Table S1. Upregulated genes in saline controls compared to fibrotic lungs at 28 days post-bleomycin treatment.

Refseq	***Symbol***	***Description***	***Fold Change***	***p value***
NM_009469	*Ulk1*	Unc-51 like kinase 1	4.4248	0.015054
NM_007527	*Bax*	Bcl2-associated X protein	3.605	0.000785
NM_053069	*Atg5*	Autophagy-related 5	3.5466	0.001619
NM_174874	*Atg4b*	Autophagy-related 4B, cysteine peptidase	3.4983	0.01307
NM_010175	*Fadd*	Fas (TNFRSF6)-associated via death domain	3.234	0.00684
NM_001002897	*Atg9b*	Autophagy-related 9B	3.2117	0.001579
NM_010480	*Hsp90aa1*	Heat shock protein 90, alpha (cytosolic), class A member 1	2.9606	0.000788
NM_010503	*Ifna2*	Interferon alpha 2	2.8481	0.001013

QPCR-based comparisons from autophagy array gene-expression profile in lungs from saline control compared to bleomycin-treated mice sacrificed after 28 days revealed significant upregulation of several genes in response to bleomycin challenge. The fold change was calculated by the $2^{-\Delta\Delta CT}$ method.

Table S2. Downregulated genes in saline controls compared to fibrotic lungs at 28 days post-bleomycin treatment.

Refseq	***Symbol***	***Description***	***Fold Change***	***p value***
NM_145570	*Eva1a*	Eva-1 homolog A	-2.1386	0.038347
NM_026693	*Gabarapl2*	Gamma-aminobutyric acid (GABA) A receptor-associated protein-like 2	-2.1835	0.001271
NM_026013	*Dram2*	DNA-damage regulated autophagy modulator 2	-2.7063	0.00015

QPCR-based comparisons from autophagy array gene-expression profile in lungs from saline control compared to bleomycin-treated mice sacrificed after 28 days revealed significant downregulation of several genes in response to bleomycin challenge. The fold change was calculated by the $2^{-\Delta\Delta CT}$ method.

Table S3. Upregulated genes in lungs from *atg4b*$^{-/-}$ compared to WT mice at 28 days post-bleomycin treatment.

Refseq	***Symbol***	***Description***	***Fold Change***	***p value***
NM_008356	*Il13ra2*	Interleukin 13 receptor, alpha 2	10.9132	0.001773
NM_007743	*Col1a2*	Collagen, type I, alpha 2	9.3697	0.000755
NM_011595	*Timp3*	Tissue inhibitor of metalloproteinase 3	7.2	0.000505
NM_009930	*Col3a1*	Collagen, type III, alpha 1	5.52	0.002442
NM_009911	*Cxcr4*	Chemokine (C-X-C motif) receptor 4	5.1982	0.000595
NM_016769	*Smad3*	SMAD family member 3	5.0095	0.003539
NM_008607	*Mmp13*	Matrix metallopeptidase 13	3.5016	0.005072
NM_013565	*Itga3*	Integrin alpha 3	3.4935	0.001528
NM_009825	*Serpinh1*	Serine (or cysteine) peptidase inhibitor, clade H, member 1	3.4774	0.001507
NM_009371	*Tgfbr2*	Transforming growth factor, beta receptor II	3.4534	0.004959
NM_016780	*Itgb3*	Integrin beta 3	2.697	0.00747
NM_009368	*Tgfb3*	Transforming growth factor, beta 3	2.5105	0.010873

QPCR-based comparisons from fibrosis array gene-expression profile in lungs from *atg4b*$^{-/-}$ mice compared to WT littermates revealed significant upregulation of several genes in response to bleomycin challenge. The fold change was calculated by the $2^{-\Delta\Delta CT}$ method.

Table S4. Downregulated genes in lungs from *atg4b*$^{-/-}$ compared to WT mice at 28 days post-bleomycin treatment.

Refseq	***Symbol***	***Description***	***Fold Change***	***p value***
NM_007616	*Cav1*	Caveolin 1, caveolae protein	-17.0142	0.019982
NM_021283	*Il4*	Interleukin 4	-2.9869	0.001497
NM_001042660	*Smad7*	SMAD family member 7	-2.3598	0.012914
NM_008877	*Plg*	Plasminogen	-2.2171	0.018787
NM_010427	*Hgf*	Hepatocyte growth factor	-2.2018	0.012668
NM_011330	*Ccl11*	Chemokine (C-C motif) ligand 11	-2.1615	0.01259

QPCR-based comparisons from fibrosis array gene-expression profile in lungs from *atg4b*$^{-/-}$ mice compared to WT littermates revealed significant downregulation of several genes in response to bleomycin challenge. The fold change was calculated by the $2^{-\Delta\Delta CT}$ method.