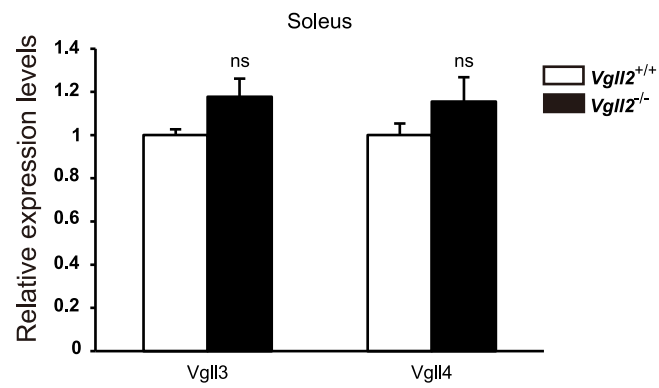
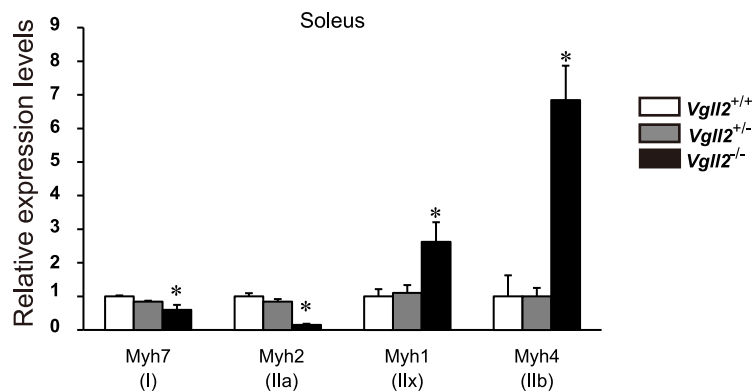


Supplementary information for:  
“Vestigial-like 2 contributes to normal muscle fiber type  
distribution in mice”

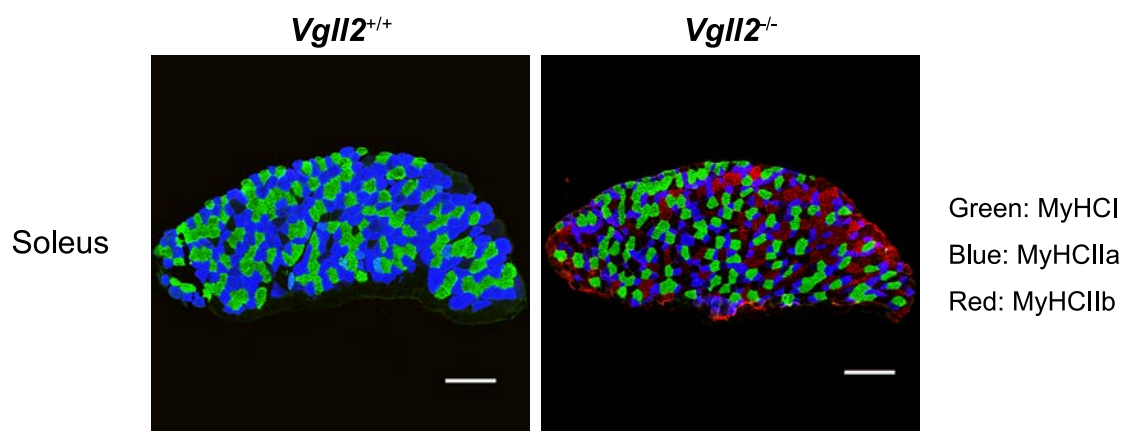
By: Masahiko Honda, Kyoko Hidaka, So-ichiro Fukada, Ryo Sugawa, Manabu  
Shirai, Masahito Ikawa, and Takayuki Morisaki



**Supplementary Figure S1. Quantification of the expression levels of Vgll family genes in adult skeletal muscle.** *Vgll3* and *Vgll4* mRNA levels were measured by qPCR in the soleus muscles from 12-week-old *Vgll2*<sup>+/+</sup> and *Vgll2*<sup>-/-</sup> mice (n = 6). ns, not significant difference. Data are presented as mean ± SEM. For comparison, the expression level in *Vgll2*<sup>+/+</sup> was arbitrarily set at 1.



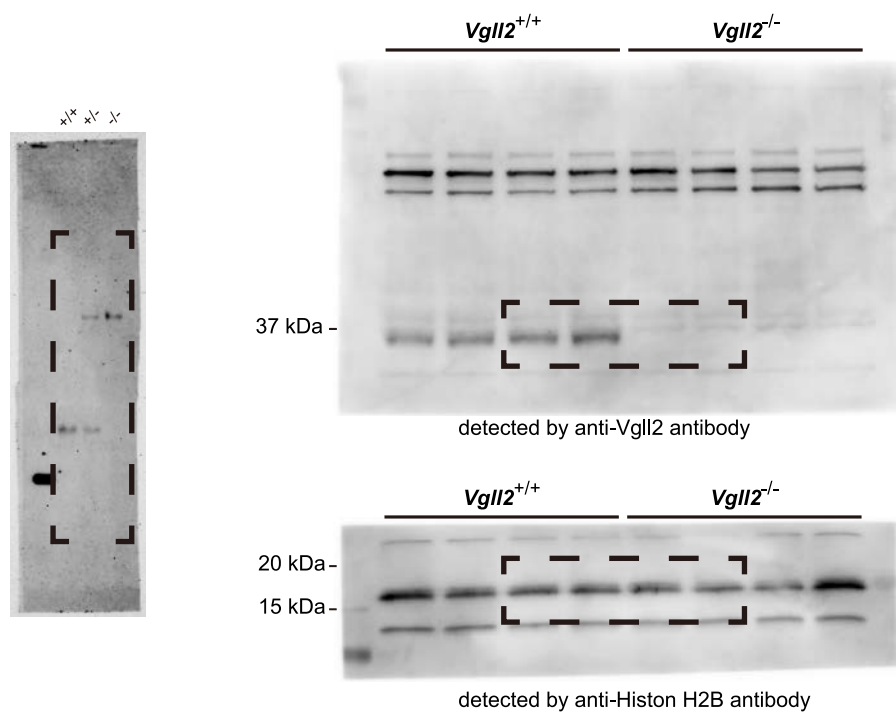
**Supplementary Figure S2. Quantification of the expression levels of myosin heavy chain isoforms in adult skeletal muscle.** Expression levels of genes encoding MyHC isoforms, *Myh7* (I), *Myh2* (IIa), *Myh1* (IIx), and *Myh4* (IIb) were measured by qPCR in the soleus muscles from 12-week-old *Vgll2*<sup>+/+</sup>, *Vgll2*<sup>+/-</sup>, and *Vgll2*<sup>-/-</sup> mice (n = 3). For comparison, the expression level of these genes in *Vgll2*<sup>+/+</sup> mice was arbitrarily set at 1. Data are presented as mean ± SEM. \**P* < 0.05 vs. *Vgll2*<sup>+/+</sup> in each muscle.



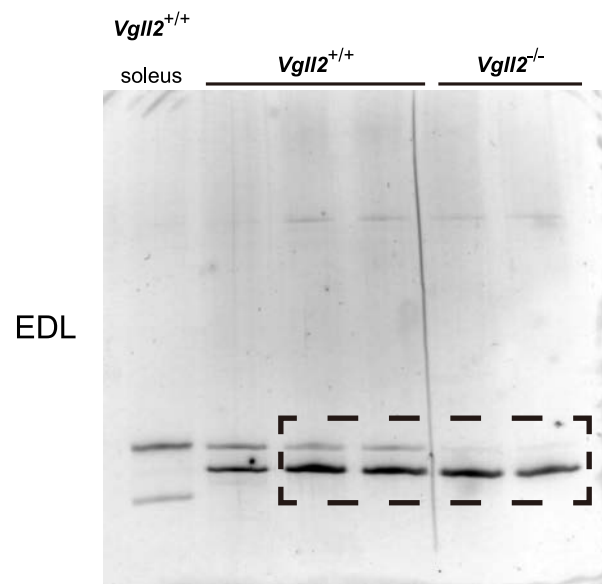
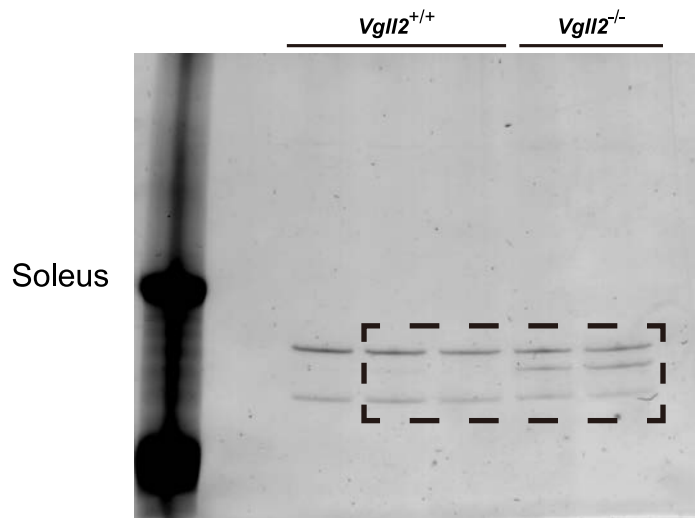
**Supplementary Figure S3. Fiber type composition analysis based on the immunostaining of myosin heavy chain isoforms in adult skeletal muscles.** Alternative images of immunostained soleus muscles presented in Figure 3. Samples are isolated from 12-week-old *Vgll2*<sup>+/+</sup> and *Vgll2*<sup>-/-</sup> mice. Scale bar: 200  $\mu$ m.



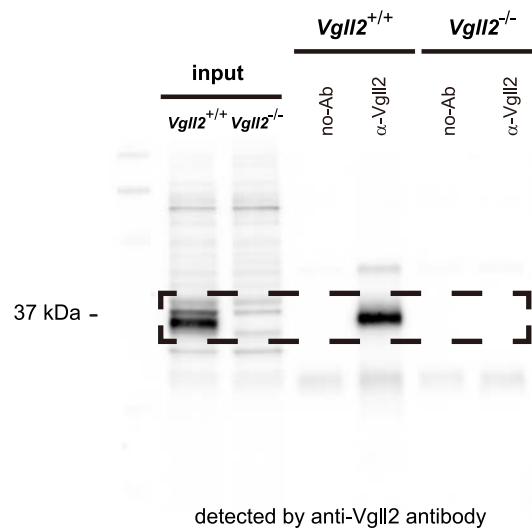
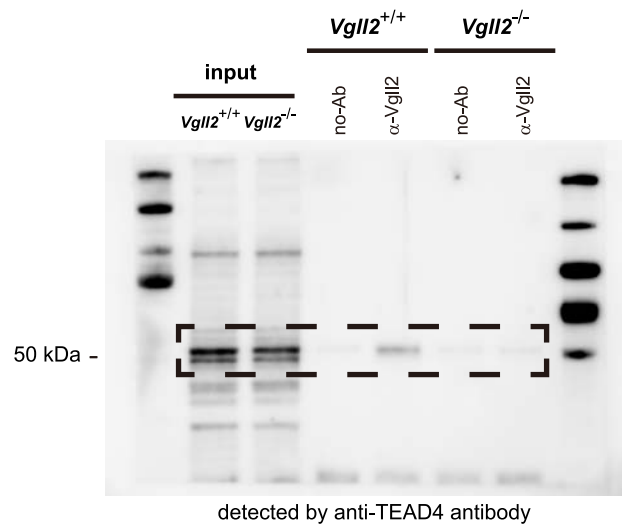
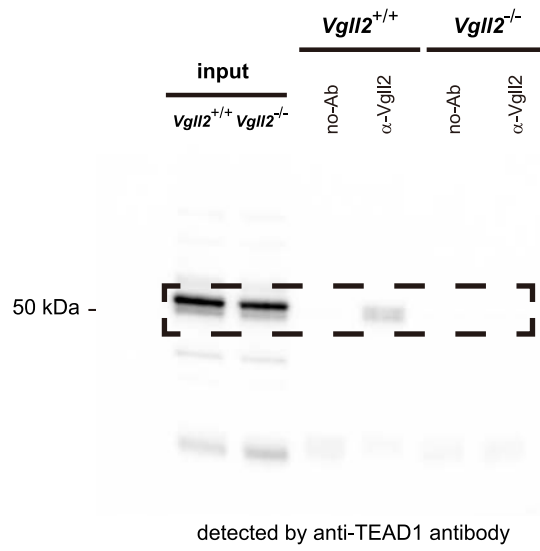
**Supplementary Figure S4. Quantification of the expression levels of cofactor of TEAD transcription factor genes in neonatal skeletal muscle.** Expression levels of cofactors of TEAD transcription factors were measured by qPCR in the gastrocnemius-plantaris-soleus (GPS) muscle complex at postnatal day 7 (P7) of *Vgll2*<sup>+/+</sup> and *Vgll2*<sup>-/-</sup> mice (n = 8). Yap and Taz mRNA expression levels were examined. For comparison, the expression level of these genes in *Vgll2*<sup>+/+</sup> mice was arbitrarily set at 1. Data are presented as mean ± SEM. ns, not significant difference.



**Supplementary Figure S5. Full-length blot images of Fig. 1c and d (with minimal contrast adjustment).** Dotted areas were cropped, processed in accordance with the guidelines, and used for the figure.

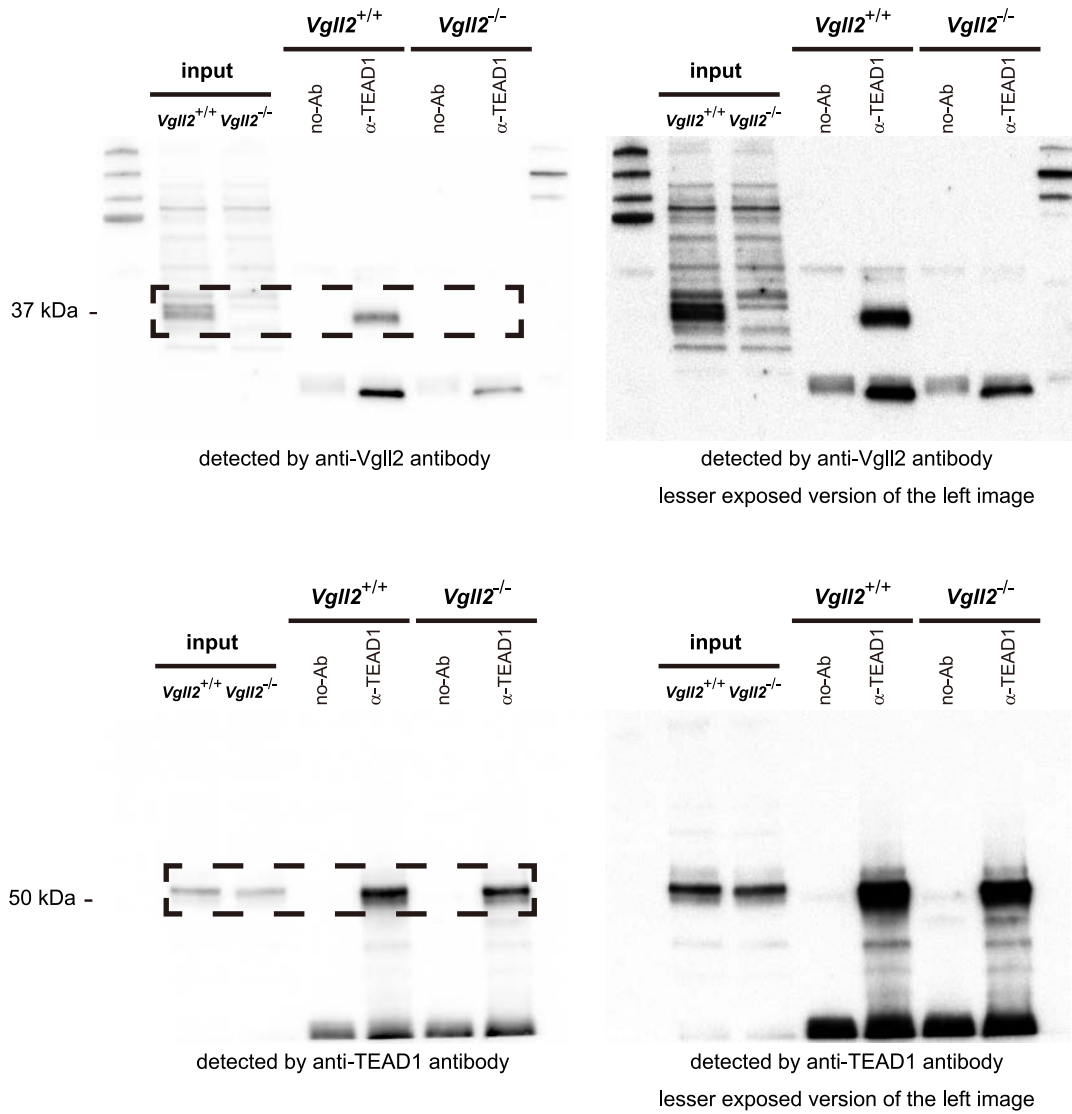


**Supplementary Figure S6. Full-length gel images of Fig. 3b (with minimal contrast adjustment).** Dotted areas were cropped, processed in accordance with the guidelines, and used for the figure.



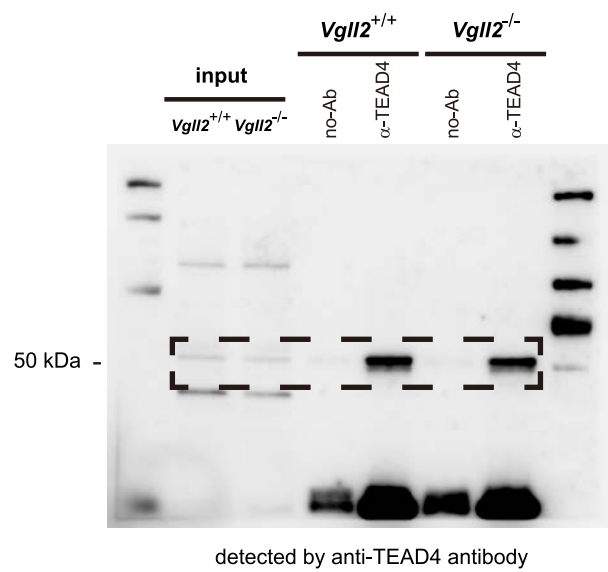
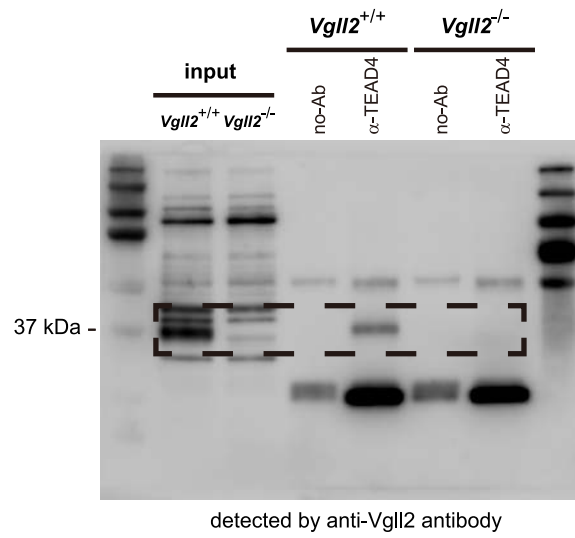
**Supplementary Figure S7. Full-length blot images of Fig. 5a (with minimal contrast adjustment).** Dotted areas were cropped, processed in accordance with the guidelines, and used for the figure.





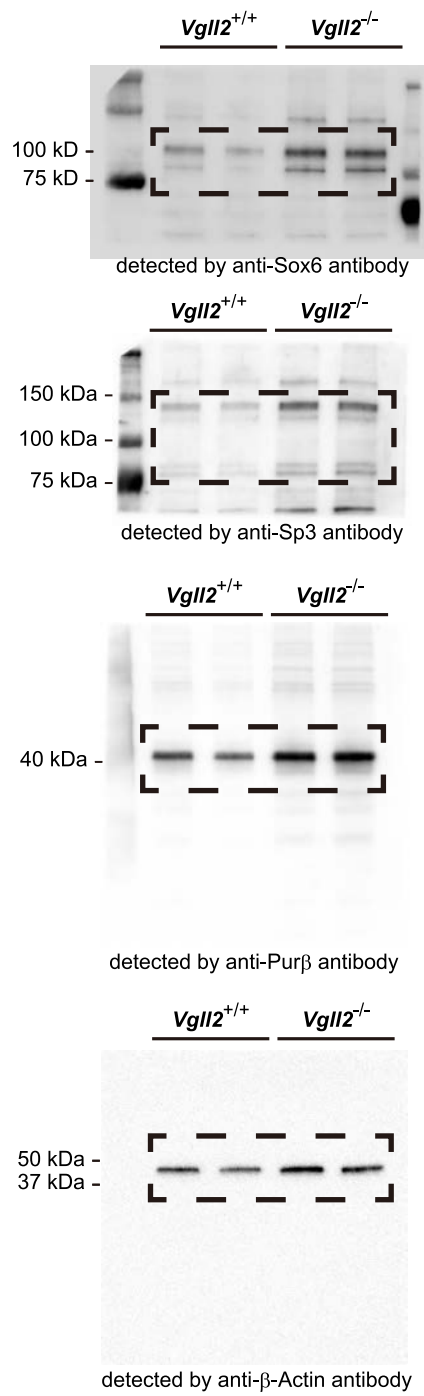
**Supplementary Figure S8. Full-length blot images of Fig. 5b (with minimal contrast adjustment).**

Dotted areas were cropped, processed in accordance with the guidelines, and used for the figure.



**Supplementary Figure S9. Full-length blot images of Fig. 5c (with minimal contrast adjustment).**

Dotted areas were cropped, processed in accordance with the guidelines, and used for the figure.



**Supplementary Figure S10. Full-length blot images of Fig. 7a (with minimal contrast adjustment).**

Dotted areas were cropped, processed in accordance with the guidelines, and used for the figure.