GENE EXPRESSION PROFILING OF CUTANEOUS INJURED AND NON-INJURED NOCICEPTORS IN SNI ANIMAL MODEL OF NEUROPATHIC PAIN

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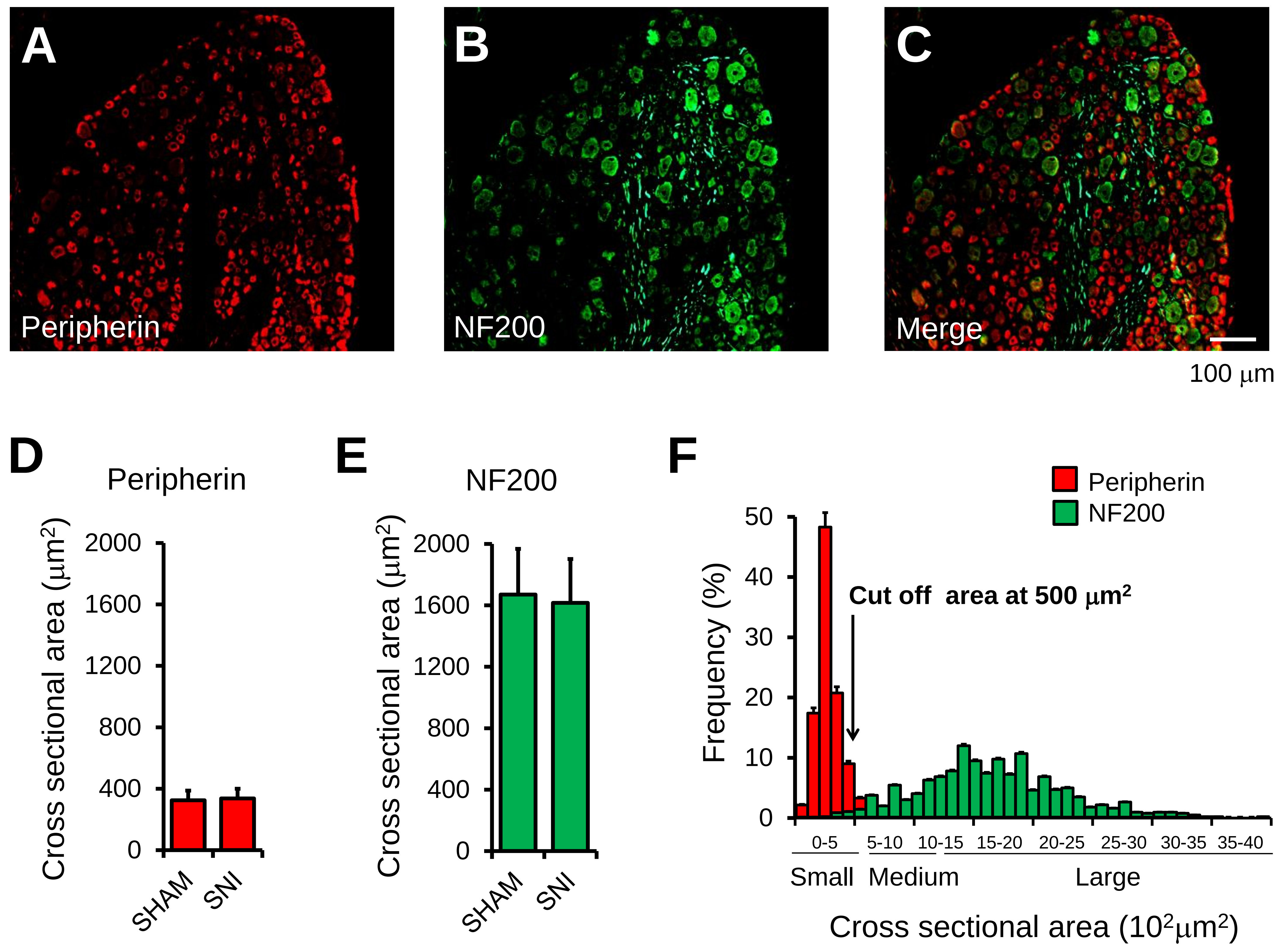
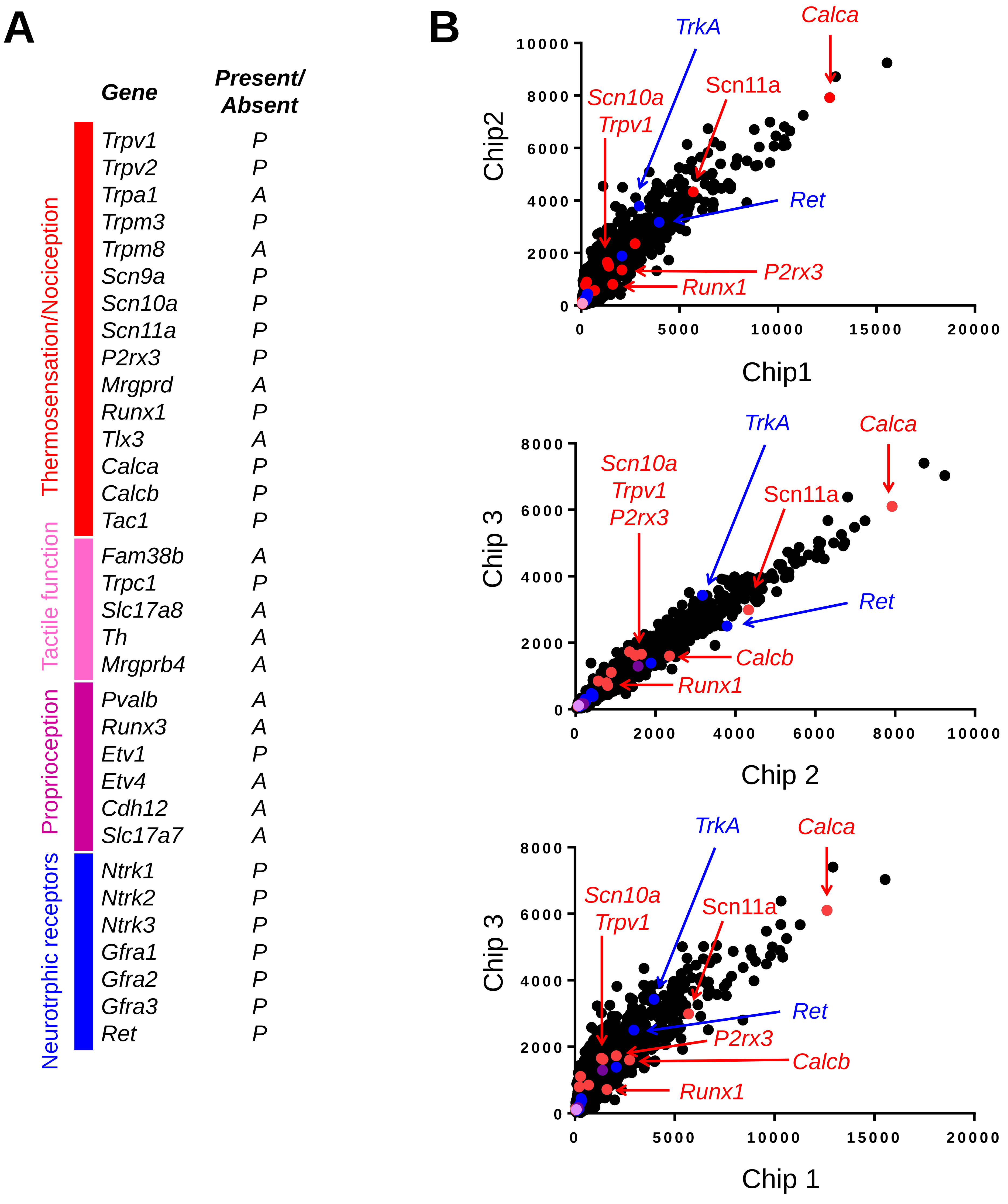
Supplementary Figures 1-3



Supplementary Fig. 1: Definition of the cell size criteria for the LCM of nociceptors. Immunohistochemistry of fresh DRG tissue for **(A)** nociceptor marker peripherin, **(B)** large-sized neuron marker NF-200 and **(C)** merged figures (scale bars = 100 μm). Analysis of average cross-sectional area for **(D)** peripherin and **(E)** NF-200 in L4-L5 sections issued from 1 week SNI or sham animals. To note no significant differences were detected between the two surgeries. **(F)** Analysis of the cross-sectional area distribution for the peripherin- and NF-200-positive neurons reveal an optimal cut off cross-sectional area of 500 μm^2, within 90% of neurons were peripherin positive and only 5% were NF-200 positive.



	Gene	Present/ Absent
Thermosensation/Nociception	*Trpv1*	*P*
	Trpv2	*P*
	Trpa1	*A*
	Trpm3	*P*
	Trpm8	*A*
	Scn9a	*P*
	Scn10a	*P*
	Scn11a	*P*
	P2rx3	*P*
	Mrgprd	*A*
	Runx1	*P*
	Tlx3	*A*
	Calca	*P*
	Calcb	*P*
	Tac1	*P*
Tactile function	*Fam38b*	*A*
	Trpc1	*P*
	Slc17a8	*A*
	Th	*A*
	Mrgprb4	*A*
Proprioception	*Pvalb*	*A*
	Runx3	*A*
	Etv1	*P*
	Etv4	*A*
	Cdh12	*A*
	Slc17a7	*A*
Neurotrphic receptors	*Ntrk1*	*P*
	Ntrk2	*P*
	Ntrk3	*P*
	Gfra1	*P*
	Gfra2	*P*
	Gfra3	*P*
	Ret	*P*

Supplementary Fig. 2: Expression of somatosensation markers on microarray analysis from LCM samples. **(A)** Analysis of transcript levels for known somatosensory mediators (list modified from Chiu *et al.* (ref)) in LCM samples from sham condition shows the presence of several markers for thermosensation and nociception. **(B)** Scatter plots of top 5% genes on the microarrays for the sham condition reveal the high expression of typical nociceptive markers, such as *Calca* (CGRP), *Scn11a* (Na$_v$1.9) and *Trpv1*.

Up-regulated genes

Fold	Non-injured	Injured
> 2	15	422
> 5	3	91
> 10	0	33

Down-regulated genes

Fold	Non-injured	Injured
> 2	6	180
> 5	0	7
> 10	0	0

Supplementary Fig. 3: Fold change of regulated gene. Number of up-regulated and down-regulated genes per conditions compared to sham and classified by fold change (for statistic see method section).