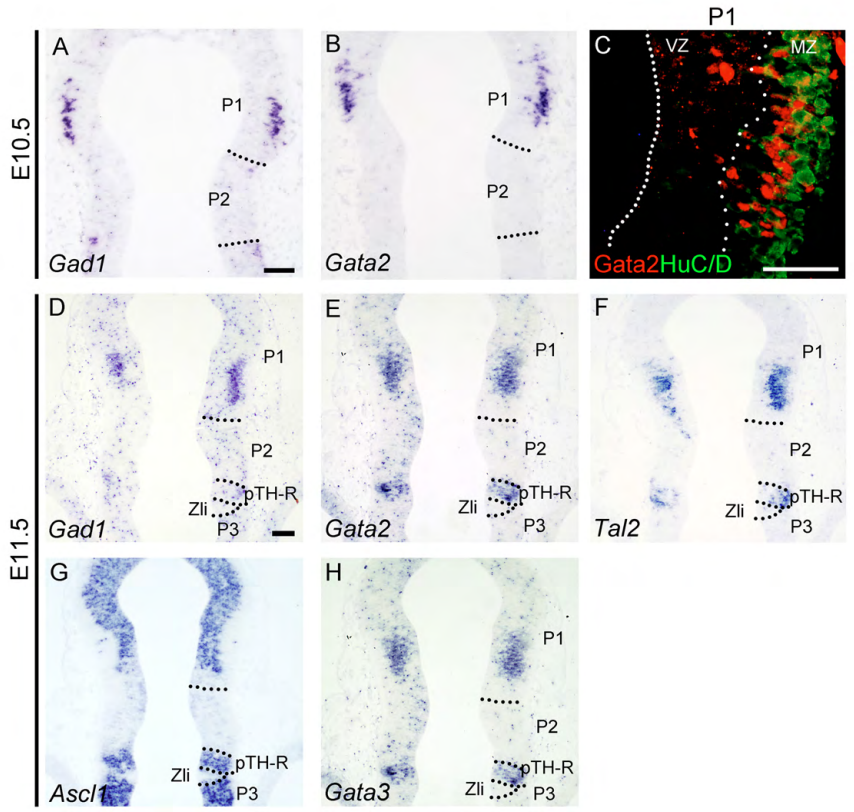

Fig. S1. Gata2 expression is initiated at ~E10.5. (**A-H**) ISH analysis of *Gad1*, *Gata2*, *Tal2*, *Ascl1* and *Gata3* expression on coronal sections of WT diencephalon at E10.5 (A,B) and E11.5 (D-H). Gata2 and HuC/D co-IHC in P1 at E10.5 (C). Scale bars: in A,D, 100 µm; in C, 50 µm.

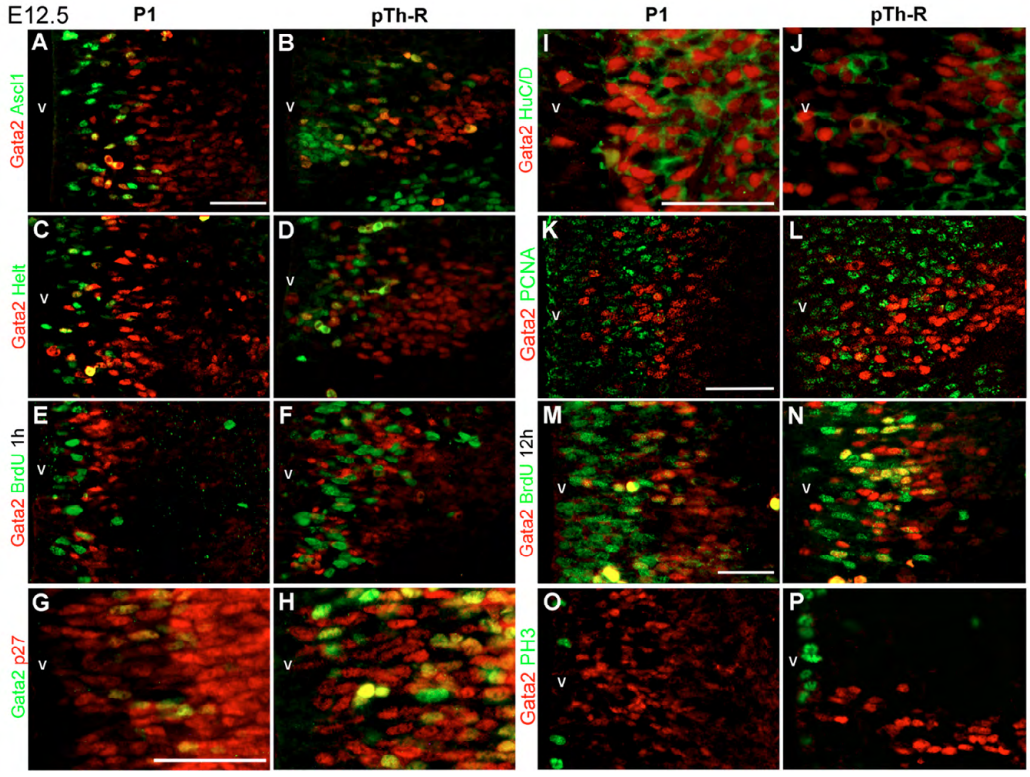

Fig. S2. Gata2 colocalizes with Ascl1 and Helt and is expressed in the postmitotic GABAergic precursors in P1 and pTh-R. (**A-P**) IHC on was used to analyse the colocalization of Gata2 and Ascl1 (A,B), Gata2 and Helt (C,D), Gata2 and p27 (G,H), Gata2 and HuC/D (I,J), Gata2 and PCNA (K,L) and Gata2 and PH3 (O,P) on coronal sections of E12.5 mouse diencephalon. BrdU incorporation in Gata2^{+} cells was analysed after a 1-hour BrdU pulse (E,F) and a 12-hour BrdU pulse (M,N). Images from the P1 and pTh-R regions are shown as indicated. v, ventricle. Scale bars: 50 µm.

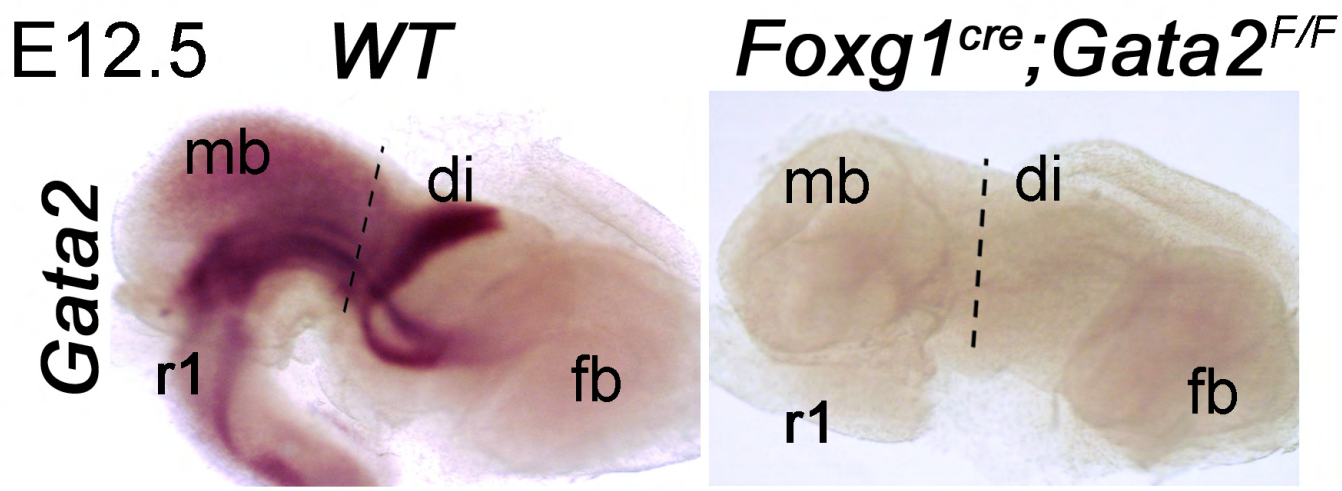

Fig. S3. Complete loss of *Gata2* expression in the *Foxg1^{cre};Gata2$^{F/F}$* brain. *Gata2* mRNA expression was analysed by whole mount in situ hybridization on E12.5 WT and *Foxg1^{cre}, Gata2$^{F/F}$* embryonic brains. di, diencephalon; fb, forebrain; mb, midbrain.

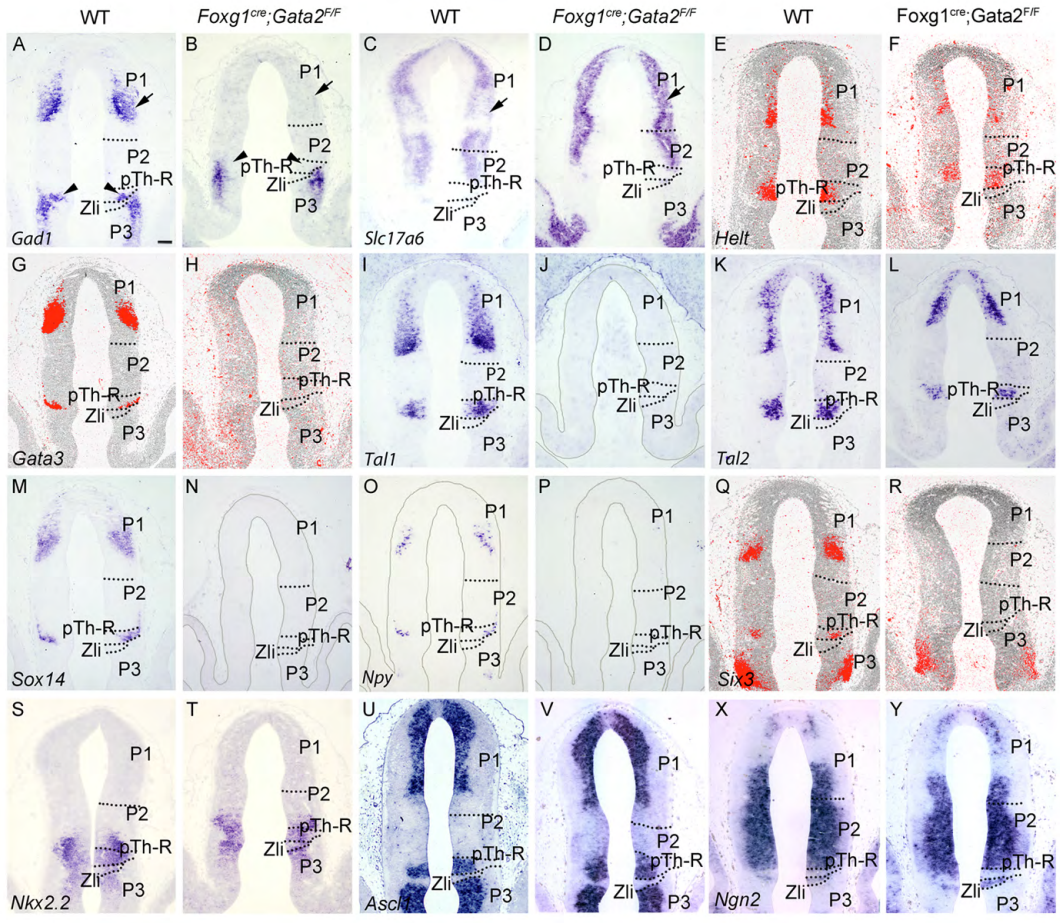

Fig. S4. GABAergic-to-glutamatergic fate transformation in the P1 and loss of GABAergic marker expression in the pTh-R in *Foxg1^{cre}; Gata2$^{F/F}$*embryos at E12.5. (**A-Y**) ISH analysis of *Gad1*, *Slc17a6*, *Helt*, *Gata3*, *Tal1*, *Tal2*, *Sox14*, *Npy*, *Six3*, *Nkx2-2*, *Ascl1* and *Ngn2* expression in WT and *Foxg1^{cre}; Gata2$^{F/F}$* embryos at E12.5. Arrows in A-D indicate the regions where the fate transformation is most apparent. Arrowheads in A and B indicate the loss of *Gad1* expression in pTh-R. The border between P1 and P2 was defined by the expression of *Gbx2* on adjacent sections. Scale bar: 100 μm.

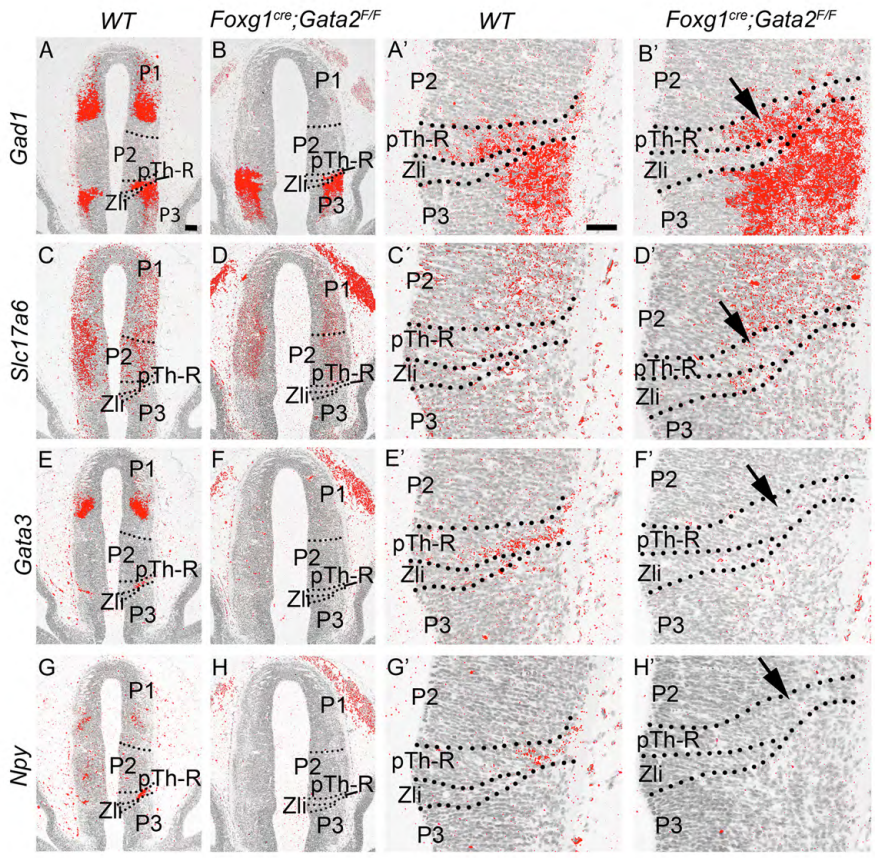

Fig. S5. pTh-R GABAergic precursors do not acquire glutamatergic phenotype in the absence of Gata2. (**A-H′**) ISH analysis of *Gad1*, *Slc17a6*, *Gata3 and Npy* in WT and *Foxg1*^{cre}*; Gata2*$^{F/F}$embryos at E13.5. Coronal view. (A′-H′) Higher magnification views from the pTh-R. Arrows in B′, D′, F′ and H′ indicate the pTh-R GABAergic progenitors that lose *Gata3* and *Npy* expression but do not upregulate *Slc17a6*. Scale bars: 100 μm.

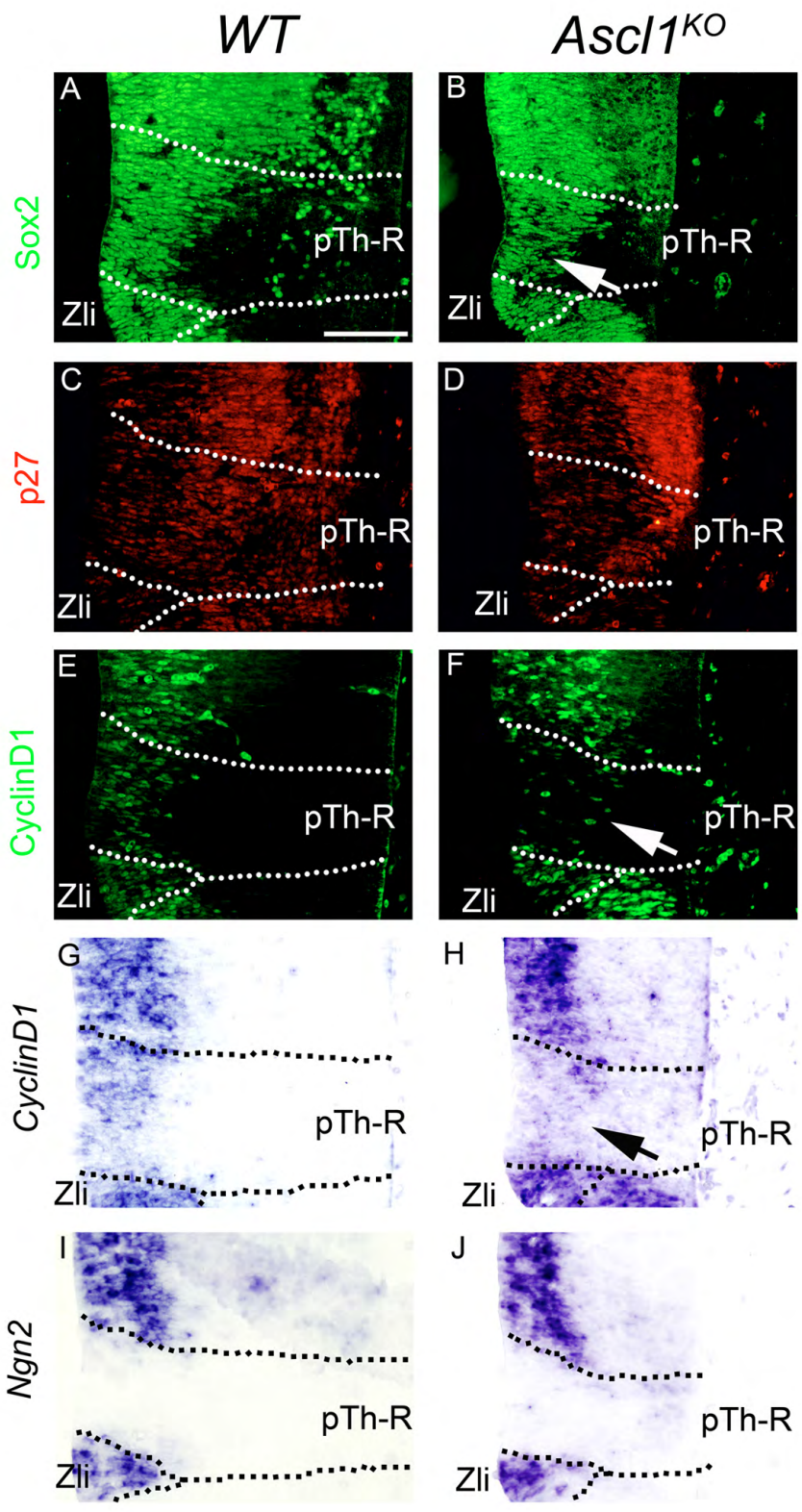

Fig. S6. Premature cell-cycle exit and reduction of progenitor cycling in the *Ascl1*^{KO} pTh-R. (**A-J**) IHC analysis of Sox2 and p27 (A-D), cyclin D1 (E,F) and ISH analysis of cyclin D1 and *Ngn2* (G-J) in the WT and *Ascl1*^{KO} pTh-R region at E12.5. Arrows indicate downregulation of Sox2 (B), cyclin D1 protein (F) and cyclin D1 mRNA (H) in the pTh-R. Scale bar: 100 μm.

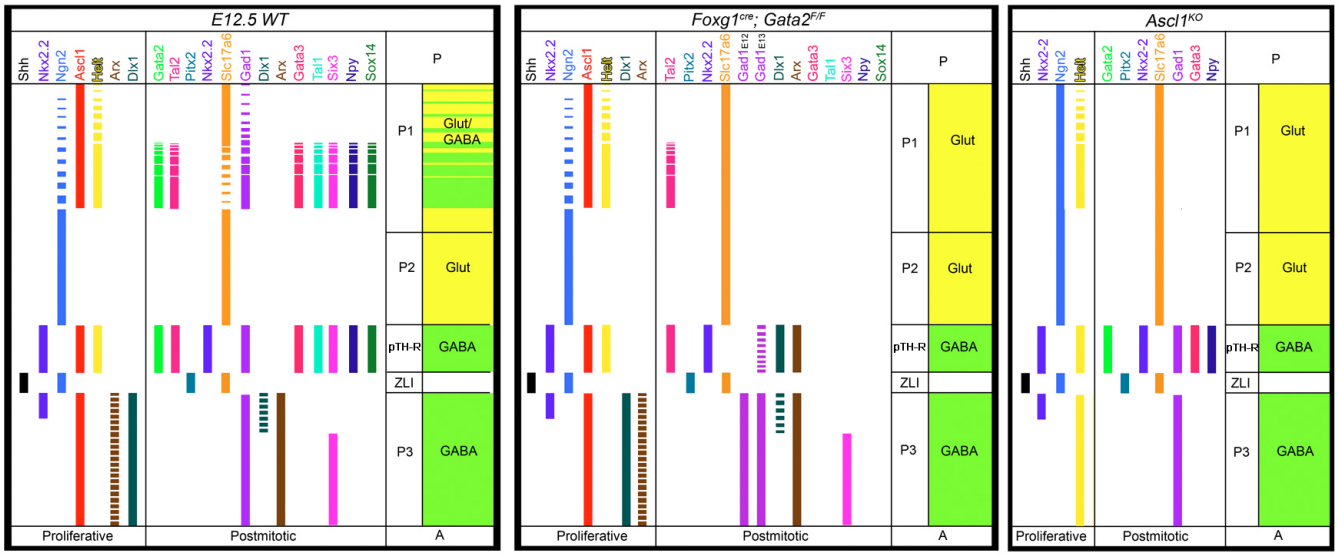

Fig. S7. Summary charts of gene expression in WT and changes in gene expression in *Foxg1^{cre}; Gata2$^{F/F}$* and *Ascl1^{KO}* diencephalon. P1-P3, diencephalic prosomeres; pTh-R, rostral part of P2; ZLI, zona limitans interthalamica; A, anterior; P, posterior.