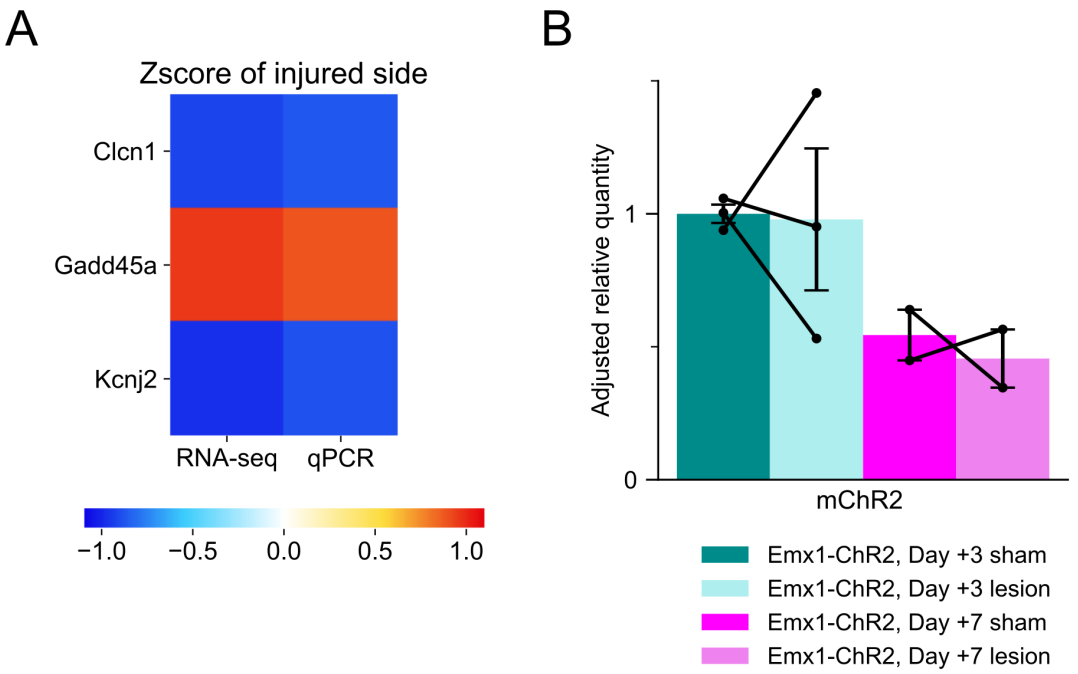

C

Name	Sequence
mClcn1_F	TACGGACTGCCCTCAGAGAA
mClcn1_R	TGGCCATATATCTGTGTTGGGT
mGadd45a_F	TGGTGACGAACCCACATTCA
mGadd45a_R	TCCATGTAGCGACTTTCCCG
mKcnj2_F	CCTGTACCAGCAACAGGACAA
mKcnj2_R	TGGGGTTCTTTTGACCAGCA
mActb_F	GGCTGTATTCCCCTCCATCG
mActb_R	CCAGTTGGTAACAATGCCATGT
mChR2_F	CCATGGGTCTGCTTGTGTCT
mChR2_R	GACCTTGACGTATCCGGTGG

Supplemental Figure 4. qPCR validation of RNA-seq data and measurements of ChR2 expression.
(A) Heatmap of differential expression of Clcn1, Gadd45a, and Kcnj2 from 3 d whisker pad for RNA-seq (left column) and qPCR (right column). qPCR values were normalized to ActB expression.
(B) qPCR data comparing ChR2 expression levels in sham and lesioned whisker pad tissue from Emx1-ChR2 mice. Lines represent data from left (sham) and right (lesion) whisker pads from individual mice. Bars and errorbars represent mean ± SEM. One of the five subjects included was unlesioned. No increases were detected at 3 d and 7 d post-lesion.
(C) Name and sequence of primers used for qPCR.