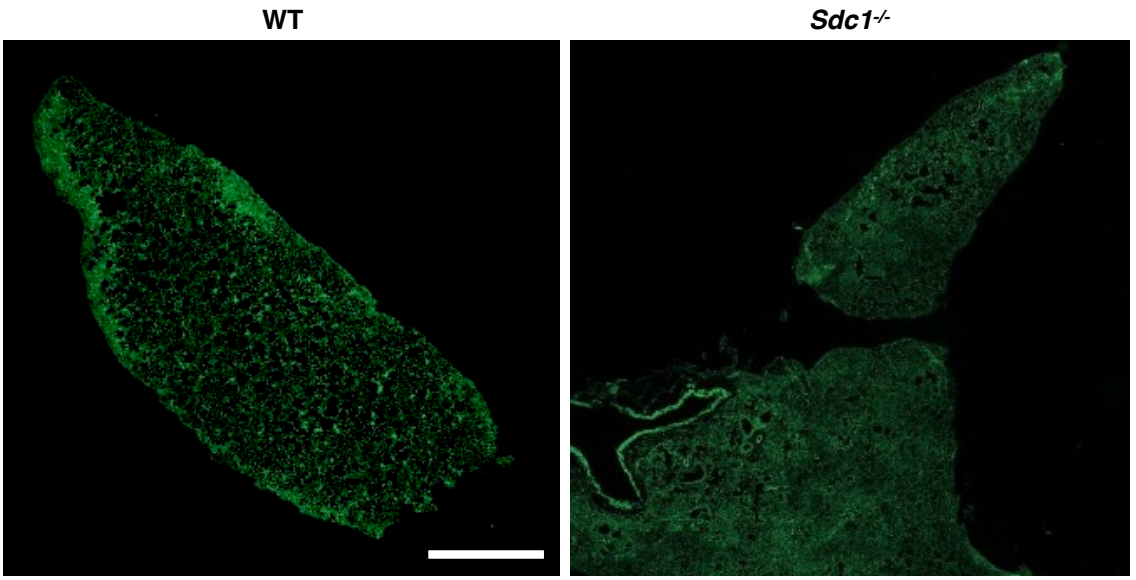
Supplemental Figure 1.

H&E staining of lungs from uninjured WT and *Sdc1*$^{-/-}$ mice. Scalebar = 200 μm.



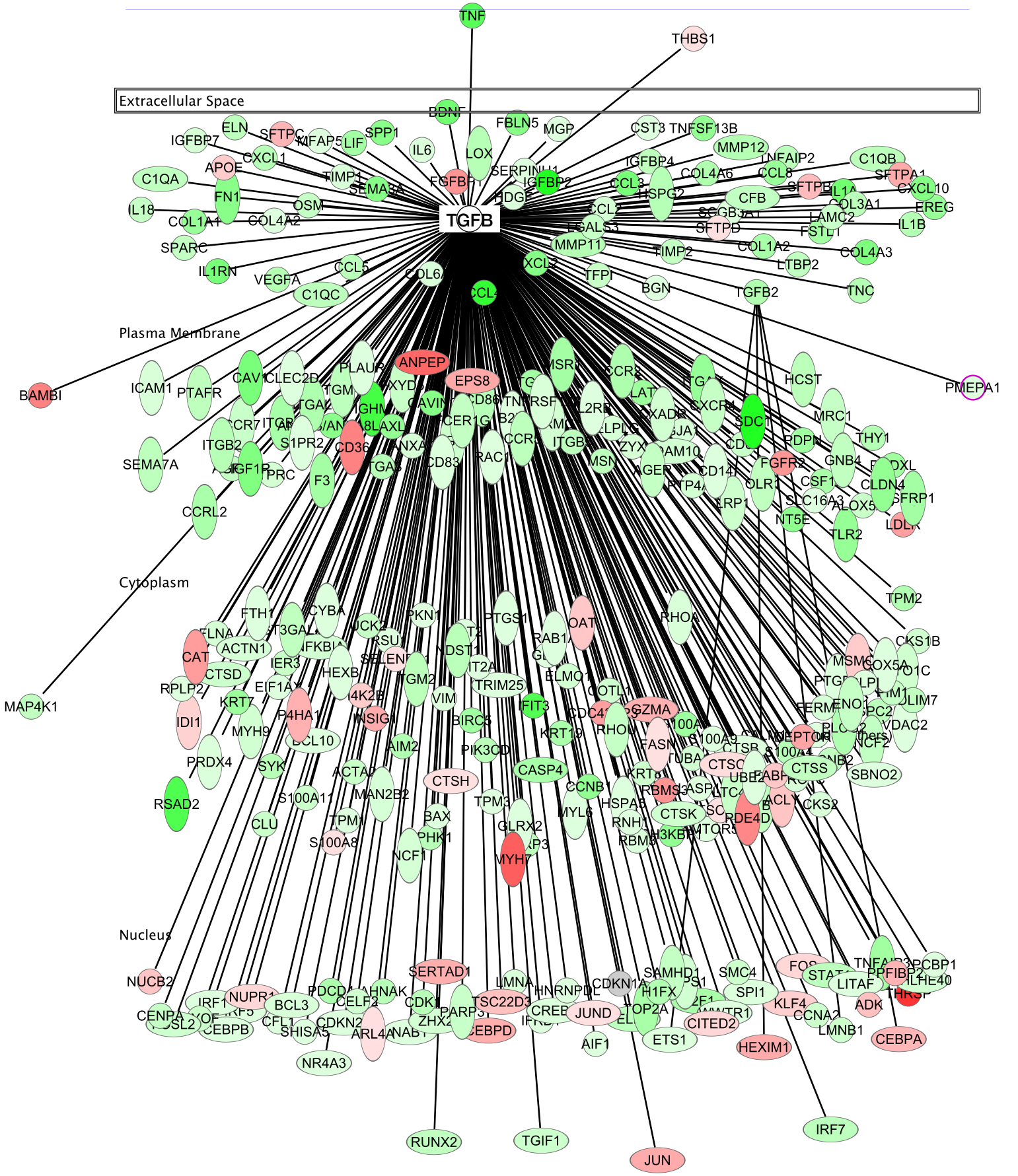
Supplemental Figure 2.

WT and *Sdc1*$^{-/-}$ mice were injured with bleomycin (0.75 units/kg). After 21 days, lungs were isolated for PCR analysis of profibrotic gene expression. *$p<0.05$ by two-tailed Student's *t*-test.



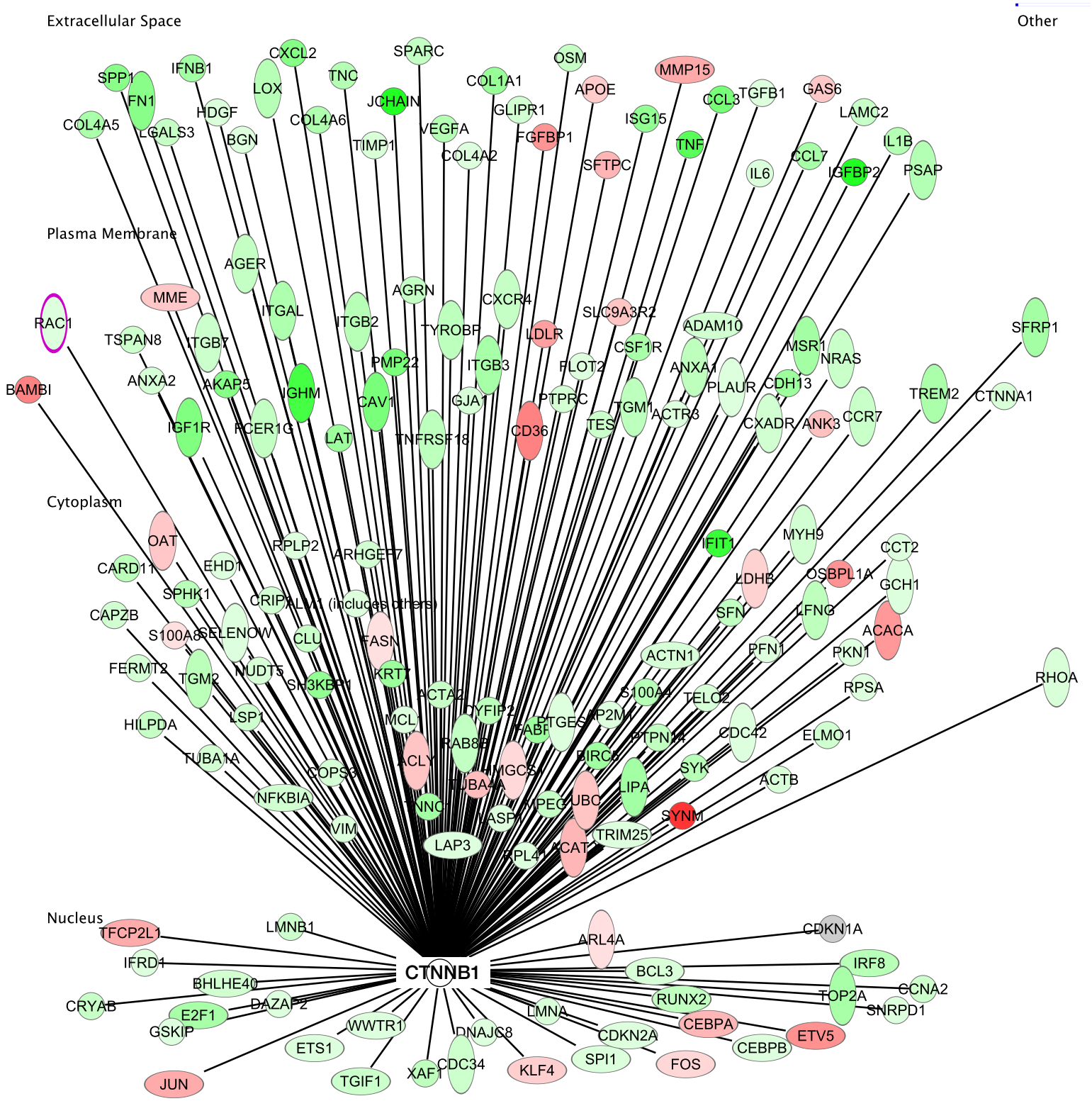
Supplemental Figure 3.

WT and *Sdc1*$^{-/-}$ mice were instilled with bleomycin (0.75 units/kg) and processed for downstream assays after 21 days of injury. Immunofluorescent staining for AMSA (αSMA) demonstrates increased staining in WT conditions.



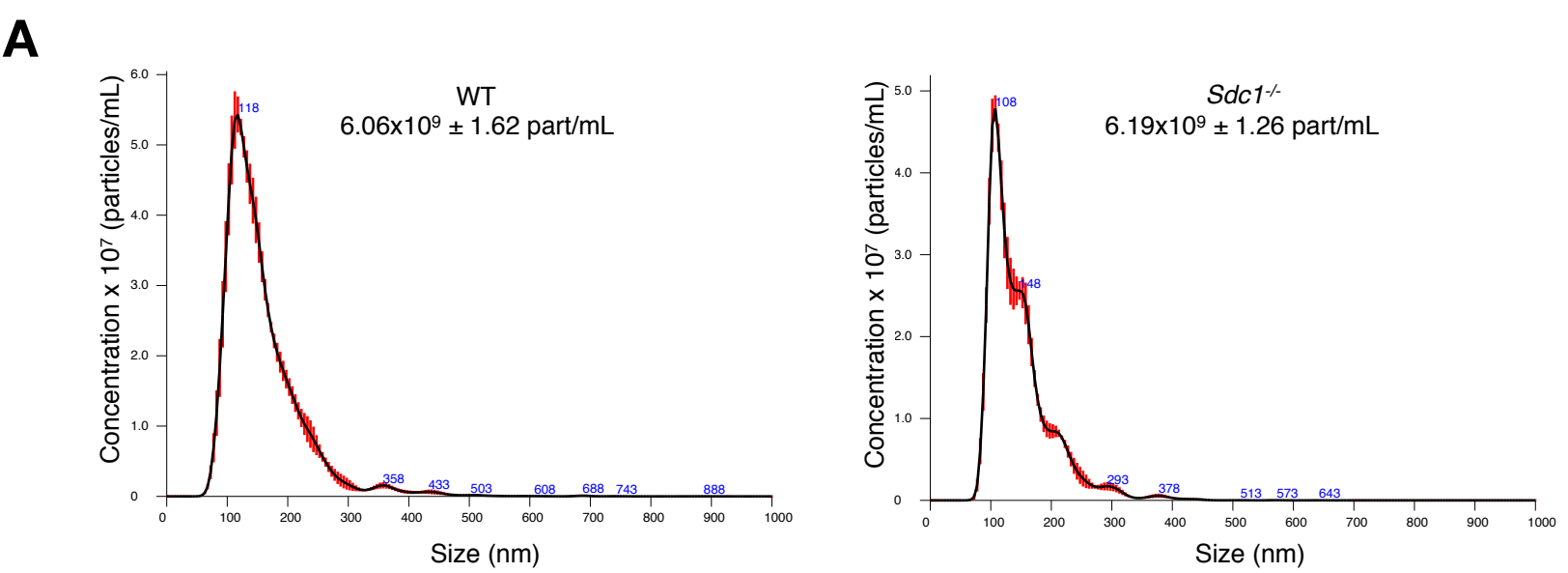
Supplemental Figure 4.

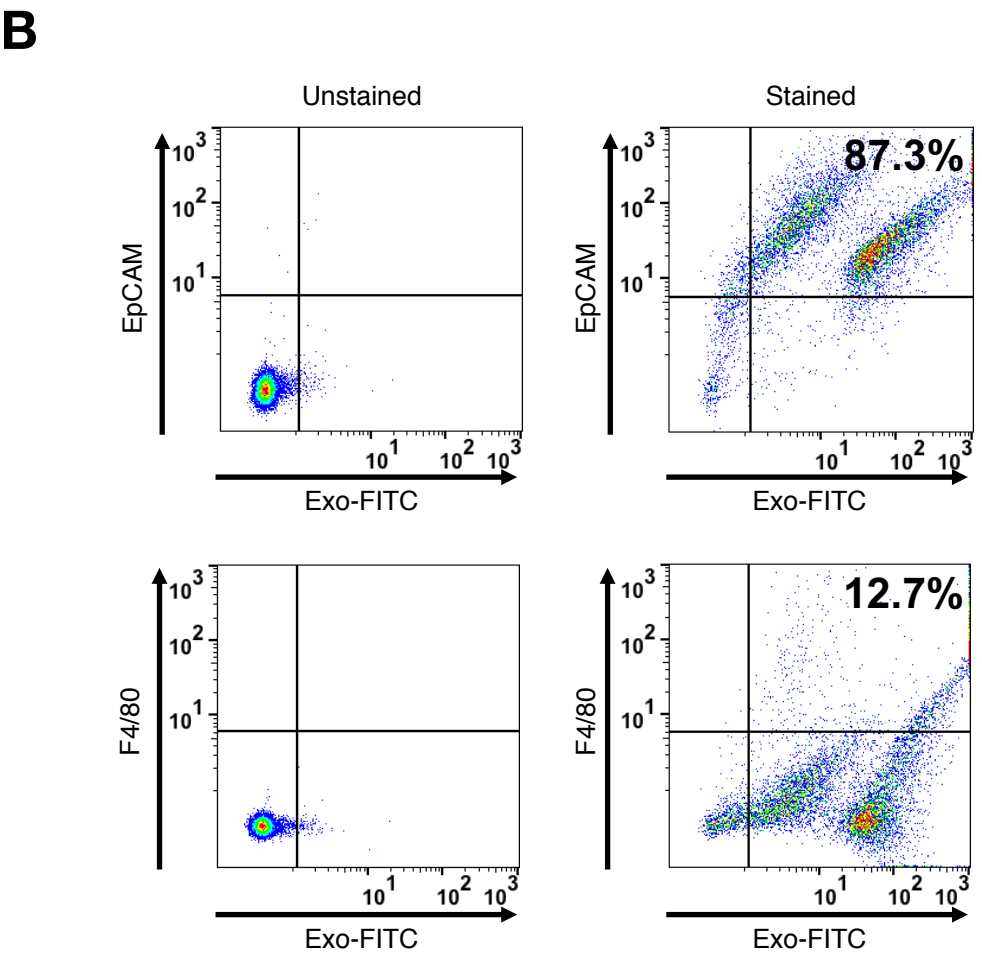
TGFβ signaling interaction network using TGFβ1 as a seed to visualize the connectivity of differentially expressed genes in ATII cells between WT and *Sdc1*$^{-/-}$ mice. The majority of genes interacting with TGFβ signaling were upregulated in WT conditions (green nodes). Red nodes are downregulated genes in WT conditions.



Supplemental Figure 5.

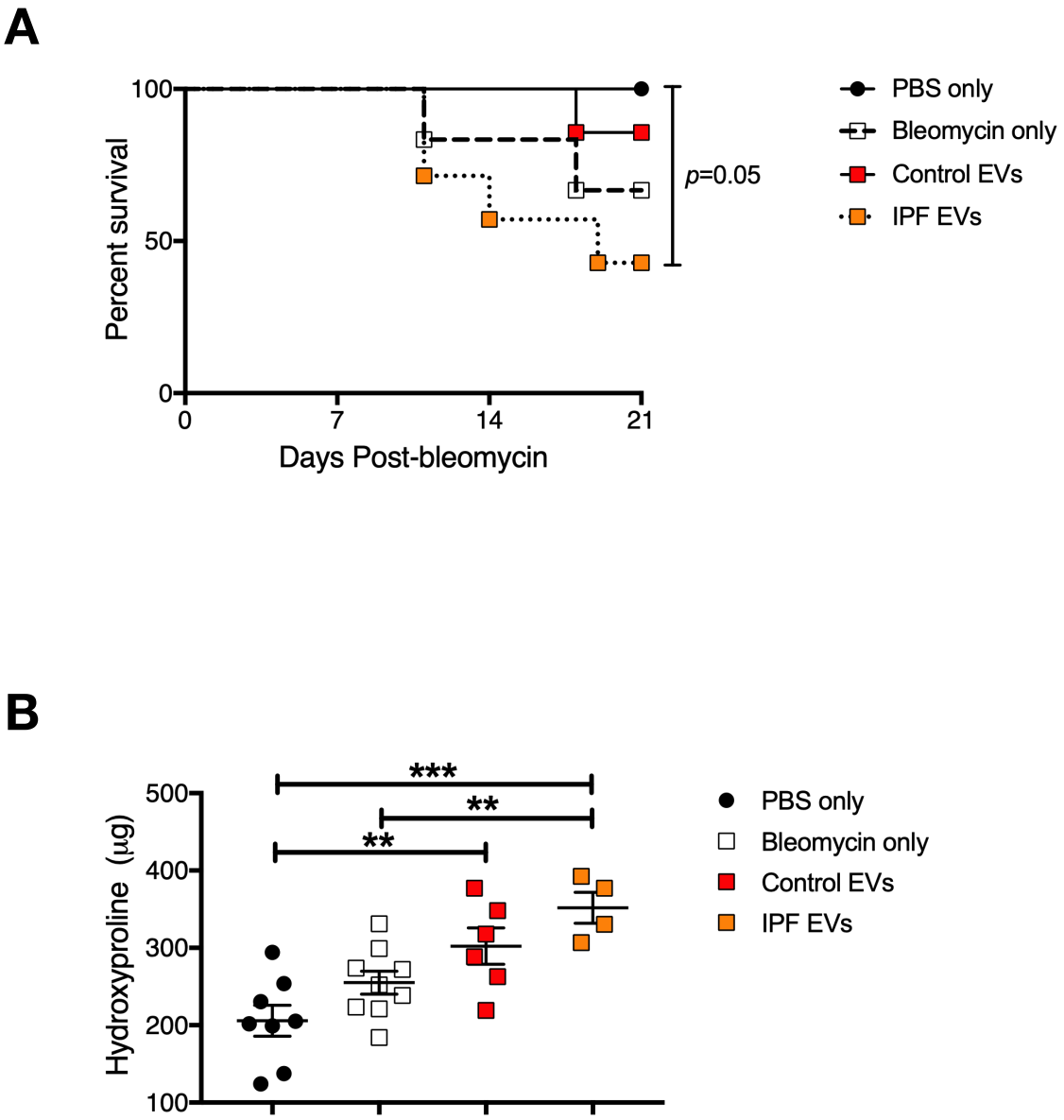
Wnt signaling interaction network using β-catenin (*CTNNB1*) as a seed to visualize the connectivity of differentially expressed genes in ATII cells between WT and *Sdc1*$^{-/-}$ mice. The majority of genes interacting with Wnt signaling were upregulated in WT conditions (green nodes). Red nodes are downregulated genes in WT conditions.





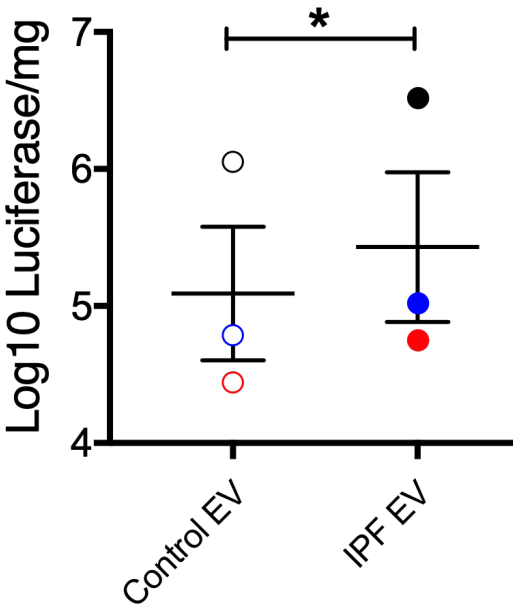
Supplemental Figure 6.

EVs were isolated from the airspaces of WT and *Sdc1*$^{-/-}$ mice. **(A)** Nanoparticle Tracking Analysis demonstrated the size distribution and numbers of EVs. **(B)** Flow cytometry of mouse fibrotic EVs labeled with Exo-FITC and co-stained for epithelial cells (EpCAM, top) and macrophages (F4/80, bottom).



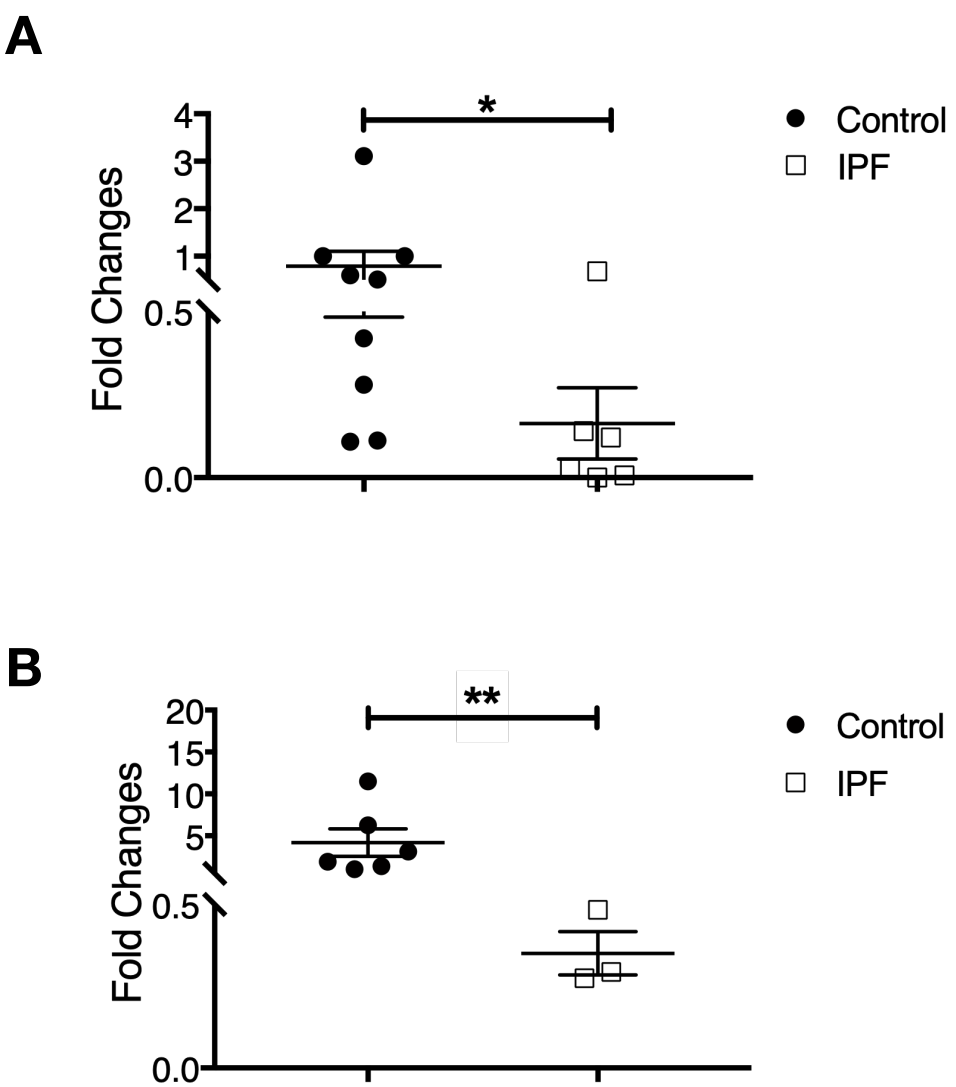
Supplemental Figure 7.

WT mice were injured with low dose bleomycin (0.25 units/kg) and then intranasally given the treatments as indicated. **(A)** Overall 21-day survival and **(B)** Whole lung hydroxyproline content (n= 4-8 in each group) on day 21 after bleomycin. ***p*<0.005*; ***p*<0.0005 by one-way ANOVA analysis.



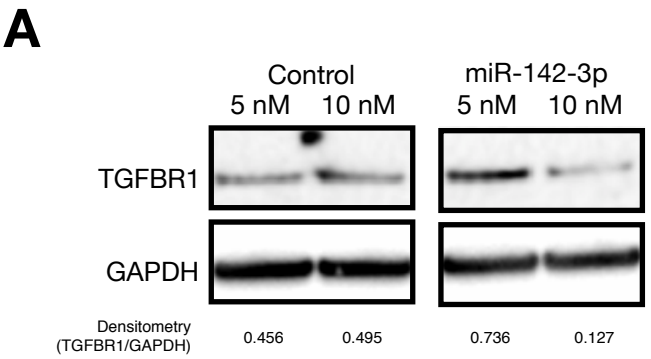
Supplemental Figure 8.

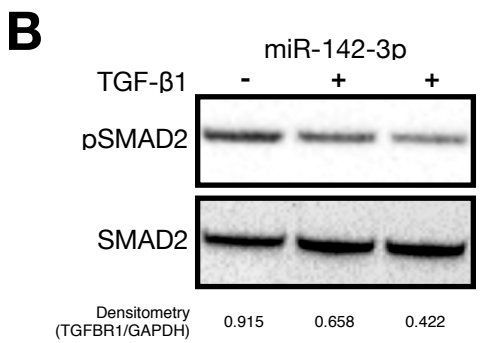
HEK cells were treated with control or IPF EVs ($1x10^8$ particles) for 24 h. Then, cells were transfected with TopFLASH plasmid and subsequently stimulated with Wnt3a proteins. Luciferase activity was measured and reported per protein content. Paired samples from independent experiments are color matched (black, blue, and red) for statistical analysis. * $p < 0.05$ by the paired ratio *t-test*.



Supplemental Figure 9.

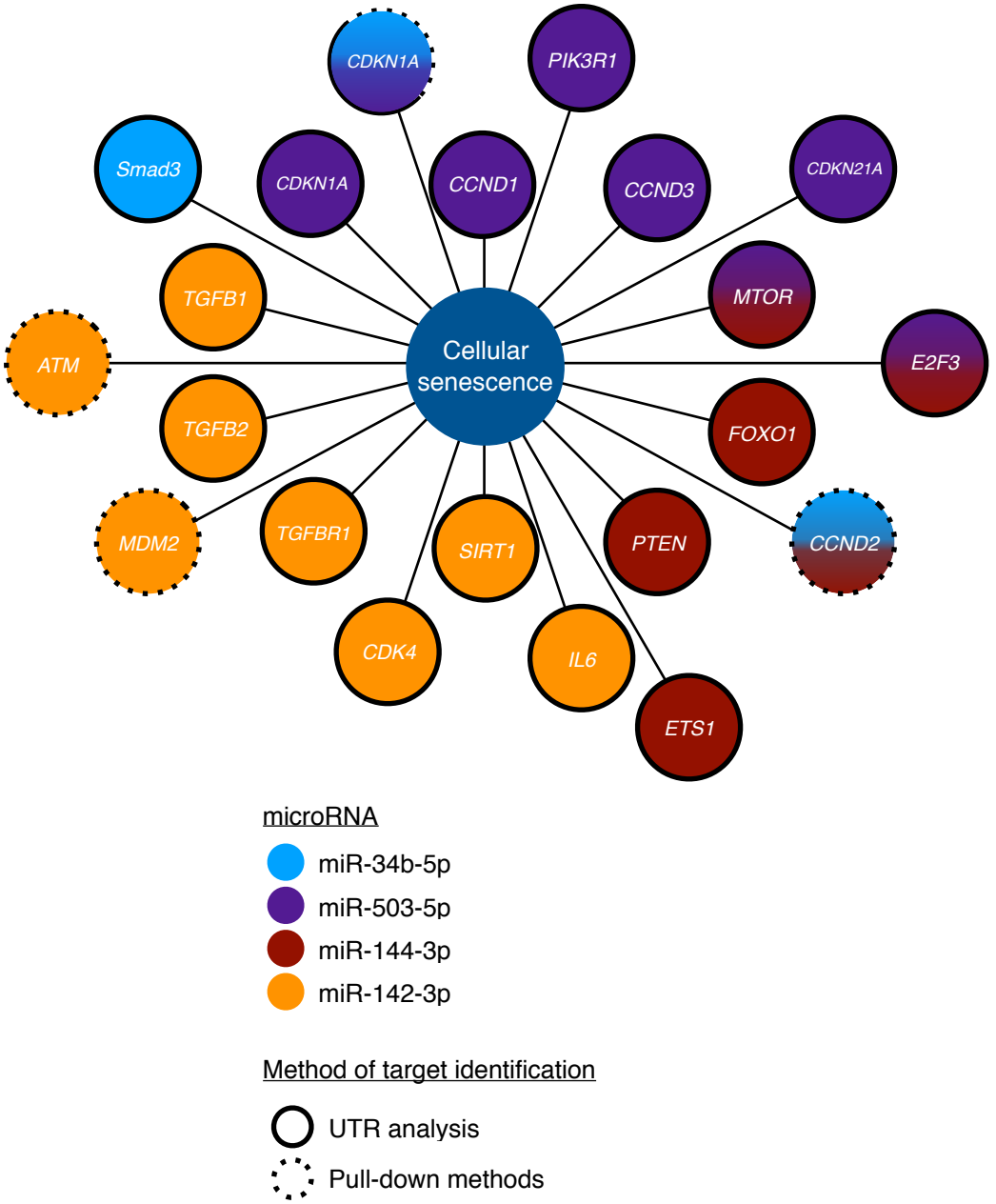
qPCR for miRNA in EVs isolated from washings of control and IPF lungs. **(A)** miR-142-3p. **(B)** miR-144-3p. **p*<0.05, ***p*<0.005 by two-tailed Student's *t*-test.





Supplemental Figure 10.

(A) TGFBR1 immunoblot of mouse lung epithelial cells transfected with the control or miR-144-3p mimics. **(B)** Immunoblot for pSMAD2 and SMAD2 using mouse lung epithelial cells transfected with control or miR-142-3p mimics followed by TGFβ stimulation.



Supplemental Figure 11.

Cellular senescence regulatory network of experimentally identified targets of miR-34b-5p (*blue*), miR-503-5p (*purple*), miR-144-3p (*brick-red*), and miR-142-3p (*orange*). These curated targets predominantly through literature search were experimentally validated either by UTR analysis (close circle) or with pull-down methods (dotted circle).