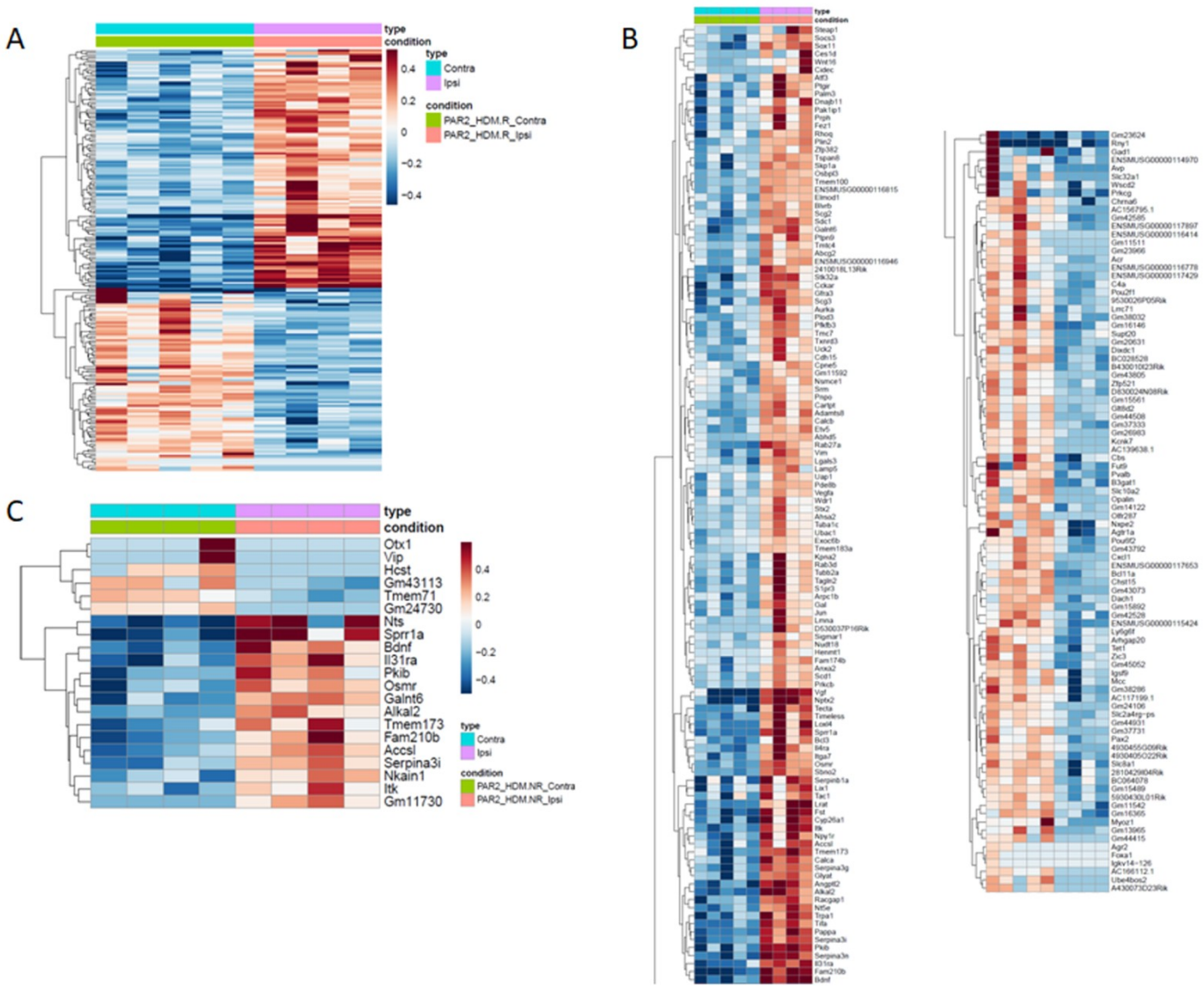
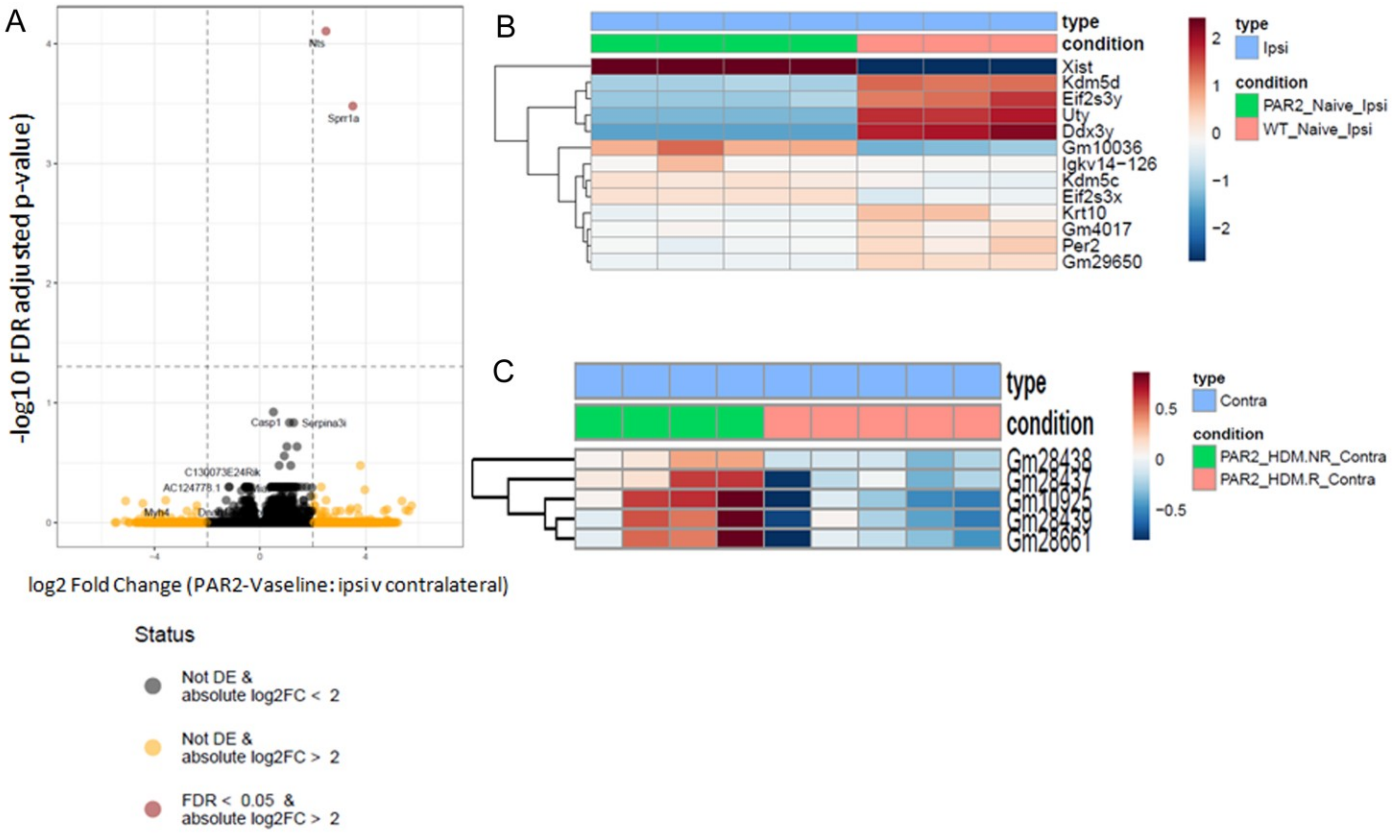


Supplementary Figure 1: Hierarchical clustering of up-(dark red) and down-(dark blue) regulated genes in HDM-treated *Grhl3*$^{PAR2/+}$ responder (A-B) and non-responder (C) mice.



Supplementary Figure 2: (A) Volcano plot illustrates that only two genes (Sprr1a and neurotensin, NTS) were significantly upregulated in the TG by Vaseline/SDS treatment in the *Grhl3*$^{PAR2/+}$ mice. (B-C) Heat map illustrates genes that were differentially expressed in the TG of untreated (naive) *Grhl3*$^{PAR2/+}$ (PAR2_Naive_ipsi) and WT (WT_Naive_ipsi) mice (B) or in the contralateral TG of HDM-treated *Grhl3*$^{PAR2/+}$ responder (PAR2_HDM.R_Contra) and non-responder (PAR2_HDM.NR_Contra) mice.

Sequencing	RIN	Reads (total)	Reads (aligned)	Alignment rate (%)	Reads (filtered)	Alignment rate filtered (%)	side	N
WT-Naive	8.3	1.13E+08	9.24E+07	82	6.54E+07	58	contra	4
WT-Naive	8.6	1.07E+08	8.68E+07	81	6.35E+07	60	ipsi	4
Ghrl3$^{PAR2/+}$ Naive	8.6	1.08E+08	8.36E+07	77	6.27E+07	58	contra	4
Ghrl3$^{PAR2/+}$ Naive	8.8	1.11E+08	8.24E+07	74	5.91E+07	54	ipsi	4
Ghrl3$^{PAR2/+}$ Vaseline	8.5	1.27E+08	8.92E+07	71	6.66E+07	53	contra	4
Ghrl3$^{PAR2/+}$ Vaseline	8.5	1.28E+07	6.64E+07	80	4.98E+07	60	ipsi	4
Ghrl3$^{PAR2/+}$ HDM/Non responder	8.7	1.30E+08	9.56E+07	75	7.35E+07	57	contra	4
Ghrl3$^{PAR2/+}$ HDM/Non responder	8.9	1.06E+08	7.71E+07	72	6.05E+07	56	ipsi	4
Ghrl3$^{PAR2/+}$ HDM/Responder	8.7	1.43E+08	9.89E+07	69	7.60E+07	53	contra	4
Ghrl3$^{PAR2/+}$ HDM/Responder	8.8	1.39E+08	9.61E+07	69	7.49E+07	54	ipsi	5

Supplementary Table 1: RNA-sequencing parameters. Results after bulk RNA-sequencing of ipsilateral and contralateral trigeminal ganglia (TG) from WT, Vaseline-treated *Grhl3*$^{PAR2/+}$ and HDM-treated *Grhl3*$^{PAR2/+}$ mice. Input RNA was of high quality (> 8 RIN) and the final, filtered sequencing depth was between 50-90 million reads.

Allele	Forward Primer (5' – 3')	Reverse Primer (5' – 3')
9130204L05Rik	GGGTGGCTCTTCTCCTTTGTA	AAAGGTGGGCAGAACTGCTT
Actb	GCCTTCCTTCTTGGGTATGGAA	CAGCTCAGTAACAGTCCGCC
Angptl2	CAGGAGAGAAGAGGCTTTCAGT	TTCATGTTGCGGCTCTCCTT
Bdnf	GACGACATCACTGGCTGACA	ATTGCGAGTTCCAGTGCCTT
Cma1	CACGGAGTGCATACCACACT	GAACCTTCTGGAAGCTCAGGG
Defb8	ATTTCTCCTGGTGCTGCTGTG	GCAGCATTTGAAAGGAGATCC
Ghrl3$^{PAR2/+}$	CACCCCCTCAGCTAAGAAGGAA	CTGGGTTTCCAATCTGCCAATAAG
Il1b	TGCCACCTTTTGACAGTGATG	AAGGTCCACGGGAAAGACAC
Il4ra	TTACTATACACACGCCGAGCC	ATGCCAGGACCCTTCTCTCT
Klk7	GGGGTGCTGGTGGACAAATA	GAGGGAAAGGTCACGTCTGG
Nptx2	AATAGGGCCTCTCCCTCGTT	CGGGGGAAATACTCGATGGG
Npy1r	CGTTCCCTGCTAGGCATCAT	AGGGACCTGTTTTGCCACTT
Ptgds2	CACTCTATCACTGGCACCCC	TTGGCACATTTCTTCCCCCA
Spink12	AGCAGGTGCCTTTCTGCTTT	AGAATGCACAGCGGTTTTGG
Tmem79	AGCTCCTTTCCGGAGATCCT	CAAGGAGCCCGAGTACGATG
Trpa1	CTCCATGGGATGACCCCTCT	AGAACCACTTCCTTGCGCTT
Vgf	CATCGCTCATACTCCAGCCA	GGGCTCTCCAGATTGACTCG

Supplementary Table 2: Sequence of the primers we used for qPCR and *Grhl3*$^{PAR2/+}$ genotyping.

Grhl3$^{PAR2/+}$	Baseline scratching (bouts/30 min)	Post-HDM scratching (bouts/30 min)
HDM-NR	2	5
HDM-NR	0	4
HDM-NR	11	14
HDM-NR	4	4
HDM-R	8	65
HDM-R	1	76
HDM-R	9	134
HDM-R	23	63
HDM-R	4	203

Supplementary Table 3: Scratching bouts of the *Grhl3*$^{PAR2/+}$ mice that were included in the RNA-Seq analysis.