SUPPLEMENTARY FIG. S3. Number of nuclei that each replicate contributed. Cell-type clustering with a *k*-nearest neighbor graph was set to $k = 50$ using the function buildSNNGraph from scran (cf. Methods: snRNA-seq—data pre-processing, nuclei clustering, and differential expression) (Lun et al., 2016). snRNA-seq, single-nuclei RNA-seq.

Supplementary Reference

Lun ATL, McCarthy DJ, and Marioni JC. (2016). A step-by-step workflow for low-level analysis of single-cell RNA-seq data with Bioconductor. F1000Res 5, 2122.