

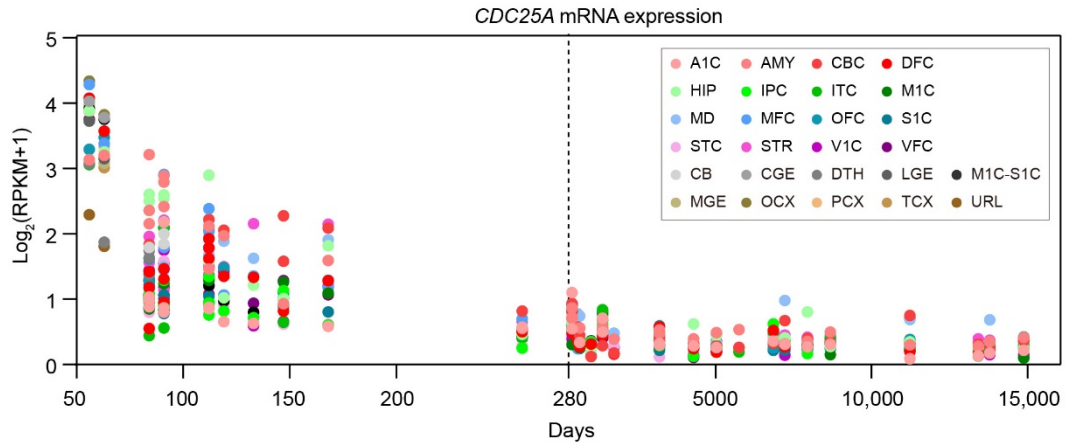
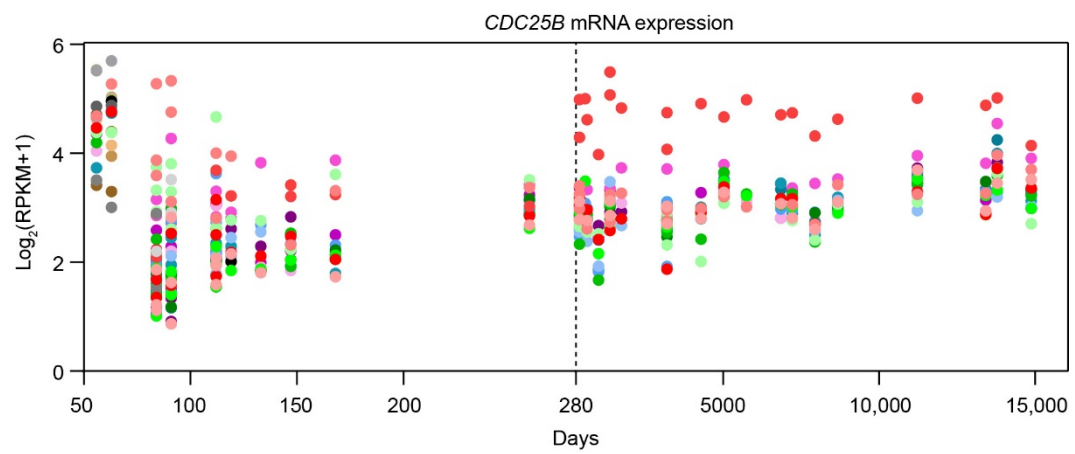
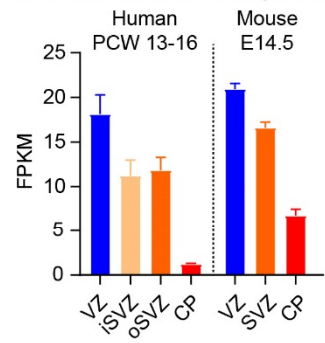
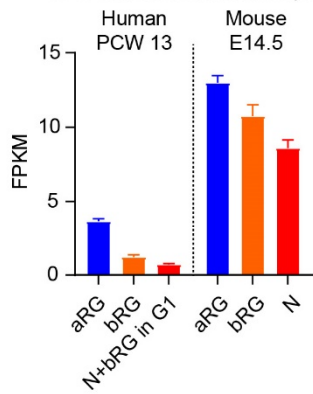
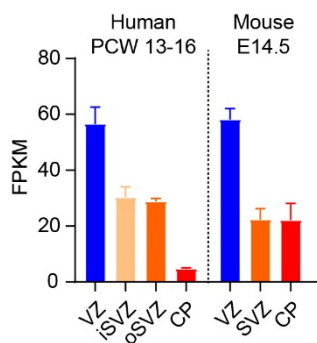
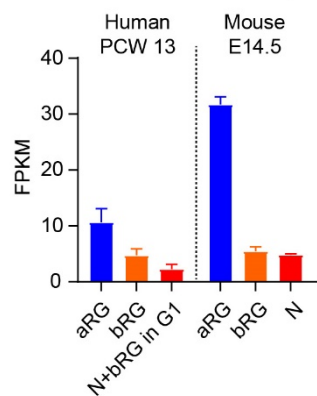
A**B****C***CDC25A/Cdc25a* mRNA expression**D***CDC25A/Cdc25a* mRNA expression**E***CDC25B/Cdc25b* mRNA expression**F***CDC25B/Cdc25b* mRNA expression

Figure S1. Related to Figure 1. (A,B) mRNA level of *CDC25A* (A) or *CDC25B* (B) across prenatal and postnatal periods from BrainSpan data. The X-axis represents the age of samples in days and Y-axis represents the log2 (RPKM + 1). The dashed line shows the day of birth. A1C, primary auditory cortex; AMY, amygdaloid complex; CBC, cerebellar cortex; DFC, dorsolateral prefrontal cortex; HIP, hippocampus; IPC, inferior parietal cortex; ITC, inferolateral temporal cortex; M1C, primary motorcortex; MD, mediodorsal nucleus of thalamus; MFC, medial prefrontal cortex; OFC, orbital frontal cortex; S1C, primary somatosensory cortex; STC, superior temporal cortex; STR, striatum; V1C, primary visual cortex; VFC, ventrolateral prefrontal cortex; CB, cerebellum; CGE, caudal ganglionic eminence; DTH, dorsal thalamus; LGE, lateral ganglionic eminence; M1C-S1C, primary motor-sensory cortex; MGE, medial ganglionic eminence; OCX, occipital neocortex; PCX, parietal neocortex; TCX, temporal neocortex; URL, upper rhombic lip. (C,D) Mean FPKM values of *CDC25A/Cdc25a* (C) and *CDC25B/Cdc25b* (D) mRNA expression in the germinal neocortical zones of fetal neocortical tissue PCW13-16 (n = 6) (left) and embryonic mouse neocortex E14.5 (n = 5) (right). FPKM values are from the dataset GSE38805. VZ, ventricular zone; SVZ, subventricular zone; iSVZ, inner subventricular zone; oSVZ, outer subventricular zone; CP, cortical plate. (E,F) Mean FPKM values of *CDC25A/Cdc25a* (E) and *CDC25B/Cdc25b* (F) mRNA expression in indicated isolated cell population of PCW13 fetal human neocortical tissue (left) and E14.5 embryonic mouse neocortex (right). aRG, apical radial glial; bRG, basal radial glial; N, neuron; N+bRG in G1, neuron fraction containing bRG in G1. FPKM values are from the dataset GSE65000.

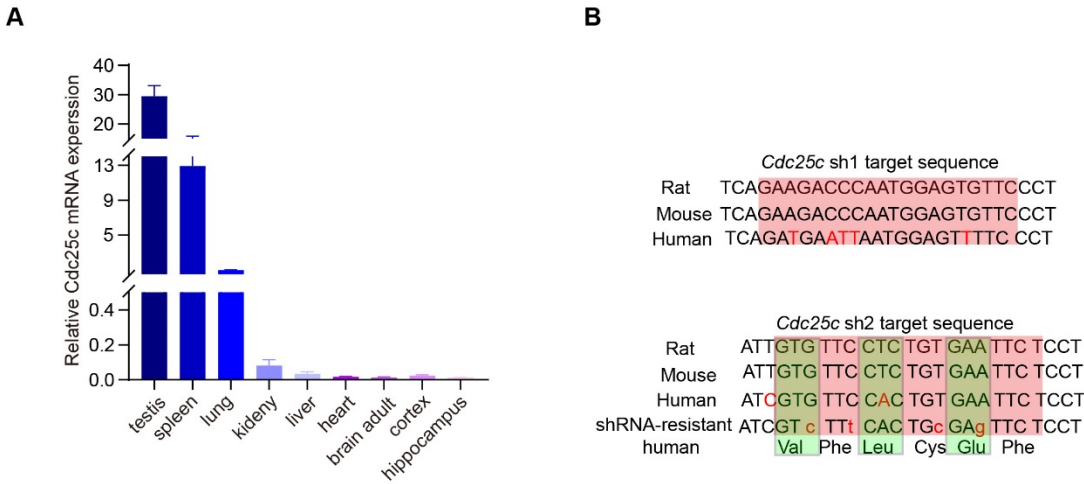


Figure S2. Related to Figure 1 and Figure 2. (A) qRT-PCR analysis of *Cdc25c* mRNA in different tissues of adult mice. (B) The nucleotide sequences of *Cdc25c* shRNA1 (sh1) and *Cdc25c* shRNA2 (sh2) target sequence in different species.

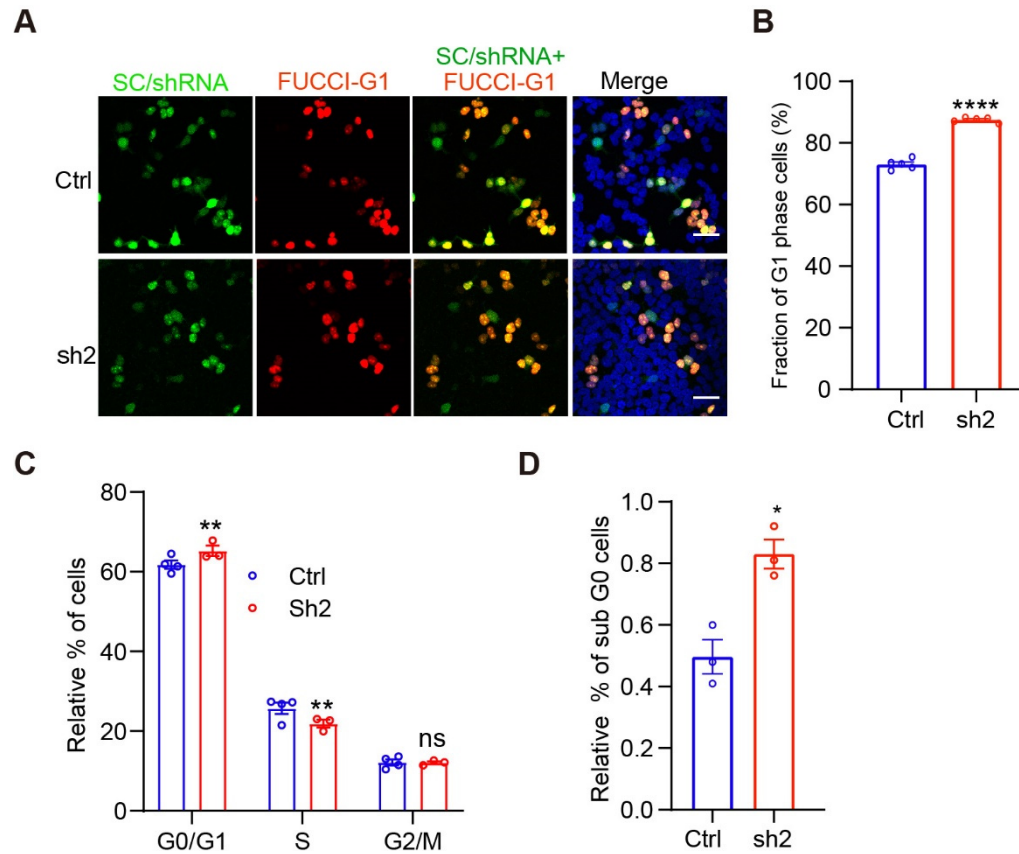


Figure S3. Related to Figure 4. (A) HEK293T were transfected with Ctrl or *CDC25C* shRNA2 (sh2) together with FUCCI-G1 fusion protein (Red), 24 h later, cells were fixed and stained with DAPI for nuclei. (B) Quantification of G1 phase cells of GFP positive cell in (A). Data are mean \pm SEM, unpaired *t*-test, **** $p < 0.0001$. (C) Quantification of cells transfected with Ctrl or *CDC25C* shRNA2 (sh2) in different cell-cycle phase as analyzed by FACS. (D) Quantification of sub G0 cells in Ctrl or *CDC25C* shRNA2 (sh2) cells. All Data are mean \pm SEM (C,D). ns, $p > 0.05$, * $p < 0.05$, ** $p < 0.01$, and *** $p < 0.0001$, unpaired *s t*-test. Results are from more than three independent experiments.