

Supplementary Information for Single-cell transcriptomic classification of rabies-infected cortical neurons

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This PDF file includes:

Supplementary text
Figures S1 to S2
Legends for supplemental tables

Other supplementary materials for this manuscript include the following:

Table S1 and S2

Supplemental Information

Supplemental tables below are provided separately as Excel files

Table S1. List of Differentially Expressed Genes in Rabies-Infected Nuclei Compared to Control, Related to Figure 1.

Table S2. List of Cell-Type-Specific Differentially Expressed Genes in Rabies-Infected Nuclei Compared to Control, Related to Figure 4.

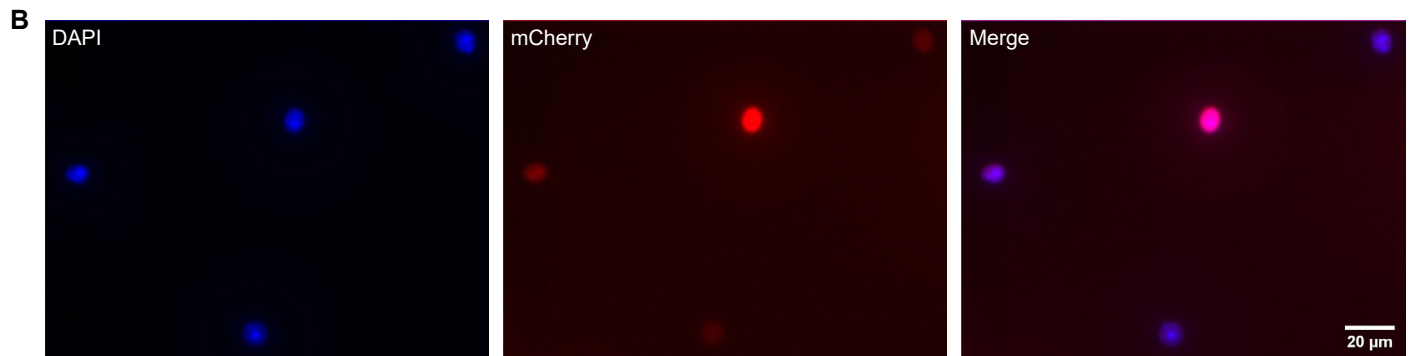
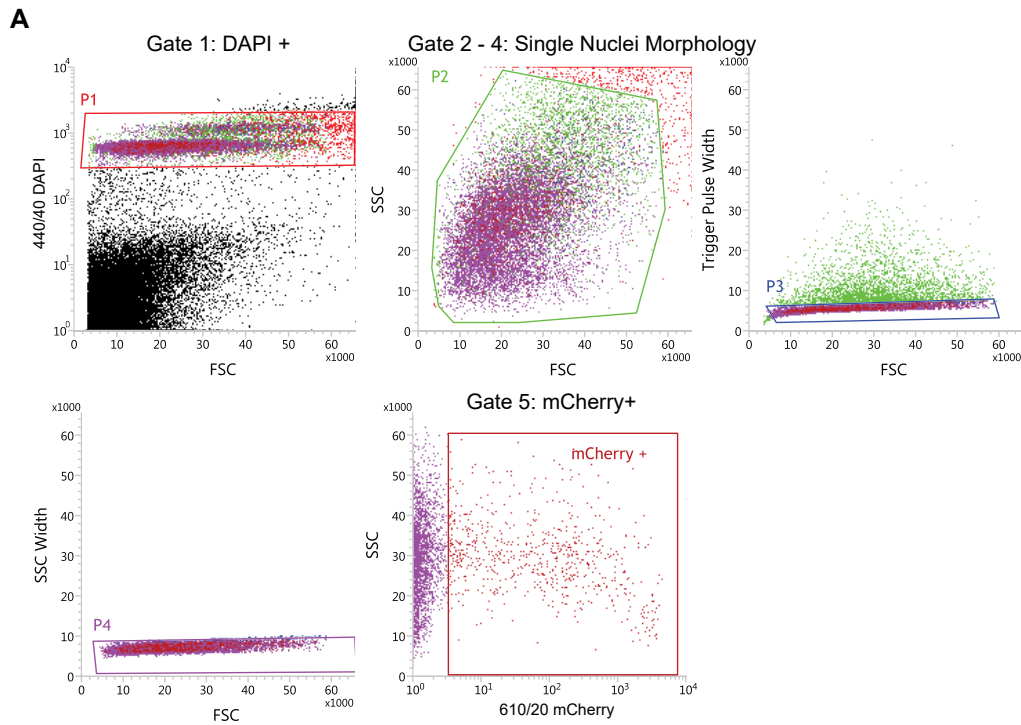


Figure S1. Details on rabies-infected fluorescence-activated nuclei sorting, related to Figure 1
 (A) Detailed gating strategy of fluorescence-activated nuclei sorting. Gate 1 selects for DAPI+ nuclei to exclude debris. Gate 2 -4 exclude cell doublets based on single nuclei morphology. Gate 5 selects for mCherry+ fluorescence.
 (B) Post-sorting visualization of sorted mCherry+ nuclei for quality control.

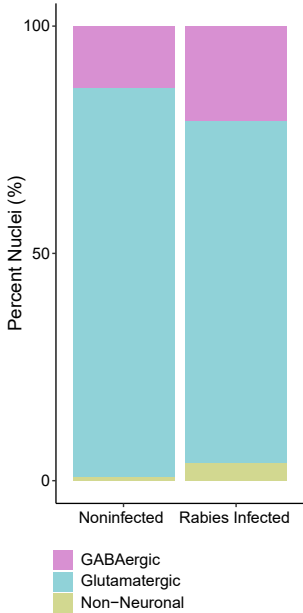
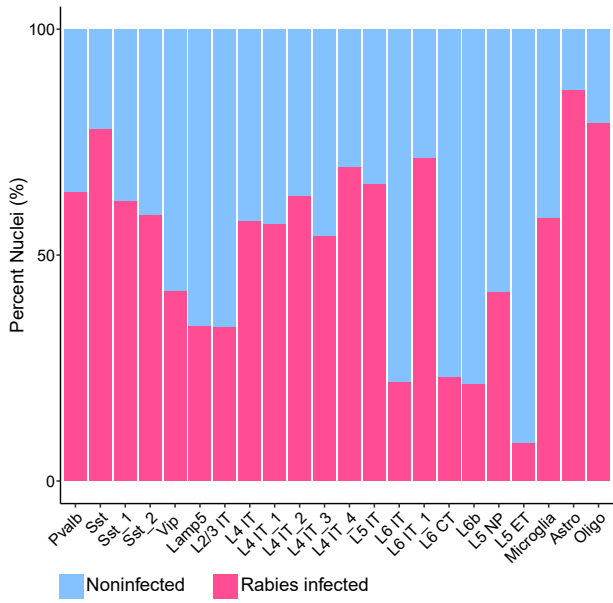
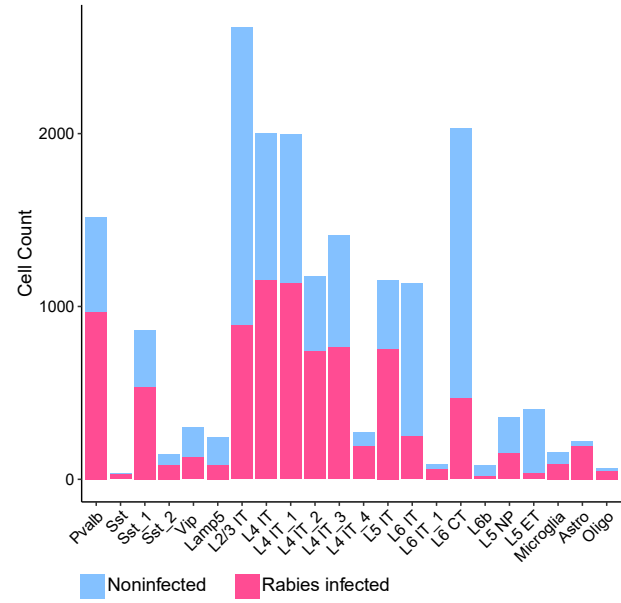
A**B****C**

Figure S2. Cell type composition of datasets, related to Figure 2

- (A) Percent of excitatory, inhibitory, and non-neuronal nuclei across experimental groups.
- (B) Percent distribution of rabies-infected and uninfected nuclei in each cluster.
- (C) Absolute count of rabies-infected and uninfected nuclei in each cluster.