# Science Advances

### Supplementary Materials for

## 4E-BP1-dependent translation in nociceptors controls mechanical hypersensitivity via TRIM32/type I interferon signaling

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#### The PDF file includes:

Figs. S1 to S3 Legend for data S1

### Other Supplementary Material for this manuscript includes the following:

Data S1



**fig. S1. Additional analyses for TRAP-seq.** Linear correlation plots show high correlation coefficients of genes between biological replicates for WT (A) and 4E-BP1 cKO (B) samples in the IP (top) and IN (bottom) fractions, suggesting high reproducibility between experiments. (C) Dual-flashlight plot of IN samples showing SSMD versus log<sub>2</sub> FC. (D) Log<sub>2</sub> IP/IN ratio of top 50 genes.



fig. S2. Type I interferon mRNAs are increased in 4E-BP1 cKO nociceptors. RNAScope images of DRG sections show increased abundance (# of puncta per cell) of *Ifnas* and *Ifnb1* mRNAs in *scn10a*-positive nociceptors of 4E-BP1 cKO mice (A) as compared to control (B) animals. (C) Quantification (n = 3 mice/group; Student's t-test, 2 tailed; scale bar: 30  $\mu$ m). All data are presented as mean ± SEM. \*\*P < 0.01.



fig. S3. shRNA knockdown of TRIM32 in nociceptors does not rescue neuropathic pain. (A) Western blots and quantification showing increased TRIM32, IFN- $\alpha$ , IFN- $\beta$  and p-S6 in DRG lysates of animals 4 days after SNI compared to sham control mice (n = 4-5 mice per group, Student's t-test, 2 tailed). (B) No difference in mechanical hypersensitivity in animals that received AAV-DIO-TRIM32-shRNAmir compared to scrambled control following SNI (n = 8 mice per group, two-way ANOVA mixed effects model followed by Bonferroni's post hoc comparison). All data are presented as mean ± SEM. \*P < 0.05.

**Data S1. Analysis of TRAP-sequencing data. Tab A**: Raw transcripts per million for INPUT and respective percentiles. **Tab B**: Raw transcripts per million for IP and respective percentiles. **Tab C**: Quantile normalized transcripts per million for IP and respective statistics. **Tab D**: Summary of differentially expressed genes between WT and 4E-BP1 cKO in IP samples.