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## ***Ascl1* is a required downstream effector of *Gsx* gene function in the embryonic mouse telencephalon**

Bei Wang<sup>1,3</sup>, Ronald R Waclaw<sup>1</sup>, Zegary J Allen II<sup>1</sup>, Francois Guillemot<sup>2</sup> and Kenneth Campbell\*<sup>1</sup>

Address: <sup>1</sup>Division of Developmental Biology, Cincinnati Children's Hospital Medical Center, University of Cincinnati College of Medicine, 3333 Burnet Avenue, Cincinnati OH45229, USA, <sup>2</sup>Division of Molecular Neurobiology, NIMR, The Ridgeway, Mill Hill, London, UK and <sup>3</sup>Nina Ireland Laboratory of Developmental Neurobiology, Center for Neurobiology and Psychiatry, Rock Hall, UCSF 1550 4th Street, San Francisco, CA 94158, USA

Email: Bei Wang - bei.wang@ucsf.edu; Ronald R Waclaw - ronald.waclaw@cchmc.org; Zegary J Allen - zegary.allen@cchmc.org; Francois Guillemot - fguille@nimr.mrc.ac.uk; Kenneth Campbell\* - kenneth.campbell@cchmc.org

\* Corresponding author

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### **Abstract**

**Background:** The homeobox gene *Gsx2* (formerly *Gsh2*) is known to regulate patterning in the lateral ganglionic eminence (LGE) of the embryonic telencephalon. In its absence, the closely related gene *Gsx1* (previously known as *Gsh1*) can partially compensate in the patterning and differentiation of ventral telencephalic structures, such as the striatum. However, the cellular and molecular mechanisms underlying this compensation remain unclear.

**Results:** We show here that in the *Gsx2* mutants *Gsx1* is expressed in only a subset of the ventral telencephalic progenitors that normally express *Gsx2*. Based on the similarities in the expression of *Gsx1* and *Ascl1* (*Mash1*) within the *Gsx2* mutant LGE, we examined whether *Ascl1* plays an integral part in the *Gsx1*-based recovery. *Ascl1* mutants show only modest alterations in striatal development; however, in *Gsx2;Ascl1* double mutants, striatal development is severely affected, similar to that seen in the *Gsx1;Gsx2* double mutants. This is despite the fact that *Gsx1* is expressed, and even expands, in the *Gsx2;Ascl1* mutant LGE, comparable to that seen in the *Gsx2* mutant. Finally, Notch signaling has recently been suggested to be required for normal striatal development. In spite of the fact that Notch signaling is severely disrupted in *Ascl1* mutants, it actually appears to be improved in the *Gsx2;Ascl1* double mutants.

**Conclusion:** These results, therefore, reveal a non-proneural requirement of *Ascl1* that together with *Gsx1* compensates for the loss of *Gsx2* in a subset of LGE progenitors.

### **Background**

The homeobox gene *Gsx2* (formerly known as *Gsh2*) has been shown to be required for correct dorsal-ventral patterning in the embryonic mouse telencephalon [1-3]. *Gsx2* accomplishes this by repressing dorsal telencephalic genes such as *Pax6* and promoting the expression of ven-

tral regulators such as *Ascl1* (*Mash1*) and *Dlx* genes within ventricular zone (VZ) and subventricular zone (SVZ) progenitors of the lateral ganglionic eminence (LGE). Although *Gsx2* mutants do not survive after birth [4], analyses at late embryonic stages have demonstrated severe reductions in markers of striatal projection neurons

as well as olfactory bulb interneurons [1-3,5,6], both of which are derived from the LGE [7-10].

The closely related *Gsx1* (*Gsh1*) is also expressed in the embryonic ventral telencephalon [11], although no telencephalic phenotype has been reported [5,6]. Despite this, removal of *Gsx1* on the *Gsx2* mutant background eliminates nearly all striatal projection neurons and olfactory bulb interneurons, suggesting that *Gsx1* can, at least in part, compensate for the loss of *Gsx2* in the development of these ventral telencephalic structures. This compensation, however, is complex because *Gsx1* is normally only present in the medial ganglionic eminence and the ventral-most portion of the LGE. In *Gsx2* mutants, *Gsx1* expression spreads dorsally to encompass the mutant LGE at mid-neurogenesis time points (for example, embryonic day (E)14), which is coincident with the re-establishment of ventral identity (for example, *Ascl1* and *Dlx* expression) in the mutant LGE [5,6]. Both *Ascl1* and *Dlx* genes are known to be required for normal development of the striatum and olfactory bulb interneurons [12-16]. Moreover, a recent study [17] suggests that *Ascl1* and *Dlx* genes control distinct and parallel pathways that act in the specification of olfactory bulb interneurons. The mechanism by which *Gsx1* compensates for the loss of *Gsx2* has not been fully elucidated. Moreover, the requirement for *Ascl1* or *Dlx* genes in this process is unclear.

In this study we have examined the molecular mechanisms underlying *Gsx1*-mediated recovery of ventral telencephalic development in *Gsx2* mutants. To do this, we have generated and analyzed *Gsx2<sup>EGFP</sup>* mice as well as *Gsx2;Ascl1* double mutants at multiple embryonic stages. Removal of *Ascl1* from the *Gsx2* mutant background results in a telencephalic phenotype nearly identical to the *Gsx1;Gsx2* double mutant [5,6]. These results thus indicate that *Ascl1* is an essential component of the *Gsx1*-mediated recovery in a subset of LGE progenitors within the *Gsx2* mutant telencephalon.

## Results

### *Gsx1* expression in the *Gsx2* mutant telencephalon

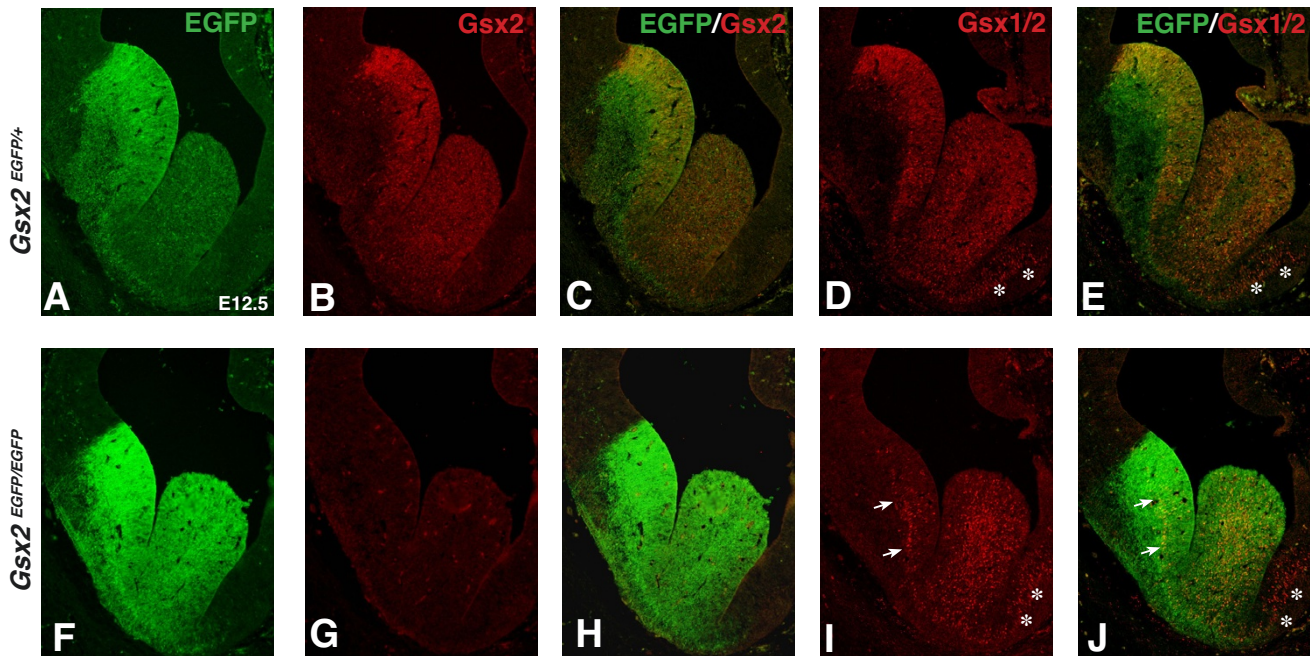
Previous studies have shown that *Gsx1* expands in the LGE of the *Gsx2* mutant [3,5,6]. Normally, the cells expressing *Gsx1* are confined to the ventral-most portion of the LGE; however, in *Gsx2* mutants the expression of this gene expands throughout the entire dorsal-ventral extent of the LGE between E11 and E14. We have generated mice in which the first exon of *Gsx2* is interrupted by an IRES-enhanced green fluorescent protein (EGFP) cassette so that EGFP is expressed in place of *Gsx2*. These mice appear to faithfully reproduce *Gsx2* expression and provide a short-term fate map of *Gsx2* derived cells that no longer express the protein (Figure 1A-C). Moreover, the *Gsx2<sup>EGFP/EGFP</sup>* embryos lack *Gsx2* protein expression, while

still delineating the portion of the LGE that the targeted *Gsx2* gene is being transcribed in by virtue of the EGFP staining (Figure 1F-H). These mutants exhibit identical patterning defects to those reported for the previously available *Gsx2* mutant allele [1-4] (data not shown). Using these mice together with an antibody that detects both *Gsx1* and *Gsx2* [18], we were able to examine the *Gsx1* recovery on a cellular level, within the context of the *Gsx2* expression domain.

While the *Gsx1/2* antibody staining looks very similar to that of *Gsx2* in the *Gsx2<sup>EGFP/+</sup>* embryos (Figure 1A-E), it reveals a rather different pattern in the *Gsx2<sup>EGFP/EGFP</sup>* embryos (Figure 1I, J). At E12.5, the cells expressing *Gsx1* in the mutant LGE are few in number and largely confined to its ventral half. This finding is in agreement with previous *Gsx1* gene expression studies [3,5]; however, the cellular resolution afforded by the immunohistochemical approach revealed that the *Gsx1* cells appear mostly at the border between the VZ and SVZ (Figure 1I, J). This is different from *Gsx2* expression in the wild-type LGE where cells throughout the apical-basal extent of the VZ express this protein, albeit at different levels of expression (Figure 1B). Previous studies have shown that the expansion of *Gsx1* throughout the *Gsx2* mutant LGE is complete between E14.5 and E16.5 [3,5,6]. This is clearly revealed by *Gsx1/2* staining in the *Gsx2<sup>EGFP/EGFP</sup>* mutants at E16.5 (Figure 2G). At this stage, only around half the LGE cells that would normally express *Gsx2* contain *Gsx1* staining. Again, the majority of the *Gsx1* expressing cells appear to line up at the VZ/SVZ boundary (Figure 2H). This is similar to *Gsx1/2* staining in the remnant of the medial ganglionic eminence in *Gsx2<sup>EGFP/+</sup>* brains (Figure 2B), and since this staining does not coincide with the EGFP from the *Gsx2* locus (Figure 2A-C), it is likely to reflect *Gsx1* expression in the wild-type medial ganglionic eminence. Thus, although *Gsx1* can at least partially compensate for *Gsx2* [5,6], it does not do so in all cells of the LGE that would normally express *Gsx2* but only in a subpopulation positioned at the VZ/SVZ boundary.

### Relationship between *Gsx1* and *Ascl1* in the *Gsx2* mutant LGE

*Ascl1* (*Mash1*) is known to be required for the normal development of the ventral telencephalon [14-16]. Furthermore, *Ascl1* is dependent on *Gsx2* for its normal expression in LGE progenitor cells [1-3], at least at early stages, before *Gsx1* expression expands into the mutant LGE. *Ascl1* is expressed by many cells within the *Gsx2<sup>EGFP/+</sup>* + VZ, although they are mainly located at the VZ/SVZ boundary (Figure 2D, E). Interestingly, the pattern of *Ascl1* expression in the *Gsx2* mutants is very similar to that of *Gsx1* (as revealed by *Gsx1/2* staining; Figure 2G-J), with scattered cells in the VZ and the majority accumulated along the VZ/SVZ boundary. In *Gsx1;Gsx2* double



**Figure 1**

**Knock-in of enhanced green fluorescent protein (EGFP) into the *Gsx2* locus.** (A, B) EGFP expression in *Gsx2*<sup>EGFP/+</sup> embryos (A) recapitulates endogenous *Gsx2* expression at E12.5 (B). (C) Note that EGFP expression persists longer than *Gsx2* protein expression in the lateral ganglionic eminence (LGE; merged image). – (D) The *Gsx1/2* antibody detects expression of *Gsx1* and *Gsx2* in the ventral telencephalon. (E) Note that the EGFP expression is absent in the septal expression domain of the *Gsx1/2* antibody (asterisks in D, E, I, J) indicating *Gsx1*-specific expression. (F–H) Homozygous knock-in of EGFP into the *Gsx2* locus (*Gsx2*<sup>EGFP/EGFP</sup>) (F) results in a loss of function of *Gsx2* with no detectable protein expression (G). Note that the EGFP expression is more intense in the *Gsx2*<sup>EGFP/EGFP</sup> embryos (H) compared to the *Gsx2*<sup>EGFP/+</sup> embryos (A). (I) The initial expansion of *Gsx1* into the LGE of *Gsx2*<sup>EGFP/EGFP</sup> embryos is detectable at E12.5 with an anti-*Gsx1/2* antibody. (J) *Gsx1* expression is not observed in all *Gsx2* mutant cells of the LGE (merged image) but found largely at the VZ/SVZ boundary (arrows in I, J).

mutants, *Ascl1* is not expressed in the LGE at early stages (for example, E12.5) but at later stages (for example, E15.5–16.5) it is found at low levels within the presumptive LGE region [5,6]. This suggests that although *Gsx* proteins are not absolutely required for *Ascl1* expression in the LGE, they are positive regulators of its expression. The overlap in *Gsx1* and *Ascl1* expression in the *Gsx2* mutant LGE (Figure 2H, J) therefore suggests that *Ascl1* may act in concert with *Gsx1* for the compensation observed in *Gsx2* mutants.

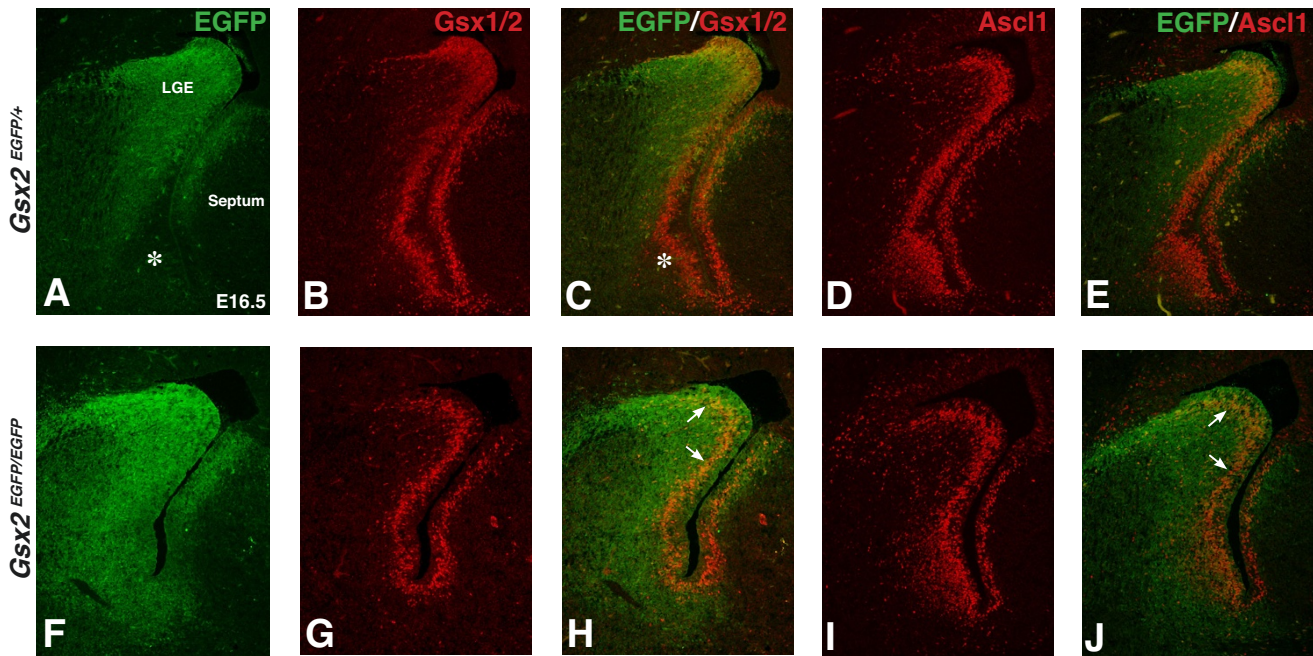
#### Expression of *Gsx2* in the *Ascl1* mutant

Although *Ascl1* expression in LGE progenitors has been shown to require *Gsx2* [1-3], the role (if any) of *Ascl1* in regulating *Gsx2* expression has not been reported. In E12.5 *Ascl1*<sup>-/-</sup> mutants, we found that *Gsx2* (and *Gsx1/2*) staining in the LGE was not significantly different from that observed in wild types (Figure 3A, D and data not shown). Conversely, at E18.5 we observed a large increase in the numbers of cells expressing *Gsx2* along the dorsal-

ventral aspect of the VZ in the *Ascl1* mutants and in certain cases clusters of *Gsx2* expressing cells were found in the forming striatum (Figure 3E). The expression of *Gsx2* coincided with Ki67 staining in many of these clusters (Figure 3E, F) on closely adjacent sections, suggesting that despite their ectopic location, these *Gsx2* cells may remain in the cell cycle. *Gsx1* expression was not changed in the LGE of *Ascl1* mutants [19] (data not shown). These findings could indicate that, in addition to being downstream of *Gsx* genes, *Ascl1* may also serve a negative feedback function to repress *Gsx2* in LGE progenitors, particularly at late embryonic stages.

#### *Gsx2*; *Ascl1* double mutants exhibit severe striatal defects

To examine the possibility that *Ascl1* is required for the *Gsx1*-mediated recovery observed in the *Gsx2* mutant, we generated *Gsx2*; *Ascl1* double homozygous mutants and analyzed the striatum at E18.5. The expression of *FoxP1* can be used to mark striatal neurons and, thus, the forming striatum at this stage [20,21]. Staining for this marker



**Figure 2**

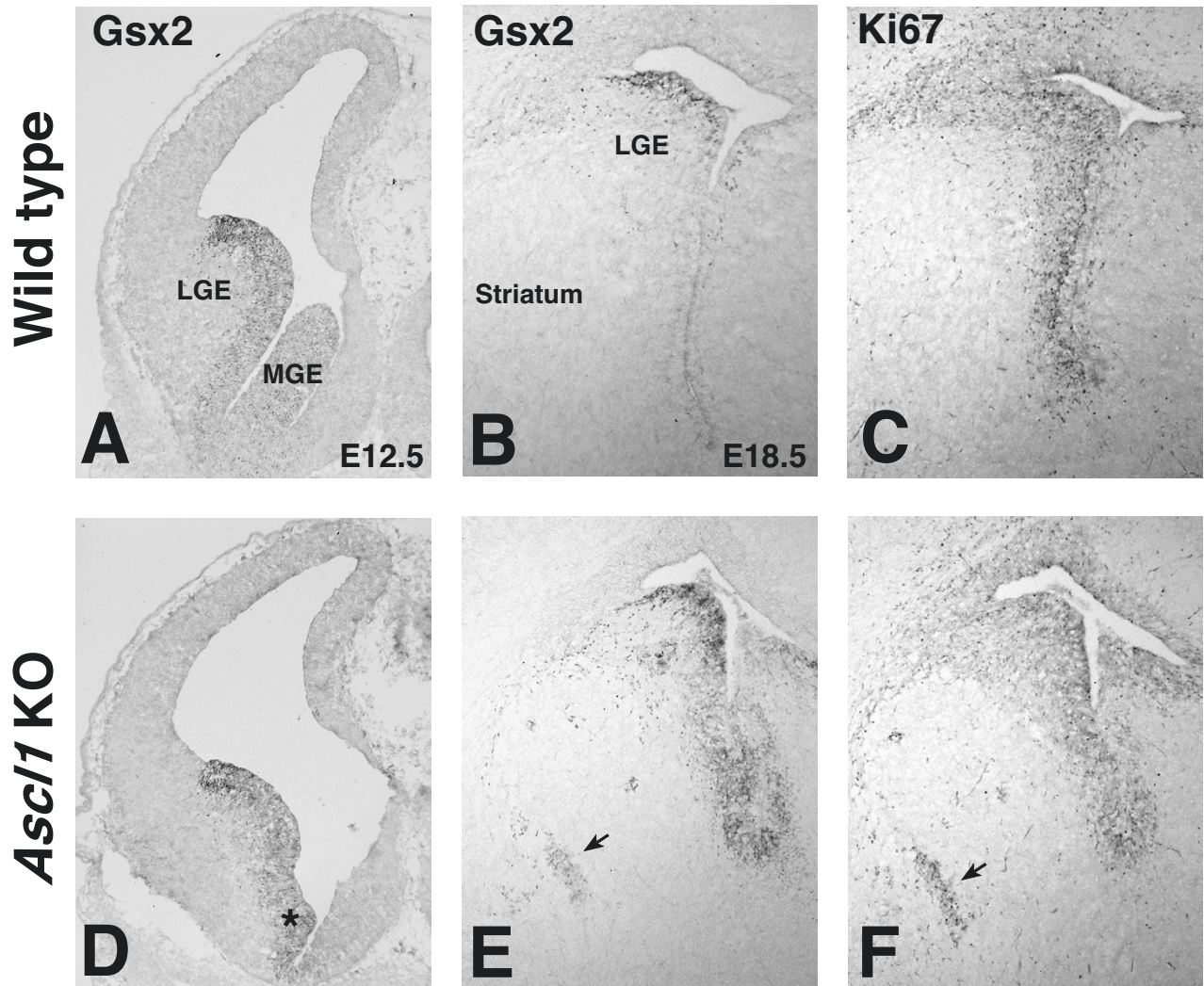
**Expansion of *Gsx1* in the *Gsx2*<sup>EGFP/EGFP</sup> lateral ganglionic eminence (LGE) occurs in only a subset of cells at the ventricular zone (VZ)/subventricular zone (SVZ) border. (A-C)** Control embryos (*Gsx2*<sup>EGFP/+</sup>) express *Gsx2* and enhanced green fluorescent protein (EGFP) throughout the VZ of the LGE at E16.5. In addition, the *Gsx1/2* antibody labels scattered cells in the SVZ (B) where EGFP expression is observed in the majority of the SVZ (A, C). Asterisks in (A, C) mark *Gsx1/2* staining in the remnant of the medial ganglionic eminence. Because EGFP expression from the *Gsx2* locus is not found in this region, it is likely that the staining reflects *Gsx1* expression. **(G)** The expansion of *Gsx1* in *Gsx2*<sup>EGFP/EGFP</sup> embryos is throughout the LGE at E16.5. **(F, H)** Note that *Gsx1* expression in *Gsx2*<sup>EGFP/EGFP</sup> embryos is observed only at the VZ/SVZ border in the LGE (arrows in merged image in (H)) whereas EGFP expression (labeling *Gsx2* mutant cells) is observed throughout the VZ and the SVZ (F, H). **(D, E)** Control embryos (*Gsx2*<sup>EGFP/+</sup>) express *Ascl1* at highest levels near the VZ/SVZ border (D) and only in scattered cells of the VZ (merged image with EGFP in (E)). **(I)** By E16.5, *Ascl1* is recovered in the LGE of *Gsx2*<sup>EGFP/EGFP</sup> embryos predominately at the VZ/SVZ border (arrows in (J)), which is similar to the expansion of *Gsx1* expression in these mutants (G).

shows that the size of the striatum in *Gsx2* mutants is severely reduced compared to wild types (Figure 4A, B), which is consistent with previous studies [1-3,5,6]. Unlike the *Gsx2* mutants, however, *Ascl1* mutants exhibit more subtle defects in striatal development [14] and, accordingly, showed a more modest reduction in FoxP1 expression (Figure 4C). Interestingly, the *Gsx2;Ascl1* double mutants showed an even more severe reduction in FoxP1 staining than the *Gsx2* mutants (Figure 4D), indicating that only a rudimentary striatum is present in these brains.

The striatum is composed of two anatomically and neurochemically distinct compartments termed the patch and matrix [22]. The striatum-enriched phosphoprotein DARPP-32 has been shown to mark the forming patch compartment at perinatal time points [23] (Figure 4E). DARPP-32 is severely reduced in the *Gsx2* mutant striatum (Figure 4F) [1,2,5,24] while its expression was only moderately reduced in the *Ascl1* mutants (Figure 4G). Interest-

ingly, no DARPP-32-positive neurons were observed in the *Gsx2;Ascl1* double mutant striatum (Figure 4H), a finding that is identical to that previously observed in the *Gsx1;Gsx2* double mutant striatum [5]. Calbindin is known to mark the matrix compartment in the mature striatum [22]. As previously reported [5], calbindin expression is increased in the forming *Gsx2* mutant striatum (Figure 4J) while a clear reduction in its expression was seen in the *Ascl1* mutant striatum (Figure 4K). The rudimentary striatum present in the *Gsx2;Ascl1* double mutant striatum did express calbindin (Figure 4L). Again, this was similar to that previously observed in the *Gsx1;Gsx2* double mutant striatum [5]. Thus, the similarities in the phenotypes observed in the *Gsx2;Ascl1* and *Gsx1;Gsx2* double mutants suggest that *Ascl1* is required for the *Gsx1*-based striatal recovery in *Gsx2* mutants.

In order to determine whether *Ascl1* is required downstream of *Gsx1* in a *Gsx2* mutant, we examined the expres-

**Figure 3**

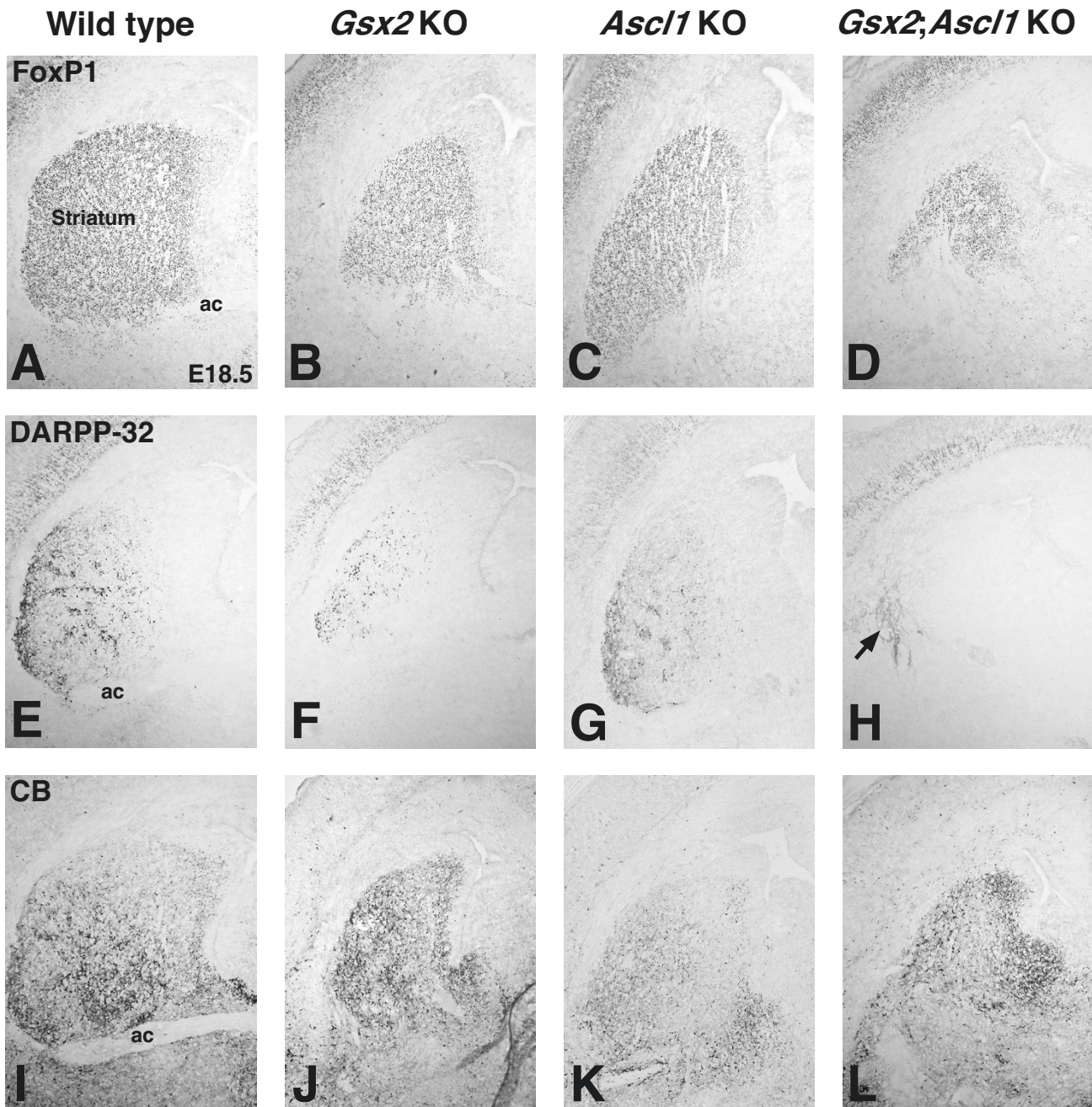
**Increase in progenitor cell markers in the lateral ganglionic eminence (LGE) of *Ascl1* mutants.** (A, D) At E12.5, *Ascl1* mutants express *Gsx2* in a relatively normal pattern in the LGE compared to wild type. Note the odd morphology in the developing medial ganglionic eminence (MGE) of *Ascl1* mutants (asterisk in (D)). (B, E) By E18.5, *Gsx2* protein expression is increased in the entire LGE region of *Ascl1* mutants (E) compared to controls (B). These ectopic *Gsx2* positive cells are observed in the SVZ and striatum, many appearing as clumps of cells stuck in the parenchyma (arrow in (E)). (C, F) Dividing cells labeled by *Ki67* expression are also increased in the *Ascl1* mutant LGE area (F) compared to control (C). Similar to *Gsx2*, many ectopic *Ki67* positive cells appear as clumps (arrow in (F)).

sion of *Gsx1* in *Gsx2;Ascl1* double mutants. If *Ascl1* is required for *Gsx1* to expand throughout the *Gsx2* mutant LGE, then the similarities in the *Gsx2;Ascl1* and *Gsx1;Gsx2* double mutant phenotypes would be easily explained by the lack of *Gsx1* in LGE progenitors. However, this is not the case, because we observed both *Gsx1* gene expression and *Gsx1/2* staining in the *Gsx2;Ascl1* double mutant LGE (Figure 5C, F). Indeed, the level and extent of this expression was very similar to that seen in the *Gsx2* mutant (Fig-

ure 5B, E). This allows us to conclude that *Ascl1* acts downstream of *Gsx1* in the *Gsx2* mutant LGE.

#### **Olfactory bulb defects in *Gsx2;Ascl1* double mutants**

Unlike striatal neurons that are largely produced at embryonic stages, olfactory bulb interneurons are generated over a protracted period, starting around E14 and with the majority produced during the first 2 weeks after birth [25]. Since *Gsx2* mutants die shortly after birth [4],



**Figure 4** (see legend on next page)

**Figure 4** (see previous page)

**Removal of *Ascl1* on the *Gsx2* mutant background exacerbates the *Gsx2* mutant phenotype in the striatum. (A)** FoxP1 expression labels striatal projection neurons at E18.5. **(B)** In *Gsx2* mutants, the expression domain of FoxP1 in the striatum is severely reduced. **(D)** Removal of *Ascl1* on the *Gsx2* mutant background (*Gsx2;Ascl1* double mutant) results in a more severe effect on the FoxP1 expression domain compared to *Gsx2* mutants (compare (D) to (B)). **(C)** *Ascl1* mutants display relatively normal expression of FoxP1 in the striatum. **(E-G)** *Gsx2* mutants also exhibit a severe reduction in DARPP-32 expression (F), which is enriched in early born striatal neurons at E18.5 in controls (E) and *Ascl1* mutants (G). **(H)** *Gsx2;Ascl1* double mutants display a more severe phenotype in DARPP-32 expression compared to *Gsx2* mutants (compare (H) to (F)). Note that *Gsx2;Ascl1* double mutants display a complete loss of DARPP-32 positive neurons in the striatum (H). The only DARPP-32 staining observed in the double mutant striatum is in fibers (arrow in (H)), which presumably arise from the cortical DARPP-32 expressing neurons. **(I, J, L)** Calbindin (CB) expression labels the later born striatal neurons at E18.5 (I) and is upregulated in the SVZ of *Gsx2* mutants (J) and *Gsx2;Ascl1* double mutants (L). **(K)** *Ascl1* mutants exhibit a noticeable reduction in CB expression in the striatum. ac, anterior commissure.

only the olfactory bulb interneurons that are generated at embryonic stages can be assayed. Previous studies [1,3,5,6] have shown that *Gsx2* mutants exhibit defects in the development of these neurons at birth. The olfactory bulb interneurons produced at embryonic time points have been suggested to originate, at least in part, from the dorsal (d)LGE [26]. We have recently shown that the zinc finger transcription factor Sp8 marks the dLGE as well as olfactory bulb interneurons [27] (Figure 6A, E). In *Gsx2* mutants, the number of Sp8 expressing cells is dramatically reduced in both the dLGE and olfactory bulb (Figure 6B, F) [27]. Although *Ascl1* mutants have been shown to have olfactory bulb interneuron defects [14,28], the expression of Sp8 in these mutants is not reduced in the dLGE at E15.5 [17]; rather, it appears as if more cells are seen in this region streaming laterally towards the ventrolateral telencephalon by E18.5 (Figure 6C). Moreover, there appear to be similar numbers of Sp8-positive cells within the *Ascl1* mutant olfactory bulb compared to wild type, although their distribution appears somewhat disorganized (Figure 6G). Conversely, in the *Gsx2;Ascl1* double mutants the expression of Sp8 is reduced, even when compared to the *Gsx2* mutants (Figure 6B, D). Indeed, most sections of the double mutant olfactory bulb lack any Sp8-positive cells (Figure 6H).

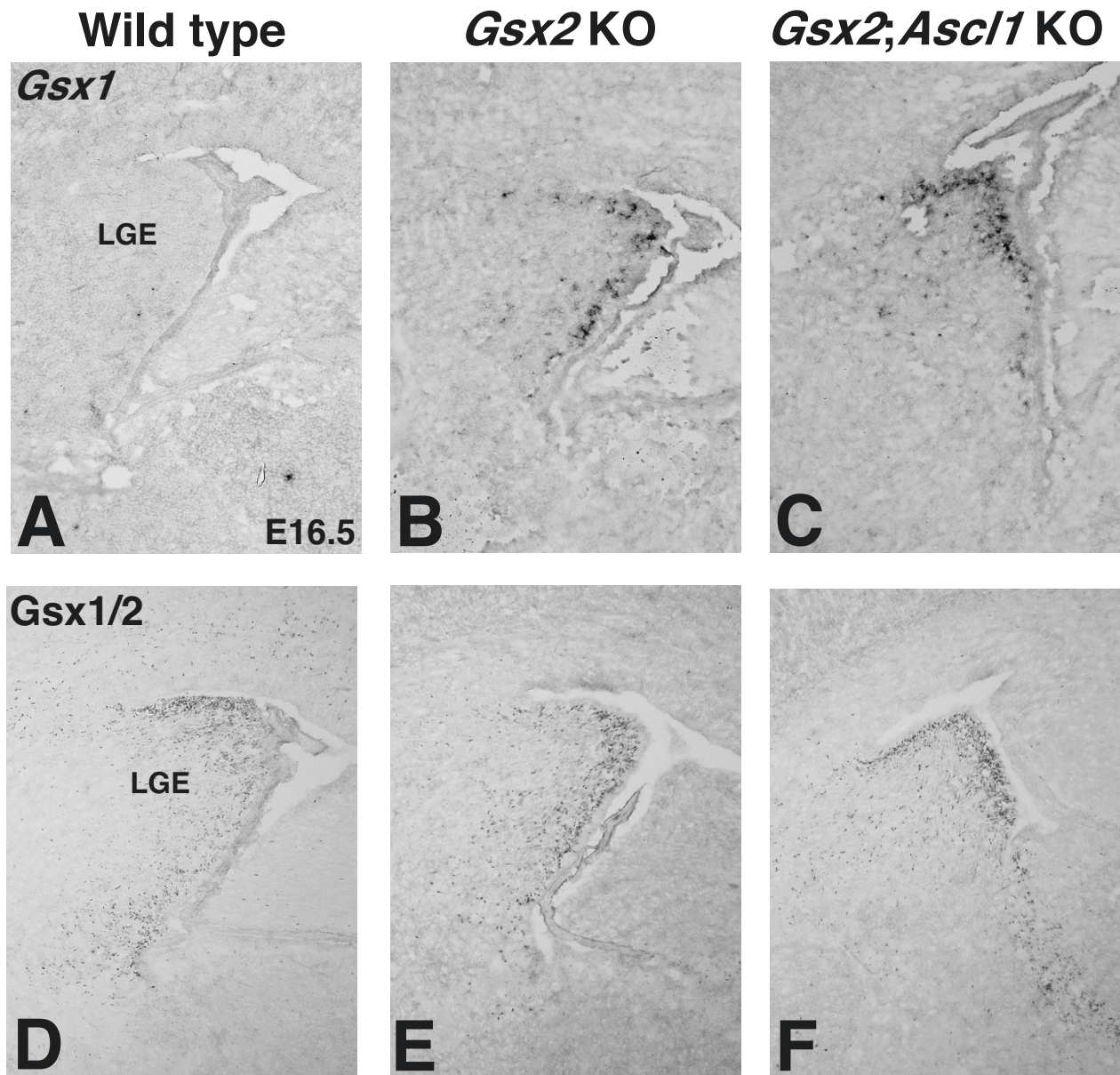
Sp8 is required for normal development of the calretinin (CR)-expressing subtype of olfactory bulb interneurons [27]. In addition to the dLGE, the septum has also been suggested to give rise to olfactory bulb interneurons [29], and more recent results suggest that the septum may also represent a region where the CR interneurons originate [30,31]. Indeed, CR positive neurons can be seen in the wild-type dLGE and even more so in the septum at E18.5 (Figure 7A) as well as in the forming glomerular layer of the olfactory bulb (Figure 7E). As might be predicted from the Sp8 staining, the *Gsx2* mutants showed reductions in CR interneurons (Figure 7B, F), while the *Ascl1* mutants did not appear to exhibit reduced numbers of CR positive cells (Figure 7G) and at least in portions of the dLGE may

even contain increased numbers of these cells (Figure 7C). Furthermore, the *Gsx2;Ascl1* double mutants showed a more severe reduction in CR staining than the *Gsx2* mutants (Figure 7D, H). Previous studies [1,3,5,6,14,28] have shown that *Gsx2* (Figure 7J) and *Ascl1* mutants (Figure 7K) exhibit reductions in glutamic acid decarboxylase (67 kDa) ( $GAD_{67}$ )-positive olfactory bulb interneurons ( $GAD_{67}$  is a rate limiting enzyme in GABA production). These appear to be compounded in the *Gsx2;Ascl1* double mutants where essentially no  $GAD_{67}$ -positive cells were observed in the olfactory bulb at this time point (Figure 7L). Taken together, these data suggest that *Ascl1* functions downstream of *Gsx2* to regulate aspects of olfactory bulb interneuron diversity. Indeed, it appears that *Gsx2* is required for many, if not all, of the interneuron subtypes to be properly generated, while *Ascl1* is more crucial for the generation of  $GAD_{67}$  (that is, GABAergic) and dopaminergic interneurons [28].

#### **Notch signaling in *Gsx2;Ascl1* double mutants**

Previous studies have shown that Notch signaling is required for normal LGE/striatal development [16,32]. Moreover, *Ascl1* mutants exhibit reduced Notch signaling [14,16]. It is possible, therefore, that the phenotypes observed in the *Gsx2;Ascl1* double mutants are a result of compound effects of a loss of Notch signaling together with distinct *Gsx2* requirements. To address this, we examined the expression of factors in the Notch signaling pathway, *Ngn2*, *Dll1* and *Hes5*, in relation to *Gsx1/2* expression. In *Gsx2* mutants, *Ngn2* was shifted ventrally into the LGE as previously described (Figure 8F) [1-3], although it appeared to be directly abutting the ventrally shifted *Gsx1/2* staining (Figure 8B). Indeed, both *Dll1* (Figure 8J) and *Hes5* (Figure 8N) were continuously expressed throughout the *Gsx2* mutant LGE. In the *Ascl1* mutants, *Gsx1/2* staining was present up to the normal pallio-subpallial boundary (Figures 3A and 8C) and *Ngn2* staining abutted it at its normal ventral position (compare Figure 8E and 8G). This theoretically leaves no proneural gene expression in the LGE and, in fact, both *Dll1* (Figure

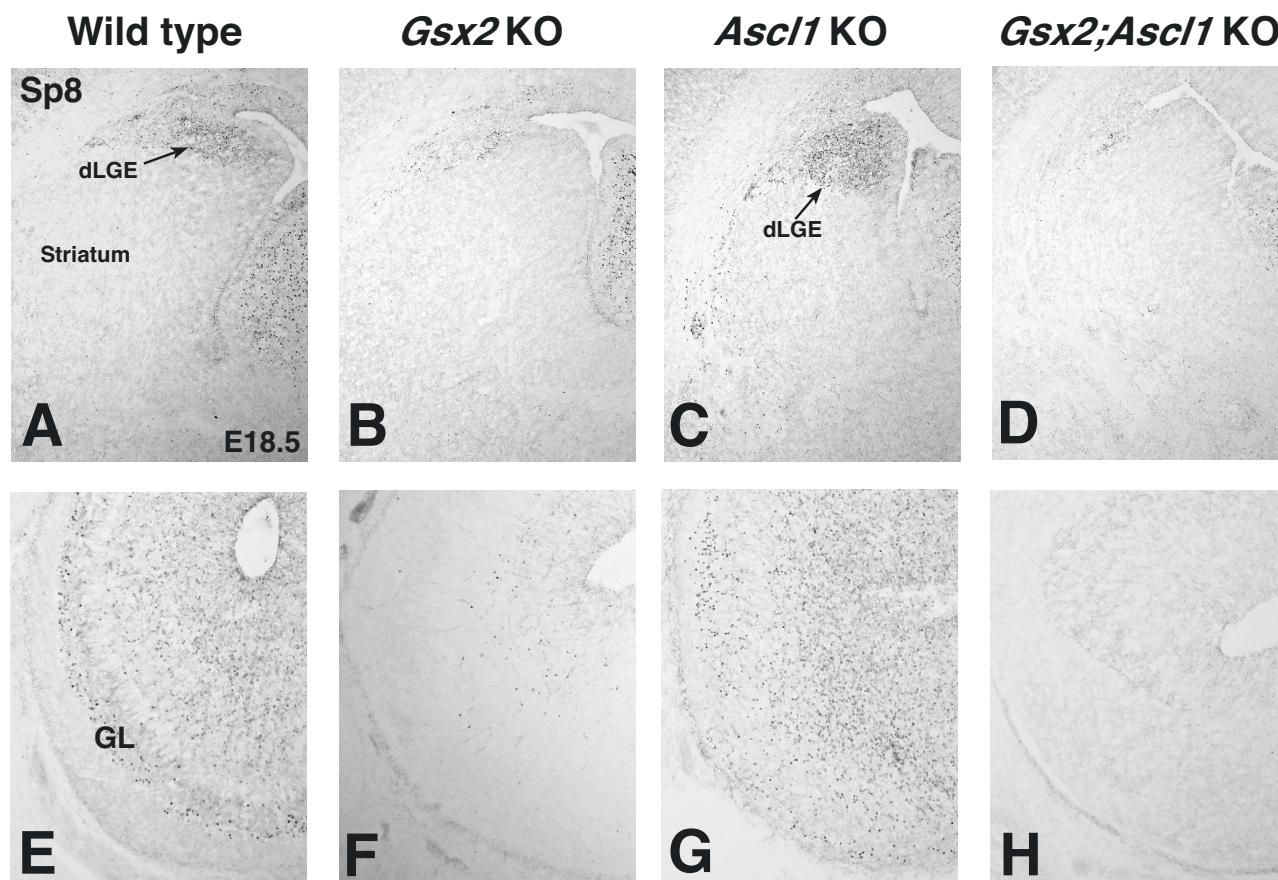


**Figure 5**

***Gsx1* expands throughout the *Gsx2;Ascl1* mutant lateral ganglionic eminence (LGE).** (A-C) *Gsx1* expression is barely present in the E16.5 wild type LGE (A) but appears to be expressed similarly in *Gsx2* (B) and *Gsx2;Ascl1* mutant (C) LGEs. (D-F) The *Gsx1/2* antibody can be used in *Gsx2* mutants to visualize *Gsx1* protein expression and not only is gene expression expanded in the mutants compared to wild type (D) but *Gsx1* protein is found in a similar pattern in the *Gsx2* mutant (E) and *Gsx2;Ascl1* mutant (F) LGEs. The *Gsx1/2* staining in the wild type mostly reflects *Gsx2* expression since very little *Gsx1* expression is seen in the wild type LGE (A).

8K) and *Hes5* (Figure 8O) staining was absent, as previously described [14]. This is not the case in *Gsx2;Ascl1* double mutants, where *Ngn2* was observed to extend ventrally into the double mutant LGE and improvement in *Dll1* (Figure 8L) and *Hes5* (Figure 8P) expression was

observed, at least within the presumptive LGE region, compared to *Ascl1* mutants. This indicates that the Notch signaling defects observed in *Ascl1* mutants are, in part, due to *Gsx2* expression remaining in the LGE. Thus, it appears that *Ascl1* performs a non-proneural function in

**Figure 6**

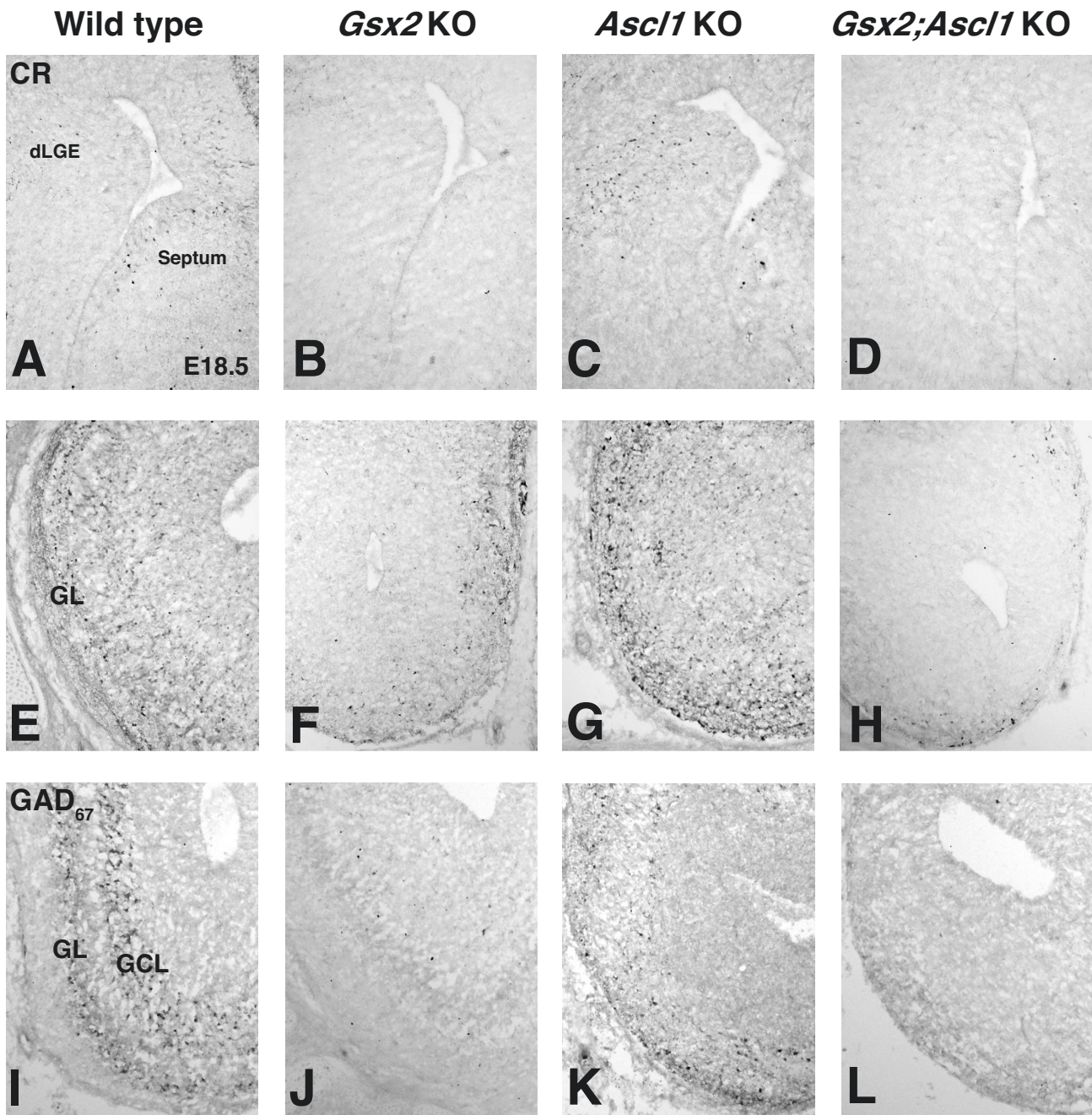
***Gsx2;Ascl1* double mutants exhibit a more severe phenotype in the formation of the dorsal lateral ganglionic eminence (dLGE) and the generation of olfactory bulb interneurons. (A, B)** The Sp8 expression domain in the dLGE is reduced in *Gsx2* mutants (B) compared to controls (A). **(D)** *Gsx2;Ascl1* double mutants exhibit a more severe reduction in the expression of Sp8 in the dLGE (D) compared to *Gsx2* mutants (B). **(C)** *Ascl1* mutants maintain Sp8 expression in the dLGE and may have a slightly expanded expression domain. **(E, F)** Sp8 expressing interneurons are reduced in *Gsx2* mutant olfactory bulb (F) compared to controls (E). **(H)** *Gsx2;Ascl1* mutant displays nearly a complete loss of Sp8 expression in the olfactory bulb. **(G)** Sp8 expression is observed in *Ascl1* mutant olfactory bulbs, but in a slightly disorganized pattern (compare (G) to (E)). gl, glomerular layer.

the *Gsx1*-mediated recovery observed in the *Gsx2* mutant. Interestingly, it also seems that *Ascl1* plays a role in the timing of the *Gsx1* expansion into the *Gsx2* mutant LGE as the *Gsx2;Ascl1* double mutants showed much less *Gsx1* (as marked by *Gsx1/2* staining) expression in the presumptive LGE at E12.5 (Figure 8D) when compared to later time points (for example, E16.5; Figure 5C, F).

### Discussion

The study of knock-out mice is essentially an investigation into the compensatory mechanisms (or lack thereof) when any given gene is inactivated. In the case of *Gsx2*, it has previously been shown that *Gsx1* is involved in the partial recovery observed in these mutants [5,6]. What

remained unclear was why the *Gsx1*-dependent compensation was not more effective in restoring normal development. In addition to a delayed upregulation of *Gsx1* in the *Gsx2* mutant LGE [5,6], we provide novel data here showing that *Gsx1* is expressed only in a subset of LGE cells that would normally express *Gsx2*. Interestingly, these cells are largely located at the boundary between the VZ and SVZ, similar in location to that of *Ascl1* expressing cells. Based on the facts that the striatal phenotype of the *Gsx2;Ascl1* mutants is nearly identical to that observed in *Gsx1;Gsx2* mutants [5,6] and that *Gsx1* expands in the *Gsx2;Ascl1* mutants in a similar way to that observed in *Gsx2* mutants, we conclude that *Ascl1* is required downstream of *Gsx1* for this recovery. These findings suggest that there

**Figure 7**

**Olfactory bulb interneuron subtype specification in *Gsx2*, *Ascl1* and *Gsx2;Ascl1* mutants.** (A-H) Calretinin (CR) staining in the dLGE (A-D) and olfactory bulb (E-H) in E18.5 wildtype (A, E), *Gsx2* mutant (B, F), *Ascl1* mutant (C, G) and *Gsx2;Ascl1* mutants (D, H). Note that CR cells in the dLGE and olfactory bulb are severely depleted in *Gsx2* and *Gsx2;Ascl1* mutants while there appear to be similar if not more numbers of CR neurons in the *Ascl1* mutants compared to wild type. (J, L)  $GAD_{67}$  (glutamic acid decarboxylase (67 kDa)) staining is severely reduced in *Gsx2* mutants (J) and nearly absent in *Gsx2;Ascl1* mutants (L). (I, K) In comparison, *Ascl1* mutants (K) show a more modest reduction in  $GAD_{67}$  staining but it is still quite severe when compared to the wild-type olfactory bulb (I). GCL, granule cell layer; GL, glomerular layer.

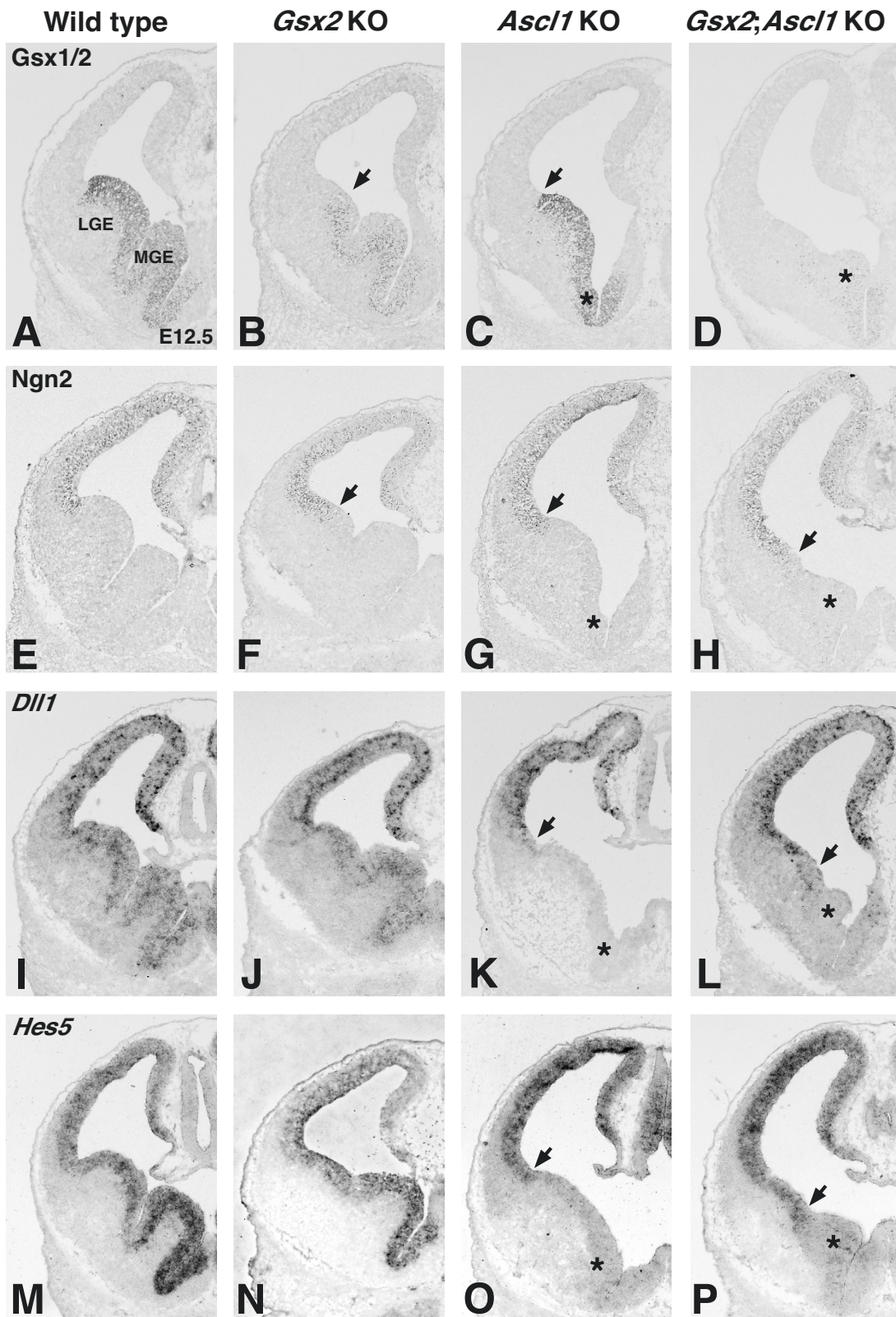


Figure 8 (see legend on next page)

**Figure 8** (see previous page)

**Notch signaling in the lateral ganglionic eminence (LGE) of *Gsx2;Ascl1* mutants is improved from that in *Ascl1* mutants.** (A) *Gsx1/2* staining in the E12.5 wild type ventral telencephalon. (B, C) *Gsx1/2* staining illustrates the expansion of *Gsx1* in the *Gsx2* mutant LGE (B) as well as the expression of *Gsx* proteins in the *Ascl1* mutant LGE (C); arrows point to the dorsal limit of *Gsx* expression. (D) Note that the *Gsx1* expansion is delayed in *Gsx2;Ascl1* mutants at this stage but, as shown earlier, this recovers at later stages. (E, F, H) The proneural protein *Ngn2* is normally expressed in pallial progenitors (E) but in the *Gsx2* (F) and *Gsx2;Ascl1* mutants (H) the ventral limit of *Ngn2* expression (arrows in (F, H)) has expanded ventrally into the mutant LGE. (G) In contrast, the ventral limit of *Ngn2* expression in *Ascl1* mutants (arrow) appears to be similar to that in wild type (E). (I-P) The status of Notch signaling can be assessed by the expression of *Dll1* and *Hes5*. In wild types, *Dll1* (I) and *Hes5* (M) are expressed in ventricular zone (VZ) progenitors along the dorsal-ventral axis of the telencephalon. As is the case in the wild types, *Gsx2* mutants appear to express *Dll1* (J) and *Hes5* (N) throughout the telencephalic VZ, while the *Ascl1* mutants exhibit expression only in the dorsal telencephalon (K, O) corresponding with *Ngn2* expression. Although the *Gsx2;Ascl1* mutants do not show *Dll1* (L) and *Hes5* (P) expression in the ventral-most telencephalon (that is, medial ganglionic eminence (MGE) remnant indicated by asterisk) these Notch effectors are expressed in the mutant LGE progenitors unlike the case in *Ascl1* mutants. Asterisks in (C, D, G, H, K, L, O, P) indicate the remnant of the MGE.

are *Ascl1*-dependent and *Ascl1*-independent pathways for LGE development. This is in agreement with recent studies by Long *et al.* [17,19] showing that *Dlx1/2* and *Ascl1* regulate parallel and overlapping pathways in LGE specification. Furthermore, our results indicate that the *Ascl1*-dependent pathway for LGE specification appears to be independent of its well-known role in regulating the Notch signaling pathway.

The mechanism by which *Gsx1* is upregulated in the *Gsx2* mutant LGE has been unclear. It does not appear that *Gsx2* represses *Gsx1* expression because only a subset of the cells that normally express *Gsx2*, particularly those at the VZ/SVZ boundary, are *Gsx1*-positive in the *Gsx2* mutant LGE. It seems possible, therefore, that *Gsx1* can only be expressed in certain cell types or in cells that have reached a particular level of maturation (that is, cells transitioning from the VZ to the SVZ). Indeed, it appears that *Gsx1*-positive cells in the medial ganglionic eminence region also reside largely in the VZ/SVZ boundary region (for example, Figure 2C). Interestingly, at early stages (that is, E12.5) in the *Gsx2* mutants, the LGE SVZ does not form, and only after *Gsx1* has expanded throughout the mutant LGE (that is, by E14–15) does it do so in this mutant [2,3,5]. Together with the current findings, these results suggest that *Gsx1* may be expressed in more mature progenitors and might even play a role in the maturation process.

*Ascl1* has previously been implicated in the development of the striatum and olfactory bulb interneurons [14–17,28]. In general, however, the requirement for *Ascl1* in striatal and olfactory bulb development is not as great as that for *Gsx2*. In fact, the striatum of the *Ascl1* mutant is only slightly reduced in size when compared to the wild type [14] (Figure 4). Moreover, the reduction in dopaminergic and GABAergic olfactory bulb interneurons [28] is not as severe as that observed in *Gsx2* mutants [5,6].

Although striatal development is only modestly affected by the loss of *Ascl1*, we show here that the added loss of *Gsx2* results in a nearly complete loss of striatal development. This result is identical to that previously reported for *Gsx1;Gsx2* double mutants [5,6]. Thus, *Ascl1* is absolutely essential for the *Gsx1*-mediated recovery observed in *Gsx2* mutants. While *Ascl1* appears to be downstream of *Gsx2* [1–3], the relationship between *Gsx1* and *Ascl1* appears to be more complex. The loss of *Gsx1* and *Gsx2* severely depletes the expression of *Ascl1* throughout embryogenesis [5,6], suggesting that both are genetically upstream; however, our findings here also demonstrate a delay in the expression of *Gsx1* in *Gsx2;Ascl1* double mutants at early stages (for example, Figure 8D), potentially implicating *Ascl1* in feedback regulation of *Gsx1* expression.

*Ascl1* is a known regulator of the Notch signaling pathway [14,16] and Notch signaling has previously been implicated in controlling striatal development [16,32]. It does not seem that the striatal defects observed in the *Gsx2;Ascl1* double mutants, described here, are simply due to compound effects of the loss of *Gsx2* and impaired Notch signaling because we observed an improvement in Notch signaling (as indicated by *Hes5* and *Dll1* expression) within LGE progenitors of the *Gsx2;Ascl1* double mutants compared to *Ascl1* mutants. Our interpretation of this result is that *Gsx2;Ascl1* mutants are similar to *Gsx2* mutants in that *Ngn2* is allowed to expand ventrally into the LGE and, as a result, Notch signaling is improved. Clearly, *Ascl1* plays a role in regulating Notch signaling within LGE progenitors [14,16]; however, the fact that striatal development is not more severely affected in the *Ascl1* mutant could suggest that *Gsx2* normally works through another gene encoding a basic helix-loop-helix (bHLH) factor to regulate aspects of LGE neurogenesis.

A somewhat surprising finding that we observed in the *Ascl1* mutants was that *Gsx2* expression appeared to be increased at perinatal stages. This is not the case at early time points (for example, E12.5) and suggests that *Ascl1* may play a role in depleting the *Gsx2* progenitors during embryogenesis. The increased *Gsx2* in the *Ascl1* mutant LGE correlated well with the expression of *Sp8*, a zinc finger transcription factor that has previously been shown to be dependent on *Gsx2* expression [27].

Previous studies have described a reduction in dopaminergic and GABAergic interneurons in the *Ascl1* mutants [14,28]; however, no data on other subtypes have been provided. We show here that unlike the dopaminergic and GABAergic subtypes, the CR interneurons are not reduced and may, in fact, be increased. The neurotransmitter of this subtype remains somewhat unclear. Recent reports suggest that as few as 14% are GABAergic [33], while others suggest that most if not all are GABAergic [30,34]. Our data seem to support the former possibility (at least at this stage of development) since the reduction in GABAergic neurons (as marked by  $GAD_{67}$ ) is not paralleled by CR-positive cells in the *Ascl1* mutant olfactory bulb. We have recently shown that the zinc finger transcription factor *Sp8* is required for the normal development of the CR interneurons in the olfactory bulb [27]. Accordingly, we found that in *Ascl1* mutants at late stages of development, *Sp8* staining is maintained in the dLGE and olfactory bulbs. Because *Gsx2* is required for *Sp8* expression in the dLGE and the latter is essential for normal CR interneuron production, it seems likely that the sequential expression of these two transcription factors cooperate to generate this interneuron subtype. However, despite that *Gsx2* appears to function upstream of *Ascl1*, this bHLH factor does not actively promote CR interneuron development.

The origin of distinct subtypes of olfactory bulb interneurons has recently been the subject of considerable attention. Kohwi *et al.* [30] have recently suggested that CR interneurons arise from pallial and septal regions but not the dLGE. On the other hand, De Marchis *et al.* [35] found that these interneurons were generated from the postnatal region of the SVZ that directly derives from the dLGE. In support of this, Merkle *et al.* [31] showed that at least some CR neurons are derived from the rostral dorsal SVZ (a likely derivative of the dLGE). Although CR interneurons start to be produced at embryonic time points, a recent study by Batista-Brito *et al.* [36] have shown that most are generated at postnatal time points. Our data show that at least a few CR neurons are present in the late embryonic dLGE and that *Ascl1* mutants appear to exhibit enhanced CR neuron production in the dLGE and possibly olfactory bulb. Thus, *Ascl1* may play a role in the temporal regulation of CR interneuron production from the dLGE and its SVZ derivatives. In any case, our findings

clearly demonstrate that the dLGE is a significant source of CR interneurons that are generated at embryonic time points; however, we cannot exclude the contribution of the septum in the generation of these interneurons as shown by Merkle *et al.* [31], particularly at early postnatal stages. Indeed, *Gsx2* is expressed at high levels in both the dLGE as well as in the dorsal portion of the septum (Figure 2) and CR staining in the septal region is also lost in the *Gsx2* mutant (Figure 7). Regardless of their origin, it seems that all subtypes of olfactory bulb interneurons, at least at embryonic time points, require *Gsx2* for their normal production.

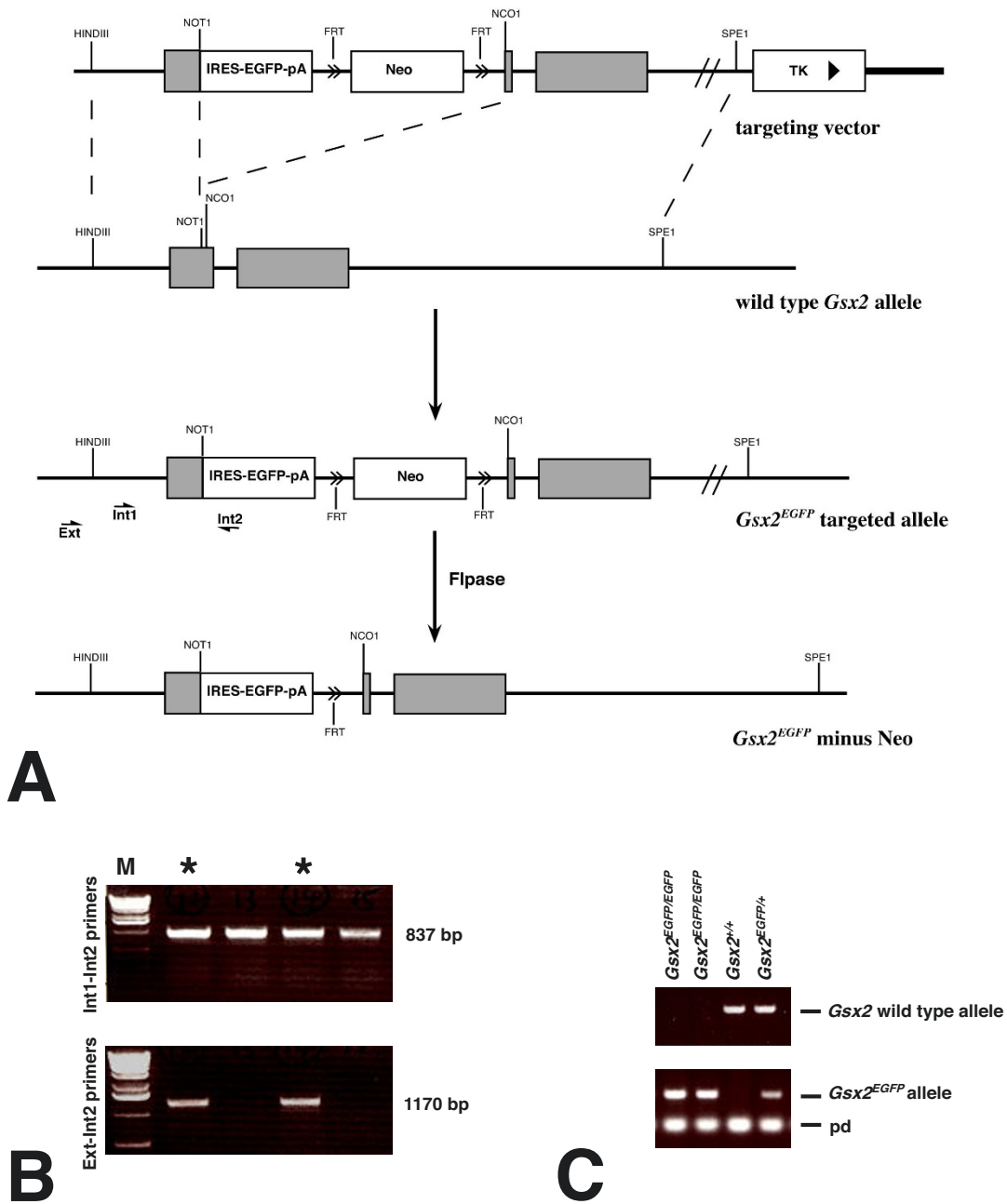
## Conclusion

Our data show that *Gsx1* compensates for the loss of *Gsx2* gene function in only a subpopulation of the LGE progenitors that normally express *Gsx2*, which may explain why the compensation is not more complete. Additionally, we show that *Ascl1* is an obligate factor for *Gsx1* in the recovery process and that this is independent of its well-known proneural function.

## Methods

*Gsx2* [4] and *Ascl1* [37] mice were genotyped as previously described [2,14]. Interbreeding between *Gsx2* and *Ascl1* heterozygotes was performed to generate *Ascl1;Gsx2* double heterozygotes, which were subsequently crossed to generate *Ascl1;Gsx2* double homozygous mutants.

*Gsx2<sup>EGFP</sup>* knock-in mice were generated by inserting an IRES-EGFP-pA cassette (Clontech, Mountain View, CA, USA) into the first exon of *Gsx2* between the *Not1* and *Nco1* sites (Figure 9A). Specifically, a 9-kb genomic fragment encompassing the *Gsx2* locus was isolated by a *HindIII* digest of a *Gsx2*-positive 129 BAC and subcloned into the *HindIII* site of pBluescript SK (Stratagene, La Jolla, CA, USA). The targeting vector backbone was previously described in Bell *et al.* [38]. A 6.4-kb *Nco1/Spe1* fragment from the 9-kb *Gsx2* genomic region was blunted and subcloned into the *Hpa1* site of cre/lox targeting vector to be used as the 3' homology arm. A 1-kb *HindIII/Not1* fragment from the 9-kb *Gsx2* genomic region was blunted and subcloned into the *Sma1* site of pBluescript SK (called 5'arm-PBS). The pIRES2-EGFP vector (Clontech) was digested with *AflIII*, blunted, and redigested with *Nhe1* to release IRES-EGFP. IRES-EGFP was cloned into 5'arm-PBS, which was digested with *Sal1*, blunted, and redigested with *Spe1* (5'arm-EGFP-PBS). The 5'arm-IRES-EGFP was released with a *Xho1* digest that was blunted and subcloned into the *Pme1* site of the cre/lox targeting vector. The *Gsx2<sup>EGFP</sup>* vector was linearized with *Sal1* and electroporated in W4 embryonic stem (ES) cells (reviewed in [39]) and selected with G418 and gancyclovir. Correctly targeted cells were identified by PCR (Figure 9A, B) using the following primer pairs to generate products spe-



**Figure 9**

**Targeting scheme to generate the *Gsx2*<sup>EGFP</sup> knock-in allele. (A)** Using homologous recombination in embryonic stem cells an IRES-enhanced green fluorescent protein (EGFP) cassette was inserted in the first exon of the *Gsx2* between an *Nco*I and *Not*I site. This removed 125 bp of the coding region of the first exon but left the exon-intron structure intact. The polyA signal at the end of the IRES-EGFP cassette effectively terminated the message and, as shown in Figure 1, no *Gsx2* protein is observed when the *Gsx2*<sup>EGFP</sup> allele is bred to homozygosity. The Neomycin (Neo) cassette was removed by breeding the mice with  $\beta$ -actin-Flpase mice [38]. These *Gsx2*<sup>EGFP</sup> minus Neo mice were exclusively used in this study. **(B)** Correctly targeted embryonic stem cells were identified using the primers indicated as half arrows in (A). **(C)** Embryos are genotyped using primers to detect the *Gsx2*<sup>EGFP</sup> allele and using *Gsx2* primers that include one sequence in the deleted region of the first exon. M, DNA marker; pd, primer dimer.

cific for the correctly targeted *Gsx2<sup>EGFP/+</sup>* allele: internal primer 1 (5'-cctccgcttctgttgact-3') with internal primer 2 (5'-cctaggaatgctcgtcaagaag-3'), which gave an 837 bp product, and an external primer (5'-cctccactacaagccacatac3') with internal primer 2, which generated a 1,170 bp product, specific for the correctly targeted *Gsx2<sup>EGFP/+</sup>* allele. Two different targeted ES cell lines were used for blastocyst injection by the Cincinnati Children's Hospital Medical Center transgenic facility. Germ-line transmission was tested by crossing the chimeras with C57/B6 mice to obtain agouti offspring. F1 *Gsx2<sup>EGFP/+</sup>* mice were bred to  $\beta$ -actin-FLPe (enhanced Flpase) mice [40] obtained from Jackson Laboratory, Bar Harbor, ME, which resulted in the Neomycin cassette flanked by FLP recombinase target (FRT) sites to be removed (Figure 9A). Embryos derived from *Gsx2<sup>EGFP/+</sup>* crosses were genotyped with the following primers: internal 2 (5'-cctaggaatgctcgtcaagaag-3') with *Gsx2* int5A (5'-catcaccatcaccagccc-3'), which generated a 225 bp product specific for the knock-in allele; and *Gsx2*-Int5B (5'-ccacggagattcactgcc 3') with *Gsx2*-1437 (5'-gcatccacccaaatctcagtc-3'), which generated a 298 bp product specific for the *Gsx2* wild-type allele (Figure 9C). The *Gsx2*-Int5b primer binds in the deleted region of exon 1 before the *Nco1* site so homozygous mutants *Gsx2<sup>EGFP/EGFP</sup>* do not have a wild-type band.

For staging of embryos, the morning of vaginal plug detection was designated as E0.5. At least three embryos of each genotype were examined for every stage studied and marker used. Embryos were fixed overnight in 4% paraformaldehyde at 4°C, rinsed extensively in phosphate-buffered saline and cryoprotected in 30% sucrose before sectioning at 12–14  $\mu$ m on a cryostat. Sections were thaw-mounted onto SuperFrost®/Plus slides (Fisher Scientific, Pittsburgh, PA, USA) and stored at -20°C until used.

For immunohistochemistry, primary antibodies were used at the following concentrations: rabbit anti-Ascl1 (Mash1; 1:1,000; provided by J Johnson); rabbit anti-calbindin (1:2,500; provided by P Emson); goat anti-calretinin (1:2,000; Millipore, Billerica, MA, USA); rabbit anti-Dll (pan DLX; 1:400; provided by J Khotz); rabbit anti-FoxP1 (1:4,000; provided by E Morissey); rabbit anti-GAD<sub>67</sub> (1:1,000; Millipore); goat anti-GFP (1:5,000; Abcam, Cambridge, MA, USA); rabbit anti-*Gsx2* (1:5,000; [2]); rabbit anti-*Gsx1/2* (1:2,000; provided by M Goulding); rabbit anti-Ki67 (1:1,000; Novocastra, Newcastle, UK); rabbit anti-Ngn2 (1:1,000; provided by M Nakafuku); rabbit anti-Sp8 (1:500; [26]). The secondary antibodies for brightfield staining were biotinylated swine anti-rabbit antibodies (1:200; DAKO, Glostrup, Denmark) and biotinylated horse anti-goat antibodies (1:200; Vector Laboratories, Burlingame, CA, USA). For visualization, the ABC kit (Vector Laboratories) followed by diaminobenzidine (DAB; Sigma, St. Louis, MO, USA) as the

final chromogen were utilized. The secondary antibodies for fluorescent staining were donkey anti-goat antibodies conjugated to Cy2 (Jackson ImmunoResearch, West Grove, PA, USA), and donkey anti-rabbit antibodies conjugated to Cy3 (Jackson ImmunoResearch).

*In situ* hybridization histochemistry was performed using digoxigenin-labeled cRNA probes as described in Toresson *et al.* [41]. Probes used were *Gsx1* [5], *Hes5* and *Dll1* [14].

### Abbreviations

bHLH: basic helix-loop-helix; CR: calretinin; E: embryonic day; ES: embryonic stem; dLGE: dorsal lateral ganglionic eminence; EGFP: enhanced green fluorescent protein; GAD<sub>67</sub>: glutamic acid decarboxylase (67 kDa); LGE: lateral ganglionic eminence; SVZ: subventricular zone; VZ: ventricular zone.

### Competing interests

The authors declare that they have no competing interests.

### Authors' contributions

BW generated the *Gsx2<sup>EGFP</sup>* mice and carried out most of the experiments. RRW helped generate and characterize the *Gsx2<sup>EGFP</sup>* mice. ZJA helped with some of the immunohistochemistry experiments. FG provided the *Ascl1* mice and helped conceive the experiments. KC supervised the studies and wrote the manuscript. All authors read and commented on the manuscript.

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