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

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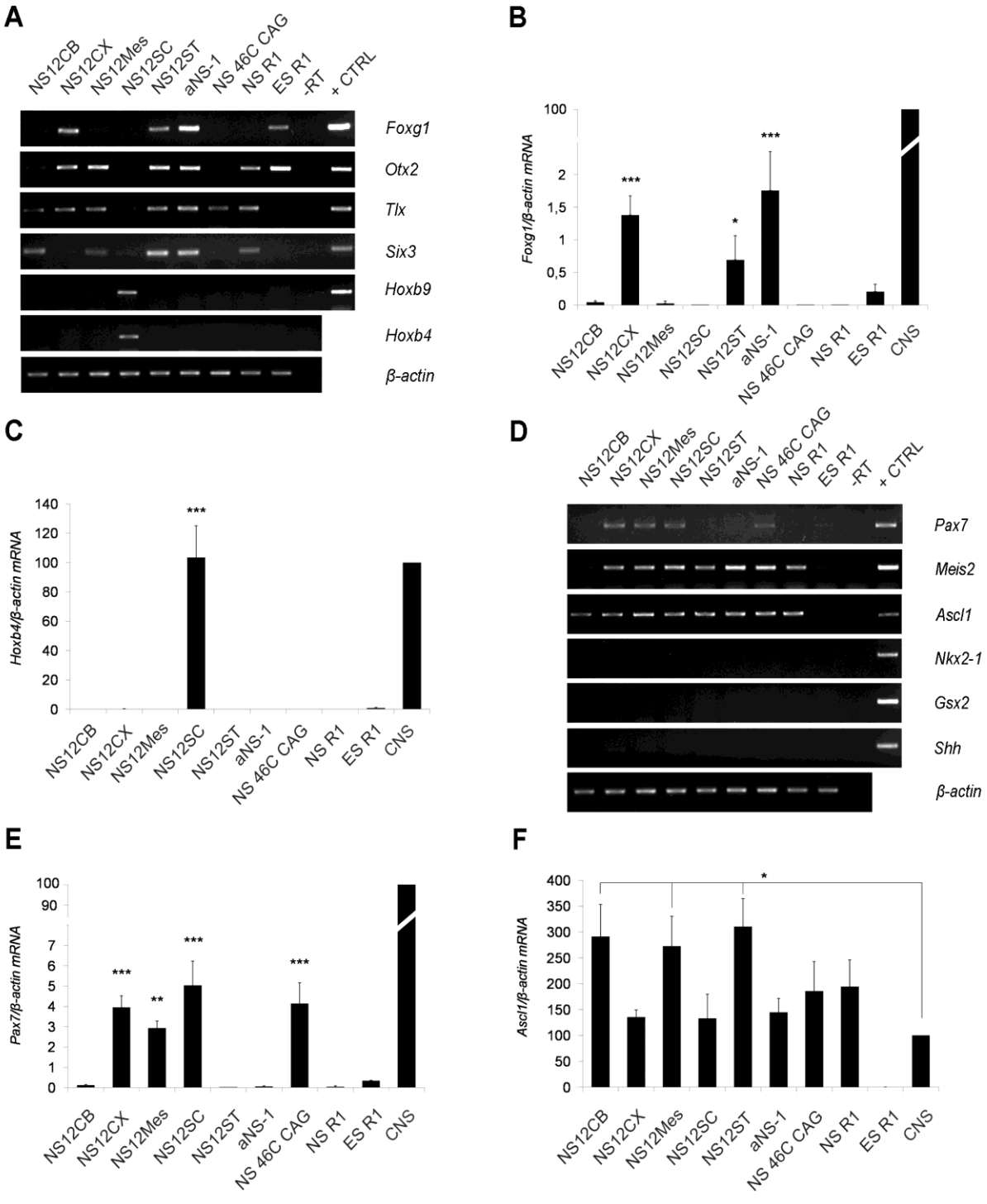
In the original publication the Figure 2A showed an RT–PCR analysis of a panel of markers expressed by 9 lines of fetus-derived NS and embryonic stem cells. The lane for *Hoxb4* gene expression contained a white bar separating the positive control (+CTRL). The band in the +CTRL was actually a duplication 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 figure we removed the duplicated +CTRL band for *Hoxb4*.

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

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 (x4, 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 = 1,068 cells for βIII-tubulin; n = 1,184 cells for MAP2 and GFAP; n = 1,645 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


A
NS12CB
NS12CX
NS12Mes
NS12SC
NS12ST
aNS-1
NS 46C CAG
NS R1
ES R1
-RT
+ CTRL
Foxg1
Otx2
Tlx
Six3
Hoxb9
Hoxb4
β-actin
B
Foxg1/β-actin mRNA
100
2
1,5
1
0,5
0
***
*
***
NS12CB
NS12CX
NS12Mes
NS12SC
NS12ST
aNS-1
NS 46C CAG
NS R1
ES R1
CNS
C
Hoxb4/β-actin mRNA
140
120
100
80
60
40
20
0
***
NS12CB
NS12CX
NS12Mes
NS12SC
NS12ST
aNS-1
NS 46C CAG
NS R1
ES R1
CNS
D
NS12CB
NS12CX
NS12Mes
NS12SC
NS12ST
aNS-1
NS 46C CAG
NS R1
ES R1
-RT
+ CTRL
Pax7
Meis2
Ascl1
Nkx2-1
Gsx2
Shh
β-actin
E
Pax7/β-actin mRNA
100
90
7
6
5
4
3
2
1
0
***
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NS12CB
NS12CX
NS12Mes
NS12SC
NS12ST
aNS-1
NS 46C CAG
NS R1
ES R1
CNS
F
Ascl1/β-actin mRNA
400
350
300
250
200
150
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*
NS12CB
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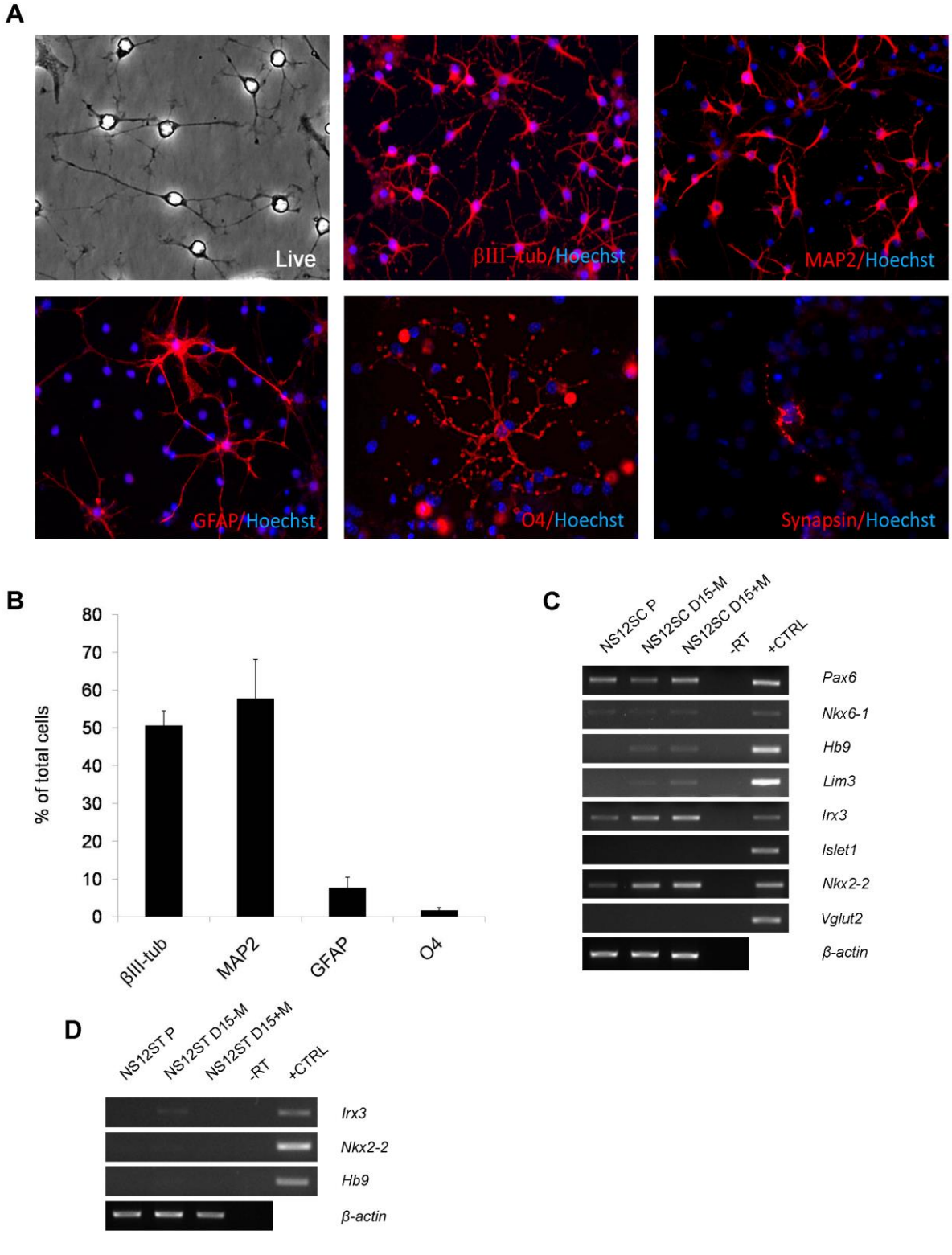
A
Live
βIII-tub/Hoechst
MAP2/Hoechst
GFAP/Hoechst
O4/Hoechst
Synapsin/Hoechst
B
% of total cells
80
70
60
50
40
30
20
10
0
βIII-tub
MAP2
GFAP
O4
C
NS12SC P
NS12SC D15-M
NS12SC D15+M
-RT
+CTRL
Pax6
Nkx6-1
Hb9
Lim3
Irx3
Islet1
Nkx2-2
Vglut2
β-actin
D
NS12ST P
NS12ST D15-M
NS12ST D15+M
-RT
+CTRL
Irx3
Nkx2-2
Hb9
β-actin