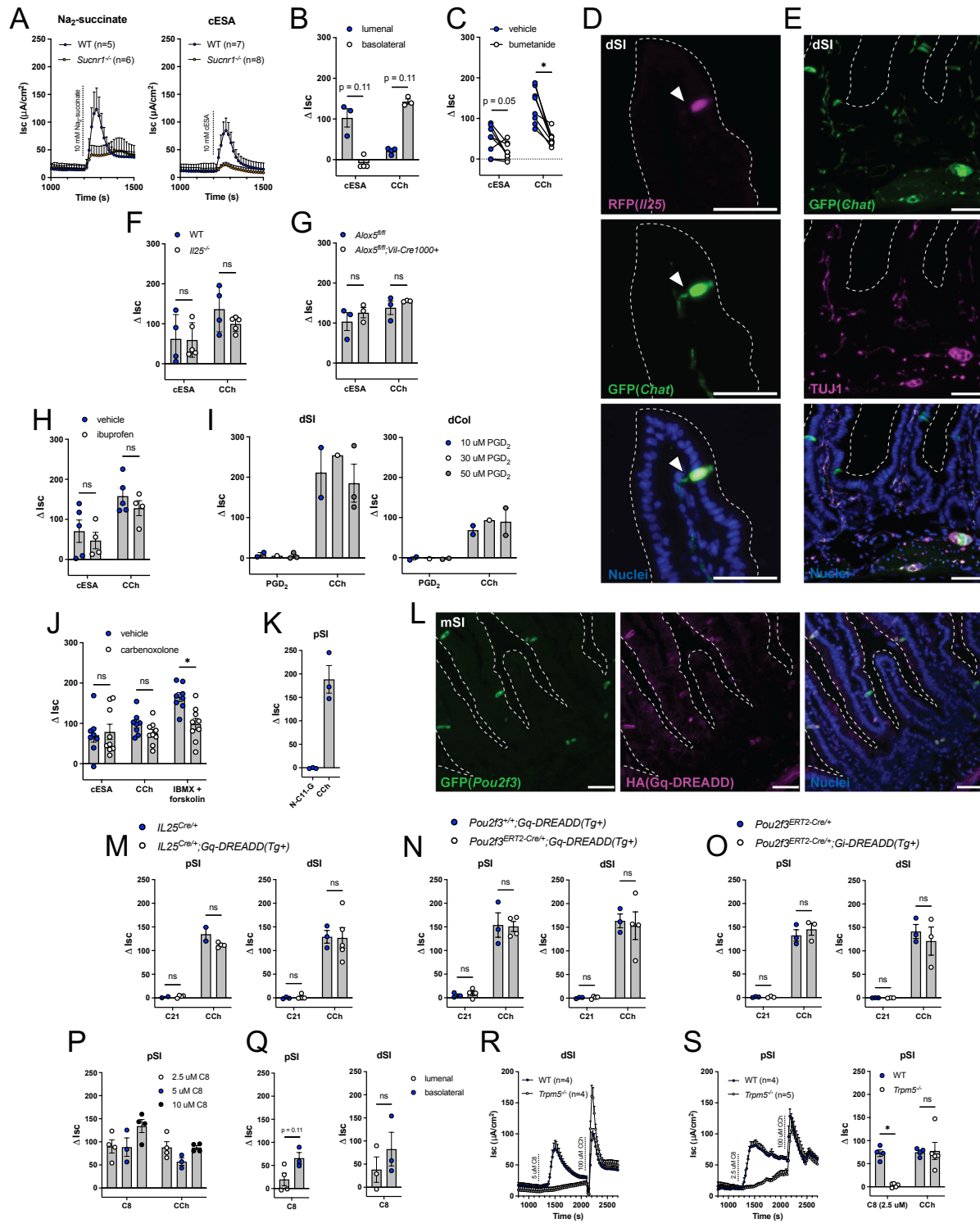
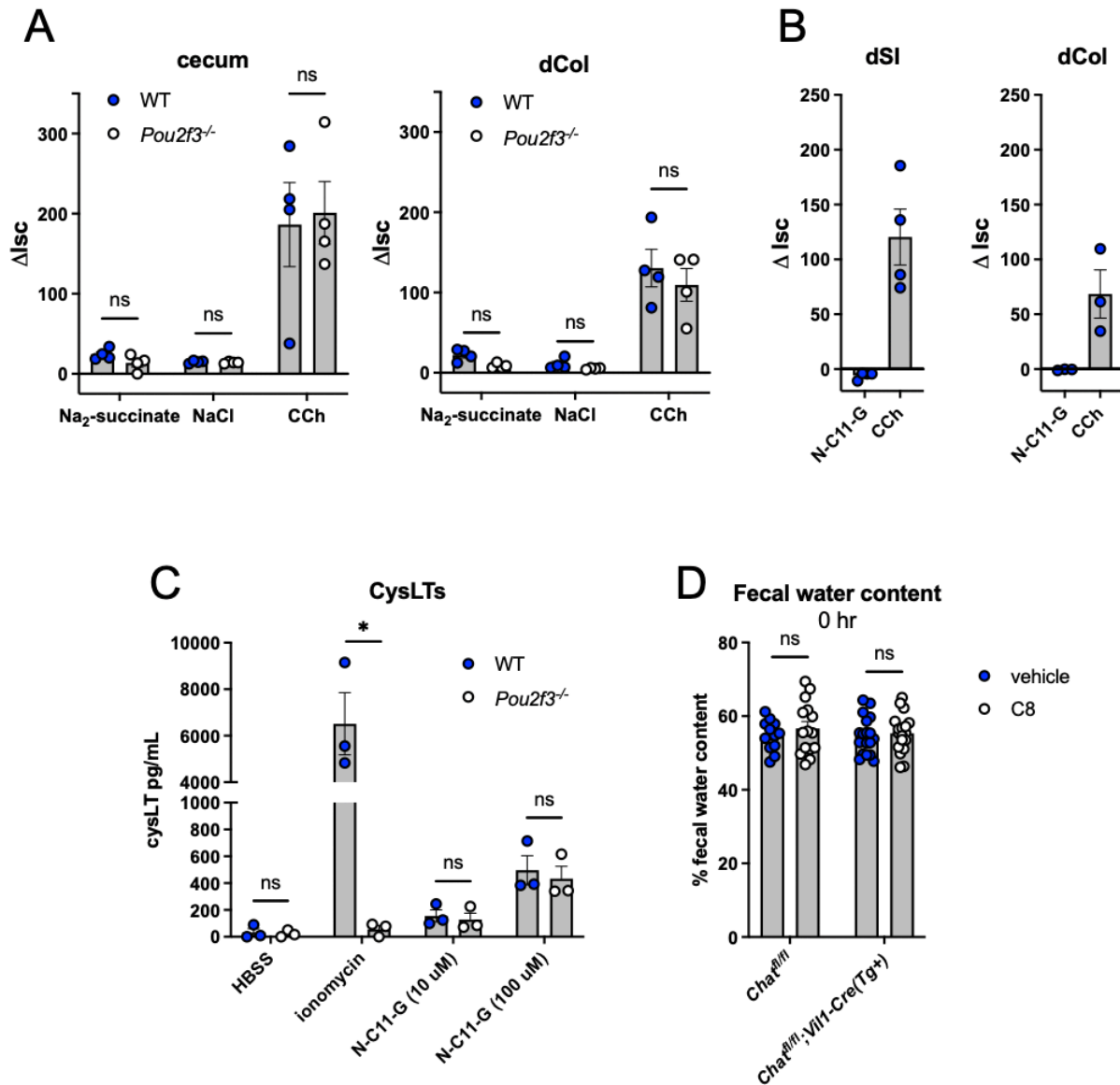


188 **Supplemental Figure 1: (A)** Quantification of GFP+ tuft cells (RFP+) from pSI and dSI of *Chat-*
189 *GFP;Il25^{RFP/+}* mice by immunofluorescence (IF). **(B)** Representative flow cytometry of traced tdTom+ tuft
190 cells (CD24+, Siglec-F+) from pSI and dSI of wild-type (WT) and *Ai9;Chat-Cre* mice. **(C)** Volcano plot
191 showing log₂FC of genes expressed in *Chat*+ tuft cells (n=4) versus *Chat-* tuft cells (n=3) sorted from
192 whole SI of *Chat-GFP;Il25^{RFP/+}* mice. **(D)** Gene set enrichment analysis comparing *Chat*+ tuft cell gene
193 expression to Tuft-1 and Tuft-2 consensus gene signatures and the dSI tuft cell signature from **(E)**
194 Volcano plot showing log₂FC of genes expressed in tuft cells sorted from the dSI (n=4) versus tuft cells
195 sorted from the pSI (n=4) of B6 mice. **(F)** Representative immunofluorescence image showing GFP+
196 (green) tuft cells (RFP+, magenta) in the SI crypt (solid white arrows), next to one GFP- tuft cell (open
197 white arrow). Nuclei stained with DAPI (blue). Scale bars: 50 μm. **(G)** Representative
198 immunofluorescence image showing a GFP- (green) tuft cell (DCLK1+, magenta) at the villus tip (open
199 white arrow), past other GFP+ tuft cells (solid white arrows). Nuclei stained with DAPI (blue). Scale bars:
200 50 μm. **(H)** Quantification of GFP(*Chat*)+ tuft cells (DCLK1+) from denoted tissues of *Il4ra^{-/-};Chat-GFP*
201 mice by immunofluorescence. In the graphs, each symbol represents an individual mouse (columns
202 represent different tissues from same mouse) from two pooled experiments. *p < 0.05, **p < 0.01, ***p <
203 0.001 by Mann-Whitney test (A) or one way ANOVA with Tukey's multiple comparisons test (G). mSI,
204 medial SI. Graphs depict mean +/- SEM.



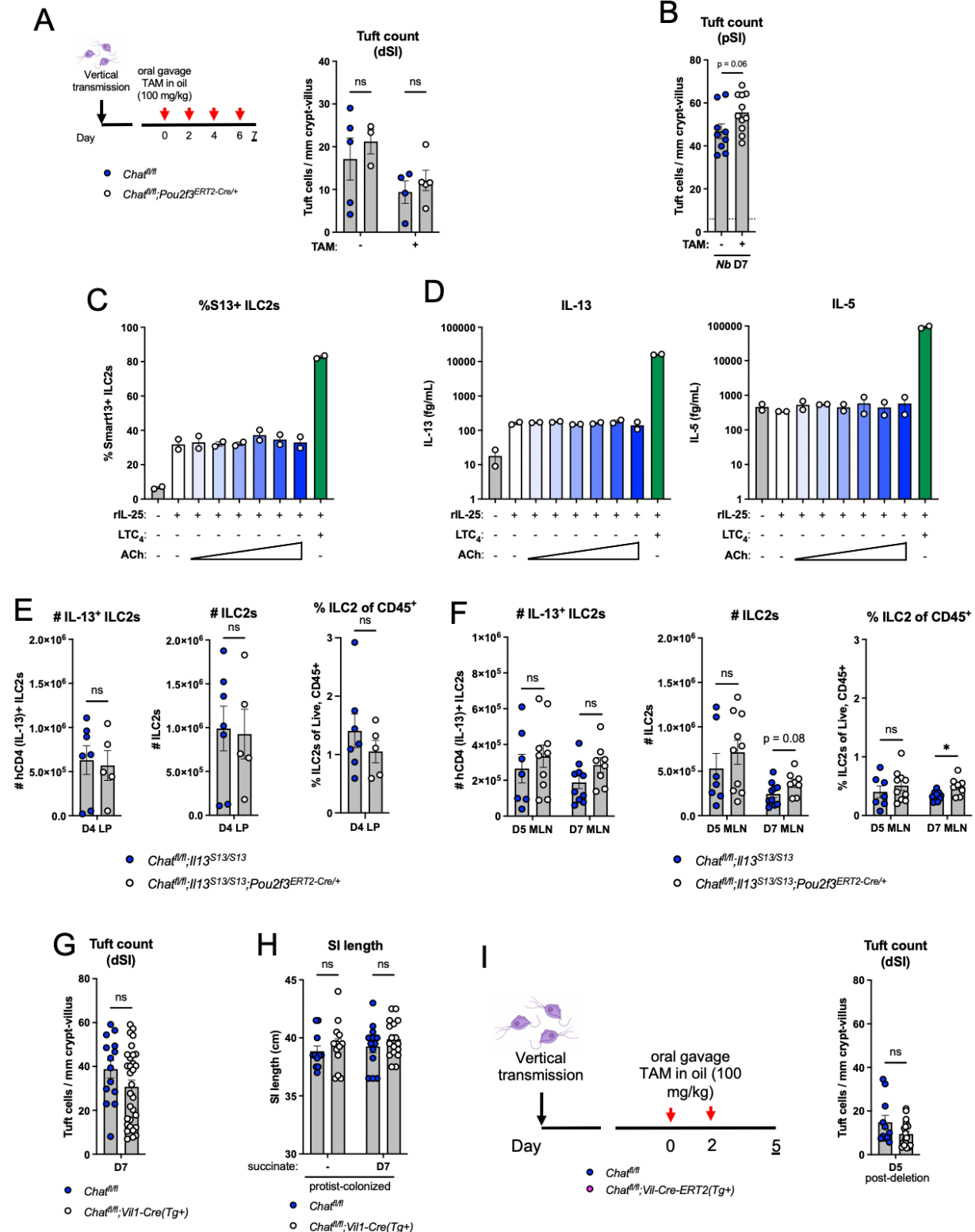
323 **Supplemental Figure 2:** (A) Average Isc traces of dSI from WT or *Sucnr1*^{-/-} mice stimulated as indicate
324 (Na₂-succinate and cESA, luminal). (B) ΔIsc values of WT dSI stimulated as indicated. (C) ΔIsc values of
325 WT dSI pretreated 15 min with vehicle or bumetanide (100 μM, basolateral), stimulated as indicated (10
326 mM cESA luminal; 100 μM CCh, basolateral). (D) Representative immunofluorescence image of a GFP+
327 (green) neuronal process (indicated by solid white arrow) approaching a GFP+/RFP+ (magenta) tuft cell
328 from the dSI of *Chat-GFP;Il25*^{RFP/+} mice. Nuclei stained with DAPI (blue). Scale bars: 50 μm. (E)
329 Representative immunofluorescence image of GFP+ (green) neurons co-stained for BIII tubulin (TUJ1,
330 magenta) in the dSI. Nuclei stained with DAPI (blue). Scale bars: 50 μm. (F, G, and H) (F and G) ΔIsc
331 values of dSI from indicated genotypes or (H) WT dSI compared to dSI pretreated 15 min with ibuprofen
332 (10 μM, bilateral), stimulated as indicated. (I) ΔIsc values of WT tissues stimulated as indicated (PGD₂,
333 basolateral). (J) ΔIsc values for WT dSI compared to dSI pretreated 15 min with carbenoxolone (1 mM,
334 luminal), stimulated as indicated (100 μM IBMX + 10 μM forskolin, bilateral). (K) ΔIsc values of WT pSI
335 stimulated as indicated (100 μM N-C11-G, luminal). (L) Representative immunofluorescence image of
336 GFP+ (green) tuft cells expressing HA+ Gq-DREADDs (magenta) in the crypts and villi of the medial SI
337 (mSI). Nuclei stained with DAPI (blue). Scale bars: 50 μm. (M, N, and O) (M) ΔIsc values of indicated
338 tissues from unmanipulated mice or (N and O) indicated tissues from mice 7 days after start of tamoxifen
339 chow, stimulated as indicated (1 μM C21, bilateral). (P) ΔIsc values of WT pSI stimulated as indicated
340 (C8, bilateral). (Q) ΔIsc values of WT tissues from pSI and dSI stimulated as indicated. (R) Average Isc
341 traces of dSI stimulated as indicated (5 μM C8, basolateral). (S) Average Isc traces and ΔIsc values of
342 pSI stimulated as indicated (2.5 μM C8, basolateral). In the graphs, each symbol represents an individual
343 mouse (one tissue or average of two) pooled from two or more experiments. Groups represent sequential
344 stimulations of the same tissue. In (C) paired vehicle and bumetanide-treated tissues are from the same
345 mouse. *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.001 by multiple Mann-Whitney tests with Holm
346 Sídák's multiple comparisons test (B, F-H, J, M-O, S), Wilcoxon matched-pairs signed rank test with Holm
347 Sídák's multiple comparisons test (C), or Mann-Whitney test (Q). ns, not significant. Graphs depict mean
348 +/- SEM.



418

419 **Supplemental Figure 3:** (A) ΔI_{sc} values of WT and *Pou2f3*^{-/-} tissues stimulated as indicated (10 mM Na₂-
 420 succinate and 20 mM NaCl, lumenal; 100 μ M CCh, basolateral). (B) ΔI_{sc} values of WT tissues stimulated
 421 as indicated (100 μ M N-C11-G, lumenal). (C) Cysteinyl leukotriene (CysLTs) production from WT and
 422 *Pou2f3*^{-/-} SI epithelial monolayers stimulated as indicated. (D) Quantification of water content of fecal
 423 pellets collected from indicated mice immediately after oral treatment with C8 (30 mg/kg). In the graphs,
 424 each symbol represents an individual mouse pooled from two or more experiments. In (A-B) groups

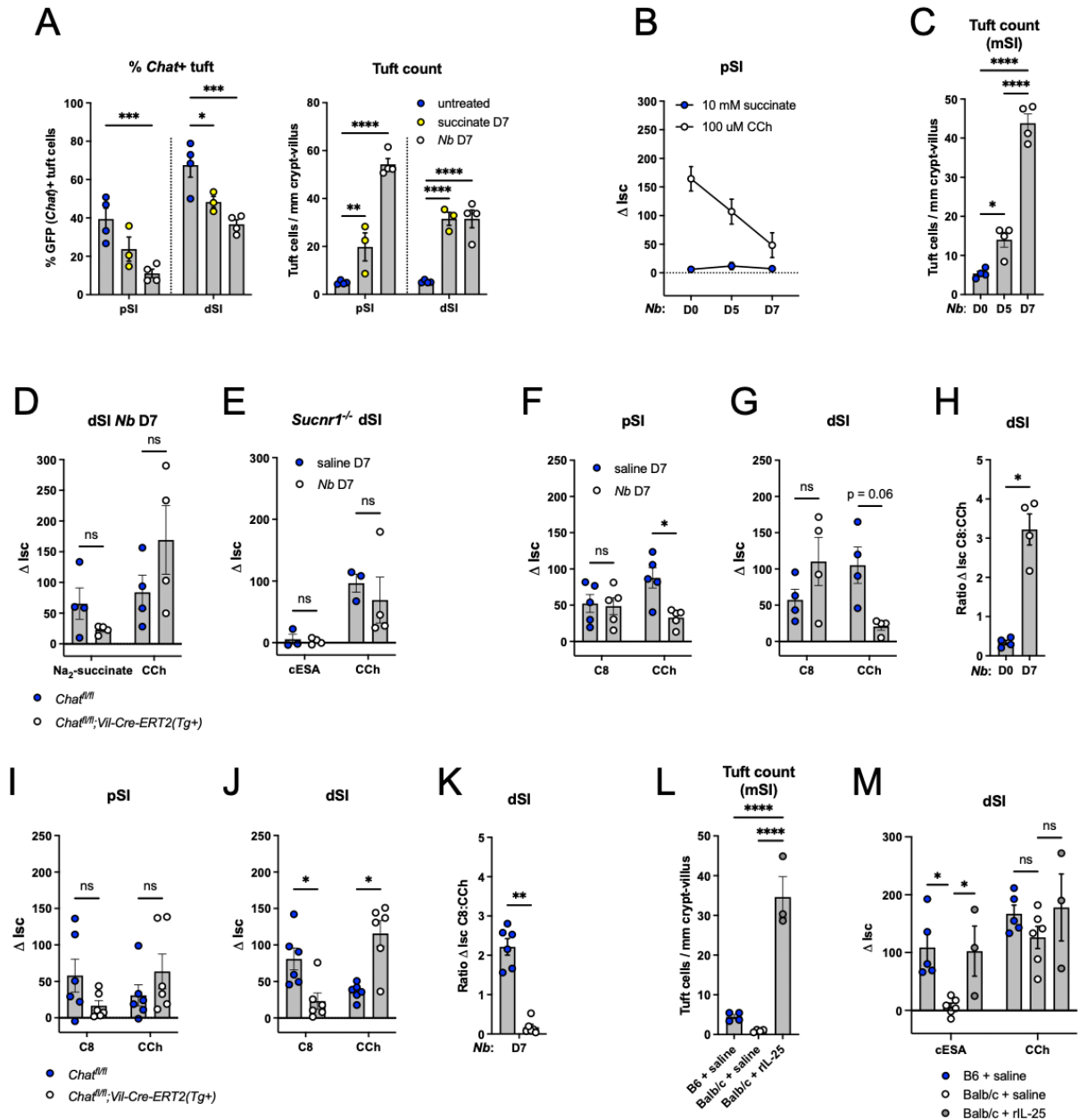
425 represent sequential stimulations of the same tissue and in (C) groups represent individual monolayers.
426 * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.001$ by multiple Mann-Whitney tests with Holm Sídák's
427 multiple comparisons test (A, D), or multiple unpaired t tests with Holm Sídák's multiple comparisons test
428 (C). ns, not significant. Graphs depict mean +/- SEM.



454

455 **Supplemental Figure 4:** (A) Schematic of tamoxifen (TAM) treatment of protist-colonized *Chat-fl;*
456 *Pou2f3^{ERT2-Cre/+}* mice and quantification of dSI tuft counts by immunofluorescence at D7 after start of
457 treatment. (B) Quantification of pSI tuft counts by immunofluorescence of WT mice treated with or without

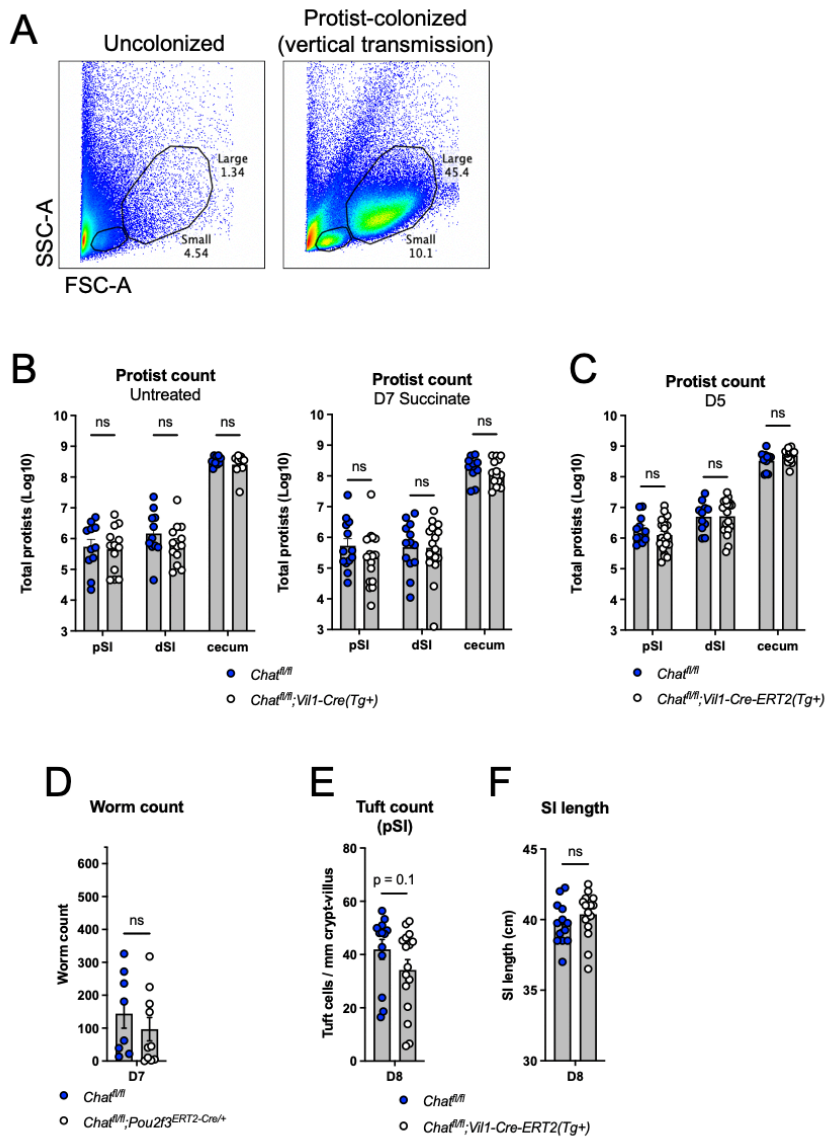
458 tamoxifen and infected with *Nb* for 7 days. **(C and D)** (C) Flow cytometric quantification of percent hCD4+
459 (IL-13+) SILP ILC2s and (D) IL-13 and IL-5 concentration in their supernatant after 6 hr *in vitro* culture
460 with the indicated conditions (0.1 ng/mL rIL-25, serial 10-fold dilutions of ACh from 10 mM to 0.1 μ M, 1
461 nM LTC₄). **(E and F)** Quantification of number of hCD4+ (IL-13+) ILC2s, total ILC2s, and percent ILC2s at
462 the indicated timepoints, tissues, and genotypes. **(G)** Quantification of dSI tuft counts by
463 immunofluorescence from indicated mice treated with 150 mM succinate drinking water for 7 days. **(H)** SI
464 length from indicated mice vertically-colonized with *T. rainier* protists with or without 7 days of additional
465 150 mM succinate drinking water treatment. **(I)** Schematic of acute deletion of *Chat* from vertically *T.*
466 *musculus* (*Tm*) -colonized mice and quantification of dSI tuft counts by immunofluorescence 5 days after
467 start of treatment. In the (A-B, E-I), each symbol represents an individual mouse from two or more pooled
468 experiments. In (C and D) each symbol represents a technical replicate of cells sorted from pooled mice.
469 *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.001 by multiple Mann-Whitney tests with Holm Sidák's
470 multiple comparisons test (A, F, H) or Mann-Whitney test (B, E, G, I). ns, not significant. Graphs depict
471 mean +/- SEM.



587

588 **Supplemental Figure 5: (A)** Quantification of percent GFP(*Chat*)+ tuft cells and RFP(*Il25*)+ tuft cells from
 589 the pSI and dSI of WT mice untreated, treated with 150 mM Na₂-succinate drinking water (succinate), or
 590 infected with *N. brasiliensis* (*Nb*) for the duration indicated. **(B)** Δ Isc values of pSI from WT mice infected
 591 with *Nb* for the indicated number of days and stimulated as indicated (10 mM succinate, luminal; 100 μ M
 592 CCh, basolateral). **(C)** Quantification of tuft cells (DCLK1+) by immunofluorescence from medial SI (mSI)
 593 of mice in (B). **(D)** Δ Isc values of dSI from mice of indicated genotypes infected with *Nb* for 7 days and
 594 stimulated as indicated. **(E)** Δ Isc values of *Sucnr1*^{-/-} dSI with or without 7 day *Nb* infection, stimulated as
 595 indicated. **(F-G)** Δ Isc values of (F) pSI and (G) dSI from WT mice with or without 7 day *Nb* infection,
 596 stimulated as indicated. **(H)** Ratio of C8 Δ Isc values to CCh Δ Isc values in (G). **(I and J)** Δ Isc values of (I)

597 pSI and (J) dSI from mice of indicated genotype infected with *Nb* for 7 days, stimulated as indicated. **(K)**
598 Ratio of C8 Δ Isc values to CCh Δ Isc values from (J). **(L)** Quantification of tuft cells (DCLK1+) by
599 immunofluorescence in the mSI of mice of indicated genotypes treated as indicated. **(M)** Δ Isc values of
600 dSI from mice in (L) stimulated as indicated. In the graphs, each symbol represents an individual mouse
601 (one tissue or average of two) from two or more pooled experiments. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$,
602 **** $p < 0.001$ by two way ANOVA with Dunnett's multiple comparisons test (A) two way ANOVA with
603 Tukey's multiple comparisons test (M), Mann-Whitney test (B, H, K), one way ANOVA with Tukey's
604 multiple comparisons test (C, L), or multiple Mann-Whitney tests with Holm Sidák's multiple comparisons
605 test (D-G, I-J). ns, not significant. Graphs depict mean +/- SEM.



620
 621 **Supplemental Figure 6:** (A) Representative flow cytometry of cecal contents from uncolonized and
 622 protist-colonized mice showing gating of protists by size. The “Large” gate contains *Tritrichomonas sp.*
 623 protists. (B) Quantification of total protists by flow cytometry in indicated tissues of vertically-colonized
 624 mice of indicated genotypes left untreated or given 150 mM Na₂-succinate in drinking water for 7 days.
 625 (C) Quantification of total protists by flow cytometry in indicated tissues of vertically-colonized mice of
 626 indicated genotypes administered tamoxifen 5 days prior to analysis. (D) Quantification of total SI *Nb*
 627 in mice of indicated genotype infected with *Nb* for 7 days without tamoxifen administration. (E and F) (E)
 628 Quantification of tuft cells (DCLK1+) by immunofluorescence and (F) total SI length 8 days post *Nb*
 629 infection of mice of indicated genotype given a single dose of tamoxifen (125 mg/kg) on day 5. In the
 630 graphs, each symbol represents an individual mouse (one tissue or average of two) from two or more
 631 pooled experiments. *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.001 by multiple Mann-Whitney tests with

632 Holm Sídák's multiple comparisons test (B-C) or Mann-Whitney test (D-F). ns, not significant. Graphs
633 depict mean +/- SEM.

1031

Table S3

Reagent or Resource	Source	Identifier
B6.Cg-Tg(RP23-268L19-EGFP)2Mik/J (Chat-GFP)	Jackson Laboratory	JAX #007902
B6. <i>Il25</i> ^{Flare25/Flare25} (Il25-RFP)	R. Locksley (PMID: 26675736)	NA
B6. <i>Il13</i> ^{Smart13/Smart13} (Smart13)	R. Locksley (PMID: 22138715)	NA
C57BL/6N-Pou2f3 ^{tm1(KOMP)Vlcg>/Tcp} (<i>Pou2f3</i> ^{-/-})	Canadian Mouse Mutant Repository	CMMR #ABDF
B6.129P2-Trpm5 ^{tm1Dgen/J} (<i>Trpm5</i> ^{-/-})	Jackson Laboratory	JAX #005848
B6. <i>Sucnr1</i> ^{-/-}	In-house (PMID: 30021144)	NA
B6. <i>Il25</i> ^{-/-}	A. McKenzie (PMID: 16606668)	NA
B6;129-Chat ^{tm1Jrs/J} (<i>Chat</i> ^{fl/fl})	Jackson Laboratory	JAX #016920
B6.Cg-Tg(Vil1-cre)997Gum/J	Jackson Laboratory	JAX #004586
B6.Cg-Tg(Vil1-cre)1000Gum/J (Vil1-Cre1000)	Jackson Laboratory	JAX #021504
B6.Cg-Tg(Vil1-cre/ERT2)23Syr/J (<i>Vil1-Cre-Ert2</i>)	Jackson Laboratory	JAX #020282
B6(129S4)- <i>Pou2f3</i> ^{tm1.1(cre/ERT2)lmt/J} (<i>Pou2f3-Cre-Ert2</i>)	Jackson Laboratory	JAX #037511
B6.129S-Chat ^{tm1(cre)Lowl/MwarJ} (<i>Chat-Cre</i>)	Jackson Laboratory	JAX #031661
B6. <i>Il25-Cre</i>	R. Locksley (PMID: 35245089)	NA
B6.Cg-Gt(<i>ROSA</i>)26Sor ^{tm9(CAG-tdTomato)Hze/J} (Ai9)	Jackson Laboratory	JAX #007909
B6N;129-Tg(CAG-CHRM3*, -mCitrine)1Ute/J (Gq-DREADD)	Jackson Laboratory	JAX #026220
B6.129-Gt(<i>ROSA</i>)26Sor ^{tm1(CAG-CHRM4*, -mCitrine)Ute/J} (Gi-DREADD)	Jackson Laboratory	JAX #026219
B6. <i>Alox5</i> ^{fl/fl}	In-house (PMID: 32160525)	NA
B6. <i>Il4ra</i> ^{fl/fl}	F. Brombacher (PMID: 15142530)	NA

1032

1033 **Table S4**

Reagent or Resource	Dilution Factor	Source	Identifier
Rabbit α -DCLK1	1:1000	Abcam	Cat#ab31704
Rabbit α -TUJ1 (Beta-III tubulin)	1:500	Abcam	Cat#ab18207
Goat α -GFP	1:500	Novus Bio	Cat#NB100-1770
Rabbit α -dsRed	1:500	Clontech	Cat#632496
Rabbit α -HA, clone 16B12	1:1000	Biolegend	Cat#901516
WGA-488	1:150	Thermo	Cat#W11261
Donkey α -Rabbit IgG AF594	1:1000	Thermo	Cat#A-21207
Donkey α -Goat IgG AF488	1:500	Thermo	Cat#A-11055
CD16 / CD32, clone 2.4G2	1:1000	Tonbo	Cat# 70-0161-M001
CD3 PerCP-Cy5.5, clone 145-2C11	1:100	Biolegend	Cat#100328
CD3 BV421, clone 145-2C11	1:400	Biolegend	Cat#100335
CD4 BV711, clone RM4-5	1:250	Biolegend	Cat#100549
CD4 eF450, clone RM4-5	1:200	eBioscience	Cat# 48-0042-80
hCD4 PE, clone RPA-T4	1:50	Biolegend	Cat#300508
CD5 PerCP-Cy5.5, clone 53-7.3	1:500	Biolegend	Cat#100624
CD5 eF450, clone 53-7.3	1:400	Biolegend	Cat#100607
CD8 PerCP-Cy5.5, clone 53-6.7	1:200	Biolegend	Cat#100724
CD8 BV421, clone 53-6.7	1:400	Biolegend	Cat#100737
CD11b AF700, clone M1/70	1:250	Biolegend	Cat#101222
CD11b BV421, clone M1/70	1:400	Biolegend	Cat# 101235
CD19 PerCP-Cy5.5, clone 6D5	1:250	Biolegend	Cat#115533
CD19 BV421, clone 6D5	1:400	Biolegend	Cat# 115537

CD24 PE, clone M1/69	1:300	Biolegend	Cat#101807
CD24 PerCP-Cy5.5, clone M1/69	1:300	Biolegend	Cat#101824
CD45 BV605, clone 30F11	1:300	Biolegend	Cat#103155
CD45 BV650, clone 30F11	1:500	Biolegend	Cat#103151
EpCAM PE-Dazzle, clone G8.8	1:300	Biolegend	Cat#118235
EpCAM AF488, clone G8.8	1:300	Biolegend	Cat#118210
EpCAM PE-Cy7, clone G8.8	1:300	Biolegend	Cat#118215
FcER1 BV421, clone Mar-1	1:400	Biolegend	Cat#334623
IL17RB APC, clone 9B10	1:100	Biolegend	Cat#146307
KLRG1 PE-Cy7, clone 2F1	1:250	Biolegend	Cat#138416
NK1.1 PerCP-Cy5.5, clone PK136	1:100	Biolegend	Cat#108728
NK1.1 BV421, clone PK136	1:200	Biolegend	Cat#108731
Siglec-F APC-Cy7, clone E50-2440	1:100	BD	Cat#565527
Siglec-F AF647, clone E50-2440	1:100	BD	Cat# 562680
Thy1.2 (CD90.2) BV605, clone 53-2.1	1:500	Biolegend	Cat#140318

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