

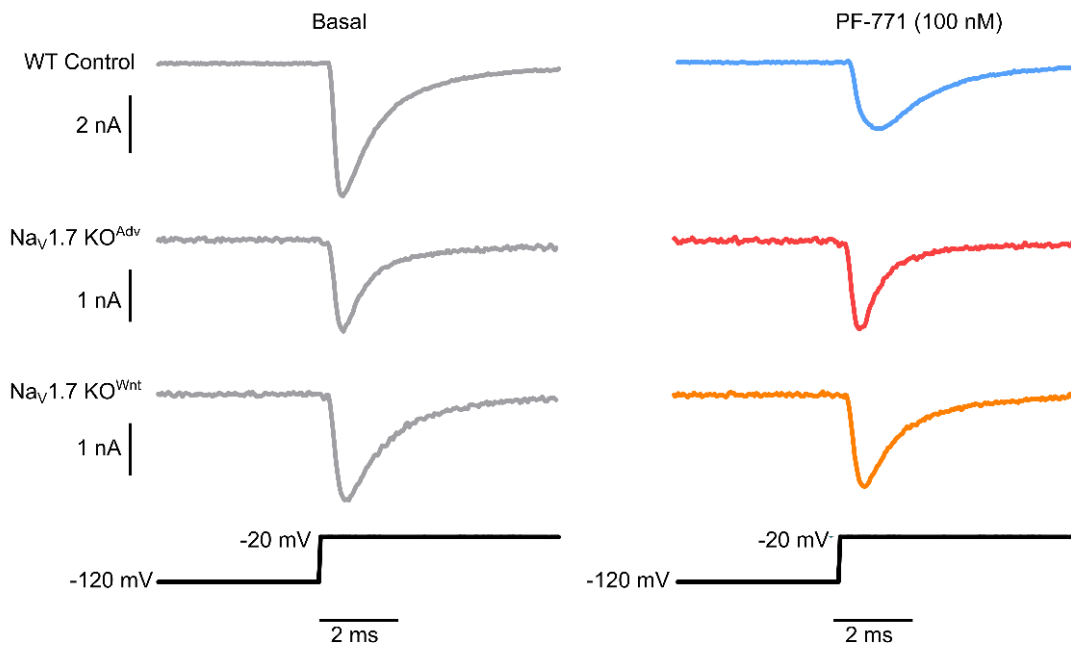
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**Supplemental information**

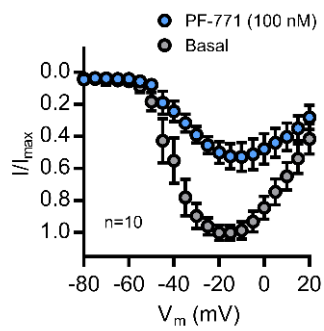
**A central mechanism of analgesia in mice  
and humans lacking the sodium channel Na<sub>v</sub>1.7**

**Donald Iain MacDonald, Shafaq Sikandar, Jan Weiss, Martina Pyrski, Ana P. Luiz, Queensta Millet, Edward C. Emery, Flavia Mancini, Gian D. Iannetti, Sascha R.A. Alles, Manuel Arcangeletti, Jing Zhao, James J. Cox, Robert M. Brownstone, Frank Zufall, and John N. Wood**

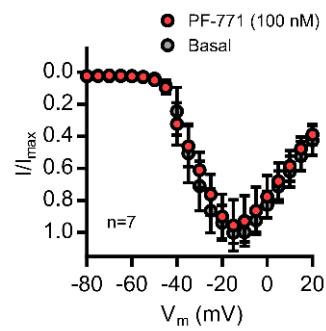
**A Voltage-gated sodium current recordings from WT and Na<sub>v</sub>1.7 KO DRG neurons**



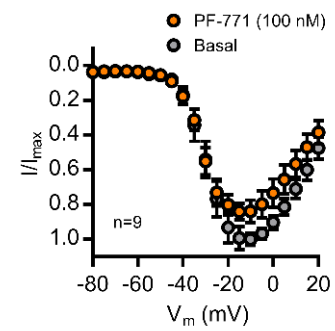
**B WT Control**



**C Na<sub>v</sub>1.7 KO<sup>Adv</sup>**



**D Na<sub>v</sub>1.7 KO<sup>Wnt</sup>**



**Figure S1 (related to Figure 1). Conditional deletion of *SCN9A* in sensory neurons abolishes voltage-gated sodium channel currents attributed to  $\text{Na}_v1.7$ .**

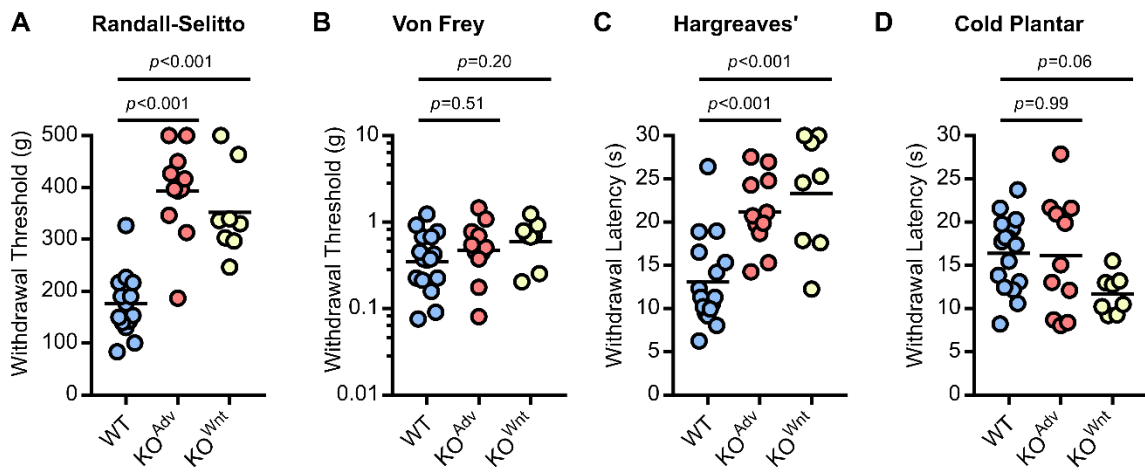
(A) Example current traces showing voltage-gated sodium channel currents activated by a 100 mV voltage-step from -120 mV to 20 mV recorded from WT and  $\text{Na}_v1.7$  KO DRG neurons (grey). Application of the  $\text{Na}_v1.7$ -specific antagonist PF-05089771 (PF-771, 100 nM for 5 minutes) caused a marked reduction in sodium currents in WT neurons (blue) but not in cells from  $\text{KO}^{\text{Adv}}$  (red) or  $\text{KO}^{\text{Wnt}}$  (orange) mice.

(B) Current-voltage (I-V) curve showing that application of the  $\text{Na}_v1.7$ -specific antagonist PF-771 reduces voltage-gated sodium currents in WT sensory neurons. n=10 cells.

(C) I-V curve showing PF-771 did not markedly affect voltage-gated sodium currents in sensory neurons from  $\text{Na}_v1.7$   $\text{KO}^{\text{Adv}}$  mice. n=7 cells.

(D) I-V curve showing PF-771 did not markedly affect voltage-gated sodium currents in sensory neurons from  $\text{Na}_v1.7$   $\text{KO}^{\text{Wnt}}$  mice. n=9 cells.

Error bars denote standard error of the mean.



**Figure S2 (related to Figure 1). Peripheral Nav1.7 knockout mice show reduced pain sensitivity.**

(A) Both Nav1.7 KO lines show increased tail withdrawal thresholds to noxious mechanical stimuli on the Randall-Selitto test.

(B) Nav1.7 deletion has no effect on withdrawal thresholds to punctate tactile stimuli on the Von Frey test

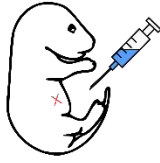
(C) Both Nav1.7 KO lines show increased withdrawal latencies to radiant heat stimuli on the Hargreaves' test.

(D) Nav1.7 KO<sup>Adv</sup> mice show unchanged withdrawal latencies to dry ice stimuli on the Cold Plantar test compared to control, however Nav1.7 KO<sup>Wnt</sup> animals display a small, but not statistically significant, hypersensitivity.

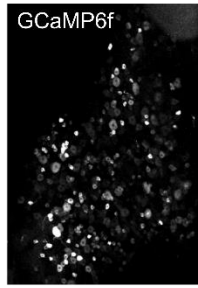
For (A) to (D), means for each KO line were compared to WT control using One-Way ANOVA followed by post-hoc Dunnett's test. n=16 mice for WT, n=11 mice for KO<sup>Adv</sup> and N=8 mice for KO<sup>Wnt</sup>.

**A Viral expression of GCaMP6f**

AAV1  
CAG-GCaMP6f  
5 $\mu$ l i.p.

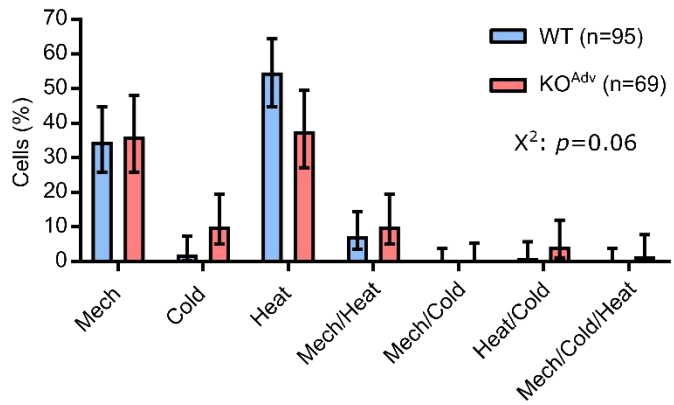


P2 mouse pup

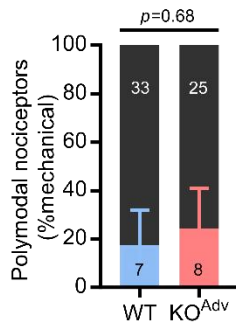


816  $\mu$ m

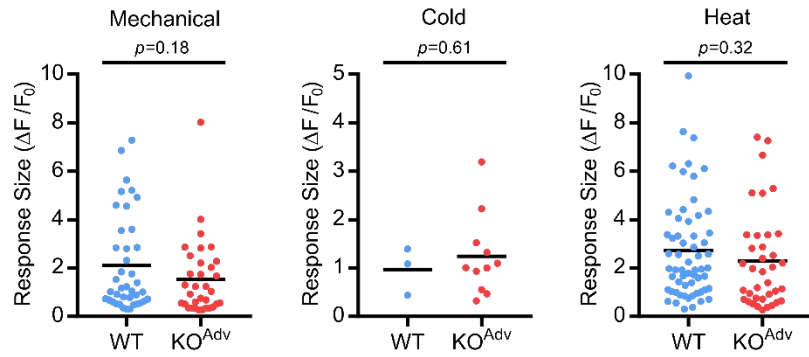
**B Distribution of noxious responses**



**C Polymodality**



**D Magnitude of noxious responses**



**Figure S3 (related to Figure 1). In vivo calcium imaging of Nav1.7-deficient sensory neurons virally expressing GCaMP6f.**

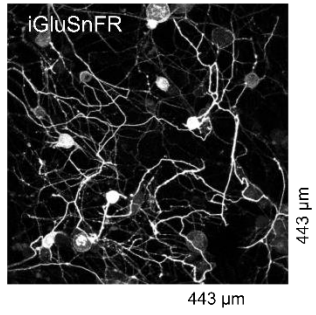
(A) Confocal z-stack of DRG imaged *in vivo* from a Nav1.7 KO<sup>Adv</sup> mouse virally expressing GCaMP6f. AAV1-CAG-GCaMP6f was delivered by intraperitoneal injection into P2 mouse pups.

(B) Bar plot summarizing the distribution of all sensory neurons that responded to different noxious stimuli in WT and KO<sup>Adv</sup> animals. The error bars represent 95% confidence intervals and proportions were compared using Chi-Square test ( $\chi^2$ ). n=95 cells from 4 WT mice (blue) and n=69 cells from 4 KO<sup>Adv</sup> mice (red). Markedly fewer cells responded to cold in these animals compared to in Pirt-GCaMP3 mice, likely due to biased expression of the virally-delivered GCaMP6f.

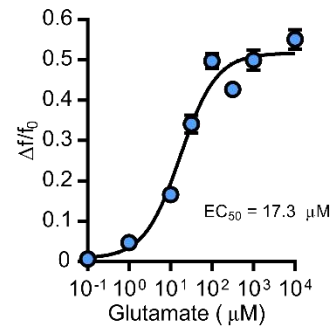
(D) Bar plot showing similar prevalence of polymodal nociceptors in WT and KO<sup>Adv</sup> mice. Polymodal nociceptors are defined as pinch-sensitive neurons that respond to any noxious thermal stimulus (colour) and are expressed as a fraction of mechanically-sensitive cells (black). The error bars represent 95% confidence intervals and proportions were compared using the Chi-Square ( $\chi^2$ ) test with Yates Correction. n=40 cells from WT and n=33 cells from KO<sup>Adv</sup>.

(E-F) Scatter plots showing similar peak calcium responses ( $\Delta F/F_0$ ) evoked by different noxious stimuli for WT and KO<sup>Adv</sup>. Mean response magnitude of KO<sup>Adv</sup> was compared to WT control using an unpaired t test. Mechanical: n=40 cells from WT and n=33 cells from KO<sup>Adv</sup>. Cold: n=3 cells from WT and n=11 cells from KO<sup>Adv</sup>. Heat: n=60 cells from WT and n=37 cells from KO<sup>Adv</sup>.

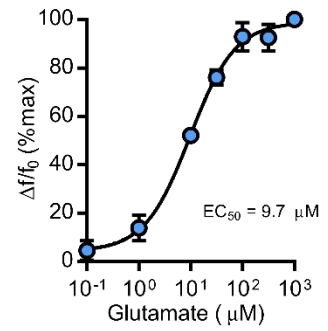
**A DRG culture**



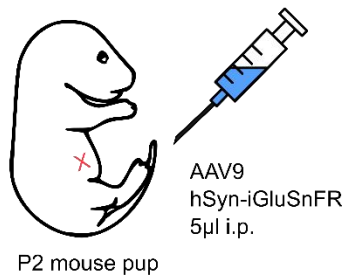
**B i. Dose-response curve**



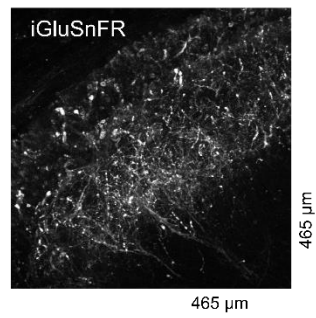
**ii.**



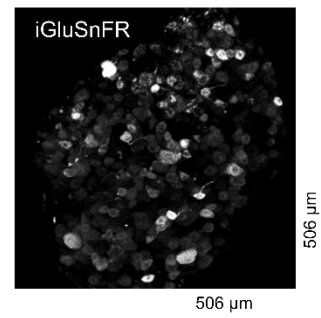
**C Neonatal AAV injection**



**D Spinal cord slice**



**E DRG in vivo**





**Figure S4 (related to Figure 4). Expression and function of iGluSnFR in sensory afferents**

(A) Confocal z-stack of iGluSnFR-expressing cultured dorsal root ganglia neurons, *in vitro*.

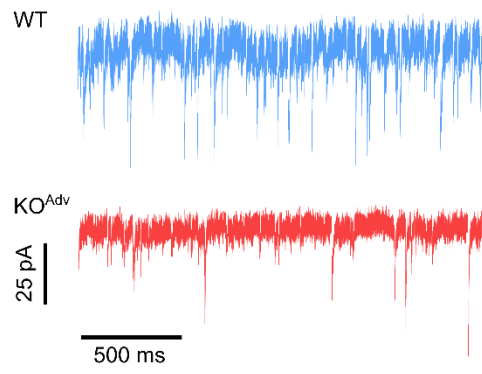
(B) Dose-response curve (i.) of iGluSnFR fluorescence ( $\Delta F/F_0$ ) in cultured DRG neurons against extracellular glutamate concentration. n=36-154 neurons depending on tested concentration.  $EC_{50}=17.3 \mu\text{M}$ .  $r^2=0.426$ . Dose-response curve (ii.) of normalized iGluSnFR fluorescence (% maximum) in cultured DRG neurons against extracellular glutamate concentration. In this experiment, each cell was exposed to all glutamate concentrations tested. n=45 neurons.  $EC_{50}=9.7 \mu\text{M}$ .  $r^2=0.625$ .

(C) Schematic of neonatal virus injection.

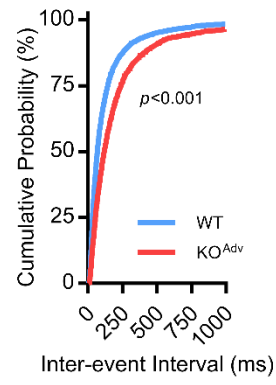
(D) Two-photon z-stack of iGluSnFR-expressing sensory afferent terminals in dorsal horn of transverse spinal cord slice, *ex vivo*. No spinal cord neuron somata express iGluSnFR.

(E) Confocal z-stack of iGluSnFR-expressing sensory afferent cell bodies in L4 dorsal root ganglion, *in vivo*.

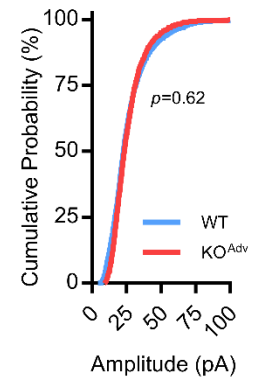
**A Spontaneous EPSCs**



**B sEPSC Frequency**



**C sEPSC Amplitude**



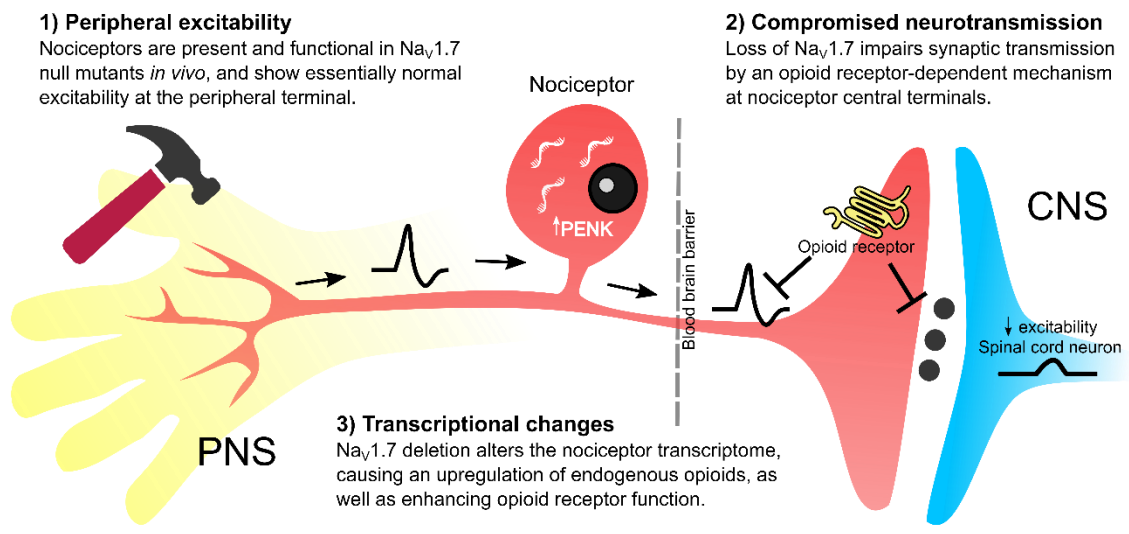
**Figure S5 (related to Figure 4). Nav1.7 deletion reduces frequency, but not amplitude, of spontaneous excitatory post-synaptic currents.**

(A) Example traces showing spontaneous excitatory post-synaptic currents (sEPSCs) recorded from lamina II neurons in WT and KO<sup>Adv</sup> mice.

(B) Cumulative probability plots showing sEPSC frequency is reduced in KO<sup>Adv</sup> animals.

(C) Cumulative probability plots showing sEPSC amplitude is unaltered in KO<sup>Adv</sup> animals.

Means were compared using unpaired t tests. n=6972 events from 40 WT slices, and n=2406 events from 23 KO<sup>Adv</sup> slices.



**Figure S6 (related to Figure 8). Mechanisms of analgesia after loss of Nav1.7.**

Cartoon showing the effects of Nav1.7 deletion on nociceptor function.

- 1) *Peripheral excitability*: Some, but not all, humans with Nav1.7 null mutations show reduced intra-epidermal fibre density, while Nav1.7-deficient sensory neurons are less excitable *in vitro*. But, *in vivo*, terminal excitability is essentially normal, and neurogenic inflammation is preserved. Thus the peripheral terminal is likely not the locus of analgesia.
- 2) *Compromised neurotransmission*: Synaptic transfer from nociceptor terminals to spinal cord dorsal horn neurons is impaired after loss of Nav1.7. These synaptic deficits depend on opioid receptors, which can suppress both synaptic release and terminal excitability. As reported by Alles *et al* (2020), dorsal horn neurons are also less excitable due to absent post-synaptic Nav1.7.
- 3) *Transcriptional changes*: Loss of Nav1.7 leads to an upregulation of PENK, encoding preproenkephalin, resulting in increased endogenous opioid signalling. Concomitantly, reduced sodium ingress following deletion of Nav1.7 leads to enhanced opioid receptor function inhibiting neurotransmitter release. Analgesia in mice and humans lacking Nav1.7 is thus dependent on opioids.

PARTICIPANT	MUTATION	CHARACTERIZATION
Male 1	c.377+5C>T (intronic) – point mutation in splice donor site in intron 3 resulting in the use of a cryptic splice donor site, leading to a frameshift and premature stop codon in exon 4 (McDermott et al., 2019; Shaikh et al., 2018).	Pathogenic (Shaikh et al., 2018).
	c.2686C>T (R896W) – amino acid change in exon 16 (McDermott et al., 2019).	No Nav1.7 current when expressed in HEK293T cells (McDermott et al., 2019).
Male 2	c.2488C>T (R830X) – premature stop codon in exon 16 (Ramirez et al., 2014).	No Nav1.7 current when expressed in HEK293T cells (McDermott et al., 2019).
	c.5318delA (FS1773) – 1 bp deletion in exon 27, that induces a frameshift at position 1773 in the C terminal domain (Ramirez et al., 2014).	8-fold reduction in Nav1.7 current density versus WT when expressed in HEK293T cells (McDermott et al., 2019).

**Table S1 (related to Figure 8). Mutations in *SCN9A* of human participants.**

Summary of previous genetic and functional characterization of the *SCN9A* mutations carried by the compound heterozygous male participants in this study.

PCR PRODUCT	FORWARD PRIMER	REVERSE PRIMER
Pirt-GCaMP3		
Pirt WT (300 b.p.)	TCCCCCTCTACTGAGA GCCAG	GGCCCTATCATCCTGAGC AC
GCaMP3 (400 b.p.)	TCCCCCTCTACTGAGA GCCAG	ATAGCTCTGACTGCGTGA CC
Nav1.7 flox		
Nav1.7 WT (382 b.p.)	CAGAGATTTCTGCAT TAGAATTTGTTC	GCAAATCATAATTAATTC ATGACACAG
Nav1.7 flox (527 b.p.)	CAGAGATTTCTGCAT TAGAATTTGTTC	GCAAATCATAATTAATTC ATGACACAG or AGTCTTTGTGGCACACGT TACCTC
Nav1.7 KO (395 b.p.)	CAGAGATTTCTGCAT TAGAATTTGTTC	GTTCTCTCTTTGAATGC TGGGCA
Advillin-Cre		
Advillin WT (480 b.p.)	CCCTGTTCACTGTGA GTAGG	AGTATCTGGTAGGTGCT TCCAG
Cre (180 b.p.)	CCCTGTTCACTGTGA GTAGG	GCGATCCCTGAACATGTC CATC
Wnt1-Cre		
Wnt1-Cre (628 b.p.)	CTCATTGTCTGTGGC CCTGA	AAATGTTGCTGGATAGTT TTTACTGCC
OMP-Cre		
OMP WT	TGGCAACAGCTGTA GCACCT	ACAGAGGCCTTTAGGTT GGC
Cre	CATTTGGGCCAGCTA AACAT	CCCGGCAAAACAGGTAG TTA

**Table S2 (related to Figures 1, 2, 3, 4, 5, 6, 7 and 8). Primers for mouse line genotyping.**  
Forward and reverse primers required for each PCR used for genotyping.