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Supplementary table 1. Cell counts mapped to specified category for tail brush (N=2), perianal brush (N=6), tail pinch (N=12) and colorectal stroke stimuli (N=15 mice).

	A LTMRs	A nociceptors	C LTMRs	C nociceptors
Tail Brush	16	1	29	6
Perianal brush	39	2	32	16
Tail Pinch	33	20	41	43
Colorectal stroke	41	31	10	42

Supplementary table 2. Pairwise comparisons statistics for post hoc analysis of defined subgroups within tested stimuli related to Fig. 3D.

Stimuli 1	Stimuli 2	Group	G-test statistics	Multiple comparison corrected p-value (Holm method)
Tail Brush	Tail Pinch	A LTMRs	3.58E-01	1.00E+00
Tail Brush	Tail Pinch	A nociceptors	9.92E-03	9.92E-02
Tail Brush	Tail Pinch	C LTMRs	1.34E-03	2.02E-02
Tail Brush	Tail Pinch	C nociceptors	5.16E-03	5.67E-02
Tail Brush	Stroke	A LTMRs	8.60E-01	8.60E-01
Tail Brush	Stroke	A nociceptors	8.17E-05	1.31E-03
Tail Brush	Stroke	C LTMRs	3.18E-11	6.37E-10
Tail Brush	Stroke	C nociceptors	2.69E-03	3.23E-02
Perianal brush	Tail Pinch	A LTMRs	2.21E-03	2.87E-02
Perianal brush	Tail Pinch	A nociceptors	2.14E-03	3.00E-02
Perianal brush	Tail Pinch	C LTMRs	3.83E-01	1.00E+00
Perianal brush	Tail Pinch	C nociceptors	2.99E-02	2.39E-01
Perianal brush	Stroke	A LTMRs	1.17E-01	7.02E-01
Perianal brush	Stroke	A nociceptors	1.56E-06	2.81E-05
Perianal brush	Stroke	C LTMRs	5.67E-07	1.08E-05
Perianal brush	Stroke	C nociceptors	1.23E-02	1.11E-01
Tail Pinch	Stroke	A LTMRs	1.30E-01	6.52E-01
Tail Pinch	Stroke	A nociceptors	4.20E-02	2.94E-01
Tail Pinch	Stroke	C LTMRs	7.99E-06	1.36E-04
Tail Pinch	Stroke	C nociceptors	6.93E-01	1.00E+00

Supplementary table 3 Pairwise comparisons statistics for post hoc analysis of defined subgroups within tested stimuli within myelination classes related to Fig. 3E.

Stimulus 1	Stimulus 2	Group	Fisher exact test.	Multiple comparison corrected p-value (Holm method)
Tail Brush	Tail Pinch	C nociceptors	8.76E-04	8.76E-04
Tail Brush	CR stroke	C nociceptors	7.59E-09	6.07E-08
Per. brush	CR stroke	C nociceptors	2.05E-06	1.23E-05
Tail Pinch	CR stroke	C nociceptors	5.37E-04	1.61E-03
Tail Brush	Tail Pinch	A nociceptors	1.43E-02	2.86E-02
Tail Brush	CR stroke	A nociceptors	4.08E-03	1.22E-02
Perianal brush	Tail Pinch	A nociceptors	1.55E-04	9.29E-04
Perianal brush	CR stroke	A nociceptors	8.83E-06	7.07E-05

Supplementary table 4 Cell counts mapped to specified transcriptomic categories for Tail pinch (N=12), hair-pull (N=4), anorectal distension (N=9), colorectal stroke (N=15 mice) stimuli in pan-neuronal CaMPARI mice and colorectal distension (N=8) and bladder stretch (N=6) in *Trpv1*^{lin-R26LSL-CaMPARI}. Related to Fig.4 and Fig. 6.

	Tail Pinch	Hair Pull	Anorectal distension	Colorectal stroke	Colorectal distension	Bladder distension
NP1 (Mrgprd)	23	13	24	8	12	8
NP2 (MRGPRA3/B4)	7	2	6	0	2	1
NP3 (Sst)	3	1	2	2	2	0
PEP1 (Sstr2)	2	1	7	6	0	2
PEP1 (Adra2a)	1	0	2	12	11	16
PEP1 (Oprk1)	7	2	4	14	11	6
C-LTMR (Th)	41	66	34	10	33	6
PEP3 (S100a16)	20	5	1	9	2	1
PEP3 (Adm)	0	1	13	22	11	33
PEP2 (Smr2)	0	1	0	0	0	2
Ab-LTMR (Calb1)	11	1	2	4	1	3
Ad-LTMR (Ntrk2h)	22	26	17	24	0	6
Prop. (Pvalb)	0	4	5	13	0	3
Unassigned	5	4	1	1	3	1

Supplementary table 5. Pairwise comparison of response pattern of C-nociceptors to high intensity stimulation related to Fig. 4C.

Stimulus 1	Stimulus 2	G-test statistics	Calculated p-value	Multiple comparison corrected p-value (Holm method)
Tail Pinch	Hair pull	1.890	8.64E-01	8.64E-01
Tail Pinch	Anorectal distension	4.213	5.19E-01	1.00E+00
Tail Pinch	CR stroke	30.743	1.05E-05	6.32E-05
Hair pull	Anorectal distension	3.393	6.40E-01	1.00E+00
Hair pull	CR stroke	26.146	8.36E-05	3.34E-04
Anorectal distension	CR stroke	30.472	1.19E-05	5.95E-05

Supplementary table 6. Post hoc pairwise comparisons of the extent of transcriptomic classes activated by different stimuli. Related to Figure 4D.

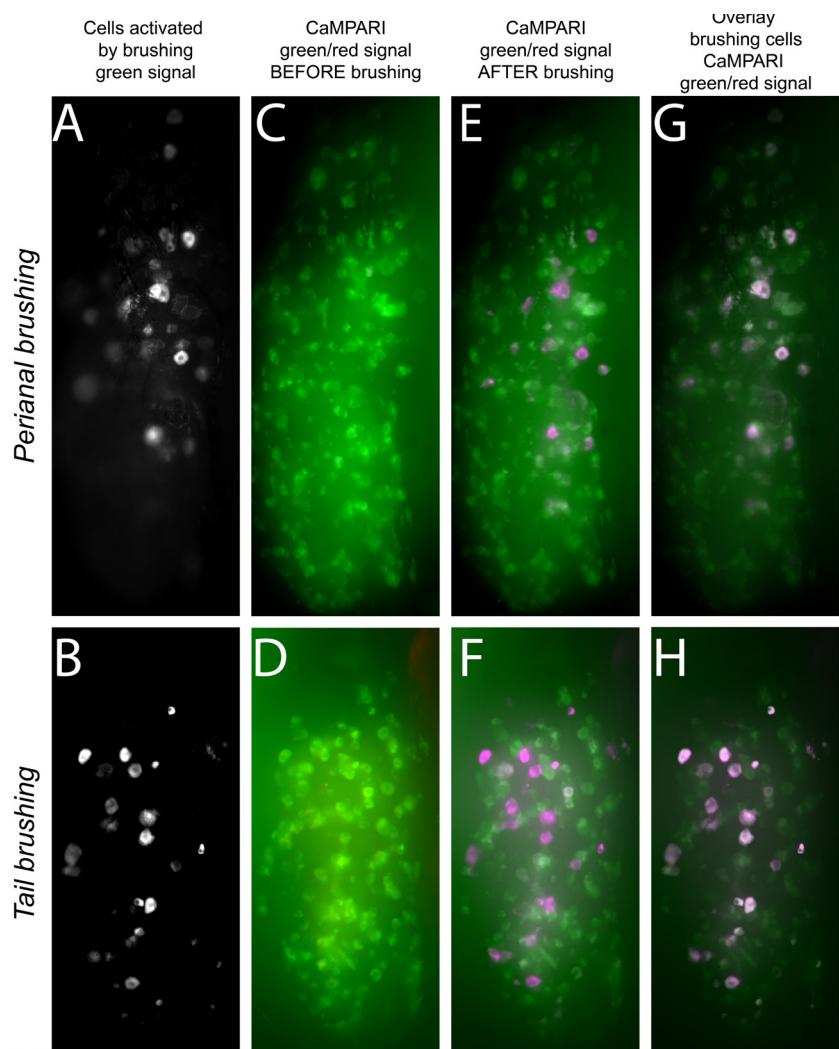
Stimulus 1	Stimulus 2	Cell class	Fisher exact test.	Multiple comparison corrected p-value (Holm method)
Hair pull	CR stroke	NP1 (Mrgprd)	3.35E-04	6.02E-03
Tail Pinch	CR stroke	NP1 (Mrgprd)	1.35E-03	2.30E-02
Anorectal distension	CR stroke	NP1 (Mrgprd)	1.63E-03	2.45E-02
Tail Pinch	CR stroke	PEP1 (Adra2a)	1.57E-03	2.51E-02
Anorectal distension	CR stroke	PEP1 (Adra2a)	2.84E-03	3.98E-02
Anorectal distension	CR stroke	PEP1 (Oprk1)	7.29E-03	9.47E-02
Tail Pinch	CR stroke	NP2 (Mrgpra3/b4)	1.19E-02	1.31E-01
Hair pull	CR stroke	PEP1 (Adra2a)	1.19E-02	1.42E-01
Anorectal distension	CR stroke	NP2 (Mrgpra3/b4)	2.65E-02	2.65E-01
Hair pull	CR stroke	NP2 (Mrgpra3/b4)	9.34E-02	8.41E-01
Tail Pinch	CR stroke	PEP1 (Oprk1)	1.29E-01	9.06E-01
Hair pull	CR stroke	PEP1 (Oprk1)	1.14E-01	9.09E-01
Tail Pinch	CR stroke	NP3 (Sst)	6.76E-01	1.00E+00
Tail Pinch	CR stroke	PEP1 (Sstr2)	2.65E-01	1.00E+00
Hair pull	CR stroke	NP3 (Sst)	1.00E+00	1.00E+00
Hair pull	CR stroke	PEP1 (Sstr2)	4.18E-01	1.00E+00
Anorectal distension	CR stroke	NP3 (Sst)	1.00E+00	1.00E+00
Anorectal distension	CR stroke	PEP1 (Sstr2)	1.00E+00	1.00E+00

Supplementary table 7. Pairwise comparison of response pattern of A-nociceptors to high intensity stimulation related to Figure 6C.

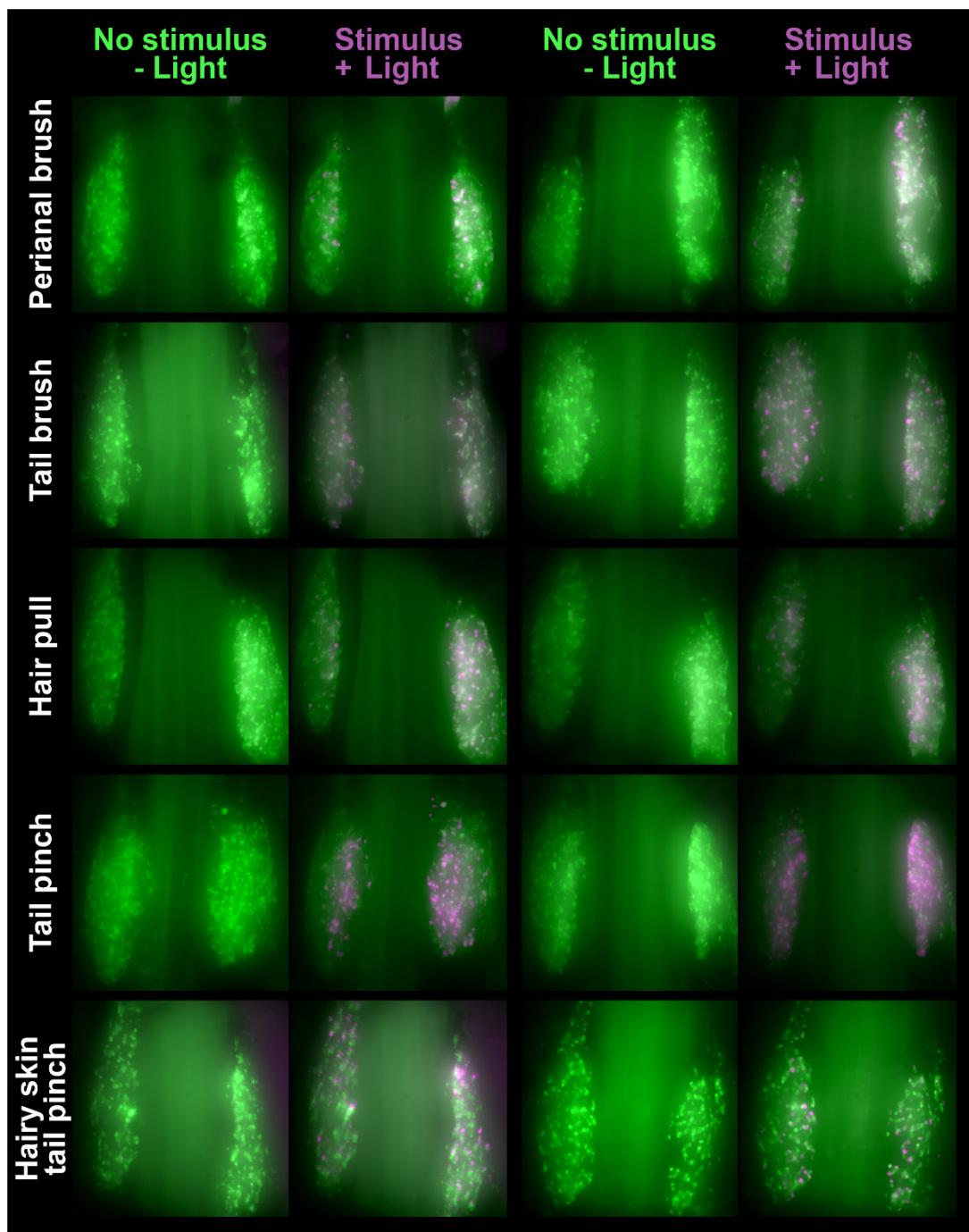
Stimulus 1	Stimulus 2	G-test statistics	Calculated p-value	Multiple comparison corrected p-value (Holm method)
Tail Pinch	Hair pull	5.883	5.28E-02	1.06E-01
Tail Pinch	CR stroke	32.386	9.28E-08	4.64E-07
Tail Pinch	Anorectal distension	38.029	5.52E-09	3.31E-08
Hair pull	CR stroke	9.831	7.33E-03	2.20E-02
Hair pull	Anorectal distension	14.122	8.58E-04	3.43E-03
CR stroke	Anorectal distension	3.117	2.10E-01	2.10E-01

Supplementary table 8. Post hoc pairwise comparisons of the extent of transcriptomic classes activated by different stimuli. Related to Figure 6D.

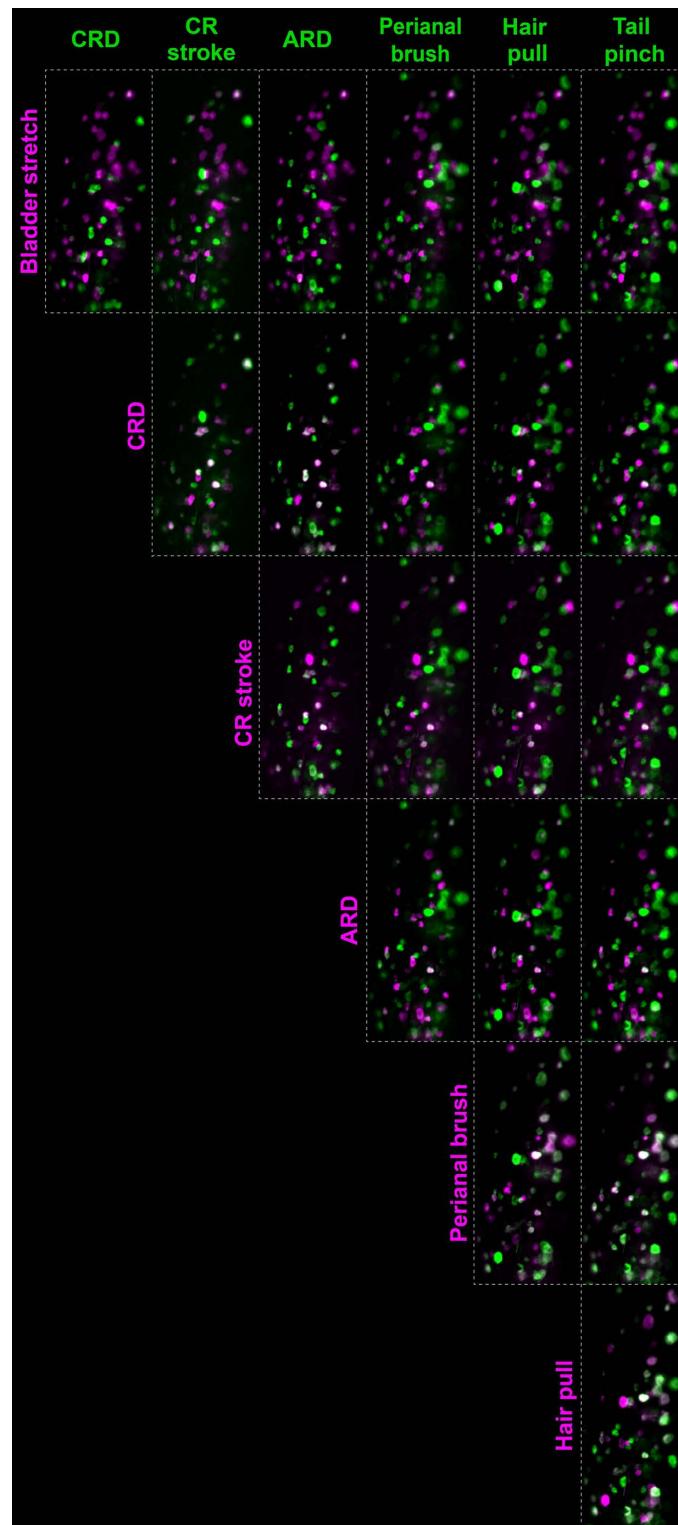
Stimulus 1	Stimulus 2	Cell class	Fisher exact test.	Multiple comparison corrected p-value (Holm method)
Tail Pinch	CR stroke	PEP3 (Adm)	1.68E-07	1.51E-06
Tail Pinch	CR stroke	PEP3 (S100a16)	1.68E-07	1.68E-06
Tail Pinch	CR stroke	PEP2 (Smr2)	1.00E+00	1.00E+00
Tail Pinch	Anorectal distension	PEP3 (Adm)	1.51E-08	1.73E-07
Tail Pinch	Anorectal distension	PEP3 (S100a16)	1.51E-08	1.73E-07
Tail Pinch	Anorectal distension	PEP2 (Smr2)	1.00E+00	1.00E+00
Hair pull	CR stroke	PEP3 (Adm)	9.63E-03	5.78E-02
Hair pull	CR stroke	PEP3 (S100a16)	7.72E-02	3.86E-01
Hair pull	CR stroke	PEP2 (Smr2)	1.84E-01	7.37E-01
Hair pull	Anorectal distension	PEP3 (Adm)	8.51E-04	6.81E-03
Hair pull	Anorectal distension	PEP3 (S100a16)	5.55E-03	3.88E-02
Hair pull	Anorectal distension	PEP2 (Smr2)	3.33E-01	1.00E+00



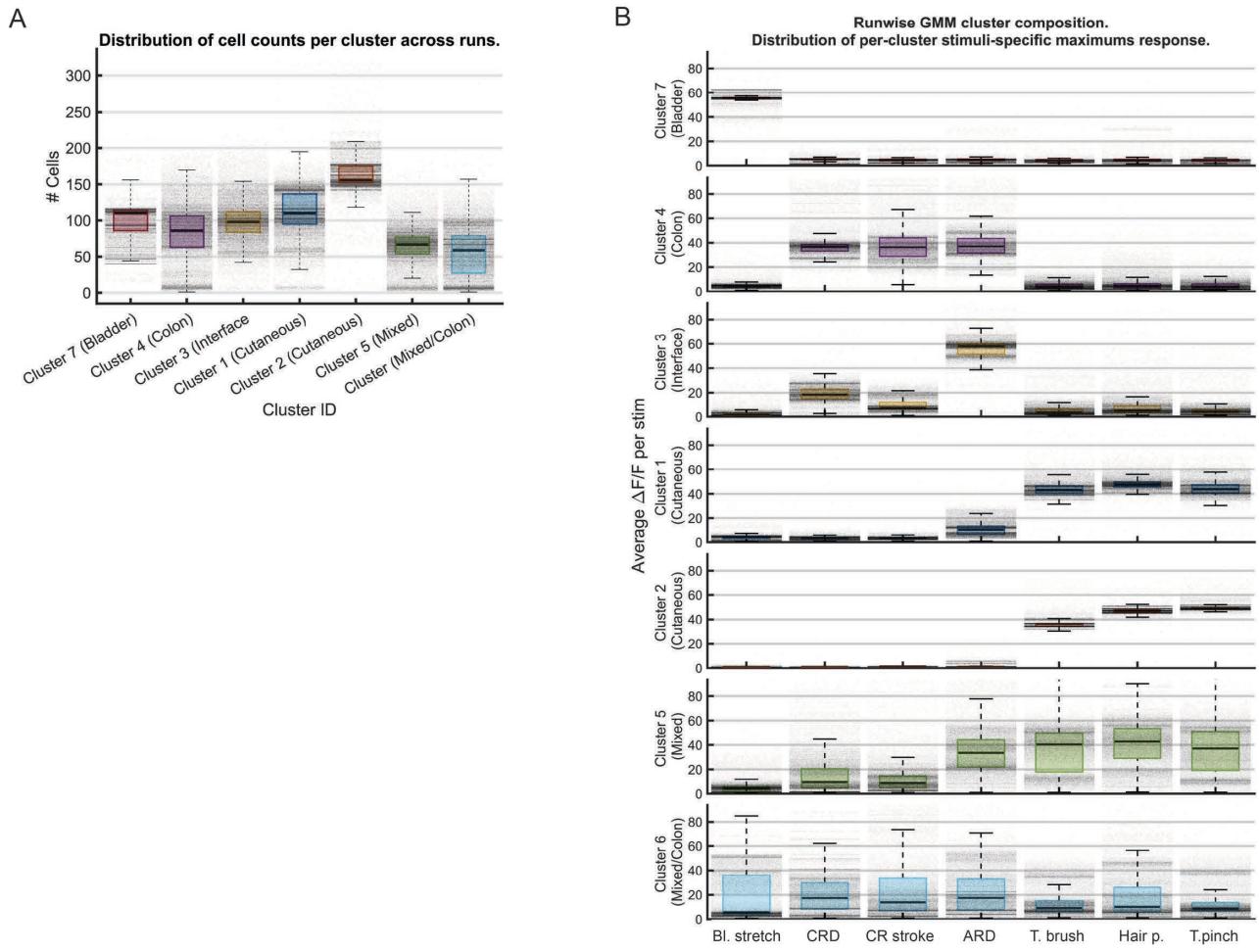
Supplementary Figure 1.1 Conversion of active cells in the L6 DRG by brushing A-B)
 CaMPARI, acting as a reverse calcium indicator, reports activity by dimming of basal green fluorescence in activated cells. Standard deviation projections of green fluorescence during stimulation visualize activated neurons in L6 DRG during perianal brushing (A) and tail brushing (B). **C-F**) Overlay of CaMPARI fluorescence in live L6 DRG, showing the basal form (green, emission $\lambda = 520$ nm) and the photoconverted form (red, emission $\lambda = 580$ nm, pseudocolored magenta). Panels C-D show pre-stimulus (before brushing), and panels E-F show post-stimulus (after brushing). **G-H**) Overlay of cells identified by acute activation during brushing through fluorescence quenching with cells photoconverted by coupling stimulation with UV illumination, showing overlap between functional activity readout and CaMPARI conversion. Look up tables (LUTs) for green and magenta are set independently for each preparation due to differences in e.g. out of focus fluorescence levels).



Supplementary Figure 1.2 Example conversions of a range of gentle and noxious cutaneous stimuli Overlays of CaMPARI fluorescence in live DRG, showing the basal form (green, emission $\lambda = 520$ nm) and the photoconverted form (red, emission $\lambda = 580$ nm, pseudocolored magenta) before and after stimuli conversion. Two representative preparations are shown for each stimulus, for a range of gentle and noxious cutaneous stimulations. Look up tables (LUTs) for green and magenta are set independently for each preparation due to differences in e.g out of focus fluorescence levels). Note 'no stimulus' images have been acquired after a mock UV stimulation.

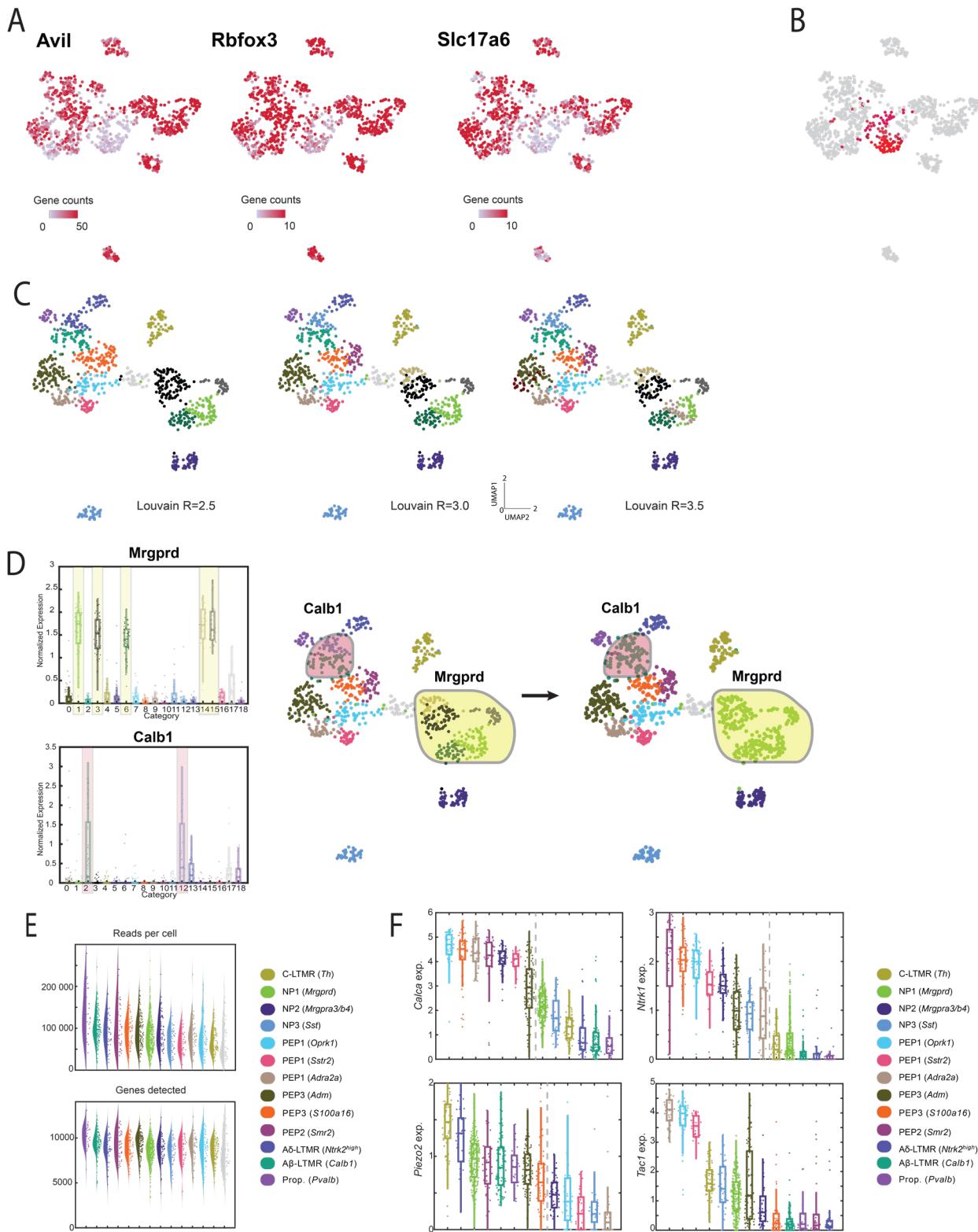


Supplementary Figure 2.1 Activation of sensory neurons by cutaneous and visceral stimuli
 Responses recorded in the mosaic GCaMP6f model. Each panel shows deviation projection visualizing cells activated by the stimulus indicated in the row (magenta) and the stimulus indicated in the column (green). Overlap (white) marks neurons activated by both stimuli. The stimulus panel included bladder stretch, colorectal distension (CRD, 80 mmHg), colorectal stroke (CR stroke), anorectal distension (ARD, 80 mmHg), perianal brushing, hair pull, and tail pinch.



Supplementary Figure 2.2 Detection of functional modules within pelvic sensory neurons

A) Comparison of Gaussian mixed model (GMM) derived clusters estimated over 50 000 algorithm realizations, graph shows average number of cells qualified into corresponding clusters. **B)** Stability of GMM cluster composition across 50 000 realizations. Box plots show the average stimulus response of cells within each cluster across all realizations; individual dots represent the mean response from a single clustering run. The most representative run was selected for further analysis in Figure 2.

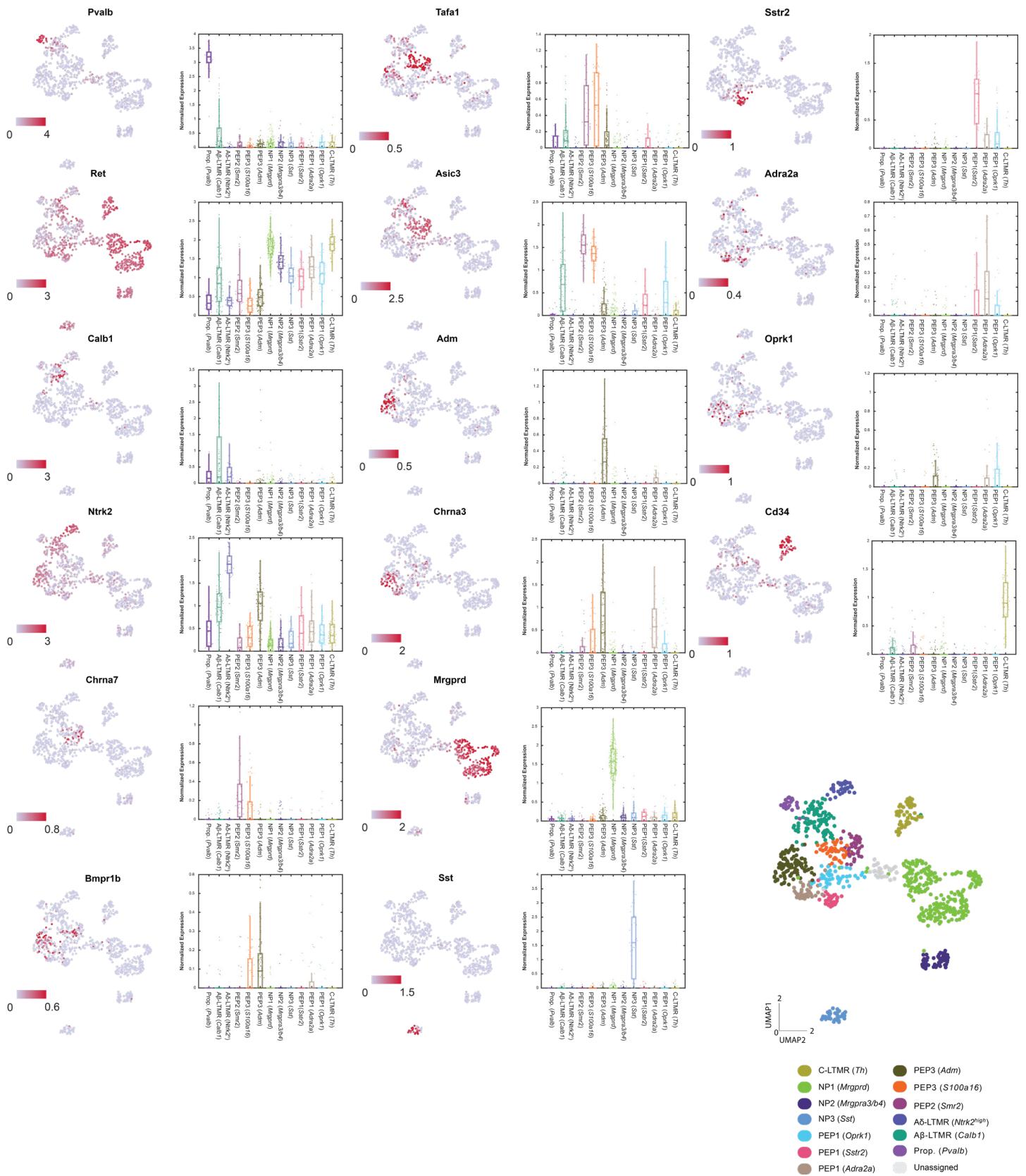


Supplementary Figure 2.3. Single-cell RNA sequencing cellular atlas preprocessing and quality control Legend continued on next page...

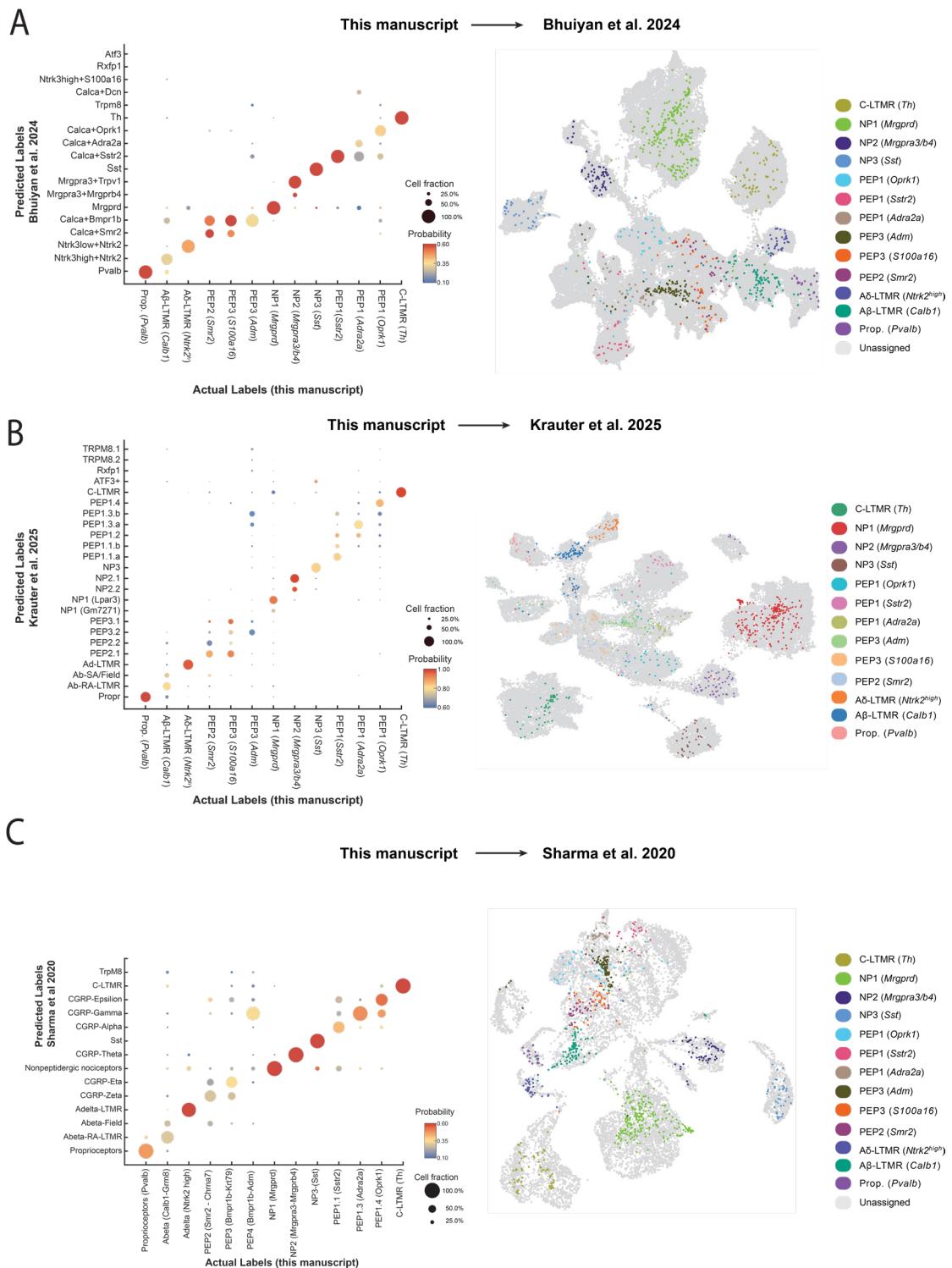
... **A–B)** Detection of clusters containing low-quality cells. After excluding cells with high mitochondrial gene content (>5%), cells were initially clustered and expression of common markers of primary sensory neurons (*Avil*, *Rbfox3*, *Slc17a6*) was assessed. Clusters with low expression of these marker genes were excluded from subsequent analysis. **C)** Clusters detected in the final atlas show little dependence on the clustering resolution parameter (R). **D)** Identification of related clusters for merging. The NP1 (*Mrgprd*) cluster was identified as fragmented based on shared *Mrgprd* expression, and the A β -LTMR (*Calb1*) cluster was identified based on shared *Calb1* expression. **E)** Characterization of sequencing depth: distribution of UMI counts per cell within each cluster (top) and number of detected genes (bottom). **F)** Differential expression analysis of representative characteristic and functionally relevant genes across detected clusters.



Supplementary Figure 2.4.
Cluster characteristic gene expression matrix Heatmap showing the expression of ten representative characteristic genes for each cluster.

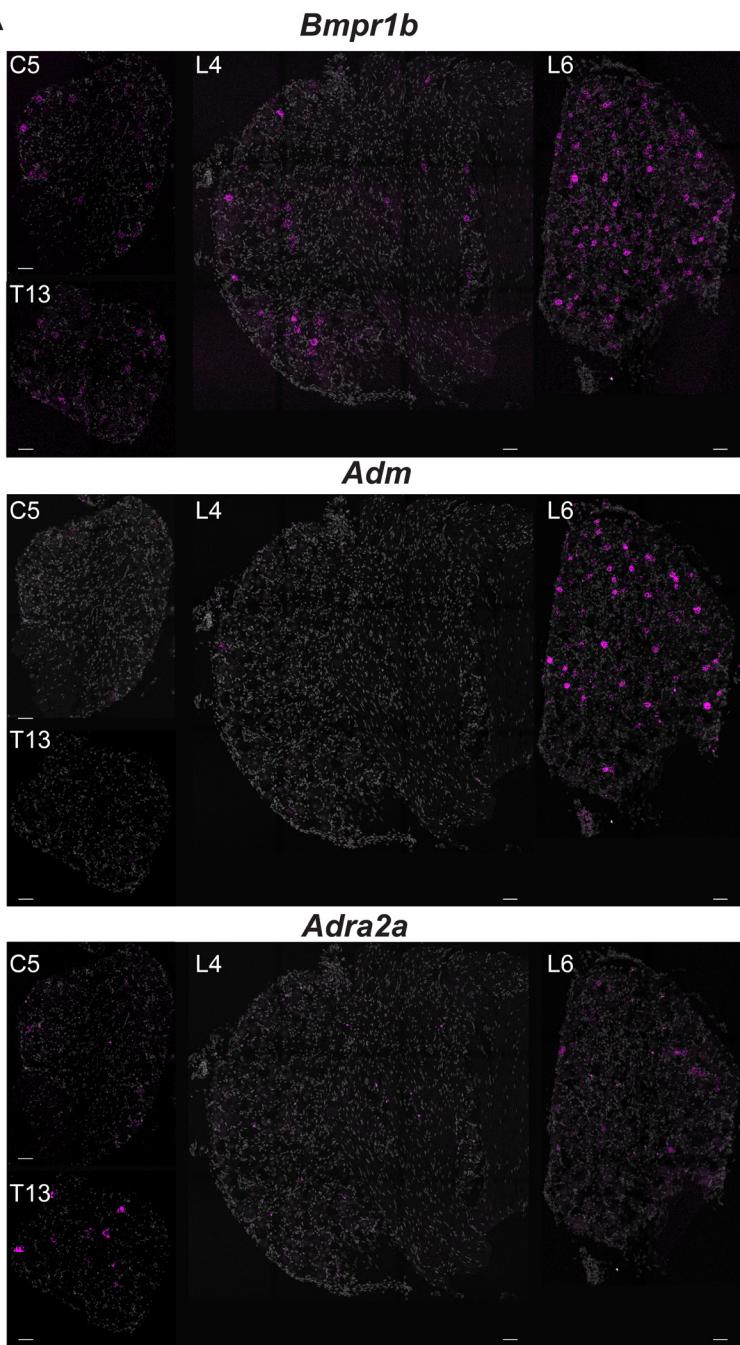


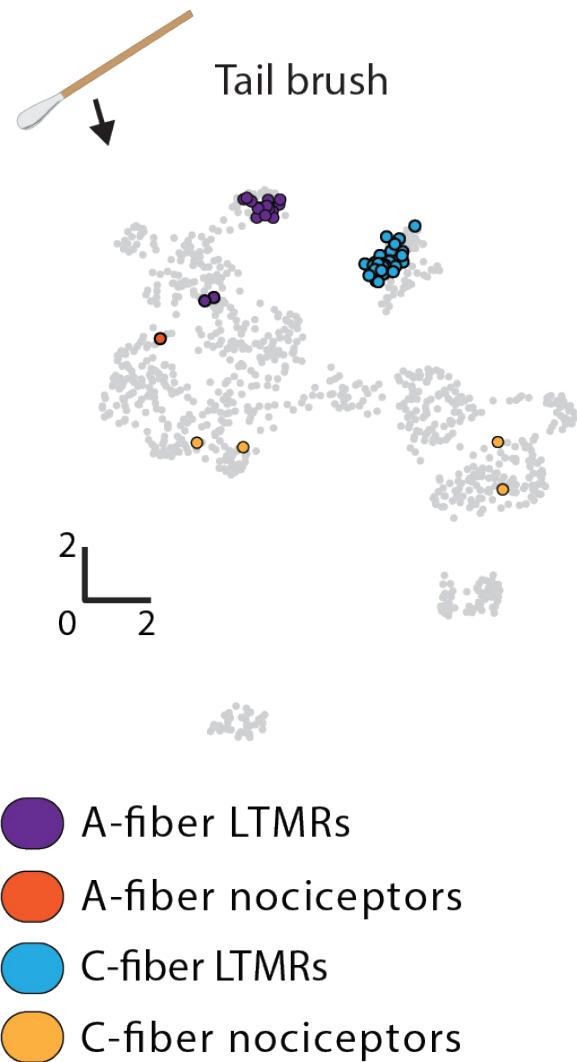
Supplementary Figure 2.5 Expression analysis of selected marker genes UMAP and bar graph representation of characteristic markers used in clusters identification. Scale indicates normalized log-transformed expression levels.



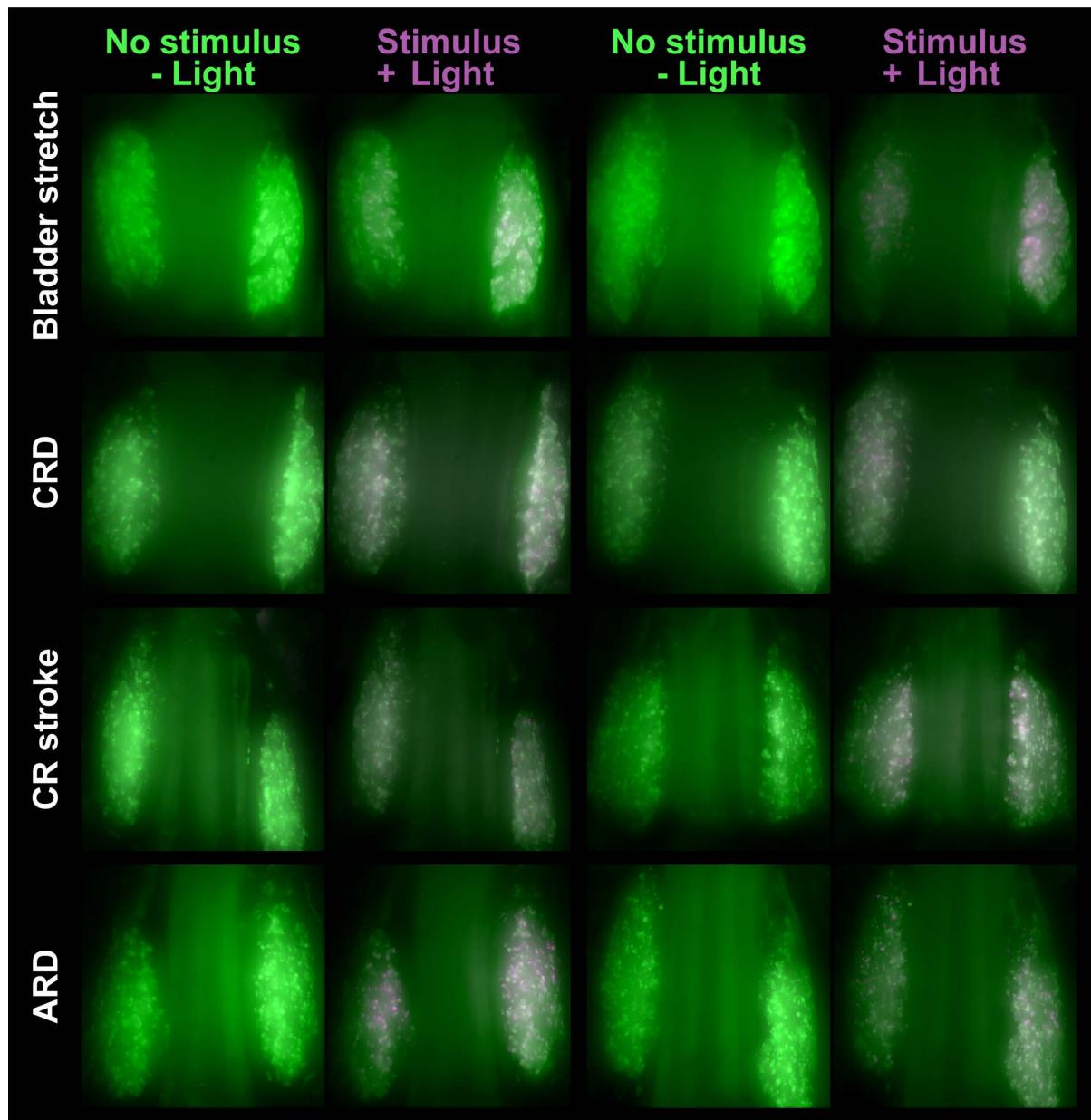
Supplementary Figure 2.6 Comparison of pelvic sensory neuron atlas with published DRG datasets Embedding of scRNA-seq pelvic neuron data into general DRG atlases from (A) Bhuiyan et al., 2024; (B) Krauter et al., 2025; and (C) Sharma et al., 2020. Left: bubble plots showing transferred cluster assignments, with labels from the reference atlases mapped onto the pelvic neuron dataset to infer class correspondence. Right: embeddings of pelvic DRG cells into the reference atlases from the source datasets.

A



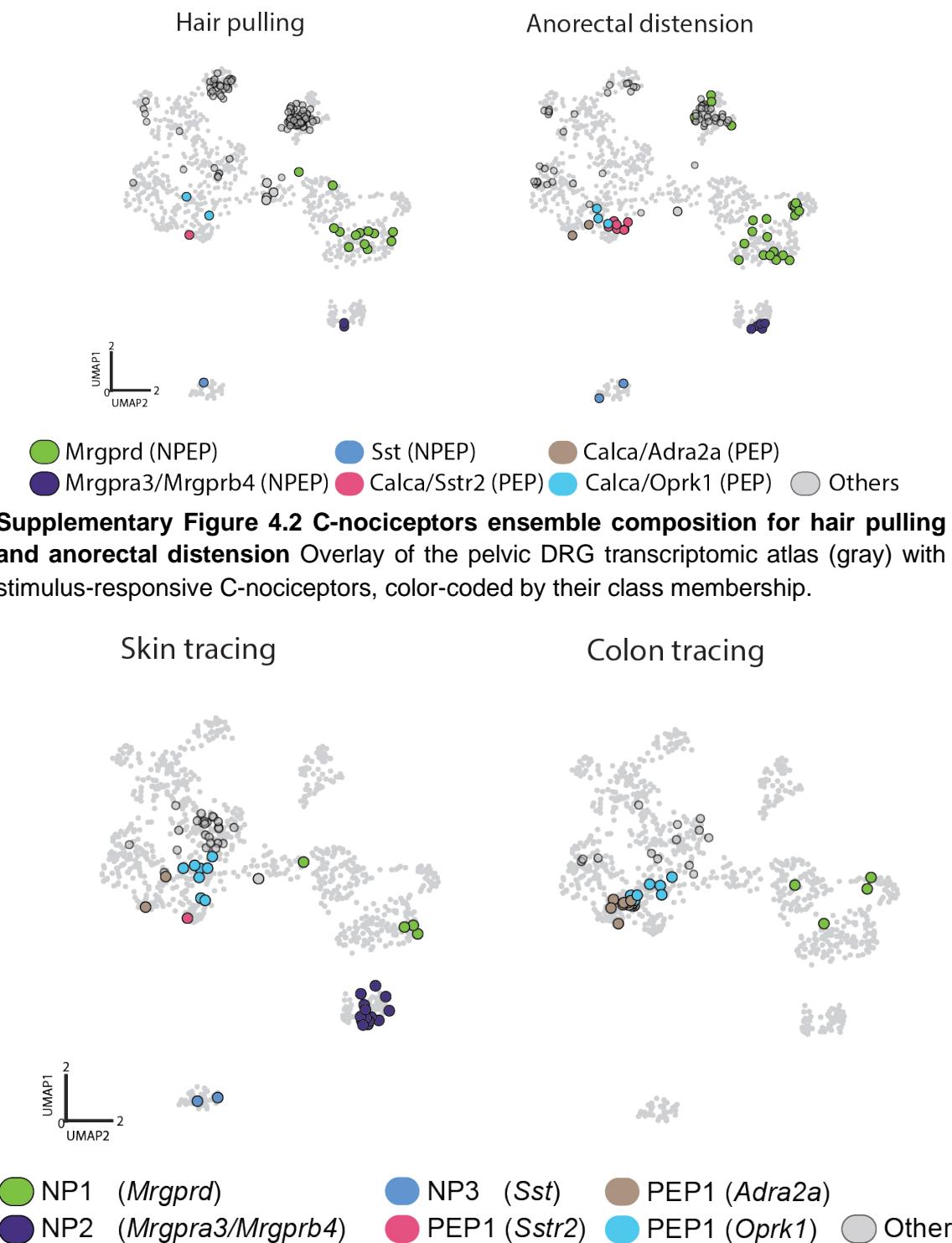


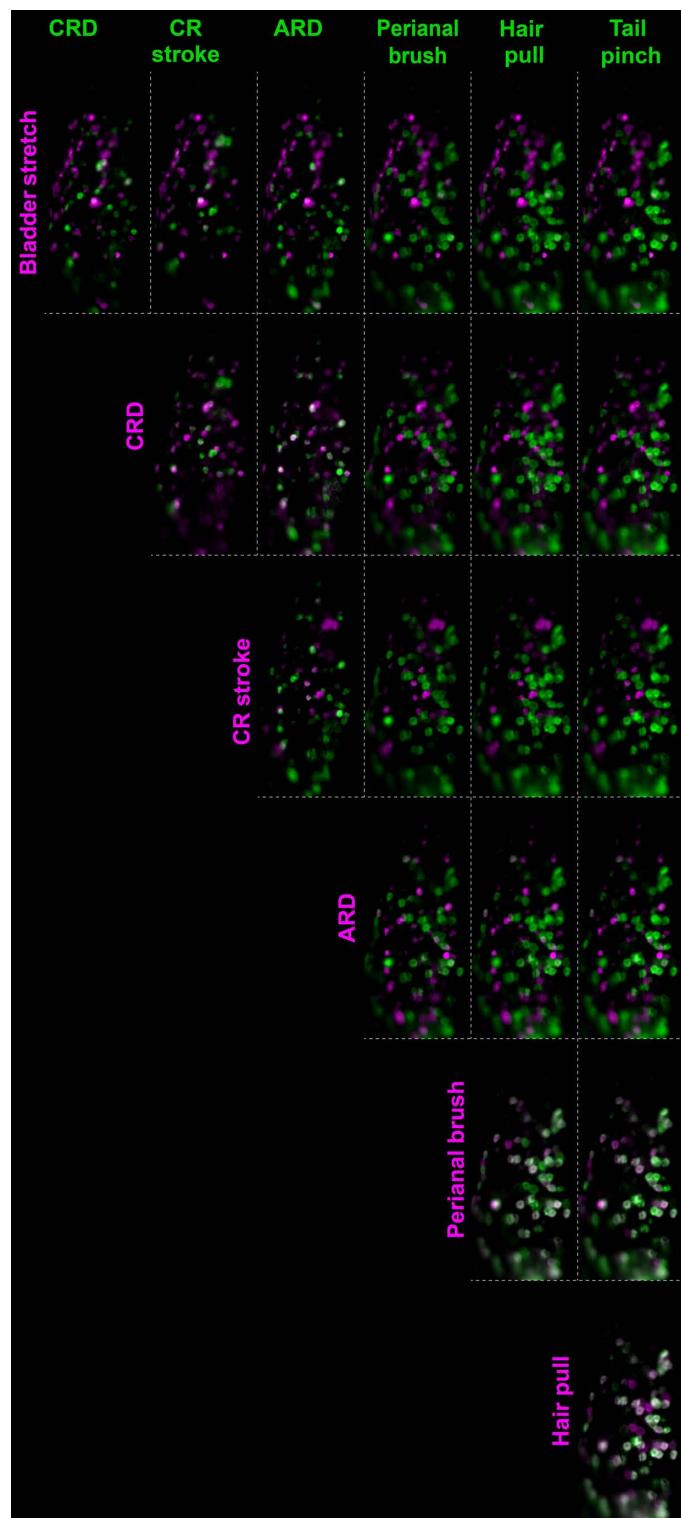
Supplementary Figure 3.1 Ensemble representation of the Tail brush stimulus
Overlay of the pelvic DRG transcriptomic atlas (gray) with labeled tail brush neurons, color-coded by their class membership.



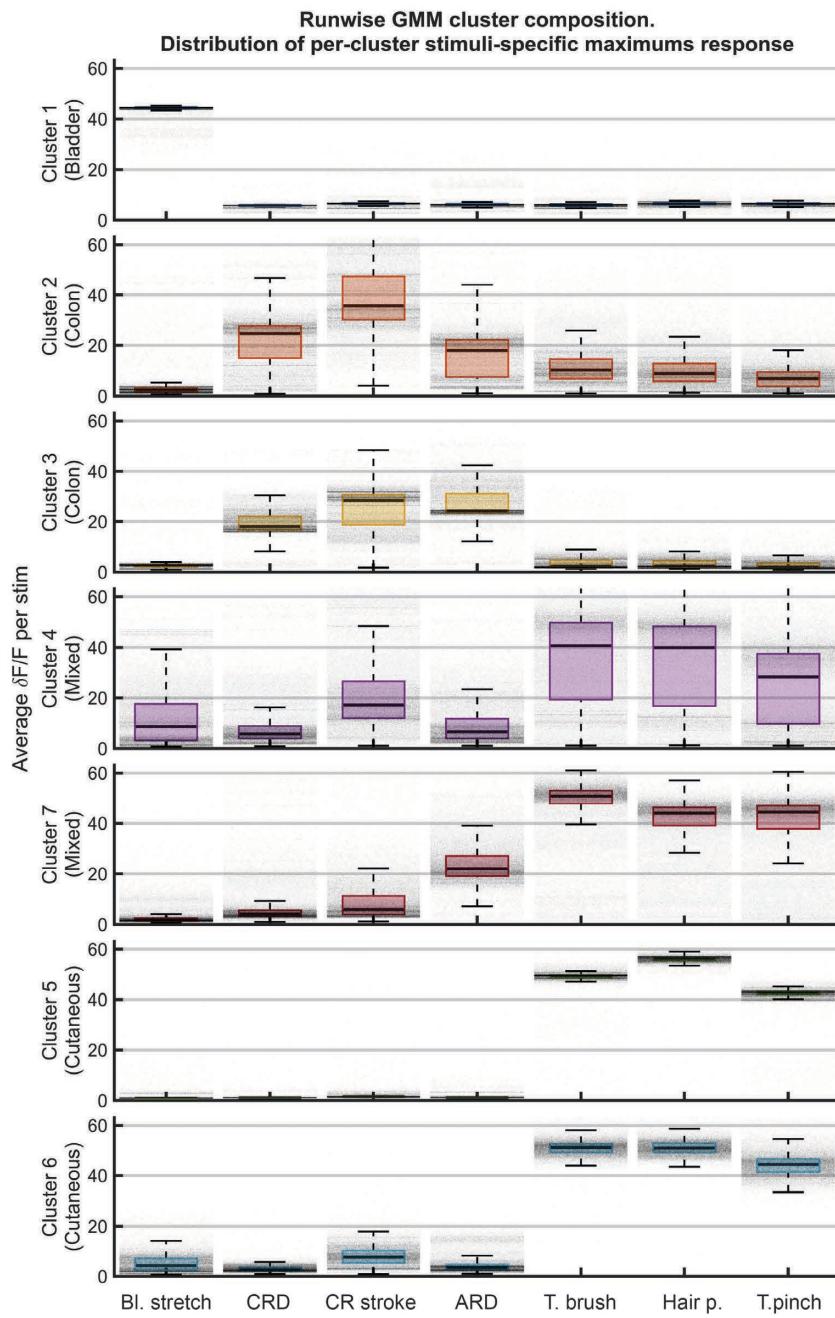
Supplementary Figure 4.1 Example conversions of noxious visceral stimuli

Overlays of CaMPARI fluorescence in live DRG, showing the basal form (green, emission $\lambda = 520$ nm) and the photoconverted form (red, emission $\lambda = 580$ nm, pseudocolored magenta) before and after stimuli conversion. Two representative preparations are shown for each stimulus, for a range visceral stimulus. Look up tables (LUTs) for green and magenta are set independently for each preparation due to differences in e.g. out of focus fluorescence levels).



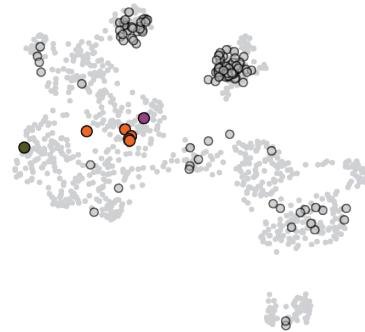


Supplementary Figure 5.1 Activation of myelinated sensory neurons by cutaneous and visceral stimuli Responses recorded in the *Nefh*^{CreER};R26^{LSL-GCaMP6f} mice. Each panel shows deviation projection visualizing cells activated by the stimulus indicated in the row (magenta) and the stimulus indicated in the column (green). Overlap (white) marks neurons activated by both stimuli. The stimulus panel included bladder stretch, colorectal distension (CRD, 80 mmHg), colorectal stroke (CR stroke), anorectal distension (ARD, 80 mmHg), perianal brushing, hair pull, and tail pinch.

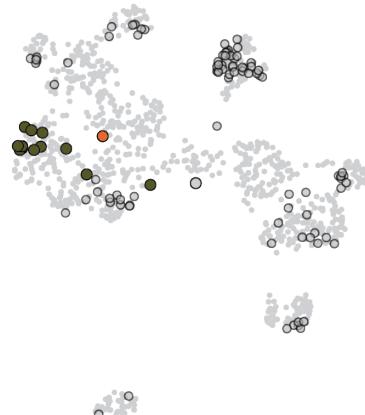


Supplementary Figure 5.2 Detection of functional cellular modules within myelinated neurons Stability of GMM cluster composition across 50 000 realizations over data obtained in *Nefh*^{CreER},*R26*^{LSL-GCaMP6f} model. Box plots show the average stimulus response of cells within each cluster across all realizations; individual dots represent the mean response from a single clustering run. The most representative run was selected for further analysis in Figure 5.

Hair pulling



Ano-rectal distension



● PEP3 (*S100a16*) ● PEP2 (*Smr2*)
● PEP3 (*Adm*) ● Others

Supplementary Figure 6.1 A-nociceptors ensemble composition for Hair pulling and Anorectal distension Overlay of the pelvic DRG transcriptomic atlas (gray) with stimulus-responsive A-nociceptors, color-coded by their class membership.