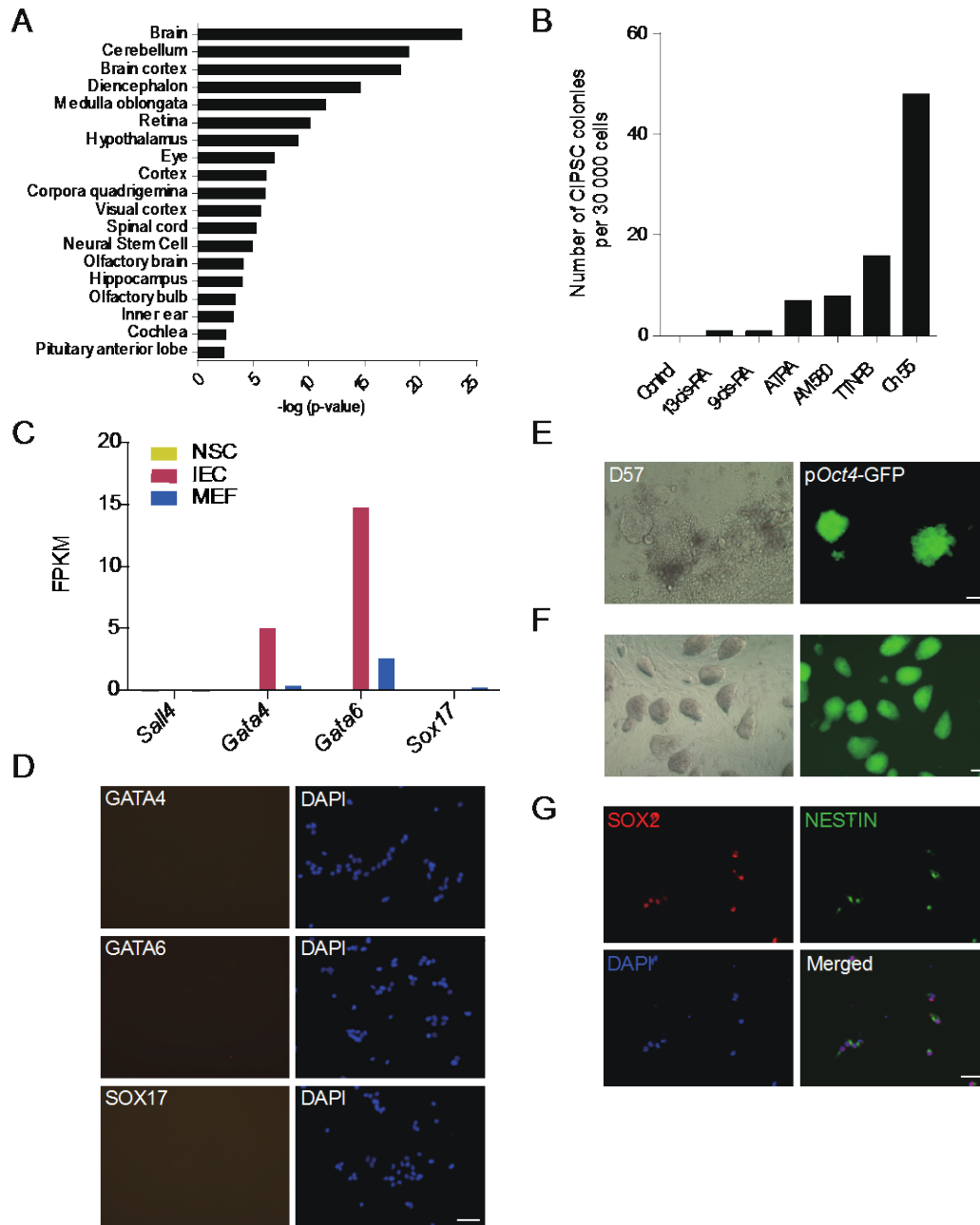


Figure S1



Supplementary information, Figure S1. Identification of Chemical Reprogramming Boosters and Further Characterization of NSCs. Related to Figure 2. (A) Gene Ontology (GO) terms for the RNA-seq analysis of isolated NSCs (passage 2), 10-fold up-regulated genes (relative to MEFs). (B) Screening of RAR agonists on chemical reprogramming of OG MEFs. 13-cis-RA, 2 μ M; 9-cis-RA, 2 μ M; ATRA, All-trans Retinoic acid, 2 μ M; AM

580, 0.01 μM ; TTNPB, 2 μM ; Ch 55, 1 μM . (C) mRNA levels of *Sall4*, *Gata4*, *Gata6* and *Sox17* genes detected by RNA-seq analysis in MEFs, IECs and NSCs. (D) Immunofluorescence staining of GATA4, GATA6 and SOX17 in initial NSCs. (E and F) Primary CiPSC colonies derived from postnatal NSCs at day 57 (D57), and passaged CiPSC colonies. (G) Immunofluorescence staining of SOX2 and NESTIN in FACS-sorted SSEA1-positive NSCs. For (D to F), scale bars, 100 μm . For (G), scale bars, 20 μm .