



**Characterization of a novel transgenic mouse line
expressing Cre recombinase under the control of the Cdx2
neural specific enhancer**

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7 **Characterization of a novel transgenic mouse line expressing Cre**
8 **recombinase under the control of the *Cdx2* neural specific enhancer**
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Running title: A Cre-driver line for the caudal neuroectoderm

Key words: Cre recombinase, *Cdx2*, neural specific enhancer, posterior neural plate, neural tube, neural crest cells.

ABSTRACT

Several genetically-modified mouse models have been generated in order to drive expression of the Cre recombinase in the neuroectoderm. However, none of them specifically targets the posterior neural plate during neurulation. To fill this gap, we have generated a new transgenic mouse line in which Cre expression is controlled by a neural specific enhancer (NSE) from the *Caudal-related homeobox 2 (Cdx2)* locus. Analyses of Cre activity via breeding with R26R-YFP reporter mice have indicated that the *Cdx2*NSE-Cre mouse line allows for recombination of LoxP sites in most cells of the posterior neural plate as soon as from the head fold stage. Detailed examination of double-transgenic embryos has revealed that this novel Cre-driver line allows targeting the entire posterior neural tube with an anterior limit in the caudal hindbrain. Of note, the *Cdx2*NSE regulatory sequences direct Cre expression along the whole dorso-ventral axis (including pre-migratory neural crest cells) and, accordingly, YFP fluorescence has been also observed in multiple non-cranial neural crest derivatives of double-transgenic embryos. Therefore, we believe that the *Cdx2*NSE-Cre mouse line represents an important novel genetic tool for the study of early events occurring in the caudal neuroectoderm during the formation of both the central and the peripheral nervous systems.

INTRODUCTION

In vertebrates, early development of the nervous system involves the concerted action of numerous tightly regulated processes in order to properly shape and pattern the neuroectoderm. Formation of a closed neural tube (NT) has to be coordinated with acquisition of positional identity (along both the antero-posterior and dorso-ventral axes) as well as with posterior elongation and induction of neural crest cells (NCC). Such synchronization is required for establishing proper interconnections between the NT-derived central nervous system and the NCC-derived peripheral nervous system. It is also noteworthy that the multipotent and migratory NCC generate in addition multiple non-neural derivatives such as melanocytes, cranio-facial chondrocytes and a subset of conotruncal heart cells, to name a few. Abnormal early nervous system development can thus result in NT defects (such as *spina bifida* and craniorachischisis) and/or neurocristopathies (NCC-associated congenital anomalies), which are amongst the most prevalent group of human congenital malformations (Bolande, 1997; Copp *et al.*, 2003; Nye *et al.*, 1999). This clinical relevance warrants a better understanding of nervous system ontogeny and the mouse has prove to be a very useful animal model in this regard.

Several mouse models based on the Cre-LoxP system have been generated to study early development of the nervous system. Genetically-modified mouse models have been developed for expressing the Cre recombinase in either the whole NT (e.g. *Nestin-Cre* or *Sox1-Cre*) (Dubois *et al.*, 2006; Takashima *et al.*, 2007) or more restricted domains along the dorso-ventral axis (e.g. *Pax3-Cre* or *Ngn1-Cre*) (Li *et al.*, 2000; Quinones *et al.*, 2010). Some other Cre-driver lines with restricted expression along the antero-posterior axis have also been generated (e.g. *Foxg1-Cre* or *Krox20-Cre*) (Hebert and McConnell, 2000; Voiculescu *et al.*, 2001). However, none of the currently existing models directs Cre expression specifically in the posterior neural plate (i.e. the prospective spinal cord territory) at the onset of neurulation.

Antero-posterior patterning of the neuroectoderm is achieved by transformation of a default anterior fate in response to posteriorizing signals. Such posteriorizing cues consist of FGF (fibroblast growth factor), RA (retinoic acid) and canonical Wnt (Wingless/*int1*-

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3 related) signaling pathways, which together regulate *Hox* gene expression via both direct
4 and indirect means (Forlani *et al.*, 2003; Kudoh *et al.*, 2002; Lumsden and Krumlauf,
5 1996). *Hox* gene products will then form the so-called Hox code, which is involved in the
6 conversion of antero-posterior positional information into morphological outcomes
7 (Deschamps and van Nes, 2005). Members of the Cdx (Caudal-related homeobox)
8 transcription factors (Cdx1/2/4) are also known to play a prominent role in this regulatory
9 cascade by acting as intermediaries between posteriorizing signals and *Hox* genes
10 (Lohnes, 2003). Murine *Cdx* genes are expressed in all three germ layers of the caudal
11 embryo during gastrulation and neurulation (Beck *et al.*, 1995; Gamer and Wright, 1993;
12 Meyer and Gruss, 1993), being notably under the direct regulation of canonical Wnt
13 signals (Pilon *et al.*, 2006; Pilon *et al.*, 2007; Sanchez-Ferras *et al.*, 2012). The most
14 anterior limit of *Cdx* expression is found in the neuroectoderm, being located around the
15 prospective hindbrain/spinal cord boundary for *Cdx1* and *Cdx2* (Sturgeon *et al.*, 2011).

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Functional analyses of cis-regulatory elements have revealed that *Cdx* gene expression is
controlled by multiple modular enhancers located in upstream, downstream or intronic
regions (Benahmed *et al.*, 2008; Gaunt *et al.*, 2003; Gaunt *et al.*, 2005; Lickert and
Kemler, 2002; Rankin *et al.*, 2004; Wang and Shashikant, 2007). Interestingly, one of
these studies identified a neural specific enhancer (NSE) located in *Cdx2* intron 1 (Wang
and Shashikant, 2007). We thus took advantage of this previous work and use a 1 kb
fragment containing this NSE in order to generate a mouse line that specifically drives
Cre expression in the caudal neuroectoderm. Characterization of this mouse line – called
*Cdx2*NSE-Cre – revealed that it allows recombination of LoxP sites in the caudal
neuroectoderm, targeting both the NT and NCC posterior to the hindbrain.

RESULTS AND DISCUSSION

In order to generate a Cre-driver mouse line that specifically targets the posterior neural
plate, we first cloned a 852bp fragment from *Cdx2* intron 1 previously reported to contain
a neural specific enhancer (NSE) (Wang and Shashikant, 2007). This fragment was then
subcloned upstream of a Cre recombinase expression cassette consisting of the *Hsp68*

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3 minimal promoter, Cre open reading frame and SV40 polyA sequences. Standard oocyte
4 microinjections of this construct yielded multiple transgenic animals from which only a
5 single male was used for establishing the *Cdx2*NSE-Cre transgenic line. Both
6 heterozygous and homozygous animals are viable, fertile and do not show any overt
7 morphological defects nor any abnormal behavior.
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12 Cre recombinase expression and activity was monitored by breeding *Cdx2*NSE-Cre
13 animals with R26R-YFP reporter mice. In this particular background, Cre-dependent
14 expression of YFP (yellow fluorescent protein) is under the control of the ubiquitous
15 ROSA26 promoter and thus occurs in cells expressing Cre as well as in their progeny
16 (Srinivas *et al.*, 2001). Using this strategy, the first sign of Cre recombinase activity was
17 traced back to the head fold stage, at which time a significant number of cells exhibited
18 YFP fluorescence in the caudal neuroectoderm of double transgenic embryos (Fig. 1A-
19 B'). By the 4-somite stage, robust Cre activity was detected in almost all cells of the
20 posterior neural plate (Fig. 1C, C'). At this stage, the anterior limit of YFP fluorescence
21 was found extending in the forming neural tube (NT) as far as in the prospective caudal
22 hindbrain territory. As expected, transverse sections of the tailbud showed that YFP
23 fluorescence was restricted to neural cells (Fig. 1D, D').
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35 At embryonic day (E) 8.5, YFP fluorescence was still observed in the whole posterior
36 neural plate and also in the closed NT with an anterior limit located between the first and
37 second somite (Fig. 2A, A'). Transverse sections at trunk level revealed that YFP-labeled
38 cells were exclusively neural, being found along the whole dorso-ventral axis of the NT
39 (Fig. 2B-B'). However, more caudally, transverse sections of the tailbud suggested an
40 expansion of Cre activity in a subset of presumptive mesoderm cells (Fig. 2C-E').
41 Immunofluorescent co-labeling with an antibody against the neural marker Sox2 was thus
42 used to confirm the non-neural identity of these cells (Fig. 3). This analysis clearly
43 revealed that a sub-population of YFP-positive cells was indeed also Sox2-negative at the
44 most caudal end of *Cdx2*NSE-Cre::R26R-YFP embryos (Fig. 3D-E').
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53 At E9.5, the pattern of YFP fluorescence was consistent with observations made at
54 previous stages. While YFP-labeled cells were exclusively neural in the caudal hindbrain
55 and anterior spinal cord regions, a subset of mesoderm cells were also YFP-positive more
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3 posteriorly (Fig. 4). These YFP-labeled mesoderm cells were displayed along a rostro-
4 caudal gradient in the most caudal quarter of the embryo, culminating in the tailbud. In
5 addition, observations at this stage revealed that *Cdx2*NSE-Cre allows targeting
6 migratory neural crest cells (NCC) (Fig. 4D'). Given that *Cdx2* is not expressed in these
7 cells, this most likely reflected a cell lineage effect subsequent to Cre activity in the pre-
8 migratory NCC population – which is located in the dorsal NT.
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15 Characterization at later stages (between E11.5 and E15.5) further demonstrated that
16 *Cdx2*NSE-Cre allows targeting every structure derived or colonized by non-cranial NCC
17 (Fig. 5). Indeed, in addition to the NT, YFP-labeled cells were found in derivatives of
18 trunk (dorsal root ganglia, peripheral nerves, sympathetic ganglia and melanoblasts; Fig.
19 5A, A' and F), cardiac (outflow tract; Fig. 5E) and vagal (enteric neural progenitors; Fig.
20 5B-D') NCC. At these later stages, the rostro-caudal gradient of YFP-labeled cells in the
21 mesoderm was found spreading from around the posterior limb down to the tip of the tail
22 (data not shown).
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31 On the other hand, it is also noteworthy that some *Cdx2*NSE-Cre::R26R-YFP double
32 transgenic embryos exhibited non-specific widespread YFP fluorescence in a genetic
33 background-dependent manner (data not shown). Interestingly, we noticed that this effect
34 occurred much less frequently when the FVB background contribution is increased. With
35 a 50% FVB contribution, it was observed in 17% of fluorescent embryos whereas with a
36 87.5% FVB contribution, it was not observed. This outcome most likely reflects the fact
37 that the regulatory sequences (NSE and *Hsp68* promoter) used to generate the *Cdx2*NSE-
38 Cre transgene were cloned from FVB genomic DNA. Consequently, it should be noted
39 that a *Cdx2*NSE-Cre mouse line having a nearly pure FVB background (backcrossed for
40 at least 5 generations) will be available to the scientific community.
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49 Taken together, our analyses have demonstrated that the *Cdx2*NSE-Cre mouse line
50 targets the whole posterior neuroectoderm (both NT and NCC) with the caudal hindbrain
51 as anterior limit. However, we have also found that this transgene is not fully neural-
52 specific since it is also active in a subset of mesoderm cells of the most caudal quarter of
53 the embryo. Given that such activity has been also observed with multiple transgenic
54 founders (5 out of 8; data not shown), this suggests that it is a true inherent property of
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3 the cloned sequences. Such hypothesis is supported by the fact that in the original
4 description of the *Cdx2* NSE, E9.5 transient transgenic embryos did not only display
5 reporter gene expression in the NT but apparently also in the whole tailbud (Wang and
6 Shashikant, 2007). Therefore, the YFP labeling of mesoderm cells in *Cdx2*NSE-
7 Cre::R26R-YFP double transgenic embryos was most likely indicative of a cell lineage
8 effect resulting from Cre activity in tailbud mesoderm precursors. Further functional
9 dissection of the NSE sequences might thus eventually lead to an improved version (i.e.
10 fully neural specific) of the *Cdx2*NSE-Cre transgene. Nonetheless, we believe that the
11 current *Cdx2*NSE-Cre mouse model represents a valuable novel genetic tool for the study
12 of early NT and NCC development specifically in the caudal embryo.
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24 MATERIALS AND METHODS

27 Ethics Statement

28 Experiments involving mice were performed following Canadian Council of Animal Care
29 (CCAC) guidelines for the care and manipulation of animals used in medical research.
30 Protocols involving the manipulation of animals were approved by the institutional ethics
31 committee of the University of Quebec at Montreal (comité institutionnel de protection
32 des animaux (CIPA)); Reference number 0512-R3-648-0513).
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41 Construction of the *Cdx2*NSE-Cre transgene

42 The neural specific enhancer was cloned by PCR as previously described (Wang et
43 Shashikant, 2007). Genomic DNA from a FVB mouse was used to amplify a 852-bp
44 fragment using a forward primer containing a *Apa*I site (5'-
45 GGGCCCGTGCTCTAAGAGCAGCATCCGTTC-3') and a reverse primer bearing a
46 *Kpn*I site (5'-GGTACCGAGGCAACTATCCTGACCAAGTGA-3'). The minimal
47 *Hsp68* promoter (315-bp) was similarly amplified with a forward primer containing a
48 *Kpn*I site (5'-GGTACCTTGGTACCCCTCCTCCGGCT-3') and a reverse primer
49 containing a *Bgl*III site (5'- AGATCTTTAGATCTGGCGCCGCGCTC -3'). Cre
50 recombinase coding sequences (1032pb) were amplified from another plasmid (Pilon *et*
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al., 2008) using a forward primer bearing a *SacI* site (5'-GAGCTCATGTCCAATTTACTGACCGTACAC-3') and a reverse primer containing a *SpeI* site (5'-ACTAGTCTAATCGCCATCTTCCAGC-3'). All amplifications were done using the Platinum Taq DNA polymerase kit (Invitrogen) in accordance with manufacturer's instructions. PCR products were cloned in pGEMT-easy vector (Promega) and verified by sequencing. Restriction sites contained in primers were then used to assemble the *Cdx2*NSE-*Hsp68p*-Cre sequences in a vector containing SV40 polyA sequences (pIRES-EGFP2; Clontech). The *Cdx2*NSE-*Hsp68p*-Cre-SV40pA transgene was finally excised with *NheI* and *PvuII* to obtain the 3150-bp fragment that was used for microinjections.

Generation and analysis of the *Cdx2*NSE-Cre transgenic mouse line

*Cdx2*NSE-Cre transgene DNA was microinjected in B6C3 oocytes in accordance with standard methods. Offspring was screened by PCR-based genotyping of tail DNA using specific Cre recombinase primers (forward: 5'-GATGAGGTTTCGCAAGAACCTGATG-3' and reverse: 5'-AACAGCATTGCTGTCACTTGGTTCG-3'). Thirteen F0 transgenic animals were identified, of which only males (eight) were tested for Cre activity as described below. A single male (R337) was then kept to generate the *Cdx2*NSE-Cre mouse line via breeding with a C57BL/6 female. *Cdx2*NSE-Cre transgenic animals are available upon request.

Cre recombinase activity was evaluated by crossing F1 *Cdx2*NSE-Cre mice with R26R-YFP animals (initially obtained from Frank Costantini and then maintained on a FVB background) as previously described (Pilon *et al.*, 2008; Srinivas *et al.*, 2001). Timed pregnancies were set up using standard vaginal plug detection, noon of the day of plug detection being considered as E0.5.

Microscopy and imaging

Embryos were dissected and fixed with 4% paraformaldehyde in PBS. Fixation time was adjusted in accordance with embryonic stages. For transverse sections, embryos were

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3 embedded in 3% agarose and 100 μ m transverse sections were realized using a vibrating
4 blade microtome Microm HM 650V (Thermo Scientific).
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8 Bright field and YFP images were obtained with a Leica DFC 495 camera mounted on a
9 Leica M205 FA microscope (Leica Microsystems). Exposure time was adjusted for
10 optimal imaging, and kept constant throughout the experimental time course.
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14 15 16 17 **Immunostaining**

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19 Following dissection and fixation, whole embryos were first incubated in blocking
20 solution (10% FBS and 0,1% triton in PBS) for 2h at room temperature. Embryos were
21 then incubated overnight at 4°C with goat anti-SOX2 primary antibody (R&D Systems,
22 #AF2018) diluted 1:200 in blocking solution. After washing, embryos were incubated 2h
23 at room temperature with bovine anti-goat Alexa Fluor 647 secondary antibody diluted
24 1:500 in blocking solution (Jackson ImmunoResearch). After final washing, transverse
25 sections were realized as described above and fluorescence from both YFP and
26 immunostaining was captured with a laser-scanning confocal microscope (Nikon A1R).
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FIGURE LEGENDS

Figure 1: Characterization of *Cdx2*NSE-Cre at the onset of neurulation. Analyses of embryos obtained from crosses between *Cdx2*NSE-Cre and R26R-YFP reporter mice at head fold (A-B') and 4-somite (C-D') stages. Images were taken under bright field (A, B, C, D) or YFP detection mode (A', B', C', D'). Lateral (A,B), dorsal (C-F) and transverse (G-H) views reveal that YFP fluorescence is restricted to the caudal neuroectoderm. The dashed line in C-C' indicates the level at which the cross section shown in D-D' was made. Abbreviations: P, posterior; A, anterior; PNP, posterior neural plate; NT, neural tube.

Figure 2: Characterization of *Cdx2*NSE-Cre during early neurulation. Detailed analysis of a 7-somite stage embryo obtained from a cross between *Cdx2*NSE-Cre and R26R-YFP reporter mice. Images were taken under bright field (A, B, C, D, E) or YFP detection mode (A', B', C', D', E'). YFP fluorescence is observed in the posterior neural plate (PNP) and the closed neural tube (NT) with an anterior limit between the first and second somite (A-A'). The dashed lines in A-A' indicates the level at which the cross sections shown in B to E' were made. These transverse sections suggest that the neural specificity of YFP fluorescence is decreasing caudally, being also found in the presumptive mesoderm territory.

Figure 3: The *Cdx2*NSE-Cre transgene is not fully neural-specific.

Immunofluorescent detection of Sox2 in a E8.5 *Cdx2*NSE-Cre::R26R-YFP double-transgenic embryo. The dashed lines in A indicate the level at which the cross sections shown on the right were made. Confocal imaging of these transverse sections show that a subset of YFP-labeled cells (green) are not labeled by an antibody against the neural marker Sox2 (red) in the most caudal end of the embryo, supporting the assumption that these cells are mesodermal. Note also that the number of these YFP-positive but Sox2-negative cells appears to form a gradient along the antero-posterior axis.

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6 **Figure 4: Characterization of *Cdx2*NSE-Cre during late neurulation.** Analysis of
7 E9.5 embryos obtained from crosses between *Cdx2*NSE-Cre and R26R-YFP reporter
8 mice. Images were taken under bright field (A, B, C, D) or YFP detection mode (A', B',
9 C', D'). Frontal (A, A') and lateral (B, B') views show YFP fluorescence in the closed
10 neural tube (NT). Blue arrowheads point to progressive mesodermal expression in the
11 caudal end of the embryo (A', B'). The dashed lines in B-B' indicate the level at which
12 the cross sections shown in C to D' were made. Note that while the tailbud is almost
13 completely labeled with YFP fluorescence (C, C'), this labeling is neuroectoderm-
14 specific in the trunk (D, D'). Note also that YFP fluorescence is observed in migratory
15 neural crest cells (NCC) of the trunk (D').
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27 **Figure 5: Characterization of *Cdx2*NSE-Cre activity in the neural crest lineage.**
28 Analyses of E11.5 (A, A'), E13.5 (B-E) and E15.5 (F) embryos obtained from crosses
29 between *Cdx2*NSE-Cre and R26R-YFP reporter mice. Bright field (A, D), YFP
30 fluorescence (A', B, C, D', F) and composite images (E) are shown. Transverse views of
31 E11.5 embryos at trunk level (A, A') indicate that YFP is expressed in the neural tube
32 (NT) as well as multiple derivatives of neural crest cells such as melanoblasts (M), dorsal
33 root ganglia (DRG), peripheral nerves (PN) and sympathetic ganglia (SG). In E13.5
34 embryos, YFP-labeled neural crest cells are also observed colonizing the cardiac outflow
35 tract (E) as well as the gut (B-D'). The dashed line in C indicates the level at which the
36 cross section shown in D-D' was made; this section shows that YFP fluorescence marks
37 enteric neural precursors (ENP). In E15.5 embryos, YFP-labeled melanoblasts can be
38 observed spreading over the whole body except the head (F).
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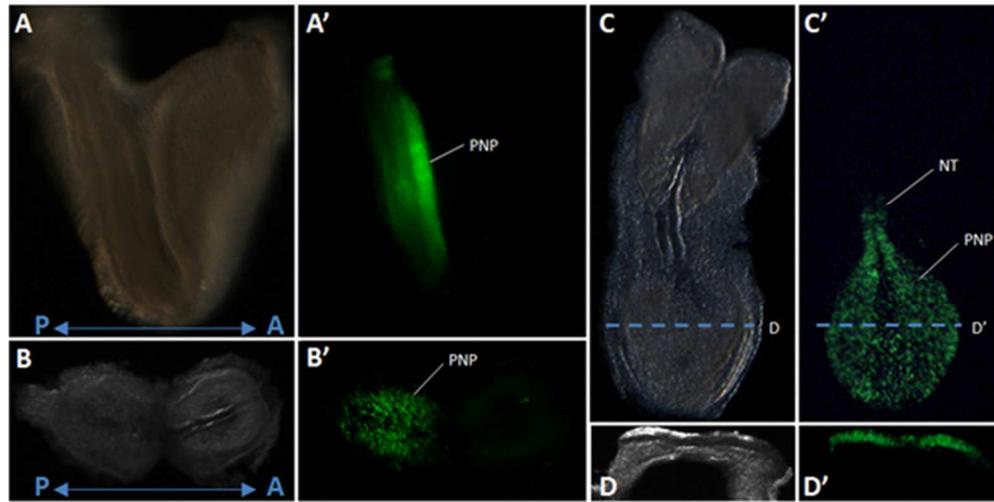


Figure 1: Characterization of Cdx2NSE-Cre at the onset of neurulation. Analyses of embryos obtained from crosses between Cdx2NSE-Cre and R26R-YFP reporter mice at head fold (A-B') and 4-somite (C-D') stages. Images were taken under bright field (A, B, C, D) or YFP detection mode (A', B', C', D'). Lateral (A,B), dorsal (C-F) and transverse (G-H) views reveal that YFP fluorescence is restricted to the caudal neuroectoderm.

The dashed line in C-C' indicates the level at which the cross section shown in D-D' was made.

Abbreviations: P, posterior; A, anterior; PNP, posterior neural plate; NT, neural tube.

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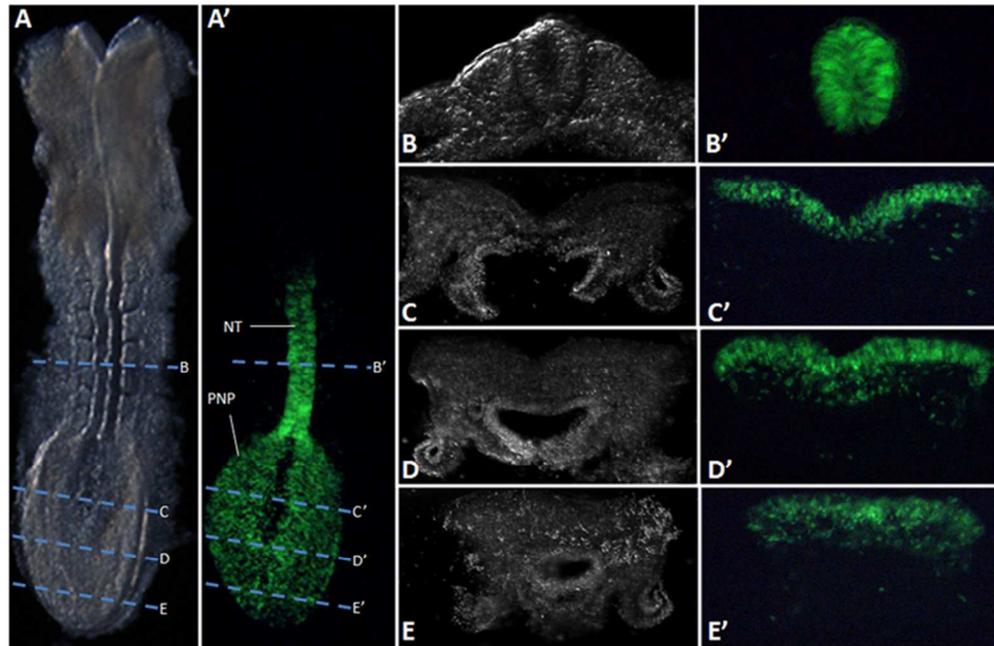


Figure 2: Characterization of Cdx2NSE-Cre during early neurulation. Detailed analysis of a 7-somite stage embryo obtained from a cross between Cdx2NSE-Cre and R26R-YFP reporter mice. Images were taken under bright field (A, B, C, D, E) or YFP detection mode (A', B', C', D', E'). YFP fluorescence is observed in the posterior neural plate (PNP) and the closed neural tube (NT) with an anterior limit between the first and second somite (A-A'). The dashed lines in A-A' indicates the level at which the cross sections shown in B to E' were made. These transverse sections suggest that the neural specificity of YFP fluorescence is decreasing caudally, being also found in the presumptive mesoderm territory.

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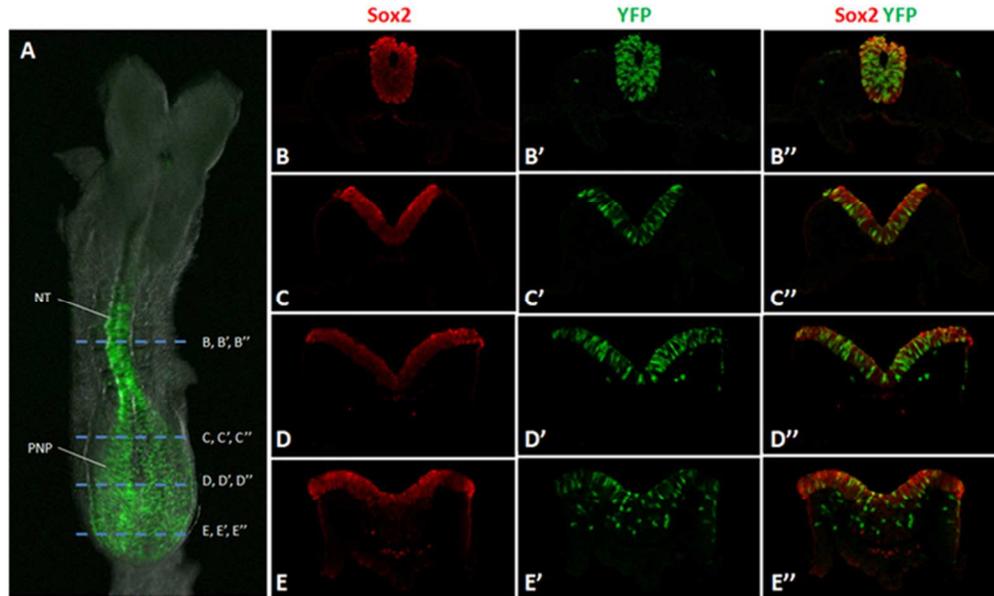


Figure 3: The *Cdx2*NSE-Cre transgene is not fully neural-specific. Immunofluorescent detection of Sox2 in a E8.5 *Cdx2*NSE-Cre::R26R-YFP double-transgenic embryo. The dashed lines in A indicate the level at which the cross sections shown on the right were made. Confocal imaging of these transverse sections show that a subset of YFP-labeled cells (green) are not labeled by an antibody against the neural marker Sox2 (red) in the most caudal end of the embryo, supporting the assumption that these cells are mesodermal. Note also that the number of these YFP-positive but Sox2-negative cells appears to form a gradient along the antero-posterior axis.

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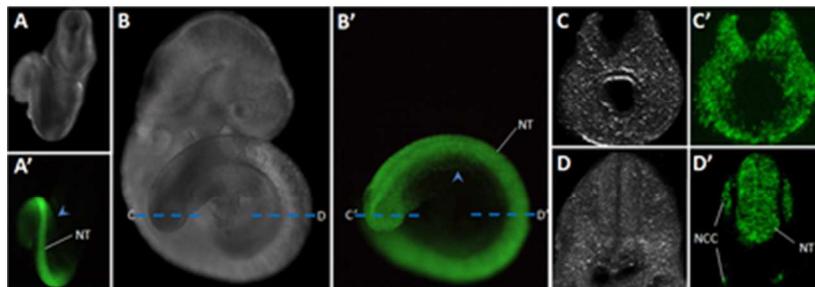


Figure 4: Characterization of Cdx2NSE-Cre during late neurulation. Analysis of E9.5 embryos obtained from crosses between Cdx2NSE-Cre and R26R-YFP reporter mice. Images were taken under bright field (A, B, C, D) or YFP detection mode (A', B', C', D'). Frontal (A, A') and lateral (B, B') views show YFP fluorescence in the closed neural tube (NT). Blue arrowheads point to progressive mesodermal expression in the caudal end of the embryo (A', B'). The dashed lines in B-B' indicate the level at which the cross sections shown in C to D' were made. Note that while the tailbud is almost completely labeled with YFP fluorescence (C, C'), this labeling is neuroectoderm-specific in the trunk (D, D'). Note also that YFP fluorescence is observed in migratory neural crest cells (NCC) of the trunk (D').

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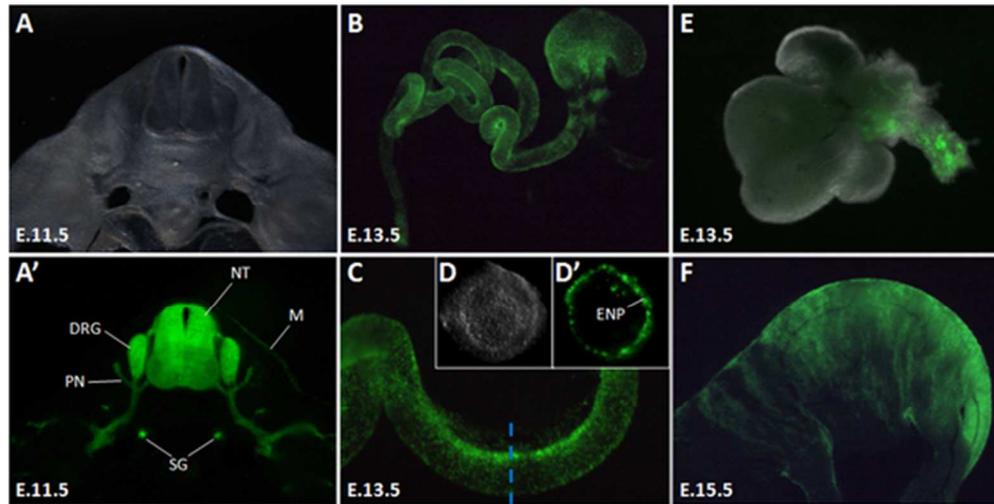


Figure 5: Characterization of Cdx2NSE-Cre activity in the neural crest lineage. Analyses of E11.5 (A, A'), E13.5 (B-E) and E15.5 (F) embryos obtained from crosses between Cdx2NSE-Cre and R26R-YFP reporter mice. Bright field (A, D), YFP fluorescence (A', B, C, D', F) and composite images (E) are shown. Transverse views of E11.5 embryos at trunk level (A, A') indicate that YFP is expressed in the neural tube (NT) as well as multiple derivatives of neural crest cells such as melanoblasts (M), dorsal root ganglia (DRG), peripheral nerves (PN) and sympathetic ganglia (SG). In E13.5 embryos, YFP-labeled neural crest cells are also observed colonizing the cardiac outflow tract (E) as well as the gut (B-D'). The dashed line in C indicates the level at which the cross section shown in D-D' was made; this section shows that YFP fluorescence marks enteric neural precursors (ENP). In E15.5 embryos, YFP-labeled melanoblasts can be observed spreading over the whole body except the head (F).

50x25mm (300 x 300 DPI)