Supplemental information

Mapping human adult hippocampal neurogenesis with single-cell transcriptomics: Reconciling controversy or fueling the debate?

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Figure S1. Heterogeneity of neurogenesis levels across individuals and its relation to inflammation in a non-human primate dataset. For each of the three macaques analyzed in the original study[1], we plotted the total number of sequenced nuclei and of identified neurogenic cells [including neuroblasts (NB), neural progenitor cells (NPC), and radial glia-like cells (RGL)], the proportion of the total neurogenic populations against the total number of nuclei, and the number of the individual subpopulations, per macaque. The astrocytic inflammation score per animal was computed as described in STAR Methods. Scores are shown as mean ± SEM. For statistical analysis, the Kruskal Wallis test and Dunn’s post hoc multiple comparison correction were performed using the GraphPad Prism software. Adjusted p-value, < 0.0001 (****); n=number of astrocytes per animal (547 in macaque 1, 1090 in macaque 2, 2559 in macaque 3). Related to Figure 5.
Figure S2. Human-specific versus human-mouse conserved gene set enrichment and additional marker gene combinations derived from meta-analysis. A. UMAP plots of data from Franjic et al.[1] representing 36 107 nuclei from macaque DG, Hao et al.[2] representing 207 785 nuclei from macaque DG, Franjic et al.[1] representing 139 187 nuclei from human DG. Cells/nuclei (dots) are labeled and colored by cluster membership labels from the original studies. B. Same UMAPs as in (A) with cells colored according to their Seurat module score calculated using conserved genes (blue) and human specific genes (red) derived from the meta-analysis, per cell type. C. Same UMAP as in (A) with cells colored according to their Seurat module score calculated using a combination of the meta-analysis-derived human markers for both ImNs and NBs as gene set, in the macaque datasets. See Table S3 for gene sets used. Precision, sensitivity and F1-scores corresponding to (C) are provided in Table S2. Related to Figure 4.
Figure S3. Top NPC and NB macaque markers in the human dataset. A. UMAP plot of data from Franjic et al.[1] representing 139 187 nuclei from human DG. Cells/nuclei (dots) are labeled and colored by cluster membership labels from the original studies. B,C. Same UMAP as in (A) with highlighted cells co-expressing at least 1 UMI of the top 4 and top 5 macaque NPC (B) and NB (C) markers derived from Hao et al.[2] and Franjic et al.[1] macaque datasets (yellow-highlighted genes in Table S1) in the Franjic et al.[1] human dataset. Related to Figure 5.
Figure S4. Marker overlap in distinct cell types across studies. NB, neuroblast; NPC, neural progenitor cell; Astro, astrocyte; ImN, immature neuron; RGL, radial glia-like. See Table S1 for gene sets used. Related to Figures 5 and 6.

Supplemental references list
