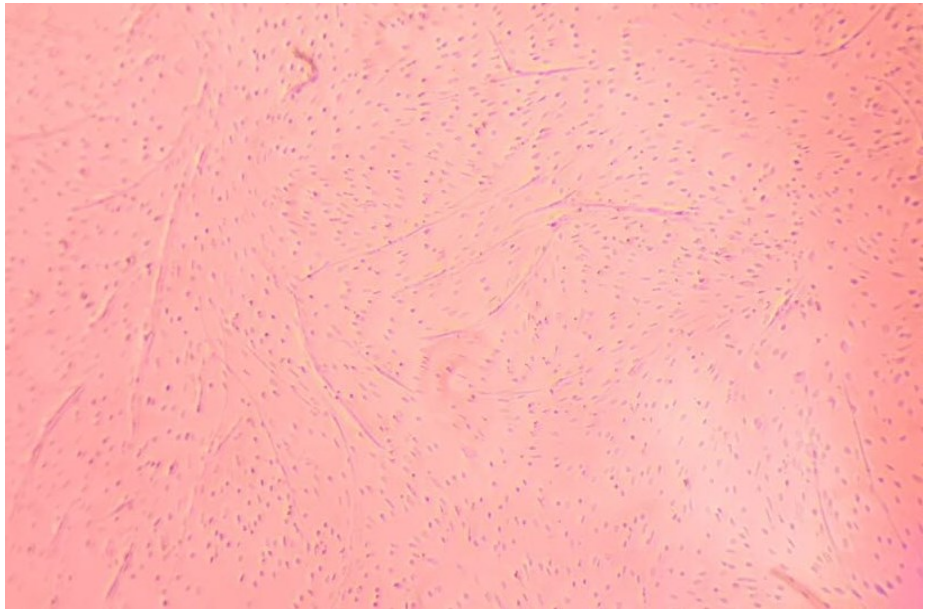
Figure S1



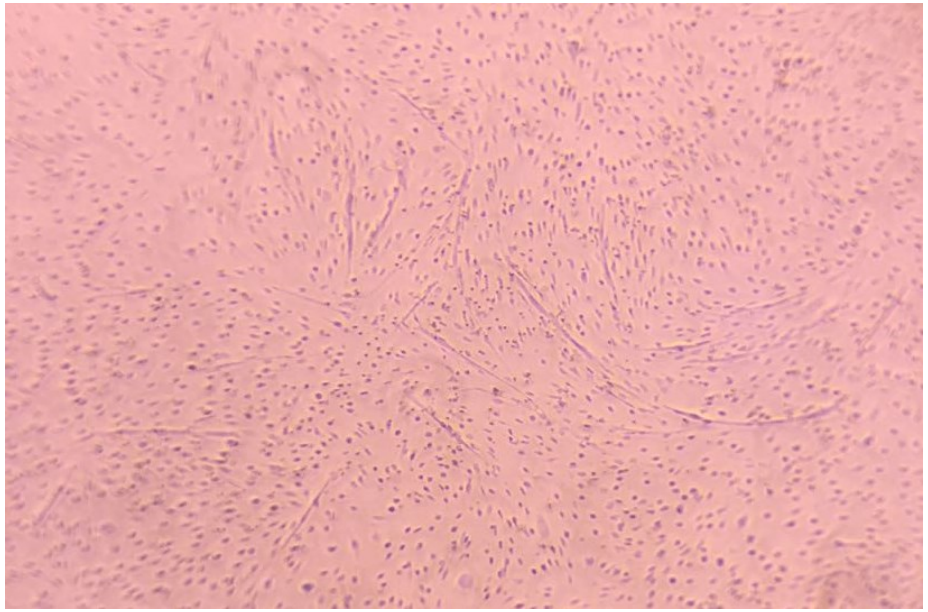


Figure S2

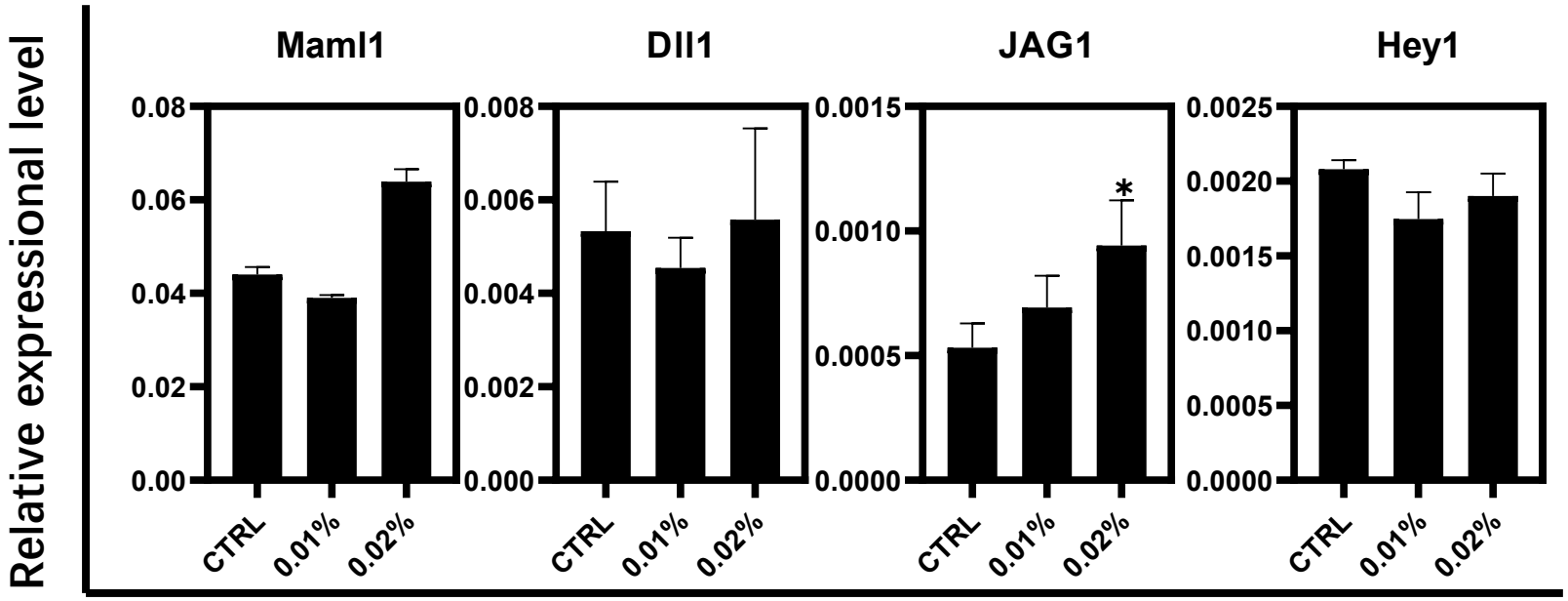
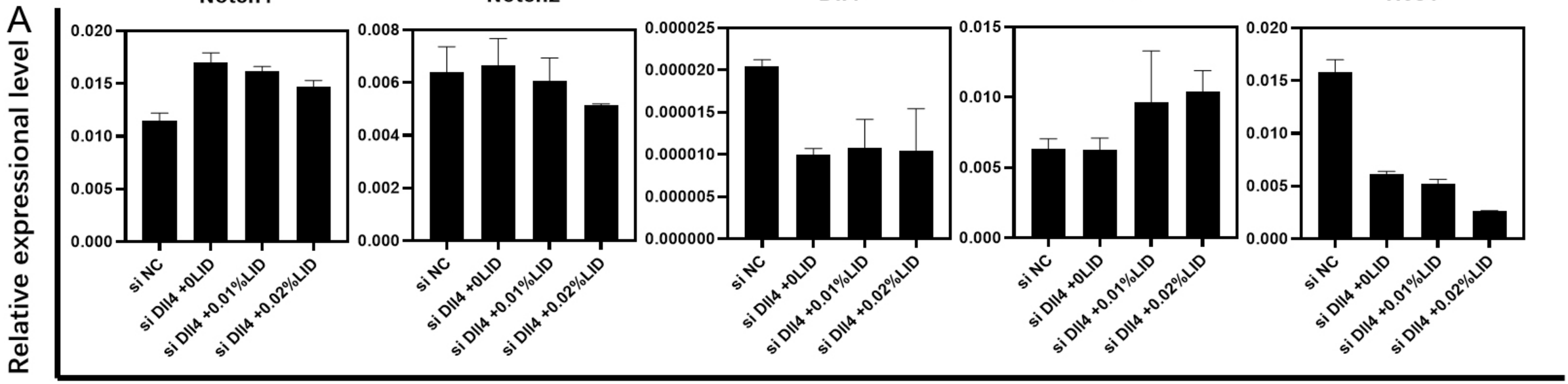
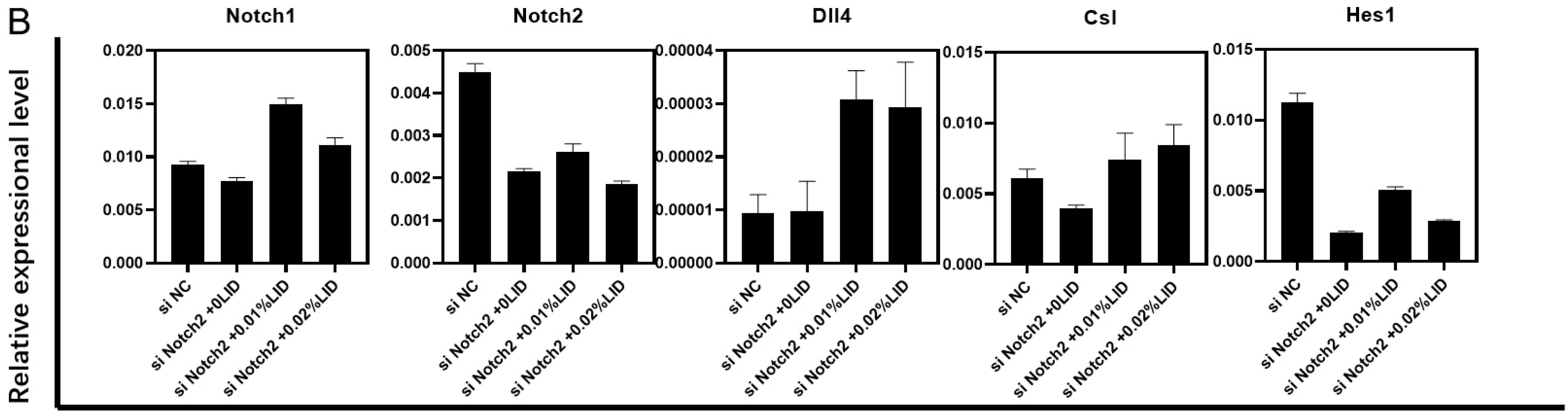

Relative expressional level
Maml1
Dll1
JAG1
Hey1
0.08
0.06
0.04
0.02
0.00
0.008
0.006
0.004
0.002
0.000
0.0015
0.0010
0.0005
0.0000
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000
*
CTRL
0.01%
0.02%

Figure S3


A
Relative expressional level
Notch1
Notch2
Dll4
Csl
Hes1
si NC
si Dll4 +0LID
si Dll4 +0.01%LID
si Dll4 +0.02%LID


B
Relative expressional level
Notch1
Notch2
Dll4
Csl
Hes1
si NC
si Notch2 +0LID
si Notch2 +0.01%LID
si Notch2 +0.02%LID

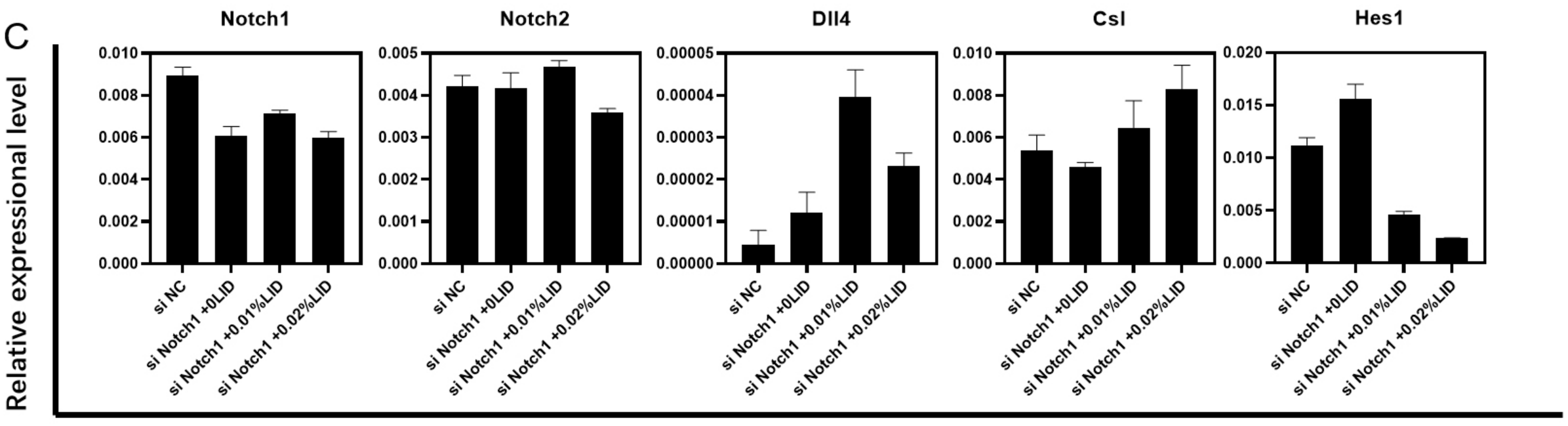
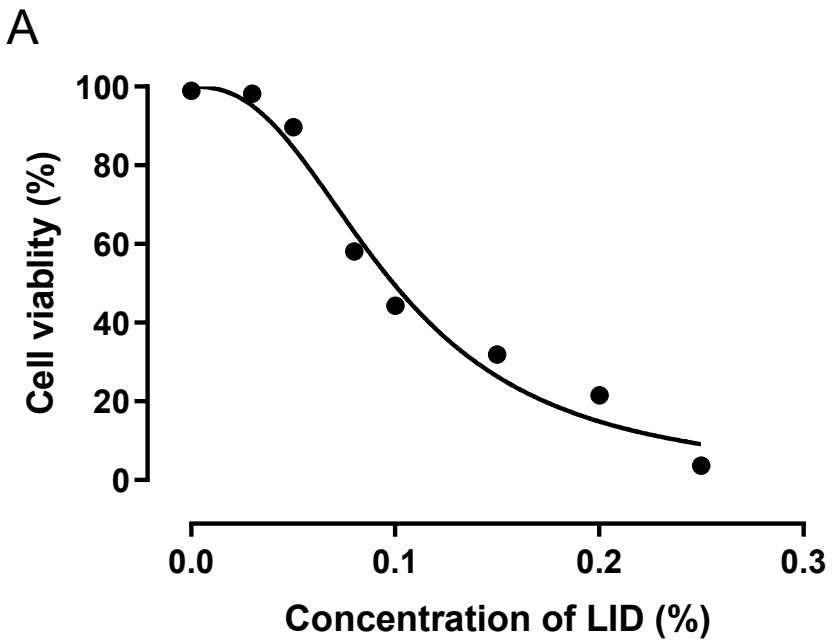

C
Relative expressional level
Notch1
Notch2
Dll4
Csl
Hes1
si NC
si Notch1 +0LID
si Notch1 +0.01%LID
si Notch1 +0.02%LID

Figure S4


A
100
80
60
40
20
0
Cell viablity (%)
0.0
0.1
0.2
0.3
Concentration of LID (%)

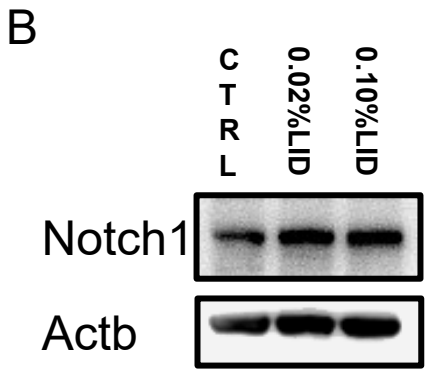
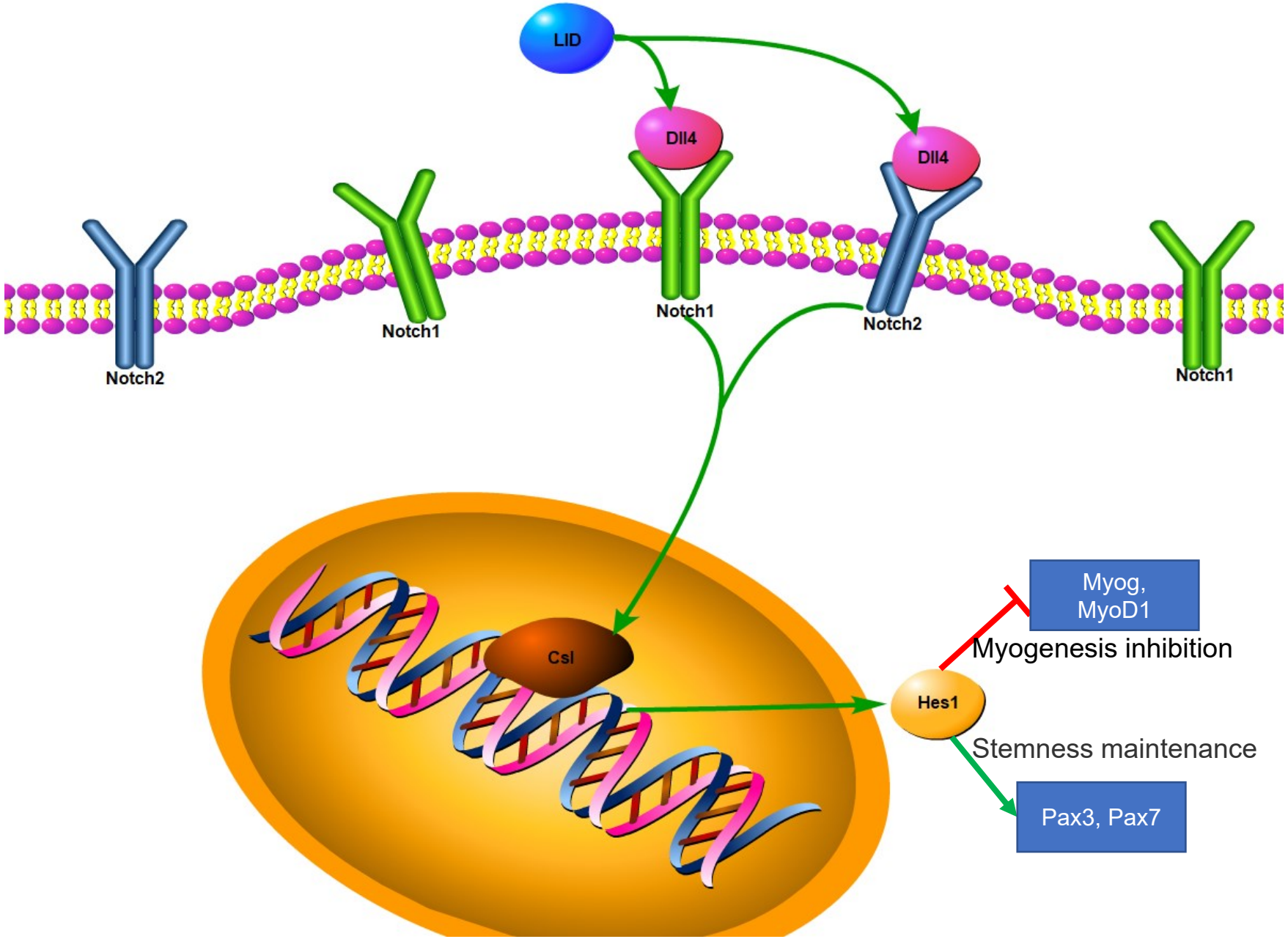

B
CTRL
0.02%LID
0.10%LID
Notch1
Actb

Figure S5


LID
Dll4
Dll4
Notch2
Notch1
Notch1
Notch2
Notch1
Csl
Hes1
Myog,
MyoD1
Myogenesis inhibition
Stemness maintenance
Pax3, Pax7

Supplemental Figure Legends

Figure S1. Primary culture EOM myoblasts were induced in differential medium. Pictures were taken in the third and fouth days. The myoblasts formed mature myotudes.

Figure S2. Some genes in the Notch signal pathway didn't show significant change after treating by lidocaine. qRT-PCR was used to measure the transcript levels of gene: Mmal1, Hey1, Dll1, Jag1. (#P>0.05, *P<0.05, **P<0.01, ***P<0.001, n=3, bars represent SD).

Figure S3. (A, B, C) Dll4, Notch2 and Notch1 were silenced respectively with siRNA. qRT-PCR was used to measure the transcript levels of gene: Notch1, Notch2, Dll4, Csl, Hes1.

Figure S4. (A) Apoptotic effects of lidocaine. (B) Protein level of Notch1 was analyzed by western blot.

Figure S5. Schematic diagram to show the involvement of Notch pathway signal. The green arrows mean activating while red arrow means inhibition.