# Appendix: Supplementary Figures

## Bronchioalveolar stem cells are a main source for regeneration of distal lung epithelia

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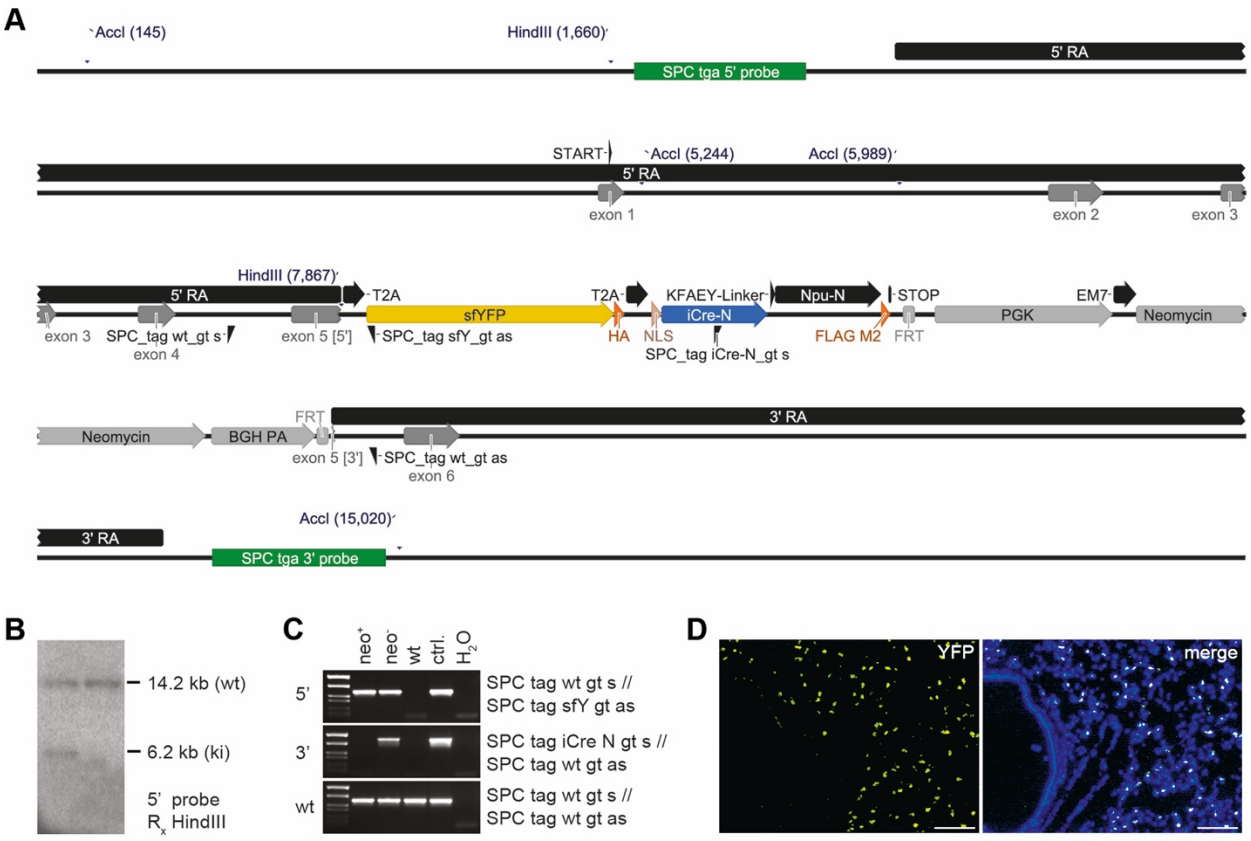
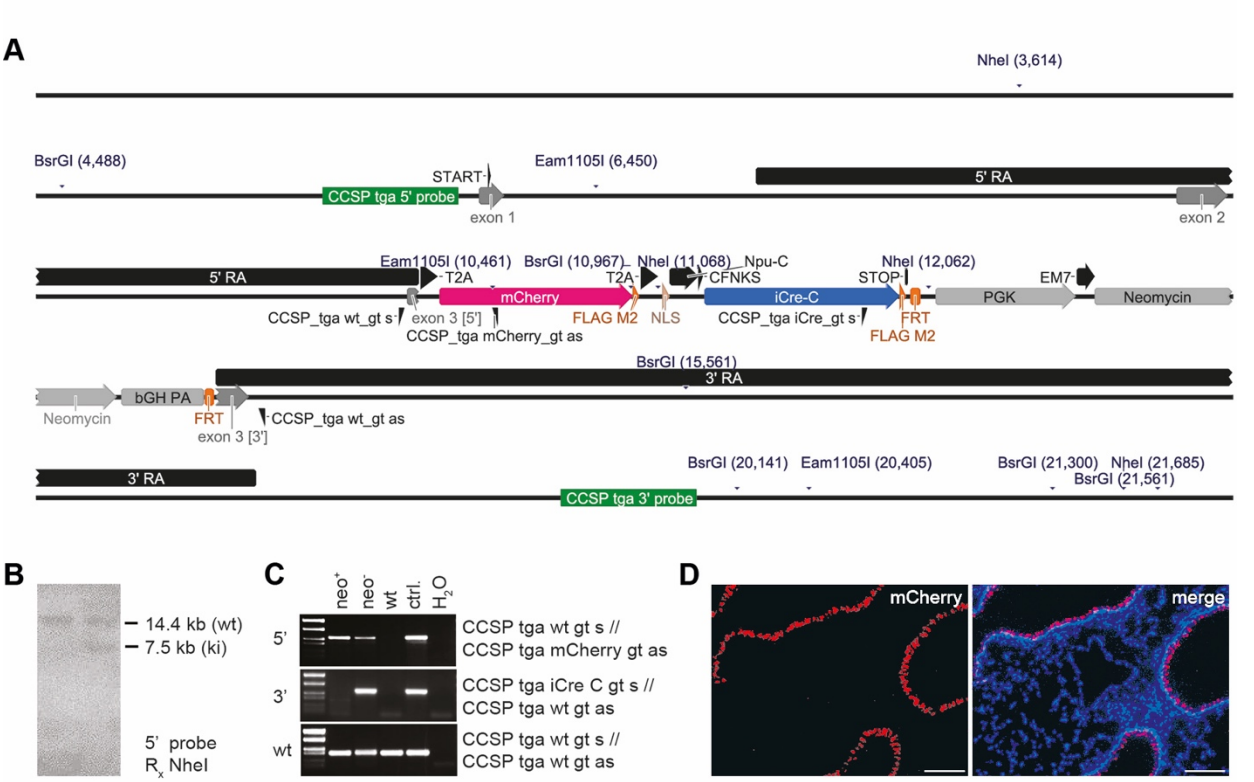
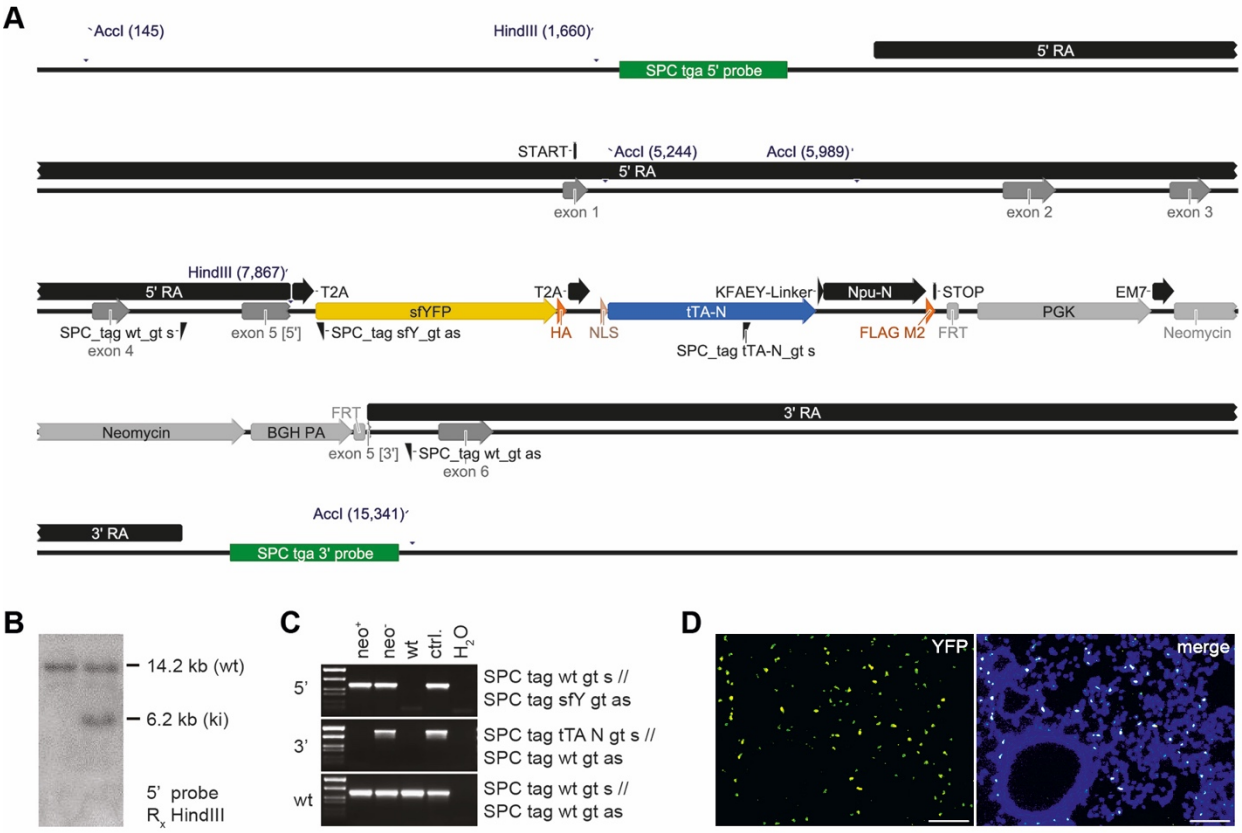
**Content:** Appendix Figures S1-S4



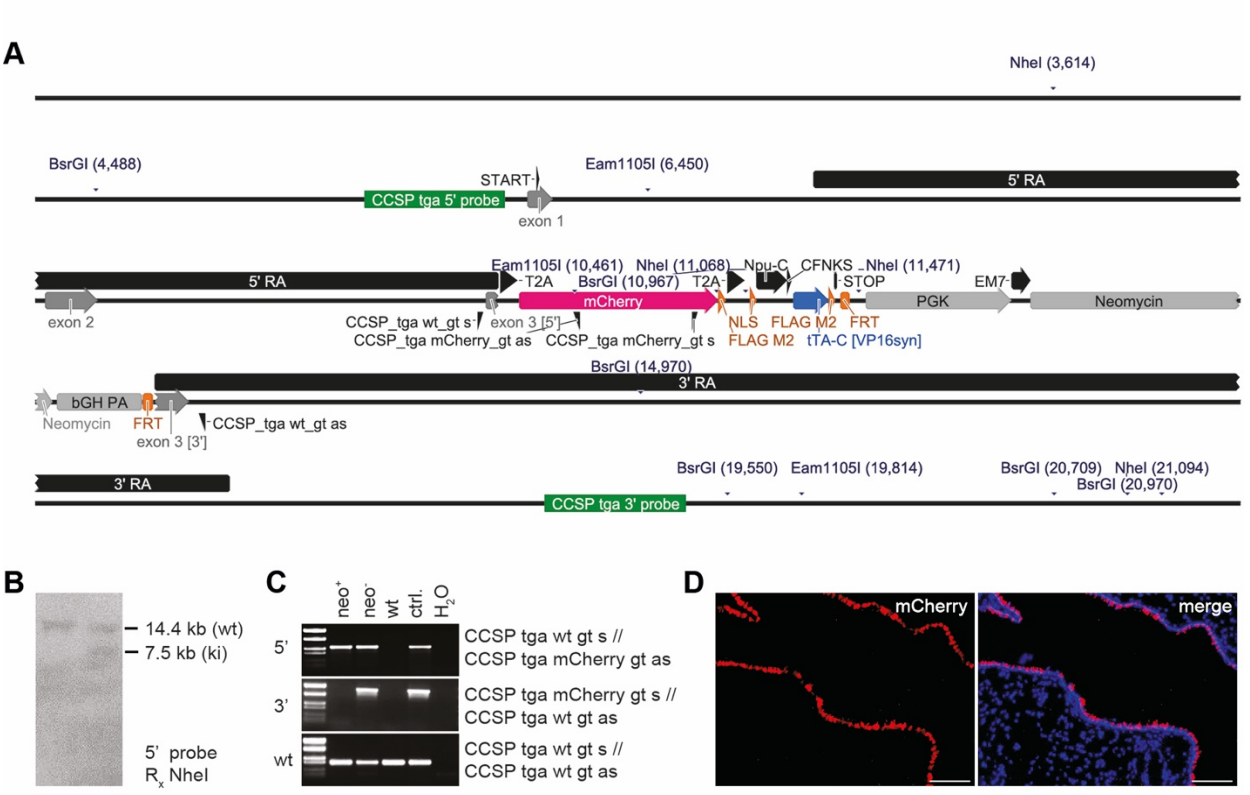

**Appendix Figure S1. Generation of the SPC$^{-2A-YFP-2A-iCre-N}$ knock-in strain. A.** Schematic representation of the SPC$^{-2A-YFP-2A-iCre-N}$ knock-in allele. Coding sequences of superfolder YFP and N-terminal split-Cre effector were inserted immediately upstream of the endogenous STOP codon of the SPC gene linked by 2A sequences. **B.** Southern Blot analysis of correct integration of the SPC$^{-2A-YFP-2A-iCre-N}$ knock-in allele. **C.** Allele-specific PCR analysis detects expected fragment sizes of 426 bp (ki 5′), 720 bp (ki 3′) and 462 bp (wt). Deletion of the neomycin selection marker was verified using the 3′ ki PCR. **D.** Epifluorescence analysis of lung sections from heterozygous SPC$^{-2A-YFP-2A-iCre-N}$ knock-in mice. YFP epifluorescence is restricted to the alveolar epithelium reflecting localization of AT2 cells. Blue: DAPI. Scale bar: 100 µm. ki – knock-in, wt – wildtype.




**Appendix Figure S2. Generation of the CCSP$^{-2A.mCherry-2A-iCre-C}$ knock-in strain. A.** Schematic representation of the CCSP$^{-2A-mCherry-2A-iCre-C}$ knock-in allele. Coding sequences of mCherry and C-terminal split-Cre effector were inserted immediately upstream of the endogenous STOP codon of the CCSP gene linked by 2A sequences. **B.** Southern Blot analysis of correct integration of the CCSP$^{-2A-mCherry-2A-iCre-C}$ knock-in allele. **C.** Allele specific PCR analysis detects expected fragment sizes of 363 bp (ki 5´), 401 bp (ki 3´) and 258 bp (wt). Deletion of the neomycin selection marker was verified using the 3´ ki PCR. **D.** Epifluorescence analysis of lung sections from heterozygous CCSP$^{-2A-mCherry-2A-iCre-C}$ knock-in mice. mCherry epifluorescence is restricted to the bronchiolar epithelium reflecting localization of Club cells. Blue: DAPI. Scale bar: 100 µm. ki – knock-in, wt – wildtype.




**Appendix Figure S3. Generation of the SPC$^{-2A\text{-}YFP\text{-}2A\text{-}tTA\text{-}N}$ knock-in strain. A.** Schematic representation of the SPC$^{-2A\text{-}YFP\text{-}2A\text{-}tTA\text{-}N}$ knock-in allele. Coding sequences of superfolder YFP and N-terminal split-tTA effector were inserted immediately upstream of the endogenous STOP codon of the SPC gene linked by 2A sequences. **B.** Southern Blot analysis of correct integration of the SPC$^{-2A\text{-}YFP\text{-}2A\text{-}tTA\text{-}N}$ knock-in allele. **C.** Allele specific PCR analysis detects expected fragment sizes of 426 bp (ki 5´), 776 bp (ki 3´) and 462 bp (wt). Deletion of the neomycin selection marker was verified using the 3´ ki PCR. **D.** Epifluorescence analysis of lung sections from heterozygous SPC$^{-2A\text{-}YFP\text{-}2A\text{-}tTA\text{-}N}$ knock-in mice. YFP epifluorescence is restricted to the alveolar epithelium reflecting localization of AT2 cells. Blue: DAPI. Scale bar: 100 µm. ki – knock-in, wt – wildtype.




**Appendix Figure S4. Generation of the CCSP$^{\text{-2A-mCherry-2A-tTA-C}}$ knock-in strain. A.** Schematic representation of the CCSP$^{\text{-2A-mCherry-2A-tTA-C}}$ knock-in allele. Coding sequences of mCherry and C-terminal split-tTA effector were inserted immediately upstream of the endogenous STOP codon of the CCSP gene linked by 2A sequences. **B.** Southern Blot analysis of correct integration of the CCSP$^{\text{-2A-mCherry-2A-tTA-C}}$ knock-in allele. **C.** Allele specific PCR analysis detects expected fragment sizes of 363 bp (ki 5´), 748 bp (ki 3´) and 258 bp (wt). **D.** Epifluorescence analysis of lung sections from heterozygous CCSP$^{\text{-2A-mCherry-2A-tTA-C}}$ knock-in mice. mCherry epifluorescence is restricted to the bronchiolar epithelium reflecting localization of Club cells. Blue: DAPI. Scale bar: 100 µm. ki – knock-in, wt – wildtype.