**Figure S1.** Generation of *Cdh1* gene-trap mice. ***a.*** A diagram depicting the gene-trapped allele of Cdh1. Arrowheads indicating the position of genotyping primers. ***b.*** PCR genotyping of embryos from an intercross of $Cdh1^{+/gt}$ mice. ***c.*** Western blotting analysis of Cdh1 in E9.5 embryo. ***d*** and ***e.*** LacZ staining of an E9.5 $Cdh1^{+/gt}$ embryo (***d***) and placenta (***e***). Scale bar, 10 μm.

**Figure S2**. Mitotic defects in $Cdh1^{gt/gt}$ MEFs. ***a.*** Distribution of mitotic phases. ***b.*** Micrographs of MEFs stained for tubulin (red) and DNA (blue). Arrows indicate binucleated cells. Scale bar, 40 μm. ***c.*** Quantitation of binucleated cells in ***b***. Results in ***a*** and ***c*** were from three independent experiments. Error bars are standard deviations.

**Figure S3.** Suppression of growth defects of *Cdh1* null MEFs by depleting *Ets2*. ***a.*** Western blot analysis of Ets2 and p16. Full scan of the gel is presented in supplemental figure 5. ***b.*** Quantitation of the results in ***a***. ***c.*** Growth curve analysis of control- and *Ets2*-shRNA treated *Cdh1* null MEFs at passage 6. Data were obtained from triplicates at each time point. Error bars represent standard deviations.

**Figure S3.** Potential function of *Cdh1* in the brain. ***a.*** β-gal staining of adult $Cdh1^{+/gt}$ brain. Scale bar, 20 μm. ***b.*** Immunoblotting of Cdh1 in adult hippocampus. ***c.*** Plot of fEPSP slope versus fiber volley amplitude. Error bars indicate SEM for ten determinations. ***d.*** Paired-pulse facilitation in wildtype and $Cdh1^{+/gt}$ mice. Shown were responses to paired pulses in which the fEPSP slope of the response to the second stimulus was expressed as a percentage of the fEPSP slope of the response to the first

stimulus plotted against the interpulse interval of the paired pulses. Error bars indicate SEM for 17 determinations.

**Figure S5.** Full gel scans of selected Western blots.

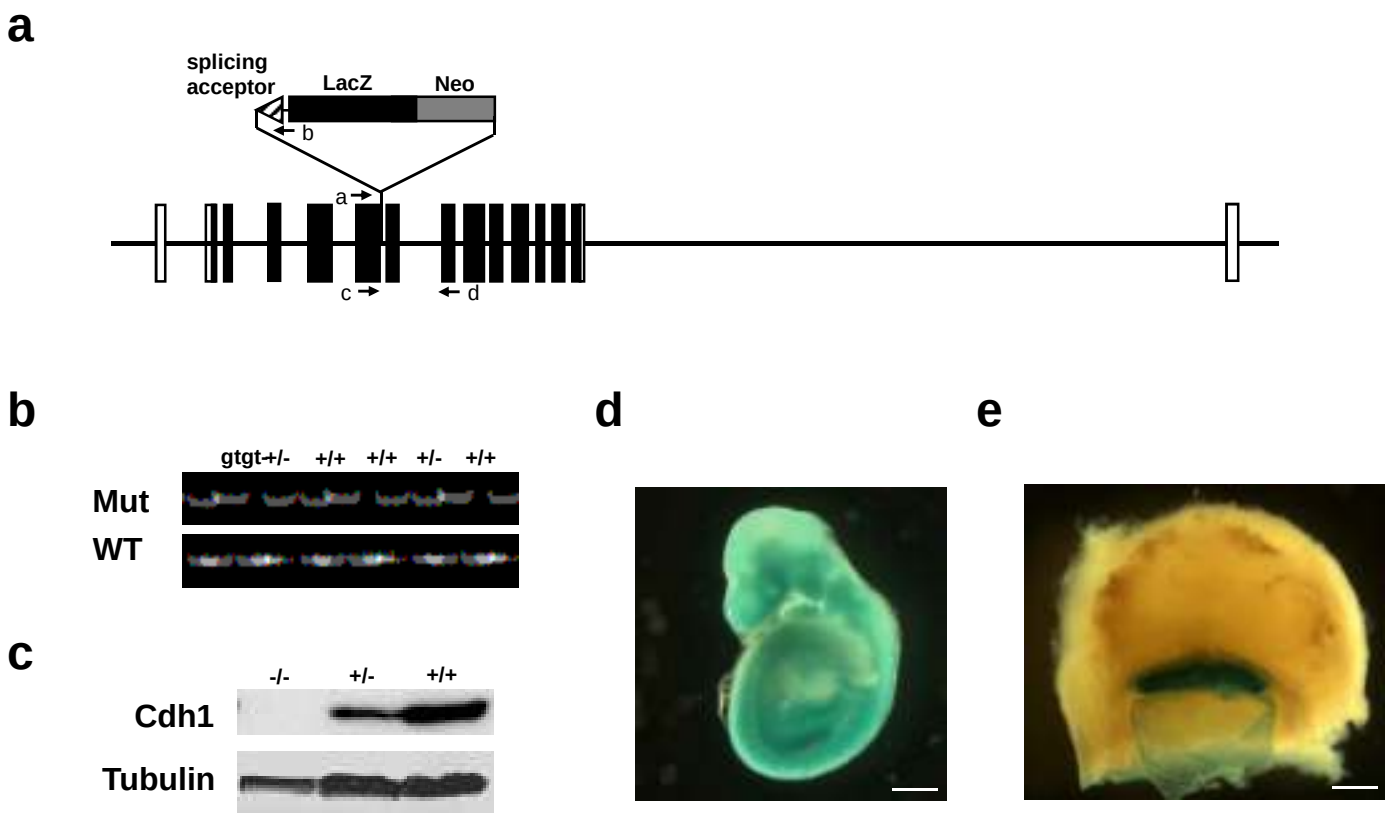

a
splicing acceptor
LacZ
Neo
b
a
c
d
b
gtgt+/-
+/+
+/+
+/-
+/+
Mut
WT
c
-/-
+/-
+/+
Cdh1
Tubulin
d
e

**Figure S1**

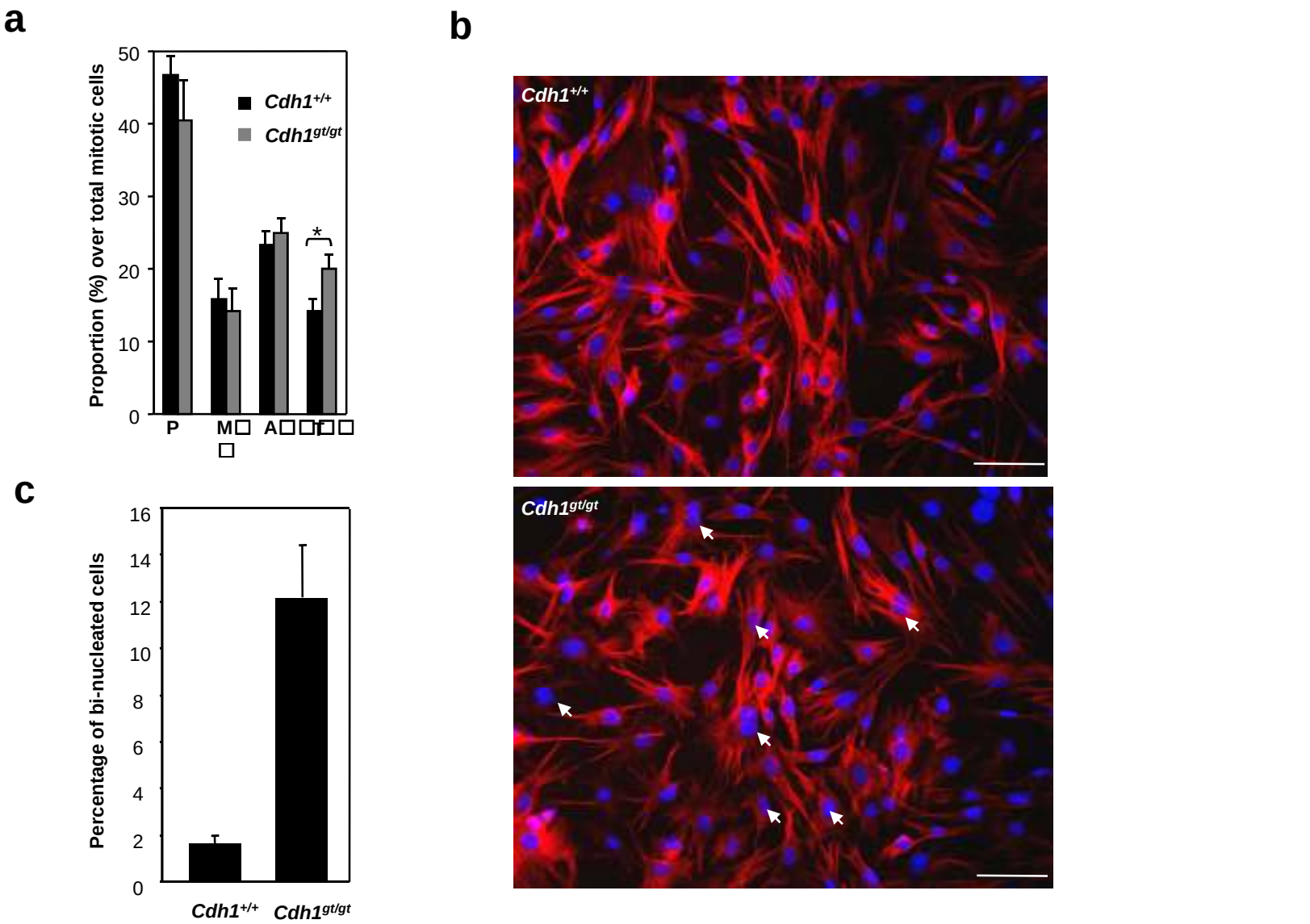

a
Proportion (%) over total mitotic cells
50
40
30
20
10
0
Cdh1+/+
Cdh1gt/gt
*
P
M
A
T
b
Cdh1+/+
Cdh1gt/gt
c
Percentage of bi-nucleated cells
16
14
12
10
8
6
4
2
0
Cdh1+/+
Cdh1gt/gt

Figure S2

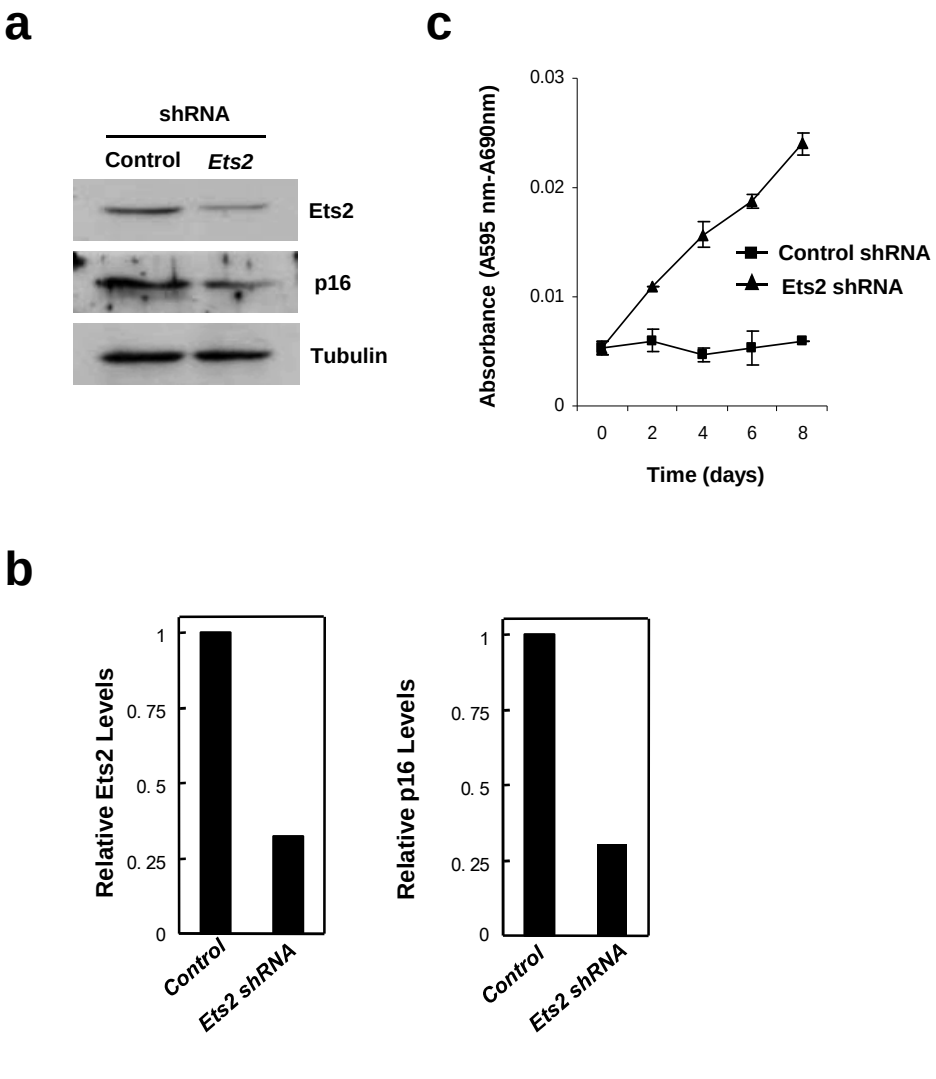
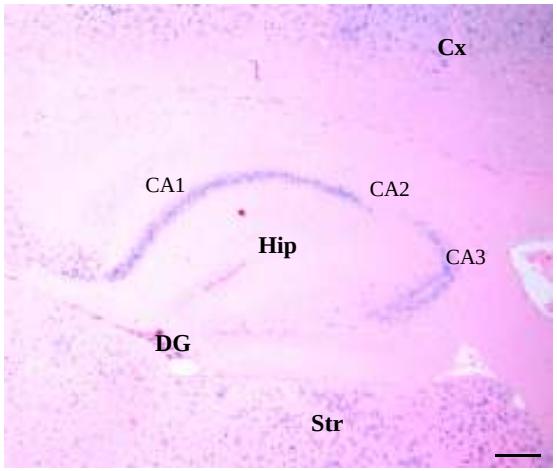
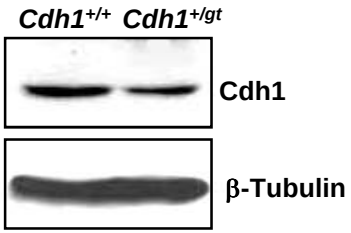

a
shRNA
Control
Ets2
Ets2
p16
Tubulin
c
Absorbance (A595 nm-A690nm)
0.03
0.02
0.01
0
0
2
4
6
8
Time (days)
Control shRNA
Ets2 shRNA
b
Relative Ets2 Levels
1
0. 75
0. 5
0. 25
0
Control
Ets2 shRNA
Relative p16 Levels
1
0. 75
0. 5
0. 25
0
Control
Ets2 shRNA

**Figure S3**

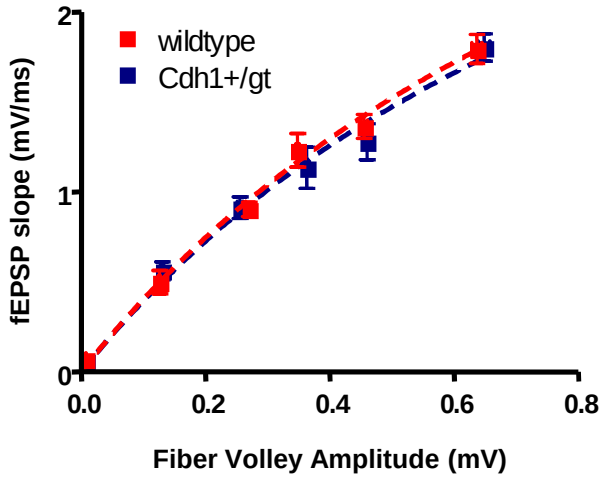
a




b




c




d

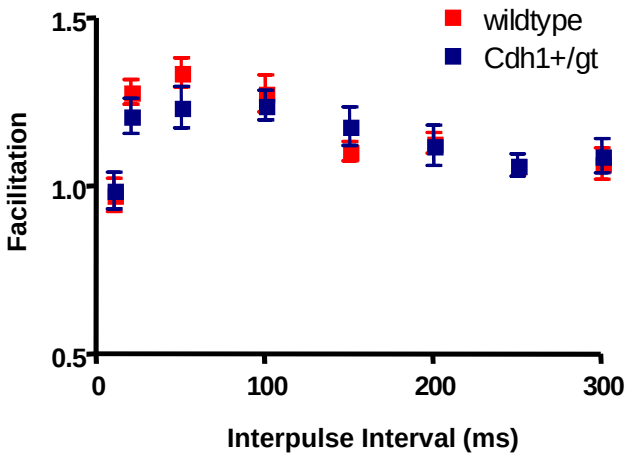
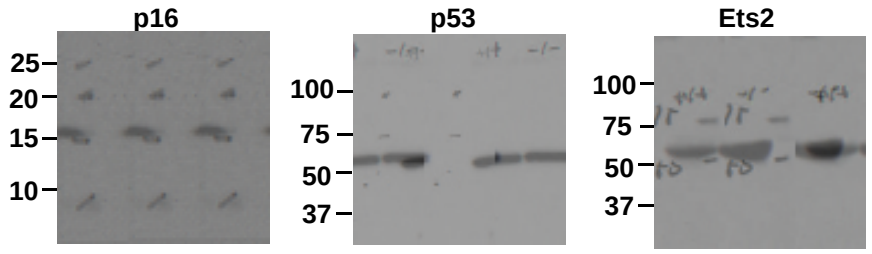
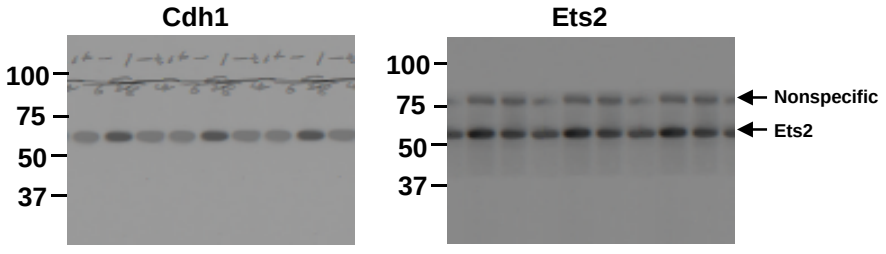



**Figure S4**

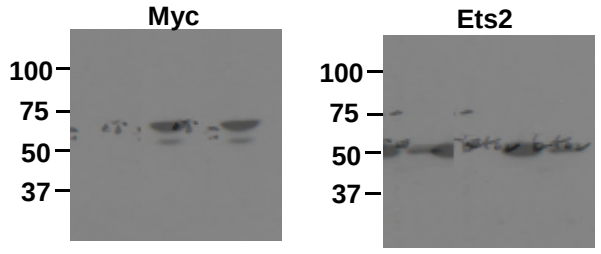
## Figure 3a



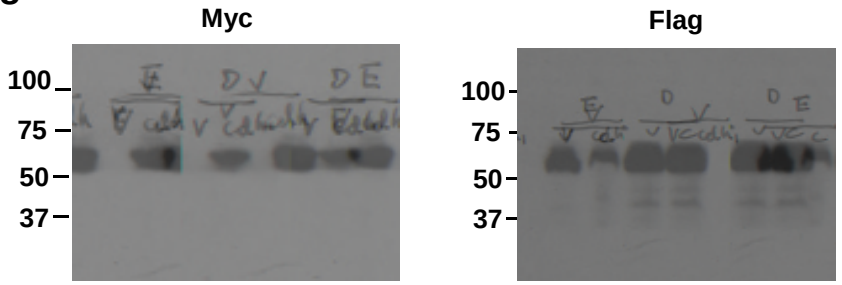

## Figure 3e



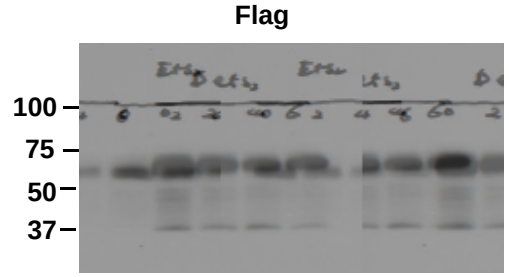

## Figure 3g



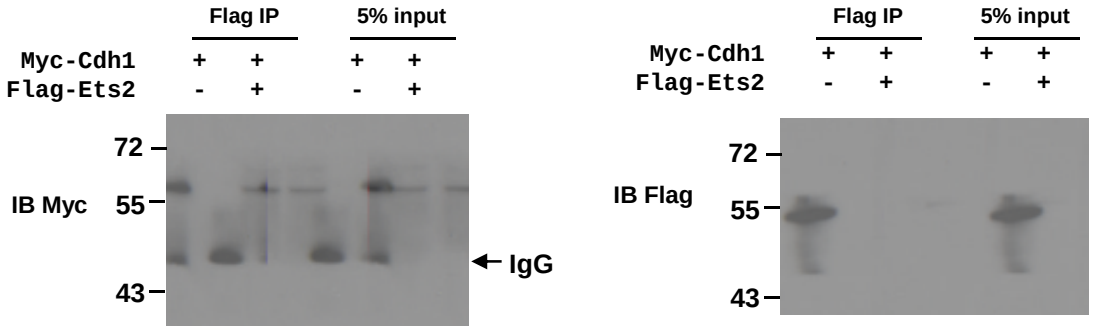

## Figure 4a



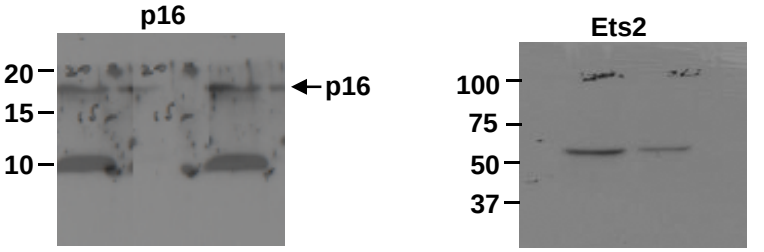

## Figure 4b




## Figure 4d




## Figure S3a




## Figure S5