Supplementary Information

Transcriptomic homogeneity and an age-dependent onset of hemoglobin expression characterize morphological PV types

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Supplementary Figures:

Fig. S1. Morphological reconstruction of different PV types. (Related to Fig. 1.)

Fig. S2. Single-cell RNAseq profiling of PV-INs. (Related to Fig. 1.)

Fig. S3. Transcriptomic clustering at low sample numbers. (Related to Fig. 1 and 4.)

Fig. S4. Transcriptomic characterization of PV-INs. (Related to Fig. 2.)

Fig. S5. Cross-comparison of electrophysiological parameters measured in PV-INs. (Related to Fig. 3.)

Fig. S6. Support vector machine classification and gene selection in morphological PV types. (Related to Fig. 4.)

Fig. S7. Expression of morphology-associated genes in the CA1-IN data set (Harris et al., 2018) (Related to Fig. 4)

Fig. S8. Morphological and electrophysiological analysis of vBC type PV-INs during circuit maturation. (Related to Fig. 6.)

Fig. S9. Age-dependent gene expression changes in PV-INs. (Related to Fig. 7.)

Fig. S10. Detection of hemoglobin expression in publicly available single-cell RNAseq datasets. (Related to Fig. 7.)

Fig. S11. Hemoglobin subunit expression at single-nucleotide level. (Related to Fig. 7.)

Supplementary Data Sheet:

Que_et_al.xlsx This file contains all numerical information referenced in the manuscript. (Related to Figs. 1-7.)