



## Supplementary Materials for

### **Scratching promotes allergic inflammation and host defense via neurogenic mast cell activation**

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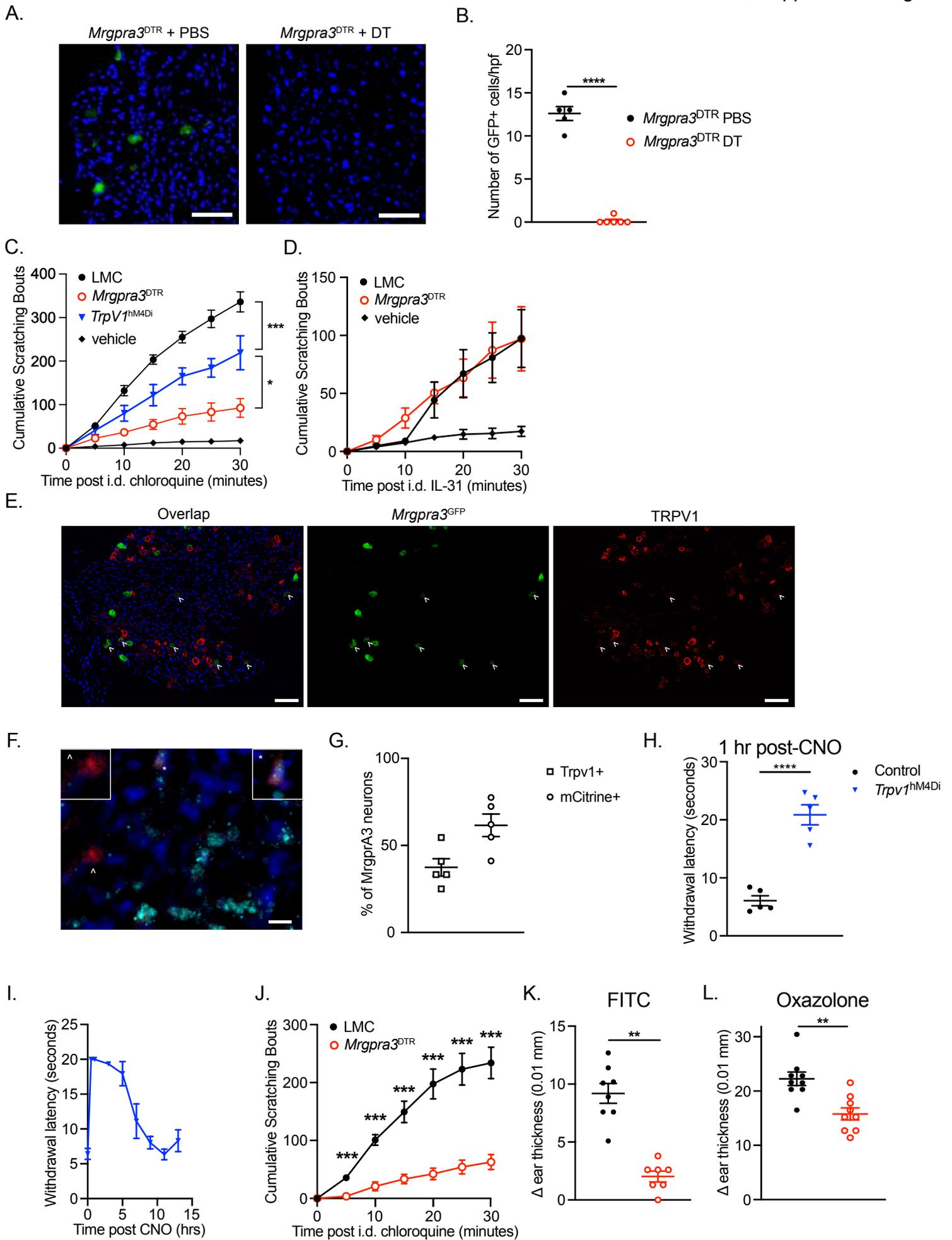
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DOI: 10.1126/science.adn9390

**The PDF file includes:**

Figs. S1 to S9

**Other Supplementary Material for this manuscript includes the following:**

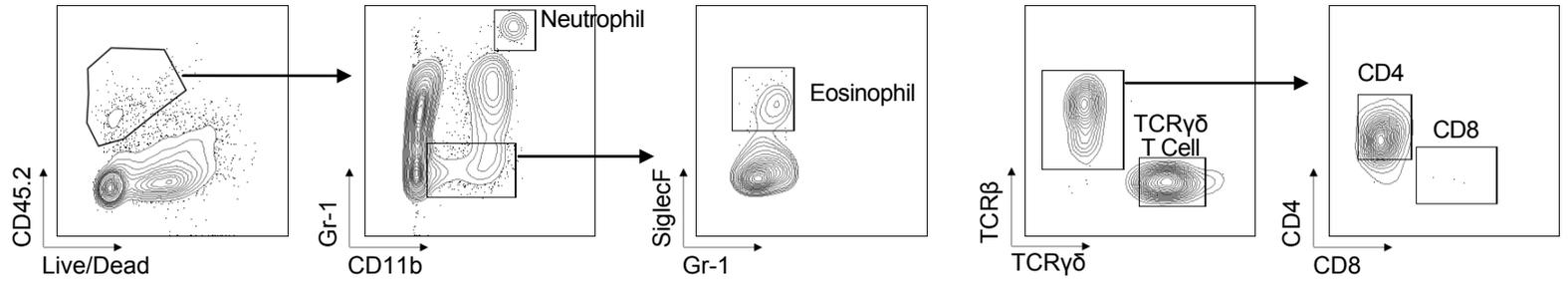
MDAR Reproducibility Checklist



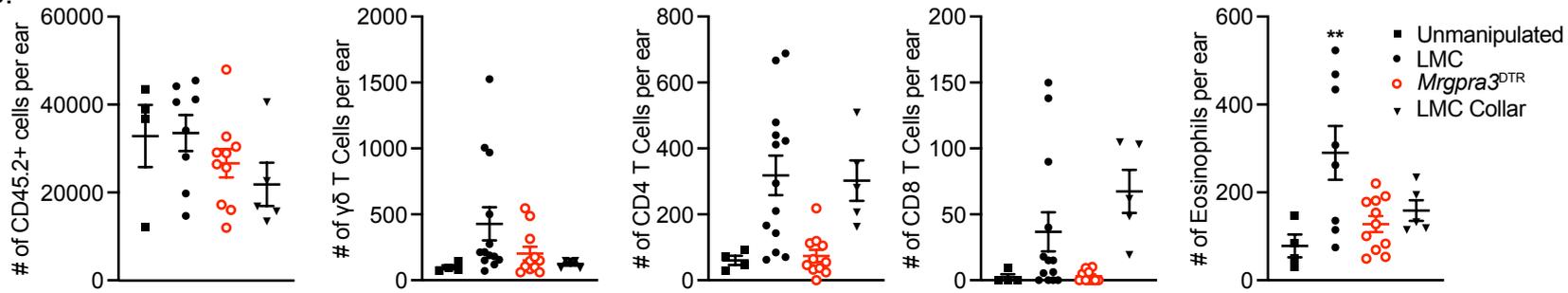
### Fig. S1. Validation of MrgprA3-DTR loss-of-function mouse model

(A) Immunofluorescent visualization of dorsal root ganglia cell bodies (DAPI, blue) and MrgprA3 (GFP, green) after 6 total 300 ng DT treatments in litter mate control (LMC, black circle) and *Mrgpra3*<sup>DTR</sup> (red circle) mice quantified in (B) (*Mrgpra3*<sup>DTR</sup> PBS n = 5 and *Mrgpra3*<sup>DTR</sup> DT n = 6) (C) Total scratching behavior at the indicated time points following injection of either PBS vehicle (black diamond) or 0.2 mg chloroquine (CQ) or (D) 0.8 µg IL-31 i.d. in the nape in LMC, *TrpV1*<sup>hM4Di</sup> (blue triangle), and *Mrgpra3*<sup>DTR</sup> mice (PBS control n = 4, LMC n = 8-16, *Mrgpra3*<sup>DTR</sup> n = 10-11, *TrpV1*<sup>hM4Di</sup> n = 7). All mice were treated with 6 i.p. injections of 300 ng DT separated by 3 days. (E) Representative images from immunofluorescent visualization of dorsal root ganglia cell bodies (DAPI, blue, MrgprA3 (GFP, green) and TrpV1 (RFP, red) in *MrgprA3*<sup>Cre</sup> Rosa26.YFP mice. MrgprA3<sup>YFP</sup> cells that co-express TrpV1 are indicated with white arrow heads. (F) Representative images of RNAscope visualization of DRG cell bodies (DAPI, blue) identifying mRNA for mCitrine (cyan) and *Mrgpra3* (red) isolated from unmanipulated *TrpV1*<sup>hM4Di</sup> mice which have mCitrine expressed in tandem with hM4Di. Asterix identifies Mrgpra3-expressing cells that co-express mCitrine and have undergone cre-mediated recombination. Arrowhead identifies cells not expressing mCitrine that have not undergone cre-mediated recombination. (G) A quantification of the percent of MrgprA3-expressing cells from (E) that co-express TrpV1 and *Mrgpra3*-expressing cells from (F) that co-express mCitrine is shown. Each symbol represents average values from 3 high powered fields from a single animal (n = 5). (H) Thermal withdrawal latency measured in CNO-injected LMC or *TrpV1*<sup>hM4Di</sup> mice 1 hour following CNO injection and (I) at the indicated time points (LMC and *TrpV1*<sup>hM4Di</sup> n = 5). (J) Total scratching behavior over 5 minute intervals at the indicated time points following injection of CQ in LMC and *Mrgpra3*<sup>DTR</sup> mice after 2 i.p. injections of 600 ng DT (LMC n = 7, *Mrgpra3*<sup>DTR</sup> n = 8). (K) Ear thickness 1 day after FITC and (L) oxazolone challenge in hapten-sensitized LMC and *Mrgpra3*<sup>DTR</sup> that were given 2 i.p. injections of 600 ng DT after sensitization and before challenge (FITC LMC n = 8, *Mrgpra3*<sup>DTR</sup> n = 7; oxazolone LMC and *Mrgpra3*<sup>DTR</sup> n = 9). Scale bar in (A and E) 200 µm and in (F) 50 µm. Results in C-D and I-J are displayed as mean +/- SEM and are representative of 3 independent experiments. Each symbol in B, H and K-L represent data from an individual animal. Significance was calculated using a one-way ANOVA with multiple comparisons (C and D), Mann-Whitney (H, J), or unpaired Student's t-test (B, K-L). \*p<0.05, \*\*p<.01, \*\*\*p<.001, \*\*\*\*p<.0001.

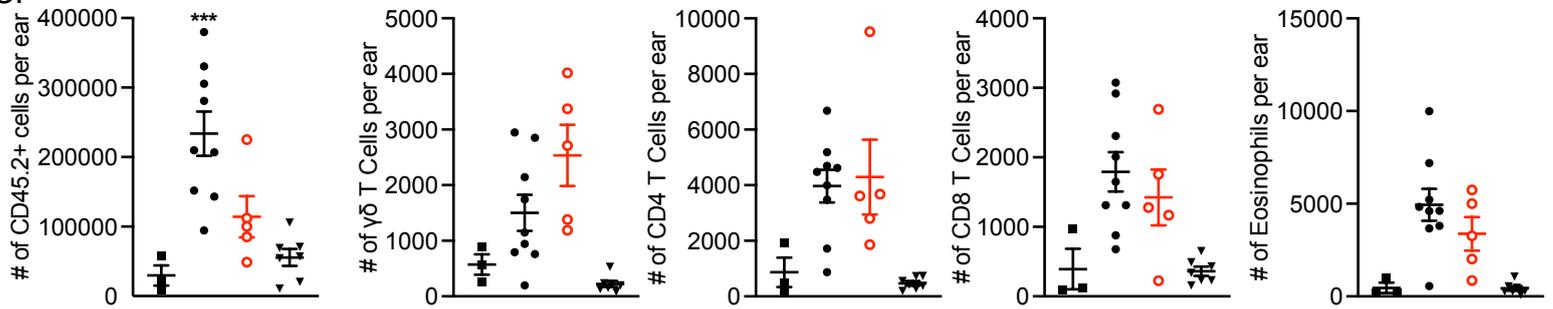
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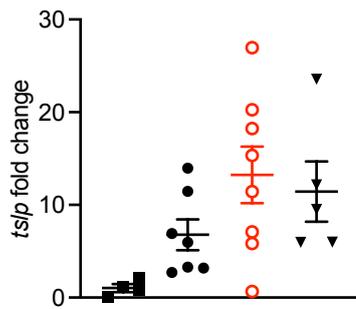
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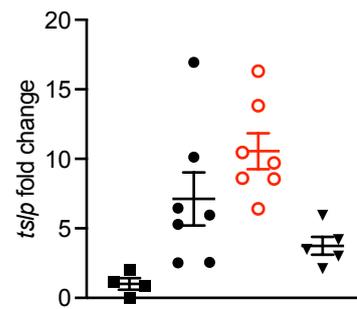
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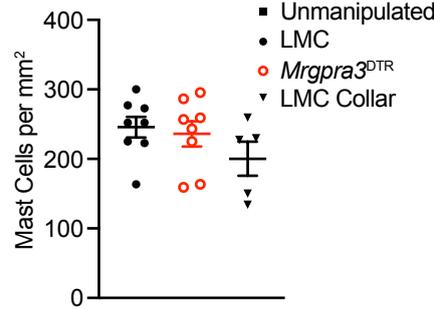
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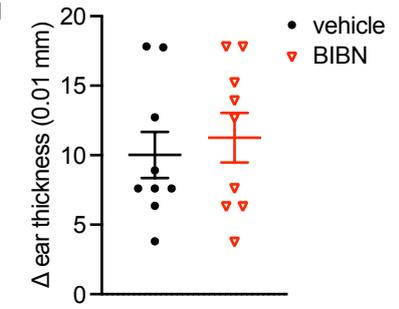
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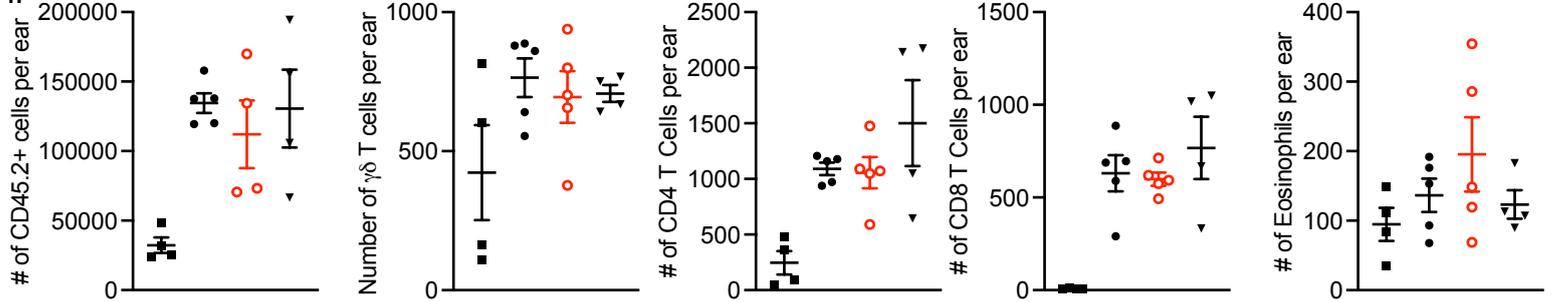
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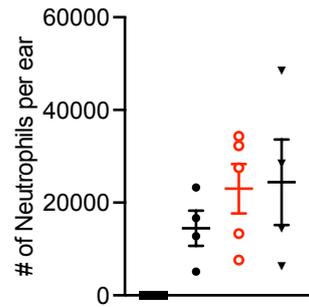
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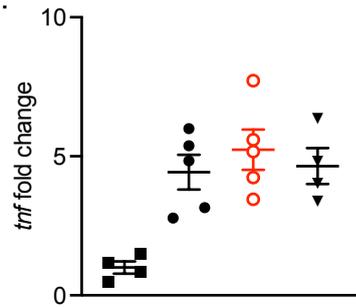
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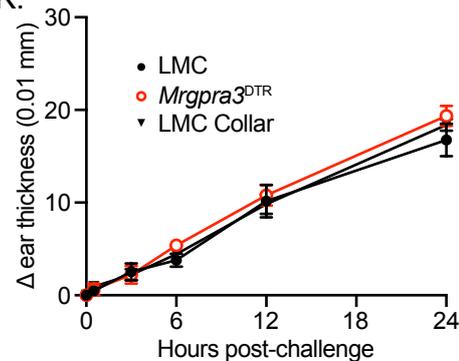
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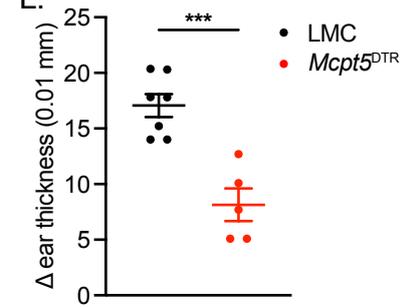
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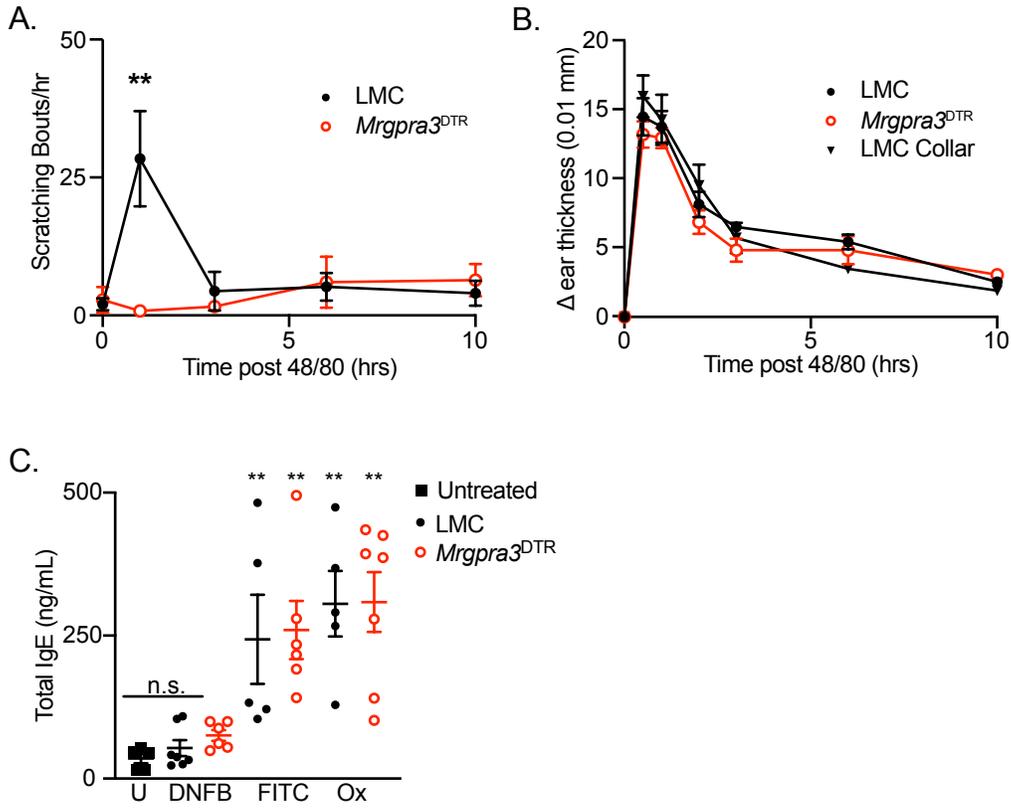


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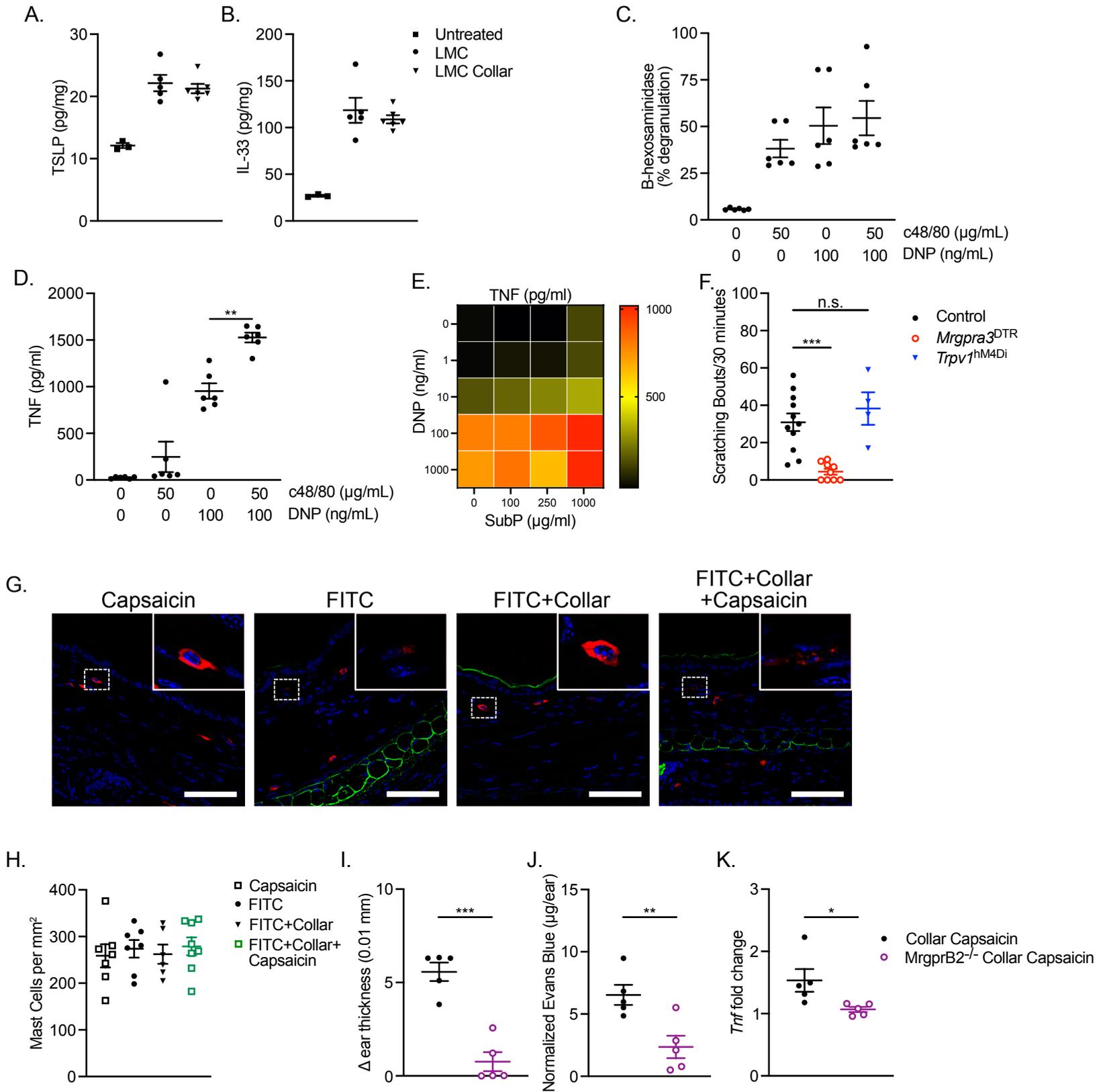
**Fig. S2. Cellular infiltrate of FITC and Oxazolone-challenged ears.**

(A) Representative gating strategy for immune cells from single cell suspensions of whole skin. Indicated cell populations in ears from unmanipulated (black square) or hapten-challenged LMC (black circle), *Mrgpra3<sup>DTR</sup>* (red circle), and LMC collared (black triangle) mice 1 day following (B) FITC or (C) oxazolone challenge. *Tslp* mRNA expression in whole ear tissue from LMC, *Mrgpra3<sup>DTR</sup>*, and LMC collared mice 1 day following (D) FITC or (E) oxazolone challenge (Unmanipulated n = 4 LMC n = 8-13, *Mrgpra3<sup>DTR</sup>* n = 5-11, collar n = 5). (F) Total number of mast cells quantified in ear skin 10 hours post-FITC challenge (LMC and *Mrgpra3<sup>DTR</sup>* n = 8, collar n = 5). (G) 80 ng BIBN4096 (red triangle) or vehicle (black circle) was given i.p. to FITC sensitized mice 1 hour prior to FITC challenge (vehicle and BIBN n = 10). Ear thickness was measured 24 hours post-challenge. (H) Indicated cell populations and (I) neutrophils in ears from unmanipulated or LMC, *Mrgpra3<sup>DTR</sup>*, and LMC collared mice 1 day following DNFB challenge of sensitized mice (Unmanipulated n = 4, LMC n = 5, *Mrgpra3<sup>DTR</sup>* n = 4, collar n = 4). (J) *Tnf* mRNA expression in whole ear tissue from unmanipulated or LMC, *Mrgpra3<sup>DTR</sup>*, and LMC collared mice 1 day following DNFB challenge. (K) Ear thickness at the indicated timepoints after DNFB challenge. (L) 120 ng DT was injected i.d. at the ear pinna in FITC-sensitized *Mcpt5<sup>DTR</sup>* (red closed circle) mice 6 and 2 days before FITC challenge (LMC n = 7, *Mcpt5<sup>DTR</sup>* n = 5). Ear thickness was measured 24 hours post-challenge. Results in K are displayed as mean +/- SEM and are representative of 3 independent experiments. Each symbol in A-J and L represent data from an individual animal. Significance was calculated using a one-way ANOVA with multiple comparisons, \*p<0.05, \*\*p<.01, \*\*\*p<.001, \*\*\*\*p<.0001.



**Fig. S3. Compound 48/80 phenocopies SP *in vivo* and Serum IgE is elevated in FITC and Ox, but not DNFB CHS**

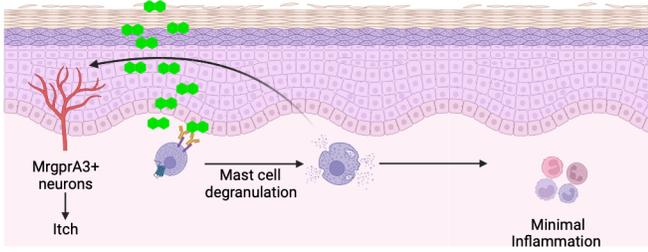
(A) The number of scratching bouts per hour in DT-treated littermate control (LMC, black circle), *Mrgpra3<sup>DTR</sup>* (red circle) after intradermal injection of 200ng compound 48/80 into the ear is shown (LMC and *Mrgpra3<sup>DTR</sup>* n = 5). (B) Ear thickness in DT-treated litter mate control (LMC), *Mrgpra3<sup>DTR</sup>*, and collared LMC mice at the indicated time following intradermal injection of compound 48/80 into the ear is shown (LMC and *Mrgpra3<sup>DTR</sup>* n = 5, Collar n = 4). (C) Total IgE levels taken from serum of untreated (black square) mice and DT-treated, hapten-sensitized LMC and *Mrgpra3<sup>DTR</sup>* mice 10 hours after DNFB, FITC, and oxazolone challenge (Unmanipulated n = 5, LMC n = 5-7, *Mrgpra3<sup>DTR</sup>* n = 6-7). Results in A-B are displayed as mean +/- SEM and are representative of 3 independent experiments. Each symbol in C represent data from an individual animal. Significance was calculated using a Mann-Whitney test (A) or by one-way ANOVA with multiple comparisons (B-C), \*p<0.05, \*\*p<.01.



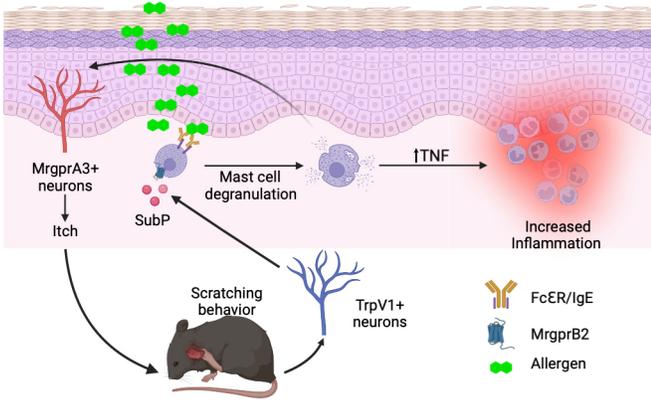
**Fig. S4. IgE cross linking and MrgprB2 agonism synergize for TNF release**

(A) TSLP and (B) IL-33 protein levels in whole ear skin from untreated (black square) mice and DNP-specific IgE sensitized LMC (black circle) and collared LMC (black triangle) mice 10 hours after DNP challenge (Untreated n = 3, LMC and collar n = 5). (C)  $\beta$ -hexosaminidase and (D) TNF protein levels from the culture supernatants of DNP-specific IgE sensitized cultured PMCs from 6 mice across 3 experiments 6 hours following treatment with the indicated doses of DNP and compound 48/80. (E) TNF protein levels from the supernatants of DNP-specific IgE sensitized cultured PMCs 6 hours following treatment with the indicated dose of DNP and Substance P. (F) Scratching behavior over 30 minutes after FITC challenge in sensitized LMC, *Mrgpra3*<sup>DTR</sup>, and *TrpV1*<sup>hM4Di</sup> mice (LMC n = 11, *Mrgpra3*<sup>DTR</sup> n = 9, *TrpV1*<sup>hM4Di</sup> n = 4). (G) Immunofluorescent visualization of ear skin 10 hours after FITC challenge in capsaicin-treated (black square), FITC-challenged (black circle), collared FITC-challenged (black triangle), and collared capsaicin-treated and FITC-challenged (green square) mice with the total number of mast cells quantified in (H) (capsaicin and FITC n = 7, collar n = 6, FITC capsaicin collar n = 8). (I) Ear thickness, (J) quantification of Evans Blue extravasation, and (K) *Tnf* mRNA measured at 10 hours following DNP and capsaicin treatment in collared WT (black circle) and *MrgprB2*<sup>-/-</sup> (purple circle) DNP-specific IgE sensitized mice (WT and *MrgprB2*<sup>-/-</sup> n = 5). Scale bar in (H) = 200  $\mu$ m. Each symbol in A-D, F and H-K represent data from an individual animal. Significance was calculated using a one-way ANOVA with multiple comparisons (C, D, F, H), or unpaired Student's t-test (I-K) \*p<0.05, \*\*p<.01.

A.

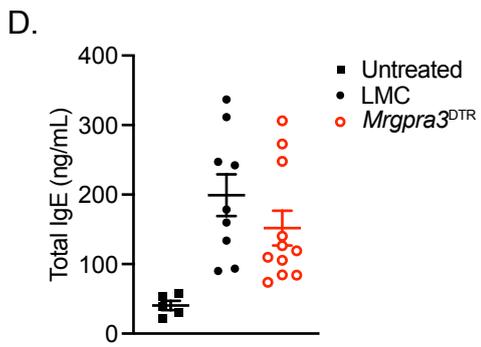
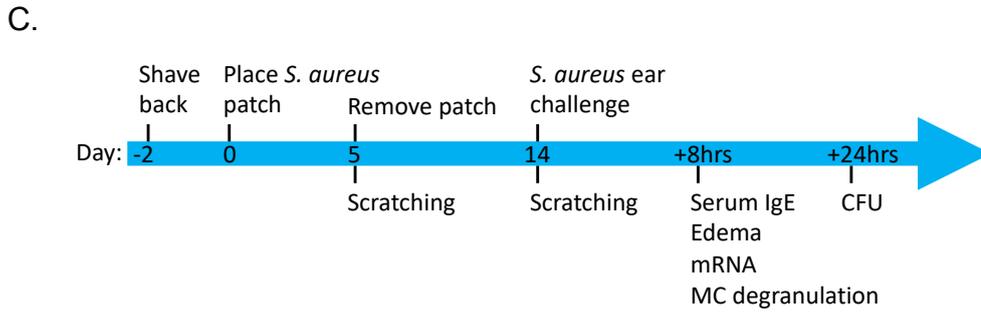
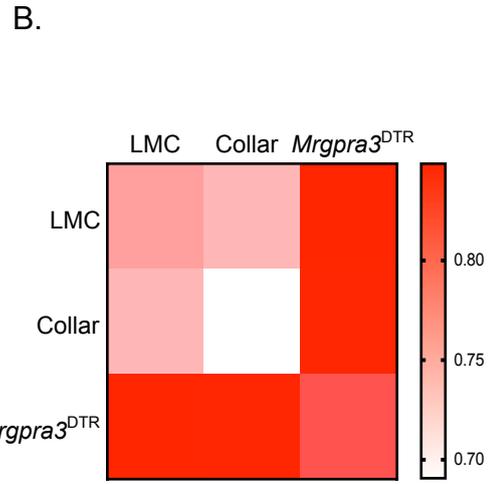
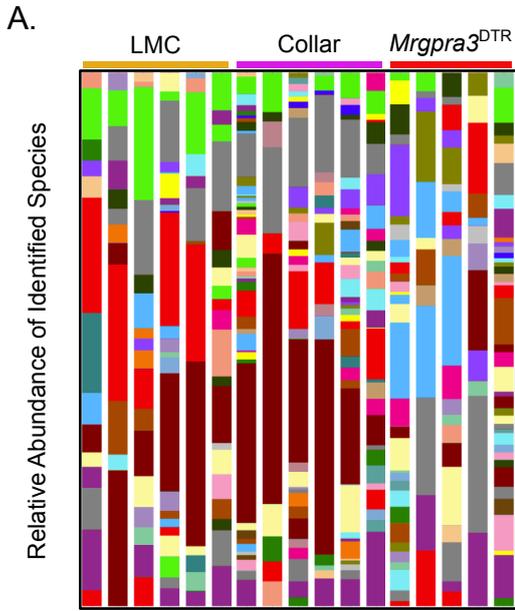


B.



**Fig. S5. Model**

(A) Following allergen challenge in an immunized host, mast cells are activated via FcεRI cross linking, resulting in degranulation and release of pruritogens that activate MrgprA3-expressing itch-sensing neurons. Mediators are also released, leading to edema (not pictured) and a small degree of inflammation. (B) Scratching in response to activation of MrgprA3-sensing neurons activates TRPV1-expressing nociceptors and the release of Substance P. Activation of mast cells via FcεRI cross linking combined with SP agonism of MrgprB2 results in increased production of TNF and exaggerated neutrophil recruitment and inflammation. Created with Biorender.com.



**Fig. S6. Experimental scheme for *S. aureus* infections and serum IgE**

(A) The relative abundance of 16S rRNA reads associated with specific bacterial species from unmanipulated ears from the indicated group is shown. The species associated with each color and its relative abundance are shown in Supplemental Figure 7. (B) Bray Curtis beta diversity comparing taxa isolated from unmanipulated ears from the indicated group is shown. (C) Experimental scheme for Figure 5. (D) Total IgE levels taken from serum of untreated (black square), LMC (black circle) and *Mrgpra3*<sup>DTR</sup> (red circle) mice 14 days after epicutaneous *S. aureus* immunization (Untreated n = 5, LMC n = 9, *Mrgpra3*<sup>DTR</sup> n = 11). Each symbol in D represent data from an individual animal..

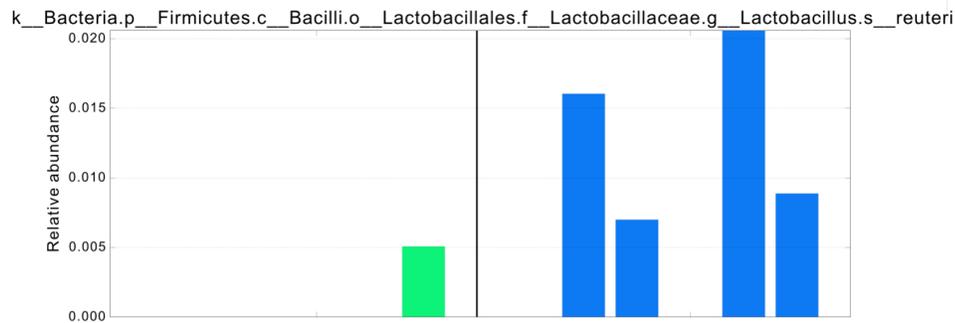
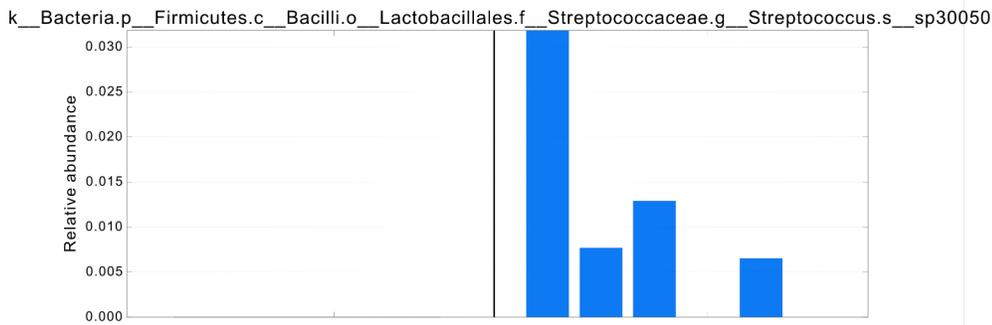
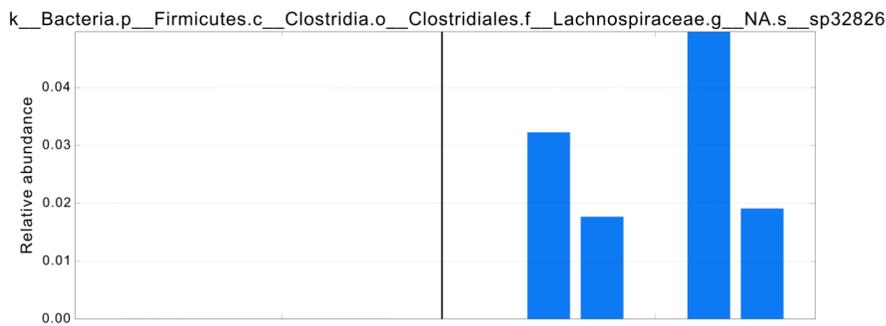
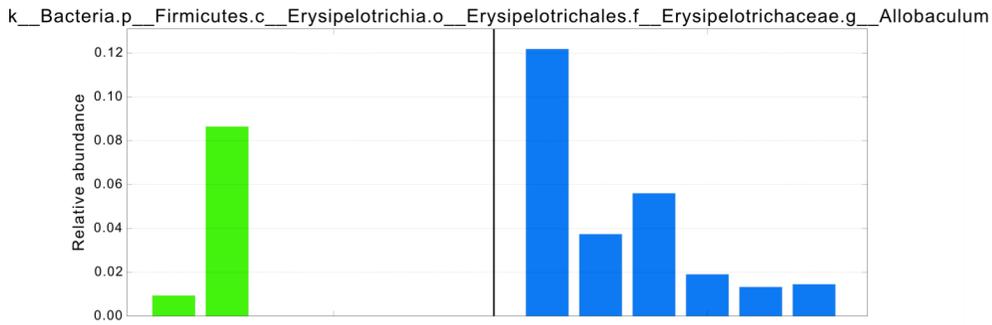
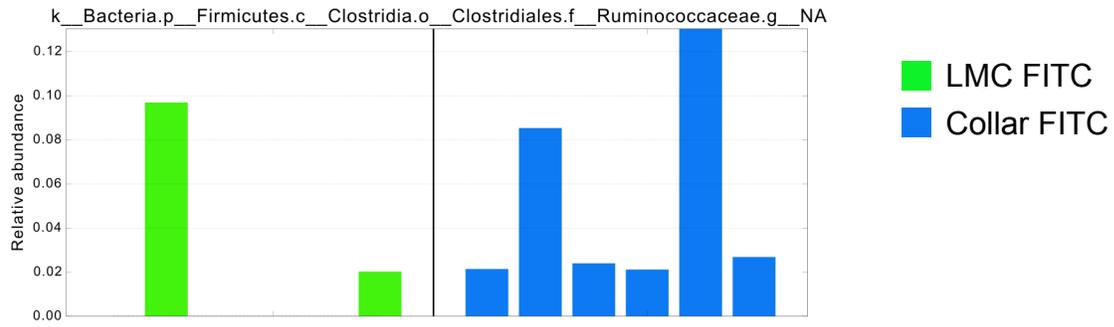
FITC MFC FITC Collar FITC Mrg

Table with columns: Legend, Taxonomy, Total, A1-A6, B1-B6, C1-C6, D1-D6, E1-E6, F1-F6. Rows list various bacterial taxa and their associated values.

FTC MC Collar Mrg

Table with 100 columns (FTC, MC, Collar, Mrg) and 1000 rows of taxonomic data. Each cell contains a percentage value representing the relative abundance of a specific taxon within a category.

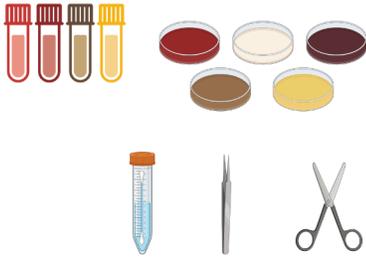
**Fig. S7. Bacterial species and percent abundance of 16S rRNA reads from Figure S6A**



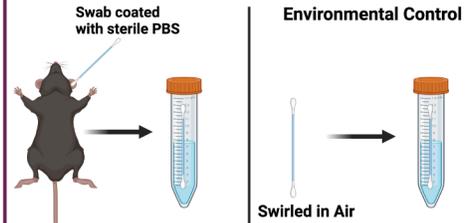
**Fig. S8. Individual 16SrRNA reads associated with decreased taxa from scratching identified by LEfSe analysis**

# Culturomics of Skin Microbiome

## Step 1: Prepare reagents & tools (autoclaved)

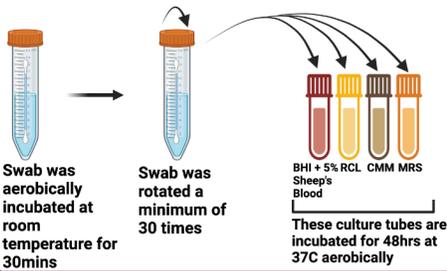


## Step 2: Ear Swabbing

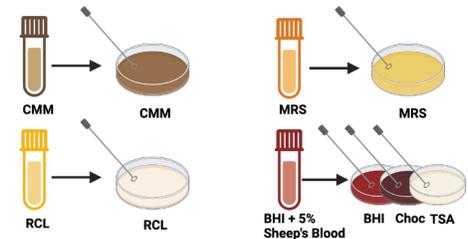


Swab was rotated in the ear for minimum 10 sec to ensure coverage of the entire ear surface

## Step 3: Inoculate Expansion Cultures

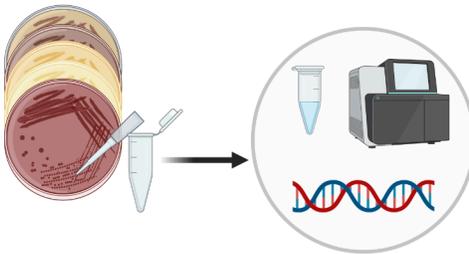


## Step 4: Plate Expansion Cultures

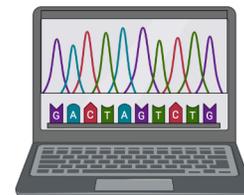


All streaked plates were incubated for 48hrs at 37C aerobically

## Step 5: Pick & Sequence Morphologically Distinct Colonies



## Step 6: Data Analysis



Data was analyzed using NCBI Blast

**Figure S9. Schema of Culturomics approach**  
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