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Cellular and Molecular Life Sciences

ERRATUM

Erratum to: Preservation of positional identity in fetus-derived neural stem (NS) cells from different mouse central nervous system compartments

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In the original publication the Fig. 2a showed an RT-PCR analysis of a panel of markers expressed by 9 lines of fetus-derived NS and embryonic stem cells. The lane for *Hoxb4* gene expression contained a white bar separating the positive control (+CTRL). The band in the +CTRL was actually a duplication of the NS12SC band. In fact, the general mouse fetal brain, used as +CTRL for all the other markers, did not express the spinal cord marker *Hoxb4*. In the new version of the Fig. 2 we removed the duplicated +CTRL band for *Hoxb4*.

Then, in Fig. 5c–d, there was a redundant duplication of the PCR for *Hb9*, *lrx3* and *Nkx2-2*, shown at first for spinal cord NS12SC in Fig. 5c, and then compared side-by-side with striatal NS12ST in Fig. 5d. In the new version, duplicated PCR analysis on NS12SC cells was removed from Fig. 5d and is referred to the data shown in Fig. 5c in the new figure legend.

The online version of the original article can be found under doi:10.1007/s00018-010-0548-7.

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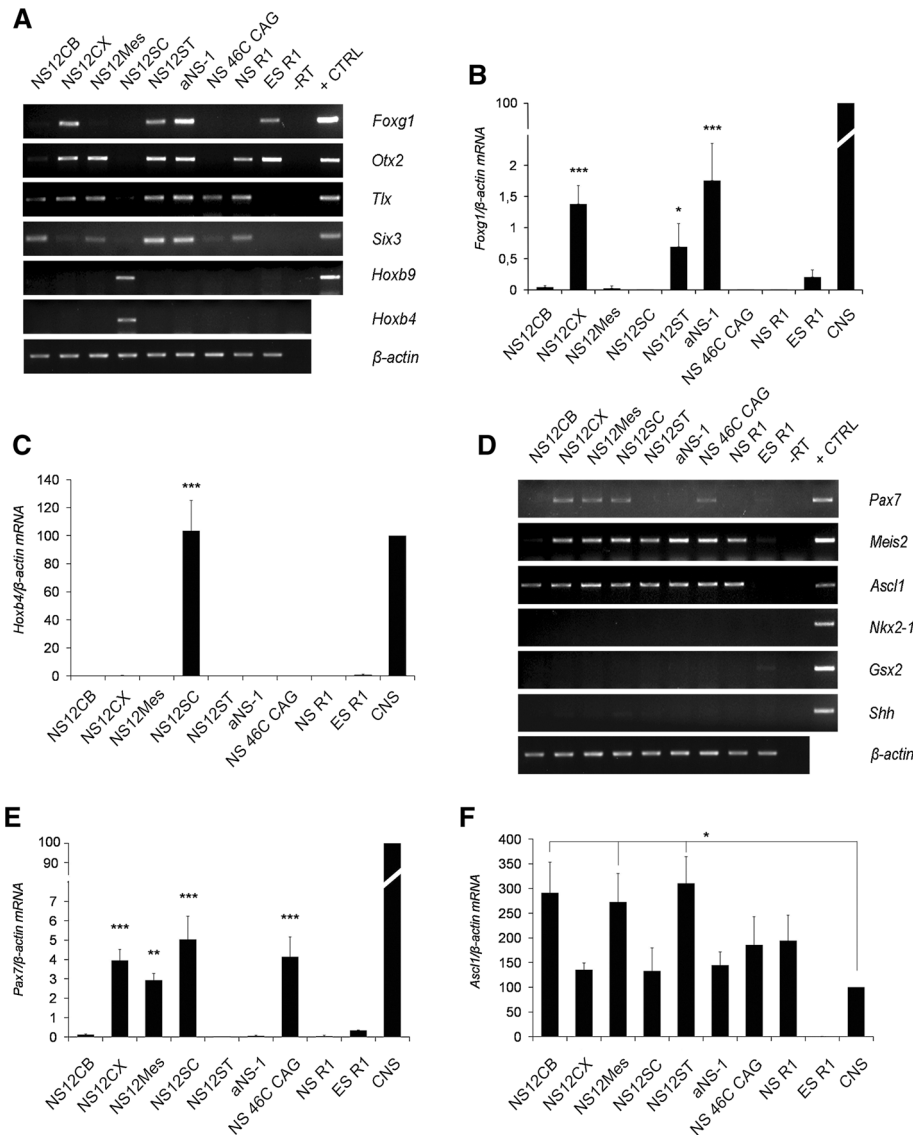

Fig. 2 Analysis of the in vitro positional identity in NS cell lines. **a** RT-PCR analysis of a subset of R-C markers shows that fetus-derived NS cells possess a region-specific transcription factor pattern: *Foxg1* is expressed in telencephalic NS lines, *Otx2* and *Six3* in anterior CNS-derived NS cells, and *Hoxb4* and *Hoxb9* in NS12SC cells. Mouse fetal brain was used as positive control (+*CTRL*); -RT was the negative control **b**, **c** RT-qPCR analysis showing the expression levels of two relevant R-C markers, *Foxg1* (**b**) and *Hoxb4* (**c**). Data are expressed as percentages (100 % was assigned to fetal CNS-E13 brain and spinal cord). **d** RT-PCR analysis of some indicative D-V markers shows constitutive expression of important ventral markers, including *Meis2* and *Ascl1*. Mouse fetal brain was used as positive control (+*CTRL*); -RT was the negative control. **e**, **f** RT-qPCR analysis showing the expression levels of two relevant D-V markers, *Pax7* (**e**) and *Ascl1* (**f**). Data are expressed as percentages (100 % was assigned to fetal CNS). $*p < 0.05$, $**p < 0.01$, $***p < 0.001$, as calculated by ANOVA using the Tukey–Kramer post-test

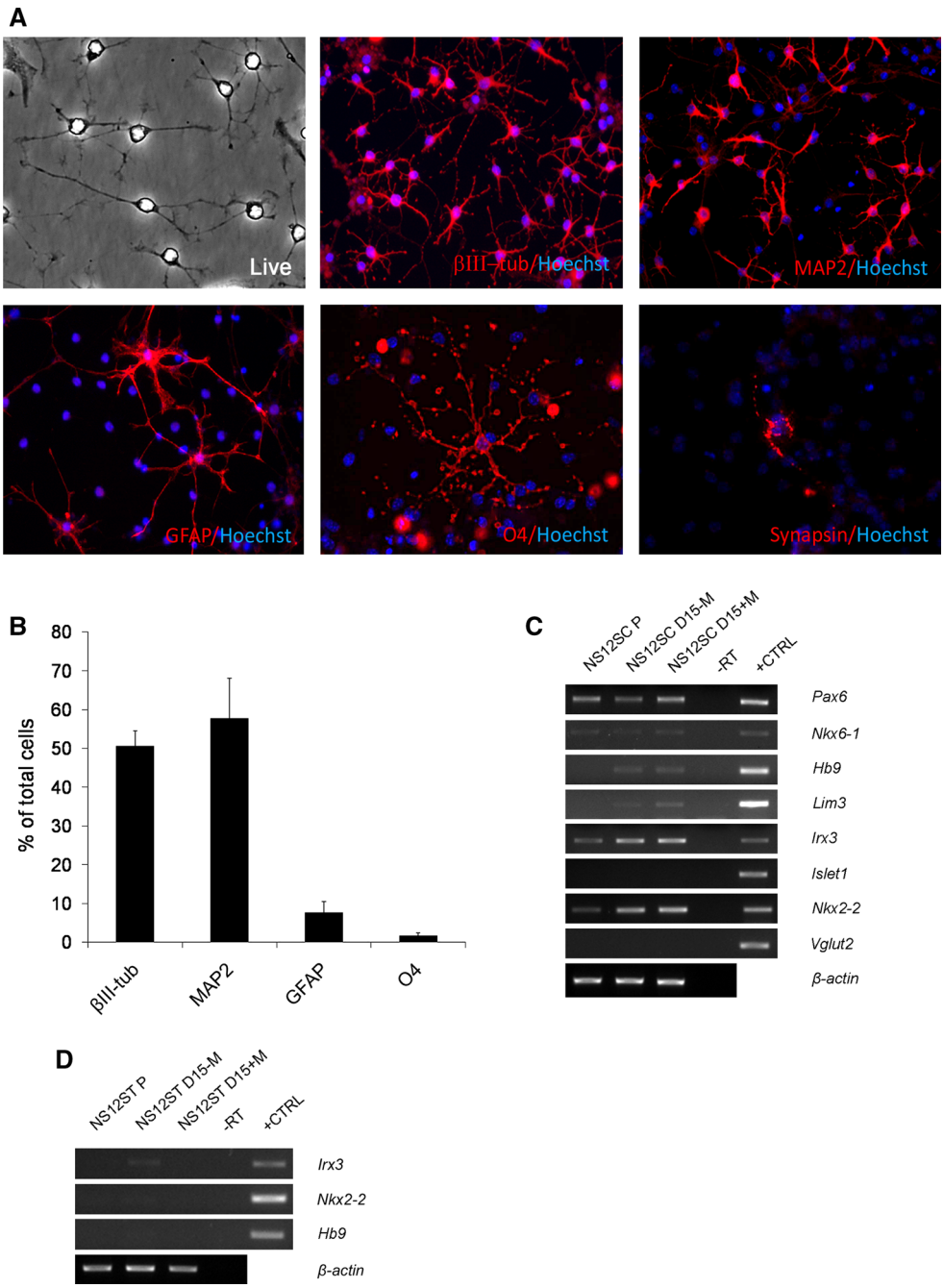

Fig. 5 Neuronal differentiation of NS12SC cells. **a** After 23 days of differentiation in vitro, NS12SC cells gave rise to βIII-tubulin-, MAP2-, GFAP-, and O4-positive cells. A representative synapsin-positive cell is shown after 21 days of differentiation (×4, magnified after acquisition). **b** At the end of differentiation, 50.5 ± 3.9 % of cells were immunopositive for βIII-tubulin, 57.7 ± 10.3 % for MAP2, 7.5 ± 2.8 % for GFAP, and 1.5 ± 0.7 % for O4 ($n = 1068$ cells for βIII-tubulin; $n = 1184$ cells for MAP2 and GFAP; $n = 1645$ cells for O4) (*columns* represent averages, *error bars* standard deviations). **c** Gene expression analysis by RT-PCR on NS12SC cells in proliferation (*P*) and after 15 days differentiation in the absence (*D15−M*) or in the presence (*D15+M*) of morphogens. **d** Spinal gene markers analyzed in **c** are not detected in NS12ST cells. Mouse fetal brain was used as positive control (+*CTRL*); -*RT* was the negative control