SUPPLEMENTAL DATA:

Supplemental Figure S1: TMC family expression in sensory ganglia. Expression values determined by real time qPCR of Tmc1-8 in DRG, JNC and TG. N=4, values are reported as mean ± SEM.

Supplemental Figure S2: Nicotinic receptor subunits expression in sensory ganglia: (A) qPCR expression values of Chrna3 and Chrnb4 subunits in DRG, TG and JNC. N=4, values are reported as mean ± SEM. **(B)** FPKM in DRG, TG and JNC of the same nicotinic receptor subunits.
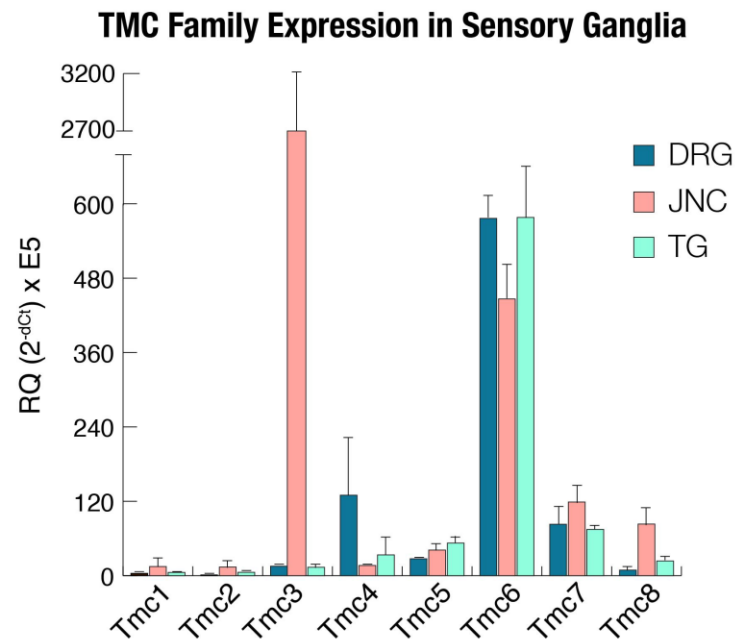
Supplemental Figure S3: RNAseq FPKM expression of JNC clusters: RNAseq expression values (FPKM) of genes identified to differentially label different nodose ganglia single cell clusters (*Cell Rep 2019, 27:2508*) comparing Fast Blue labeled (lung innervating) JNC population to the non-labeled (non lung-innervating) negative population. N=4, values are reported as mean ± SEM; * p < 0.05.

Supplemental Table S1: Alignment Fast Blue positive and negative: RNAseq read alignment and total cell values for the Fast Blue traced populations. The Fast Blue traced neurons represented ~2% of the total population of neurons in the JNC. Veh = vehicle, LSP = lipopolysaccharide, FB+ = Fast Blue positive JNC neurons, FB- = Fast Blue negative JNC neurons. N=2, each N represents 5 pooled mice.

Supplemental Table S2: Distribution of JNC-enriched transcripts in Fast Blue positive and negative cells: RNAseq expression values in FPKM of the 7 gene transcripts highly enriched in JNC as compared to DRG and TG. Expression levels in whole JNC ganglia (WG) are compared to the lung-innervating Fast Blue positive neurons (FB+), and the Fast Blue unstained cells that include the non-lung innervating neurons (FB-). Data are shown from 2 experiments with ganglia or cells pooled from 5 mice each, values reported as mean ± SEM.
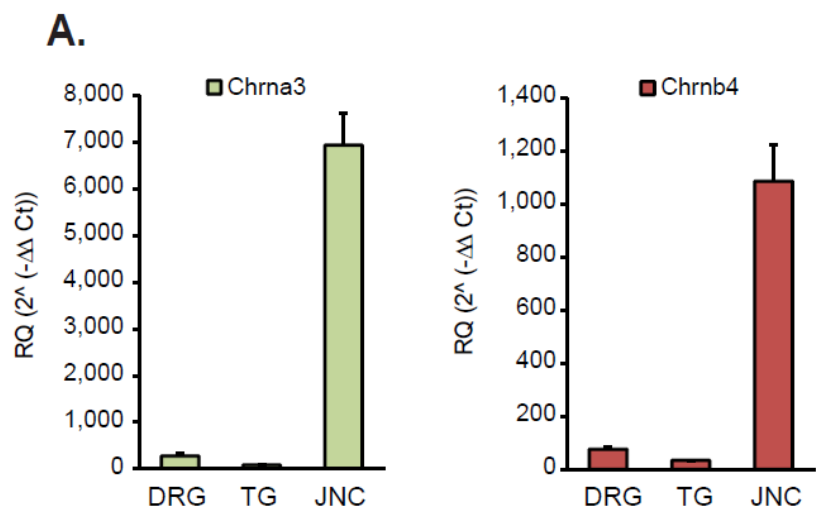
Supplemental Video S1: Airway-innervating JNC neurons traced with Fast Blue: Three-dimensional reconstruction of JNC ganglion. Neurons are labeled by Fast Blue that was exposed intranasally one week before collection.
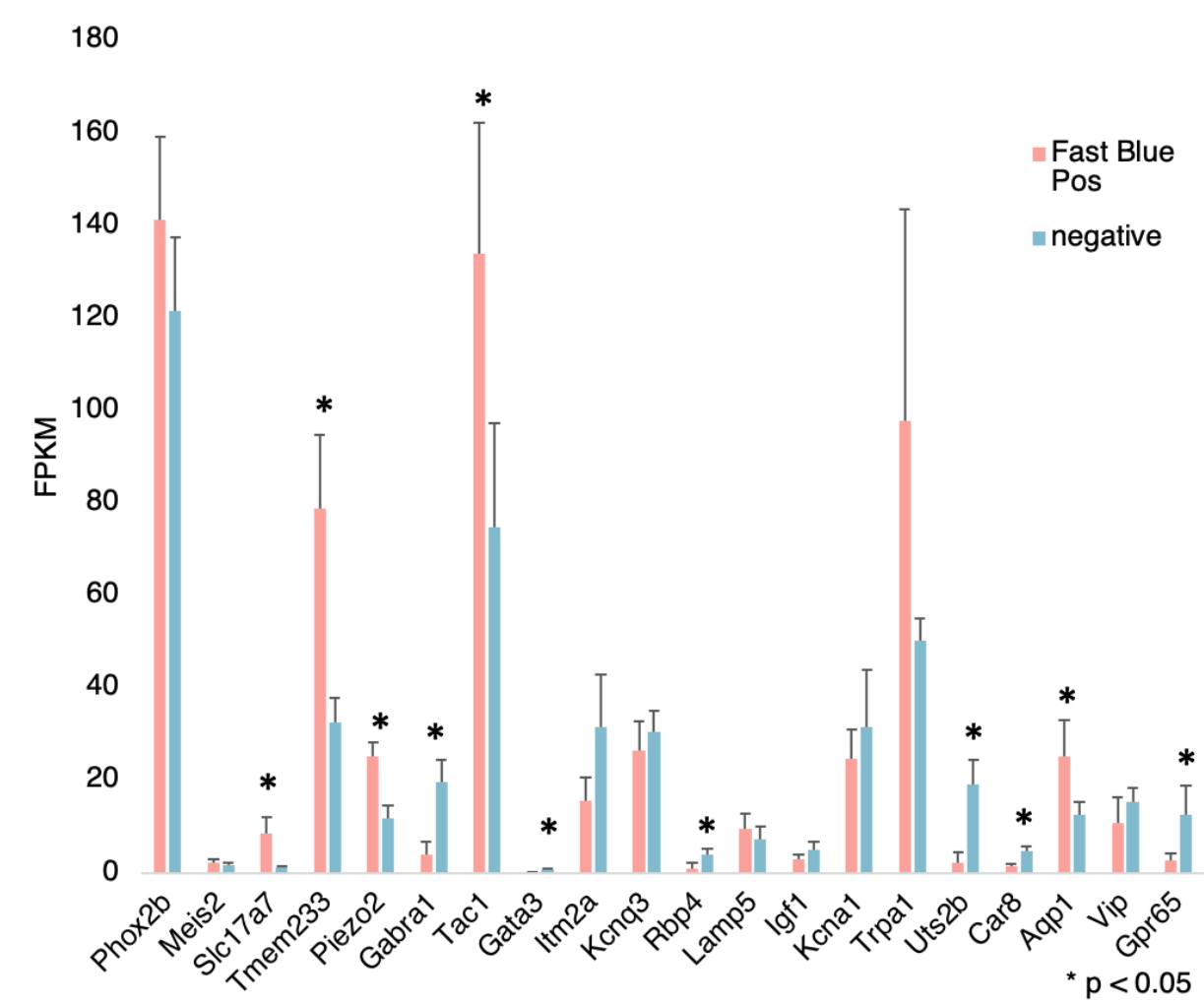
Supplemental Figure S1

TMC Family Expression in Sensory Ganglia

Supplemental Figure S2

Expression of nicotinic receptor subunits in sensory ganglia

A.

B.

Gene	FPKM			Description
	DRG	TG	JNC	
Chrna3	6.92 ± 0.33	2.63 ± 0.30	161.83 ± 4.14	Cholinergic Receptor Nicotinic Alpha 3 Subunit
Chrnb4	5.17 ± 0.70	1.25 ± 0.20	83.57 ± 2.83	Cholinergic Receptor Nicotinic Beta 4 Subunit

Supplemental Figure S3

Supplemental Table S1

Sample	# Cells	Total reads	% reads aligned	% Multiple alignments	# Reads with ≥ 20 alignments
Veh1 FB+	785	29,322,446	83.8%	6.0%	745
Veh1 FB-	38,650	33,463,139	84.3%	5.3%	1,566
LPS1 FB+	752	31,198,754	83.3%	6.9%	905
LPS1 FB-	26,266	30,231,450	85.5%	5.1%	1,170
Veh2 FB+	1,355	30,723,914	84.3%	5.8%	1,078
Veh2 FB-	54,963	29,977,479	85.2%	3.5%	2,855
LPS2 FB+	1,390	32,572,505	82.6%	7.0%	1,189
LPS2 FB-	57,212	38,033,182	87.4%	4.2%	2,533

Supplemental Table S2

Gene	WG	FB+	FB-
Phox2b	90.98 ± 2.29	155.83 ± 6.25	113.10 ± 2.78
P2rx2	90.37± 3.04	70.91 ± 5.99	94.43 ± 26.19
Tmem255b	28.78 ± 4.00	10.07 ± 2.53	38.25 ± 11.98
Gpr65	26.62 ± 0.42	1.91 ± 0.71	13.59 ± 5.69
Uts2b	34.77 ± 5.09	1.92 ± 1.73	23.24 ± 2.30
Tmc3	59.74 ± 7.26	36.02 ± 1.49	74.60 ± 6.74
Actb	647.8 ± 31.7	679.4 ± 3.41	592.52 ± 114.1