

*Preclinical modeling of chronic inhibition of the Parkinson's disease associated kinase LRRK2 reveals altered function of the endolysosomal system in vivo*

Article

Supplemental Material

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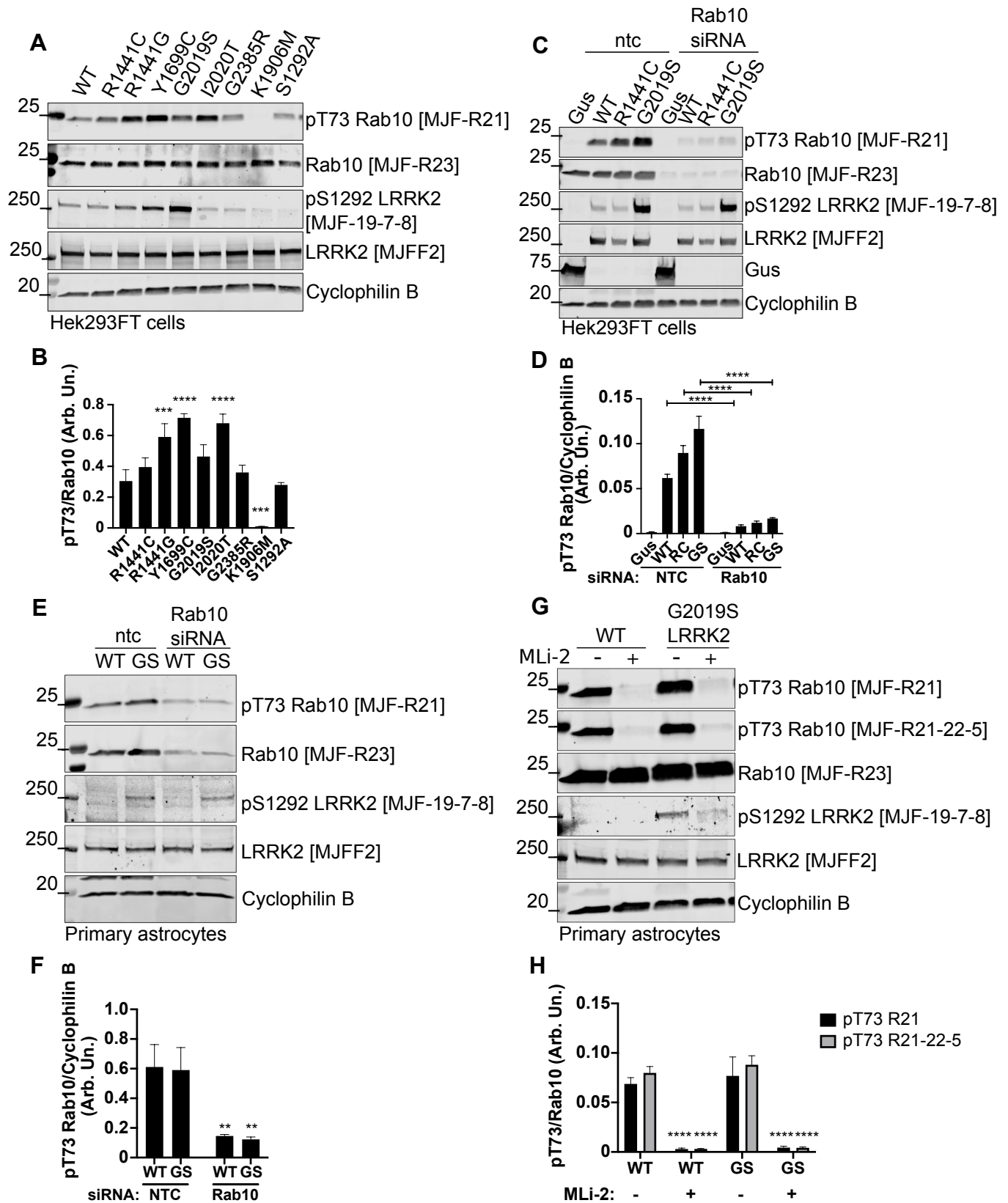


Figure S2

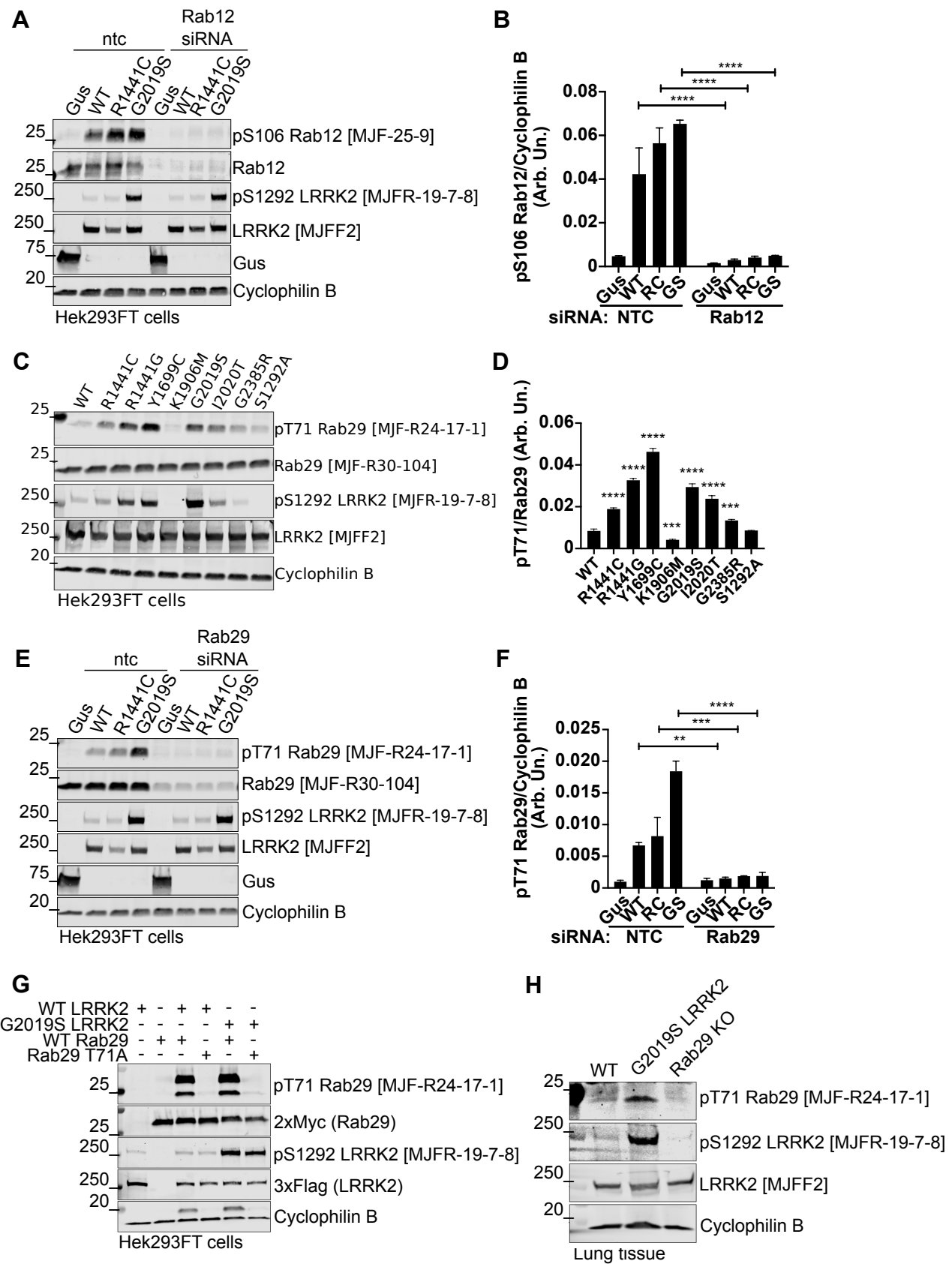
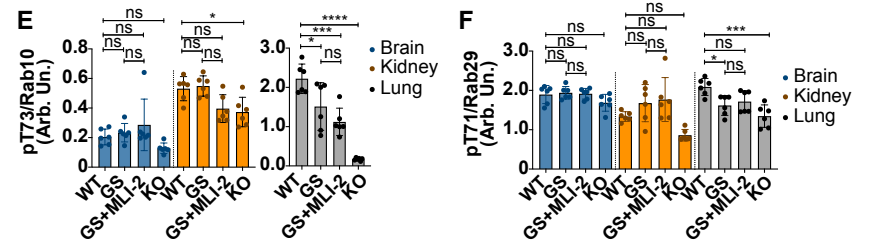
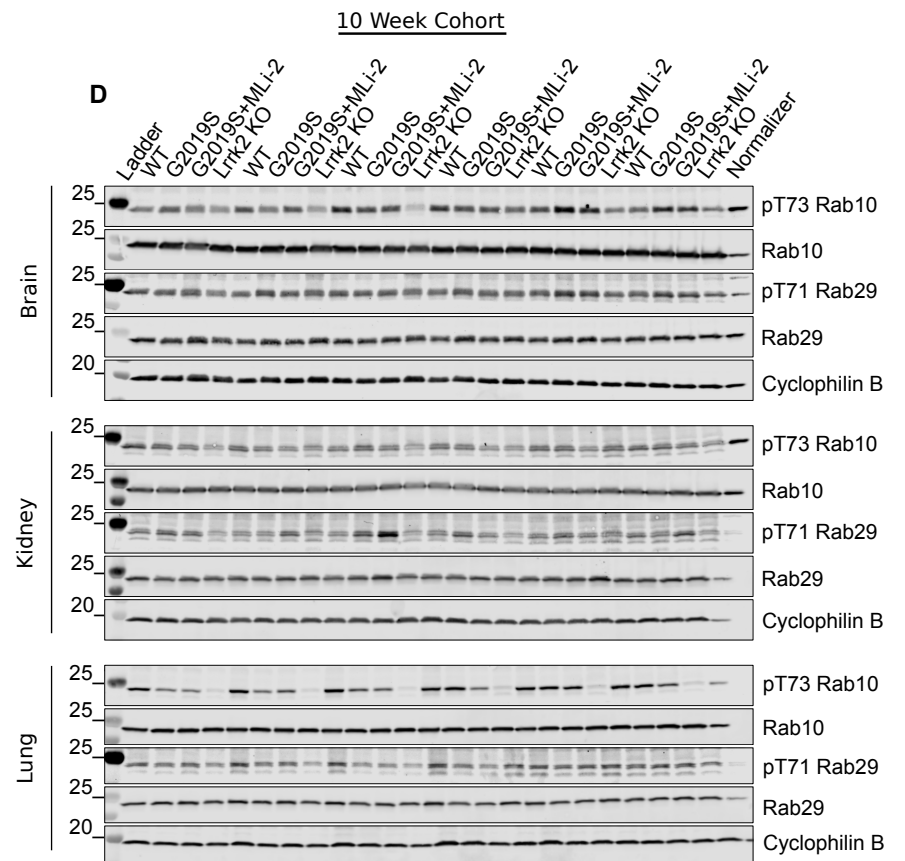
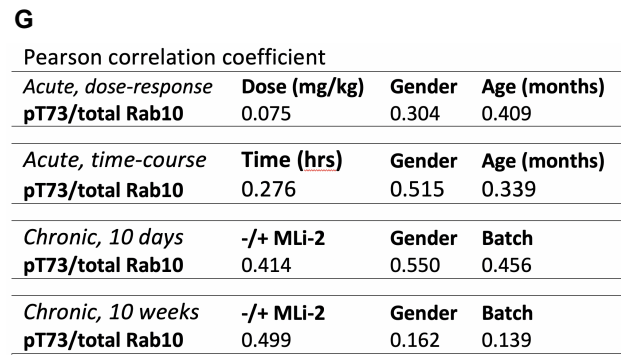
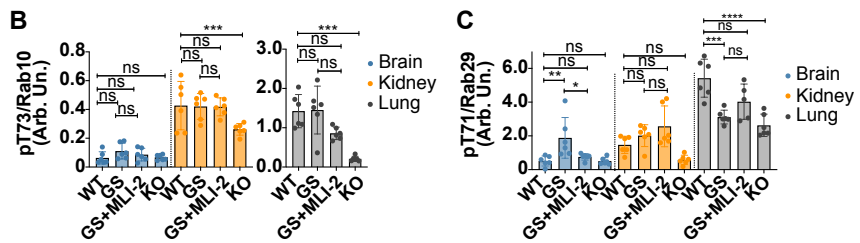
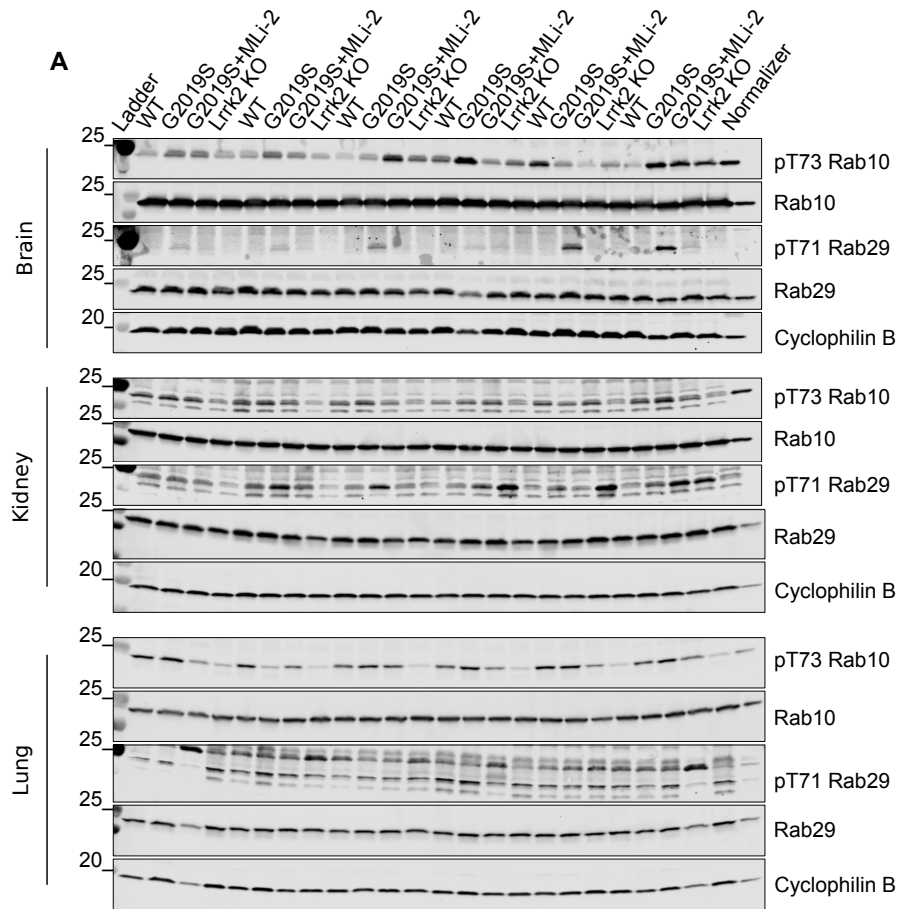


Figure S3



## 10 Day Cohort



## Figure S4

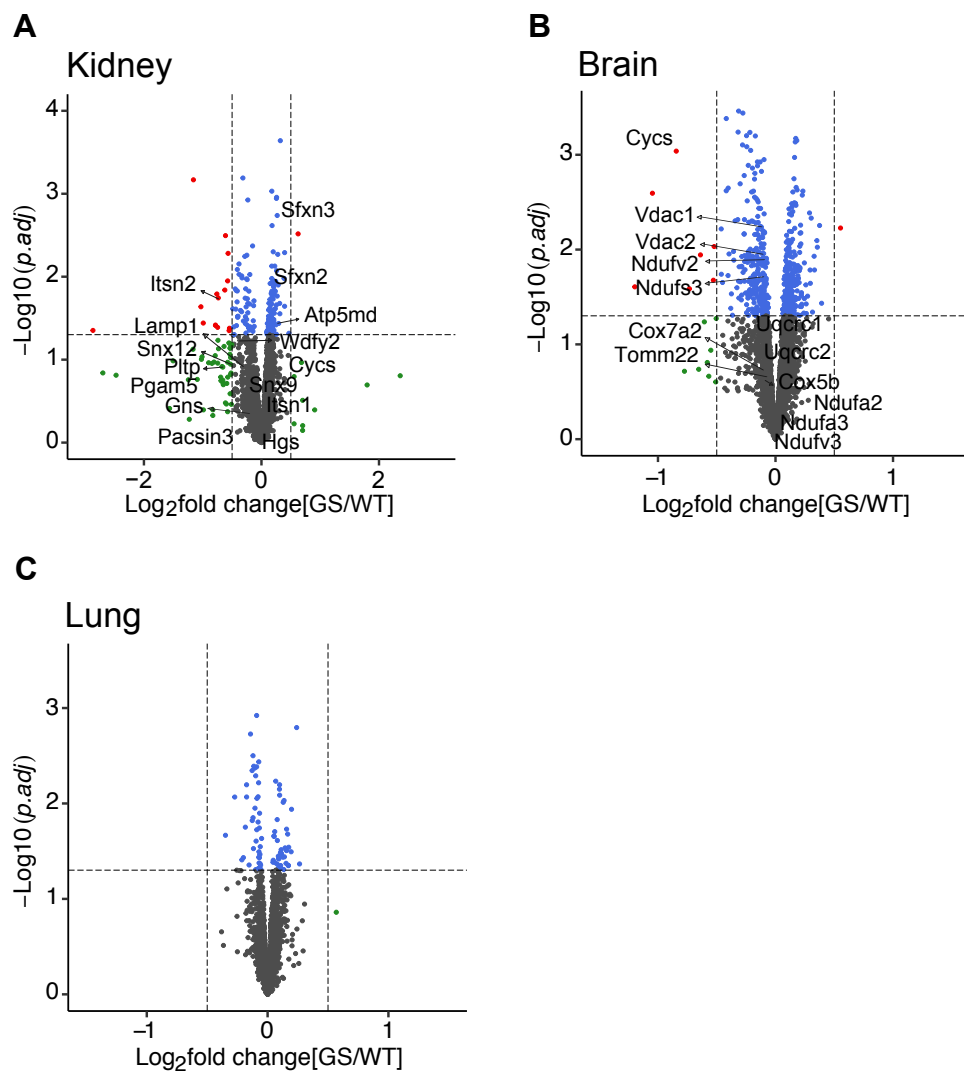


Figure S5

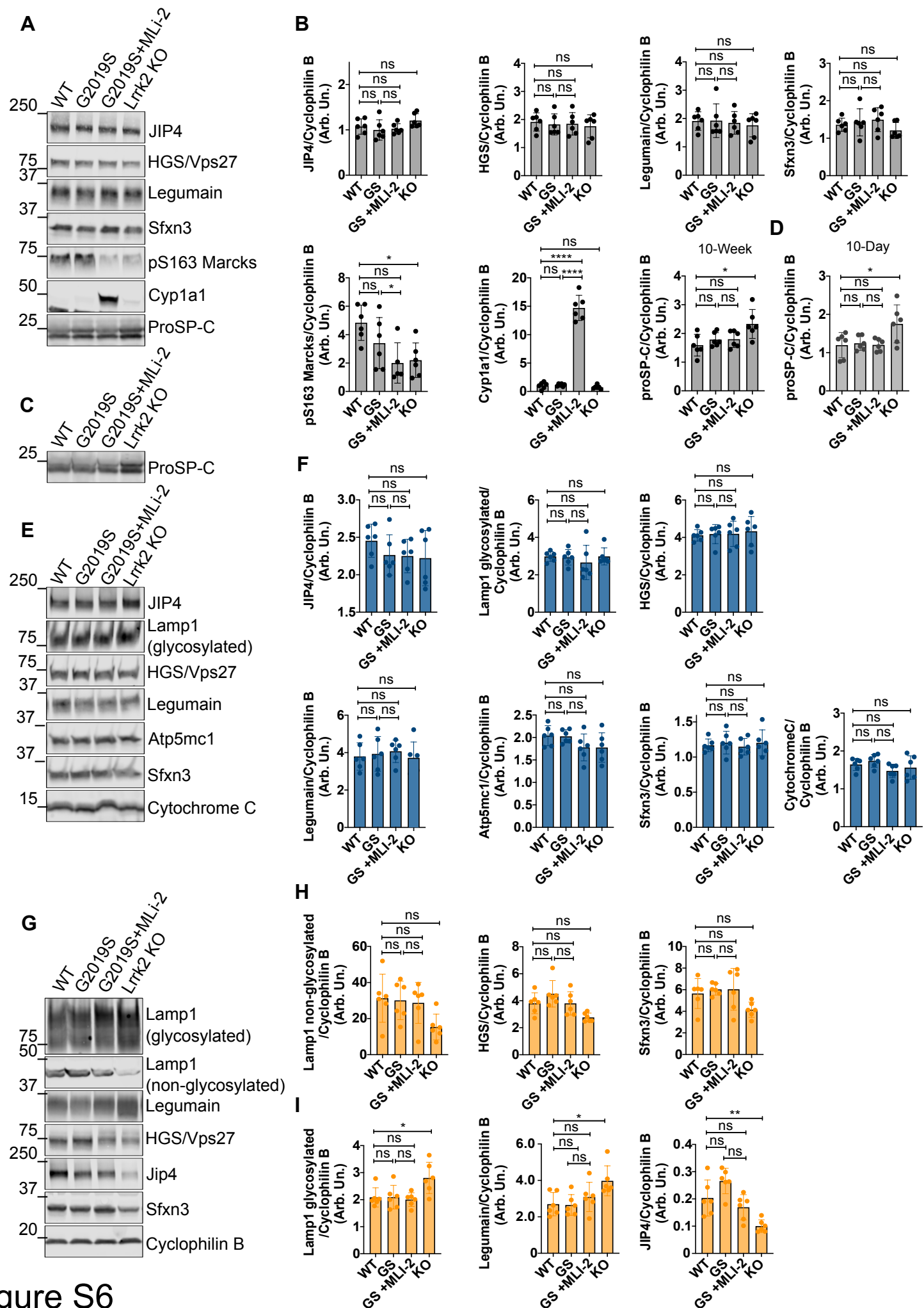


Figure S6

Legend:

- Direct interactor of LRRK2, total protein
- Direct interactor of LRRK2, phospho-site
- 1 step from LRRK2, total protein
- 1 step from LRRK2, phospho-site

1 step of bridge nodes

Network diagram showing interactions between LRRK2 and various proteins. LRRK2 is a central purple node. It has direct interactors (green nodes) and phospho-site interactors (blue nodes). A box labeled '1 step of bridge nodes' points to a large circular network of nodes, which includes both direct interactors and phospho-site interactors of the bridge nodes.

[illegible]

Figure S7