Summary of supplementary information

The Supplementary Information contains some experimental methods (Supplementary methods), some supplementary results of the experimental (Supplementary figure1-9), antibody information (Supplementary table1) used in western and Immunofluorescence staining, primer information (Supplementary table2, 3) and the contribution of each author.

Supplementary methods

Stereotaxic injections

The mice were anesthetized with 20ng/ml AVER(0.02ml/g) (Aladdin) delivered through intraperitoneal injection and placed in a stereotaxic frame. The area around the incision was trimmed, and then, treated the meninges with 3% hydrogen peroxide (Aladdin) and find the bregma to locate the origin. Virus were injected bilaterally into the DG of the dorsal hippocampi using the following coordinates: (from bregma) anterior = −1.75mm, lateral = ± 1.75mm, (from skull surface) height = −2.06mm. A 2 μl volume was injected stereotaxically over 10 min (injection speed: 0.20μl/min) using a 5 μl 33s gauge Hamilton syringe. To limit reflux along the injection track, the needle was maintained in situ for 10 minutes, slowly pulled out. The skin was closed using silk suture. Mice were single-housed and monitored during recovery.

Novel Object Recognition

Mice were habituated in the room for behavior detection for 1d. For novel-object recognition training, the mice were handed into a black Plexiglas rectangular chamber (31 × 24 cm, height 27 cm), and two identical objects were presented to mice to explore for 20 min, after which mice were returned to the home cage. Twenty-four hours later, one object was replaced by one novel object and the mouse was again placed in the chamber 6min. The novel object had the same height and volume as the object it replaced, but different shape and appearance. To control for odor cues, the open field arena and the objects were thoroughly cleaned with ethanol, dried, and ventilated between mice. Exploration of the objects was defined as sniffing of the objects (with nose contact or head directed toward the object) within a 2-cm radius of the objects. Sitting or standing on the objects was not scored as exploration. Behavior was recorded from cameras positioned above the training chamber.). The discrimination index (DI) was computed as DI = (novel-object exploration time – familiar-object exploration time/total exploration time) × 100. The discrimination ratio (DR) of novel-object was computed as DR = (novel-object exploration time /total exploration time) × 100.

Water maze

Mice were habituated in the room for behavior detection for 1d. The water maze consisted of a circular pool (120 cm diameter) filled with water (22 ± 2 °C) surrounded by Curtains. The platform (10 cm wide) was located approximately 1 cm below the water level. On the first 4 d (d, days), the mice were trained to locate a visible platform. Each mouse was given four trials (at different quadrants) per day. Each trial began by placing the mouse in the water, near and facing the wall of the pool. The starting points for each subject were chosen randomly from any of the three quadrants other than the one with the platform. Each subject was allowed 60 s to find the platform and, if it failed to reach the platform within 60 s, it was guided by the experimenter to the platform and allowed to stay on the platform for 20 s. The mice that did not reach the platform during a trial were assigned a latency of 60 s. Upon removal from the maze, the mice were dried with fresh towel, placed on a warm platform and returned to their home cages. After the visible platform test was completed, the mice were then tested with no platform, each subject was allowed 60 s to find the platform and record the data with the

camera. The entire travel of the mouse was tracked and analyzed off-line with EthoVision XT software. The number of mice through the platform area during the the probe trial or the time of mice arrival in platform during learning was used as a measure of spatial memory retention. Mice with more than 20 s of floating during learning acquisition were excluded from analysis.

Frozen section

Three weeks after stereotaxic injection, mice transcranial perfusion with 4% paraformaldehyde (PFA), brains were removed and postfixed for a further 16 h in 4% PFA and then transferred to 30% sucrose in PBS until saturated. The brain was embedded in Tissue-Tek O.C.T. compound. Coronal frozen slices 30 μm thick were prepared on a freezing microtome (Leica) and stored the brain slices in the brain freezing medium which contains 30% sucrose and 30% ethanediol, 11.36% Na2HPO4 and 2.4% NaH2PO4.

Figure S1

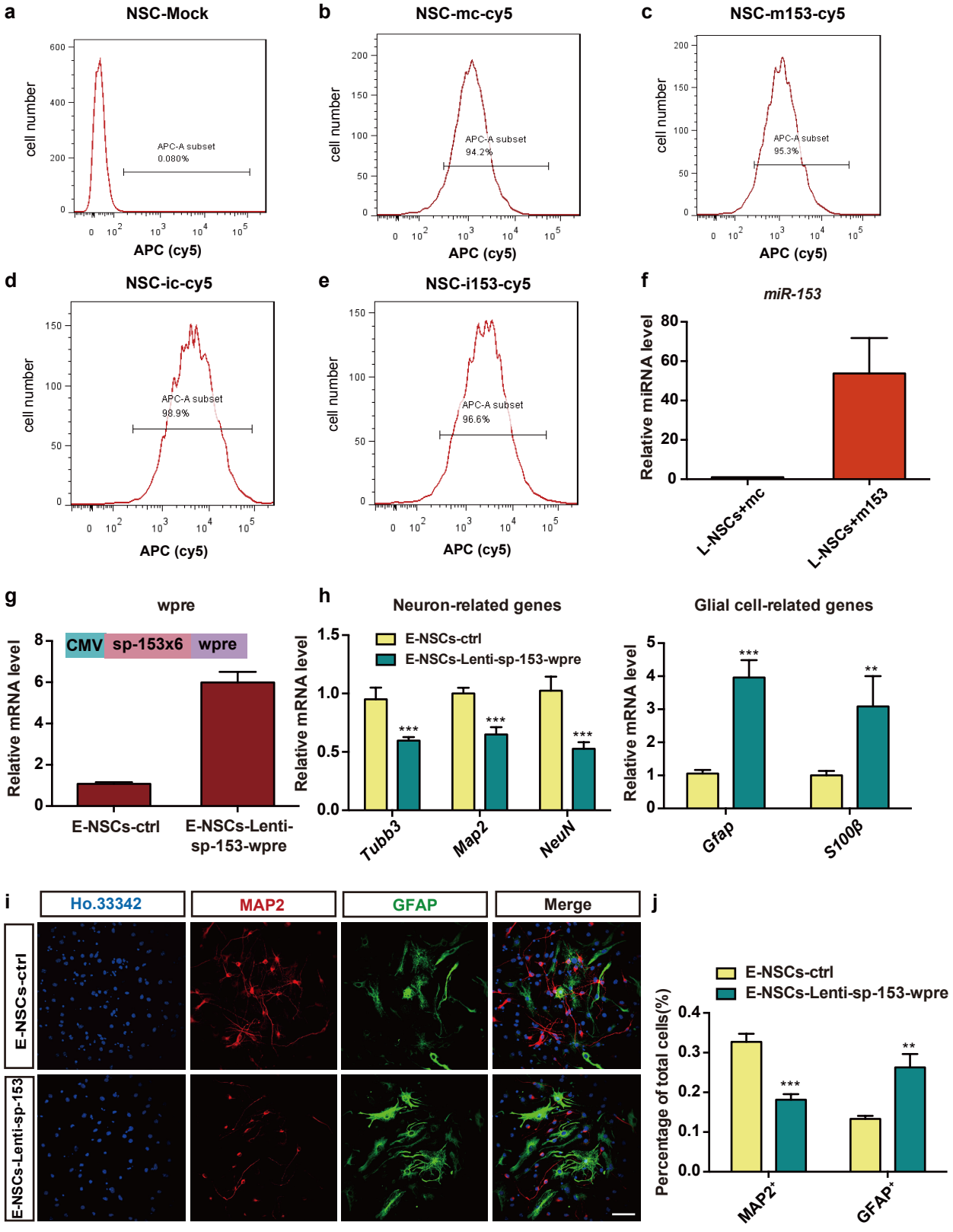

a
NSC-Mock
cell number
APC-A subset
0.080%
APC (cy5)
b
NSC-mc-cy5
APC-A subset
94.2%
c
NSC-m153-cy5
APC-A subset
95.3%
d
NSC-ic-cy5
APC-A subset
98.9%
e
NSC-i153-cy5
APC-A subset
96.6%
f
miR-153
Relative miRNA level
L-NSCs+mc
L-NSCs+m153
g
wpre
CMV
sp-153x6
wpre
Relative mRNA level
E-NSCs-ctrl
E-NSCs-Lenti-sp-153-wpre
h
Neuron-related genes
Tubb3
Map2
NeuN
Glial cell-related genes
Gfap
S100β
i
Ho.33342
MAP2
GFAP
Merge
E-NSCs-ctrl
E-NSCs-Lenti-sp-153
j
Percentage of total cells(%)
MAP2+
GFAP+

Figure S2

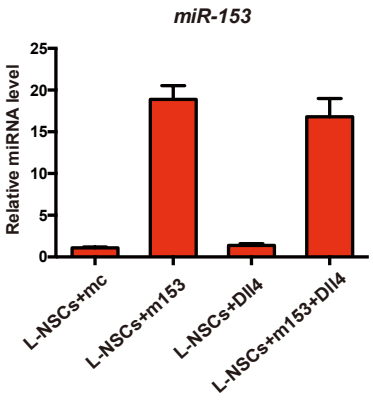

miR-153
Relative miRNA level
25
20
15
10
5
0
L-NSCs+mc
L-NSCs+m153
L-NSCs+Dll4
L-NSCs+m153+Dll4

Figure S3

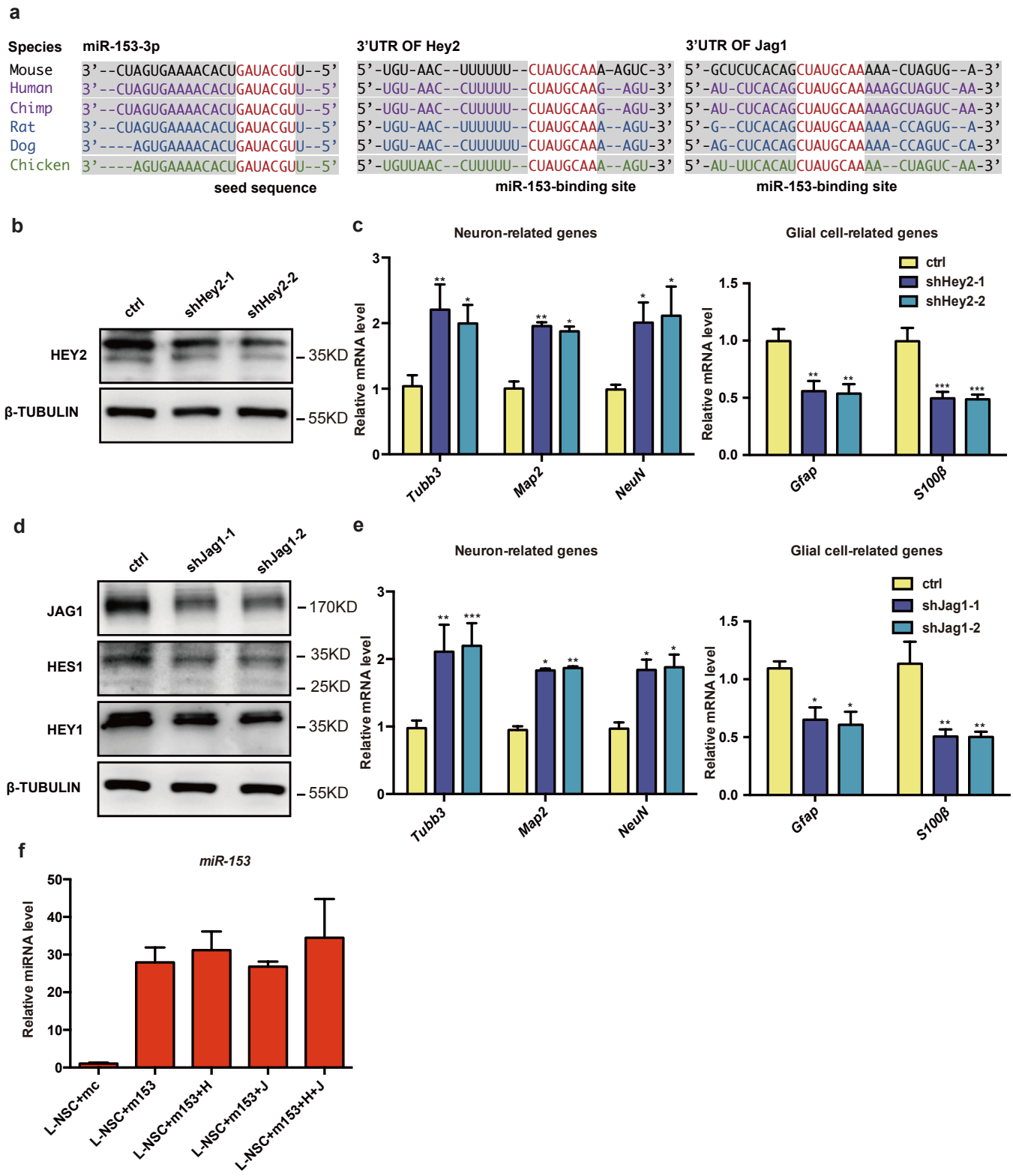

a
Species
miR-153-3p
3'UTR OF Hey2
3'UTR OF Jag1
Mouse
Human
Chimp
Rat
Dog
Chicken
3'--CUAGUGAAAACACUGAUACGUU--5'
3'--CUAGUGAAAACACUGAUACGUU--5'
3'--CUAGUGAAAACACUGAUACGUU--5'
3'--CUAGUGAAAACACUGAUACGUU--5'
3'----AGUGAAAACACUGAUACGUU--5'
3'----AGUGAAAACACUGAUACGUU--5'
5'-UGU-AAC--UUUUUU--CUAUGCAAA-AGUC-3'
5'-UGU-AAC--CUUUUU--CUAUGCAAG--AGU-3'
5'-UGU-AAC--CUUUUU--CUAUGCAAG--AGU-3'
5'-UGU-AAC--UUUUUU--CUAUGCAAA--AGU-3'
5'-UGU-AAC--CUUUUUU-CUAUGCAAA--AGU-3'
5'-UGUUAAC--CUUUUU--CUAUGCAAA--AGU-3'
5'-GCUCUCACAGCUAUGCAAAAA-CUAGUG--A-3'
5'-AU-CUCACAGCUAUGCAAAAAGCUAGUC-AA-3'
5'-AU-CUCACAGCUAUGCAAAAAGCUAGUC-AA-3'
5'-G--CUCACAGCUAUGCAAAAA-CCAGUG--A-3'
5'-AG-CUCACAGCUAUGCAAAAA-CCAGUC-CA-3'
5'-AU-UUCACAUCUAUGCAAAA--CUAGUC-AA-3'
seed sequence
miR-153-binding site
miR-153-binding site
b
ctrl
shHey2-1
shHey2-2
HEY2
β-TUBULIN
35KD
55KD
c
Neuron-related genes
Glial cell-related genes
ctrl
shHey2-1
shHey2-2
Relative mRNA level
Tubb3
Map2
NeuN
Gfap
S100β
d
ctrl
shJag1-1
shJag1-2
JAG1
HES1
HEY1
β-TUBULIN
170KD
35KD
25KD
35KD
55KD
e
Neuron-related genes
Glial cell-related genes
ctrl
shJag1-1
shJag1-2
Relative mRNA level
Tubb3
Map2
NeuN
Gfap
S100β
f
miR-153
Relative miRNA level
L-NSC+mc
L-NSC+m153
L-NSC+m153+H
L-NSC+m153+J
L-NSC+m153+H+J

Figure S4

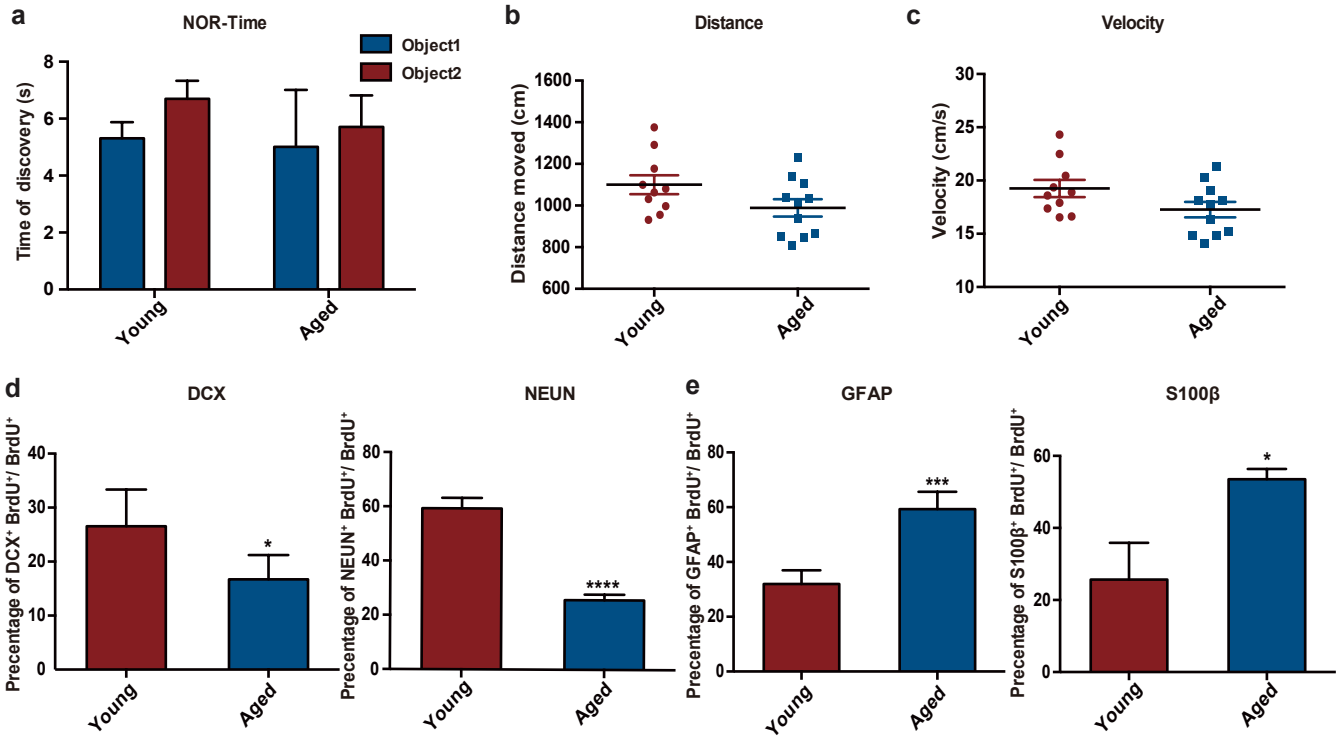

a
NOR-Time
Object1
Object2
Time of discovery (s)
Young
Aged
b
Distance
Distance moved (cm)
Young
Aged
c
Velocity
Velocity (cm/s)
Young
Aged
d
DCX
Precentage of DCX+ BrdU+/ BrdU+
*
Young
Aged
NEUN
Precentage of NEUN+ BrdU+/ BrdU+
****
Young
Aged
e
GFAP
Precentage of GFAP+ BrdU+/ BrdU+
***
Young
Aged
S100β
Precentage of S100β+ BrdU+/ BrdU+
*
Young
Aged

Figure S5

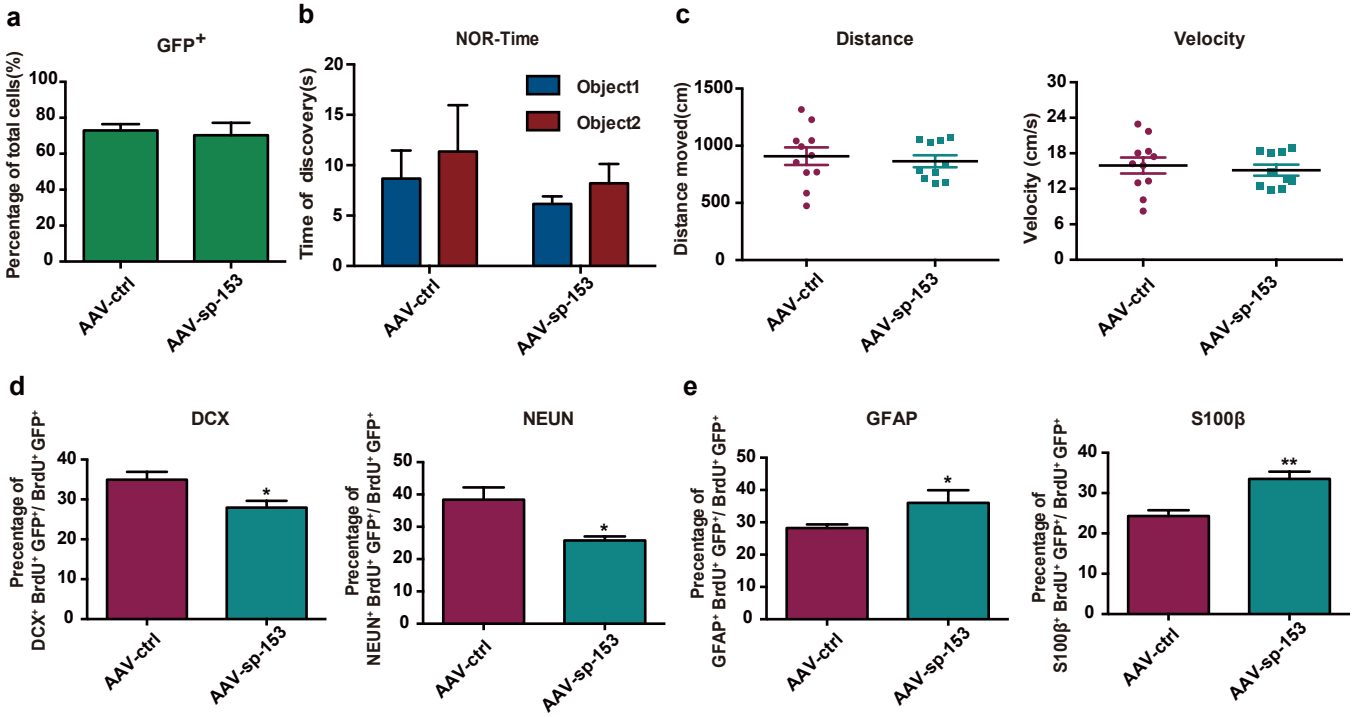

a
GFP+
Percentage of total cells(%)
AAV-ctrl
AAV-sp-153
b
NOR-Time
Time of discovery(s)
Object1
Object2
AAV-ctrl
AAV-sp-153
c
Distance
Distance moved(cm)
AAV-ctrl
AAV-sp-153
Velocity
Velocity (cm/s)
AAV-ctrl
AAV-sp-153
d
DCX
Precentage of DCX+ BrdU+ GFP+/ BrdU+ GFP+
AAV-ctrl
AAV-sp-153
NEUN
Precentage of NEUN+ BrdU+ GFP+/ BrdU+ GFP+
AAV-ctrl
AAV-sp-153
e
GFAP
Precentage of GFAP+ BrdU+ GFP+/ BrdU+ GFP+
AAV-ctrl
AAV-sp-153
S100β
Precentage of S100β+ BrdU+ GFP+/ BrdU+ GFP+
AAV-ctrl
AAV-sp-153

Figure S6

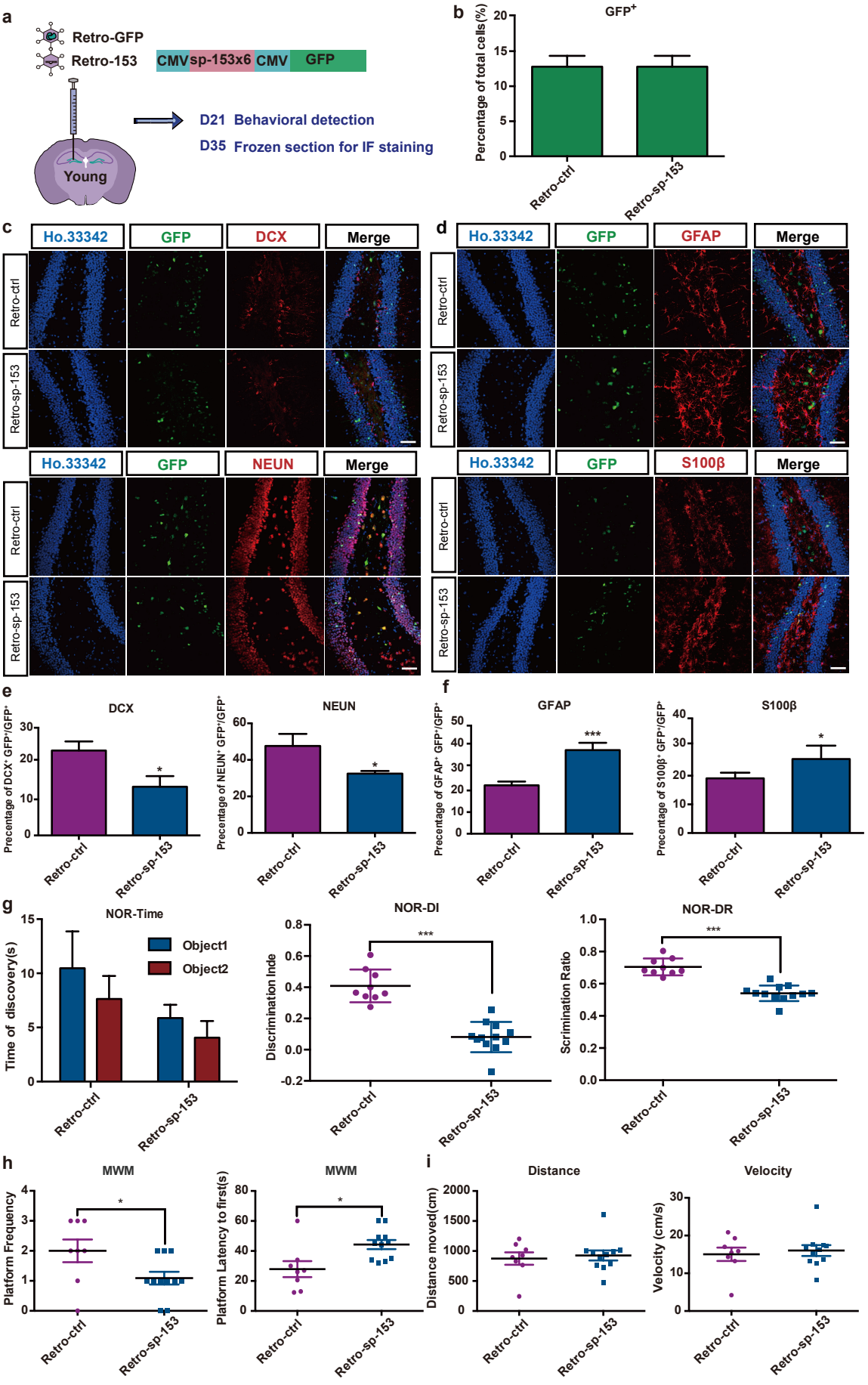

a
Retro-GFP
Retro-153
CMV sp-153x6 CMV GFP
D21 Behavioral detection
D35 Frozen section for IF staining
Young
b
GFP+
Percentage of total cells (%)
Retro-ctrl
Retro-sp-153
c
Ho.33342
GFP
DCX
Merge
NEUN
d
GFAP
S100β
e
DCX
NEUN
f
GFAP
S100β
g
NOR-Time
Object1
Object2
Time of discovery(s)
NOR-DI
Discrimination Inde
NOR-DR
Scrimination Ratio
h
MWM
Platform Frequency
Platform Latency to first(s)
i
Distance
Distance moved(cm)
Velocity
Velocity (cm/s)

Figure S7

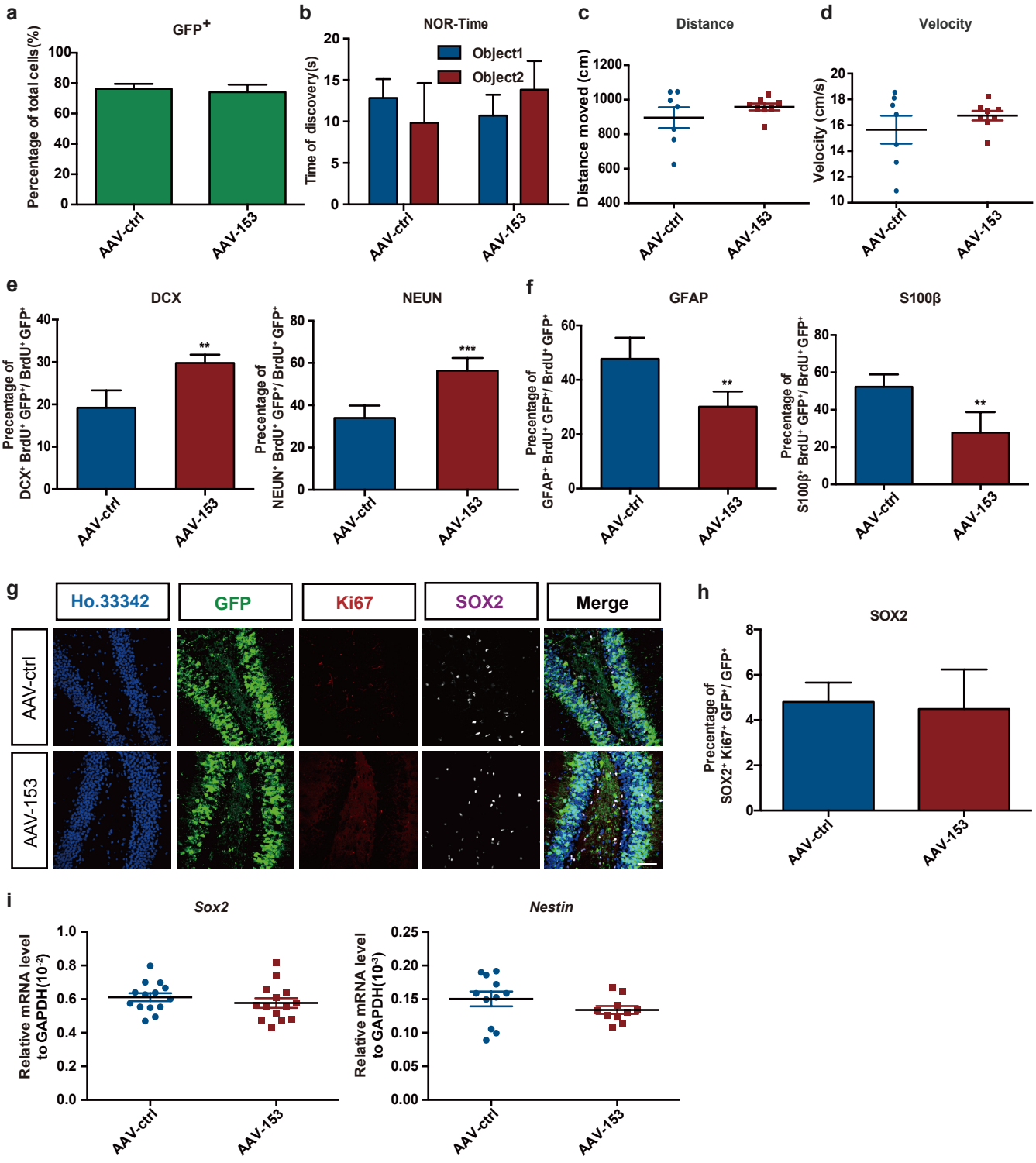

a
GFP+
Percentage of total cells(%)
AAV-ctrl
AAV-153
b
NOR-Time
Object1
Object2
Time of discovery(s)
c
Distance
Distance moved (cm)
d
Velocity
Velocity (cm/s)
e
DCX
Precentage of DCX+ BrdU+ GFP+/ BrdU+ GFP+
NEUN
Precentage of NEUN+ BrdU+ GFP+/ BrdU+ GFP+
f
GFAP
Precentage of GFAP+ BrdU+ GFP+/ BrdU+ GFP+
S100β
Precentage of S100β+ BrdU+ GFP+/ BrdU+ GFP+
g
Ho.33342
GFP
Ki67
SOX2
Merge
AAV-ctrl
AAV-153
h
SOX2
Precentage of SOX2+ Ki67+ GFP+/ GFP+
i
Sox2
Nestin
Relative mRNA level to GAPDH(10-2)
Relative mRNA level to GAPDH(10-3)

Figure S8

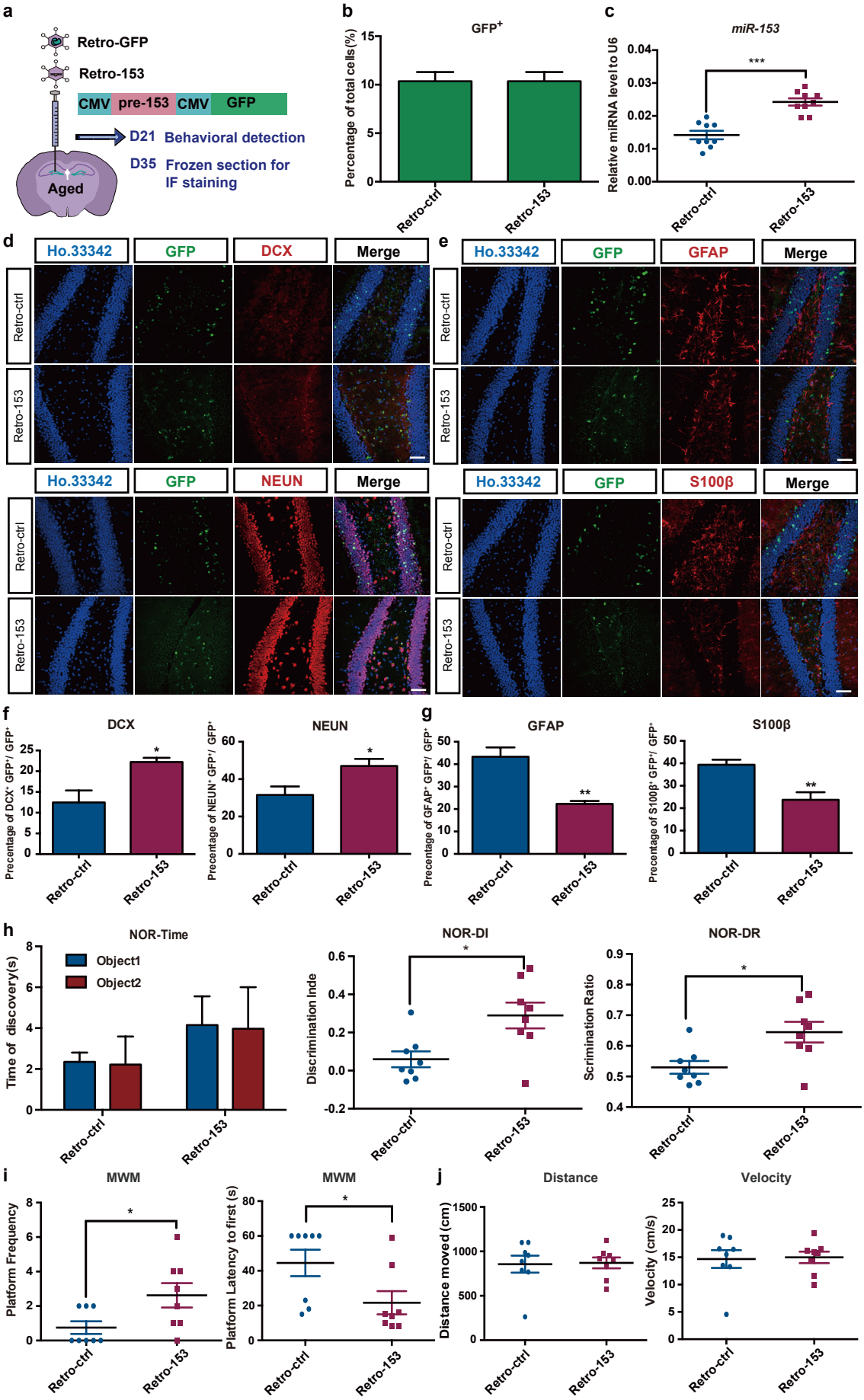
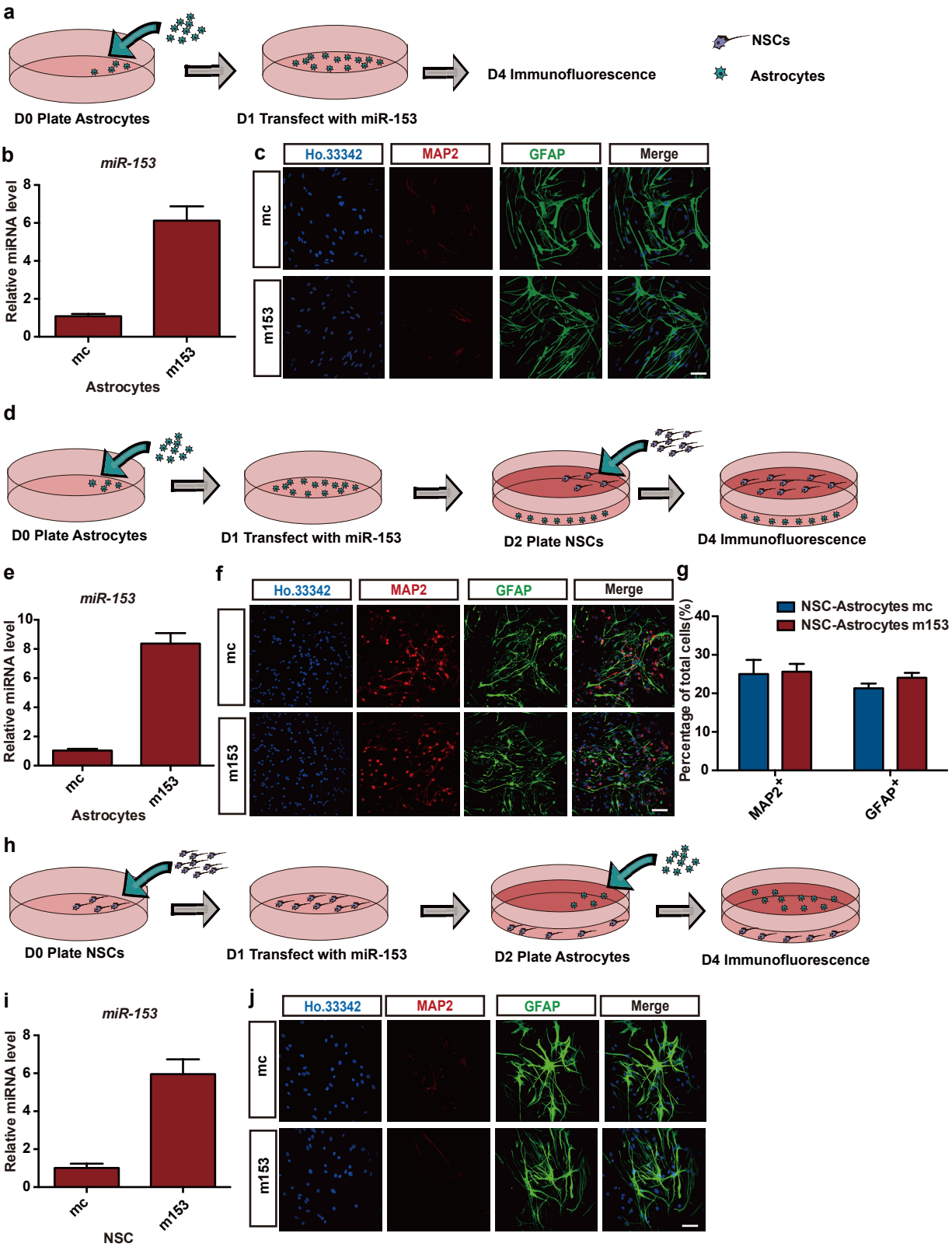

a
Retro-GFP
Retro-153
CMV pre-153 CMV GFP
D21 Behavioral detection
D35 Frozen section for IF staining
Aged
b
GFP+
Percentage of total cells (%)
Retro-ctrl
Retro-153
c
miR-153
Relative miRNA level to U6
***
d
Ho.33342
GFP
DCX
Merge
NEUN
e
GFAP
S100β
f
DCX
NEUN
Precentage of DCX+ GFP+/ GFP+
Precentage of NEUN+ GFP+/ GFP+
g
GFAP
S100β
Precentage of GFAP+ GFP+/ GFP+
Precentage of S100β+ GFP+/ GFP+
h
NOR-Time
Object1
Object2
Time of discovery(s)
NOR-DI
Discrimination Inde
NOR-DR
Scrimination Ratio
i
MWM
Platform Frequency
Platform Latency to first (s)
j
Distance
Velocity
Distance moved (cm)
Velocity (cm/s)

Figure S9


a
D0 Plate Astrocytes
D1 Transfect with miR-153
D4 Immunofluorescence
NSCs
Astrocytes
b
miR-153
Relative miRNA level
mc
m153
Astrocytes
c
Ho.33342
MAP2
GFAP
Merge
mc
m153
d
D0 Plate Astrocytes
D1 Transfect with miR-153
D2 Plate NSCs
D4 Immunofluorescence
e
miR-153
Relative miRNA level
mc
m153
Astrocytes
f
Ho.33342
MAP2
GFAP
Merge
mc
m153
g
NSC-Astrocytes mc
NSC-Astrocytes m153
Percentage of total cells(%)
MAP2+
GFAP+
h
D0 Plate NSCs
D1 Transfect with miR-153
D2 Plate Astrocytes
D4 Immunofluorescence
i
miR-153
Relative miRNA level
mc
m153
NSC
j
Ho.33342
MAP2
GFAP
Merge
mc
m153

Supplementary figure legends

Figure S1. Related to Figure 2. a-e Flow cytometry detection of percentage of cy5-positive cells at 48h post transfection with mock(a), mc-cy5(b), m153-cy5(c), ic-cy5(d), i153-cy5(e). **f** Quantitative RT-PCR detection of miR-153 in L-NSC+mc and L-NSC+m153. U6 was used as an internal control for the normalization in quantitative RT-PCR. **g** Quantitative RT-PCR detection of wpre in E-NSCs-ctrl and E-NSC-Lenti-sp-153-wpre (infection with Lenti-sp-153-wpre virus). **h** Quantitative RT-PCR detection of neuron-related genes and glial cell-related genes in the neural differentiation of E-NSCs-ctrl or E-NSC-Lenti-sp-153-wpre. **i** Immunofluorescence analysis of neural differentiation with E-NSCs-ctrl or E-NSC+Lenti-sp-153-wpre as evaluated by MAP2 (red), GFAP (green) and Ho.33342 (blue). Scale bar: 50 μm. **j** Percentage of MAP2-positive or GFAP-positive cells in neural differentiation. Data information: The data shown are the mean±SEM, n=3; ANOVA; ***p<0.001, **p<0.01. Abbreviations: L-NSCs, late NSCs; E-NSCs, early NSCs; mc, control mimics; m153, miR-153 mimics; ic, control inhibitor; i153, miR-153 inhibitor; Lenti-sp-153-wpre, Lenti-sponge-153-wpre.

Figure S2. Related to Figure 3. Quantitative RT-PCR detection of miR-153 in L-NSC+mc, L-NSC+m153, L-NSC+Dll4 and L-NSC+m153+Dll4 groups; Data shown are the mean±SEM, n=3; U6 was used as an internal control for the normalization in quantitative RT-PCR. Abbreviations: L-NSCs, late NSCs; E-NSCs, early NSCs; mc, control mimics; m153, miR-153 mimics.

Figure S3. Related to Figure 4. a The sequence of miR-153-3p and the binding sites of miR-153-3p in 3'UTR of Hey2 and Jag1 in different species. **b** Western blot assay for measuring the HEY2 protein levels normalized to β-TUBULIN in ctrl, shHey2-1 and shHey2-2 groups of NSCs. **c** Quantitative RT-PCR detection of neuron-related genes (*Tubb3, Map2, NeuN*) and glial cell-related genes (*Gfap, S100β*) in neural differentiation of ctrl, shHey2-1 and shHey2-2 groups. **d** Western blot assay for measurements of JAG1, HEY1 and HES1 proteins in ctrl, shJag1-1 and shJag1-2 groups of NSCs, normalized to β-TUBULIN. **e** Quantitative RT-PCR detection of neuron-related genes and glial cell-related genes in neural differentiation of ctrl, shJag1-1 and sh Jag1-2 groups. **f** Quantitative RT-PCR detection of miR-153 in L-NSCs+mc, L-NSCs+m153, L-NSCs+m153+H, L-NSCs+m153+J and L-NSCs+m153+H+J groups. Data information: The data shown are the mean±SEM, n=3; ANOVA; ***p<0.001, **p<0.01, *<0,05. Abbreviations: L-NSCs, late NSCs; E-NSCs, early NSCs; mc, control mimics; m153, miR-153 mimics; H, Hey2; J, Jag1.

Fig. S4 Related to Figure 5. a Exploration time for different objects in young and aged mice; young, n = 9; aged, n = 9. **b, c** Movement distance and speed of young and aged mice during the water maze test; young, n = 10; aged, n = 10. **d, e** Percentage of BrdU+ cells expressing either DCX, NEUN, GFAP, or S100β; n = 3 brains; ANOVA; ****p<0.0001,

***p<0.001, *p<0.05. Data information: The data shown are the mean±SEM. Abbreviations: young mice, 8-10 weeks old; aged mice, 16-18 months old; NOR, novel object recognition.

Fig S5. Related to Figure 6. a Percentage of GFP positive cells in hippocampus three weeks post injection AAV-ctrl or AAV-sp-153; n = 3 brains. **b** Exploration time for different objects for the AAV-ctrl or AAV-sp-153 mice; AAV-ctrl, n=9; AAV-sp-153, n=9. **c** Movement distance and speed of the AAV-ctrl or AAV-sp-153 mice during the water maze test; AAV-ctrl, n = 11; AAV-sp-153, n = 10. **d, e** Percentage of GFP^+/$BrdU^+$ cells expressing either DCX, NEUN, GFAP, or S100β; n = 3 brains; ANOVA; **p<0.01, *p<0.05. Data information: The data shown are the mean±SEM. Abbreviations: AAV-sp-153, AAV-sponge-153; young mice, 8-10 weeks old; NOR, novel object recognition.

Fig S6. Inhibition of miR-153 with Retro-sp-153 decreases hippocampal neurogenesis and impairs the cognitive function of young mice. a Schematic of virus injection into the hippocampi of young mice and the process diagram of detection. **b** Percentage of GFP positive cells in hippocampus three weeks post injection Retro-ctrl or Retro-sp-153; n = 3 brains. **c** Immunofluorescence analysis of neurons in the hippocampi of Retro-ctrl or Retro-sp-153 young mice, as evaluated by GFP (green), DCX (red), NEUN (red), and Ho.33342 (blue). Scale bar: 50 μm. **d** Immunofluorescence analysis of astrocytes in the hippocampi of Retro-ctrl or Retro-sp-153 mice, as evaluated by GFP (green), GFAP (red), S100β (red), and Ho.33342 (blue). Scale bar: 50 μm. **e, f** Percentage of GFP^+ cells expressing either DCX, NEUN, GFAP, or S100β; n = 3 brains; ANOVA; ***p<0.001, *p<0.05. **g** Exploration time for different objects and discrimination index and discrimination ratio of novel objects; Retro-ctrl, n=9; Retro-sp-153, n=12; Student's t test; ***p<0.001. **h** Platform crossings and the amount of time for the mice to first reach the platform area during the water maze test; Retro-ctrl, n=8; Retro-sp-153, n=11; Student's t test; *p<0.05. **i** Movement distance and speed of the Retro-ctrl or Retro-sp-153 mice during the water maze test; Retro-ctrl, n=8; Retro-sp-153, n=11. Data information: The data shown are the mean±SEM Abbreviations: Retro-sp-153, Retro-sponge-153. Abbreviations: young mice, 8-10 weeks old; NOR, novel object recognition; MWM, Morris water maze.

Fig S7. Related to Figure 7. a Percentage of GFP positive cells in hippocampus three weeks post injection AAV-ctrl or AAV-sp-153; n = 3 brains. **b** Exploration time for different objects for the AAV-ctrl or AAV-153 mice during testing; AAV-ctrl, n=7; AAV-153, n=11. **c, d** Movement distance and speed of AAV-ctrl and AAV-153during the water maze test; Data shown are the mean ± SEM; AAV-ctrl, n = 7; AAV-153, n = 8. **e, f** Percentage of GFP+/BrdU+ cells expressing either DCX, NEUN, GFAP, or S100β; n = 3 brains; ANOVA; ***p<0.001, **p<0.01. **g** Immunofluorescence analysis of NSCs in the hippocampi of AAV-ctrl or AAV-153 mice, as evaluated by GFP (green), Ki67 (red), SOX2 (white), and Ho.33342 (blue). Scale bar: 50 μm. **h** Percentage of GFP^+ cells expressing either SOX2/Ki67; Data shown are the mean percentage ± SEM; n = 3 brains. **i** Quantitative RT-PCR detection of the NSCs markers *Sox2*; AAV-ctrl, n=14; AAV-153, n=14; and *Nestin*; AAV-ctrl, n=11; AAV-153, n=10; in the hippocampi of young or aged mice. Data

information: The data shown are the mean±SEM. Abbreviations: aged mice, 16-18 months old; NOR, novel object recognition.

Fig S8. Retro-153 increases adult neurogenesis in the hippocampus and enhances the cognitive ability of aged mice. a Schematic of retro virus injection into the hippocampi of aged mice and the process diagram of detection. **b** Percentage of GFP positive cells in hippocampus three weeks post injection Retro-ctrl or Retro-153; n = 3 brains. **c** Quantitative RT-PCR detection of miR-153 in the hippocampi of Retro-ctrl or Retro-153 mice; Retro-ctrl, n=9; Retro-153, n=9; Student's t test; ***p<0.001. **d** Immunofluorescence analysis of neurons in the hippocampi of Retro-ctrl or Retro-153 young mice, as evaluated by GFP (green), DCX (red), NEUN (red), and Ho.33342 (blue). Scale bar: 50 μm. **e** Immunofluorescence analysis of astrocytes in the hippocampi of Retro-ctrl or Retro-153 mice, as evaluated by GFP (green), GFAP (red), S100β (red), and Ho.33342 (blue). Scale bar: 50 μm. **f, g** Percentage of GFP^+ cells expressing either DCX, NEUN, GFAP, or S100β; n = 3 brains; ANOVA; **<0.01, *p<0.05. **h** Exploration time for different objects and discrimination index and discrimination ratio of novel objects; Retro-ctrl, n=8; Retro-153, n=8; Student's t test; *p<0.05. **i** Platform crossings and the amount of time for the mice to first reach the platform area during the water maze test; Retro-ctrl, n=8; Retro-153, n=8; Student's t test; *p<0.05. **j** Movement distance and speed of the Retro-ctrl or Retro-153 mice during the water maze test; Retro-ctrl, n=8; Retro-153, n=8. Data information: The data shown are the mean±SEM. Abbreviations: aged mice, 16-18 months old; NOR, novel object recognition; MWM, Morris water maze.

Fig S9. MiR-153 could not convert astrocytes into neurons. a Schematic of transdifferentiation of astrocytes with miR-153 overexpression. **b** Quantitative RT-PCR detection of miR-153 in astrocytes. **c** Immunofluorescence analysis of transdifferentiation of astrocytes after 4 days transfection with mc or miR-153, as evaluated by GFAP (green), MAP2 (red), and Ho.33342 (blue). Scale bar: 50 μm. **d** Schematic of neural differentiation of NSCs co-culture with astrocytes. **e** Quantitative RT-PCR detection of miR-153 in astrocytes. **f** Immunofluorescence analysis of neural differentiation of NSCs co-culture with astrocytes transfection with mc or m153, as evaluated by MAP2 (red), GFAP (green) and Ho.33342 (blue). Scale bar: 50 μm. **j** Percentage of MAP2-positive or GFAP-positive cells in neural differentiation. **h** Schematic of transdifferentiation of astrocytes co-culture with NSCs. **i** Quantitative RT-PCR detection of miR-153 in NSCs. **g** Immunofluorescence analysis of neural transdifferentiation of astrocytes co-culture with NSCs transfection with mc or m153, as evaluated by MAP2 (red), GFAP (green) and Ho.33342 (blue). Scale bar: 50 μm. Data information: The data shown are the mean±SEM; n=3.

Supplementary table 1. Antibodies list

Antibody	Company	Cat	Concentration
β-tubulin	Bioworld	ap0064	1:2 000
Hey2	Proteintec	10597-1-AP	1:1 000
Hey1	Abcam	ab154077	1:1 000
Hes1	Abcam	ab71559	1:1 000
NICD	Cell Signaling technology	4147S	1:1 000
Jag1	Cell Signaling technology	2620S	1:1 000
Map2	Abcam	ab32454	1:3 000
Gfap	Millipro	MAB360	1:1 000
NeuN	Millipro	ABN78	1:1 000
Dcx	Abcam	ab18723	1:1 000
S100β	Abcam	ab11178	1:1 000
BrdU	Abcam	ab6326	1:1 000
Sox2	R&D systems	AF2018	1:1 000
Ki67	Abcam	ab15580	1:1 000

Supplementary table 2. Primers list1

Application	Gene	Forward primer	Reverse primer	The efficacy of primer	The value of Ct in cell	The value of Ct in tissues
QPCR	Gapdh	AGGTCGGTGTGA ACGGATTTG	TGTAGACCATGT AGTTGAGGTCA	108.0%	17-19	14-16
QPCR	Tuj1	TAGACCCCAGCG GCAACTAT	GTTCCAGGTTCC AAGTCCACC	98.9%	24-27	／
QPCR	Map2	GGTCACAGGGCA CCTATTCA	TGTTCACCTTTC AGGACTGC	102.4%	21-24	／
QPCR	NeuN	GGGTATGGGTAG GATTGGGG	GTGGAAGGTTTC ACTACAACAGA	97.0%	28-31	21-23
QPCR	Dcx	GGCCAAGAAGGT ACGTTTCTAC	AGCAACGCATCA AAACTACGAA	100.8%	／	23-25
QPCR	Gfap	ACCAGCTTACGG CCAACAG	CCAGCGATTCAA CCTTTCTCT	97.8%	25-28	18-20
QPCR	S100β	TGGTTGCCCTCAT TGATGTCT	CCCATCCCCATC TTCGTCC	111.5%	21-24	22-23.5
QPCR	Sox2	GCGGAGTGGAAA CTTTTGTCC	CGGGAAGCGTGT ACTTATCCTT	104.3%	／	21-22.5
QPCR	Nestin	CTGCAGGCCACT GAAAAGTT	GACCCTGCTTCT CCTGCTC	106.7%	／	26-28
QPCR	Wpre	CCTTTTACGCTAT GTGGATACGCTG	CGTCAGCAAACA CAGTGCACACC	109.1%	19-23	／
QPCR	Hey2	AGTCAACCCCAT GTCGCCTAT	TGGCATCCGAAG AGCAGAATC	110.6%	28-29	／
QPCR	Jag1	CCTCGGGTCAGTT TGAGCTG	CCTTGAGGCACA CTTTGAAGTA	104.5%	25-26	／
QPCR	miR-153	Obtained from RiboBio company	Obtained from RiboBio company	99.2%	20-27	14-27
QPCR	U6	Obtained from RiboBio company	Obtained from RiboBio company	103.5%	14-16	11-13

Supplementary table 3. Primers list2

Application	Gene	Forward primer	Reverse primer
PCR	Pre-miR-153	TTTGAGCTGCTCCTTGTAATGTGTC	AAAAATTAGACTCCAAGCTGGGCGT
Sponge	Sponge-miR-153	AATTCGATCACTTTTACTCTATGCAACCGGATCACTTTTACTCTATGCAAGCGGATCACTTTTACTCTATGCAAG	GATCCTTGCATAGAGTAAAAGTGATCCGCTTGCATAGAGTAAAAGTGATCCGGTTGCATAGAGTAAAAGTGATCG
ShRNA	ShHey2-1	CCGGCCTCTCAGATTATGGCAAGAACTCGAGTTCTTGCCATAATCTGAGAGGTTTTTG	AATTCAAAAACCTCTCAGATTATGGCAAGAACTCGAGTTCTTGCCATAATCTGAGAGG
ShRNA	ShHey2-2	CCGGCTCTCAGATTATGGCAAGAAACTCGAGTTTCTTGCCATAATCTGAGAGTTTTTG	AATTCAAAAACTCTCAGATTATGGCAAGAAACTCGAGTTTCTTGCCATAATCTGAGAG
ShRNA	ShJag1-1	CCGGACATCTGCCAGCGGTCCTAATCTCGAGATTAGGACCGCTGGCAGATGTTTTTTG	AATTCAAAAAACATCTGCCAGCGGTCCTAATCTCGAGATTAGGACCGCTGGCAGATGT
ShRNA	ShJag1-2	CCGGGCTCTGTCTTAACAGTGGCTTCTCGAGAAGCCACTGTTAAGACAGAGCTTTTTG	AATTCAAAAAGCTCTGTCTTAACAGTGGCTTCTCGAGAAGCCACTGTTAAGACAGAGC

DECLARATION OF CONTRIBUTIONS TO ARTICLE

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Author(s): Jing Qiao , Jinping Zhao, Shujuan Chang, Qiaoyi Sun, Nana Liu, Jianfeng Dong, [illegible] (the 'Authors')

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Any person who cannot be shown to have made a substantial contribution to the article cannot be listed as an author in the final version. The name of any person who is deemed to have made a minor contribution can, however, appear in the Acknowledgments section of the article.

Please complete the table below to indicate the contributions of all named authors to the manuscript.

Author Full Name:	Specification of Contribution to the Manuscript:
Jing Qiao	Designed experiments, performed most of the experiments, [illegible]
Jiuhong Kang, Jiajie Xi	Designed experiments and helped write the manuscript
Jinping Zhao, Shujuan Chang,	Helped complete the animal experiments
Nana Liu	Helped complete the animal experiments and acquisition of [illegible]
Jianfeng Dong	Helped complete the animal experiments and acquisition of data [illegible]
Yafang Chen	Performed sectional experiments and acquisition of sectional [illegible]
Dandan Yang	Helped design the experiments
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Xiaoqin Liu, Yangyang Yu	Helped complete the molecule experiments
Wen Chen	Helped design the experiments
Songcheng Zhu	Helped complete the hippocampal positioning injection
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Figure 1:

Jing Qiao generated the data of A-G, prepared panel A-G and assembled the figure
Yafang Chen generated the data of AJing Qiao generated the data of A-F, prepared panel A-F and assembled the figure
Jiuhong Kang and Jiajie Xi helped assembled the figure

Figure 2:

Jing Qiao generated the data of A-F, prepared panel A-F and assembled the figure
Jiuhong Kang and Jiajie Xi helped assembled the figure

Figure 3:

Jing Qiao generated the data of A-K, prepared panel A-K and assembled the figure
Jiuhong Kang and Jiajie Xi helped assembled the figure

Figure 4:

Jing Qiao generated the data of A-J, prepared panel A-J and assembled the figure
Yafang Chen generated the data of panel A and B
Jiuhong Kang and Jiajie Xi helped assembled the figure

Figure 5:

Jing Qiao generated the data of A-I, prepared panel A-I and assembled the figure
Jinping Zhao helped complete the animal experiments inculde C,D,G
Nana Liu helped generated the data of A,B
Jianfeng Dong helped generated the data of A,B
Jiuhong Kang and Jiajie Xi helped assembled the figure

Figure 6:

For Figure6, Jing Qiao generated the data of A-I, prepared panel A-I and assembled the figure
Shujuan Chang and Qiaoyi Sun helped complete the animal experiments inculde B-D
Jiuhong Kang and Jiajie Xi helped assembled the figure

For Figure7

Signed for and on behalf of the Author(s):	Print Name:	Date:
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