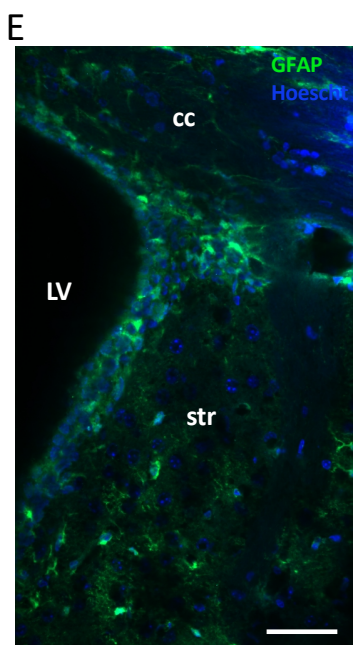
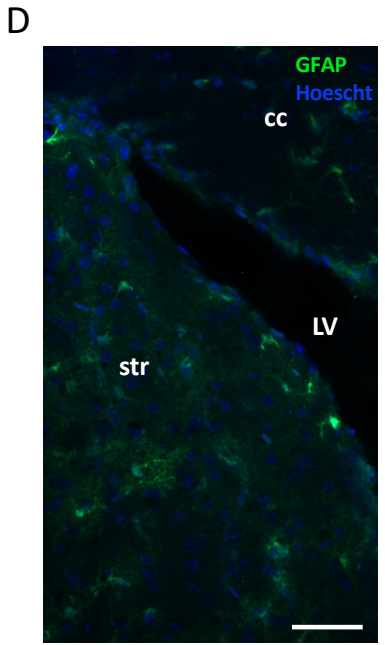
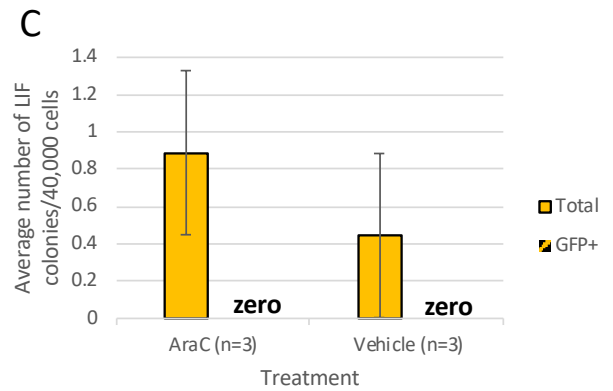
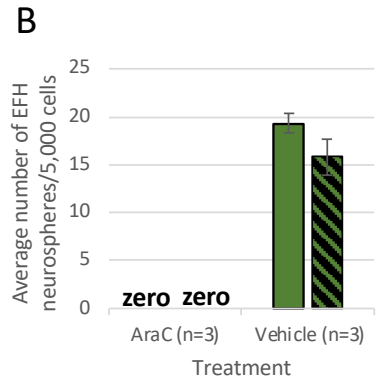
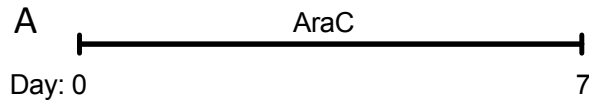


Lineage tracing reveals the hierarchical relationship between neural stem cell  
populations in the mouse forebrain

Nadia Sachewsky<sup>1\*</sup>, Wenjun Xu<sup>1,2\*</sup>, Tobias Fuehrmann<sup>4</sup>, Derek van der Kooy<sup>2,3</sup> and Cindi M  
Morshead<sup>1,2,4,5</sup>



**Supplemental Figure 1: GFAP expressing dNSCs are ablated following AraC infusion**

**a**, Schematic of the experimental paradigm. **b**, Number of dNSC derived neurospheres (EFH) following ablation with AraC or vehicle infusion in GFAP-gfp mice (n=3 per group) and the number that are gfp+. **c**, pNSC derived colonies (LIF) derived following ablation with AraC or vehicle infusion in GFAP-gfp mice (n=3 per group) and the number that are gfp+. **d**, Lateral ventricle image from sections of ablated mice with loss of GFAP expressing cells in the subependyma of GFAP-gfp mice. **e**, Lateral ventricle image from sections of vehicle infused mice with normal distribution of GFAP expressing cells in the subependyma of GFAP-gfp mice. Scalebar = 100µm. LV = lateral ventricle, str = striatum, cc = corpus callosum. Green = GFAP, Blue = Hoescht.