

## **Description of Additional Supplementary Files**

**Supplementary Data 1.** RNA-sequencing meta-analysis. Data is compiled from 3 datasets: de Rus Jacquet et al., Booth et al. and di Domenico et al.. The tabs "All genes\_Downregulated" and "All genes\_Upregulated" show the combined dysregulated genes for these 3 datasets (duplicates removed) and compares LRRK2 G2019S vs control iPSC-derived astrocytes. Gene Ontology tabs: sub-categories are extracted from DAVID Gene Ontology analysis. The fold change value of LRRK2 G2019S vs. control astrocytes are provided in this supplementary file, and these are the data used to generate the heatmaps provided in Figure 1. The genes that are dysregulated in at least 2 datasets were used to generate the histograms provided in Figure 1.