A respiratory noise comparison between p73KO and WT mice.

B: Relative expression of Muc5ac and Muc5b genes in 3-month and 6-month-old WT and TAp73KO mice.

C: Relative expression of Muc5b gene in 3-month and 6-month-old WT and TAp73KO mice.

D: Relative expression of Mmp12 gene in 3-month and 6-month-old WT and TAp73KO mice.

E: Forced vital capacity comparison between WT, TAp73KO, aging, and old mice.

F: Tissue elastance comparison between WT, TAp73KO, aging, and old mice.
Supplemental Figure S1 (related to Fig. 1). TAp73 deficiency causes chronic bronchitis leading to marked impairment of pulmonary function

(A) Coughing/sneezing phenotype of p73KO mice. Audiograms of KO and WT mice recorded and processed with identical settings for 90 sec. WT mice are completely silent. The occasional small amplitudes in the WT track are due to extraneous noises from the microphone scratching the cage wall and from the rustling of bedding material (see also Fig. 1B and Supplemental Movie S1).

(B and C) As a result of chronic airway inflammation, expression of Muc5ac and Muc5b is increased in TAp73KO mice, reflecting goblet cell hyperplasia and mucus accumulation in airways.

(D) Likewise, levels of tissue-destructive enzymes such as matrix metalloproteinase (Mmp12, aka macrophage elastase) are increased in TAp73KO mice, consistent with the observed macrophage- promoted secondary emphysema. B-D, qRT-PCR on whole lung lysates of age-matched TAp73KO and WT mice; 3 months old cohorts, n=6-7 mice per genotype; 6 months old cohorts, n=3 mice per genotype.

(E and F) TAp73 deficiency results in a spontaneous chronic obstructive pulmonary disease (COPD)-like phenotype in barrier-maintained mice. Mice were subjected to pulmonary function testing with the FlexiVent system that applies negative pressure to the lungs of freshly sacrificed animals. TAp73KO mice show typical signs of emphysema, indicated by an increase in forced vital capacity (E, FVC) and a decrease in tissue elastance (F). The increase in FVC and decrease in elastance progresses with age. ‘Aging’ cohort 385 days, ‘Old’ cohort 630 days; n= 4 mice per genotype.