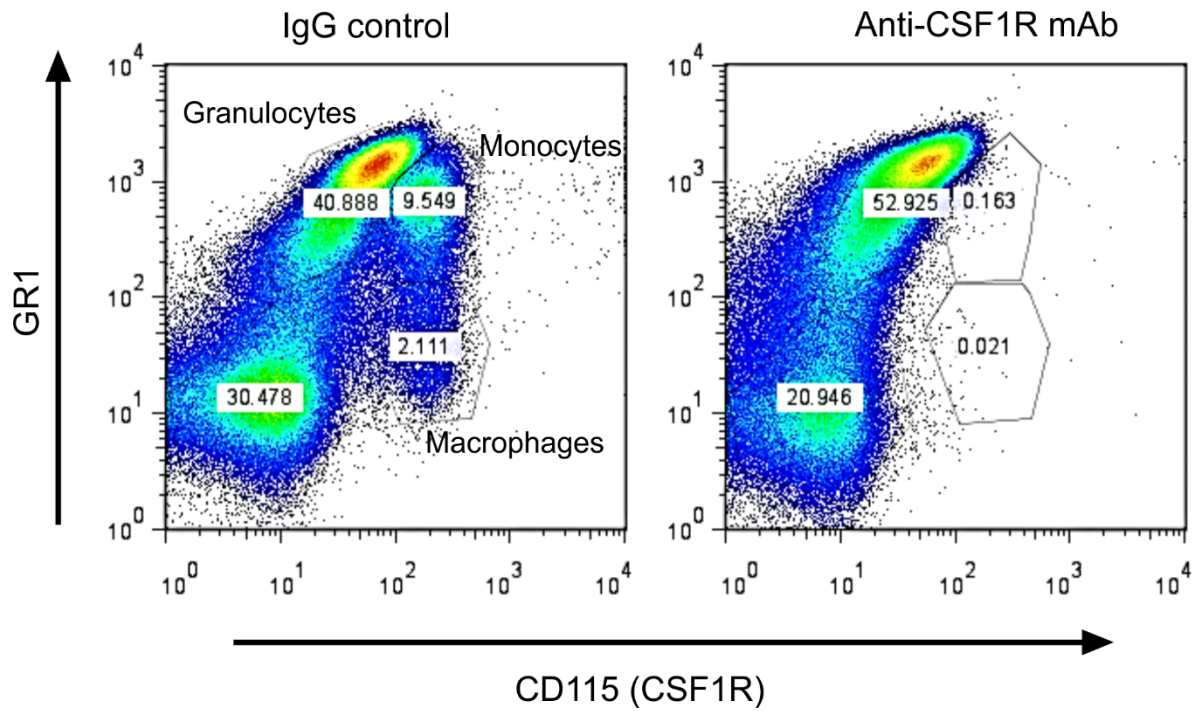


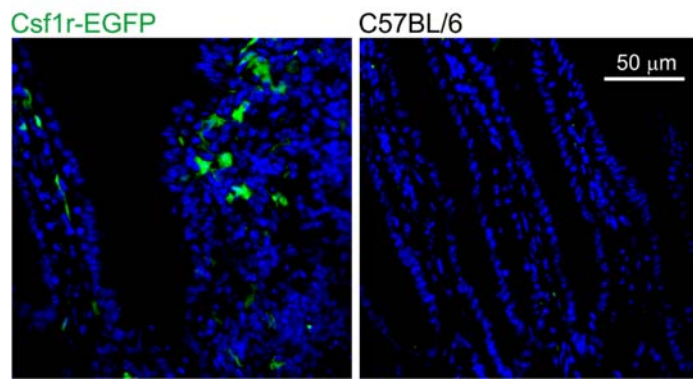
The role of CSF1R-dependent macrophages in control of the intestinal stem-cell niche

Anuj Sehgal, David S. Donaldson, Clare Pridans, Kristin A. Sauter, David A. Hume & Neil A. Mabbott

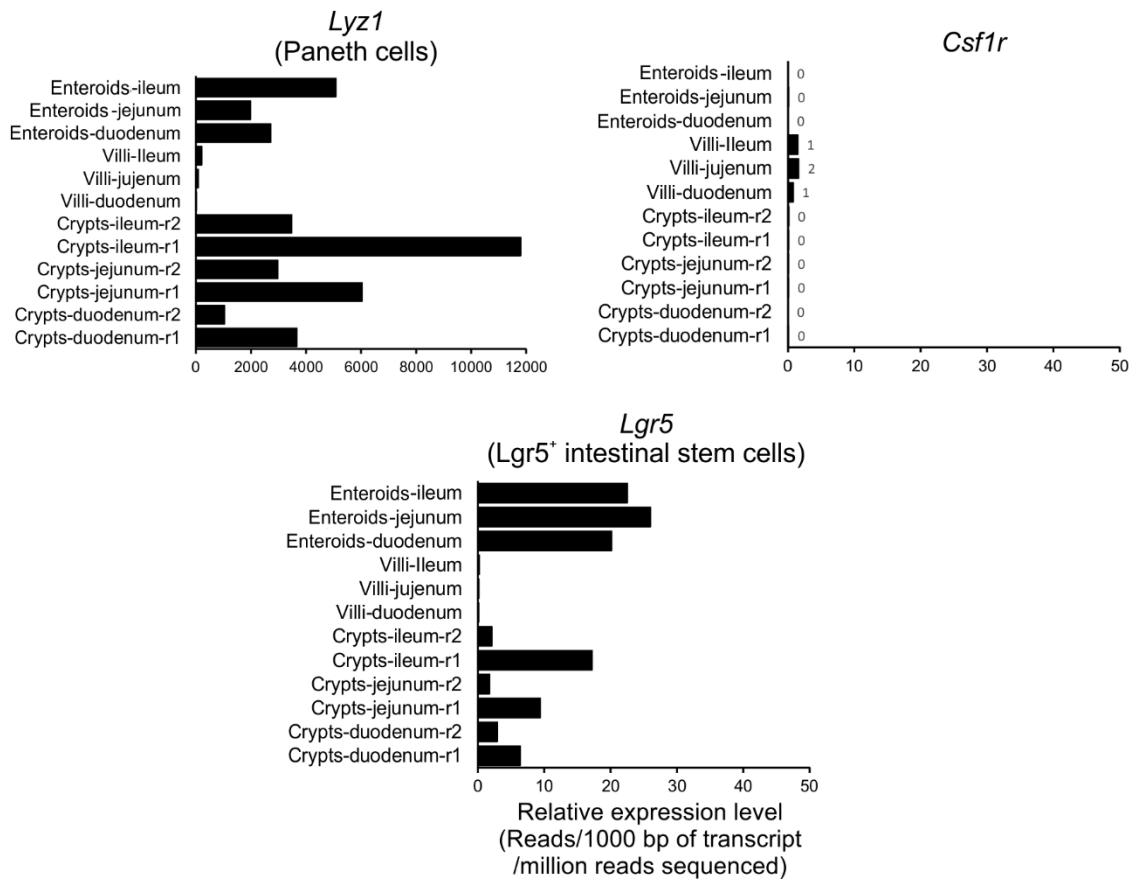
Supplementary Figures and Tables



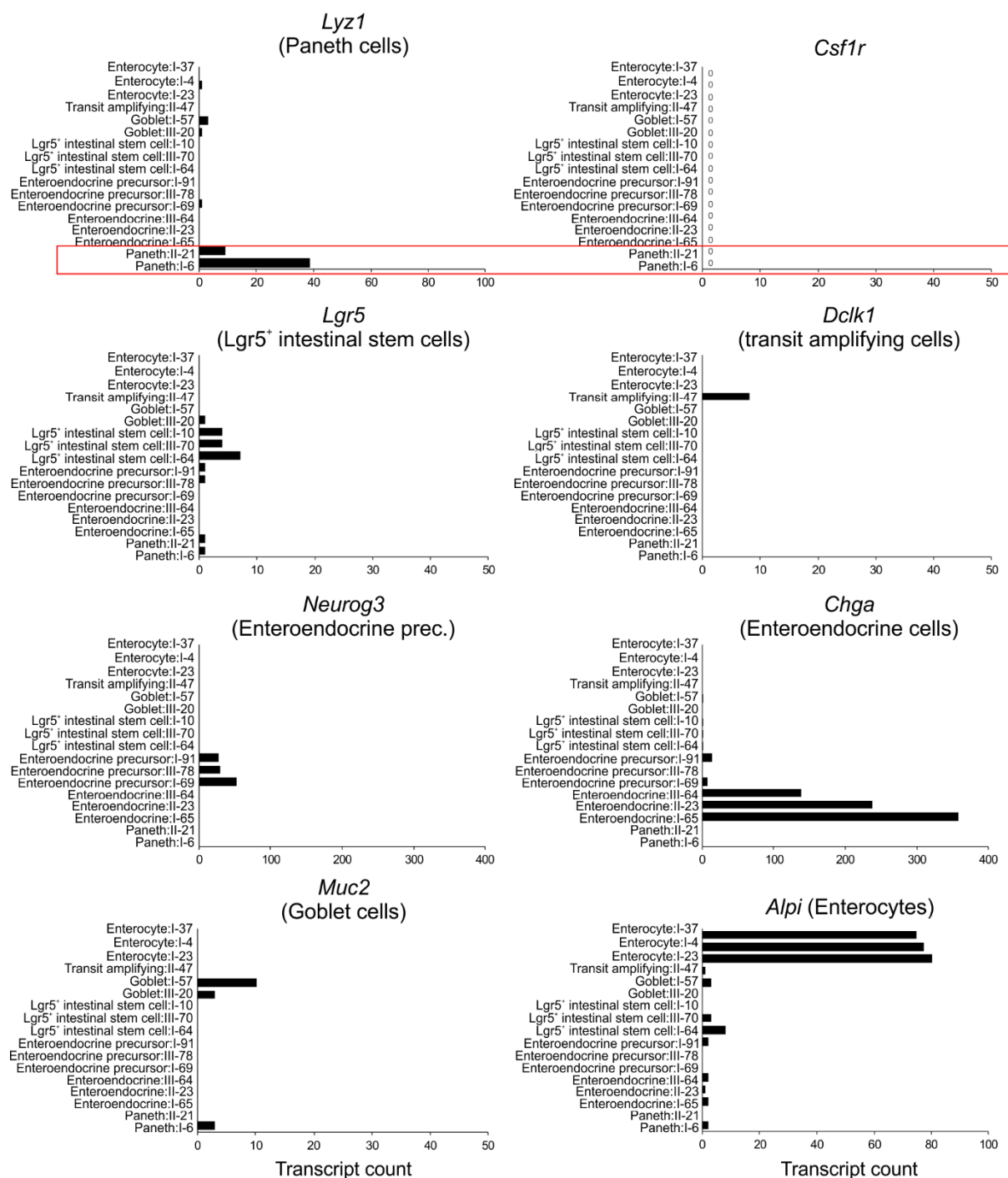
Supplementary Figure 1. Depletion of macrophages in the bone marrow of anti-CSF1R-treated mice. Representative FACS profiles of bone marrow preparations from control rat IgG or anti-CSF1R-treated mice ($n=3$ and $n=4$ mice/group). GR1/CSF1R profiles highlighting the almost complete reduction of cells with monocyte and macrophage characteristics.



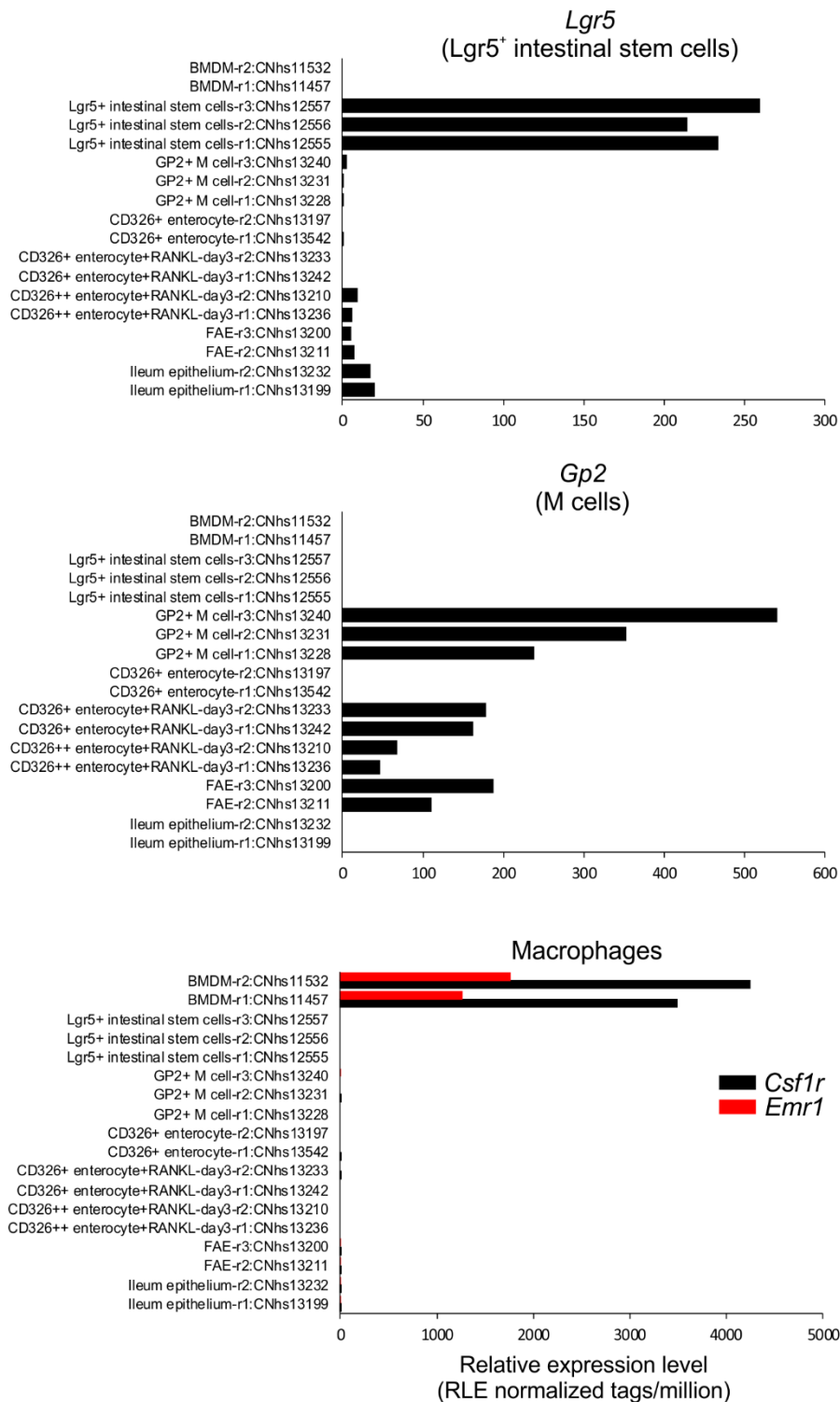
Supplementary Figure 2. Fluorescence microscopical analysis of the intestines from *Csf1r*-EGFP mice and C57BL/6J control mice. Sections were counterstained with DAPI to detect cell nuclei (blue). Scale bar, 50 μ m.



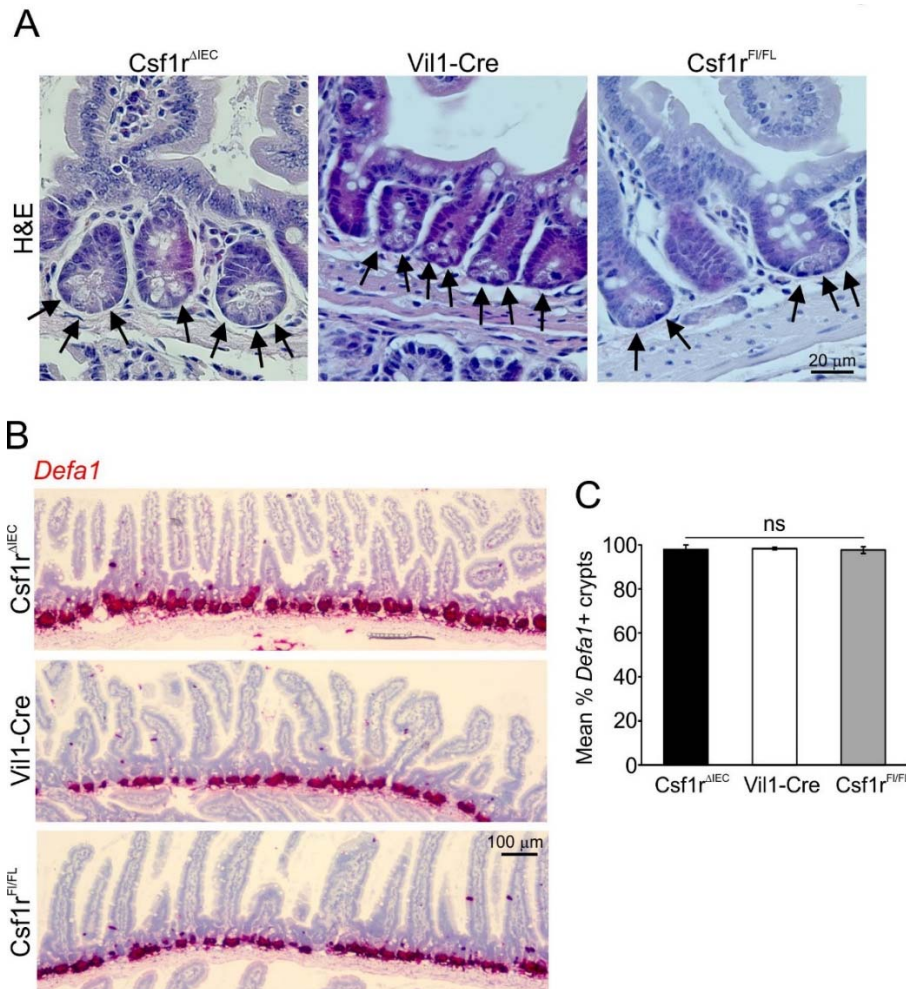
Supplementary Figure 3. Absence of *Csf1r* mRNA expression in isolated small intestinal crypts. Comparison of *Csf1r* mRNA expression in individual data sets from independent mRNA sequencing studies of enteroids, villi and isolated intestinal crypts¹ (GEO data set: GSE53297).



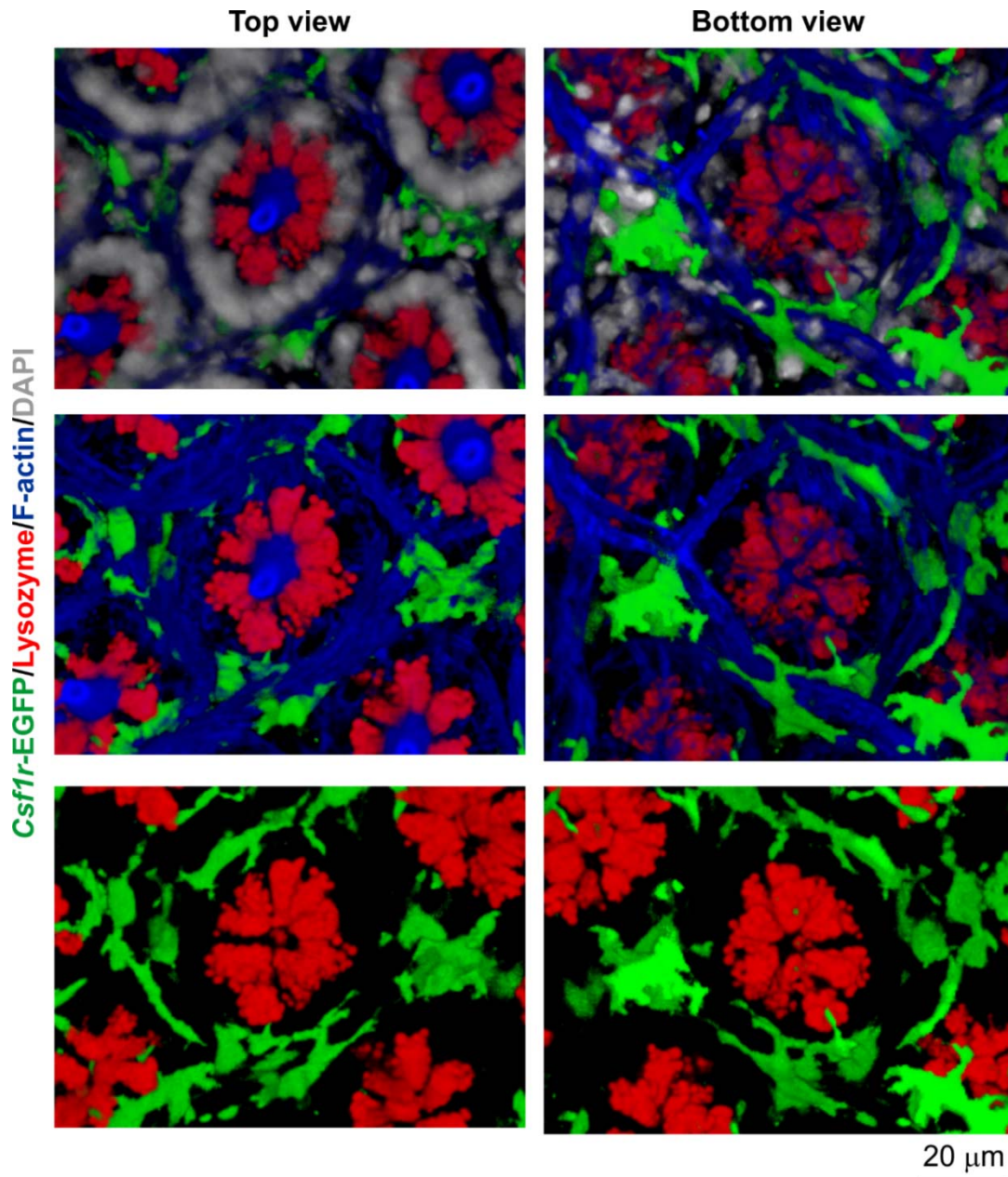
Supplementary Figure 4. Paneth cells and other crypt epithelial cell lineages do not express *Csf1r* mRNA. Comparison of *Csf1r* mRNA expression and other crypt epithelial cell lineage-related genes in data from independent mRNA sequencing studies of individual cell populations derived from intestinal crypts².



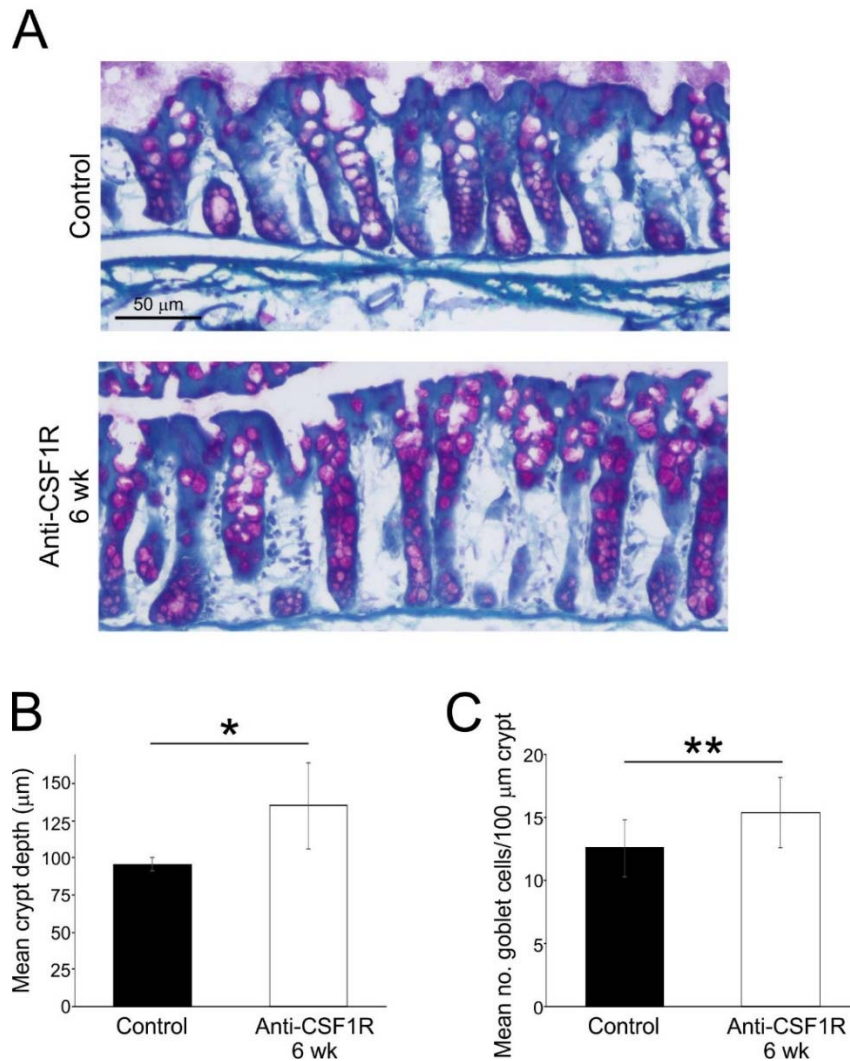
Supplementary Figure 5. Epithelial cell lineages, including M cells, do not express *Csfr1* mRNA. Comparison of *Csfr1*, *Emr1*, *Gp2* and *Lgr5* mRNA expression in individual cell populations in deep CAGE sequence data from the FANTOM5 project of the FANTOM consortium³ (<http://fantom.gsc.riken.jp/zenbu>).



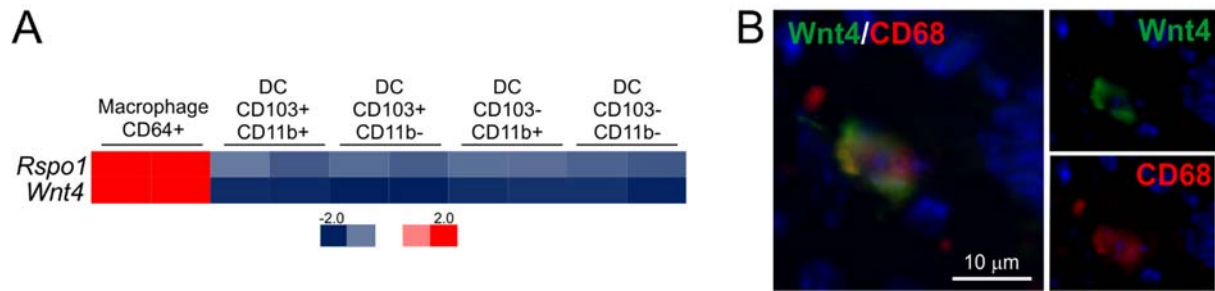
Supplementary Figure 6. Analysis of Paneth cell status in the intestines of Csfr1^{ΔIEC}, Vil1-Cre and Csfr1^{FL/FL} mice. **A)** Analysis of H&E stained intestines revealed that Paneth cells containing secretory granules (arrows) were present in the intestines of mice from each group. Representative images from the intestines of 3 mice/group are shown. Scale bar, 20 μ m. **(B)** RNA *in situ* hybridisation analyses showed that *Defa1* mRNA (red) was abundantly expressed in the intestinal crypts of Csfr1^{ΔIEC}, Vil1-Cre and Csfr1^{FL/FL} mice. Representative images from the intestines of 3 mice/group are shown. Scale bar, 100 μ m. **(C)** Morphometric analysis confirmed that the % crypts with *Defa1*-expressing Paneth cells was similar in the crypts of mice from each group. Data were obtained from 3 mice/group and 98-100 crypts/mouse. ns, one-way ANOVA with Tukey's post-hoc test.



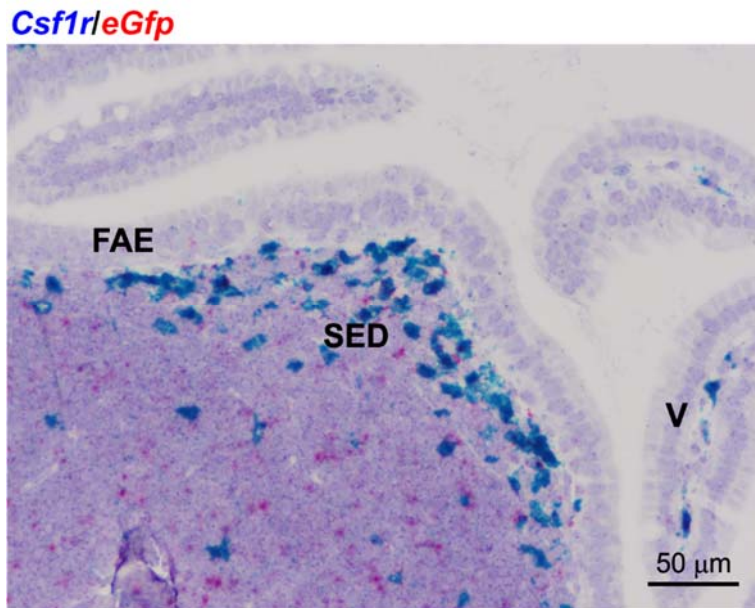
Supplementary Figure 7. Paneth cells do not express CSF1R. Representative whole-mount IHC analysis of intestinal crypts in the intestines of untreated *Csf1r*-EGFP mice shows the lysozyme expressing Paneth cells (red) do not express CSF1R (EGFP, green). In the crypt EGFP-expression was only detected in cells with macrophage morphology. Tissues are counterstained to detect F-actin (blue) and cell nuclei (DAPI, white/grey). Left-hand panels show crypts viewed from the luminal (upper) surface. Right-hand panels show the same crypts viewed from the serosal (bottom) surface. Scale bar, 20 μm.



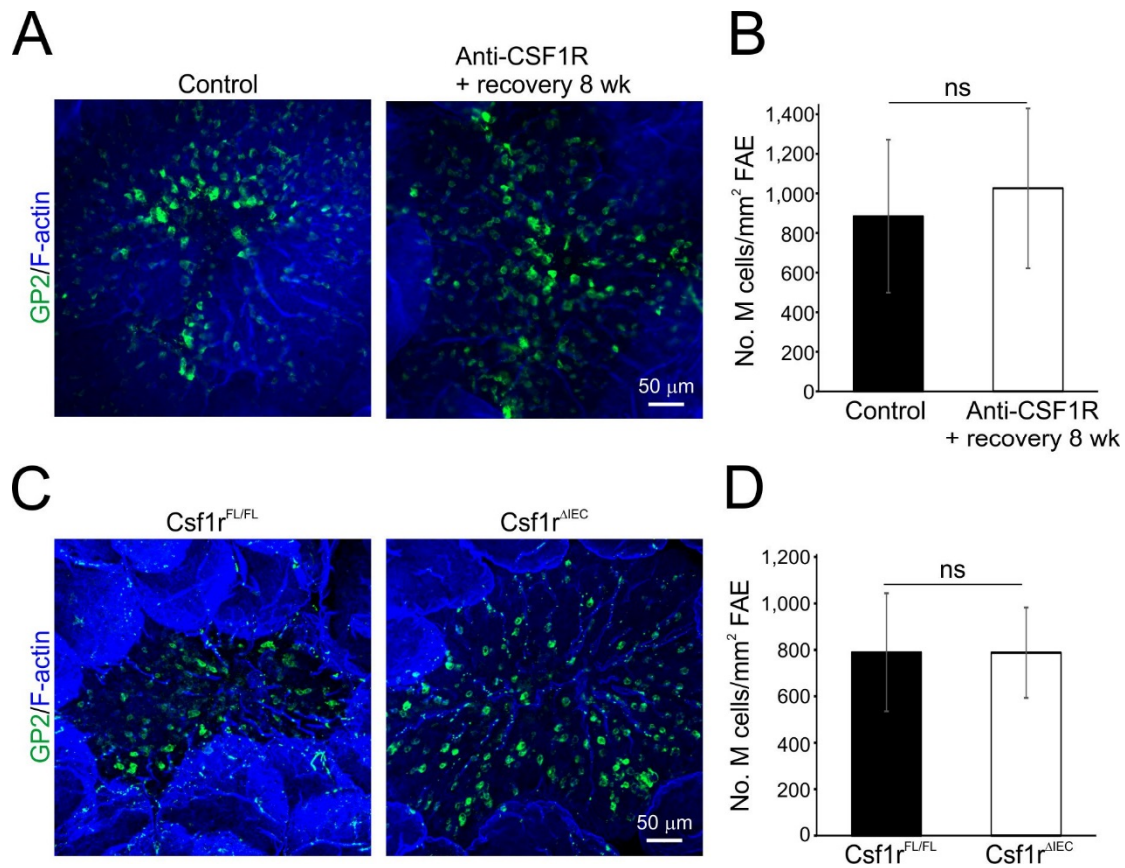
Supplementary Figure 8. Effect of prolonged CSF1R-blockade in the colon. Mice were treated with anti-CSF1R mAb or control-IgG (control) for 6 weeks before colons from 4 mice from each group were removed for analysis. (A) Histological analysis of PAS-stained sections from the colons of mice from each treatment group. Representative images from 4 mice/group, from 3 independent experiments are shown. Scale bar, 50 μm . (B) Morphometric analysis revealed that crypt depth was significantly longer following prolonged CSF1R-blockade. Data were obtained from 4 mice/group and 36-73 crypts/mouse. (C) A significant increase in goblet cell density was also observed in the colonic crypts following prolonged CSF1R-blockade. Data are derived from 4 mice/group and 29-59 crypts/mouse, and representative of 2 independent experiments. *, $P < 0.05$; **, $P < 0.01$, two-tailed unpaired Student's t test.



Supplementary Figure 9. (A) Heat map showing relative expression of *Rspo1* (upper row) and *Wnt4* (lower row) in microarray data from distinct mononuclear phagocyte populations isolated from the small intestine (GEO data set: GSE100393). DC, dendritic cells. (B) IHC analysis of Wnt4 expression (green) by CD68⁺ macrophages (red) in the gut wall. Sections were counterstained with DAPI to detect cell nuclei. Scale bar, 10 μ m.



Supplementary Figure 10. Two colour mRNA *in situ* hybridisation analysis showed that the follicle-associated epithelium (FAE) overlying the Peyer's patch lacked expression of *Csf1r* (blue) and (red) *eGfp* mRNA. SED, subepithelial dome; V, villous. Scale bar, 50 μm.



Supplementary Figure 11. (A&B) Mice were treated with anti-CSF1R mAb or control-IgG (control) for 6 weeks and then allowed to recover for 8 wk before analysis. (A) Peyer's patches were whole-mount immunostained to detect M cells (GP2⁺ cells, green) and f-actin (blue). Scale bar, 50 μ m. (B) Morphometric analysis showed that the density of GP2⁺ M cells was restored within an 8 wk recovery period after prolonged CSF1R-blockade. Data were obtained from 2-4 mice/group, 2-3 Peyer's patches/mouse, with 2-3 follicle-associated epithelia analysed from each Peyer's patch. ns, two-tailed unpaired Student's *t* test. (C) Peyer's patches from *Csf1r^{FL/FL}* mice (left-hand panel) and *Csf1r ^{Δ IEC}* mice (right-hand panel) were whole-mount immunostained to detect M cells (GP2⁺ cells, green) and f-actin (blue). Scale bar, 50 μ m. (D) Morphometric analysis showed that similar densities of GP2⁺ M cells were detected in the Peyer's patches *Csf1r^{FL/FL}* mice and *Csf1r ^{Δ IEC}* mice. Data were

obtained from 3 mice/group, 1-3 Peyer's patches/mouse with 4-10 follicle-associated epithelia analysed from each Peyer's patch. ns, two-tailed unpaired Student's *t* test.

Supplementary Table 1. Primary antibodies used for immunohistochemistry

Target	Antibody details	Clone	Source	Dilution used
Anxa5	Rabbit anti-annexin V	polyclonal	Abcam (Cambridge, UK)	1/400
CCL20	Rabbit anti-mouse CCL20	polyclonal	R&D Systems (Abingdon, UK)	1/200
CD11c	Hamster anti-mouse CD11c	HL3	BD Biosciences (Oxford, UK)	1/100
CD45R (B220)	Rat anti-mouse B220	RA3-6B2	Invitrogen (Paisley, UK)	1/100
CD68	Rat anti-mouse CD68	FA-11	Biologend	1/100
GP2	Rat anti-mouse GP2	2F11-C3	MBL International, Woburn, MA)	1/250
Ki67	Rabbit anti-Ki67	polyclonal	Abcam	1/100
Lysozyme	Rabbit anti-lysozyme	polyclonal	Abcam	1/200
RANKL	Rat anti-mouse CD254	IK22/5	eBioscience (Hatfield, UK)	1/250
SpiB	Sheep anti-mouse SpiB	polyclonal	R&D Systems	1/500
SOX9	Rabbit anti-mouse SOX9	EPR14335-78	Abcam	7 µg/ml
Wnt4	Rabbit anti-Wnt4	polyclonal	Abcam	1.25 µg/ml

Supplementary Table 2. Primers used for RT-qPCR analysis

Gene	Forward primer	Reverse primer
<i>Anxa5</i>	TTTCCGTTGCACGGAGTTGT	TTTCCTGGCGCTGAGCATT
<i>Bmi1</i>	AATTAGTTCCAGGGCTTTTCAA	CTTCATCTGCAACCTCTCCTCT AT
<i>Ccl9</i>	TACTGCCCTCTCCTTCCTCA	TTGAAAGCCCATGTGAAACA
<i>Cd68</i>	GCAACTCGAGCATCATTCTTTCA CC	GATGAGAGGCAGCAAGATGGA C
<i>Csf1r</i>	CCTGAAGGTGGCTGTGAAGATG	GCTCCCAGAAGGTTGACGATG
<i>Emr1</i>	ATGTGGGGCTTTTGGCTGCT	TGAGTCACTTTGAAGACATT
<i>Gapdh</i>	GATACTGCACAGACCCCTCCA	GCAGTTCCGGTCATTGAGGTA
<i>Gp2</i>	GATACTGCACAGACCCCTCCA	GCAGTTCCGGTCATTGAGGTA
<i>Lgr5</i>	GGGAGCGTTCACGGGCCTTC	GGTTGGCATCTAGGCGCAGGG
<i>Lyz1</i>	GAGACCGAAGCACCGACTATG	CGGTTTTGACATTGTGTTTCGC
<i>Lyz2</i>	ATGGAATGGCTGGCTACTATGG	ACCAGTATCGGCTATTGATCTG A
<i>Marcksl1</i>	TTTTGCCCTCCTGTGGATTCT	CCACTAGGCACAGCACAAGAG A
<i>Olfm4</i>	AGTGACCTTGTGCCTGCC	CACGCCACCATGACTACA
<i>Sgne1</i>	ACGGTTAAAAATGGCCTCAAGG	AAGGACCCAGATGCTGAAGAC C
<i>SpiB</i>	AGCGCATGACGTATCAGAAGC	GGAATCCTATACACGGCACAG G
<i>Tnfs11</i>	GAAGGCTCATGGTTGGATGTGG	GTGACTTTATGGGAACCCGAT G
<i>Tnfrsf11a</i>	CTGCCTCTGGGAACGTGACTGG	GGCTGACATACACCACGATG
<i>Tnfrsf11b</i>	CACCTTGAAGGGCCTGATGT	TTTTGGGAAAGTGGGATGTTTT
<i>Wnt3</i>	TCCTCCTCGGCGCTGCTTCT	CCAGGGCCAGGGACCACCAA
<i>Wnt3a</i>	TCAGGGGTGATACCAAGACC	GGGACTGCAAATCTTCCTCA

Supplementary Table 3. RNAscope RNA *in situ* hybridisation probes used

Gene	Probe target region	Supplier catalogue no.
<i>Bmi1</i>	3096-3549	466021
<i>Csf1r</i>	241-1212	428191
<i>Defa1</i>	2-427	445751
<i>eGfp</i>	628-1352	400751
<i>Emr1</i>	85-1026	317961
<i>Lgr5</i>	2165-3082	312171

References

1. Middendorp S, Schneeberger K, Wiegerinck CL, et al. Adult stem cells in the small intestine are intrinsically programmed with their location-specific function. *Stem Cells* 2014;32:1083-1091.
2. Grun G, Lyubimova A, Kester L, et al. Single-cell messenger RNA sequencing reveals rare intestinal cell types. *Nature* 2015;525:251-255.
3. FANTOM Consortium and the RIKEN PMI and CLST (DGT), Forrest AR *et al.* A promoter-level mammalian expression atlas. *Nature* 2014;507:462-470.