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Hbp1 regulates the timing of neuronal differentiation during cortical development by controlling cell cycle progression

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ABSTRACT
In the developing mammalian brain, neural stem cells (NSCs) initially expand the progenitor pool by symmetric divisions. NSCs then shift from symmetric to asymmetric division and commence neurogenesis. Although the precise mechanisms regulating the developmental timing of this transition have not been fully elucidated, gradual elongation in the length of the cell cycle and coinciding accumulation of determinants that promote neuronal differentiation might function as a biological clock that regulates the onset of asymmetric division and neurogenesis. We conducted gene expression profiling of embryonic NSCs in the cortical regions and found that expression of high mobility group box transcription factor 1 (Hbp1) was upregulated during neurogenic stages. Induced conditional knockout mice of Hbp1, generated by crossing with Nestin-CreERT2 mice, exhibited a remarkable dilatation of the telencephalic vesicles with a tangentially expanded ventricular zone and a thinner cortical plate containing reduced numbers of neurons. In these Hbp1-deficient mouse embryos, neural stem/progenitor cells continued to divide with a shorter cell cycle length. Moreover, downstream target genes of the Wnt signaling, such as cyclin D1 (Ccnd1) and c-jun (Jun), were upregulated in the germinal zone of the cortical regions. These results indicate that Hbp1 plays a crucial role in regulating the timing of cortical neurogenesis by elongating the cell cycle and that it is essential for normal cortical development.

KEY WORDS: Hbp1, Brain morphology, Cell cycle, Cortical development, Neural stem cells, Neuronal differentiation, Mouse

INTRODUCTION
During mammalian cortical development, neural stem cells (NSCs) gradually alter their characteristics and generate a variety of cell types, which establishes the functional complexity of the brain (Temple, 2001). In early developmental stages, a sheet of NSCs vigorously expands through repeated symmetric divisions, and the neural tube distends like a balloon, with a thin wall composed of short neuroepithelial cells. After expanding the progenitor pool for several cycles, NSCs in the cortical regions begin to produce neurons by converting from symmetric to asymmetric division, which initiates neurogenesis (Takahashi et al., 1995, 1999). The timing of this transition is crucial for determining the overall number of NSCs and the size of ventricles, which largely determines the eventual size and morphology of the brain. However, the precise mechanisms that regulate the switch from symmetric to asymmetric division and the onset of neurogenesis have not been fully elucidated.

It has been reported that the length of the G1 phase of the cell cycle (T\textsubscript{G1}) in neural stem/progenitor cells gradually rises over the course of cortical development. This elongation of T\textsubscript{G1} is accompanied by downregulation of cyclin E (Ccne1 – Mouse Genome Informatics) and p21 (Cdkn1a – Mouse Genome Informatics), along with upregulation of p27 (Cdkn1b – Mouse Genome Informatics), cdk2 and cyclin B (Delalle et al., 1999; Caviness et al., 2003). Moreover, the forced reduction of T\textsubscript{G1} by manipulation of cyclin D1 led to an expansion of neural progenitor cells in the developing and adult brain (Lange et al., 2009; Pilaz et al., 2009; Artega et al., 2011). One proposed mechanism for the transition from symmetric proliferative to asymmetric neurogenic division is that an elongation of T\textsubscript{G1} allows fate determinants that promote neuronal differentiation to accumulate during the G1 phase and exert their neurogenic functions (Calegari and Huttner, 2003; Calegari et al., 2005; Götz and Huttner, 2005; Dehay and Kennedy, 2007).

To identify temporal alterations in the transcriptional properties of embryonic NSCs, we previously carried out DNA microarray-based gene expression profiling of embryonic NSCs prepared from the cortical regions at different developmental stages by using pHes1-d2EGFP transgenic mice, which express enhanced green fluorescent protein (EGFP) in NSCs (Ohtsuka et al., 2006, 2011). Among a variety of genes that were differentially expressed during the course of development, we hypothesized that high mobility group box transcription factor 1 (Hbp1) might be an important regulator of neurogenesis, given that it was upregulated during neurogenic stages around embryonic day 13.5 (E13.5) through embryonic day 15.5 (E15.5). Previous studies demonstrated that Hbp1 acts as a transcriptional repressor that functions as a cell cycle inhibitor by repressing downstream targets of the Wnt signaling and cell cycle-related genes, cyclin D1 (Ccnd1), c-jun (Jun), N-myc (Mycn) and p21 (Cdkn1a) (Gartel et al., 1998; Sampson et al., 2001; Kim et al., 2006; Elfert et al., 2013; Yan et al., 2014).

Here, we analyzed the molecular function of Hbp1 in neuronal differentiation during cortical development. We found that Hbp1 controls the length of the cell cycle in neural stem/progenitor cells by modulating the expression levels of cyclin D1, thereby regulating the timing of neuronal differentiation during early cortical development.

RESULTS
Hbp1 is expressed in the germinal zone during cortical neurogenesis
By evaluating our gene expression profiling data for embryonic NSCs in the developing cortex (Ohtsuka et al., 2011), we selected
candidate genes expected to be involved in the regulation of neuronal differentiation based on their upregulation during the neurogenic period. Among these genes, we observed that Hbp1 was prominently expressed in the germinal zone that comprises the ventricular zone (VZ) and subventricular zone (SVZ) in the developing telencephalon (Fig. 1A). The expression pattern of Hbp1 was characterized by a lateral high-dorsal low gradient at E11.5 corresponding to the propagation of neurogenesis, similar to Hbp1 developing telencephalon (Fig. 1A). The expression pattern of ventricular zone (VZ) and subventricular zone (SVZ) in the prominently expressed in the germinal zone that comprises the microarray analysis (Fig. 1C).

**Overexpression of Hbp1 suppresses cell proliferation, but inhibits terminal neuronal differentiation**

We conducted overexpression experiments by *in utero* electroporation. *Hbp1* expression vectors (pEF-Hbp1) and control vectors (pEF-EGFP) were co-introduced into ventricular cells in the cortical regions of E13.5 mouse embryos, and the fates of transfected cells were subsequently examined at E14.5 and E16.5. As shown in our previous paper (Ohtsuka et al., 2011), cells transfected with pEF-Hbp1 mainly remained in the SVZ and the intermediate zone (IZ) at E16.5. Noticeably, a majority of transfected cells differentiated into neurons positive for neuronal markers, such as Tuj1 (Tubb3 – Mouse Genome Informatics) and Map2. In addition, they were negative for Ki67 (Mki67 – Mouse Genome Informatics), a marker of proliferating cells, or phospho-histone H3 (pH3), a marker of dividing cells in the M phase; moreover, they stagnated in the IZ and failed to migrate into the cortical plate (CP) (Fig. 2A; supplementary material Fig. S1A-D), indicating that neuronal migration was inhibited. The proportions of transfected cells positive for Pax6, a specific marker of NSCs during this period of development, and Tbr2 (Eomes – Mouse Genome Informatics), a marker of intermediate progenitor cells (IPs), were significantly lower than in the control at E16.5. Transfected cells that incorporated BrdU administered 4 h after *in utero* electroporation at E13.5 exited the VZ earlier than control cells at E15.5. However, the majority of cells still remained in the IZ at E16.5 (supplementary material Fig. S1E,F), suggesting that overexpression of Hbp1 promoted initial neuronal differentiation but impaired terminal neuronal differentiation and migration.

Next, we evaluated the rate of cell proliferation by administering the thymidine analog EdU intraperitoneally to the pregnant mice 30 min before sacrifice at E14.5 to mark cells in the S phase. In cells transfected with pEF-Hbp1, EdU incorporation was suppressed compared with control (Fig. 2B), indicating that overexpression of Hbp1 caused an attenuation of cell proliferation or premature cell cycle exit. We then carried out a calculation of cell cycle kinetics by BrdU/EdU double-labeling protocol (modified from a previously described IdU/BrdU double-labeling method (Martynoga et al., 2005; Mairet-Coello et al., 2012)] and estimated the cell cycle length. Cells transfected with pEF-Hbp1 showed a slightly longer cell cycle length compared with control (Fig. 8F; supplementary material Table S3); however, the effect on the cell cycle was minimal in comparison with Hbp1 knockdown or Hbp1-deficient cells.

**Co-expression of Rb1 de-represses terminal neuronal differentiation and migration**

Hbp1 has been shown to be a target of retinoblastoma 1 (Rb1) and p130, also known as Rbl2 (Tevosian et al., 1997). Shih et al. reported that muscle cell differentiation was blocked when Hbp1 was overexpressed in C2C12 cells without interfering with cell cycle exit, and the expression of MyoD (Myod1 – Mouse Genome Informatics) and myogenin (Myog), but not of Myf5, was inhibited in Hbp1-expressing cells; however, full differentiation occurred when Rb1 was co-expressed with Hbp1 and the ratio of Rb1/Hbp1 was elevated, suggesting that the relative ratio of Rb1 to Hbp1 is important as a determinant of whether cell cycle exit or full differentiation occurs (Shih et al., 1998). Thus, we introduced a mixture of pEF-Hbp1 and pCAGGS-HA-human Rb1 (hRb1) vectors at ratios of 3:1 or 1:3 by *in utero* electroporation, and found that transfected cells were released from the stagnation and significantly more transfected cells reached the CP when Hbp1 and Rb1 were co-expressed (Fig. 2C,D).
Next, we examined the expression levels of proneural bHLH genes by *in situ* hybridization 24 h after *in utero* electroporation. We found that *Neurod1* expression was downregulated in the regions transfected with *pEF-Hbp1* (Fig. 2E), and the repression was rescued to some extent by co-expression of *Rb1*, whereas expression of *Neurog2* was not significantly affected. Taken together, these results supported findings from a previous study of muscle cell differentiation (Shih et al., 1998) and also suggested that overexpression of Hbp1 promoted cell cycle exit but impaired terminal neuronal differentiation required for full migration due to the low Rb1/Hbp1 ratio. Conversely, a higher Rb1/Hbp1 ratio obtained by co-expressing Rb1 promoted terminal differentiation and neuronal migration.

**Knockdown of Hbp1 inhibits neuronal differentiation and activates cell cycle progression**

Next, we carried out knockdown experiments using expression vectors of shRNA targeting Hbp1 (*shHbp1*), in addition to scrambled shRNA control vectors (*scrambled*) (supplementary material Fig. S2A,B). When we introduced *shHbp1* into ventricular cells together with *pEF-EGFP* by *in utero* electroporation at E13.5, most cells transfected with *shHbp1* remained in the VZ/SVZ/IZ, whereas those transfected with *pEF-EGFP* migrated into the cortical plate and formed the cortical mantle (Fig. 2C). Knockdown of Hbp1 inhibits neuronal differentiation and activates cell cycle progression.

![Fig. 2. Inhibition of terminal neuronal differentiation and migration by overexpression of Hbp1.](image-url)

*In utero* electroporation (ep) was performed with control vectors (*pEF-EGFP*) alone or with a combination of Hbp1 expression vectors (*pEF-Hbp1*) at E13.5. The fates of transfected cells were analyzed at E14.5 (B) or E16.5 (A,C) by immunohistochemistry (IHC). (A) Coronal sections of dorsolateral telencephalon were double-stained using anti-GFP (green) and anti-Tuj1/Tbr2/Pax6 (red) antibodies. (B) EdU was administered intraperitoneally to pregnant mice 30 min before sacrifice, and incorporated EdU (red) was detected by a fluorogenic click reaction. (C) pCAGGS-HA-hRb1 vectors were co-transfected with *pEF-Hbp1* at ratios of 3:1 or 1:3 by *in utero* electroporation at E13.5, and the fates of transfected cells were analyzed at E16.5. (D) The proportions of transfected cells that migrated into the cortical plate are shown in bar graphs. (E) *In situ* hybridization for neurogenic bHLH genes such as *Neurog2* and *Neurod1* was performed on coronal brain sections 24 h after *in utero* electroporation at E14.5. Brackets indicate regions transfected with expression vectors. *n*=3, error bars: s.e.m.; *P*<0.05, **P*<0.01; Student’s t-test; N.S., not significant. Scale bars: 200 µm.
with only a few cells observed in the CP at E16.5 (supplementary material Fig. S2C). However, neuronal differentiation occurred later and most transected cells in the IZ were Tuj1 and Map2-positive and negative for Ki67 or pH3 (supplementary material Fig. S1A,C and Fig. S2C), although the number of pH3+ cells increased in the VZ and SVZ in regions transfected with shHbp1 (supplementary material Fig. S1C,D). Knockdown cells that incorporated BrdU administered 4 h after electroporation exhibited slower exits from the VZ than in the control at E15.5 (supplementary material Fig. S1E,F), indicating that Hbp1 knockdown inhibited and delayed neuronal differentiation. Whereas most cells transfected with scrambled shRNA differentiated into Cux1+ neurons (layer II-IV) and settled in the CP at E18.5, a majority of cells transfected with shHbp1 still remained in the VZ/SVZ/IZ (supplementary material Fig. S2D). The number of Cux1+ cells in the superficial layers of the CP decreased markedly in the regions transfected with shHbp1, whereas the number of Ctip2+ cells (layer V) was comparable to the control.

To evaluate the specificity of the Hbp1 knockdown, we performed rescue experiments by co-electroporation of shHbp1 and pEF-Hbp1 at ratios of 3:1, 1:1 or 1:3, and found that pEF-Hbp1 rescued the phenotype of Hbp1 knockdown (inhibition of neuronal differentiation and migration) at a 1:1 ratio (supplementary material Fig. S2E,F). However, the neuronal migration defect was observed again at a 1:3 ratio, similar to our observations in the case of Hbp1 overexpression.

We performed immunostaining with anti-phosphorylated vimentin (p-Vim) antibody but did not observe a significant increase in p-Vim+ mitotic radial glial cells outside the VZ (supplementary material Fig. S1C,D). In addition, we found that cell death (as measured bycleaved-caspase 3+ cells) was not enhanced by either overexpression or knockdown of Hbp1 at 3 days after electroporation (supplementary material Fig. S1G,H). Estimation of the cell cycle length revealed that Hbp1 knockdown cells showed a considerably shorter cell cycle length compared with control (Fig. 8F; supplementary material Table S3), indicating that knockdown of Hbp1 shortened the cell cycle length, in particular the duration of the G2-M-G1 phase, and activated cell cycle progression.

**Deficiency of Hbp1 in neural stem/progenitor cells impairs cortical morphogenesis**

To analyze the function of Hbp1 over the course of brain development, we generated Hbp1 induced conditional knockout (icKO) mice, in which tamoxifen-inducible Cre recombinase is expressed specifically in neural stem/progenitor cells in the embryonic brain (see supplementary materials and methods and Fig. S3A,B). We confirmed by real-time RT-PCR that expression of Hbp1 in the telencephalon of Hbp1 icKO mice was downregulated by E11.5 when tamoxifen was administered at E9.5 (supplementary material Fig. S3C).

The whole brain size of Hbp1 icKO embryos was comparable to that of the negative controls (NC) but the telencephalic wall appeared to be thinner (Fig. 3A). The telencephalic vesicles of mutant embryos were remarkably dilated, although the ventricular dilatation was not prominent at E12.5 (Fig. 3A,B). The volume of the ventral telencephalon was severely diminished and the wall of the dorsal telencephalon was significantly thinner than that of the control after E14.5 (Fig. 3B). Notably, the ventricular surface area in the dorsolateral telencephalon (cortical region) was substantially enlarged; thus, the VZ appeared to be stretched in the tangential direction. The thickness of both the VZ (Pax6+ and the neuronal layer (Tuj1+)) were thinner than in the control. The midline and medial structures of the telencephalon, such as hippocampus and corpus callosum, were hypoplastic or missing at E18.5. The measurements of each structure are summarized in Fig. 3C (see supplementary materials and methods).

**Hbp1-deficiency leads to delayed neuronal differentiation and tangential expansion of NSCs**

Next, we investigated the dynamics of cortical development in the Hbp1-deficient mice. We determined the number of distinct cell types through immunolabeling with various cell- and layer-specific markers within a radial column of constant width (200 µm) in the cortical regions (Fig. 4A-C; supplementary material Fig. S4A,B). At E12.5, the thickness of the VZ (Pax6+ and Hes1+) was similar to that in the control mice. Noticeably, the number of Tbr2+ cells and early-born neurons (Tuj1+ and Tbr1+) was reduced in the icKO mice at E12.5, indicating that the onset of neurogenesis was delayed. Instead, the NSC population was still expanding by symmetric divisions, thus leading to the tangential extension of the VZ and ventricular dilatation that became prominent after E14.5. We determined the number of Pax6+ NSCs throughout the cortical regions in multiple coronal sections at constant intervals along the antero-posterior axis of lateral ventricle. Through this method, we estimated and compared the total number of NSCs in the hemisphere of control and mutant brains, and found that the total number of NSCs was increased in the icKO at E14.5 (Fig. 3C).

As the generation of Tbr2+ IPs and neurons commences after the transition from symmetric to asymmetric division mode of NSCs (Sessa et al., 2008), these results suggested that the Hbp1-deficiency delayed this transition and the onset of neurogenesis. Thus, we analyzed the fates of cells after cell divisions by administering EdU 12 h before sacrifice (Fig. 5A). A majority of cells that incorporated EdU remained Pax6+ NSCs in the cortical regions of icKO embryos at E12.5, whereas the number of EdU+ cells that differentiated into Tbr2+ IPs was much higher in the control (Fig. 5B). Given the significantly higher frequency of cell divisions in Pax6+ cells than in Tbr2+ cells, as demonstrated by pH3 staining (Fig. 5C), these results indicated that the symmetric proliferative divisions of Pax6+ NSCs were maintained in the icKO at a population level, although it was not revealed at a single-cell level, whereas many NSCs had shifted to asymmetric neurogenic division in the control at E12.5. Estimation of the proportions of Ki67+/EdU+/EdU− (cell cycle re-entry) and Ki67−/EdU+/EdU+ (cell cycle exit) also indicated that more cells re-entered the cell cycle in the icKO, whereas more cells exited the cell cycle in the control at E12.5 and E14.5 (Fig. 5D).

**Cortical neurons are reduced in number proportionately throughout all layers**

Immunostaining with anti-Pax6 and anti-Hes1 antibodies revealed that the thickness of the VZ was reduced in the icKO mice compared with control at E14.5 and thereafter (Fig. 4A-C; supplementary material Fig. S4A,B). Intriguingly, the number of Tbr2+ cells remarkably increased in the mutant cortex by E14.5 (Fig. 4A-C), and EdU incorporation experiments revealed that those Tbr2+ cells were highly proliferative at E14.5 (Fig. 5A,B); however, Tbr2+ IPs rapidly reduced in number between E14.5 and E16.5. These results indicated a drastic thinning of the germinal zone composed of NSCs and IPs at later stages. We found that cell death was enhanced in Pax6+, Tbr2+ and Tuj1+ populations in the icKO (supplementary material Fig. S5A,B), suggesting that the cell death somewhat
masked the expansion of NSCs through continued symmetric divisions and caused the reduction of neural stem/progenitor cells at later stages. Enhanced cell death was also observed in the ventral telencephalon (supplementary material Fig. S5C,D). However, in the cortical regions, no significant difference was observed in the number of GABA (γ-aminobutyric acid)-positive GABAergic interneurons, which are generated in the ventral telencephalon (data not shown).

The thickness of the cortical neuronal layers was reduced in the icKO throughout embryonic stages, as estimated by Tuj1 expression in the IZ/CP and expression of NeuN (Rbfox3), a neuronal marker, in the CP (supplementary material Fig. S4A,B). We counted the number of cells positive for each marker and then normalized to the number of all DAPI+ nuclei. We found that the subsets of layer-specific neurons were proportionately reduced in the icKO at all stages analyzed (Fig. 4C). It is likely that the significant cell death and rapid depletion of the neural stem/progenitor cell pool contributed to the reduced thickness of cortical layers.

In situ hybridization and real-time RT-PCR revealed that the expression levels of Neurog2 and Neurod1 were prominently upregulated around E14.5-16.5 in the mutant cortex (Fig. 6A,B), whereas expression of Ascl1 (achaete-scute complex homolog 1) was...
Fig. 4. Perturbed cortical neurogenesis in Hbp1-deficient mice. (A) Immunohistochemistry on coronal sections of the cortical regions of negative control (NC) and Hbp1 icKO mice at different developmental stages with markers specific to each cortical layer (Cux1 for layer II-IV, Ctip2 for layer V and Tbr1 for layer VI), Tbr2, a marker for IPs, and Pax6, a marker for NSCs. (B) The number of cells immunoreactive for each antibody was counted within a radial column of 200 µm width in the middle part of dorsolateral telencephalon. (C) The proportions of cells positive for each marker of all DAPI+ cells within the radial column. Cux1+ cells in the VZ/SVZ/IZ are shown in yellow bars and those in the CP are shown in red. n=3, error bars: s.e.m.; *P<0.05, **P<0.01, ***P<0.001; Student’s t-test. Scale bar: 100 µm.
not significantly affected. We further assessed whether neurogenesis terminated earlier and gliogenesis began precociously in the icKO. Although aberrant generation of astrocytes (GFAP+) or oligodendrocytes (Olig2+) was not observed at either E16.5 or E18.5 (data not shown), the number of oligodendrocyte precursor cells (PDGFRα+) decreased in the mutant cortex (supplementary material Fig. S4C,D), probably due to enhanced cell death and shrinking of the ventral telencephalon. It is possible that the sustained expression of neurogenic bHLH factors prevented precocious gliogenesis in the mutant brain (Sun et al., 2001). We also did not observe any significant increase of p-Vim+ basal radial glial cells in the SVZ/OSVZ (outer subventricular zone) of mutant cortex at either E16.5 or E18.5 (supplementary material Fig. S4C,D).

Neural stem/progenitor cells are actively dividing in Hbp1-deficient mice

It was previously reported that Hbp1 is involved in regulation of the Wnt signaling by inhibiting the function of TCF4-β-catenin complex via physical blockade of TCF/LEF-mediated DNA binding, and functions as a growth suppressor by repressing downstream genes of the Wnt signaling and cell cycle-related genes (Tevosian et al., 1997; Gartel et al., 1998; Sampson et al., 2001; Shih et al., 2001; Kim et al., 2006; Elfert et al., 2013; Yan et al., 2014). We therefore assessed cell proliferation activity in neural stem/progenitor cells in the developing cortex. The number of cycling cells that incorporated EdU for 30 min before sacrifice, as well as proliferating cells (Ki67+) and mitotic cells (pH3+), was significantly higher in the icKO at E14.5 (Fig. 7A,B). We then calculated the proportions of proliferating and mitotic Pax6+ cells and Tbr2+ cells separately, and determined that both cell types were more proliferative than in the control (Fig. 7C). The proportions of Ki67+ cells that co-expressed Pax6 or Tbr2, and the proportions of Pax6+ or Tbr2+ cells that co-expressed Ki67, are shown in supplementary material Fig. S6.

Furthermore, we found that the cell cycle length was much shorter in neural stem/progenitor cells (Ki67+) in the mutant cortex at each developmental stage (Fig. 7D; supplementary material Table S3). Intriguingly, the length of the overall cell cycle (TC) was gradually elongated as development proceeded in both the control and the mutant cortex. The length of the S phase (TS) was also shortened in the mutant cortex, although it was less prominent than the reduction in TC and comparatively constant during this period. These results indicate that the duration of the G2-M-G1 phase was significantly shortened in the icKO mice. We then analyzed the cell cycle length separately in either Pax6+ NSCs or Tbr2+ IPs and found that both populations exhibited a shorter cell cycle (Fig. 7E,F; supplementary material Table S3).

Growth regulatory genes are upregulated in Hbp1 knockdown and Hbp1-deficient cells

We next searched for genes that prospectively lay downstream of Hbp1. Immunohistochemistry and in situ hybridization revealed that cyclin D1 expression was remarkably upregulated in Hbp1
knockdown cells (Fig. 8A,B; supplementary material Fig. S7A). In addition, we estimated cyclin D1 expression levels and found that the proportion of cyclin D1-expressing GFP+ cells was not significantly changed, but that the signal intensity of cyclin D1 staining in the GFP+ area was lower in Hbp1 overexpression and higher in Hbp1 knockdown (Fig. 8B).

In line with the above findings, expression levels of cyclin D1 were strikingly upregulated and c-Jun expression was also upregulated in the cortical regions of Hbp1 icKO mice at E12.5 and E14.5 (Fig. 8C,D). Double-labeling with Pax6 or Tbr2 revealed that enhanced cyclin D1 expression was observed in most NSCs and a subset of IPs (data not shown). Real-time RT-PCR confirmed the significant upregulation of cyclin D1 expression in the icKO at E12.5 and E14.5 (Fig. 8E). The expression levels of cyclin E1 (Ccne1 – Mouse Genome Informatics) and N-myc were slightly upregulated and sustained until later stages in the icKO (supplementary material Fig. S7B). Immunohistochemistry using antibodies against phosphorylated Rb (p-Rb) (Ser 780, Ser 807/811), a major target of cyclin D1/Cdk4/6 complexes (Kitagawa et al., 1996; Zarkowska and Mittnacht, 1997; Ely et al., 2005), revealed that the proportions of M phase cells that were strongly positive for p-Rb (Ser 780) were significantly higher in both Pax6+ NSCs and Tbr2+ IPs in the mutant cortex at E12.5 and E14.5, and the signal intensity of p-Rb (Ser 807/811) was slightly higher throughout the VZ of icKO at E14.5 (supplementary material Fig. S8A,B). Western blot analysis revealed the increased levels of p-Rb (Ser 807/811) in the mutant cortex at E14.5 (supplementary material Fig. S8C,D).

Cyclin D1 is a crucial factor involved in the regulation of cell cycle length by Hbp1

To address whether the upregulation of cyclin D1 is causative of the phenotype of Hbp1 deficiency, we performed rescue experiments by co-transfecting shHbp1 and knockdown vectors against cyclin D1 (shCcnd1) by in utero electroporation (supplementary material Fig. S9A,B). We introduced a mixture of shHbp1 and shCcnd1 at ratios of 3:1, 1:1 or 1:3, and found that co-transfection of shCcnd1 rescued the shortening of cell cycle caused by Hbp1 knockdown (Fig. 8F). However, the co-expression of shCcnd1 could not rescue the effects of Hbp1 knockdown on neuronal differentiation/migration (supplementary material Fig. S9C,D), suggesting that Hbp1 has crucial functions not only in the regulation of cyclin D1 but also in the regulation of neuronal differentiation.

We then performed real-time RT-PCR using total RNAs prepared from NSCs in the embryonic cortex of pHes1-d2EGFP transgenic mice and found that cyclin D1 expression was downregulated threefold between E11.5 and E13.5 (Fig. 8G). Intriguingly, the temporal dynamics of cyclin D1 expression exhibited a striking contrast to Hbp1 expression (see Fig. 1C). We further performed a reporter assay using a cyclin D1 promoter (3.3 kb)-luciferase construct. Expression of Hbp1 by co-transfection of pCAG-HA-Hbp1 vectors in HEK293T cells significantly repressed the cyclin D1 promoter activity (Fig. 8H).

Collectively, these data suggest that upregulation of cyclin D1 caused active proliferation with a short cell cycle length in neural stem/progenitor cells in the developing cortex of Hbp1-deficient
mice, and that cyclin D1 is a crucial factor involved in the regulation of cell cycle length by Hbp1 during cortical development.

**DISCUSSION**

**Rapid proliferation of NSCs delays the onset of neurogenesis**

In the developing embryonic cortex, NSCs gradually alter their characteristics and give birth to distinct cell types in a precise temporal order (McConnell, 1989; Temple, 2001; Ohtsuka et al., 2011). In particular, the timing of the transition from symmetric proliferative to asymmetric neurogenic division is crucial in determining the onset of neurogenesis and the size of the initial stem cell pool. One possible mechanism underlying regulation of the timing of this transition is that the number of cell divisions intrinsically functions as a biological clock to determine their competence and to mark developmental steps in NSCs. If so, rapid proliferation of NSCs with a shorter cell cycle will result in a precocious transition from symmetric to asymmetric division and an early onset of neurogenesis. An alternative possibility is that the gradual elongation of cell cycle length in NSCs during cortical development allows determinants for neuronal differentiation to accumulate to the threshold level that initiates asymmetric neurogenic division and thus acts as a regulator of the biological clock (Calegari and Huttner, 2003; Calegari et al., 2005; Götz and Huttner, 2005; Dehay and Kennedy, 2007). If this is the case, rapid cycling of NSCs inhibits these determinants from reaching the threshold needed to drive neuronal differentiation.

Our data support the latter hypothesis, because rapidly proliferating NSCs in the cortex of Hbp1 icKO mice were maintained as cycling NSCs, and the generation of Tbr2+ IPs and neurons was delayed (Fig. 4A-C and Fig. 5A,B). Our results suggest
that Hbp1 is required to elongate the cell cycle length and facilitate the attainment of the threshold length required to commence neurogenesis, as illustrated in Fig. 7G.

As observed in the mutant cortex at later stages, when NSC proliferation shifted to the asymmetric neurogenic division mode, the aberrantly rapid cell cycle accelerated the production of Tbr2+ IPs and their proliferation in the SVZ. This resulted in the premature exhaustion of the neural stem/progenitor cell pool, rendering the neurogenic period shorter in the Hbp1-deficient mice. This raises the possibility that the number of cell divisions in neural stem/progenitor cells is intrinsically limited after the transition to the neurogenic mode.
Hbp1 inhibits cell cycle progression by suppressing cyclin D1 expression

Our observations revealed that Hbp1 knockdown and Hbp1-deficiency led to cyclin D1 upregulation and accelerated cell cycle progression in neural stem/progenitor cells in the cortical regions, where reduction in T_C was more substantial than reduction in T_S (Fig. 7D-F and Fig. 8F). Given that cyclin D1 is required for the G1/S transition and that the durations of the G2 and M phases are relatively constant in distinct cell types, it is likely that T_G1 was mainly reduced via upregulation of cyclin D1. Indeed, the primary phenotypes observed in the Hbp1-deficient mice were consistent with the cyclin D1 overexpression phenotype, in which T_G1 was shortened, and inhibition of neurogenesis and expansion of IPs were observed (Lange et al., 2009; Pilaz et al., 2009).

It has been reported that T_C in neural progenitors is gradually elongated as development proceeds and is approximately doubled over the period between E11 and E15, mostly due to the elongation of T_G1 (Miyama et al., 1997). Here, we found contrasting expression dynamics between Hbp1 and cyclin D1 in NSCs over the course of cortical development (Fig. 1C and Fig. 8G), and revealed that Hbp1 repressed the cyclin D1 promoter activity (Fig. 8H). Together, these findings support our model that Hbp1 is involved in the elongation of T_G1 in NSCs during early cortical development by regulating the expression of growth regulatory genes, including cyclin D1. Future genome-wide expression analysis comparing gene expression in the wild-type and Hbp1-deficient cortex will provide new insights into novel targets or effectors of Hbp1.

Rb1 cooperates with Hbp1 to promote terminal differentiation

It was speculated that Hbp1 induces cell cycle exit and promotes neuronal differentiation when overexpressed in neural stem/progenitor cells. However, overexpression of Hbp1 alone failed to promote terminal neuronal differentiation (Fig. 2A). We hypothesized that overexpression of Hbp1 alone would lead to cell cycle exit without tissue-specific gene expression, due to a low Rb1/Hbp1 ratio. We found that Neurod1 expression was downregulated by Hbp1 overexpression (Fig. 2E) and that the repression was partly rescued by co-expression of Rb1, whereas expression of Neurog2 was not significantly affected. It has been shown that Neurod1 regulates terminal neuronal differentiation (Lee et al., 1995; Schwab et al., 2000; Gao et al., 2009) and that Neurod1 expression is activated by the Wnt signaling in adult hippocampal neurogenesis (Kuwabara et al., 2009). Therefore, it is possible that overexpression of Hbp1 repressed Neurod1 expression via inhibition of the Wnt signaling. We found that the expression levels of Neurod1 were significantly upregulated in the cortex of Hbp1-deficient mice (Fig. 6A,B), suggesting that Hbp1 has a role in repressing Neurod1 expression in neural stem/progenitor cells. Although it is likely that the cell cycle length was too short in the Hbp1-deficient mice for Neurog2 and Neurod1 to induce neuronal differentiation at earlier stages, the enhanced expression of these genes might have accelerated the production of Tbr2+ IPs after the transition to the asymmetric neurogenic division mode (Fig. 4A-C). Thus, our present study further corroborates the finding that Hbp1 promotes cell cycle exit but blocks terminal differentiation if the Rb1/Hbp1 ratio is low. Confirming this hypothesis, an increased ratio of Rb1/Hbp1 promoted terminal neuronal differentiation, similar to observations for muscle cell differentiation (Shih et al., 1998).

G1 elongation by Hbp1 is essential for cortical development

We previously reported that expression of the bHLH transcriptional repressor Hes1 is oscillatory with a period of 2-3 h in neural stem/progenitor cells in the developing cortex, and that expression of neurogenic bHLH genes such as Neurog2 and Ascl1 is also oscillating (Shimojo et al., 2008, 2011; Imai et al., 2013). Thus, it is likely that some neurogenic bHLH factors or their downstream effectors gradually accumulate during the phase of oscillation when Hes1 expression is low. If the G1 phase is elongated, such determinants have a greater chance to reach the threshold necessary to exert their neurogenic functions. Therefore, it is presumed that the duration of the G1 phase is crucial in determining the onset of cortical neurogenesis.

Increases in the number of cell divisions during the symmetric proliferative division phase will cause the exponential expansion of NSCs as neuroepithelial cells (a non-neurogenic form of NSCs) and the increase in radial units composed of each stem cell and its progeny, thus leading to expansion of brain vesicles/ventricles and tangential extension of the VZ (Noctor et al., 2001). Once NSCs shift to the asymmetric neurogenic division mode, they transform into radial glial cells (a neurogenic form of NSCs), and the number of NSCs does not increase any further. Our findings demonstrate that in the absence of Hbp1 neuroepithelial cells continued to proliferate rapidly by symmetric proliferative divisions and expanded the neuroepithelial sheet, leading to the expansion of the ventricular surface and the VZ.

Taken together, our results indicate that the elongation of cell cycle length by Hbp1 mediated by repression of cyclin D1 is a key mechanism regulating the proper timing of neuronal differentiation. As such, Hbp1 is a key factor in determining the onset of cortical neurogenesis and the duration of neurogenic period, thus being essential for normal cortical development.

MATERIALS AND METHODS

**In situ hybridization**

Preparation of digoxigenin-labeled antisense RNA probes and in situ hybridization were performed as described previously (Ohtsuka et al., 2011). We used partial-length cDNA of Neurog2 (NM_009718.2) (0.87 kb) and full-length coding sequence of Hbp1 (NM_153198.2). Neurod1 (NM_010894.2), Ascl1 (NM_008553.4), Ccnal (NM_007631.2), Cccn1 (NM_007633.2) and M야n (NM_008709.3) as templates of the RNA probes.

**Quantitative real-time RT-PCR**

Total RNA samples were extracted from FACS-sorted embryonic NSCs prepared from the cortical regions of pHes1-d2EGFP transgenic mice as described previously (Ohtsuka et al., 2011). Reverse transcription of the total RNA and real-time RT-PCR were performed as previously described (Tan et al., 2012), using the primers listed in supplementary material Table S1. β-actin (Actb) was used as internal control.

**Plasmid construction**

For overexpression of Hbp1, full-length coding sequence of Hbp1 (NM_153198.2) was cloned into the pEF (human elongation factor 1α promoter)-MM expression vector, which was modified from pEF-BOS vector (Mizushima and Nagata, 1990). The pCAGGS-HA-hRb1 vector, in which HA (hemagglutinin)-tagged human Rb1 was inserted into pCAGGS vector, was kindly provided by Dr Chiaki Takahashi and Dr Nobunari Sasaki (Kanazawa University, Japan). The pCAG-HA-Hbp1 vector was created by inserting HA-tagged Hbp1 into pCAGEN (Matsuda and Cepko, 2004). For the reporter assay, Ccnal promoter region (from −3281 to −232) was inserted into pGL4.10 (Promega), and the LacZ in pGL4.10 was then replaced for the ubiquitylated luciferase fused with two nuclear localization sequences (NL2-UB-Luc2). For knockdown experiments, expression vectors were generated from annealed oligonucleotides
for shRNA targeting Hbp1 (shHbp1) or Cnd1 (shCnd1) (Hbp1: 5′-acct-cGGACTCTTCCGGTGTCTATGCTcaagagACATAGACCGCAGAAGAGTCCg-3′ and 5′-ccaaatGGACTCTTCCGGTGTCTATGTtcaagagACATAGACCGCAGAAGAGTCCtt-3′; Cnd1: 5′-acctGTCGATCATACCTAGCACAATGTTCTAGTGATGATCCAC3′ and 5′-ccaaatGTGCATCTACACTGACAACTctcttgaAGTTGTCAGTGTAGATGCA-3′) inserted into the BbsI site of pSRNA-h7SKneo G1 plasmid vector (InvivoGen), with the 20-21 nucleotide target sequence shown in uppercase letters, as described previously (Ohtsuka et al., 2011). Randomly scrambled sequence of the target was used for the negative control. The knockdown efficiency was confirmed in HEK293T cell lines.

**In utero electroporation**

Pregnant ICR mice were obtained from Japan SLC and CLEA Japan. In utero electroporation was performed with E13.5 ICR pregnant mice as described previously (Ohtsuka et al., 2011). All animals were handled in accordance with the Kyoto University Guide for the Care and Use of Laboratory Animals.

**Immunohistochemistry**

Immunohistochemistry was performed as described previously (Ohtsuka et al., 2011). The primary antibodies used are listed in supplementary material Table S2. Primary antibodies were detected with Alexa Fluor-conjugated secondary antibodies (1:200; Molecular Probes). To visualize the cell nuclei, 4′,6-diamidino-2-phenylindole (DAPI; Sigma-Aldrich) was added to slides. Fluorescent staining was analyzed with LSM510 and LSM780 confocal microscopes (Zeiss).

**Analysis of cell cycle length**

To estimate the cell cycle length, we conducted a dual-pulse-labeling of DNA synthesis using 5-bromo-2′-deoxyuridine (BrdU; Sigma-Aldrich) and 5-ethynyl-2′-deoxyuridine (EdU; Molecular Probes), referring to the previous methods (Martynoga et al., 2005; Mair et al., 2012). Previous reports used EdU first, followed by BrdU, but here we administered BrdU first, followed by EdU. Using the anti-BrdU antibody MoBU-1 (Molecular Probes), we confirmed that the reverse order of injection produced the same results. BrdU (50 μg BrdU/g body weight) and EdU (125 μg EdU/g body weight) were injected intraperitoneally to the pregnant mice 2 h and 30 min before sacrifice, respectively, and the ratios of cells that incorporated either or both BrdU and EdU were analyzed to estimate the cell cycle length. The detection of EdU-labeled cells was performed based on a fluorogenic click reaction (Salic and Mitchison, 2008). Length of the S phase cycle length. The detection of EdU-labeled cells was performed based on a fluorogenic click reaction (Salic and Mitchison, 2008). Length of the S phase cycle length. The detection of EdU-labeled cells was performed based on a fluorogenic click reaction (Salic and Mitchison, 2008). Length of the S phase cycle length. The detection of EdU-labeled cells was performed based on a fluorogenic click reaction (Salic and Mitchison, 2008). Length of the S phase cycle length.

**Reporter assay**

The luciferase reporter of Cnd1 (0.1 μg) and the expression plasmids (1.0 μg) were transfected into HEK293T cells. The pRL-SV40 vector (1 μg; Promega) was co-transfected to normalize the transfection efficiency. Cells were harvested after 48 h and the reporter assay was performed as described previously (Sakamoto et al., 2003).

**Statistical analysis**

Each experiment was performed with at least three independent samples. Results are shown as mean±s.e.m. Statistical differences were examined with Student’s t-test.

**Acknowledgements**

We thank Dr Hitoshi Miyachi for his help in the generation of Hbp1-flox mice, Dr Chiaki Takahashi and Dr Nobunari Sasaki for pCAGGS-HA-Hrp1 vectors, Dr Itaru Imayoshi for Nestin-CreER2 mice, NLS2-UB-Luc2pBS vectors and for critical discussion, Dr Takahiko Matsuda for pCAGEN and pCAG-mCherry vectors, and Mr Yuhei Yasueda for technical assistance.

**Competing interests**

The authors declare no competing or financial interests.

**Author contributions**

N.W. developed the concepts, and performed experiments and data analysis. R.K. developed the concepts and performed data analysis. T.O. developed the concepts, performed experiments and data analysis, and wrote the manuscript.

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**Supplementary material**

Supplementary material available online at http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.120477/-/DC1

**References**


Supplementary Materials and Methods

Generation of Hbp1 induced conditional knockout mice

The construction of targeting vector and gene targeting in TT2 ES cell line were conducted as previously described (Imayoshi et al., 2013). For the generation of the targeting vector for FRT-neomycin-FRT cassette-inserted Hbp1-floxed mice, in which LoxP site and LoxP-FRT-neomycin-FRT cassette were inserted into intron 1 and 2 of Hbp1 gene, respectively, BAC (bacterial artificial chromosome) carrying Hbp1 genomic locus of the C57BL/6J background was purchased from BACPAC Resource Center (Children's Hospital Oakland Research Institute, Clone ID: RP23-193M19). For screening of successfully targeted ES cell clones, Hbp1-targeted allele (Hbp1-floxed-neo) was evaluated by Southern blot analysis of genomic DNA of the ES cells as described previously (Imayoshi et al., 2010). For preparing probes for Southern blot, PCR fragments amplified by using the primers listed in supplementary material Table S1 were cloned into pTA2 vector (TOYOBO), and the vectors were double-digested with ClaI and SalI and then purified by electrophoresis and QIAquick Gel Extraction Kit (QIAGEN). After creating the chimeric mice carrying Hbp1-floxed-neo allele by using the ES cells obtained, we crossed them with CAG-FLPe\textsuperscript{+/o} mice (Kanki et al., 2006) to remove the neomycin cassette. PCR-based genotyping for Hbp1-floxed allele was performed using genomic DNA from mouse tails as a template. The specific primers used were listed in supplementary material Table S1. We generated Hbp1\textsuperscript{flox/+} mice by removing CAG-FLPe transgene by crossing mice. By crossing them with Nestin-CreER\textsuperscript{T2} L5-1\textsuperscript{+/o} transgenic mice (Imayoshi et al., 2006), we obtained Nestin-CreER\textsuperscript{T2} L5-1\textsuperscript{+/o};Hbp1\textsuperscript{flox/flox} mice. These mice were maintained on a mixed C57BL/6J and ICR background. For activation of CreER\textsuperscript{T2}, 5.2 mg of tamoxifen (Sigma-Aldrich) per 40 g of body weight was administered by oral gavage to the pregnant mice at E9.5 as described previously (Imayoshi et al., 2010). We used the tamoxifen-induced Nestin-CreER\textsuperscript{T2} L5-1\textsuperscript{+/o} mice as a negative control (NC).

Western blot analysis

HEK293T cells and the brains of embryos were disrupted and homogenized with lysis buffer [50 mM Tris-HCl pH 8.0, 100 mM NaCl, 5 mM MgCl\textsubscript{2}, 0.5% NP-40, 1× Complete Proteinase Inhibitor Cocktail (Roche), 1 mM phenylmethanesulfonylfluoride, 250 U/ml Benzonase (Sigma-Aldrich)] and incubated on ice for 30 min before adding 1/10 volume
of 10% SDS to the lysates, and then the samples were boiled for 3 min. SDS-PAGE and Western blotting were performed as described previously (Harima et al. 2013). The primary antibodies used were listed in supplementary material Table S2.

**Measurement**

The signal intensity of the immunoreaction for anti-cyclin D1 antibody in GFP$^+$ area and DAPI$^+$ nuclei was analyzed by using the modules of “IdentifyPrimaryObjects”, “MaskImage” and “MeasureImageIntensity” in CellProfiler 2.1.1 (Broad Institute). The measurement of the length and area was performed by using ImageJ 1.48 (Wayne Rasband, NIH, USA). The cell counting, including the counting of double and triple-positive cells, was conducted manually by using the plug-in of “Cell Counter” in ImageJ 1.48. For Pax6$^+$ cell counting in the lateral cortices, single-plane confocal images of coronal sections were obtained using motorized XY-scanning stage of LSM780 (Zeiss), and then the Pax6$^+$ fluorescence signals were counted automatically using the function of “Spots” in Imaris 7.6.5 (Bitplane). The number of Pax6$^+$ NSCs throughout the cortical regions in multiple coronal sections at constant intervals was summed up along the antero-posterior axis of lateral ventricle; thus the total number of NSCs in the hemisphere was estimated and compared between the control and icKO. In the scanned sections containing the ventricles, vesicle area, length of brain surface and ventricular surface of dorsolateral telencephalon, area of ventral telencephalon, and thickness of the VZ/SVZ/IZ+CP in the dorsolateral telencephalon were measured at the interval of 544 μm at E14.5.

**References**


Figures

A

ep:E13.5→IHC:E16.5

GFP  Map2  Merge  high magnif.

pEF-EGFP

pEF-Hbp1

shHbp1

B

Graph showing the percentage of Map2-GFP/GFP for different conditions:

- pEF-EGFP
- pEF-Hbp1
- shHbp1

Statistical significance indicated by asterisks:

**

***

C

ep:E13.5→IHC:E16.5

GFP  KI67  Merge

pEF-EGFP

pEF-Hbp1

shHbp1

GFP

pH3

Merge

GFP + p-Vim

D

Graphs showing various biological parameters:

- Ki67-GFP/GFP percentage
- pH3-GFP/GFP percentage
- Number of pH3-positive cells in VZ + SVZ
- p-Vim-GFP/GFP outside of VZ

Statistical significance indicated by asterisks:

**

N.S.

N.S.
Fig. S1. Characterization of transfected cells in overexpression and knockdown experiments. In utero electroporation (ep) was performed with control vectors (pEF-EGFP) only or with a combination of pEF-Hbp1 or shHbp1 at E13.5, and the fates of transfected cells were analyzed by immunohistochemistry (IHC). (A) Coronal sections of dorsolateral telencephalon were double-stained using anti-GFP (green) and anti-Map2 (red) antibodies. (B) The proportions of Map2+ cells of transfected (GFP+) cells. (C) Double-staining using anti-GFP (green) and anti-Ki67/pH3/p-Vim (red)
antibodies. (D) The proportions of Ki67+ or pH3+ cells of transfected (GFP+) cells, the numbers of pH3+ cells in the VZ/SVZ within a radial column of 200 μm width, and the proportions of p-Vim+;GFP+ cells outside the VZ of GFP+ cells. (E) BrdU was administered intraperitoneally to pregnant mice 4 h after in utero electroporation and sacrificed after 24 h at E14.5, 48 h at E15.5 and 72 h at E16.5. Coronal sections of dorsolateral telencephalon were double-stained using anti-GFP (green) and anti-BrdU (red) antibodies. (F) Graphs showing the proportions of BrdU+;GFP+ cells in the VZ, SVZ or IZ of total BrdU+;GFP+ cells. (G) Triple-staining using anti-GFP (green) and anti-cleaved-caspase 3 (red) antibodies and DAPI (blue) at E15.5 and E16.5. (H) The numbers of cleaved-caspase 3+ cells within a radial column of 200 μm width. n=3, error bars: s.e.m.; *P<0.05, **P<0.01, ***P<0.001; Student’s t-test; N.S., not significant. Scale bars: 200 μm.
Fig. S2. Inhibition of neuronal differentiation by knockdown of *Hbp1*. (A) Knockdown efficiency of *shHbp1* was evaluated by western blot. HEK293T cells were co-transfected with expression vectors (*pEF-HA-Hbp1*) that express HA (hemagglutinin)-tagged Hbp1 and expression vectors of either shRNA targeting *Hbp1* (*shHbp1*) or scrambled shRNA control vectors (*scrambled*), and proteins were extracted from cells 24 h later. HA-Hbp1 protein was detected with anti-HA antibodies. (B) Expression levels of HA-Hbp1 protein in knockdown cells were estimated as 2.14 ±
0.00% compared with the control. β-Actin was used as an internal control, and the values were normalized to that in the control. (C,D) shHbp1 or scrambled shRNA vectors were introduced into ventricular cells by in utero electroporation at E13.5. Coronal sections of dorsolateral telencephalon were immunostained to analyze the fates of transfected cells at E16.5 (C) or E18.5 (D). Anti-GFP (green) and anti-Tuj1/Tbr2/Pax6 (C) or anti-Cux1/Ctip2 (D) (red) antibodies were used for double-labeling. The proportions of cells positive for each marker (Tuj1, Tbr2 or Pax6) (C) and the proportions of Cux1+ or Ctip2+ cells (D) of the Hbp1 knockdown or control cells, and the numbers of Cux1+ or Ctip2+ cells in the CP within a radial column of 200 μm width (D) were shown in bar graphs. (E) pEF-Hbp1 vectors were co-introduced with shHbp1 at ratios of 3:1, 1:1 or 1:3 by in utero electroporation at E13.5, and the fates of transfected cells were analyzed at E16.5. Coronal sections of dorsolateral telencephalon were stained using anti-GFP (green) and anti-Tuj1/Tbr2/Pax6 (red) antibodies and DAPI (blue). (F) Graphs showing the proportions of Tuj1+, Tbr2+ or Pax6+ cells of transfected (GFP+) cells. n=3, error bars: s.e.m.; *P<0.05, **P<0.01, ***P<0.001; Student’s t-test; N.S., not significant. Scale bars: 200 μm.
Fig. S3. Generation and validation of Hbp1 icKO mice. (A) Schematic drawing of the strategy for generating Hbp1 icKO mice. (B) Southern blot analysis of genomic DNA from wild-type and Hbp1-targeted ES cell clones by using EcoRV-digested DNA hybridized with 5’ probe, which detected wild-type allele (wt): 21.8 kb and Hbp1-floxed-neo allele (flx-neo): 9.1 kb, and EcoRI and NotI-digested DNA hybridized with 3’ probe, which detected wt: 17.2 kb and flx-neo: 11.8 kb. (C) Expression levels of Hbp1 in the telencephalon of negative control (NC) and Hbp1 icKO mice. Tamoxifen (Tam) was administered at E9.5, embryos were sacrificed at E11.5, E12.5 and E14.5, and real-time RT-PCR was performed using total RNAs prepared from the telencephalon. β-actin was used as internal control, and the values were normalized to that in NC at E11.5. n=3, error bars: s.e.m.; **P<0.01, ***P<0.001; Student’s t-test.
Fig. S4. Cortical development in Hbp1-deficient mice. (A) Immunohistochemistry on coronal sections of the cortical regions of control and Hbp1 icKO mice at different developmental stages with neuronal markers such as NeuN and Tuj1, and Hes1, a marker for NSCs. (B) The number of cells immunoreactive for each antibody was
counted within a radial column of 200 μm width in the middle part of dorsolateral telencephalon. (C) Immunostaining on coronal sections of the cortical regions at E16.5 and E18.5 with antibodies against PDGFRA, a marker for oligodendrocyte precursor cells, and p-Vim, a marker for mitotic radial glial cells. (D) The numbers of PDGFRA+ cells within a radial column of 200 μm width, and the numbers of p-Vim+ cells in the VZ or SVZ/OSVZ within a radial column of 200 μm width. n=3, error bars: s.e.m.; **P<0.01, ***P<0.001; Student’s t-test; N.S., not significant. Scale bars: 200 μm in A; 100 μm in C.
Fig. S5. Estimation of cell death in Hbp1 icKO mice. (A) Cell death in neural stem/progenitor cells and neurons in the cortical regions of the control and the icKO was analyzed by immunohistochemistry using anti-cleaved-caspase 3 antibodies at different developmental stages. (B) The numbers of cleaved-caspase 3+ cells in NSCs (Pax6+), IPs (Tbr2+) or neurons (Tuj1+) in the control and the icKO embryos. (C) Analyses of cell death in the ventral telencephalon in the control and the icKO at different developmental stages. (D) The numbers of cleaved-caspase 3+ cells within a 200 μm square in the ventral telencephalon. n=3, error bars: s.e.m.; *P<0.05, **P<0.01, ***P<0.001; Student’s t-test; N.S., not significant. Scale bars: 200 μm.
Fig. S6. Analysis of cell proliferation properties in *Hbp1* icKO mice. The proportions of Pax6+ or Tbr2+ cells of Ki67+ cells, and Ki67+ cells of Pax6+ or Tbr2+ cells in the cortical regions of the control and the icKO mice at different developmental stages. *n*=3, error bars: s.e.m.; **P<0.01, ***P<0.001; Student’s *t*-test; N.S., not significant.
Fig. S7. Altered expression of cell cycle-related genes under modified Hbp1 expression levels. (A) *In situ* hybridization (ISH) for cyclin D1 on coronal brain sections from mice subjected to overexpression or knockdown of Hbp1. Brackets indicate regions transfected with expression vectors. (B) *In situ* hybridization for cyclin E1 and N-myc on coronal brain sections of the cortical regions of the control and the Hbp1 icKO mice at different embryonic stages. Dashed lines indicate the ventricular surface. Scale bars: 200 μm in A; 100 μm in B.
Fig. S8. Analysis of expression levels of phosphorylated Rb. (A) Immunohistochemistry showing the expression levels of phosphorylated Rb (p-Rb) (Ser 780, Ser 807/811) in the cortical regions of the control and the icKO mice at E12.5 and E14.5. (B) Graphs showing the proportions of p-Rb (Ser 780 or Ser 807/811)⁺ cells of Pax6⁺ or Tbr2⁺ cells. (C) Western blot comparing the expression levels of p-Rb in the dorsolateral telencephalon of the control and the icKO mice at E12.5 and E14.5. (D) Graphs showing the expression levels of p-Rb protein. β-Actin was used as internal control, and the values were normalized to that in the control at E12.5. n=3, error bars: s.e.m.; *P<0.05, **P<0.01, ***P<0.001; Student’s t-test; N.S., not significant. Scale bar: 100 μm.
Fig. S9. Rescue experiments by knockdown of cyclin D1. (A) Knockdown efficiency of shCcn1 was evaluated by western blot. HEK293T cells were co-transfected with expression vectors (pEF-HA-Ccn1) that express HA-tagged cyclin D1 and expression vectors of shRNA targeting cyclin D1 (shCcn1) or negative control vectors (psiRNA),
and proteins were extracted from cells 24 h later. HA-cyclin D1 was detected with anti-HA antibodies. (B) Expression levels of HA-cyclin D1 protein were estimated as 25.58 ± 0.01% compared with the control. β-Tubulin was used as internal control, and the values were normalized to that in the control. (C) shCcdnl were co-introduced with shHbp1 at ratios of 3:1, 1:1 or 1:3 by in utero electroporation at E13.5, and the fates of transfected cells were analyzed at E16.5 by immunohistochemistry using anti-GFP (green) and anti-Tuj1/Tbr2/Pax6 (red) antibodies and DAPI (blue). (D) Graphs showing the proportions of Tuj1+, Tbr2+ or Pax6+ cells of transfected (GFP+) cells 3 days after in utero electroporation at E16.5. n=3, error bars: s.e.m.; *P<0.05, **P<0.01; Student’s t-test; N.S., not significant. Scale bar: 200 μm.
### Table S1. Primers used for PCR

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(PrimerBank ID: 6671509a1)

### Primers used for preparing probes for Southern blot of genomic DNA of the ES cells

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### Primers used for PCR-based genotyping for Hbp1-floxed allele

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### Table S2. Primary antibodies

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Table S3. Estimation of the length of the cell cycle

The length of the cell cycle in Ki67+ proliferating cells (Fig. 7D)

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<td>$T_C$ (h)</td>
<td>10.91 ± 0.26</td>
<td>8.54 ± 0.02</td>
<td>14.41 ± 0.12</td>
<td>10.47 ± 0.13</td>
<td>17.64 ± 0.31</td>
<td>13.25 ± 0.11</td>
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<tr>
<td>$T_S$ (h)</td>
<td>4.72 ± 0.17</td>
<td>5.09 ± 0.09</td>
<td>5.72 ± 0.01</td>
<td>4.68 ± 0.16</td>
<td>4.12 ± 0.02</td>
<td>3.43 ± 0.03</td>
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The length of the cell cycle in Pax6+ neural stem cells (Fig. 7E)

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<td>$T_C$ (h)</td>
<td>10.10 ± 0.16</td>
<td>6.87 ± 0.01</td>
<td>14.48 ± 0.06</td>
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<td>17.44 ± 0.68</td>
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<tr>
<td>$T_S$ (h)</td>
<td>5.70 ± 0.09</td>
<td>4.22 ± 0.02</td>
<td>5.73 ± 0.04</td>
<td>4.12 ± 0.01</td>
<td>5.72 ± 0.29</td>
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The length of the cell cycle in Tbr2+ neural progenitor cells (Fig. 7F)

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<td>$T_C$ (h)</td>
<td>21.37 ± 0.08</td>
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<td>25.38 ± 1.12</td>
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<tr>
<td>$T_S$ (h)</td>
<td>7.38 ± 0.09</td>
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<td>5.04 ± 0.17</td>
<td>5.26 ± 0.12</td>
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The length of the cell cycle in overexpression and knockdown experiments (Fig. 8F)

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<th>$T_S$ (h)</th>
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<td>pEF-Hbp1</td>
<td>15.82 ± 0.10</td>
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<td>shHbp1</td>
<td>8.54 ± 0.29</td>
<td>4.09 ± 0.28</td>
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<td>shHbp1 : shCcnd1 3:1</td>
<td>11.47 ± 0.28</td>
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<td>shHbp1 : shCcnd1 1:1</td>
<td>12.10 ± 0.06</td>
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<td>shHbp1 : shCcnd1 1:3</td>
<td>13.46 ± 0.24</td>
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Data are mean ± s.e.m., n = 3.