A genetically defined injured C-fibre nociceptor associated with neuromas

drives chronic spontaneous neuropathic pain

Xiangsunze Zeng[1,2], Rosa I. Martinez-Garcia[2,3], Shamsuddin A. Bhuiyan[4], Keunjung Heo[1,2],

Natalie MacKinnon-Booth[1], Elke Bentley[1], Emily Shea[1], Kangling Wu[5], Omer Barkai[1,2], Bruna

Lenfers Turnes[1,2], Selwyn S. Jayakar[1,2], Barbara Gomez-Eslava[1], Mustafa Q. Hameed[1], Celine

Santiago[2,3], Karina Lezgiyeva[2,3], Emmanuella Osei-Asante[2,3], Ivan Furfaro[5], Alexander

Rotenberg[1], Benjamin R. Johnston[6], Brian J. Wainger[7,8], William Renthal[4], Stéphanie P. Lacour[5],

David D. Ginty[2,3]* & Clifford J. Woolf[1,2]*

[1]F.M. Kirby Neurobiology Center, Boston Children's Hospital, Boston, MA, USA

[2]Department of Neurobiology, Harvard Medical School, Boston, MA, USA

[3]Howard Hughes Medical Institute, Boston, MA, USA

[4]Department of Neurology, Brigham and Women's Hospital, and Harvard Medical School, Boston, MA,

USA

[5]Laboratory for Soft Bioelectronic Interfaces (LSBI), Neuro-X Institute, École Polytechnique Fédérale de

Lausanne, Geneva, Switzerland

[6]Department of Neurosurgery, Mass General Brigham, and Harvard Medical School, Boston, MA, USA

[7]Department of Anesthesiology, Critical Care and Pain Medicine and Department of Neurology,

Massachusetts General Hospital, Harvard Medical School, Boston, MA, USA

[8]Broad Institute of MIT and Harvard, Cambridge, MA, USA

*Corresponding authors. email:

david_ginty@hms.harvard.edu (D.D.G);

clifford.woolf@childrens.harvard.edu   (C.J.W.)

Abstract

Spontaneous pain is a common but poorly understood consequence of peripheral nerve injury[1-3], including injuries that lead to the formation of neuromas[4,5]. We developed a chronic neuroma model for measuring spontaneous pain-related behaviours in mice, which revealed that limb flicks - emerging predominantly 2 months post-injury - reflect spontaneous paroxysmal pain. Ectopic activity of injured dorsal root ganglia (DRG) sensory neurons whose axonal endings terminate within the neuroma drives this spontaneous pain. *In vivo* imaging showed that a subset of small-diameter DRG sensory neurons are the source of spontaneous neural signals emanating from the neuroma, and these spontaneously active neurons are distinct from the intact larger diameter sensory neurons that mediate stimulus-evoked mechanical allodynia from spared nerves. Cell-type–specific gain- and loss-of-function studies identified a genetically- and functionally-defined subtype of small-diameter C-fibre nociceptors whose injured axons in neuromas drive spontaneous limb flicks/neuropathic pain. These findings establish the neurobiological basis of spontaneous pain enabling targeted pain management strategies and define a cellular and mechanistic separation between spontaneous and evoked neuropathic pain.

Introduction

Peripheral nerve injury is a major cause of chronic neuropathic pain, resulting in persistent suffering and disability. Spontaneous pain is among the most common and debilitating clinical feature of neuropathic pain[1-3], yet its underlying mechanisms remain largely unknown. Most preclinical research emphasizes stimulus-evoked withdrawal responses[6], which poorly captures the chronic and fluctuating nature of spontaneous neuropathic pain. This knowledge gap stems

from the fact that spontaneous pain arises sporadically and unpredictably, posing challenges for

comprehensive quantitative investigations[7] and mechanistic discovery.

Existing measures of spontaneous pain are inadequate. For example, the grimace scale performs

well in acute pain settings but not for neuropathic pain[8]. Conditioned place preference can indicate

ongoing pain[9], but fails to capture the paroxysmal nature of spontaneous pain—characterized by

sudden, episodic bouts—which is a hallmark in patients with peripheral nerve trauma who develop

neuromas[10]. Consequently, studies have relied on intermittent pain-like behaviours such as paw

biting or guarding to infer spontaneous paroxysmal pain after nerve injury[11,12]. These measures,

however, typically depend on short-term video observations and do not provide a comprehensive

view of sporadic and unpredictable pain episodes over prolonged periods.

Neuropathic pain research has predominantly centered on acute and subacute post-nerve injury

(e.g., 1–4 weeks), leaving its chronic features relatively underexplored[13], even though chronic pain

is the major clinical issue. Furthermore, the cellular sources of aberrant activity are unclear: early

electrophysiological studies demonstrated that both injured and neighboring uninjured sensory

fibres generate ectopic discharges soon after axotomy[12,14,15], but the genetically defined and

physiologically distinct sensory subtypes that drive chronic spontaneous neuropathic pain have not

been identified. Finally, a longstanding clinical puzzle is why patients with comparable peripheral

nerve insults experience different outcomes, with some developing severe chronic pain while

others exhibiting moderate or no pain[4,5,16]. Although risk factors, including genetic predisposition,

psychosocial context, prior injury, age, and sex, have been proposed[16,17], the cellular and molecular

bases for this variability are still elusive.

By integrating long-term home-cage behavioural studies with a novel measure of spontaneous

pain, *in vivo* calcium imaging, cell-type–specific optogenetic and chemogenetic manipulations,

and transcriptomic profiling in mice, we now identify injured axons of a genetically and

functionally defined C-fibre nociceptor subtype as the driver of chronic spontaneous neuropathic

pain in animals with painful neuromas. Our findings also reveal a clear cellular and mechanistic

distinction between spontaneous and evoked neuropathic pain.

Results

Painful neuromas drive chronic spontaneous pain after peripheral nerve injury

We sought to understand the mechanistic basis of spontaneous neuropathic pain by analysing

defined spontaneous behaviours in mice using a machine-learning–based platform[18] following

different types of sciatic nerve injury (Extended Data Fig. 1a,b). Guarding, biting/licking,

scratching, rearing, and grooming behaviours were monitored using 30-minute recording sessions

conducted once per week for up to two months after injury. All of these behaviours remained

unchanged post-injury, except for guarding, where mice lift and hold the paw ipsilateral to the

nerve injury, which increased relative to sham controls from one week after the injury (Extended

Data Fig. 1c), in line with previous studies[11,12].

While the conventional behavioural measures did not provide a reliable measurement of

spontaneous pain, the long-term videography analysis revealed an unexpected "limb flick"

behaviour that was very rare in the first 4 weeks after the nerve injury, but then progressively

increased, becoming most prominent at 8 weeks post-injury across all the nerve transection injury

models (Extended Data Fig. 1d). This spontaneous limb flick behaviour was characterized as

having a stereotyped pattern of rapid, repetitive hindlimb shaking (Supplementary Video 1). The

incidence of limb flicks scaled with injury severity, being most pronounced after a full sciatic nerve

transection (SNT) and intermediate in the spared nerve injury (SNI) model, where the common

peroneal and tibial nerves are injured and the sural nerve remains intact (Extended Data Fig. 1a,d).

Limb flicks were also observed after a sural nerve transection (SuNT) (Extended Data Fig. 1a,d),

which selectively damages sensory fibres[19], and they were suppressed by gabapentin (Extended

Data Fig. 2a), supporting that this behaviour likely reflects pain and not motor dysfunction. By

contrast, limb flicks were absent in acute nociceptive or inflammatory pain models (Extended Data

Fig. 2b). These observations suggest that spontaneous limb flicks arise from chronic pathological

changes in injured sensory nerve fibres.

Because the limb flick is a chronic pain-associated behaviour that emerged most robustly in the

SNT model, we focused on this nerve injury model for subsequent analyses. To move beyond

short-term measures of limb flicks, we established a quantitative framework for long-term home-

cage monitoring. Given the stereotyped high-frequency muscle activity underlying limb flicks, we

implemented a wireless electromyography (EMG) system using electrodes placed in the vastus

lateralis, the largest quadriceps muscle, coupled with video recording, to reliably capture injured

hindlimb behaviours over extended time periods (Fig. 1a). The EMG system faithfully detected

repetitive limb flick oscillations (Supplementary Video 1), with an average peak frequency of ~13

Hz and most events lasting <1 second (Extended Data Fig. 3a–c), without any apparent motor

impairment from the recording electrode implantation (Extended Data Fig. 3d). To determine

whether prolonged monitoring reduces behaviour variability, we performed continuous 24-hour

recording at 8 weeks post-SNT and assessed intra-animal variation by binning the data into time

windows of increasing length. As the window size increased, variability progressively declined,

and extending the recording period up to 48 hours did not yield a further reduction when compared

with 24 hours (Fig. 1b). These results demonstrate that 24-hour monitoring provides a stable

measure of limb flicks and also reveal a circadian component to this spontaneous neuropathic pain

behaviour[20].

Using 24-hour recordings, we tracked limb flicks longitudinally. Group averages rose gradually,

reaching a peak around 8 weeks post-SNT and remaining at a plateau thereafter, with most

increases occurring during the dark phase (7 p.m.–7 a.m.) (Fig. 1c,d). Between mice, the flick

prevalence varied, with some mice displaying dramatic increases and others remaining at moderate

or low levels throughout the 16-week post-SNT period (Fig. 1d). Unlike the intra-animal

variability attributable to recording length, this inter-animal variability likely reflects biological

differences and is reminiscent of the different pain phenotypes in patients who develop painful or

non-painful neuromas after peripheral nerve injury or an amputation[4,5]. Histology confirmed the

formation of terminal neuromas proximal to the nerve transection, appearing as bulbous structures

filled with exuberant but disorganized axons within fibrotic tissue by 8 weeks post-SNT (Fig. 1e),

as described previously[21]. To test whether the neuromas trigger the limb flicks, we used a

transcutaneous poke test, analogous to the clinical Tinel sign evoked by gentle tapping the skin

over a peripheral nerve[22]. Our poke test involved indenting the skin overlying the SNT lesion with

a 15 g von Frey filament to mechanically stimulate the underlying neuroma (hereafter referred to

as "transcutaneous neuroma poke"). This stimulus increasingly induced limb flicks over time

across the nerve injury models, with the strongest responses in SNT animals, and minimal

responses in sham controls or when applied to the side contralateral to the SNT surgery (Extended

Data Fig. 4a and Supplementary Video 2). EMG implantation did not affect this outcome

(Extended Data Fig. 3e). We also assessed flick probability to the transcutaneous neuroma poke in

the same mice that were used for the 24-hour spontaneous flick recordings. This analysis revealed

comparable inter-animal variability as spontaneous limb flicks (Fig. 1f) and also demonstrated a

strong positive correlation in the chronic phase: mice with more spontaneous limb flicks were also

highly sensitive to the poke test, whereas those with few spontaneous limb flicks showed little or

no flick response to a poke (Fig. 1g). To test causality, we injected lidocaine locally at the neuroma

site, a standard clinical intervention[23]. This virtually abolished the poke-induced flicks in mice

with a high neuroma pain behaviour. In addition, lidocaine treatment markedly reduced

spontaneous flicks (Fig. 1h), indicating that activity originating in neuromas is the major driver of

this chronic spontaneous pain behaviour.

To quantify the incidence of the high-pain phenotype, we performed the transcutaneous

neuroma poke test in 144 mice at 8–12 weeks post-SNT. Thirty-two percent of SNT mice exhibited

a high response probability ($\geq$0.7; hereafter referred to as high-pain), twenty-seven percent

exhibited low probability ($\leq$0.3; low-pain), and forty-one percent displayed an intermediate pain

phenotype (0.4–0.6; medium-pain), with no sex differences or correlation with the neuroma size

(Extended Data Fig. 4b,c). Finally, neither poke-induced nor spontaneous limb flicks required the

mechanosensitive channel Piezo2, as evaluated in Piezo2 conditional knockout mice (Extended

Data Fig. 5).

Injured small-diameter sensory axons exhibit ectopic activity arising from their terminals in

the neuroma

To investigate the neuronal basis of the spontaneous pain, we performed *in vivo* calcium imaging

from the L4 dorsal root ganglia (DRG) 8–12 weeks after SNT using *Vglut2^{Cre}::GCaMP6f* mice, in

which primary DRG sensory neurons across all subtypes are labelled. The neuroma or contralateral

intact nerve was surgically exposed to allow direct stimulation with von Frey filaments of varying

force (Fig. 2a). Poking neuromas induced calcium responses almost exclusively in small-diameter

neurons (<25 μm soma diameter), whereas stimulation of the contralateral intact nerve rarely

activated neurons of any size, with the 1.4 g filament producing the most discriminating response

(largest effect size determined by Cohen's d) (Fig. 2b,c). Neuroma-poke responses also varied

across animals: the response amplitude of small-diameter neurons induced by the 1.4 g probe

stimulus differed substantially across mice and was positively correlated with their behavioural

pain responsiveness, assessed by transcutaneous neuroma poke immediately prior to the imaging

(Fig. 2d), supporting a peripheral contribution to the differential pain outcomes in individual mice.

We next assessed spontaneous activity in the same DRG and found that the L4 DRG ipsilateral

to the neuroma contained more spontaneously active cells than the contralateral L4 DRG

containing neurons with an intact sciatic nerve, specifically within the small-diameter population

(Fig. 2e). Comparing the ipsilateral spontaneously active neurons with those responsive to a

neuroma poke showed that the majority—both spontaneously active and those responsive to a

poke—were small-diameter neurons (Fig. 2f,g). Moreover, topical lidocaine applied directly at the

neuroma largely abolished the spontaneous activity (Fig. 2h), demonstrating that the origin of this

spontaneous neural activity is in the neuroma rather than the DRG. These findings establish injured

small-diameter sensory axons as the principal source of ectopic activity and the likely drivers of

spontaneous neuropathic pain.

Pain arising from injured versus uninjured fibres requires distinct sensory neuron cell types

Peripheral nerve injury induces ectopic activity in both injured and adjacent uninjured fibres across

different sensory neuron subtypes[12,14,24,25]. We next asked whether activity originating from injured

fibres in neuromas and uninjured fibres jointly contribute to a common pain phenotype or act

through distinct mechanisms. Because the entire sciatic nerve is severed in the SNT model, we

assessed mechanosensitivity of the medial plantar paw which is innervated by the intact saphenous

nerve [26]. Tactile allodynia associated with the medial plantar paw emerged 4 weeks post-SNT (Fig.

3a), well before spontaneous limb flicks became prevalent. No correlation was found between the

intact saphenous nerve-evoked pain and neuroma pain intensity (Fig. 3b), pointing to independent

mechanisms. Direct imaging of DRG activity confirmed this separation: completely distinct

populations of sensory neurons were engaged in the two pain models. Medium- and large-diameter

DRG neurons were the primary responders to medial plantar stimulation, whereas small-diameter

neurons were predominately associated with neuroma stimulation (Fig. 3c–f; and Supplementary

Video 3). Locally silencing the neuroma or saphenous nerve endings with lidocaine selectively

inhibited responses initiated from each region, respectively (Fig. 3g,h), providing evidence that

pain arising from injured and uninjured fibres is initiated through distinct mechanisms.

A genetically defined subtype of C-nociceptor axons in neuromas drives limb flicks

Transcriptomic studies have identified at least 16 genetically distinct DRG sensory subtypes[27-31]

with unique physiology and morphology[28]. We performed single-nucleus RNA sequencing

(snRNA-seq) of DRG from mice 10 weeks post-SNT and confirmed the presence of all these cell

types in both high- and low-pain conditions (Fig. 4a and Extended Data Fig. 6a). To identify

specific sensory subtypes whose activation may drive spontaneous limb flicks, we conducted an

optogenetic gain-of-function screen, using transgenic mouse lines that collectively encompass the

majority of sensory subtypes with soma diameters <25 μm [28]. Because neuromas reside deep

within fibrotic tissue, we adapted a miniaturized LED cuff [32] for localized epineural activation of

sensory axons, either in neuromas or contralateral intact nerves (Fig. 4b and Extended Data Fig.

7). In mice expressing opsins in a subset of small-diameter C-fibres marked by *Sstr2* expression

(SSTR2; *Sstr2[T2a-CreER];Calca-FlpE;R26[LSL-FSF-ReaChR::mCitrine]*), a single 10-ms 470-nm pulse

delivered to the neuroma induced limb flicks and, to a lesser extent, other pain-related behaviours

(vocalization, jump, licking, and avoidance, either individually or in combination)[7], with

significantly lower activation thresholds than those needed to evoke behavioural responses on the

contralateral intact nerve (Fig. 4c,d). The nomenclature for this cell type varies across the literature,

depending on the response modality assessed in intact tissue: C-Heat thermonociceptor (C-Heat

[SSTR2]) from skin[28]; C-high threshold mechanoreceptors (C-HTMR) from colon[33], lineage

subtype (CGRP-α)[29], marker gene expression in mice (*Calca* + *Sstr2*)[30], hierarchical

transcriptomic clustering within the peptidergic branch (PEP1.1) [31], and putative human

homologues (C-PEP.TAC1/CACNG5)[34]. Here, we refer to this genetically defined, neuroma-

hypersensitive C-fibre subtype as 'Neuroma C-Nociceptors (SSTR2)'. In contrast, Aδ-

HTMR/Heat (SMR2) neurons, which are myelinated mechanonociceptors[35], elicited behavioural

responses when intact nerves were stimulated but rarely when neuromas were activated (Fig. 4c,d).

This discrepancy likely reflects the preferential loss of the axons of these Aδ-HTMR/Heat (SMR2)

neurons in neuromas (Extended Data Fig. 8). Other subtypes showed little or no nocifensive

behavioural responses when activated: activating Aδ-low-threshold mechanoreceptors (Aδ-

LTMRs), C-LTMRs, and C-HTMR/Heat (CYSLTR2/SST) neurons elicited no consistent

behaviours from either neuromas or intact nerves, whereas stimulating C-HTMR/Heat

(MRGPRA3), C-HTMR/Heat (MRGPRB4), C-HTMR/Heat (MRGPRD), C-Cold (TRPM8) axons

with strong optical power occasionally evoked avoidance, guarding, or licking behaviours from

either site, but rarely induced limb flicks (Fig. 4c,d; and Supplementary Video 4).

Anatomical analyses revealed denser Neuroma C-Nociceptor (SSTR2) fibres in neuromas than

in contralateral intact nerves, but a reduced presence of Aδ-HTMR/Heat (SMR2), C-HTMR/Heat

(MRGPRA3), and C-HTMR/Heat (MRGPRD) nerve fibres, with C-HTMR/Heat (MRGPRD)

axons almost completely absent (Extended Data Fig. 8), likely reflecting cell death in this

population after peripheral nerve trauma[36].

Because activation of the Neuroma C-Nociceptor (SSTR2) injured axons robustly induced limb

flicks, we further characterized how their activity relates to different pain-related behaviours and

response dynamics. High-frequency or prolonged optogenetic stimulation did not change the

incidence of limb flicks or most other behaviours, except audible vocalizing - a response uniquely

triggered by activation of the Neuroma C-Nociceptors (SSTR2) - showed an increased occurrence

under these stimulation patterns, suggesting a dependence on summation of activity (Extended

Data Fig. 9a). Response latency analyses showed that the limb flicks occurred with an average

latency of 259 ms, which was longer than the latency to jump or avoid the stimulus but

considerably shorter than the latency for self-licking (Fig. 4e, left). These temporal distinctions

suggest that limb flicks represent a pain-related behavioural output that is dissociable from rapid

withdrawal reflexes[35] and from delayed coping behaviours. Lastly, we noted from the snRNA-seq

analysis that *Scn10a* (encoding voltage-gated sodium channel $Na_v1.8$) and *Scn3a* ($Na_v1.3$) were

selectively upregulated in Neuroma C-Nociceptors (SSTR2) under high-pain conditions (Extended

Data Fig. 6b,c), potentially linking these ion channels to hyperexcitability of this population in

painful neuromas. Related to this, we analysed the optical stimulation strength required to induce

limb flicks in high-, medium-, and low-pain mice. We used a Cox proportional hazards model with

optical power as the ordered exposure variable and the first limb flick to optogenetic stimulation

as the event. This analysis revealed that the flick probability determined by the transcutaneous

neuroma poke test significantly predicted optogenetic threshold (*hazard ratio = 198.8, p = 0.0023*);

high-pain mice flick at a lower optical power, whereas low-pain mice require a higher optical

power to elicit flicks (Fig. 4e, right). This result is consistent with increased excitability of

Neuroma C-Nociceptors (SSTR2) in high-pain neuromas potentially mediated by upregulation of

voltage-gated sodium channels[24].

We next asked whether activity of the Neuroma C-Nociceptors (SSTR2) is necessary for

neuroma-driven pain behaviours. We acutely silenced this neuronal population using

chemogenetic inhibition highly specific to the $Sstr2^+$ population ($Sstr2^{T2a\text{-}CreER}$;$R26^{LSL\text{-}}$

$^{hM4Di::mCitrine}$) (Extended Data Fig. 9b). This manipulation significantly suppressed transcutaneous

neuroma poke–induced limb flicks in high-pain mice but not in littermate controls (Fig. 4f).

Notably, motor function and mechanical allodynia arising from the intact saphenous nerve-

innervated area were unaffected (Fig. 4f and Extended Data Fig. 9c), indicating a specific role for

activity in injured Neuroma C-Nociceptors (SSTR2) in driving pain arising from the neuroma.

These findings define a specific nociceptor subtype whose injured axons become hypersensitive

in painful neuromas to drive a chronic spontaneous pain-related behaviour.

Discussion

The mechanisms of spontaneous neuropathic pain are obscure, largely because of the lack of

reliable measures, particularly over chronic timescales. Most mechanistic insights into neuropathic

pain have been derived from stimulus-evoked pain arising from uninjured afferents[26], potentially

biasing interpretation toward spared-nerve pathways after injury. By establishing a long-term

recording platform, we identified limb flicks as a robust behavioural readout of chronic

paroxysmal spontaneous pain and traced their origin to injured axons of a genetically defined

sensory subtype within painful neuromas. These findings support the conclusion that the

spontaneous and evoked components of neuropathic pain arise from distinct peripheral drivers.

This distinction reframes prevailing models of neuropathic pain and has direct implications for

treatment. Prior work indicates that mechanical allodynia mediated by spared nerves after injury

is primarily initiated by Aδ/Aβ-LTMRs whose central afferents reroute into nociceptive circuits

through dorsal horn plasticity[37,38], with Piezo2-dependent mechanotransduction playing a central

role[39]. By contrast, our model identifies injured Neuroma C-Nociceptors (SSTR2) as the principal

drivers of neuropathic pain, and with neuroma mechanical hypersensitivity occurring

independently of Piezo2 (Extended Data Fig. 5), which is consistent with minimal expression of

Piezo2 in this neuronal subtype[28-31]. Defining the pain transduction mechanisms at neuroma

terminals[24], and how Neuroma C-Nociceptors (SSTR2) engage central circuits to generate pain

perception, will advance our understanding of the underlying mechanisms of spontaneous

neuropathic pain.

Consistent with the mechanistic separation of spontaneous and evoked pain, both preclinical

and clinical evidence suggests that spontaneous pain and stimulus-evoked hypersensitivity are

distinct in their pharmacological responsiveness[40-43]. However, current diagnostic frameworks

lump these manifestations under a single "neuropathic pain" label, and treatment guidelines

recommend single agents without any delineation for evoked or spontaneous pain. This likely

contributes to variable therapeutic efficacy through a mechanism–therapy mismatch. Our findings

support the need to revisit diagnostic criteria to explicitly distinguish between spared-fibre evoked

allodynia and injured-fibre triggered spontaneous pain, and develop specific targeted interventions

aligned with the dominant mechanistic driver in individual patients.

A second key implication is that identifying the peripheral driver of spontaneous pain provides

a rational framework for cell-targeted intervention[44]. Because Neuroma C-Nociceptors (SSTR2)

are both necessary and sufficient to drive neuroma pain, and their selective silencing suppresses

neuroma pain without impairing sensory modalities from spared nerves or motor function (Fig. 4f

and Extended Data Fig. 9c), therapeutic strategies that act selectively within this population,

particularly those enabling localized, subtype-specific delivery[45], offer a means to alleviate

pathological pain while preserving desired sensory function and minimizing central exposure in

patients. Although the Neuroma C-Nociceptors (SSTR2) identified here are defined by *Sstr2*

expression in mice—a marker with minimal expression in human DRG neurons—the model

recapitulates key clinical features of neuropathic pain, suggesting the existence of an evolutionarily

conserved homologous human nociceptor subtype, which is supported by transcriptomic

observations[34]. Defining the analogous mechanisms operating in humans and identifying

molecular access points to suppress neuroma-associated hyperexcitability will be essential for

translation.

Beyond symptomatic control, preventing the formation of painful neuromas may be a new

treatment strategy. The emergence of high-pain versus low-pain phenotypes that can be decoded

at the level of sensory neuron activity (Fig. 2d) points to peripheral heterogeneity in how neuromas

are primed after injury. Such variability may reflect differences in stochastic perturbations of gene

expression during the early injury response[46,47], local trophic and inflammatory signaling[48], and

interactions with diverse non-neuronal cell types[48-52]. Defining the determinants that govern

painful neuroma maturation during the subacute formation phase may therefore enable early

protective strategies that can intercept pathological trajectories before chronic spontaneous pain

becomes established, enabling its prevention[44].

Methods

Mice

All experiments were conducted in accordance with the guidelines of the Boston Children's

Hospital Institutional Animal Care and Use Committee (IACUC) under protocols 00001507 and

00002403, or by the Harvard Medical School IACUC under protocol IS00001036-9. Mice were

housed under temperature-controlled conditions on a 12-hour light/dark cycle (lights on at 7:00

a.m., off at 7:00 p.m.) with ad libitum access to food and water. Both male and female mice were

used in all experiments. The C57BL/6J strain (JAX #000664; The Jackson Laboratory) was used

unless otherwise specified, with transgenic strains detailed in the relevant sections below.

Peripheral nerve injury models

Surgeries were performed on 8–9-week-old mice under aseptic conditions. Anaesthesia was

induced and maintained with 2% isoflurane (Patterson Veterinary, #07-890-8115) delivered via a

nose cone. Throughout the procedure, body temperature was maintained at 37°C using a heated

pad to prevent hypothermia. Sciatic nerve injuries were performed using standardized protocols as

follows. 1. The surgical site was shaved, and residual hair was completely removed using Nair.

The area was then sterilized with 70% ethanol and Betadine. 2. A small skin incision was made

over the lateral thigh, above the biceps femoris. The underlying musculature was carefully

separated and retracted to expose the sciatic nerve. 3. For sham controls, the sciatic nerve was

gently freed from surrounding connective tissue using curved forceps without causing any damage.

For SNT injury, a segment of the sciatic nerve trunk 5 mm above the sural, common peroneal, and

tibial nerves was ligated with 6-0 sutures (Ethicon, #K889H) followed by a complete transection

proximal to the ligation using microsurgical scissors. An additional 5 mm segment of the distal

nerve stump was excised. For SNI injury, the common peroneal and tibial nerve branches were

ligated and transected in the same manner, leaving the sural nerve intact. For SuNT injury, the

sural nerve branch was ligated and transected in the same manner, leaving the common peroneal

and tibial nerve branches intact (Extended Data Fig. 1a). 4. The musculature was then folded back

to cover the sciatic nerve with the skin closed with 6-0 sutures. 5. Mice were placed on a 37°C

heated pad postoperatively until they fully recovered before being returned to their home cages.

Automated behavioural screening

The recording setup and analytic platform were identical to those previously described[18]. Briefly,

mice were recorded inside a black acrylic enclosure (18 × 18 × 15 cm; length × width × height),

which was closed on all sides except for the bottom and positioned on a 25-cm square piece of 5-

mm thick glass floor. To ensure consistent illumination from below, two independent 850-nm near-

infrared (NIR) LED strips (SMD5050-300-IR, Huake Light Electronics Co., Ltd., Shenzhen,

China) were mounted 10 cm beneath the glass floor. These were carefully positioned to prevent

reflections from interfering with the recorded images. The LED strips were powered by a 12-V

DC power supply. Video recordings were acquired in darkness using an NIR camera (Basler

acA2000-50gmNIR GigE, Basler AG, Ahrensburg, Germany) positioned 30 cm below the glass

surface. Pylon viewer software (v4.1.0.3660, Basler) was used to capture videos under

standardized camera settings. All recordings were conducted at 25 Hz with an initial resolution of

1000 × 1000 pixels, which was subsequently downsized to 500 × 500 pixels for high throughput

analysis. For each injury type, four male and four female C57BL/6J mice were used. To minimize

stress and ensure natural behaviour, mice were habituated for 30 minutes in the recording chamber

followed by a 30-minute recording session at each time point (Extended Data Fig. 1c,d). Only one

mouse was placed in the chamber at a time.

To analyse behaviours from the recordings, we used BAREfoot, a supervised machine learning

algorithm that integrates pose estimation with light-based measurements of body-part pressure and

distance[18]. For behaviours without pre-existing classifiers, training datasets were generated by

manual annotation of videos by experienced scorers, and new classifiers were subsequently trained.

The resulting library of trained classifiers enabled automated, frame-by-frame scoring of a

behavioural repertoire that included spontaneous rearing, grooming, scratching, biting/licking,

guarding, and limb flicks in freely moving mice.

Home-cage EMG/video recording system

Implantation of wireless telemetry transmitters and recording was performed aseptically in 8-

week-old C57BL/6J mice under 2% inhaled isoflurane anaesthesia. Wireless telemetry transmitters

(PhysioTel ETA-F10; Data Sciences International, St. Paul, MN) were implanted by making a short

skin incision along the dorsal aspect of the left hindlimb. A subcutaneous pocket was created by

blunt dissection over the back, cephalad to the hindlimb, to house the transmitter body. For EMG

recording, a pair of recording and reference electrode leads were stripped of silicone insulation

over a 2–3 mm segment, inserted into the vastus lateralis muscle, and secured to the muscle surface

with 5-0 nylon sutures to prevent displacement. The incision was closed with surgical staples and

tissue adhesive, and mice were returned to their home cages to recover for ~2 weeks before

undergoing the SNT procedure. For experiments shown in Fig. 1d,f, sham controls included 3

males and 2 females, and the SNT group included 6 males and 4 females. Mice in the sham group

were also used to assess weight bearing and gait parameters post-implantation (Extended Data Fig.

3d) using a previously reported behavioural platform [53]. In a separate cohort, 3 high-pain and 3

low-pain mice at 8 weeks post-SNT were implanted with transmitters to evaluate the impact of

implantation on neuroma pain sensitivity (Extended Data Fig. 3e).

Mice were housed in custom-designed home cages equipped with overhead video cameras with

night-vision, maintained under a 12-hour light/12-hour dark cycle (lights on at 7 a.m. and off at 7

p.m.) in temperature- and humidity-controlled chambers, with ad libitum access to food and water

(Fig. 1a). In a subset of animals, four additional side-view IP cameras (M1145-L Network Camera,

Axis) were used. Video/EMG recordings (sampled at 1000 Hz) were acquired in real time using

the DSI Ponemah data acquisition platform (Data Sciences International, St. Paul, MN).

To examine the frequency-domain characteristics of EMG signals representing different

behaviours, we performed fast Fourier transform (FFT) analysis on raw EMG time series data with

Python's scipy.fft module to determine dominant frequency for each behaviour defined by video

observations (Extended Data Fig. 3a). The raw amplitude values of the corresponding time series

were first transformed into the frequency domain. The resulting spectrum was computed over the

range of 0 to 200 Hz. To facilitate comparison across time series and to highlight relative peak

frequencies independent of absolute amplitude differences, the FFT magnitude spectrum for each

trace was normalized by dividing all frequency amplitudes by the maximum amplitude within that

trace. This rescaled the values to a range between 0 and 1, allowing identification of the dominant

frequency peaks while minimizing inter-sample variability in absolute signal strength (Extended

Data Fig. 3c, right). Event amplitudes were defined as the absolute peak-to-peak value during each

event (Extended Data Fig. 3b). Autocorrelation was computed using the autocorrelation function

up to 1000 ms using FFT-based methods. The first positive peak after lag 0 was identified to extract

both the dominant periodicity and its autocorrelation strength (Extended Data Fig. 3b).

For scoring limb flicks, raw EMG signals were bandpass filtered at 5–30 Hz. Limb flicks were

defined as bouts of repetitive spikes in the filtered EMG trace (Fig. 1a and Supplementary Video

1). Based on features distinguishing limb flicks from other behaviours (Extended Data Fig. 3a,b),

we implemented a two-step semi-manual scoring pipeline. First, EMG traces were screened using

a dynamic threshold–based automated spike detection algorithm in NeuroScore CNS Data

Analysis Software (v3.6; DSI, Data Sciences International, St. Paul, MN) with broad parameters

as follows. Threshold ratio: 1.2; Maximum ratio: 3; Minimum value: 5 µV; minimum spike

duration: 1 ms; Maximum spike duration: 1000 ms; Minimum inter-spike interval: 10 ms;

Maximum inter-spike interval: 1000 ms; Minimum spike train duration: 10 ms; and Minimum

number of spikes: 2. This automated step detected >95% of true-positive events as confirmed in

pilot observations. Second, automatically detected events were reviewed by an experimenter

blinded to the experimental condition (sham vs. SNT and time point post-surgery), who cross-

referenced detection timestamps with simultaneous video recordings to exclude false positives.

The coefficient of variation was calculated as the standard deviation divided by the mean of flick

counts within each binned time window. Ten 24-hour recordings of SNT mice were randomly

selected to compute variation across bin sizes ranging from 0.5 to 12 hours. A subset of five mice

was recorded for 6 consecutive days to compute CV across extended 12-, 24-, and 48-hour

windows (Fig. 1b).

Transcutaneous neuroma poke test

Mice were shaved around the thigh area before behavioural assay. Acclimation was conducted over

two consecutive days prior to the actual test. During acclimation, mice were placed on a laboratory

bench while the investigator gently held their tails. A series of pokes (20–50 repetitive trials

covering the entire thigh area, ~15 minutes per mouse) were applied using a 15 g von Frey filament

(Stoelting Co, #58011) to familiarize the animals with the testing environment. This acclimation

step was crucial, as mice otherwise exhibited escaping behaviour in response to mechanical

stimulation, even in the absence of injury. Following acclimation, mice typically remained calm

and stationary, indicating readiness for the actual behavioural test (Supplementary Video 2). If

mice continued to display escaping or excessive movements, acclimation was extended until they

reached a stable state. Additionally, trials during this acclimation process enabled the investigators

to identify a 'target point'—the area on the thigh that elicited the most consistent flicking response.

This point often corresponded to the precise location of the neuroma, as later confirmed by *post-*

hoc dissection. In mice that did not exhibit a flicking response throughout acclimation, the 'target

point' was set on the skin area directly above the site of the nerve transection.

For the behavioural test, 10 trials of mechanical stimulation were applied to the identified 'target

point' using the 15 g von Frey filament, with an inter-stimulus interval of >5 seconds. If a stimulus

did not evoke an immediate flicking response, it was maintained for 3 seconds. Trials with no

response after this duration were counted as non-responsive (Supplementary Video 2). Since

injured mice sporadically exhibited spontaneous flicking behaviours, any response occurring more

than 2 seconds after stimulus offset was not counted, and the trial was repeated. Occasionally, mice

exhibited other behaviours to pokes (e.g., licking or guarding), which were not quantified as they

were rare and also occurred on the contralateral side. Flicking probability to poke was quantified

as the proportion of trials that elicited flicking behaviours relative to the total number of trials. For

animals tested repeatedly on different days, investigators were blinded to their previously assessed

pain phenotype.

Plantar von Frey assay

Mice were placed individually in transparent plastic chambers on a wire mesh grid and acclimated to the testing environment for 60 minutes on two consecutive days. Calibrated von Frey filaments (0.008–4.0 g) were applied to the medial plantar surface (saphenous nerve territory) of the injured side using the Up-Down method[54]. Testing was performed 1 day before SNT and weekly thereafter up to 8 weeks post-SNT, and 50% withdrawal thresholds were calculated (Fig. 3a).

For plantar von Frey testing in Piezo2 conditional knockout mice generated from *Cdx2^Cre^* (JAX #009350)[55], *Piezo2^flox^* (JAX #027720) and *Piezo2^flox/Null^* strains[56], the contralateral central plantar area was targeted using the same Up-Down method (Extended Data Fig. 5).

Drug treatments and chemogenetic silencing experiments

For the drug-related tests, spontaneous behavioural assessments were performed in the black box recording system (Extended Data Fig. 1b) for 30 minutes rather than in the home-cage monitoring setup, as the effective window of drug action is on the scale of hours. To mitigate intra-animal variability and ensure robust statistical power, a larger sample size was included. Gabapentin (Medisca, #60142-96-3) was administered intraperitoneally at 30 mg/kg. Spontaneous behaviours were recorded in the black box for 30 minutes before injection (pre) and again for 30–60 minutes post-injection (Extended Data Fig. 2a). Compound 21 (Hello Bio, #HB4888) was administered intraperitoneally at 3 mg/kg to mice carrying either the hM4Di allele (B6.129-*Gt(ROSA)26Sor^tm1(CAG-CHRM4,-mCitrine)Ute^*/J; JAX #026219) alone, *Sstr2^T2a-CreER^* alone, or hM4Di under the control of *Sstr2^T2a-CreER^*. Transcutaneous neuroma poke tests were conducted 40–50 minutes post-injection (Fig. 4f). 50 µl 1% lidocaine hydrochloride monohydrate (Sigma-Aldrich, #L5647) was administered via deep intramuscular–perineural injection around the lateral upper

thigh where the neuroma resides. Spontaneous behaviours were recorded for 30 minutes beginning

15 minutes after injection, immediately followed by transcutaneous neuroma poke tests conducted

45–55 minutes post-injection (Fig. 1h). For calcium imaging experiments, 10 µL of 1% lidocaine

hydrochloride monohydrate was applied either topically to surgically exposed neuromas (Fig. 2h

and Fig. 3g) or via intraplantar injection (Fig. 3h), and von Frey assessments were performed 5

minutes after administration. Capsaicin (Sigma-Aldrich, #M2028), zymosan (Sigma-Aldrich,

#Z4250), and CFA (Sigma-Aldrich, #F5881) were administered as described in the legend to

Extended Data Fig. 2b. Spontaneous limb flicks and paw biting/licking behaviours were manually

counted by investigators blinded to the treatments.

***In vivo* imaging of DRG activity**

DRG imaging was performed as described previously[38]. Mice carrying both *Vglut2-ires-Cre*

(B6J.129S6(FVB)-*Slc17a6^{tm2(cre)Lowl}*/MwarJ;   JAX   #28863)   and   *Ai95D*   (B6J.Cg-

Gt(ROSA)26Sor^{tm95.1(CAG-GCaMP6f)Hze}/MwarJ; JAX #028865) alleles were used for imaging at 8–12

weeks post-SNT. Anaesthesia was induced with 2.5% isoflurane and maintained at 2% via a nose

cone. Mice were placed on a heated pad to maintain the body temperature at 37 °C, and ophthalmic

ointment was applied to the eyes throughout the surgery and imaging. The back was shaved, and

a rectangular incision was made between the lumbar enlargement and pelvic bone with the skin

folded away. A dorsal laminectomy was performed in four steps. First, a 1.5-cm midline incision

caudal to the lumbar enlargement area was made to create space for clamping. Second, a 3–4 mm

incision was made approximately 1 cm rostral to the pelvic bone to expose the spine where the L4

DRG is situated. Third, muscles and connective tissues were removed with scissors and forceps.

Fourth, the L4 transverse process was excised using rongeurs, and small vertebral fragments were

carefully trimmed with fine forceps to fully expose the DRG. Bleeding was controlled using

absorbent paper points (Electron Microscopy Sciences, #71011-01). To minimize motion artifacts

from respiration, a custom spinal clamp was used to secure the spine over the vertebrae 5 mm

rostral to the L4 DRG. Illumination was provided with a collimated 470 nm light-emitting diode

through a 10x, 0.3 numerical aperture air objective. The clamp was adjusted to ensure the DRG

surface was as level as possible, visualizing the maximum surface area in the focal plane, typically

covering ~80% of the entire DRG. A single focal plane was selected to maximize the number of

clearly resolvable neurons across the DRG exhibiting robust calcium responses to indentation of

the medial hindpaw (saphenous nerve territory). A 30-minute imaging session without external

stimulation was conducted to assess spontaneous activity. The neuroma was then surgically

exposed following a procedure similar to sciatic nerve exposure during SNT injury. Mechanical

stimuli of varying forces were applied to the neuroma using von Frey filaments. Each force was

delivered in five trials, with an interstimulus interval of >5 seconds. After imaging the ipsilateral

L4 DRG, the same procedure was repeated for the contralateral L4 DRG, except that mechanical

stimuli were applied to the intact sciatic nerve at a location corresponding to the neuroma site on

the ipsilateral side. The imaging order (i.e., ipsilateral or contralateral first) was randomized to

minimize potential variability due to anaesthesia duration. Images were acquired at 10 Hz with a

99 ms exposure time during neuroma stimulation. The stimulation was also recorded

simultaneously at 25–30 Hz using a digital camera, with the video output time-stamped to

synchronize with GCaMP imaging data. For imaging spontaneous activity, exposure time was

reduced to 35 ms to minimize photobleaching during long-term recordings. Isoflurane

concentration was reduced to 1% throughout the imaging process.

Imaging data were analysed using the open-source CaImAn package[57]. Briefly, data were first

corrected for motion using the NoRMCorre algorithm. Regions of interest (ROIs) were identified

using a constrained non-negative matrix factorization (CNMF) framework, which jointly estimates

spatial footprints and temporal activity traces. Extracted fluorescence traces were detrended to

correct for bleaching and converted to $\Delta F/F$ on a per-cell basis, with baseline (F) defined as the

average of the lowest 10% of fluorescence values. Automatically extracted ROIs were reviewed

by an investigator to correct false positives and false negatives. The corresponding calcium traces

were then evaluated against quality criteria, including spatial correlation, temporal signal-to-noise

ratio ($\Delta F/F$ exceeding 3× the standard deviation of baseline fluctuation for ≥0.5 s), appropriate rise

and decay kinetics, and consistent morphology. Only ROIs meeting these criteria were retained for

analysis.

To classify spontaneously active cells, neuroma poke–responsive cells, and dual-active cells

based on calcium activity, we used an unsupervised clustering approach with Gaussian Mixture

Models (GMMs) implemented in Python's scikit-learn package. The model estimated the

probability of each cell belonging to one of three classes (Fig. 2g) or two classes (Fig. 3d)

according to its peak $\Delta F/F$ across the corresponding imaging sessions, with final cluster

assignment determined by maximum posterior probability (decision boundary).

Miniaturized LED cuff and epineural optogenetic activation

We adapted a previously developed wireless LED array[32] into a wired device to enable behavioural

screening across multiple Cre lines (Fig. 4b and Extended Data Fig. 7). The fabrication process for

the LED cuff began with the spin-coating of a 3 μm-thick polyimide (PI) layer (HD Microsystems

GmbH, catalog no. PI2611) onto a silicon (Si) wafer coated with an aluminum (Al) layer. The

underlying Al acted as a sacrificial layer for subsequent device release. The PI was then baked at

300 °C for 2 hours to complete the imidization process. A 130 nm-thick silicon carbide (SiC) layer

was then deposited via plasma-enhanced chemical vapor deposition (PECVD) using an Oxford

PlasmaLab System 100 under the following conditions: 133 sccm Ar, 60 sccm CH_4, and 375 sccm

of 2% SiH_4 in Ar; RF power of 25 W; substrate temperature of 300 °C; and deposition time of

10 minutes. Next, a metal stack composed of Titanium/Platinum/Gold/Platinum/Titanium

(Ti/Pt/Au/Pt/Ti, thicknesses: 10/10/200/10/10 nm) was sputtered using an AC450 system

(Alliance-Concept) and patterned by lift-off in an ultrasonic acetone bath (80 kHz, 100% power,

10 minutes). A second 130 nm SiC layer was deposited, followed by spin-coating and baking of an

additional PI layer using the same parameters as before. A Titanium/Silicon Oxides (Ti/SiO_2)

bilayer (10/25 nm) was subsequently sputtered onto the top PI surface. The final device patterning

was carried out using an ICP-RIE etch system (Corial 210IL), defining the shape of the cuff and

opening windows for LED integration and soldering. Following the microfabrication steps, solder

paste bumps (~50 μm diameter, Chipquik, catalog no. SMDLTLFP10T5) were manually deposited

onto the exposed contact pads. Micro-LEDs (Cree Inc., catalog no. DA2432) were placed using a

pick-and-place system (JFP Microtechnic) and bonded by heating the wafer on a hotplate at 165 °C,

ensuring both electrical and mechanical connections. To improve hermetic sealing, a 15 wt%

solution of poly(isobutylene) (PIB, Oppanol, BASF) in cyclohexane (Sigma-Aldrich) was applied

to the die surface via pneumatic dispensing. Finally, a 60 μm-thick encapsulating layer of

polydimethylsiloxane (PDMS) was printed, baked at 70 °C for 12 hours, and patterned by blade

cutting. DC voltage was measured using a source meter (Keithley 2400) while sweeping the input

current from 0.5 to 17 mA. Simultaneously, the total optical power output at 470 nm was measured

using a calibrated photodiode (S170C, Thorlabs) connected to a power meter console (PM100D,

Thorlabs). During measurements, the distance between the photodiode and the micro-LEDs was

maintained at approximately 1 mm.

The neuroma or intact sciatic nerve was exposed as described in the sciatic nerve injury

procedure. The LED cuff was positioned beneath the neuroma or intact sciatic nerve at a

perpendicular angle, and its distal end was folded 180° to wrap around the target site. This

configuration placed one set of LEDs on the front and the other on the back of the neuroma or

nerve (Fig. 4b, right). To secure the device, the two proximal anchoring points were sutured to

each other and to the adjacent proximal muscles, while the distal anchoring points were sutured to

the upper thigh muscle for additional stabilization (Fig. 4b, right). 10-0 sutures (Ethicon, #2794G)

were used for these anchoring sites. The wires with a female nano-miniature circular connector

(Omnetics, #A79103-001) were routed subcutaneously to the backside, where a small skin pocket

was created to externalize the connector. The thigh incision was closed using 6-0 sutures, while

the skin pocket was sealed with tissue adhesive (3M Vetbond, #1469). After each experiment, the

placement of the LEDs was confirmed. If displacement occurred (e.g., slippage from the neuroma),

the animal was excluded from analysis.

The following transgenic lines were used to target sensory neuron subtypes: $Sstr2^{T2a\text{-}}$

^{CreER};$Calca\text{-}FlpE$;$R26^{LSL\text{-}FSF\text{-}ReaChR::mCitrine}$ for the Neuroma C-Nociceptor (SSTR2) subtype,

$Mrgprd^{CreER}$;$R26^{LSL\text{-}ReaChR::mCitrine}$ for the C-HTMR/HEAT (MRGPRD) subtype, $Th^{T2a\text{-}}$

^{CreER};$Avil^{FlpO}$;$R26^{LSL\text{-}FSF\text{-}ReaChR::mCitrine}$ for the C-LTMR subtype, $Smr2^{T2a\text{-}Cre}$;$Calca\text{-}FlpE$;$R26^{LSL\text{-}}$

$^{FSF\text{-}ReaChR::mCitrine}$ for the Aδ-HTMR/Heat (SMR2) subtype, $TrkB^{CreER}$;$Avil^{FlpO}$; $R26^{LSL\text{-}FSF\text{-}}$

$^{ReaChR::mCitrine}$ for the Aδ-LTMR subtype, $Mrgpra3^{Cre}$;$R26^{LSL\text{-}ReaChR::mCitrine}$ for the C-HTMR/Heat

(MRGPRA3) subtype, $Mrgprb4^{Cre}$;$R26^{LSL\text{-}ReaChR::mCitrine}$ for the C-HTMR/Heat (MRGPRB4)

subtype, $Cysltr2^{Cre}$;$R26^{LSL\text{-}ReaChR::mCitrine}$ for the C-HTMR/Heat (CYSLTR2/SST) subtype,

Trpm8^{T2a-FlpO}; R26^{FSF -ReaChR::mCitrine} for the C-Cold (TRPM8) subtype. All the mouse lines used to

generate these genetic crosses have been previously described: *Sstr2^{T2a-CreER}* (JAX #039563)[28],

Mrgprd^{CreER} (JAX #031286)[58], *Th^{T2a-CreER}* (JAX #025614)[59], *Smr2^{T2a-Cre}* (JAX #039562)[28],

TrkB^{CreER} (JAX #027214)[60], *Mrgpra3^{Cre61}*, *Mrgprb4^{Cre62}*, *Cysltr2^{Cre}* (JAX #039985)[28], *Trpm8^{T2a-FlpO}*

(JAX #039564[28], *Calca-FlpE^{63}*, *Avil^{FlpO63}*, *R26^{LSL-FSF-ReaChR::mCitrine}* (JAX #024846), *R26^{LSL-}*

^{ReaChR::mCitrine} (JAX #026294), *R26^{FSF-ReaChR::mCitrine}* (derived from JAX #024846 by germline

excision of LSL cassette). All transgenic mouse lines were maintained on a mixed background and

included males and females. CreER lines were induced by a single intraperitoneal injection of

tamoxifen dissolved in sunflower seed oil, prepared as previously described[28]. For *Sstr2^{T2a-CreER}*;

Calca-FlpE; R26^{LSL-FSF-ReaChR::mCitrine}, we administered 3 mg of tamoxifen at 3–4 weeks;

Mrgprd^{CreER};R26^{LSL-ReaChR::mCitrine}, 2 mg at 3-4 weeks; *Th^{T2a-CreER};Avil^{FlpO};R26^{LSL-FSF-ReaChR::mCitrine}*,

2 mg at 3-6 weeks; *TrkB^{CreER}; Avil^{FlpO}; R26^{LSL-FSF-ReaChR::mCitrine}*, 0.5 mg at postnatal day 3 to day 5.

For optogenetic activation, the external connector was coupled to an adapter linked to a

stimulator (AM-Systems, Grass Instruments S88). When mice were in a calm, awake state, a single

10 ms pulse was delivered at various voltages corresponding to different optical power levels with

behaviours recorded by a high-speed camera at 120 Hz. Each power level was tested in 10 trials

with an inter-stimulus interval of >1 minute. Behaviours occurring during stimulation or within 2

s after stimulus offset were counted as positive responses. Response probability was calculated as

the proportion of trials with a behavioural response out of 10 trials for each animal (Fig. 4c). The

occurrence rate of each behaviour type was calculated as the number of trials in which that

behaviour was induced from the ipsilateral neuroma site at 60 mW across all animals, divided by

the total number of trials (i.e., 10 × number of animals) (Fig. 4d). Response latency (Fig. 4e, left)

was defined as the time between opto-stimulation onset (single 10 ms pulse at 60 mW) and the

initiation of the behaviour. Single 10 ms pulses were used for all optogenetic experiments except

in Extended Data Fig. 9a, where repetitive 10 ms pulses at 10 Hz or continuous light (60 mW)

were delivered for 5 s. Cre expression in all animals was verified *post hoc* by histological analysis

following completion of optogenetic experiments (Extended Data Fig. 8).

Survival analysis using a Cox proportional hazards regression model was used to assess whether

flick probability to transcutaneous neuroma pokes predicted the optical threshold for evoked limb

flicks. During optogenetic stimulation, optical power (mW) was increased monotonically and

treated as the ordered analysis variable, with the first limb flick defined as the event. Animals that

did not flick at the maximum tested power (60 mW) were right-censored. Von Frey flick

probability (0–1) was included as a continuous covariate. Hazard ratios with 95% confidence

intervals were reported, and significance was assessed using the likelihood-ratio test (Fig. 4e, right).

Histology

Neuromas, contralateral intact sciatic nerves, or DRG were fixed in 4% paraformaldehyde (PFA)

in PBS at 4 °C overnight. Nerves were cryoprotected in 30% sucrose in PBS at 4 °C for one to two

days, embedded in OCT compound (Sakura Finetek) on dry ice, and cryosectioned longitudinally

(parallel to the axon trajectory) at 50 μm. DRG were fixed and processed for whole-mount staining.

Sections or whole DRG were permeabilized in 1% Triton X-100 in PBS for 20 minutes and blocked

in 10% normal donkey with 0.3% Triton X-100 in PBS overnight at 4 °C. Primary antibody

incubation was performed overnight at 4 °C in blocking solution (1:500) using anti-GFP (Thermo

Fisher, #A10262) and anti-PGP9.5 (Abcam, #ab108986). Secondary antibodies were incubated for

2 hours at room temperature or overnight at 4 °C in blocking solution (1:500): Cy5-conjugated

donkey anti-rabbit (Jackson ImmunoResearch, #711-175-152) and Alexa Fluor 488–conjugated

donkey anti-chicken (Jackson ImmunoResearch, #703-545-155). Images were acquired on a Leica

SP8 confocal microscope at 1024 × 1024 resolution. Whole DRG were imaged in 60 mm glass-

bottom dishes using 10× or 20× air objectives with 2–5 µm z-steps. Neuromas and contralateral

nerves were captured by tile scan using a 10× air objective with 2 µm z-steps. Post-processing was

performed with LAS X Life Science software (Leica).

fibre density (Extended Data Fig. 8) was quantified from mCitrine reporter signal in neuromas

and contralateral sciatic nerves using ImageJ. Each neuroma and contralateral nerve typically

yielded ~20 and ~12 longitudinal cryosections, respectively; the middle three consecutive slices

were selected to minimize epineural tissue interference. Images were converted to 8-bit grayscale,

background-subtracted, and thresholded to generate binary masks of axonal fibres. A 50 × 50 µm

region of interest (ROI) was placed at the neuroma tip or corresponding contralateral nerve center,

and the axon-occupied area within this ROI was measured. fibre density was expressed as the

fraction of axon-positive area relative to total ROI area. Values from three slices were averaged to

obtain one measurement per sample.

***In situ* hybridization combined with immunohistochemistry**

L4 DRG were dissected under 2% isoflurane anaesthesia and embedded in OCT on dry ice. The

tissues were then cryosectioned at a thickness of 20 µm and stored at -80°C until processing. To

assess the co-expression of *Sstr2* mRNA and mCitrine protein (Extended Data Fig. 9b), *in situ*

hybridization (ISH) was performed using the RNAscope (Advanced Cell Diagnostics) combined

with immunohistochemistry (IHC). Sections were processed according to the manufacturer's ISH

instructions using the RNAscope H2O2 and Protease Reagents, the RNAscope Multiplex

Fluorescent Detection Kit v2, with *Sstr2* (Cat. # 437681-C2) detected via Akoya Opal Dye 570.

Immediately following the RNAscope protocol, IHC was performed to detect mCitrine expression.

Briefly, slides were blocked with 10% Normal Donkey Serum with PBST (1X PBS with 0.1%

Tween20) for 15 minutes at room temperature. Primary antibody incubation was performed for 1

hr at room temperature in blocking solution using goat anti-GFP antibody (1:500; US Biological

Life Sciences, G8965-01E). Following two 5-minute rinses in PBST, secondary antibodies

incubation was performed for 40 min at room temperature in blocking solution using Donkey anti-

Goat Alexa Fluor 488 (ThermoFisher Scientific, A-11055). After the final washes, sections were

counterstained with DAPI and coverslipped. Confocal images were acquired using a Zeiss LSM

900 microscope equipped with 10X and 20X air objectives.

snRNA-seq of DRG across pain conditions

From a parent cohort of 60 mice, L4 and L5 DRG were collected from 18 mice (9 males and 9

females) that consistently exhibited a high-pain phenotype across 8–10 weeks post-SNT, with

phenotyping performed weekly and tissue collected at 10 weeks, and from 18 mice (9 males and

9 females) that consistently exhibited a low-pain phenotype over the same period. 36 contralateral

L4 and L5 DRG from both high- and low-pain mice were combined as the control group.

All nuclear extraction steps were performed on ice, or at 4 °C. Frozen L4 and L5 DRG, collected

on dry ice in DNA/RNA LoBind tubes (Qiagen) were homogenized in NST buffer: 50 ml NST

buffer contained 25 ml of 2x ST buffer, 1ml of 10% IGPAL, 1.4 ml of 35% BSA, and 22.6 ml

nuclease-free water, and was prepared from ST buffer, containing 146 mM NaCl, 10 mM Tris-HCl,

pH 7.5, 1 mM $CaCl_2$, and 21 mM $MgCl_2$[64]. For each sample, 7.5 ml of ST and 7.5 ml of NST

buffer were prepared and 10 µl of Rnasin was added to each. For each sample, 1 ml cold NST

buffer (on ice) was added directly to the tube containing frozen DRG, allowed to thaw for 15–30

seconds, and DRG were transferred to a 7 ml Dounce Wheaton homogenizer containing 4 ml of

NST buffer, and homogenized with 5 strokes with the loose pestle and 15 strokes with the tight

pestle. The homogenate was then filtered through a 40 μm cell filter into a 50 ml Falcon tube on

ice. 5 ml of ST buffer was added to the homogenizer, and any remaining homogenate was collected

and also pipetted through the 40 μm cell filter. 10 ml of filtered homogenate then filtered through

a 20 μm cell filter into a 15 ml Falcon tube on ice. The homogenizer was thoroughly rinsed between

samples. Samples were centrifuged at $500 \times g$ for 10 minutes at 4 °C. The supernatant was removed

and the pellet was resuspended in 1 ml of ST buffer. 10 µl of Hoechst was added for a final

concentration of 0.5 µg/ml, and the samples were FACS sorted to isolate nuclei.

Nuclei suspensions were sequenced using 10x Genomics assays, resuspended, and loaded into

the 10x Chromium device for snRNA-seq (10x Genomics 3' v3). Libraries were prepared for

snRNA-seq according to the manufacturer's protocol. Libraries were sequenced on an Illumina

NovaSeqX (Azenta). Sequencing data were processed and mapped to the mouse (mm10) genome

using 10x Genomics cellranger v9 using default parameters. We ran the remove-background

function of Cellbender (v0.3.0) to remove ambient RNA and empty droplets from raw expression

matrices using default parameters.

We followed a similar cell type annotation and clustering approach as previously described[30,47],

and adopted the established physiological nomenclature for each neuronal subtype as shown in

Table 1 in a reference study[28]. Seurat v4 was used to perform quality control, data normalization,

cell type annotation and comparison between neuroma conditions[65]. Nuclei with >1000 genes and

<10% of mitochondrial counts were included for analysis. We found 2000 variable genes for each

library after log-normalization, and then integration anchors were selected across all libraries. The

data were then scaled, and we selected PCs on the basis of the point where the PC only contributes

to 5% of SD of highly variable gene expression and all PCs cumulatively contributed to 90% of

the SD of highly variable gene expression. The libraries were then integrated using Seurat's CCA

algorithm, and nuclei were clustered and plotted in UMAP space at a resolution of 0.5. A Wilcoxon

rank sum test was performed between the clusters to identify marker genes. We annotated clusters

that were $Snap25^+$ ($\log_2$FC > 0.5 and adjusted P value < 0.05 relative to all other clusters) as

"neurons" and clusters that were $Sparc^+$ ($\log_2$FC > 0.5 and adjusted P value < 0.05 relative to all

other clusters) as "non-neurons." Neurons were then separated and reintegrated using a resolution

of 1. We annotated neurons using marker gene expression (Extended Data Fig. 6a; $\log_2$FC > 0.5;

adjusted p-value < 0.05 relative to all other clusters). Clusters were labelled as doublets if they

contained both expression of $Snap25$, Mpz, and $Sparc$ ($\log_2$FC > 0.5 and adjusted P value < 0.05

relative to all other clusters). Doublets were then removed, and the nuclei were reintegrated using

the same parameters as described and then reannotated for a final time. To identify genes

differentially expressed between conditions within each subtype, we used the Wilcoxon rank-sum

test.

Directional concordance scores for each gene within each cell type were computed from its $\log_2$

fold-change ($\log_2$FC) values between the high-pain vs. low-pain and high-pain vs. control

comparisons (Extended Data Fig. 6c), defined as:

725
$$\begin{cases} +\sqrt{|\log_2\text{FC}_{\text{high pain/low pain}} \cdot \log_2\text{FC}_{\text{high pain/control}}|}, \text{if both } \log_2\text{FC} > 0 \text{ (upregulated in both)} \\ -\sqrt{|\log_2\text{FC}_{\text{high pain/low pain}} \cdot \log_2\text{FC}_{\text{high pain/control}}|}, \text{if both } \log_2\text{FC} < 0 \text{ (downregulated in both)} \\ 0, \text{otherwise (opposite directions or no change)} \end{cases}$$

For gene ontology (GO) analysis, we used EnrichR [66] to assess functional enrichment. We

selected genes significantly enriched in the Neuroma C-Nociceptor (SSTR2) population under the

high pain condition ($\log_2$FC > 0.5; adjusted p < 0.05), compared to either the Neuroma C-

Nociceptor (SSTR2) cells in the low-pain condition or the contralateral control condition. As the

background gene list, we used all genes expressed in the Neuroma C-Nociceptor (SSTR2)

population.

Statistical analysis

All statistical analyses, except for snRNA-seq data, were performed using GraphPad Prism, with

the exact tests and P values reported in the figures, figure legends, or source data.

Data availability

All data supporting the findings of this study are available within the manuscript. Reagents are

available from the corresponding authors upon reasonable request. snRNA-seq will be deposited

into GEO upon manuscript acceptance.

Acknowledgements We thank Dr. Bruce P. Bean and members of the Ginty and Woolf laboratories for their constructive feedback. We thank Kitwa Ng for helpful comments on the manuscript. We also thank the IDDRC Animal Behavior and Physiology Core, funded by NIH/NICHD P50HD105351 and IDDRC Cellular Imaging Core, funded by NIH P50 HD105351 at Boston Children's Hospital. Schematics and illustrations were created with BioRender.com. This work was supported by the International Human Frontier Science Program Organization LT0026/2023-L (X.Z.), NIH grants R35NS105076 (C.J.W.), R35NS097344 (D.D.G.), R35NS132196 (D.D.G.), and R01AT011447 (D.D.G. and C.J.W.), the Edward R. and Anne G. Lefler Center for Neurodegenerative Disorders (D.D.G.), and the K. Lisa Yang Brain Body Center at Harvard Medical School (D.D.G.). D.D.G. is an investigator of the Howard Hughes Medical Institute. This article is subject to HHMI's Open Access to Publications policy. HHMI lab heads have previously granted a nonexclusive CC BY 4.0 license to the public and a sublicensable license to HHMI in their research articles. Pursuant to those licenses, the author-accepted manuscript of this article can be made freely available under a CC BY 4.0 license immediately upon publication.

Author contributions X.Z., D.D.G., and C.J.W. conceived the study. X.Z. performed all experiments and analysed the data, with assistance from R.M.G. (generation of transgenic mouse lines and *in situ* hybridization), S.A.B. (snRNA-seq), K.H. (histology), N.M.B., E.B., E.S. (behavioural studies and histology), K.W. (LED cuff design), O.B. (automated behavioural screen), B.L.T. (acute pain experiments), S.S.J., B.G.E. (tissue collection for snRNA-seq), M.Q.H. (home-cage EMG setup), C.S. (Piezo2-knockout experiments), K.L. (generation of transgenic mouse lines and *in situ* hybridization), E.O.A. (generation of transgenic mouse lines), and I.F. (LED cuff calibration). A.R. provided resource for the home-cage EMG experiments. B.R.J. provided

expertise on and assisted with the transcutaneous neuroma poke tests. B.J.W. provided expertise on the behavioural experiments. W.R. provided resource and oversight of the snRNA-seq experiments. S.P.L. provided resource and oversight of LED cuff design. D.D.G. and C.J.W. supervised the project. X.Z., D.D.G., and C.J.W. wrote the manuscript with input from all authors.

Competing interests X.Z., D.D.G., and C.J.W. are consultants for Alive Molecular Technologies, Inc. D.D.G. is a founder of Krause Therapeutics, and C.J.W. is a founder of Nocion Therapeutics, Quralis, and BlackBox Bio, and serves on the scientific advisory boards of Lundbeck Pharma, Axonis, Niroda, Mimetic Medicine, Tenvie Therapeutics, and Tafalgie Therapeutics.

References

References

1   Bouhassira, D. *et al.* Comparison of pain syndromes associated with nervous or
somatic lesions and development of a new neuropathic pain diagnostic
questionnaire   (DN4).   *Pain*   **114**,   29-36   (2005).
https://doi.org/10.1016/j.pain.2004.12.010
2   Bouhassira, D. *et al.* Development and validation of the Neuropathic Pain Symptom
Inventory. *Pain* **108**, 248-257 (2004). https://doi.org/10.1016/j.pain.2003.12.024
3   Maier, C. *et al.* Quantitative sensory testing in the German Research Network on
Neuropathic Pain (DFNS): somatosensory abnormalities in 1236 patients with
different   neuropathic   pain   syndromes.   *Pain*   **150**,   439-450   (2010).
https://doi.org/10.1016/j.pain.2010.05.002
4   Buch, N. S., Qerama, E., Brix Finnerup, N. & Nikolajsen, L. Neuromas and
postamputation   pain.   *Pain*   **161**,   147-155   (2020).
https://doi.org/10.1097/j.pain.0000000000001705
5   Hwang, C. D. *et al.* Biology and pathophysiology of symptomatic neuromas. *Pain* **165**,
550-564 (2024). https://doi.org/10.1097/j.pain.0000000000003055
6   Sandkuhler, J. Models and mechanisms of hyperalgesia and allodynia. *Physiol Rev* **89**,
707-758 (2009). https://doi.org/10.1152/physrev.00025.2008
7   Tappe-Theodor, A. & Kuner, R. Studying ongoing and spontaneous pain in rodents--
challenges   and   opportunities.   *Eur   J   Neurosci*   **39**,   1881-1890   (2014).
https://doi.org/10.1111/ejn.12643
8   Langford, D. J. *et al.* Coding of facial expressions of pain in the laboratory mouse. *Nat*
Methods **7**, 447-449 (2010). https://doi.org/10.1038/nmeth.1455
9   King, T. *et al.* Unmasking the tonic-aversive state in neuropathic pain. *Nat Neurosci*
12, 1364-1366 (2009). https://doi.org/10.1038/nn.2407
10   Attal, N. *et al.* Neuropathic pain: are there distinct subtypes depending on the
aetiology   or   anatomical   lesion?   *Pain*   **138**,   343-353   (2008).
https://doi.org/10.1016/j.pain.2008.01.006
11   Zheng, Q. *et al.* Synchronized cluster firing, a distinct form of sensory neuron
activation,   drives   spontaneous   pain.   *Neuron*   **110**,   209-220 e206   (2022).
https://doi.org/10.1016/j.neuron.2021.10.019
12   Djouhri, L., Koutsikou, S., Fang, X., McMullan, S. & Lawson, S. N. Spontaneous pain,
both neuropathic and inflammatory, is related to frequency of spontaneous firing in
intact   C-fiber   nociceptors.   *J   Neurosci*   **26**,   1281-1292   (2006).
https://doi.org/10.1523/JNEUROSCI.3388-05.2006
13   Gangadharan, V. *et al.* Neuropathic pain caused by miswiring and abnormal end
organ targeting. *Nature* **606**, 137-145 (2022). https://doi.org/10.1038/s41586-022-
04777-z
14   Wu, G. *et al.* Early onset of spontaneous activity in uninjured C-fiber nociceptors after
injury   to   neighboring   nerve   fibers.   *J   Neurosci*   **21**,   RC140   (2001).
https://doi.org/10.1523/JNEUROSCI.21-08-j0002.2001

15   Wu, G. *et al.* Degeneration of myelinated efferent fibers induces spontaneous activity
in uninjured C-fiber afferents. *J Neurosci* **22**, 7746-7753 (2002).
https://doi.org/10.1523/JNEUROSCI.22-17-07746.2002
16   Kehlet, H., Jensen, T. S. & Woolf, C. J. Persistent postsurgical pain: risk factors and
prevention. *Lancet* **367**, 1618-1625 (2006). https://doi.org/10.1016/S0140-
6736(06)68700-X
17   Fillingim, R. B. Individual differences in pain: understanding the mosaic that makes
pain personal. *Pain* **158 Suppl 1**, S11-S18 (2017).
https://doi.org/10.1097/j.pain.0000000000000775
18   Barkai, O. *et al.* A machine learning tool with light-based image analysis for automatic
classification of 3D pain behaviours. *Cell Rep Methods*, 101145 (2025).
https://doi.org/10.1016/j.crmeth.2025.101145
19   Su, P. P., He, L., Zhang, L., Yu, J. & Guan, Z. Saphenous-sural nerve injury: a sensory-
specific rodent model of neuropathic pain without motor deficits. *Pain* (2025).
https://doi.org/10.1097/j.pain.0000000000003722
20   Bumgarner, J. R., Walker, W. H., 2nd & Nelson, R. J. Circadian rhythms and pain.
Neurosci Biobehav Rev **129**, 296-306 (2021).
https://doi.org/10.1016/j.neubiorev.2021.08.004
21   Oliveira, K. M. C. *et al.* Time course of traumatic neuroma development. *PLoS One* **13**,
e0200548 (2018). https://doi.org/10.1371/journal.pone.0200548
22   Arnold, D. M. J. *et al.* Diagnostic Criteria for Symptomatic Neuroma. *Ann Plast Surg*
82, 420-427 (2019). https://doi.org/10.1097/SAP.0000000000001796
23   Miclescu, A., Schmelz, M. & Gordh, T. Differential analgesic effects of subanesthetic
concentrations of lidocaine on spontaneous and evoked pain in human painful
neuroma: A randomized, double blind study. *Scand J Pain* **8**, 37-44 (2015).
https://doi.org/10.1016/j.sjpain.2015.04.026
24   Roza, C., Laird, J. M., Souslova, V., Wood, J. N. & Cervero, F. The tetrodotoxin-resistant
Na+ channel Nav1.8 is essential for the expression of spontaneous activity in
damaged sensory axons of mice. *J Physiol* **550**, 921-926 (2003).
https://doi.org/10.1113/jphysiol.2003.046110
25   Choi, D. *et al.* Spontaneous activity in peripheral sensory nerves: a systematic review.
Pain **165**, 983-996 (2024). https://doi.org/10.1097/j.pain.0000000000003115
26   Decosterd, I. & Woolf, C. J. Spared nerve injury: an animal model of persistent
peripheral neuropathic pain. *Pain* **87**, 149-158 (2000). https://doi.org/10.1016/S0304-
3959(00)00276-1
27   Usoskin, D. *et al.* Unbiased classification of sensory neuron types by large-scale
single-cell RNA sequencing. *Nat Neurosci* **18**, 145-153 (2015).
https://doi.org/10.1038/nn.3881
28   Qi, L. *et al.* A mouse DRG genetic toolkit reveals morphological and physiological
diversity of somatosensory neuron subtypes. *Cell* **187**, 1508-1526 e1516 (2024).
https://doi.org/10.1016/j.cell.2024.02.006
29   Sharma, N. *et al.* The emergence of transcriptional identity in somatosensory neurons.
Nature **577**, 392-398 (2020). https://doi.org/10.1038/s41586-019-1900-1

30   Bhuiyan, S. A. *et al.* Harmonized cross-species cell atlases of trigeminal and dorsal
root ganglia. *Sci Adv* **10**, eadj9173 (2024). https://doi.org/10.1126/sciadv.adj9173

31   Krauter, D. *et al.* Spatial organization, chromatin accessibility and gene-regulatory
programs defining mouse sensory neurons. *Commun Biol* **8**, 908 (2025).
https://doi.org/10.1038/s42003-025-08315-1

32   Michoud, F. *et al.* Epineural optogenetic activation of nociceptors initiates and
amplifies inflammation. *Nat Biotechnol* **39**, 179-185 (2021).
https://doi.org/10.1038/s41587-020-0673-2

33   Wolfson, R. L. *et al.* DRG afferents that mediate physiologic and pathologic
mechanosensation from the distal colon. *Cell* **186**, 3368-3385 e3318 (2023).
https://doi.org/10.1016/j.cell.2023.07.007

34   Bhuiyan, S. A. *et al.* A Reference Atlas of the Human Dorsal Root Ganglion. *bioRxiv*
(2025). https://doi.org/10.1101/2025.11.05.686654

35   Lezgiyeva, K. *et al.* Fast-conducting mechanonociceptors uniquely engage reflexive
and affective pain circuitry to drive protective responses. *bioRxiv* (2025).
https://doi.org/10.1101/2025.11.11.687663

36   Cooper, A. H. *et al.* Peripheral nerve injury results in a biased loss of sensory neuron
subpopulations. *Pain* **165**, 2863-2876 (2024).
https://doi.org/10.1097/j.pain.0000000000003321

37   Dhandapani, R. *et al.* Control of mechanical pain hypersensitivity in mice through
ligand-targeted photoablation of TrkB-positive sensory neurons. *Nat Commun* **9**,
1640 (2018). https://doi.org/10.1038/s41467-018-04049-3

38   Yarmolinsky, D. A. *et al.* Differential modification of ascending spinal outputs in acute
and chronic pain states. *Neuron* **113**, 1223-1239 e1225 (2025).
https://doi.org/10.1016/j.neuron.2025.01.031

39   Murthy, S. E. *et al.* The mechanosensitive ion channel Piezo2 mediates sensitivity to
mechanical pain in mice. *Sci Transl Med* **10** (2018).
https://doi.org/10.1126/scitranslmed.aat9897

40   Gottrup, H., Bach, F. W., Juhl, G. & Jensen, T. S. Differential effect of ketamine and
lidocaine on spontaneous and mechanical evoked pain in patients with nerve injury
pain. *Anesthesiology* **104**, 527-536 (2006). https://doi.org/10.1097/00000542-
200603000-00021

41   Murai, N. *et al.* Spontaneous and evoked pain-associated behaviours in a rat model
of neuropathic pain respond differently to drugs with different mechanisms of action.
Pharmacol Biochem Behav **141**, 10-17 (2016).
https://doi.org/10.1016/j.pbb.2015.11.008

42   Deseure, K. & Hans, G. H. Differential drug effects on spontaneous and evoked pain
behaviour in a model of trigeminal neuropathic pain. *J Pain Res* **10**, 279-286 (2017).
https://doi.org/10.2147/JPR.S124526

43   Hung, C. H., Wang, J. C. & Strichartz, G. R. Spontaneous Chronic Pain After
Experimental Thoracotomy Revealed by Conditioned Place Preference: Morphine
Differentiates Tactile Evoked Pain From Spontaneous Pain. *J Pain* **16**, 903-912 (2015).
https://doi.org/10.1016/j.jpain.2015.06.006

44   Zeng, X., Powell, R. & Woolf, C. J. Mechanism-based nonopioid analgesic targets. *J*
Clin Invest **135** (2025). https://doi.org/10.1172/JCI191346
45   Madigan, V., Zhang, F. & Dahlman, J. E. Drug delivery systems for CRISPR-based
genome   editors.   *Nat   Rev   Drug   Discov*   **22**,   875-894   (2023).
https://doi.org/10.1038/s41573-023-00762-x
46   Raj, A. & van Oudenaarden, A. Nature, nurture, or chance: stochastic gene expression
and   its   consequences.   *Cell*   **135**,   216-226   (2008).
https://doi.org/10.1016/j.cell.2008.09.050
47   Renthal, W. *et al*. Transcriptional Reprogramming of Distinct Peripheral Sensory
Neuron   Subtypes   after   Axonal   Injury.   *Neuron*   **108**,   128-144   e129   (2020).
https://doi.org/10.1016/j.neuron.2020.07.026
48   Znaor, L., Lovric, S., Hogan, Q. & Sapunar, D. Association of neural inflammation with
hyperalgesia following spinal nerve ligation. *Croat Med J* **48**, 35-42 (2007).
49   Yan, H., Gao, W., Pan, Z., Zhang, F. & Fan, C. The expression of alpha-SMA in the
painful traumatic neuroma: potential role in the pathobiology of neuropathic pain. *J*
Neurotrauma **29**, 2791-2797 (2012). https://doi.org/10.1089/neu.2012.2502
50   Deininger, S. *et al*. Nerve injury converts Schwann cells in a long-term repair-like state
in   human   neuroma   tissue.   *Exp   Neurol*   **382**,   114981   (2024).
https://doi.org/10.1016/j.expneurol.2024.114981
51   Khan, J., Noboru, N., Young, A. & Thomas, D. Pro and anti-inflammatory cytokine
levels (TNF-alpha, IL-1beta, IL-6 and IL-10) in rat model of neuroma. *Pathophysiology*
24, 155-159 (2017). https://doi.org/10.1016/j.pathophys.2017.04.001
52   Austin, P. J. *et al*. Evidence for a distinct neuro-immune signature in rats that develop
behavioural   disability   after   nerve   injury.   *J Neuroinflammation* **12**,   96   (2015).
https://doi.org/10.1186/s12974-015-0318-4
53   Zhang, Z. *et al*. Automated preclinical detection of mechanical pain hypersensitivity
and   analgesia.   *Pain*   **163**,   2326-2336   (2022).
https://doi.org/10.1097/j.pain.0000000000002680
54   Chaplan, S. R., Bach, F. W., Pogrel, J. W., Chung, J. M. & Yaksh, T. L. Quantitative
assessment of tactile allodynia in the rat paw. *J Neurosci Methods* **53**, 55-63 (1994).
https://doi.org/10.1016/0165-0270(94)90144-9
55   Santiago, C. *et al*. Activity-dependent development of the body's touch receptors.
Neuron **113**, 1758-1773 e1759 (2025). https://doi.org/10.1016/j.neuron.2025.04.015
56   Nonomura, K. *et al*. Piezo2 senses airway stretch and mediates lung inflation-
induced apnoea. *Nature* **541**, 176-181 (2017). https://doi.org/10.1038/nature20793
57   Giovannucci, A. *et al*. CaImAn an open source tool for scalable calcium imaging data
analysis. *Elife* **8** (2019). https://doi.org/10.7554/eLife.38173
58   Olson, W. *et al*. Sparse genetic tracing reveals regionally specific functional
organization   of   mammalian   nociceptors.   *Elife*   **6**   (2017).
https://doi.org/10.7554/eLife.29507
59   Abraira, V. E. *et al*. The Cellular and Synaptic Architecture of the Mechanosensory
Dorsal   Horn.   *Cell*   **168**,   295-310   e219   (2017).
https://doi.org/10.1016/j.cell.2016.12.010

60 Rutlin, M. *et al*. The cellular and molecular basis of direction selectivity of Adelta-
LTMRs. *Cell* **159**, 1640-1651 (2014). https://doi.org/10.1016/j.cell.2014.11.038

61 Han, L. *et al*. A subpopulation of nociceptors specifically linked to itch. *Nat Neurosci*
16, 174-182 (2013). https://doi.org/10.1038/nn.3289

62 Vrontou, S., Wong, A. M., Rau, K. K., Koerber, H. R. & Anderson, D. J. Genetic
identification of C fibres that detect massage-like stroking of hairy skin in vivo. *Nature*
493, 669-673 (2013). https://doi.org/10.1038/nature11810

63 Choi, S. *et al*. Parallel ascending spinal pathways for affective touch and pain. *Nature*
587, 258-263 (2020). https://doi.org/10.1038/s41586-020-2860-1

64 Slyper, M. *et al*. A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen
human tumors. *Nat Med* **26**, 792-802 (2020). https://doi.org/10.1038/s41591-020-
0844-1

65 Hao, Y. *et al*. Integrated analysis of multimodal single-cell data. *Cell* **184**, 3573-3587
e3529 (2021). https://doi.org/10.1016/j.cell.2021.04.048

66 Chen, E. Y. *et al*. Enrichr: interactive and collaborative HTML5 gene list enrichment
analysis tool. *BMC Bioinformatics* **14**, 128 (2013). https://doi.org/10.1186/1471-
2105-14-128

67 Burek, D. J. *et al*. Inflammatory pain in mice induces light cycle-dependent effects on
sleep architecture. *Neuropsychopharmacology* **50**, 1595-1605 (2025).
https://doi.org/10.1038/s41386-025-02152-w

Fig.1

Fig. 1 | Neuromas drive chronic spontaneous neuropathic pain. a, Schematic of the home-cage EMG/video recording system (top) and representative EMG trace of limb flick bouts (bottom) after SNT. **b**, Coefficient of variation (CV) of spontaneous limb flick counts following binning of 24-hour recordings into different time windows (0.5, 1, 2, 4, 6, and 12 hours). Each dot represents one recording from an SNT mouse (n = 10). A subset of five mice was recorded for 6 consecutive days to compute CV across extended 12-, 24-, and 48-hour windows. Data are mean ± SEM. *P* values from one-way ANOVA with Tukey's multiple comparisons within each dataset. **c**, Spontaneous limb flick counts quantified in 4-hour bins over 24 hours at indicated time points post-SNT. Light phase: 7:00 a.m.–7:00 p.m.; dark phase: 7:00 p.m.–7:00 a.m. Solid lines and shaded bands represent mean ± SEM across n = 10 SNT mice. **d**, Total 24-hour spontaneous flick counts in individual mice after sham surgery (n = 5) or SNT (n = 10). Data are mean ± SEM; dashed lines connect individual mice. *P* values from two-way ANOVA with Tukey's multiple comparisons (figure shows the interaction effect of sham vs SNT over time). **e**, Confocal images of a neuroma (8 weeks post-SNT) and contralateral intact nerve labelled with a neuronal axonal marker PGP9.5. **f**, Flick probability in response to transcutaneous neuroma poke after sham surgery or SNT in the same mice shown in (**d**). **g**, Pearson's correlation between spontaneous flick counts (**d**) and flick probability (**f**) at indicated time points post-SNT. **h**, Flick probability to poke (top) and spontaneous flick counts over 30 minutes (bottom) before and after local lidocaine injection at the neuroma site (8–12 weeks post-SNT, n = 10 high-pain mice). Data are mean ± SEM; dashed lines connect individual mice. *P* values from two-sided Wilcoxon matched-pairs signed-rank test.

Fig.2

a *VgluT2^Cre^;GCaMP6f (8–12 weeks SNT)*

b Neuroma poke (ipsilateral L4 DRG)

Cell 1–8

ΔF/F
0   0.5   1.0

Intact nerve poke (contralateral L4 DRG)

Cell 1–6

10 seconds

c
- - - Intact nerve poke
—— Neuroma poke

● Small (<25μm)   Neuroma poke vs intact nerve poke:
● Medium (25–40μm)   *p = 0.0012*
● Large (>40μm)   *p = 0.1337*
                            p = 0.1792

Cohen's d

0.68   0.76   1.47   1.32   1.77   1.75   1.94   1.82   1.66

# of responsive cells to poke (y-axis, 0–15)

Mechanical force (g): 0.04 0.07 0.16 0.4 0.6 1 1.4 2 4

d Small-diameter neurons

r = 0.76
p = 0.0018

Cumulative peak ΔF/F (y-axis, 0–8)
Flick probability to poke (behavior) (x-axis, 0.0–1.0)

e Spontaneous activity (ipsilateral L4 DRG)

Cell 1–11

ΔF/F
0   0.25   0.50

Spontaneous activity (contralateral L4 DRG)

Cell 1–5

1 minute

Small   Medium   Large

p = 0.03   *p = 0.78*   *p = 0.43*

# of spontaneously active cells (y-axis, 0–15)
Contra. Ipsi. Contra. Ipsi. Contra. Ipsi.

f Ipsilateral L4 DRG

Neuroma poke responsive
Spontaneously active
Dual-active (overlap)

25 μm

g
Spontaneous activity (peak ΔF/F) (y-axis 0–1.5)
GMM decision boundary

Dual-active
5 cells
Small (60%)
Medium (23%)
Large (0%)
45 cells

GMM decision boundary

Neuroma poke-induced activity (peak ΔF/F) (x-axis 0–1.5)

h 1% lidocaine, 10μl

p = 0.0078

# of spontaneously active cells (y-axis, 0–15)
Pre   Post

Fig. 2 | Small-diameter DRG neurons respond to neuroma poke and exhibit ectopic spontaneous activity. a, Schematic of the *in vivo* DRG imaging setup. **b**, Calcium activity heatmaps from individual DRG neurons from one representative mouse in response to a 1.4 g von Frey filament applied to the neuroma or to the contralateral intact nerve. Arrowheads indicate stimulus timing. For intact nerve poke, cells were defined by responses to plantar paw stimulation with the same filament, as no cells showed detectable responses to the nerve poke. **c**, Quantification of responsive cells by soma diameter, small (<25 μm), medium (25–40 μm), and large (>40 μm), across a range of mechanical forces applied with von Frey filaments. Data are mean ± SEM from 14 ipsilateral and contralateral L4 DRG (n = 14 mice). *P* values from two-way ANOVA with Tukey's multiple comparisons (figure shows the interaction effect of neuroma poke vs intact nerve poke across mechanical forces). Cohen's d effect sizes are shown for small-diameter neurons (neuroma poke versus intact nerve poke). **d**, Pearson's correlation between the cumulative peak ΔF/F of responsive small-diameter DRG neurons to neuroma poke (1.4 g von Frey) and behavioural flick probability to transcutaneous neuroma poke. Each dot represents one mouse. **e**, Representative heatmaps of spontaneous calcium activity from individual neurons from one representative mouse in ipsilateral and contralateral L4 DRG (top), and quantification of spontaneously active cells of each size during 30-minute recordings (bottom). Data are mean ± SEM; each dot represents one L4 DRG (n = 14 DRG from 14 mice). *P* values from two-sided paired t-tests. **f**, Example overlay of cells spontaneously active (blue) and cells responsive to neuroma poke (yellow); dual-active cells are overlaid (white). **g**, Classification of cells solely responsive to neuroma poke, solely spontaneously active, or dual-active, based on peak activity amplitude determined by Gaussian Mixture Model (GMM) boundaries (dashed lines). Percentages indicate the proportion of dual-active cells relative to the total number of cells of each size. Pie chart depicts the cell distribution within the dual-active category. Each dot represents one cell. **h**, Number of spontaneously active small-diameter cells before and 5 minutes after topical application of lidocaine to the neuroma. Data are mean ± SEM; dashed lines connect ipsilateral L4 DRG from individual mice (n = 8). *P* value from two-sided Wilcoxon matched-pairs signed-rank test.

Fig.3

1010

Fig. 3 | Distinct DRG neuron populations mediate pain from intact versus injured sensory fibres. a, Schematic of the plantar von Frey assay targeting the medial plantar area innervated by the intact saphenous nerve (left) and quantification of the 50% withdrawal threshold (right). Each dot represents one mouse (n = 20). Data are mean ± SEM. *P* values from one-way ANOVA with Tukey's multiple comparisons. **b**, Pearson's correlation between the 50% withdrawal threshold from medial plantar poke and flick probability to transcutaneous neuroma poke at 8 weeks post-SNT. Each dot represents one mouse. **c**, Schematic of the *in vivo* L4 DRG calcium imaging setup for neuroma or medial plantar poke with a 1.4 g von Frey filament (top), and an example overlay showing cells responsive to neuroma poke and medial plantar poke (bottom). **d**, Classification of cells responsive to neuroma poke or medial plantar poke based on peak ΔF/F amplitude determined by GMM boundaries (dashed lines). Each dot represents one cell; no dual-responsive cells were observed. **e**, Calcium traces from neuroma poke-responsive (yellow) and medial plantar poke-responsive (blue) cells. Shaded bands indicate mean ± SEM from n = 5 mice (neuroma poke) and n = 4 mice (medial plantar poke). **f**, Quantification of response amplitude, duration, rising time, and falling time for each group. Each dot represents one cell. *P* values from two-sided Mann–Whitney tests. **g,h**, Number of cells responsive to a neuroma poke (yellow) or a medial plantar poke (blue) before and after topical lidocaine application to the neuroma (**g**) or intraplantar injection (**h**). Tests were performed 5 minutes after lidocaine administration. Data are mean ± SEM; dashed lines connect individual mice (n = 8 for neuroma application, n = 6 for medial plantar injection). *P* values from two-sided Wilcoxon matched-pairs signed-rank tests.

Fig.4

1029

Fig. 4 | **Neuroma C-Nociceptors (SSTR2) drive limb flicks. a**, UMAP projections of DRG snRNA-seq

showing nuclei from contralateral DRG (control), ipsilateral DRG from low-pain, and high-pain mice (left)

and annotated sensory-neuron subtype identities (right). 10 weeks post-SNT mice were used for snRNA-

seq. **b**, Photograph of the miniaturized blue LED cuff (top), schematic cross-section of the interconnects

showing layered materials (bottom left; softness and flexibility were achieved by miniaturizing metal

interconnects and incorporating soft polymer layers; see Extended Data Fig. 7 for details), and illustration

of the implantation site for neuroma or intact sciatic nerve stimulation (right). **c**, Optogenetic activation of

genetically defined neuronal subtypes (see Methods for the transgenic lines targeting each subtype). Optical

power versus response probability for individual transgenic lines (10 trials per animal; single 10 ms pulse).

Data are mean ± SEM; dashed lines connect individual mice. *P* values from two-way ANOVA with Tukey's

multiple comparisons (figure shows the interaction effect of neuroma versus intact nerve stimulation across

optical powers). **d**, Histograms showing the occurrence of different behaviours evoked at maximum optical

neuroma stimulation (60 mW) using single 10-ms pulses. Note that multiple behaviours could occur in a

single trial. **e**, Left: response latencies of individual behaviours relative to stimulus onset; data are mean ±

SEM, each dot represents a single trial across n = 10 mice. Right: Cumulative flick probability (1 − Kaplan-

Meier estimate) as a function of optical power for high-, medium-, and low-pain mice determined by

transcutaneous neuroma poke. Cross mark at 60 mW indicates right-censoring for animals who did not

show a flick at the maximum optical power. **f**, Limb flick probability to transcutaneous neuroma poke (left)

and 50% withdrawal threshold from medial plantar poke before and after intraperitoneal (i.p.) injection of

compound 21 (C21) in *Sstr2^{CreER};hM4Di* mice (n = 7) for selective chemogenetic silencing of Neuroma C-

Nociceptors (SSTR2) and littermate controls (*Sstr2^{CreER}* alone or *hM4Di* alone, n = 10). Data are mean ±

SEM; dashed lines connect individual mice. *P* values from two-sided paired t-tests.

Extended Data Fig. 1

 Extended Data Fig. 1 | Automated behavioural screening reveals limb flick as a prominent behaviour

in the chronic phase after peripheral nerve injury. a, Schematics of three sciatic nerve injury models:

sciatic nerve transection (SNT), spared nerve injury (SNI), and sural nerve transection (SuNT). **b**,

Experimental setup for 30-minute recordings of spontaneous behaviours using a bottom-up near-infrared

(NIR) camera and machine-learning–based automated scoring[18]. **c,d**, Total time spent on each indicated

behaviour on the injured side, measured weekly for up to 8 weeks post-injury. Lines represent group means,

error bars indicate ± SEM. For each injury type, n = 8 mice (4 males, 4 females).

Extended Data Fig. 2

Extended Data Fig. 2 | Limb flicks are suppressed by gabapentin and are absent in acute pain conditions. a, Spontaneous limb flicks quantified over 30 minutes before and after intraperitoneal gabapentin (30 mg/kg) at 8–12 weeks post-SNT (n = 13 mice). Data are mean ± SEM; dashed lines connect individual mice. *P* value from two-sided Wilcoxon matched-pairs signed-rank test. **b**, Schematic of intraplantar injection (left) and quantification of biting/licking events and spontaneous limb flicks (right) following capsaicin (0.01%, 10 µL), Zymosan (100 µg in 10 µL), or complete Freund's adjuvant (CFA, 100%, 10 µL) injection. Behaviours were recorded for 30 minutes at peak-response windows defined from literature: immediately after capsaicin[18], 4 hours after Zymosan[53], and 24 hours after CFA[67]. Limb flicks are absent across all acute pain models, while biting and licking of the affected paw is the predominant behaviour in the capsaicin model. Each dot represents one mouse (n = 5 per model). Data are mean ± SEM; *P* values from one-way ANOVA with Tukey's multiple comparisons.

Extended Data Fig. 3

1071

Extended Data Fig. 3 | 24-hour EMG-based home-cage monitoring captures spontaneous limb flicks.

a, Representative EMG traces during various home-cage behaviours. Gray bars indicate periods when the

behaviours occurred as confirmed by corresponding videos. **b**, Feature plots of peak amplitude, frequency,

and autocorrelation coefficient (first non-zero positive peak) of EMG trace for each behaviour. Periodic

movements such as limb flicks showed higher autocorrelation values. Each dot represents the average of

20 events from one mouse (n = 10 mice, 12 weeks post-SNT). Elev, elevation; azim, azimuth. **c**, Left:

histogram showing the duration distribution of individual limb flick bouts, with an inset expanding the 0–

1% vs 1–7 seconds range. Most events occurred within 1 s. Right: Fast Fourier Transform (FFT) of limb

flicks showing a dominant frequency at 13.3 Hz. **d**, Weight bearing and gait parameters measured by

luminance ratio (left) and paw angle ratio (right)[53] before and two weeks after implantation of the wireless

telemetry device without nerve injury (n = 5 mice). **e**, Flick probability to poke before and two weeks after

implantation of the wireless EMG device (n = 6 mice at 8–10 weeks post-SNT). Data are mean ± SEM;

dashed lines connect individual mice. *P* values from two-sided Wilcoxon matched-pairs signed-rank tests

in (**d**,**e**).

Extended Data Fig. 4

Extended Data Fig. 4 | Neuroma pain emerges across peripheral nerve injury models and shows differential pain severity. a, Flick probability in response to transcutaneous neuroma poke measured weekly for up to 8 weeks after injury. Lines represent group means; error bars indicate ± SEM. For each injury type, n = 8 mice (4 males and 4 females, as in Extended Data Fig. 1). **b**, Pie chart showing the distribution of high-pain, low-pain, and medium-pain phenotypes. **c**, Histogram showing the size of neuromas in each pain condition. Each dot represents a neuroma (n = 5 mice for each condition). *P* value from one-way ANOVA.

Extended Data Fig. 5

a Von Frey on contralateral glabrous paw

b *p > 0.99*

c *p = 0.51*

Extended Data Fig. 5 | Spontaneous limb flicks and flicks evoked by transcutaneous poke are

independent of Piezo2. a-c, Von Frey filament evoked responses from contralateral glabrous paw (**a**), flick

probability to transcutaneous neuroma poke (**b**), and spontaneous flick count over 30 minutes (**c**) at 8 weeks

post-SNT in control and Piezo2 conditional knockout mediated by *Cdx2*[Cre55]. Data are mean ± SEM; each

dot represents one mouse (n = 8 controls, 6 knockouts). *P* values in (**a**) from two-way ANOVA with Tukey's

multiple comparisons (figure shows the interaction effect of control vs knockout across von Frey forces),

and from two-sided Mann–Whitney tests in (**b**,**c**).

Extended Data Fig. 6

Extended Data Fig. 6 | Transcriptomic profiling of DRG across pain conditions. a, Violin plots showing

quality control metrics, including the number of genes detected per nucleus (nFeature cutoff = 1,000), total

RNA counts, and percentage of mitochondrial transcripts, and dot plots showing expression of canonical

marker genes across neuronal populations. Dot size represents the percentage of nuclei expressing the gene,

and dot colour reflects average expression level. Cell-type annotations follow previously described criteria[30].

b, Gene Ontology enrichment within the Neuroma C-Nociceptor (SSTR2) population. Left: top 10 Cellular

Component terms for high-pain vs. low-pain; right: top 10 Cellular Component terms for high-pain vs.

control, ranked by adjusted *P* values. Middle column lists DEGs contributing to each term; solid magenta

lines connect genes shared between contrasts, gray dashed lines connect genes appearing in only one

contrast. **c**, Concordance scores for *Scn10a* and *Scn3a* across sensory neuron subtypes. The score is positive

when a gene is up-regulated in both comparisons (high-pain vs. low-pain and high-pain vs. control),

negative when down-regulated in both, and zero when regulation is inconsistent or observed in only one

comparison; larger magnitude indicates stronger concordance (see Methods for formula).

Extended Data Fig. 7

Extended Data Fig. 7 | Fabrication and characterization of the miniaturized LED cuff. a, Schematic of the fabrication process. A 3-µm polyimide (PI) layer is spin-coated onto an aluminum (Al)/silicon (Si) wafer, serving as a sacrificial substrate, and baked to complete imidization. A 130-nm silicon carbide (SiC) layer is deposited by plasma-enhanced chemical vapor deposition (PECVD). Metal interconnects consisting of Titanium/Platinum/Gold/Platinum/Titanium (Ti/Pt/Au/Pt/Ti) (10/10/200/10/10 nm) are sputtered and patterned by lift-off, followed by deposition of a second SiC layer and an additional PI layer. A Ti/SiO$_2$ bilayer (10/25 nm) is sputtered on the surface, and final device patterning is performed by inductively coupled plasma–reactive ion etching (ICP-RIE) to define cuff geometry and electrode windows. **b**, Electrical and optical performance of the integrated blue micro-LEDs (470 nm). Representative current–voltage (I–V), current–power (I–P), and voltage–power (V–P) curves. Solid lines and shaded bands represent mean ± SEM across n = 24 devices.

Extended Data Fig. 8

Extended Data Fig. 8 | Differential density of sensory fibre subtypes in neuromas. a, Representative images of reporter expression (ReaChR::mCitrine) in neuromas, contralateral intact nerves, and L4 DRG neurons from transgenic lines, including Neuroma C-Nociceptors (SSTR2), C-HTMR/Heat (MRGPRD), C-HTMR/Heat (MRGPRA3), C-HTMR/Heat (MRGPRB4), Aδ-HTMR/Heat (SMR2), C-Cold (TRPM8), C-LTMR, and Aδ-LTMRs. **b**, Quantification of fibre density, expressed as the percentage of axon-occupied area. Note that the increased density in neuromas labelled by the C-LTMR reporter may reflect contributions from both C-LTMRs and Th$^+$ sympathetic nerves. C-HTMR/Heat (CYSLTR2/SST) fibres were not quantified because the transgenic line (*Cysltr2^{Cre}*) labels a mixture of axons and non-neuronal cells in peripheral nerves. Data are mean ± SEM; each dot represents one nerve/neuroma. *P* values from two-sided

1135   paired t-tests are shown for each population. All these histology studies were performed following the

1136   optogenetic activation experiments at 8–12 weeks post-SNT.

Extended Data Fig. 9

Extended Data Fig. 9 | Gain- and loss-of-function analyses of Neuroma C-Nociceptors (SSTR2). a, Occurrence of behaviours in response to a 5-s stimulation, delivered either as a 10 Hz train of 10-ms pulses or as continuous light. **b**, Representative images and quantification of combined *in situ* hybridization for *Sstr2* and immunolabeling of hM4Di::mCitrine in the ipsilateral L4 DRG of *Sstr2*[T2a-CreER]*; R26*[LSL-hM4Di::mCitrine] mice. Twenty L4 DRG sections from two *Sstr2*[T2a-CreER]*; R26*[LSL-hM4Di::mCitrine] mice were used to quantify the overlap ratio between *Sstr2* mRNA and hM4Di::mCitrine expression. **c**, Quantification of distance traveled and locomotor speed before and after acute chemogenetic silencing using a previously reported behavioural platform[53]. Data are mean ± SEM; each dot represents one mouse (n = 7 mice). *P* values from two-sided paired t-tests.