

## **Supplemental Material to:**

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**Pathogenic role of BECN1/Beclin 1 in the development  
of amyotrophic lateral sclerosis**

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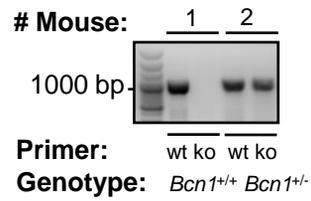
**TableS1.** Visual observation scores. One of the disease parameters evaluated to determinate the onset and duration of the disease is the visual symptoms.

Code	Visual observation	Scores
C1	slight limb-clasping	1
C2	moderated limb-clasping	3
C3	severe limb-clasping	5
T1	slight tremor felt in one of the hind-limbs	1
T2	moderated tremor felt in one of the hind-limbs	3
T3	severe tremor felt in one of the hind-limbs	5
S1	moderated dirty appearance	1
S2	severe dirty appearance	3
A1	moderated backbone arching	2
A2	obvious backbone arching	5
P1	slight paralysis	2
P2	moderated paralysis	3
P3	severe paralysis	5

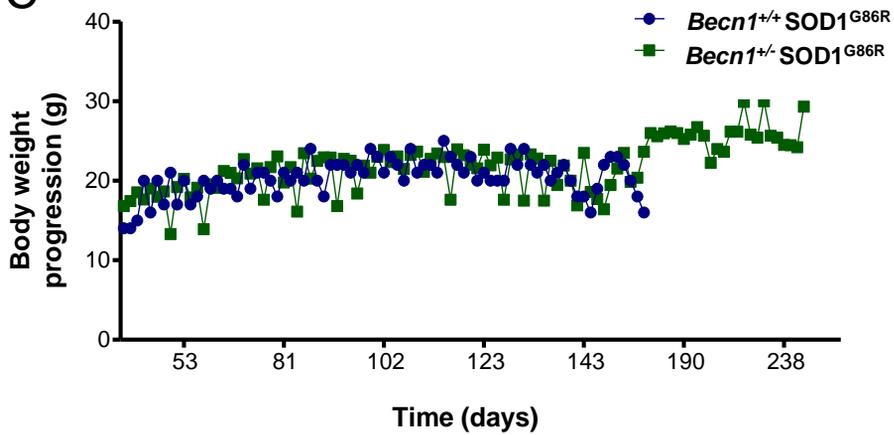
A



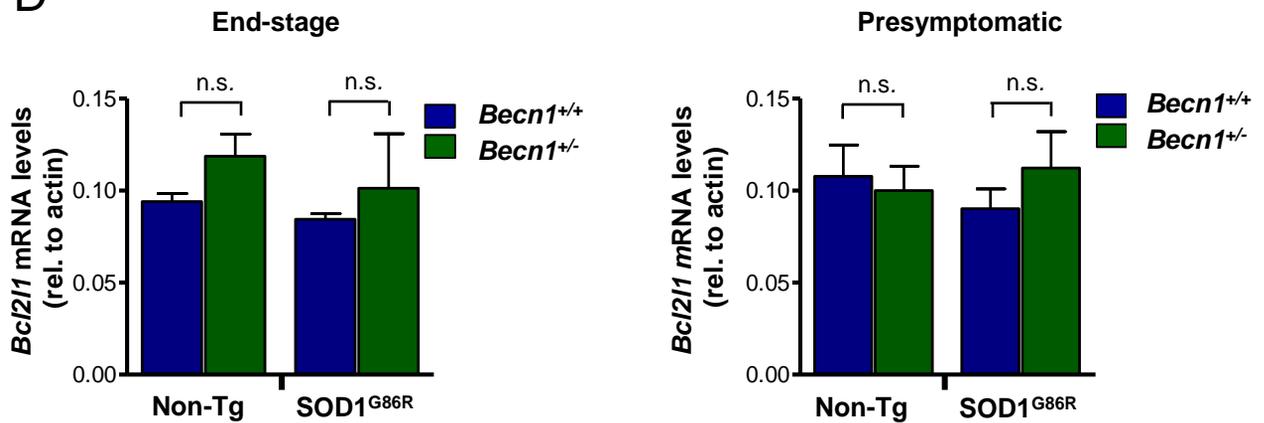
B



C



D



E

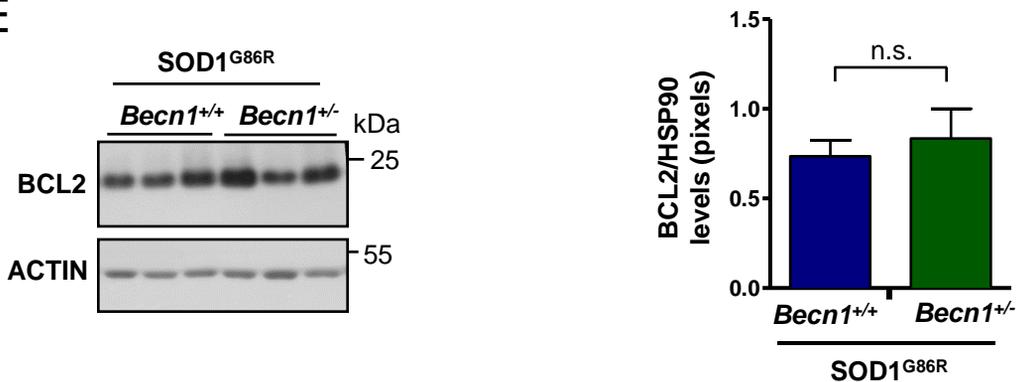


Figure S1

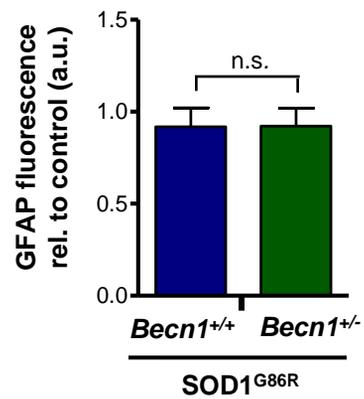
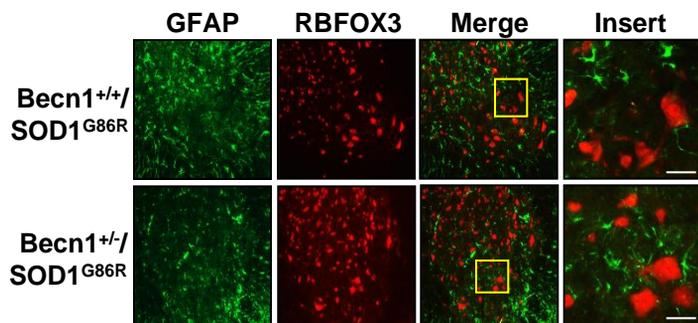
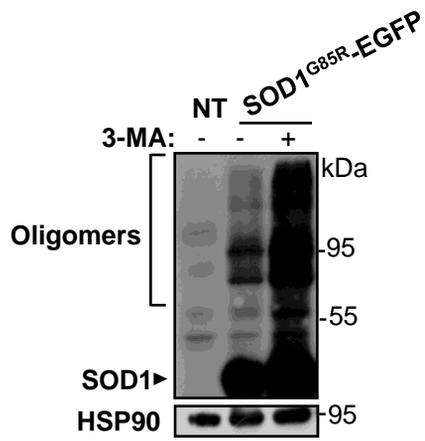
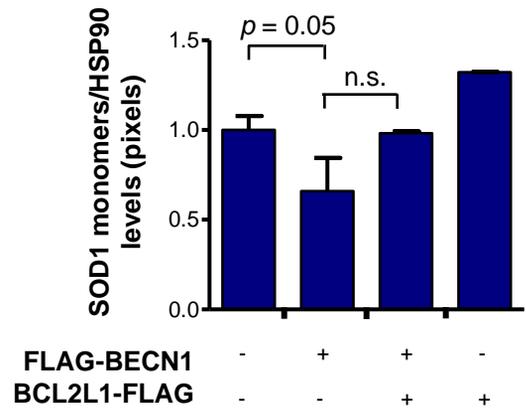


Figure S2

A



B



C

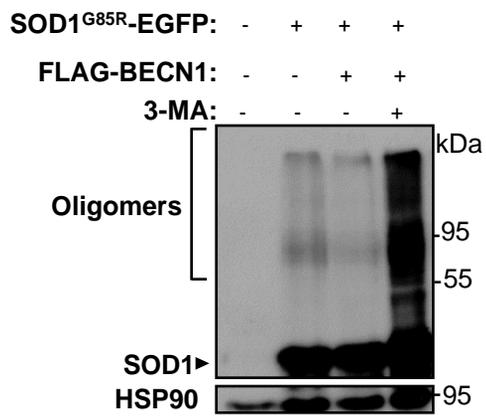
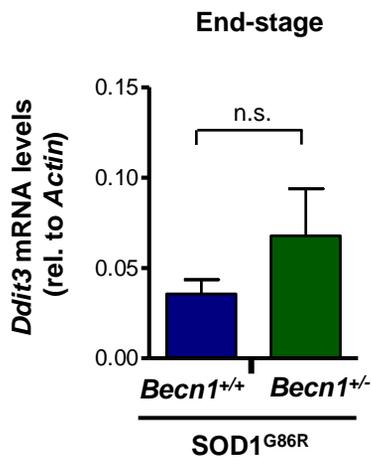
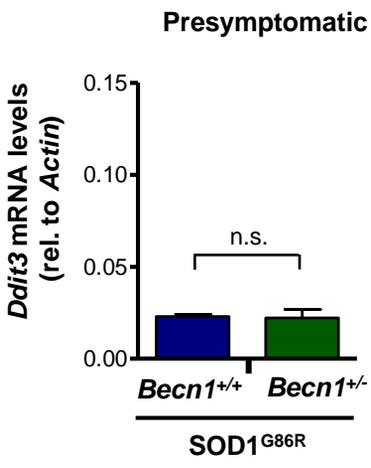
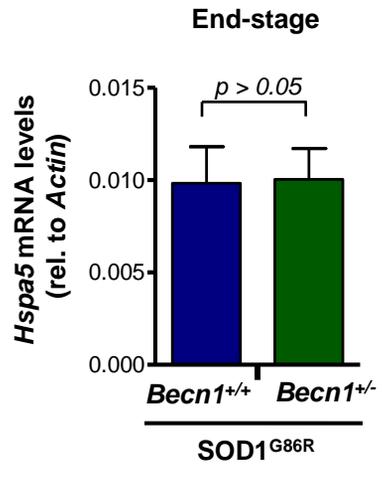
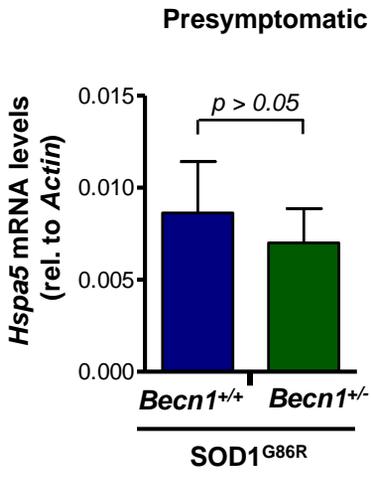


Figure S3



**Figure S4**

**Figure S1.** *Becn1* heterozygous mice. (A) To confirm the functional reduction of BECN1 1 in *Becn1*<sup>+/-</sup> animals, the levels of BECN1 were monitored in spinal cord extracts from *Becn1*<sup>+/+</sup> and *Becn1*<sup>+/-</sup> mice by western blot. HSP90 was used as a loading control. (B) Example of a DNA-tail genotyping by PCR followed by an electrophoresis on an agarose gel. In the figure we show the representative genotyping of 2 animals, a *Becn1*<sup>+/+</sup> and *Becn1*<sup>+/-</sup> mouse. Two separate PCR reactions were performed for each DNA-tail, with 2 pairs of primers to amplify the wild-type allele (monitored as a loading control) or the “knockout” (ko) allele. (C) Variation of the body weight over time in experimental *Becn1*<sup>+/+</sup> SOD1<sup>G86R</sup> and *Becn1*<sup>+/-</sup> SOD1<sup>G86R</sup>. Mice started to be monitored from 30 d old until the day of their sacrifice. (D) Levels of *Bcl2l1* were determined by real-time PCR in *Becn1*<sup>+/+</sup> SOD1<sup>G86R</sup> and *Becn1*<sup>+/-</sup> SOD1<sup>G86R</sup> and non-transgenic spinal cord tissue at the presymptomatic and end-of-disease stages. Mean and standard error are presented for the analysis of 4 animals per group. The *P* value was calculated with the Student *t* test. n.s., nonsignificant differences. (E) BCL2 levels were evaluated in spinal cord tissue from *Becn1*<sup>+/+</sup> SOD1<sup>G86R</sup> and *Becn1*<sup>+/-</sup> SOD1<sup>G86R</sup> mice in the same samples/gel shown in Figure 4F. Actin was used a loading control (same image from Figure 4F). Right panel: Quantification of BCL2 levels. Mean and standard error are presented.

**Figure S2.** GFAP and RBFOX3 in presymptomatic SOD1<sup>G86R</sup> mice. (A) Immunofluorescence analysis of the expression of GFAP (astrocytes, green) and RBFOX3 (neurons, red) after indirect immunofluorescent staining of spinal cord tissue derived from *Becn1*<sup>+/+</sup> SOD1<sup>G86R</sup> and *Becn1*<sup>+/-</sup> SOD1<sup>G86R</sup> at the presymptomatic stage of disease. A merged image is also presented together with a zoom of the selected area (yellow square). A representative image is presented of the analysis of 3 independent animals for group. Scale bars: 10 μm. Right panel: Quantification of the GFAP signal intensity is presented for 3 animals from each genotype.

Mean and standard deviation are presented. *P* value was calculated with the Student *t* test. n.s., nonsignificant differences.

**Figure S3.** Autophagy inhibition increases SOD1<sup>G85R</sup>-EGFP aggregation. **(A)** NSC34 cells expressing SOD1<sup>G85R</sup>-EGFP were treated with 10 mM 3-MA for 16 h or left untreated (control), and then the generation of mutant SOD1 aggregation was analyzed by western blot. Results are representative from at least 3 independent experiments. **(B)** NSC34 cells were cotransfected with SOD1<sup>G85R</sup>-EGFP, FLAG-BECN1 in the presence or absence of FLAG-BCL2L1 expression vectors. After 72 h, SOD1 protein oligomers were measured in cell extracts prepared in 1% Triton X-100?? by western blot. HSP90 levels were monitored as loading control. Then quantification of relative SOD1 levels of the monomeric species from 3 independent experiments was performed, normalized to the values obtained in control cells only expressing mutant SOD1. Mean and standard error are presented. Western blots are shown in Figure 6C. **(C)** NSC34 cells expressing SOD1<sup>G85R</sup>-EGFP together with FLAG-BECN1 were treated with 10 mM 3-MA for 16 h or left untreated (control), and then the generation of mutant SOD1 aggregation was analyzed by western blot. HSP90 levels were monitored as loading control.

**Figure S4.** Expressions of ER stress markers in SOD1<sup>G86R</sup> mice heterozygous for *Becn1*. Expression levels of the mRNA of *Hspa5* and *Ddit3* were determined by real-time PCR in *Becn1*<sup>+/+</sup> SOD1<sup>G86R</sup> and *Becn1*<sup>+/-</sup> SOD1<sup>G86R</sup> spinal cord in presymptomatic and end-stage of the disease. Mean and standard error are presented for the analysis of 4 animals per group. *P* value was calculated with the Student *t* test. n.s., nonsignificant differences.