

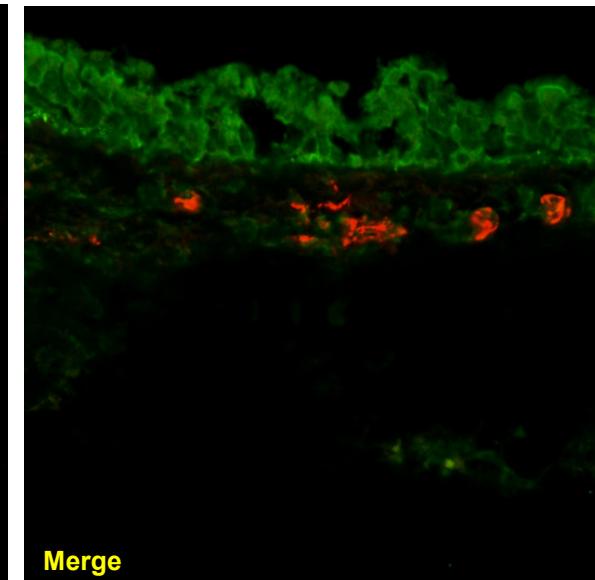
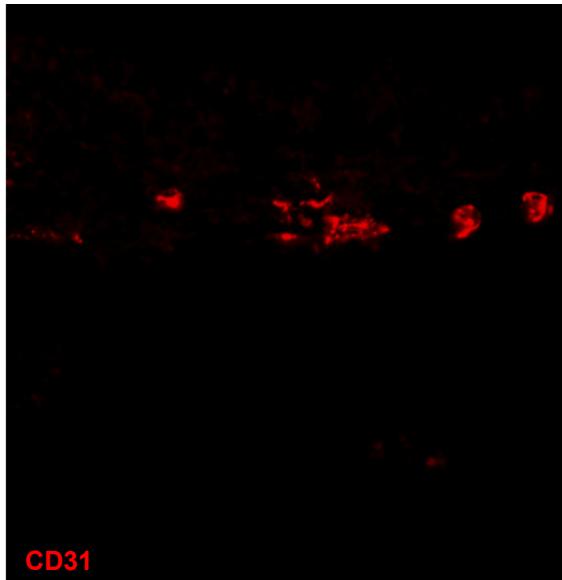
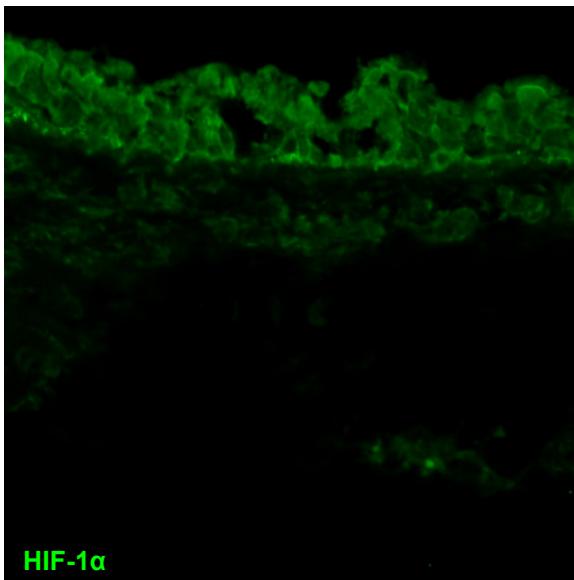
**Tie2-dependent VHL knockdown promotes airway
microvascular regeneration and attenuates invasive growth of
*Aspergillus fumigatus***

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Olcholski³, Vinicio de Jesus Perez³, Gregg L. Semenza⁴, Mark R.
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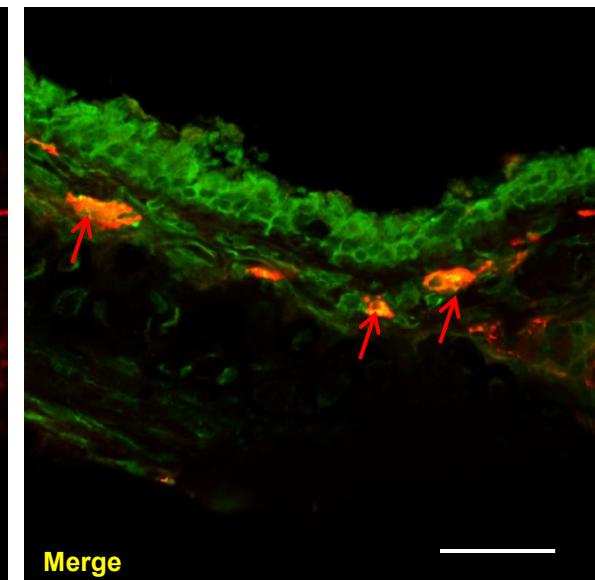
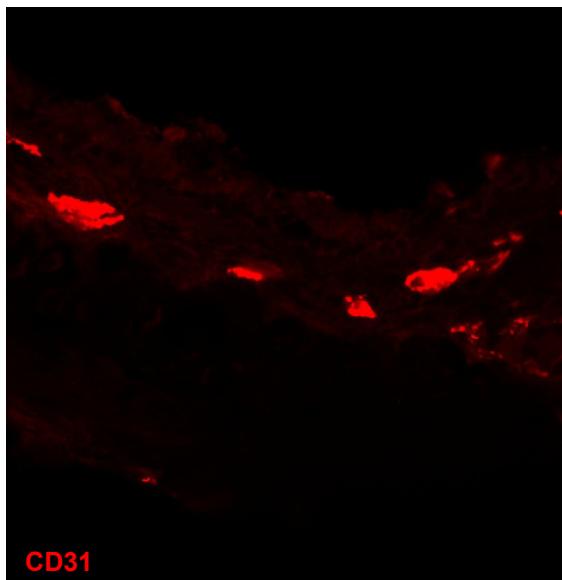
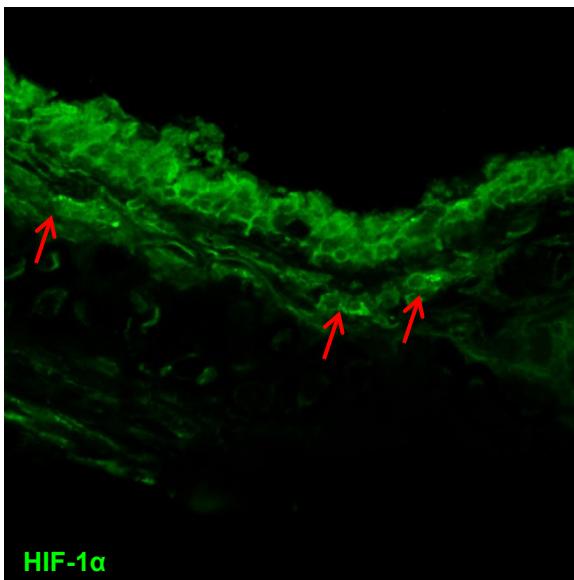
Supplementary Fig. 1

Tie2Cre(-)VHL(fli/+)



Subepithelium

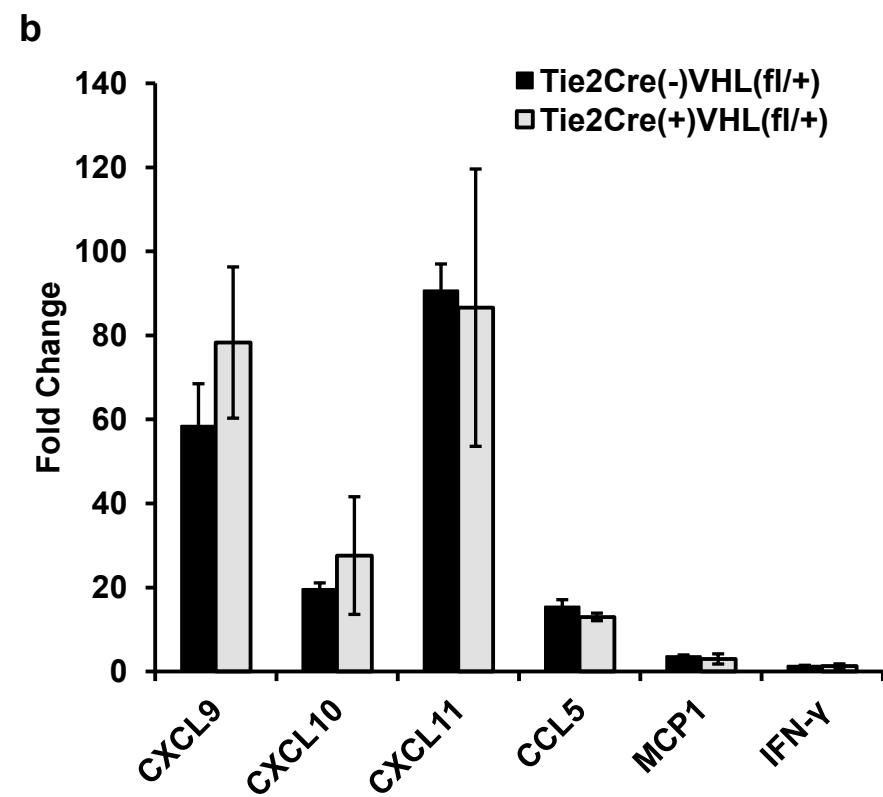
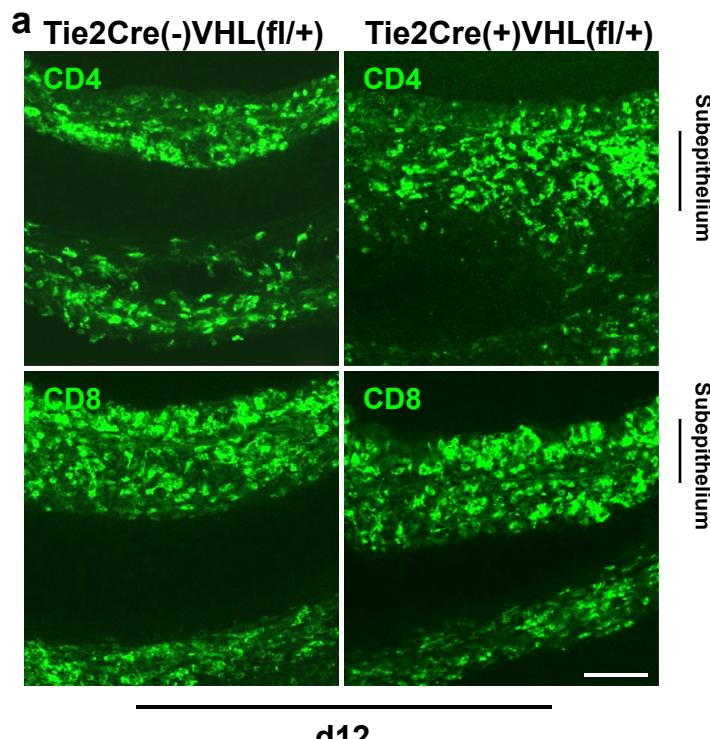
Tie2Cre(+)VHL(fli/+)



Subepithelium

Supplementary Fig. 1 Increased HIF-1 α expression in ECs of VHL-haplodeficient trachea. Immunofluorescence staining shows HIF1 α protein expression in ECs from VHL-haplodeficient mice. Red arrows denote HIF-1 α -positive cells. Scale Bar: 20 μ M.

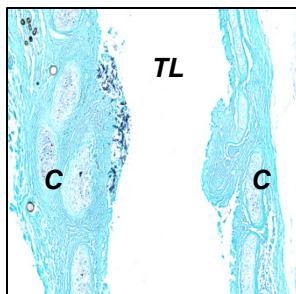
Supplementary Fig. 2



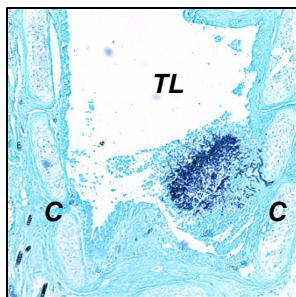
Supplementary Fig. 2 Comparable infiltration of immune cells and expression of common inflammatory cytokines in tracheas transplanted into both control and VHL haplodeficiency recipients. **a** CD4 and CD8 staining are similar in tracheas transplanted into both control and VHL-haplodeficient recipients at day 12. **b** mRNA expression levels of common inflammatory cytokines are similar in both control and VHL-haplodeficient groups at day 12. Scale bar: 20 μ M. (**a**). Data are shown as means \pm SEM.

Supplementary Fig. 3

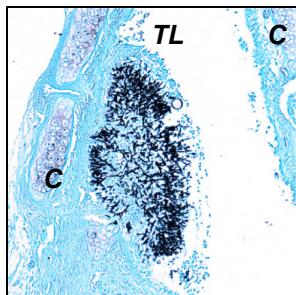
a



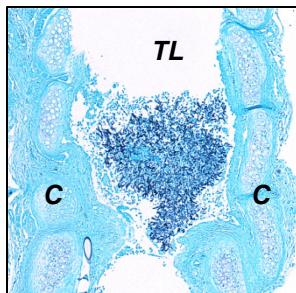
1: minimal, <25%



2: mild, 25%-49%

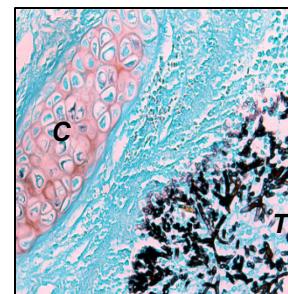


3: moderate, 50-74%

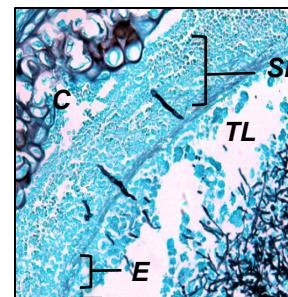


4: severe, >75%

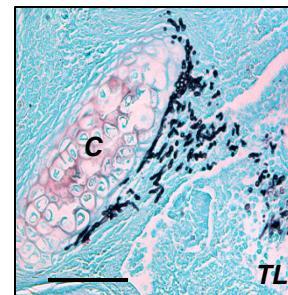
b



1: minimal, epithelium



2: mild, subepithelium



3: moderate, cartilage ring

Supplementary Fig. 3 Semiquantitative scale histopathological definitions. a Degree of fungal infection was determined using a semiquantitative scoring system as follows: 0, no fungal elements, 1 (minimal), fungal hyphae in less than 25% of the luminal area, 2 (mild) hyphae. Scale Bar: 20 μ M.

Supplementary Table 1. Sequences of primers for qRT-PCR analysis

Gene	Forward Primer	Reverse Primer
CXCL9	CACCAGCCGAGGCACGATCC	TGCAATTGGGGCTTGGGGCA
CXCL10	TCTCGCAAGGACGGTCCGCT	CGTGGCAGGATAGGCTCGC
CXCL11	GCCATAGCCCTGGCTGCGAT	CATCCCGGGGCCGATGCAA
CCL5	CATCCTCACTGCAGCCGCC	AGCGCGAGGGAGAGGTAGGC
MCP-1	GAAGGCCAGCCCAGCACAG	GTGGATGCTCCAGCCGGCAA
IFN-γ	CACAGGTCCAGCGCCAAGCA	CCCACCCCCAATCAGCAGCG
HIF-1α	GCTCATCAGTTGCCACTTCCCC	CGGCATCCAGAAGTTTCTCACACG
SDF-1	GAGAGCCACATGCCAGAG	TTTCGGGTCAATGCACACTG
ANGPT1	CTACCAACAACAACAGCATCC	CTCCCTTAGCAAAACACCTTC
ANGPT2	CTGTGCGGAAATCTTCAAGTC	TGCCATCTTCTCGGTGTT
VEGF	GGCTGCTGTAACGATGAAG	CTCTCTATGTGCTGGCTTG
PLGF	GGATGTGCTCTGTGAATGC	CCTCTGAGTGGCTGGTTAC
Tie2	GTGTAGTGGACCAGAAGG	CTTGAGAGCAGAGGCATC
VEGFR2	GCGGGCTCCTGACTACAC	CCAAATGCTCCACCAACTCTG
CXCR4	AGCATGACGGACAAGTACC	GATGATATGGACAGCCTTACAC
18S	GAATCGAACCTGATTCCCCGTC	CGGCGACGACCCATTGAAAC