Figure S1. Coomassie blue staining of purified recombinant LRRK2 and NLRC4 proteins (NLRC4 WT and S533A mutant).
Mass spectrometry identified phosphorylation at Ser533 of NLRC4. (a) Phosphorylation site analysis of NLRC4. Immunoprecipitated NLRC4 from HEK293T cells cotransfected with NLRC4 and LRRK2 was used for mass spectrometric analysis following standard procedures. (b) Protein coverage of NLRC4. NLRC4 peptides detected by mass spectrometry covered 66.5% of the NLRC4 protein sequence. Residues covered are highlighted in blue font. Phosphorylation was detected only on Ser533 (boxed in red) of NLRC4.
Figure S3. **Genotyping of LRRK2 G2019S transgenic mice.** (a) RT-PCR to examine human LRRK2 mRNA expression in LRRK2 G2019S transgenic mice. RNA was extracted from peritoneal macrophages and brain tissue of G2019S transgenic mice, cDNA was synthesized, and human-specific primers to LRRK2 were used for RT-PCR. Data are representative of two independent experiments. $n = 3$ mice/group. Mr. represents the DNA marker used. (b) Sequence result of LRRK2 cDNA$_{5751-6540}$ from peritoneal macrophages of G2019S transgenic mice. Three base pairs of the GGC (Gly) to TCG (Ser) transition (between 6,055–6,057 bp) were detected and are highlighted in the red box.