SUPPLEMENTAL MATERIAL

Liu et al., https://doi.org/10.1084/jem.20170014

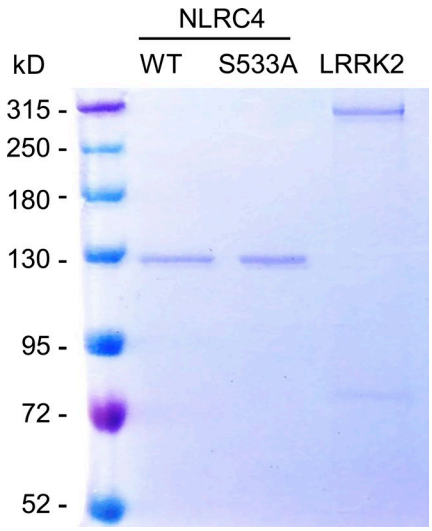

Figure S1. **Coomassie blue staining of purified recombinant *LRRK2* and NLRC4 proteins (NLRC4 WT and S533A mutant).**

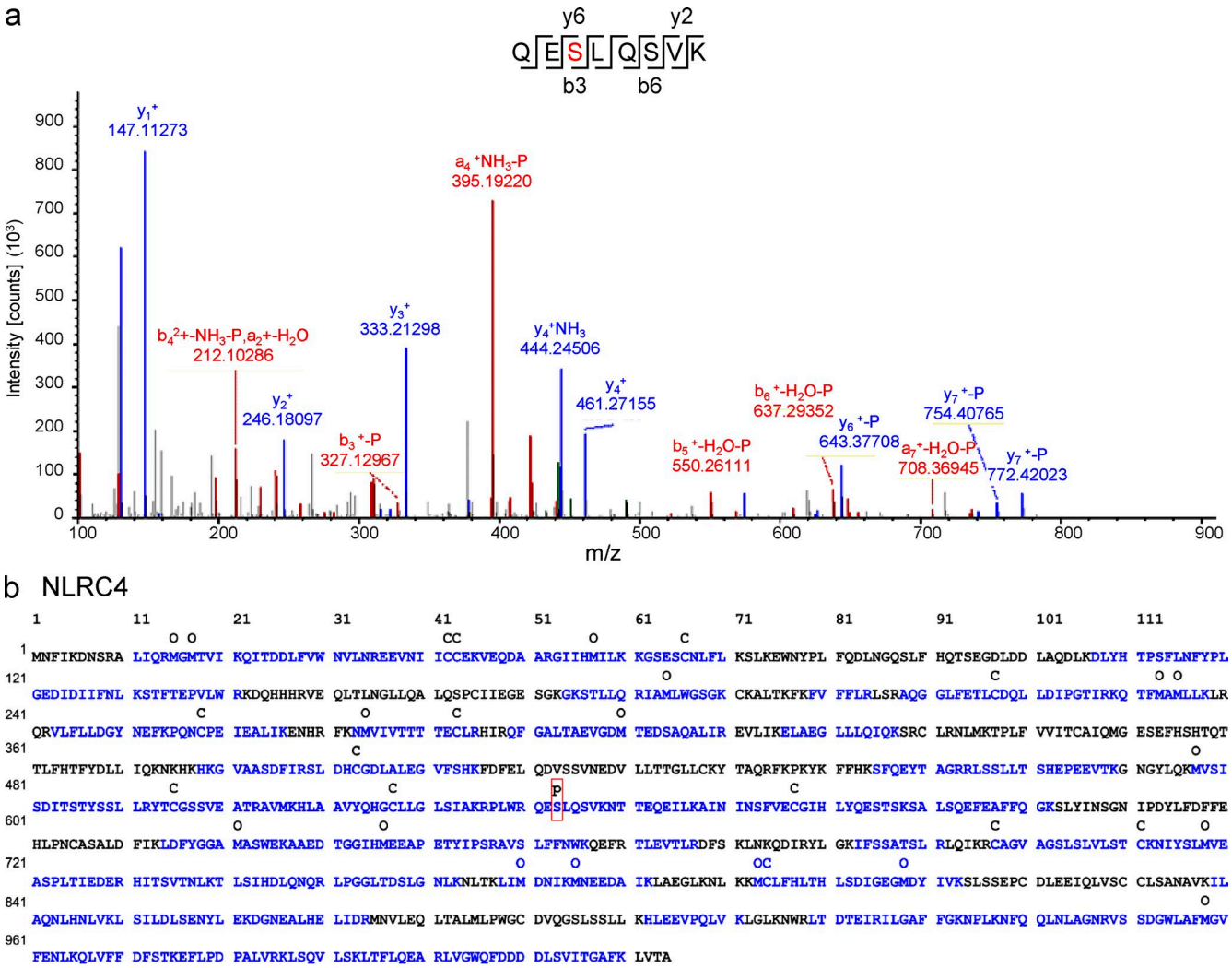

Figure S2. **Mass spectrometry identified phosphorylation at Ser533 of NLRC4.** (a) Phosphorylation site analysis of NLRC4. Immunoprecipitated NLRC4 from HEK293T cells cotransfected with NLRC4 and *LRRK2* was used for mass spectrometric analysis following standard procedures. (b) Protein coverage of 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.

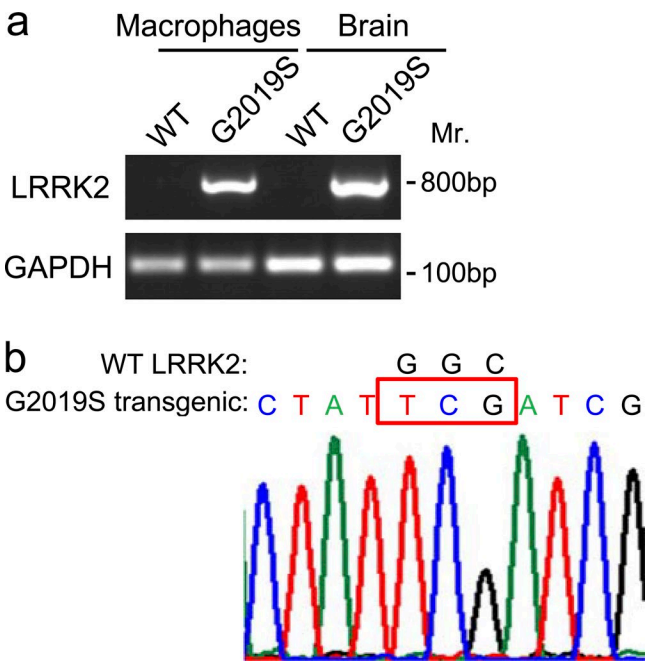

Figure S3. **Genotyping of *LRRK2* G2019S transgenic mice.** (a) RT-PCR to examine human *LRRK2* mRNA expression in *LRRK2* G2019S transgenic mice. RNA was extracted from peritoneal macrophages and brain tissue of G2019S transgenic mice, cDNA was synthesized, and human-specific primers to *LRRK2* were 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.