

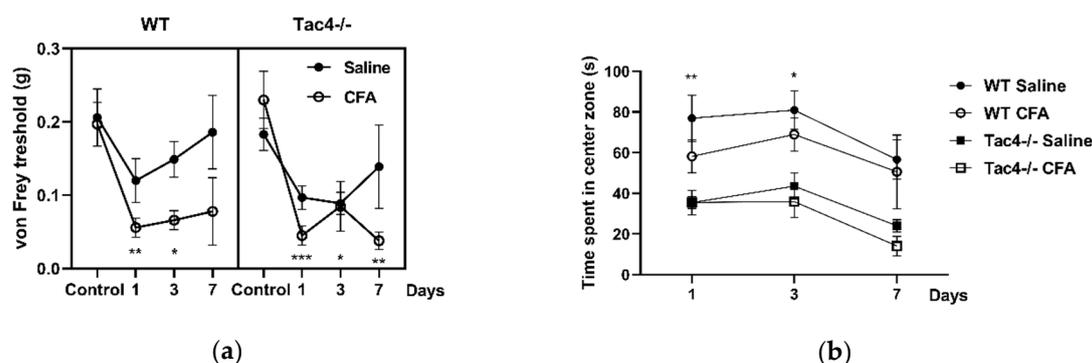


Supplementary Materials for *Hemokinin-1 Gene Expression is Upregulated in Trigeminal Ganglia in an Inflammatory Orofacial Pain Model: Potential Role in Peripheral Sensitization*

1. Supplementary Results

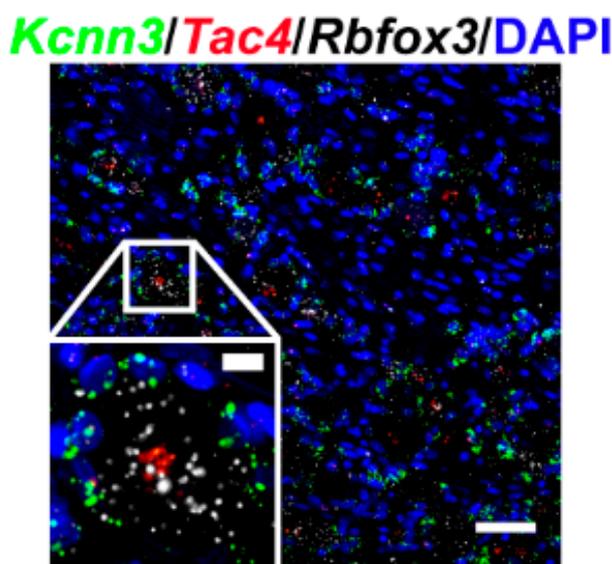
1.1. Behavioural tests in *Tac4*^{-/-} gene-deficient mice

CFA administration caused significantly decreased facial mechanonociceptive threshold 1 and 3 days after injection in both wild-type (WT) and *Tac4*^{-/-} mice. However, saline injection caused similar, although non-significant changes. No significant changes were observed between the thresholds of WT and *Tac4*^{-/-} mice. No significant change in spontaneous behavior was seen as a consequence of CFA injection, although *Tac4*^{-/-} mice spent less time in the centre zone of the open-field box, suggesting an anxiety-like behavior compared to their littermates (Supplementary Figure 1).



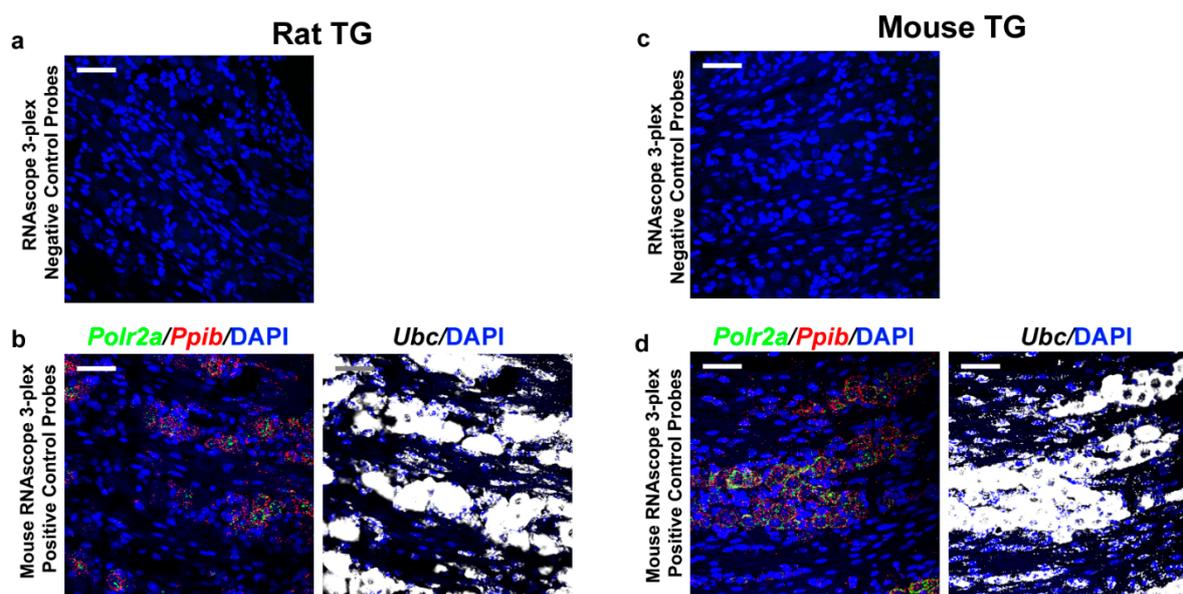
Supplementary Figure 1. (a) Changes in von Frey threshold before and 1, 3, 7 days after CFA (10 μ l s. c. complete Freund's adjuvant) inflammation. Mean of the orofacial thresholds in both sides were calculated. Data are means \pm S.E.M. ($n = 7$ –18). Asterisks denote statistically significant differences between control and saline/CFA-treated groups (* $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$) as analyzed by two-way ANOVA followed by Tukey's multiple comparison tests; (b) Changes in spontaneous behavior measured in the open field test. Data are means \pm S.E.M. ($n = 3$ –15; WT vs. *Tac4*^{-/-}; * $p < 0.05$, ** $p \leq 0.01$, two-way ANOVA followed by Tukey's multiple comparison tests).

1.2. RNAscope



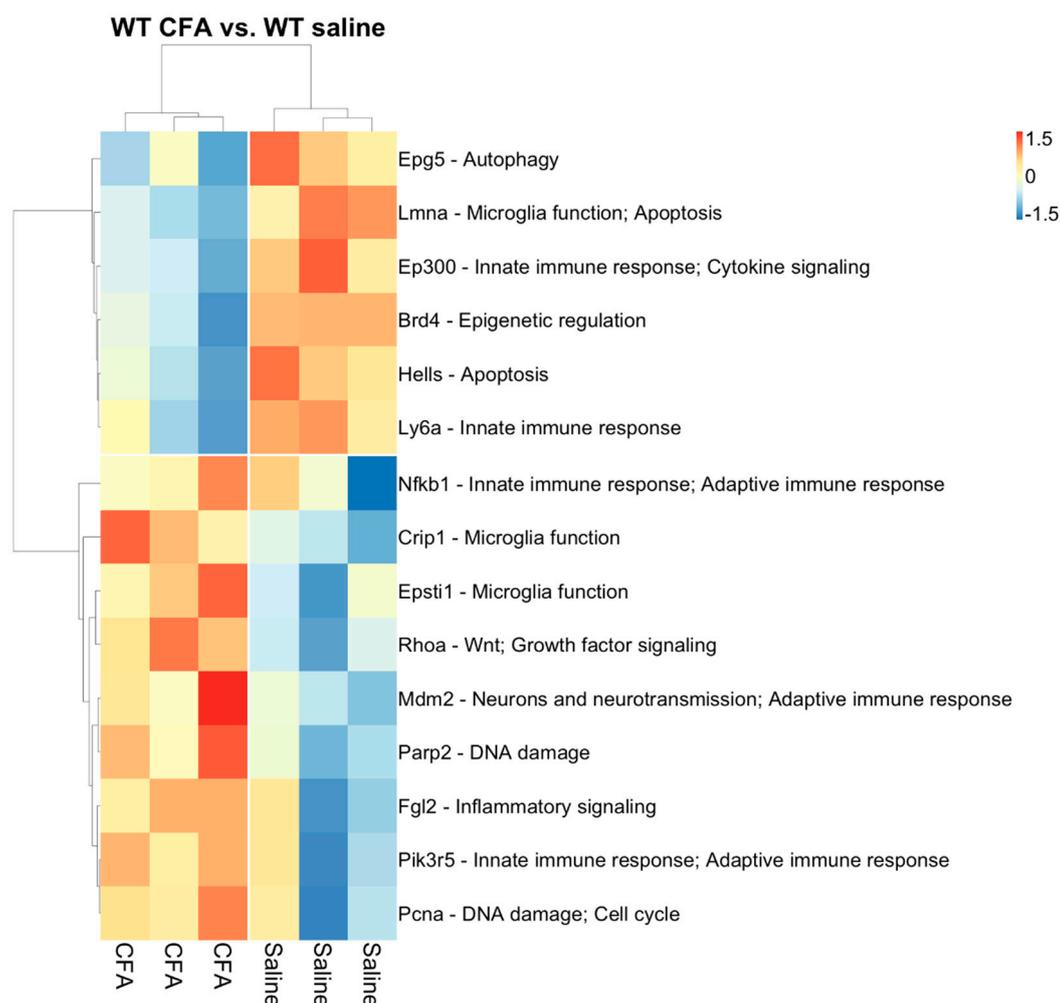
Supplementary Figure 2. Representative confocal image of rat longitudinal TG section. RNAscope probes specific to *Kcnn3* (in green encoding SK3) to detect SGCs, and to *Rbfox3* (in white encoding NeuN) to visualize sensory neurons were used to colocalize with *Tac4* mRNA (in red). Scale bar: 50 μ m, inset scale bar 10 μ m.

1.3. RNAscope technical controls

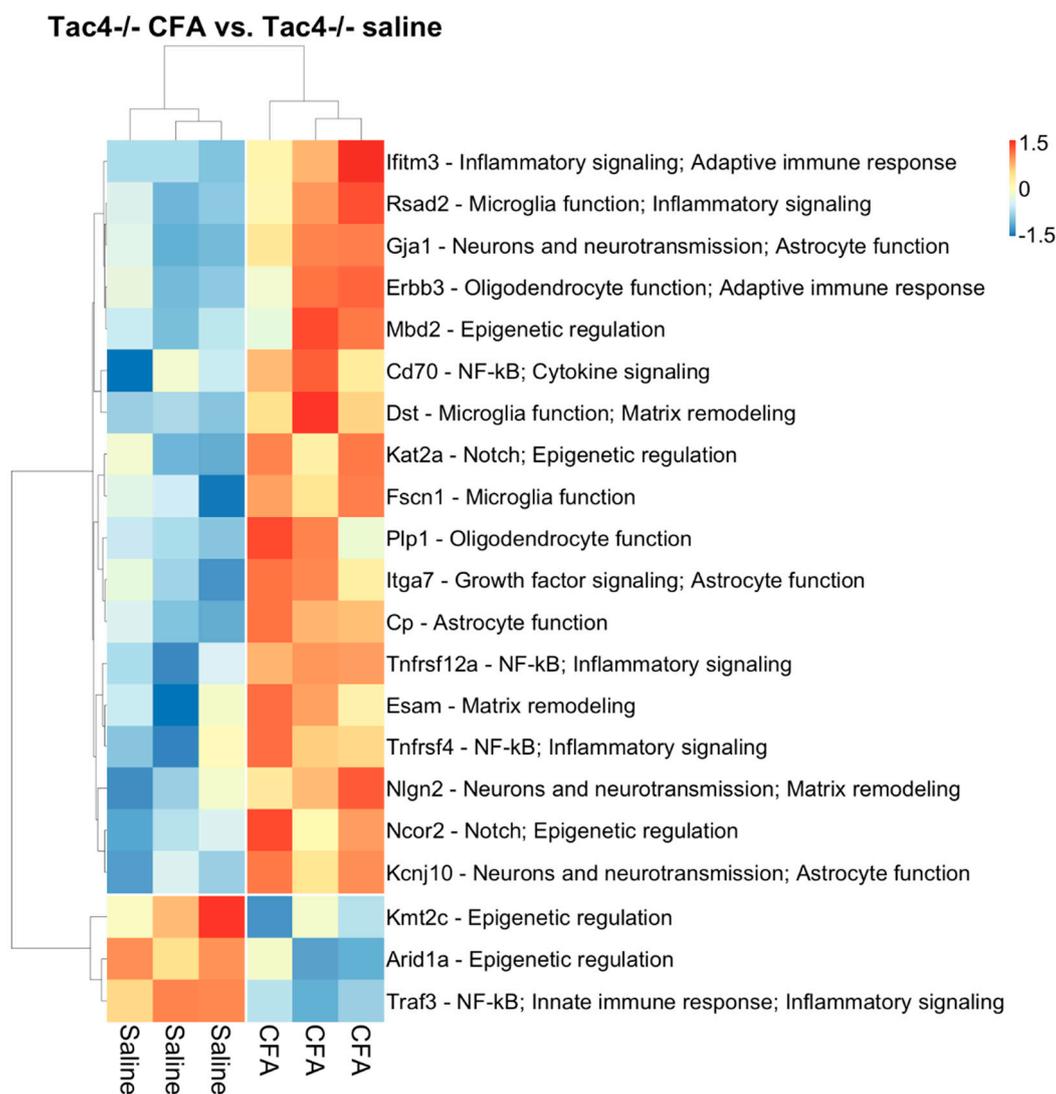


Supplementary Figure 3. RNAscope control conditions performed on saline-injected rat and mouse longitudinal TG sections counterstained with DAPI. (a) Representative confocal image of 3-plex negative control probes specific to the bacterial *dabP* gene giving no specific signal on rat TG; (b) Representative confocal images of 3-plex positive control probes specific to mouse *Polr2a* (in green), *Ppib* (in red) and *Ubc* (in white) mRNA targets on rat TG; (c) Representative confocal image of 3-plex negative control probes specific to the bacterial *dabP* gene giving no specific signal on mouse TG; (d) Representative confocal images of 3-plex positive control probes specific to mouse *Polr2a* (in green), *Ppib* (in red) and *Ubc* (in white) mRNA targets on mouse TG. Scale bar: 50 μ m. Note that sensitivity of mouse 3-plex positive control probes applied on rat tissue samples reflects on the highly conserved mouse and rat genome.

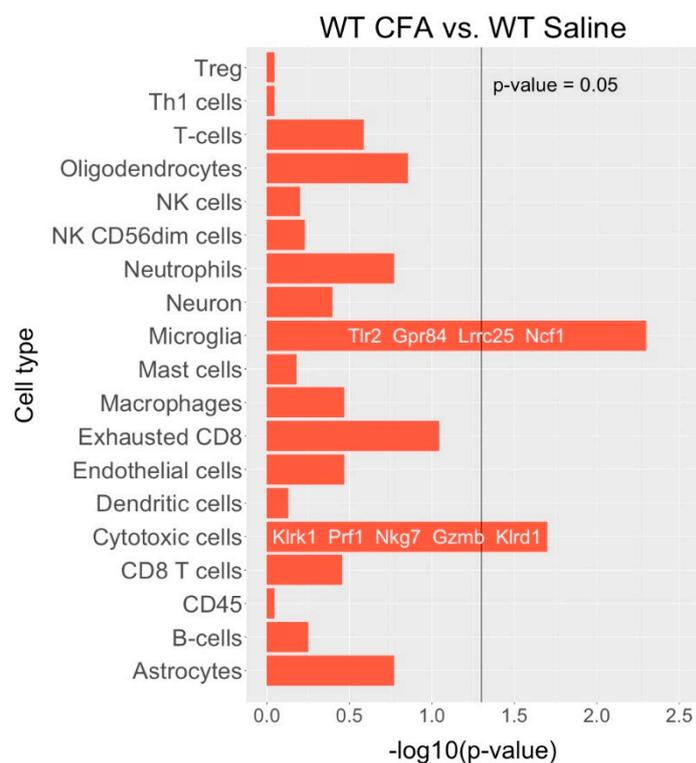
1.3. Nanostring



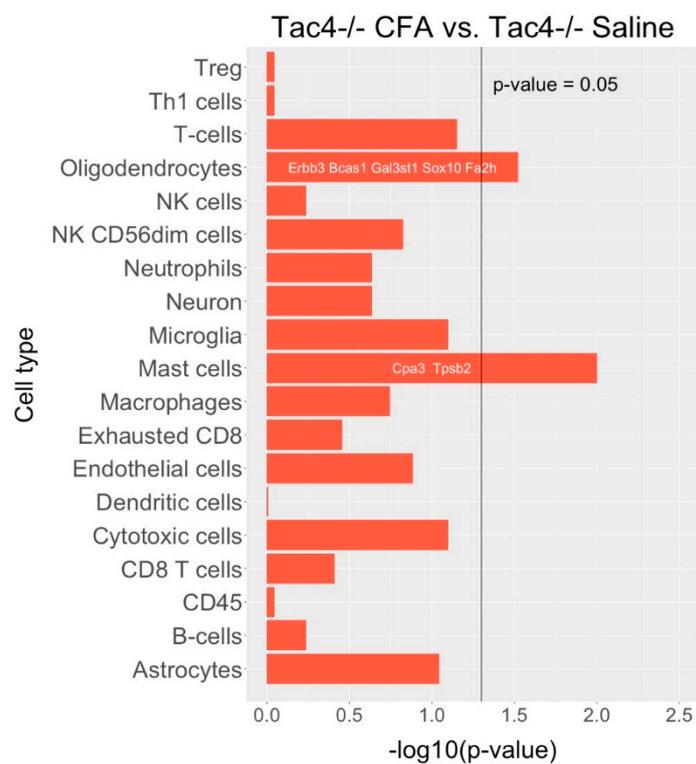
Supplementary Figure 4. Heat map representation of the differentially expressed genes with annotations between TG samples of CFA and saline-treated WT mice. Rows represent genes and columns represent TG samples (n = 3). Normalized gene counts data are shown as row-wise z-scores (scale is shown on legend). Rows and columns were hierarchically clustered using Pearson correlation distance measure and average method. Distances are shown as dendrograms.



Supplementary Figure 5. Heat map representation of the differentially expressed genes with annotations between TG samples of CFA- and saline-treated *Tac4^{-/-}* mice. Rows represent genes and columns represent TG samples (n = 3). Normalized gene counts data are shown as row-wise z-scores (scale is shown on legend). Rows and columns were hierarchically clustered using Pearson correlation distance measure and average method. Distances are shown as dendrograms.



Supplementary Figure 6. Barplots of p-values for correlation of cell-type-specific gene expression as compared between CFA- and saline-treated WT mice. Barplots of p-values across cell types. p-values are $-\log_{10}$ transformed. Statistically significant cell types ($p < 0.05$) are shown.



Supplementary Figure 7. Barplots of p-values for correlation of cell-type-specific gene expression as compared between CFA- and saline-treated *Tac4^{-/-}* mice. Barplots of p-values across cell types. p-values are $-\log_{10}$ transformed. Statistically significant cell types ($p < 0.05$) are shown.

2. Supplementary Materials and Methods

2.1. Open Field test

The open-field test was used to assay spontaneous activity and anxiety levels of mice. The mice were placed into the same area of a box (60 cm x 40 cm), then their behavior was recorded for 10 min. Recorded videos were evaluated using Ethovision software (Noldus Information Technology, Wageningen, Netherlands).

2.2. RNAscope

Supplementary Table 1. Probes, applied dilutions of fluorophores

Target	Catalog number	Fluorophores	Dilutions
<i>Tac4</i>	449651-C2	TSA Plus Cyanine 3	1:750
<i>Kcnn3</i>	427961	TSA Plus Fluorescein	1:750
<i>Rbfox3</i>	313311-C3	TSA Plus Cyanine 5	1:750
Mm-3-plex positive ctrl probes	320881		
3-plex negative ctrl probes	320871	TSA Plus Fluorescein, Cyanine 3, 5	1:750

2.3. Quantitative real-time PCR (RT-qPCR)

Supplementary Table 2. Sequences of primers for real-time PCR

Gene symbol	Species	Accession number	Forward primer sequence (F, 5' - 3')
			Reverse primer sequence (R, 5' - 3')
<i>Aif1 (Iba1)</i>	mouse	NM_001361501.1	F: CAA CAA GCA ATT CCT CGA TGA TCC R: CTC CAG CAT TCG CTT CAA GG
<i>β2m</i>	mouse	NM_009735.3	F: TTC TGG TGC TTG TCT CAC TGA R: CAG TAT GTT CGG CTT CCC ATT C
<i>FosB</i>	mouse	NM_001347586.1 NM_008036.2	F: CGA GAA GAG ACA CTT ACC CCA R: GTT TCC GCC TGA AGT CGA TCT
<i>Gapdh</i>	mouse	AY618199.1	F: GTG GAG TCA TAC TGG AAC ATG TAG R: AAT GGT GAA GGT CGG TGT G
<i>Gfap</i>	mouse	NM_010277.3	F: CGG AGA CGC ATC ACC TCT G R: TGG AGG AGT CAT TCG AGA CAA
<i>Hprt1</i>	mouse	NM_013556.2	F: CCC CAA AAT GGT TAA GGT TGC R: AAC AAA GTC TGG CCT GTA TCC
<i>Ppia</i>	mouse	NM_008907.2	F: GAG CTG TTT GCA GAC AAA GTT R: CCC TGG CAC ATG AAT CTT GG
<i>Tac4</i>	mouse	NM_053093.2	F: CCG TGA ACC TGA AGG GAA T R: CCC ATC AGA CCA TAG AAC TGG
<i>B2m</i>	rat	NM_012512	F: CCC ACC CTC ATG GCT ACT TC R: CCA CTT CAC TTC ACT CTG GCA
<i>Gapdh</i>	rat	NM_017008	F: GTA ACC AGG CGT CCG ATA C R: TCC TCT GCT CCT CCC TGT TC
<i>Hprt1</i>	rat	NM_012583	F: GCT TTT CCA ACT TTC GCT GAT G R: GGT GAA AAG GAC CTC TCG AAG
<i>Ppia</i>	rat	NM_017101	F: CCA TTA TGG CGT GTG AAG TC R: GCA GAC AAA GTT CCA AAG ACA G
<i>Tac4</i>	rat	NM_172328.2	F: CTG TCC CCA GCA TCG AAC TT R: CCA GCT GAT ACC CCG TTC TC

Supplementary Table 3. A summary of sample numbers in each experiment. Samples for RT-qPCR were collected from animals participating in the behavioral measurements

<i>Rat</i>				
Method	Treatment	Day 1	Day 3	Day 7
von Frey	CFA	16	10	5
	saline	6	6	6
RT-qPCR	CFA	3	3	3
	saline	3		
RNAscope	CFA		6	
	saline		4	

<i>Mouse</i>				
WT				
Method	Treatment	Day 1	Day 3	Day 7
von Frey/Open field	CFA	18/13	18/13	8/3
	saline	16/13	16/13	7/4
RT-qPCR	CFA	5	10	3
	saline	5	9	4
RNAscope	CFA		5	
	saline		4	
Nanostring	CFA		3	
	saline		3	

Tac4 ^{-/-}				
Method	Treatment	Day 1	Day 3	Day 7
von Frey /Open field	CFA	16/13	16/13	8/5
	saline	18/14	18/15	8/5
RT-qPCR	CFA	5	7	5
	saline	5	10	5
Nanostring	CFA		3	
	saline		3	