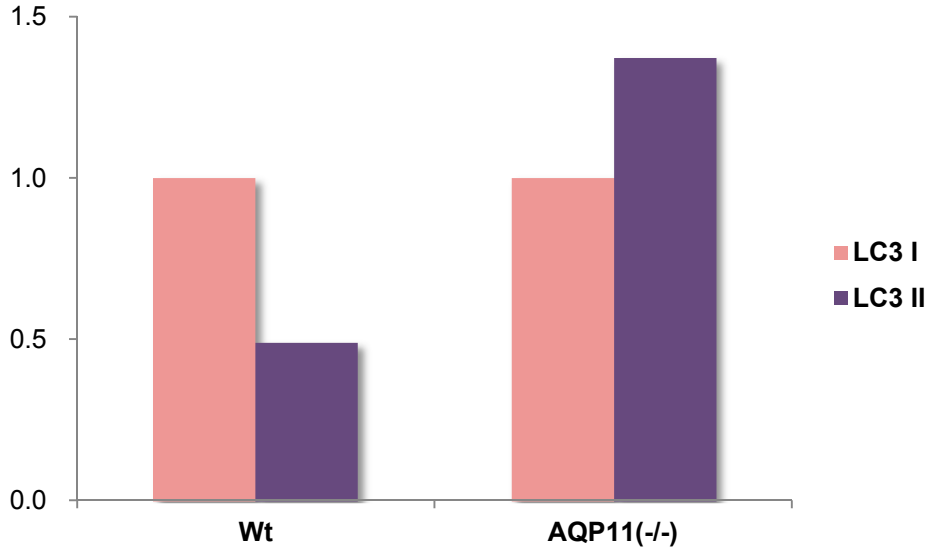
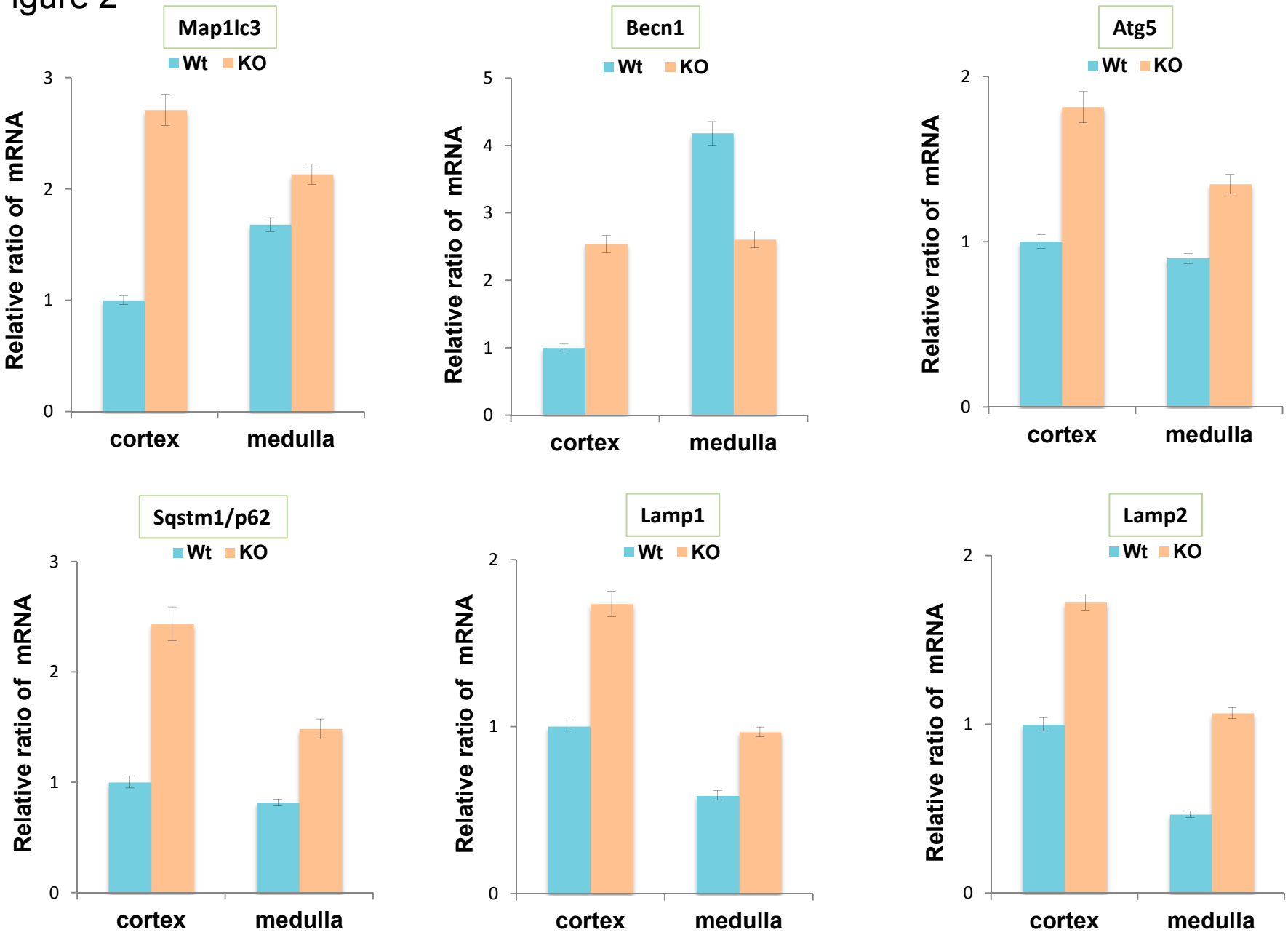
Supplementary information
Figure 1



The western blotting of Fig1.B was analyzed by graphical method (ImageJ). It was showed that inactive form LC3 I of wild mice was in the standard (=1). The inactive form of both mice was the same density. The active form of LC3 II was half density for the inactive form of LC3 I in wild mice. In contrast, the expression of LC3 II in AQP11(-/-) mice was increased to 2.8 times for the expression of LC3 I in wild mice. The results suggest that autophagy was enhanced in the kidney of AQP11 (-/-).

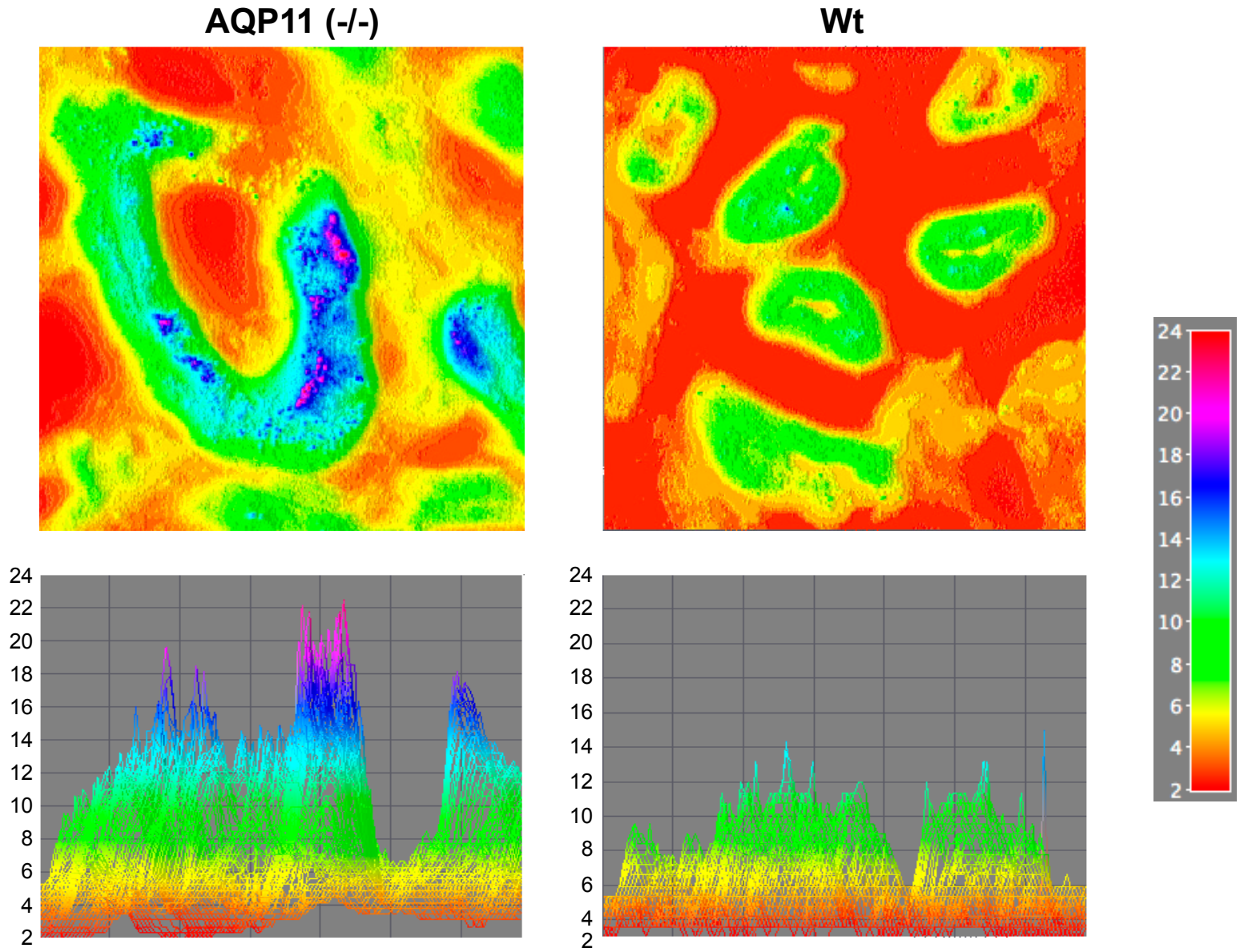
Supplementary Information
Figure 2



Supplementary figure 2

Quantitative analysis (qRT-PCR) for Map1lc3b (an autophagy marker), Becn1, Atg5 and Sqstm1/p62 (early augophagosome markers) , and Lamp1 and Lamp2 (late autophagosome markers) in the kidney of 3 week old mice. The expression level of each gene was compared between AQP11(-/-) and wild type in the cortex and the medulla. The expression levels in the cortex of the wild type are arbitrarily normalized to one. The results are the mean +/- SE of three separate sets of experiments.

Supplementary Information
Figure 3



Supplementary figure 3

The GFP expression of puncta were analyzed by interactive 3D surface plot of Image J for the proximal tubule in Fig.3D and Fig.3J. The intensity of fluorescence was shown as a heat map indicator on the right. The level of heat map under 12 indicates a background.