

1 **Supplementary Information**

2 **Supplementary Figures**

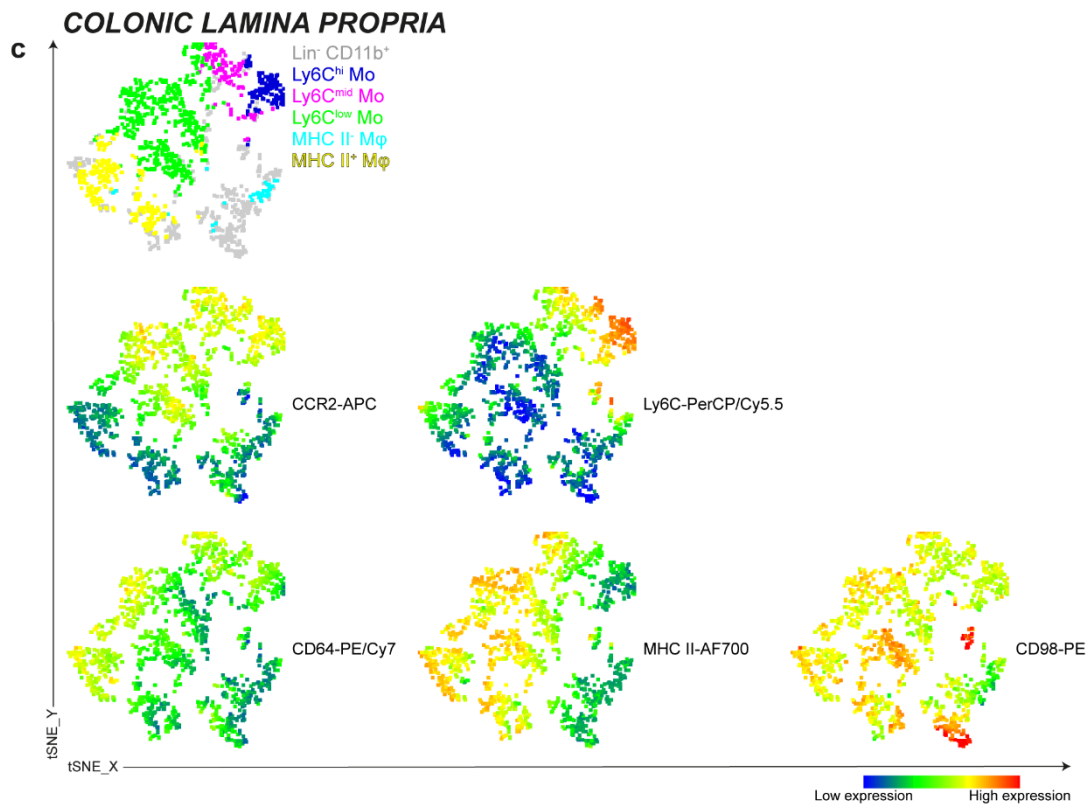
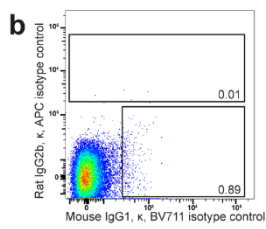
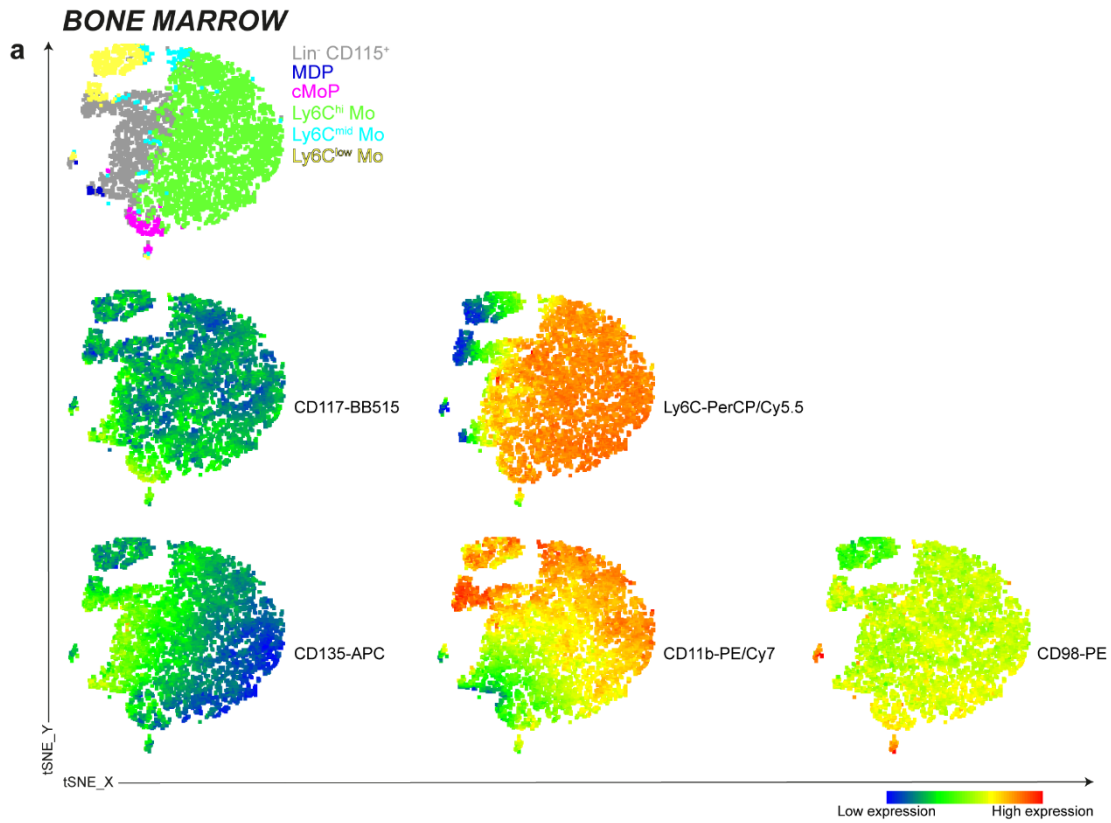
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4 **Supplementary Figure 1. Characterization of bone marrow and colonic lamina propria**
5 **monocytes and macrophages.**

6 **(a)** Representative tSNE visualization of bone marrow cells displaying the indicated markers
7 used for the identification of respective cell populations from one out of eight analyzed animals.

8 **(b)** Staining control for figure 1d. **(c)** Representative tSNE visualization of colonic lamina
9 propria (cLP) showing the distribution of indicated markers used for the identification of
10 respective cell populations in the colonic lamina propria from one animal out of eight analyzed
11 mice.

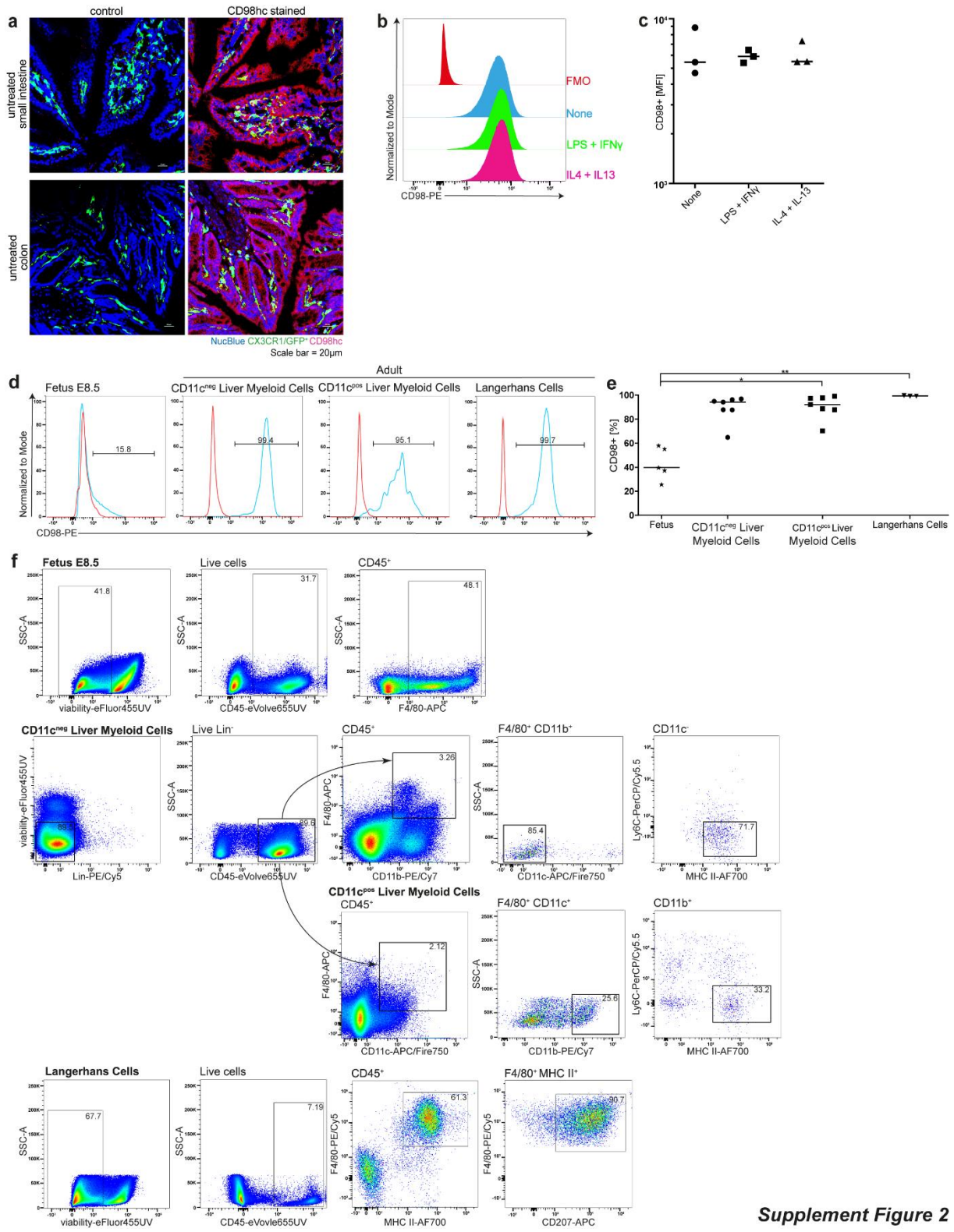
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14 **Supplementary Figure 2. CD98hc is expressed in the small and large intestine.**

15 (a) The small intestine and the colon of naïve Cx3cr1-GFP mice were stained for CD98hc and
16 counterstained with NucBlue. (b and c) Bone marrow derived macrophages (BMDM) were
17 stimulated either with LPS + IFN- γ or with IL-4 + IL-13 and surface CD98 expression assessed
18 by flow cytometry. Histogram and mean fluorescence intensity (MFI) are shown. (d) Histogram
19 and (e) MFI of yolk sac macrophages from embryos (E8.5), CD11c⁻ and CD11c⁺ liver myeloid
20 cells and Langerhans cells isolated from naïve adult mice and stained for CD98. Red histograms
21 show FMO control, blue histograms cells stained for CD98. Number within plots indicated the
22 percentage of CD98⁺ macrophages, liver myeloid cells and Langerhans cells. (f) Gating strategy
23 for the identification of the yolk sac macrophages, CD11c⁻ and CD11c⁺ liver myeloid cells and
24 Langerhans cells. Statistical significance was calculated with a Kruskal-Wallis test followed by
25 Dunn's correction; *p<0.05, **p<0.01. Experiments performed thrice for the CD98hc staining,
26 thrice for the CD98hc expression in fetus and Langerhans cells, and seven times for liver
27 myeloid cells.

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Supplement Figure 2

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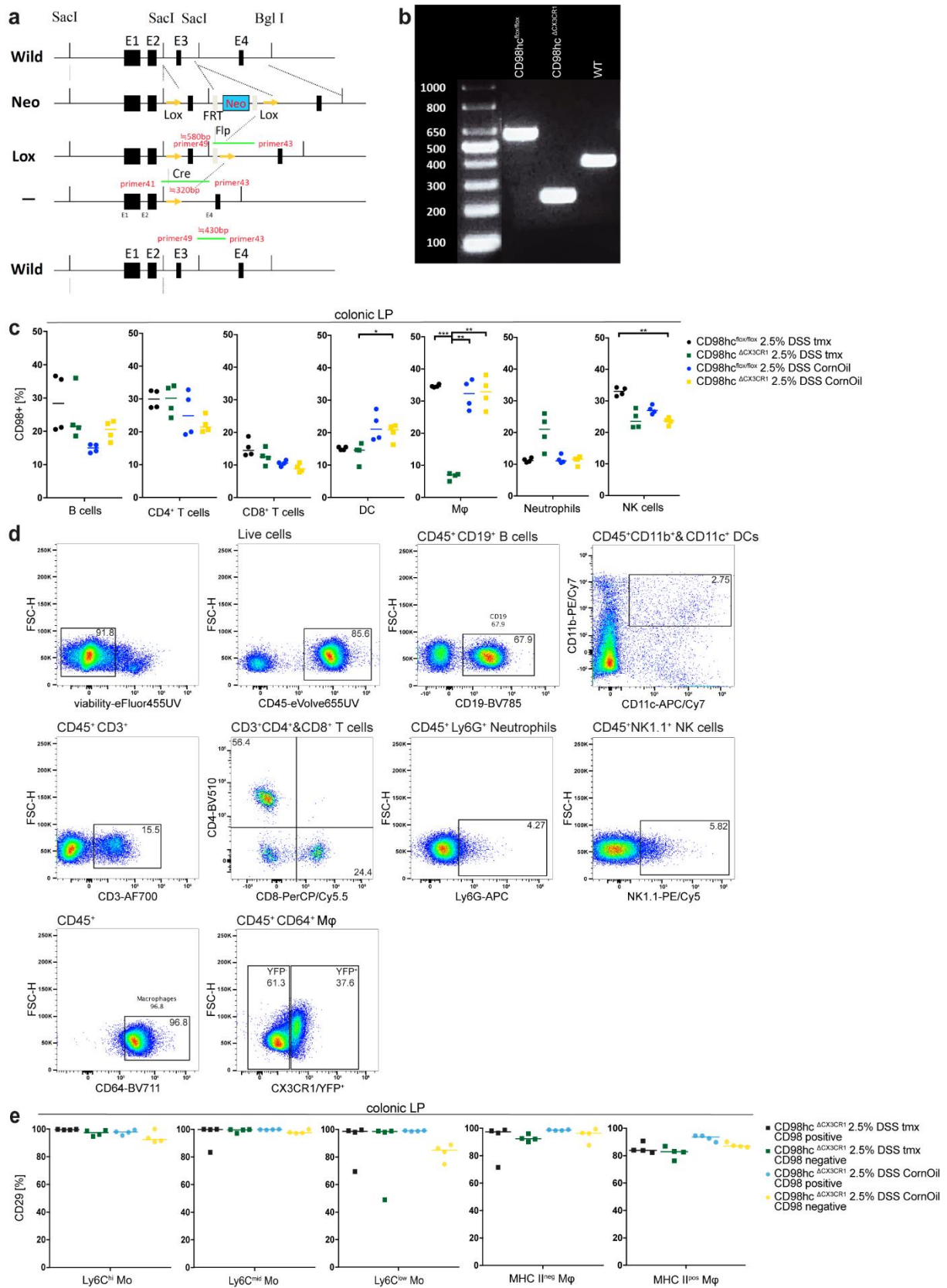
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33 **Supplementary Figure 3. Tamoxifen induced Cre recombinase deletes CD98hc in**
34 **monocytes and macrophages but not in T cells in CD98hc^{ΔCX3CR1} animals.**

35 (a) CD98hc^{flox/flox} mouse construct that were breed with Cx3cr1^{CreER} mice. (b) Genotyping of,
36 CD98hc^{flox/flox}, CD98hc^{ΔCX3CR1} and wildtype (WT) animals. (c) Percentage of CD98 expression
37 by B cells, CD4⁺ and CD8⁺ T cells, dendritic cells (DC), macrophages, neutrophils isolated
38 from the colonic lamina propria of corn oil- or tamoxifen-treated C57BL/6 WT or
39 CD98hc^{ΔCX3CR1} animals. (d) Gating strategy for the identification of B cells, CD4⁺ and CD8⁺ T
40 cells, dendritic cells (DC), macrophages, neutrophils isolated from the colonic lamina propria.
41 (e) Percentage of integrin β1/CD29⁺ monocytes and macrophages in indicated animals treated
42 with corn oil or tamoxifen. Data was analyzed by two-way ANOVA followed by Sidak's
43 correction; *p<0.05, ****p<0.0001. Experiments performed twice.

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Supplement Figure 3

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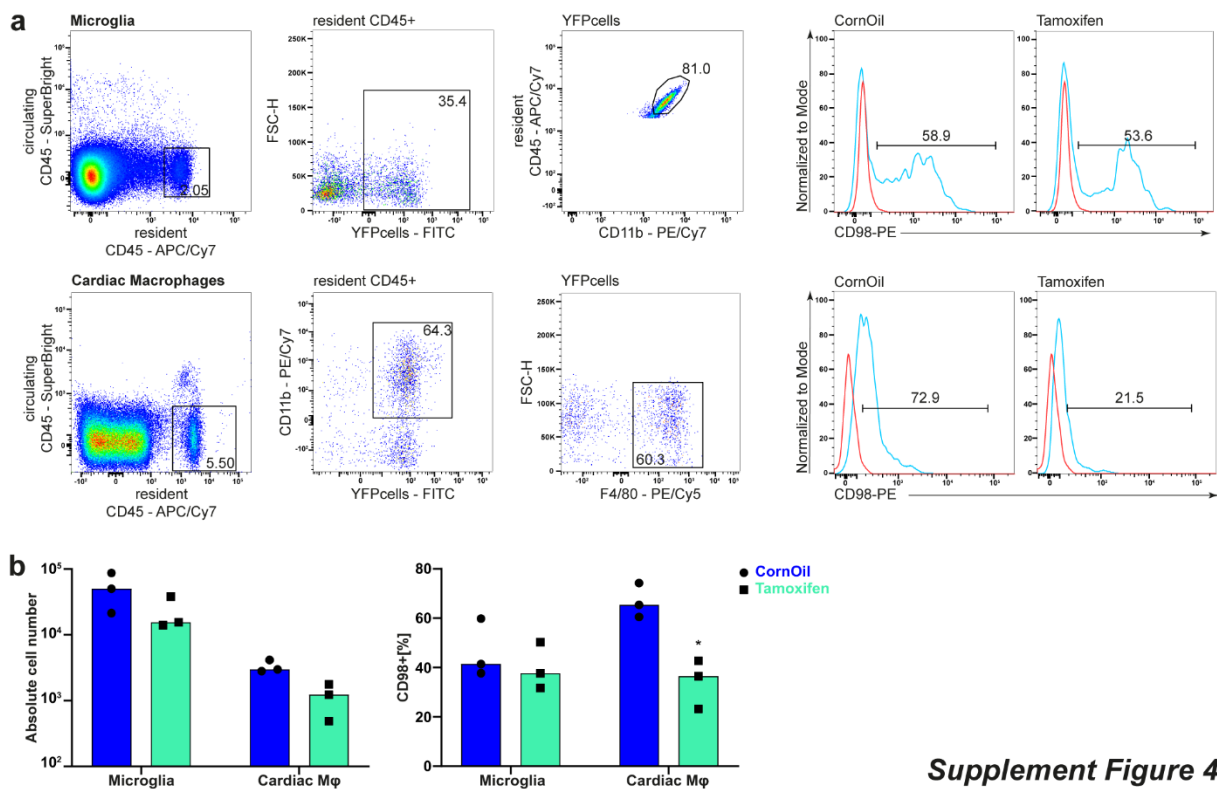
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48 **Supplementary Figure 4. CD98hc deletion in cardiac macrophages but not in microglia.**

49 (a) Gating strategy for the identification of microglia and cardiac macrophages obtained after
 50 exclusion of dead cells. Red histograms show FMO control, blue histograms present cells
 51 stained for CD98hc. Circulating cell of hematopoietic origin were excluded after i.v. injection
 52 of an anti-CD45 SuperBright antibody into the animals at least 5 min before isolation. (b)
 53 Absolute cell numbers of microglia and cardiac macrophages and percentage of CD98hc
 54 expressing macroglia and cardiac macrophages after intraperitoneal corn oil or tamoxifen
 55 injection in CD98hc^{ΔCX3CR1} mice (n=3) and analyzed by two-way ANOVA followed by Sidak's
 56 correction; *p<0.05. Experiments performed once with three biological replicates.

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Supplement Figure 4

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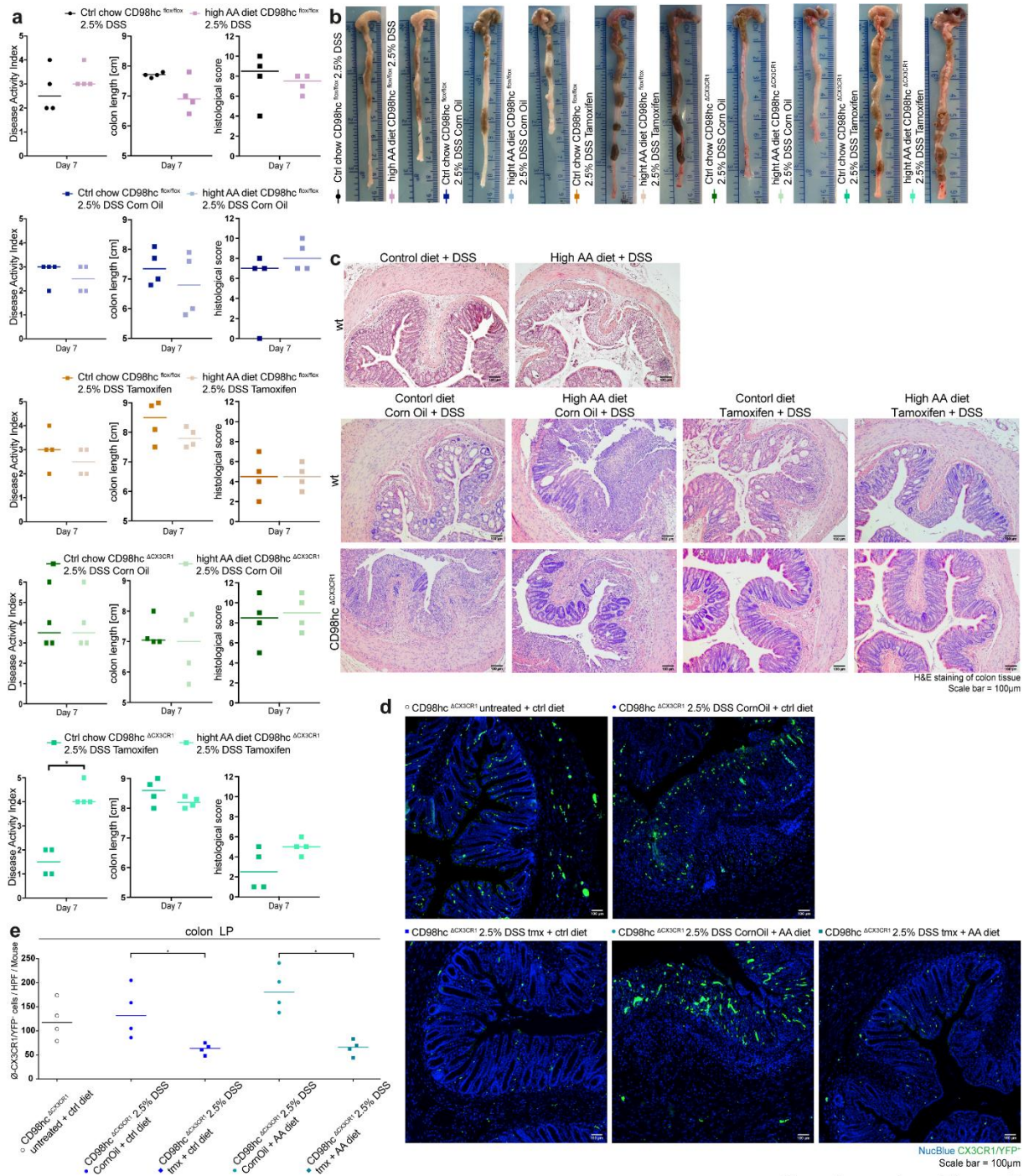
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64 **Supplementary Figure 5. Animals fed with regular chow or L-leucin/L-isoleucine**
65 **enriched chow before and after the deletion of CD98hc during DSS-induced colitis.**

66 Colitis was induced by adding 2.5% dextran sodium sulfate (DSS) to CD98hc^{flox/flox} and
67 CD98hc^{ΔCX3CR1} mice which were treated either with corn oil or tamoxifen two days before DSS
68 administration and fed with either regular chow or regular chow enriched with 5% L-leucine
69 and 5% L-isoleucine. **(a)** Disease activity index, colon length, and histological scores of
70 indicated groups. The data were analyzed by two-way ANOVA followed by Sidak's correction;
71 ****p<0.0001. Histological scores were assessed in a blinded fashion by two independent
72 investigators. The mean histological score was determined for each animal after H&E staining
73 of colonic tissues, presented as individual dot and analyzed with a Mann-Whitney U test;
74 *p<0.05. The colon length was determined at day 7 after start of DSS administration, colon
75 length is shown for each individual animal, the mean indicated and analyzed with a Mann-
76 Whitney U test; *p<0.05. **(b)** A representative image of the colon from each group is shown.
77 **(c)** H&E staining of colonic tissues. **(d)** A representative image of the colonic CX3CR1/YFP⁺
78 cells counterstained with NucBlue. **(e)** Quantification of the colonic CX3CR1/YFP⁺ cells per
79 high power field (HPF) per mouse. The Experiment was performed once.

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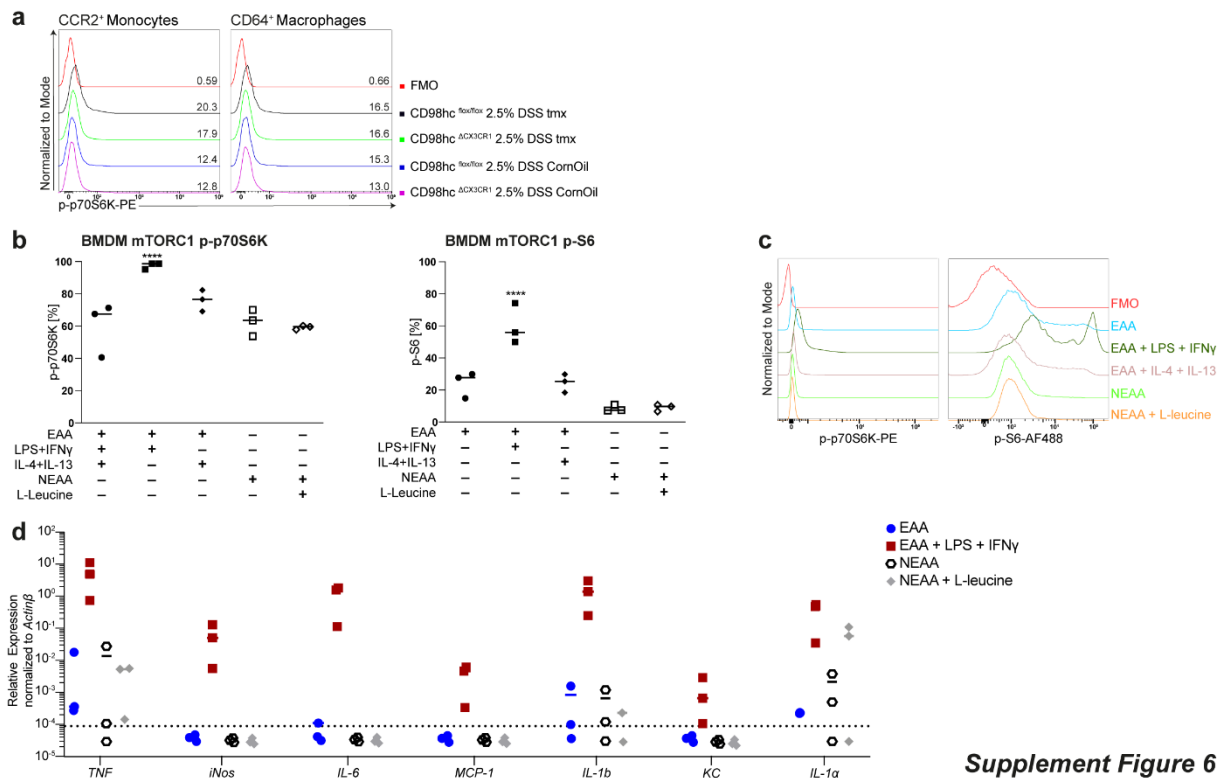
Supplementary Figure 5

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88 **Supplementary Figure 6. mTORC1 pathway is not influenced by CD98hc deletion.**

89 (a) Colitis was induced by adding 2.5% dextran sodium sulfate (DSS) to CD98hc^{fllox/fllox} and
 90 CD98hc^{ΔCX3CR1} mice which were treated either with corn oil or tamoxifen two days before DSS
 91 administration. Histogram of the phosphorylation of p70S6K. Numbers indicate the percentage
 92 of positive cells. (b) Percentage of phosphorylated p70S6K and S6 in bone marrow derived
 93 macrophages (BMDM), which were cultured in RPMI 1640 medium containing essential amino
 94 acids (EAA), EAA and either LPS + IFN γ or IL-4 + IL-13 stimulation, non-essential amino
 95 acid (NEAA) medium, and NEAA supplemented with L-leucine (0.05 g/L). (c) Changes in
 96 normalized p70S6K and S6 phosphorylation in BMDM. (d) qRT-PCR of indicates cytokines,
 97 *iNos*, *Mcp1* and *Kc* of BMDM cultured in EAA, EAA and LPS + IFN γ stimulated, NEAA, and
 98 NEAA supplemented with L-leucine (0.05 g/L). Experiment performed with three biological
 99 replicates or in duplicates, respectively.

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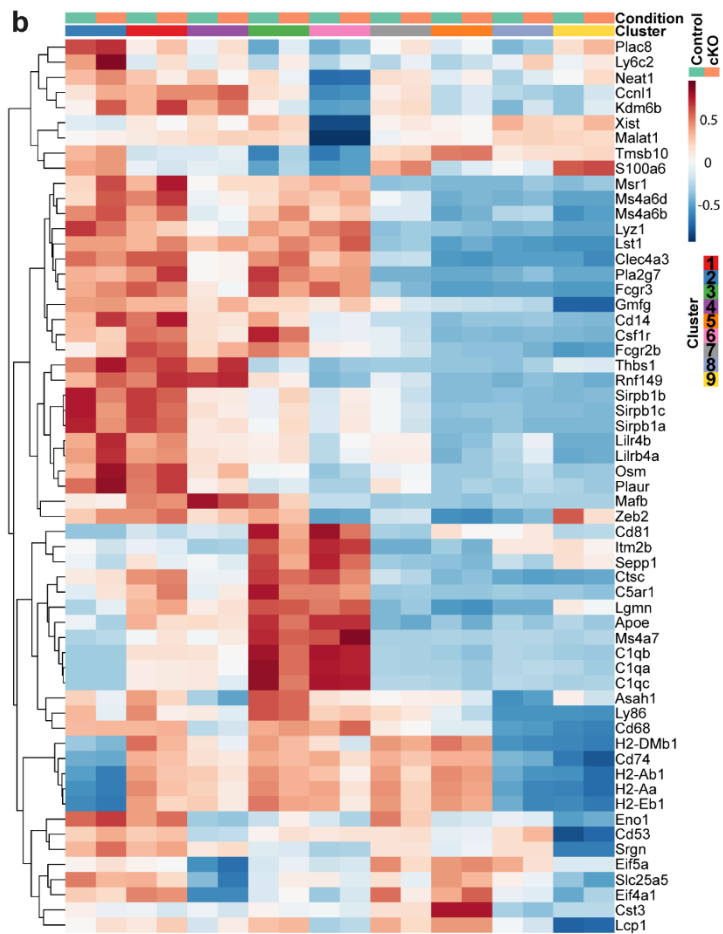
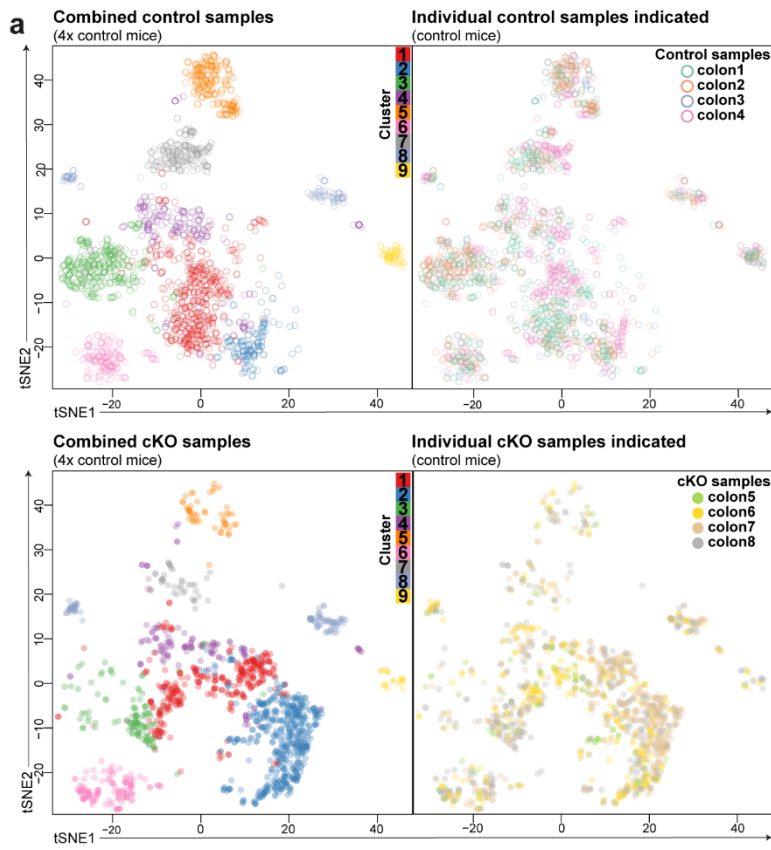
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Supplement Figure 6

104 **Supplementary Figure 7. Verification of relevant patterns observed in the scRNA-seq**
105 **data.**

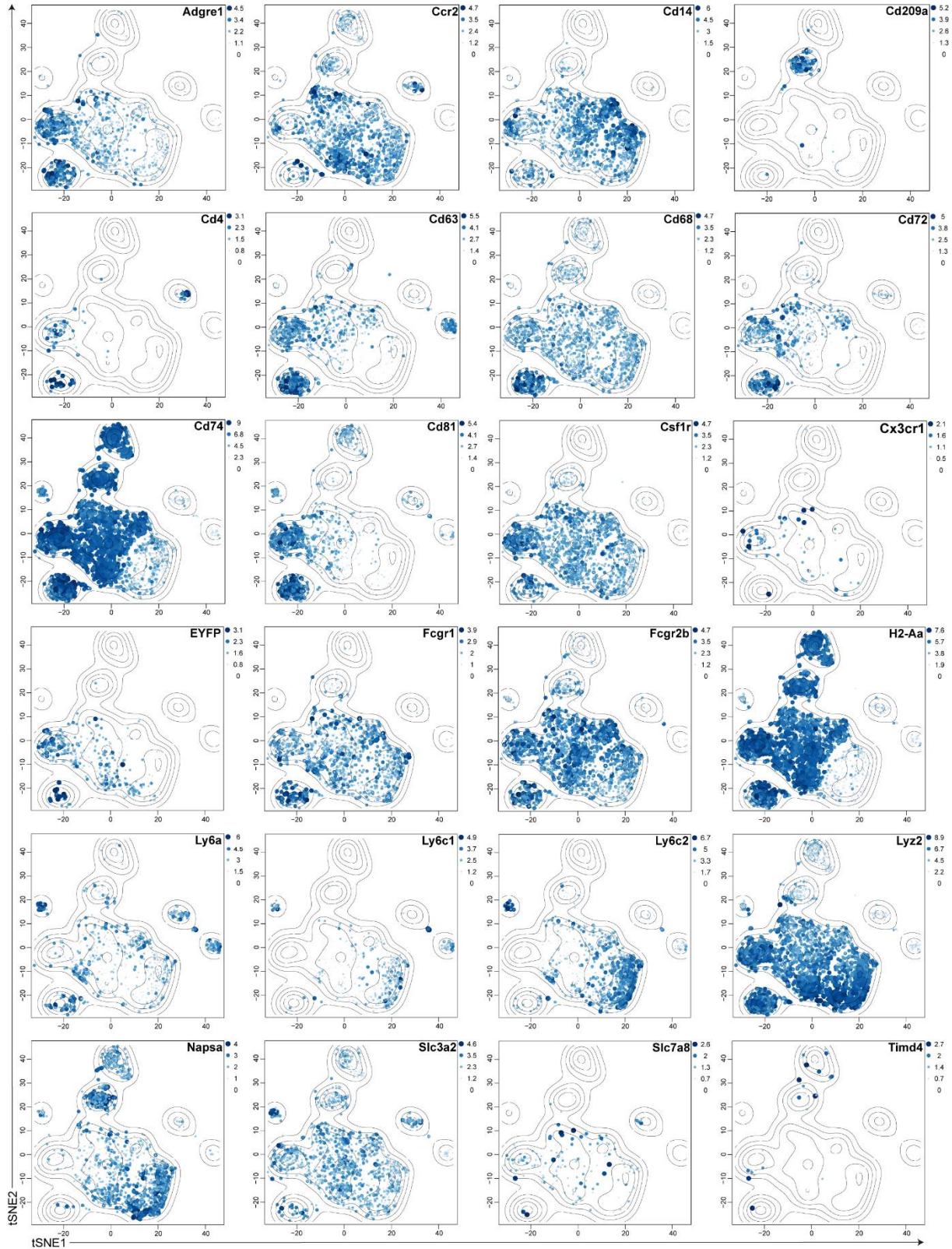
106 (a) tSNE plots of control (corn oil-treated CD98hc^{ΔCX3CR1} mice) and CD98hc cKO (tamoxifen-
107 treated CD98hc^{ΔCX3CR1} mice) and control and CD98hc cKO tSNE plots, where the individual
108 samples per condition have been annotated. (b) Heatmap of cluster specific genes by cells from
109 corn oil (control) and tamoxifen (cKO) treated animals. The clusters are shown in different
110 colors. Heatmaps are showing the centered and scaled average expression (normalized log-
111 counts values) across cells of each cluster in each condition. The experiment was performed
112 once (scRNA-seq) with four biological replicates per group.

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115 **Supplementary Figure 8. tSNE visualization of the expression of arbitrarily chosen**
116 **markers.**

117 The experiment was performed once (scRNA-seq) with four biological replicates per group.



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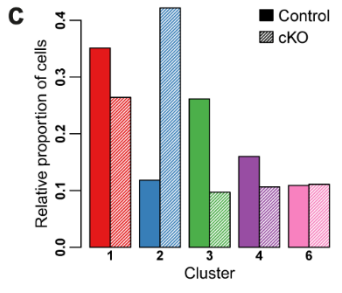
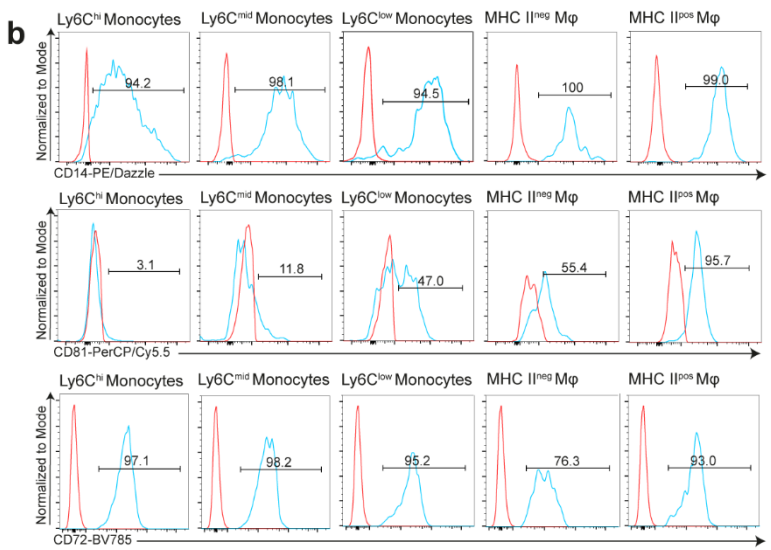
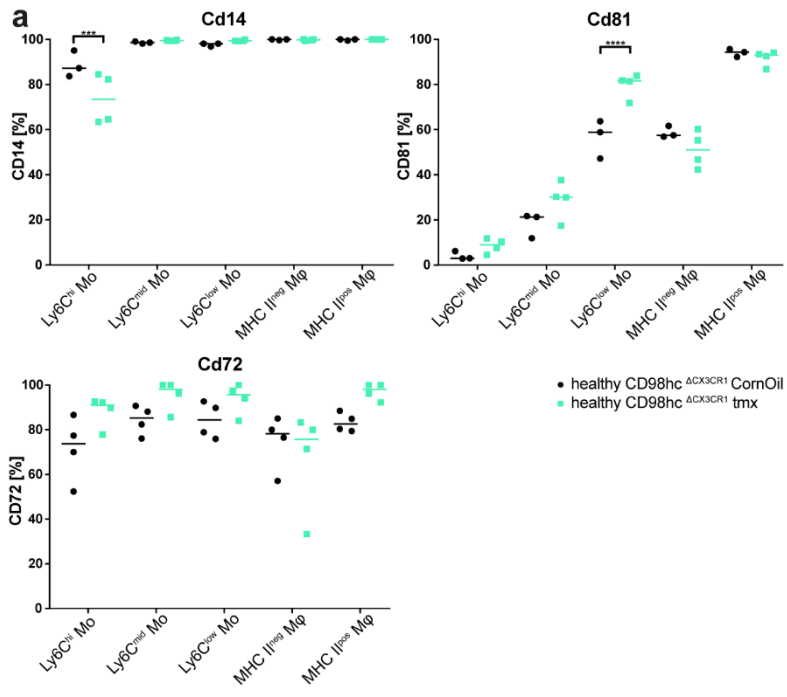
Supplement Figure 8

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120 **Supplementary Figure 9. Chosen marker expression by flow cytometry.**

121 (a) Percentage of CD14⁺, CD81⁺, and CD72⁺ colonic lamina propria monocytes and
122 macrophages as determined by flow cytometry. Each dot represents an individual animal and
123 the median value is shown. Data was analyzed by two-way ANOVA followed by Sidak's
124 correction; ***p<0.001, ****p<0.0001. (b) Histogram plot of monocytes and macrophages
125 after CD14, CD81, and CD72 staining. Red line represents the FMO control and blue line shows
126 stained cells. Numbers in histograms indicate the percentage of CD14⁺, CD81⁺, and CD72⁺
127 monocytes and macrophages. (c) Relative frequency of control and cKO cells within the
128 different clusters defined based on the scRNA-seq experiment. Experiments performed once
129 with three to four biological replicates per group.

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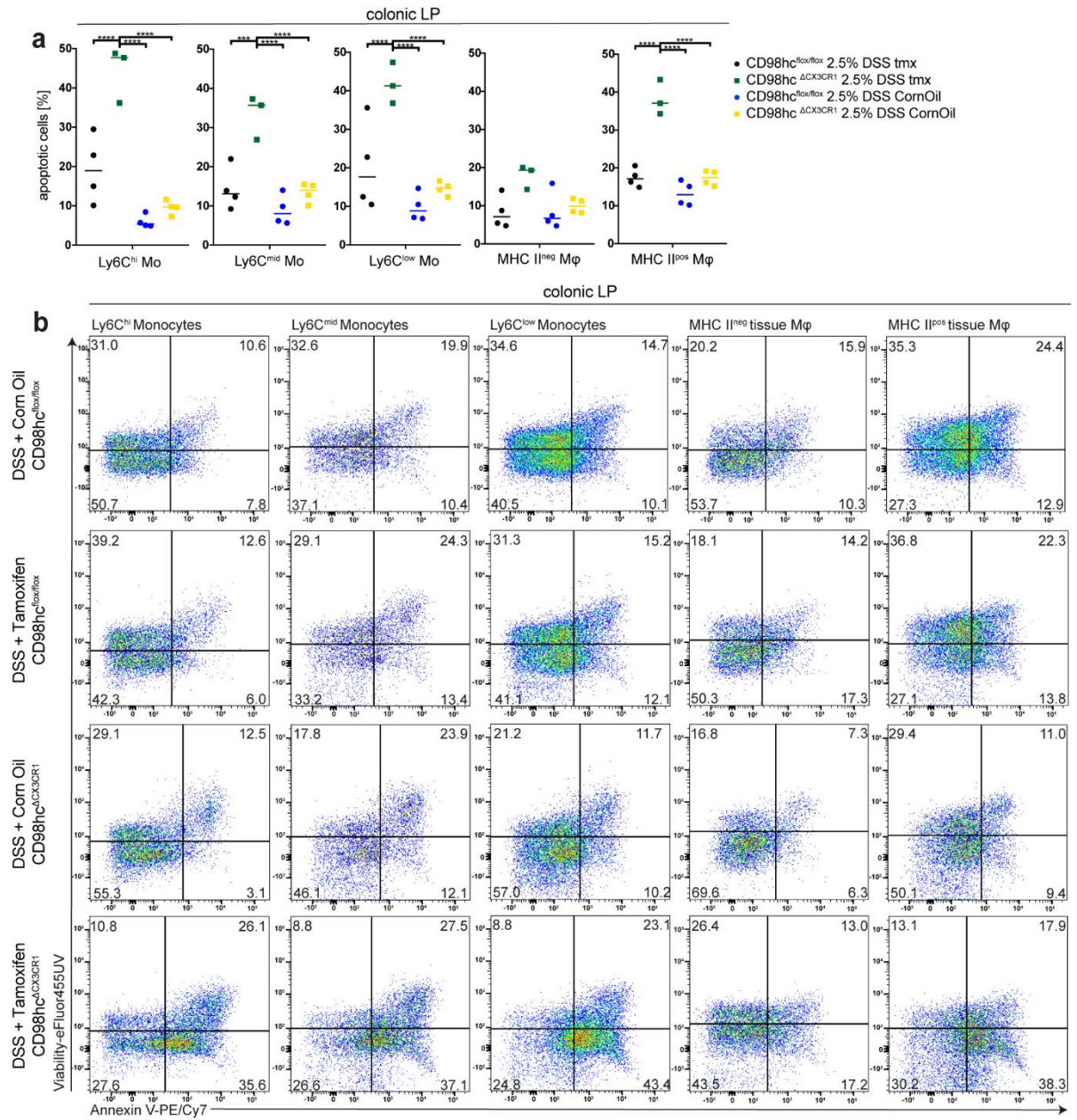
Supplement Figure 9

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136 **Supplementary Figure 10. Deletion of CD98hc leads to increased apoptosis and reduced**
137 **cell number in colonic macrophages.**

138 **(a)** Percentage of apoptotic cells determined by flow cytometry after Annexin V/viability
139 staining by indicated monocytes and macrophages isolated from corn oil- or tamoxifen treated
140 CD98hc^{flox/flox} or CD98hc^{ΔCX3CR1} animals. **(b)** Annexin V/viability staining of indicated
141 experimental groups are presented by dot plot graphs. Data is shown as the mean and analyzed
142 by two-way ANOVA followed by Sidak's correction; ***p<0.001, ****p<0.0001. The
143 experiment was performed once.

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Supplement Figure 10

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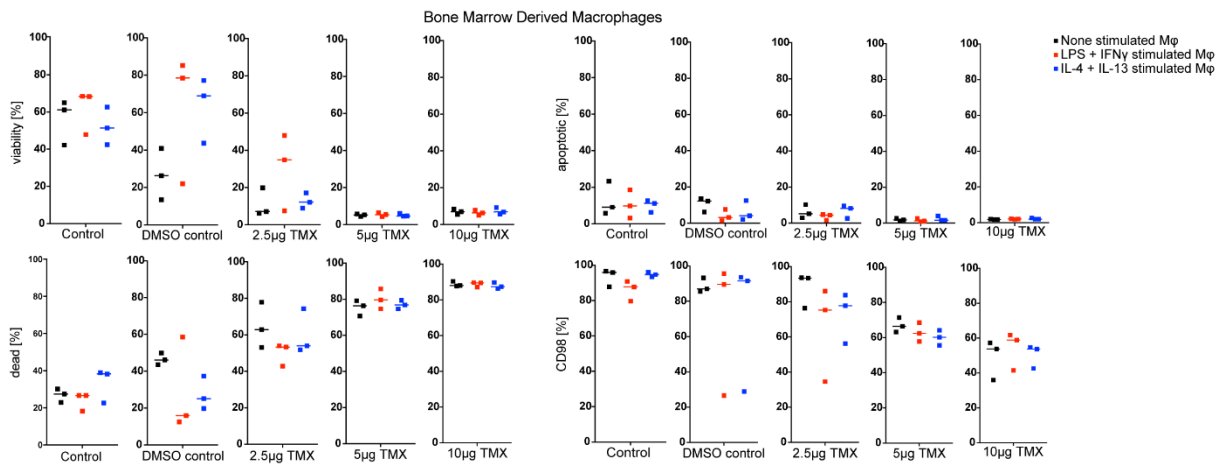
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154 **Supplementary Figure 11. *In vitro* deletion of CD98hc results in BMDM cell death.**

155 Non-stimulated, LPS + IFN γ , or IL-4 + IL-13 stimulated bone marrow-derived macrophages
156 (BMDM) were cultured in RPMI 1640 medium containing: none (control), 100 μ g dimethyl
157 sulfoxide (DMSO control), 2.5 μ g, 5 μ g, and 10 μ g tamoxifen dissolved in DMSO. Annexin
158 V/viability and CD98 staining were performed and analyzed by flow cytometry to assess dead
159 or apoptotic cells along with CD98 expression. The experiment was performed thrice.

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Supplement Figure 11

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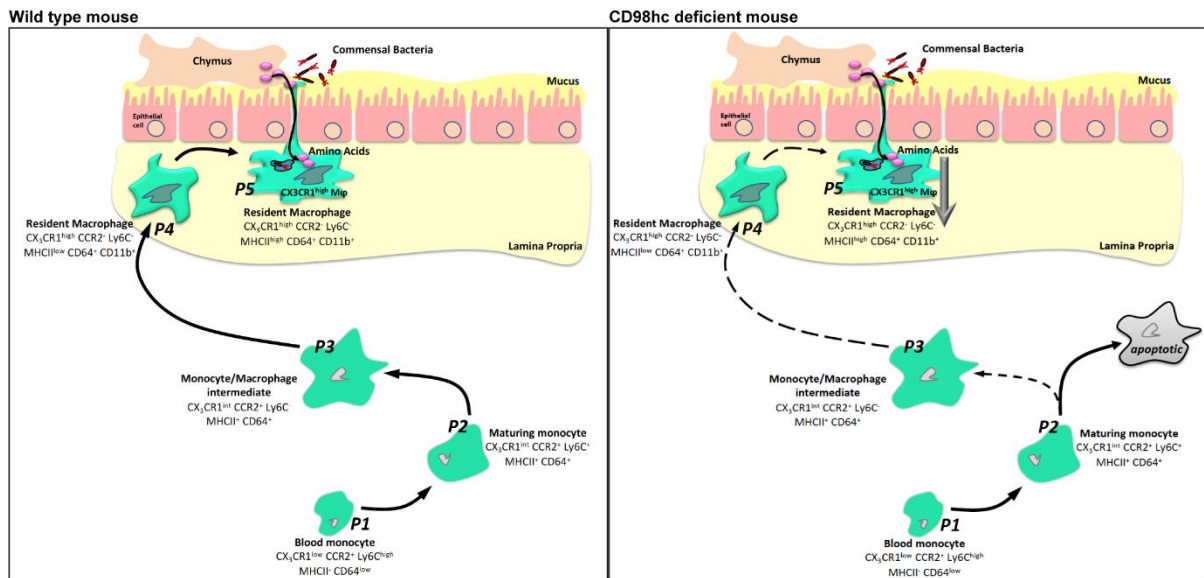
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173 **Supplementary Figure 12.**

174 Schematic representation of the ‘monocyte waterfall’-development to gut macrophages in

175 C57BL/6 WT and CD98hc deficient mice.

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Supplement Figure 12

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178 **Supplementary Tables**

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180 **Supplementary Table 1.**

181 Depicted 10× genomics web summaries.

Treatment	CD98hc^{ACX3CR1} Colon #	Estimated Number of Cells	Mean Reads per Cell	Median Genes per Cell
Corn Oil	1	696	63.153	1.657
	2	495	74.116	1.794
	3	94	320.447	1.630
	4	536	53.893	1.666
Tamoxifen	5	95	455.324	1.476
	6	387	103.541	1.378
	7	506	65.280	1.680
	8	435	97.441	1.614

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199 **Supplementary Table 2.**

200 Annotated cell types per cluster.

Source Name	Cell Type
Cluster 1	Monocytes, Macrophages
Cluster 2	Monocytes
Cluster 3	Macrophages
Cluster 4	Monocytes, Macrophages, Endothelial cells, Epithelial cells
Cluster 5	Dendritic cells
Cluster 6	Macrophages
Cluster 7	Monocytes, Macrophages, Dendritic cells
Cluster 8	B cells, Innate lymphoid cells (ILC), T cells
Cluster 9	Fibroblast, Stromal cells

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219 **Supplementary Table 3.**

220 Characteristics of healthy patients and patients with Crohn's disease (CD) or ulcerative colitis
 221 (UC), who provided biopsies to the Swiss IBD cohort used for *CD98hc/SLC3A2* and
 222 *CD98lc/SLC7A5* expression analysis.

Baseline Group characteristics					
	<i>Healthy</i>	<i>Crohn' disease</i>		<i>Ulcerative colitis</i>	
	n=7	Quiescent (n=20)	Active (n=11)	Quiescent (n=20)	Active (n=11)
Gender, male/female, n (%)	71/29% 5 m, 2 f	60/40 % 12 m, 8 f	36/64% 4 m, 7 f	35/65% 12 m, 8 f	54/45% 6 m, 5 f
Median age (range), yr	42 (18-52)	56 (32-81)	39 (31-71)	58 (31-81)	53 (24-68)
Mean BMI (SD), kg/m ²	23,6 (2,57)	24.15 (3)	25.55 (4.9)	24.70 (2.99)	23.89 (4.08)
Median age at diagnosis (range), yr	–	33.5 (18-60)	21 (14-34)	28.5 (14-65)	30 (16-60)
Median disease duration (range), yr	–	21.5 (6-45)	19 (7-37)	26 (8-44)	16 (7-38)
	<i>Healthy</i>	CD extent, n (%)			
Ileum isolated	–	5 (25%)	2 (18%)	–	–
Colon isolated	1 (14%)	2 (10%)	3 (27%)	–	–
Ileocolonic	1 (14%)	2 (10%)	5 (46%)	–	–
unknown	–	11 (55%)	1 (9%)	–	–
Colon ascending	2 (29%)	–	–	–	–
Sigmoid	1 (14%)	–	–	–	–
random	2 (29%)	–	–	–	–
	<i>Healthy</i>	UC extent, n (%)			
Proctitis	–	–	–	1 (5%)	1 (10%)
Left-sided colitis	–	–	–	3 (20%)	5 (45%)
Pancolitis	–	–	–	5 (25%)	5 (45%)
Unknown	–	–	–	–	–
	<i>Healthy</i>	Current medical treatment, n (%)			
No treatment	–	5 (25%)	–	5 (25%)	1 (9%)
5-ASA	–	6 (30%)	–	13 (65%)	9 (81%)
Steroids	–	–	6 (54%)	–	4 (36%)
Immunosuppressants	–	11 (55%)	1 (9%)	4 (20%)	1 (9%)
Anti-TNF	–	–	1 (9%)	–	3 (27%)
		Smoking status			
Non-smoker, n (%)	1 (14%)	12 (60%)	6 (54%)	15 (75%)	9 (81%)
Active smoker, n (%)	3 (43%)	6 (30%)	5 (46%)	1 (5%)	1 (9.5%)
unknown	3 (43%)	2 (10%)	0	4 (20%)	1(9.5%)

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229 **Supplementary Table 4.**

230 Characteristics of healthy patients and patients with IBD of the Basler IBD cohort, biopsy

231 donors from healthy, inflamed, and non-inflamed regions for immunofluorescence staining.

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	<i>Healthy</i>					<i>Ulcerative colitis</i>			<i>Crohn's disease</i>		
Sample #	5266	5268	5269	5270	5272	504	535	619	558	568	620
Gender	male	female	female	male	male	female	female	unknown	female	male	female
Age	61	30	61	42	58	50	71	unknown	72	68	69
BMI	20,1	un-known	23,5	31,7	30,6	25,6	27,3	unknown	19	32	21,6
Age at diagnosis	–					34	56	unknown	23	52	56
Smoking status	un-known	un-known	Yes	former	former	un-known	un-known	unknown	non-smoker	active	active
Localisation inflamed	–					sigmoid/rectum	rectum/sigmoid	sigmoid/rectum	unknown	sigmoid	terminal Ileum
Localisation non-inflamed	–					transversal colon	colon	ascending/transversal colon	rectum	colon descending	colon ascending
Medical treatment at time of study	–					none	none	none at time of study, but received Salofalk 10 days before	Quantalan, Immodium	Spiricort, Aldactone, Orfiril	unknown
Clinical disease activity index	–					5	6	unknown	unknown	74	70

233 *Note: age calculated as of 2019 (healthy) and 2018 (IBD patient), not the year of sample*

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242 **Supplementary Table 5.**

243 Primers used for qPCR in this study.

Primer (mouse)	Sequence (5'-3')	Tm (°C)	Product size (bp)
<i>Actβ</i> -fwd	TTC TTT GCA GCT CCT TCG TT	56,4	149
<i>Actβ</i> -rev	ATG GAG GGG AAT ACA GCC C	59,5	
<i>Il1β</i> -fwd	TGT GAA ATG CCA CCT TTT GA	54,3	94
<i>Il1β</i> -rev	GGT CAA AGG TTT GGA AGC AG	58,4	
<i>Il6</i> -fwd	TCG GAG GCT TAA TTA CAC ATG TTC T	62,5	94
<i>Il6</i> -rev	GCA TCA TCG TTG TTC ATA CAA TCA	60,3	
<i>Mcp-1</i> -fwd	AGG TCC CTG TCA TGC TTC TG	60,5	249
<i>Mcp-1</i> -rev	TCT GGA CCC ATT CCT TCT TG	58,4	
<i>Tnf</i> -fwd	CCA CCA CGC TCT TCT GTC TAC	63,2	103
<i>Tnf</i> -rev	AGG GTC TGG GCC ATA GAA CT	60,5	
<i>Il-1α</i> -fwd	CGC TTG AGT CGG CAA AGA AAT	59,5	271
<i>Il-1α</i> -rev	CTT CCC GTT GCT TGA CGT TG	60,5	
<i>iNos</i> -fwd	GTT CTC AGC CCA ACA ATA CAA GA	60,9	127
<i>iNos</i> -rev	GTG GAC GGG TCG ATG TCA C	61,6	
<i>Kc</i> -fwd	CTG GGA TTC ACC TCA AGA ACA TC	62,9	117
<i>Kc</i> -rev	CAG GGT CAA GGC AAG CCT C	61,6	
Primer (human)	Sequence (5'-3')	Tm (°C)	Product size (bp)
<i>GAPDH</i> -fwd	TCG ACA GTC AGC CGC ATC TTC TTT	65,2	104
<i>GAPDH</i> -rev	GCC CAA TAC GAC CAA ATC CGT TGA	65,2	
<i>SLC3A2</i> -fwd	GAC CCC TGT TTT CAG CTA CG	60,5	108
<i>SLC3A2</i> -rev	TCA GGG AAG CTG GAC TCA TC	60,5	
<i>SLC7A5</i> -fwd	TCC TGG ATC ATC CCC GTC TT	60,5	88
<i>SLC7A5</i> -rev	CCA CGA AGA AGA GCC TGG AG	62,5	

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