

Vascular-resident CD169-positive Monocytes and Macrophages Control Neutrophil Accumulation in the Kidney with Ischemia-reperfusion Injury

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Supplemental discussion

Supplementary Figures S1-S7

Supplementary Table S1

Supplemental discussion

Time course of gene recombination by Cre recombinase

In CD169-Cre-YFP mice, YFP⁺ cells may not correspond to CD169-expressing cells because Cre recombinase remains active even after the cells cease to express CD169. Thus, YFP-positive cells may not necessarily express CD169. On the other hand, activation of CD169 gene promoter does not instantly initiate YFP expression. When ES cells expressing tamoxifen-inducible modified estrogen receptor were cultured *in vitro* in the presence of tamoxifen, fluorescence intensity continued to increase up to day 4¹. Hori et al generated mice that express GFP-Cre fusion protein under the control of Foxp3 promoter and crossed them with ROSA26-red fluorescent protein (RFP) mice. In those mice, Foxp3⁺, CD4⁺ thymocytes contained many RFP⁻ or ^{lo} cells until 4 days after the birth, indicating the presence of newly developed Foxp3⁺ cells that have initiated Foxp3 transcription but have not fully accumulated RFP². Compatible with the reported kinetics, M-CSF-cultured BM cells express YFP more than 3 days after CD169 expression (**Fig. S3**). Disappearance of monocytes in CD169-DTR mice was more profound than the frequency of YFP-positive cells in the peripheral blood. We argue that the gap results from a delayed gene recombination in peripheral blood CD169⁺ monocytes. Due to the rapid turnover of peripheral blood monocytes, they may differentiate into tissue macrophages before they express YFP in blood stream.

The interaction of perivascular kidney CD169 macrophages with vascular endothelial cells

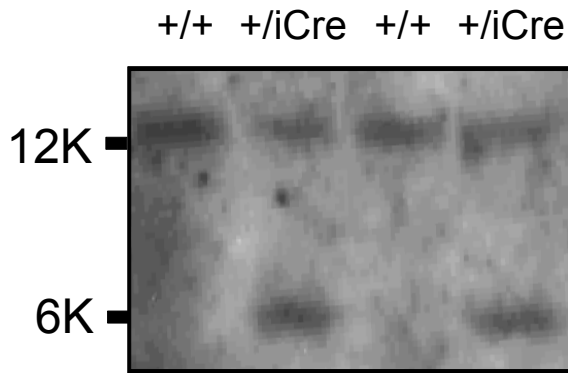
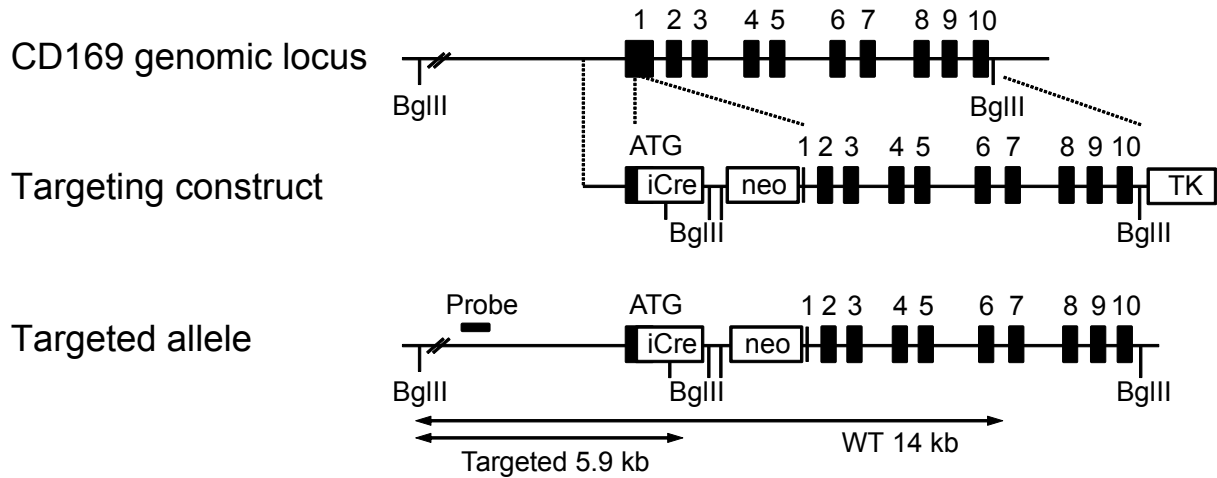
Our results strongly suggest that some CD169 monocytes attach to vascular endothelial cells from the luminal side, whereas perivascular kidney CD169 macrophages interact with vascular endothelial cells from the side of basal lamina. Although we have not determined

the details of interaction between perivascular macrophages and capillary endothelial cells, we speculate that the mechanism of interaction might be similar to that of interaction between pericytes and capillary endothelial cells. The capillary wall consists of vascular endothelial cells, the basal lamina, and pericytes. Pericytes are located in the perivascular region, and have been recently reported to interact closely with endothelial cells and to regulate the functions of these cells^{3, 4}. From these findings, it is possible for perivascular macrophages to interact with vascular endothelial cells, and to regulate these functions.

References

1. Schlenner, SM, Madan, V, Busch, K, Tietz, A, Laufle, C, Costa, C, Blum, C, Fehling, HJ, Rodewald, HR: Fate mapping reveals separate origins of T cells and myeloid lineages in the thymus. *Immunity*, 32: 426-436, 2010.
2. Miyao, T, Floess, S, Setoguchi, R, Luche, H, Fehling, HJ, Waldmann, H, Huehn, J, Hori, S: Plasticity of Foxp3(+) T cells reflects promiscuous Foxp3 expression in conventional T cells but not reprogramming of regulatory T cells. *Immunity*, 36: 262-275, 2012.
3. Armulik A, Genové G, Betsholtz C: Pericytes: developmental, physiological, and pathological perspectives, problems, and promises. *Dev Cell*, 21: 193-215, 2011.
4. Armulik A, Abramsson A, Betsholtz C: Endothelial/pericyte interactions. *Circ Res*, 97: 512-23, 2005

Karasawa et al. Fig.S1.



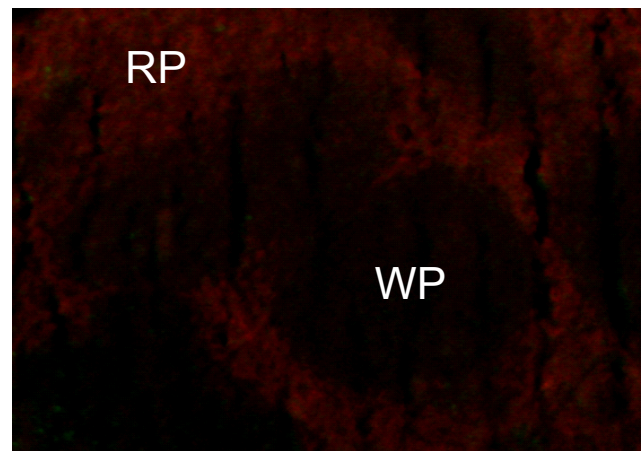
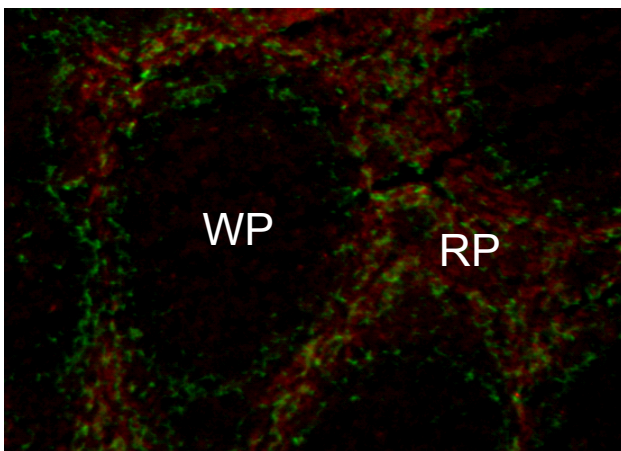
Supplementary Fig S1. CD169-Cre-YFP mice

Schematic diagram of the CD169-Cre targeting construct. Exons of the CD169 gene (*siglec1*) are indicated by solid boxes. The improved Cre recombinase cDNA (iCre), the neomycin resistant gene (neo), and the HSV-thymidine kinase (TK) gene are indicated by open boxes. The probe used for Southern blot analysis is indicated by a solid line together with the predicted hybridization fragments. Genomic Southern blot analysis of WT (+/+) and CD169-Cre (+/iCre) mice was carried out using Bgl II digest.

Karasawa et al. Fig.S2.

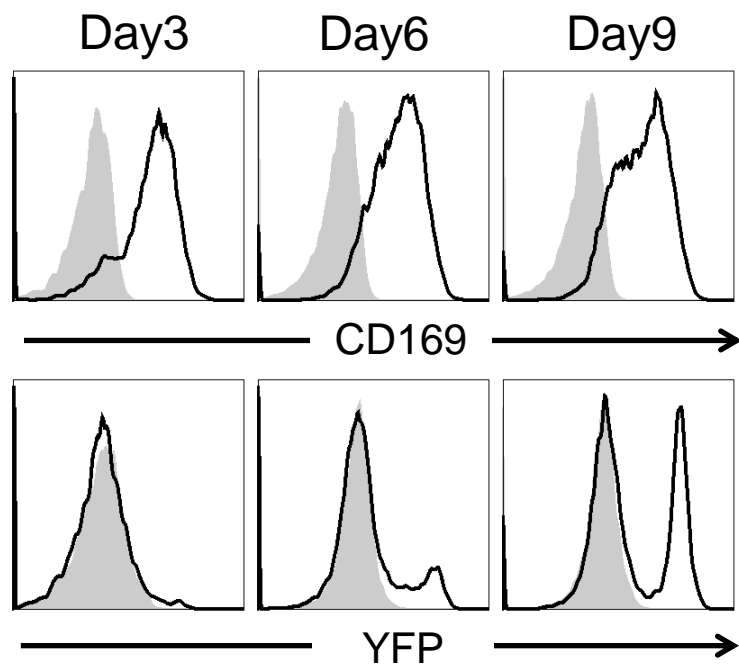
CD169-Cre-YFP

ROSA26-YFP

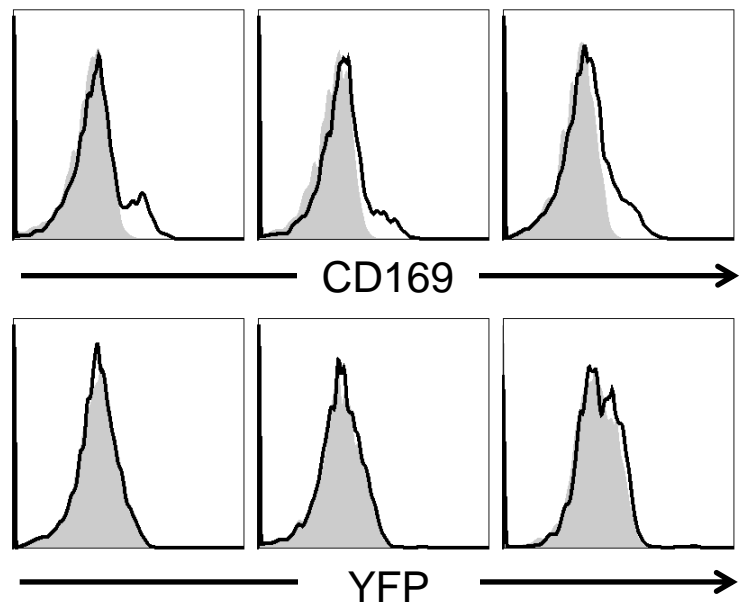


Supplementary Fig S2. Immunohistochemical analysis of the spleen of CD169-Cre-YFP mice Cryosections of spleens from CD169-Cre-YFP mice (left) or ROSA26-YFP mice (right) were stained for YFP (Green) and F4/80 (red). WP: white pulp, RP: red pulp. Original magnification, x 40.

M- CSF



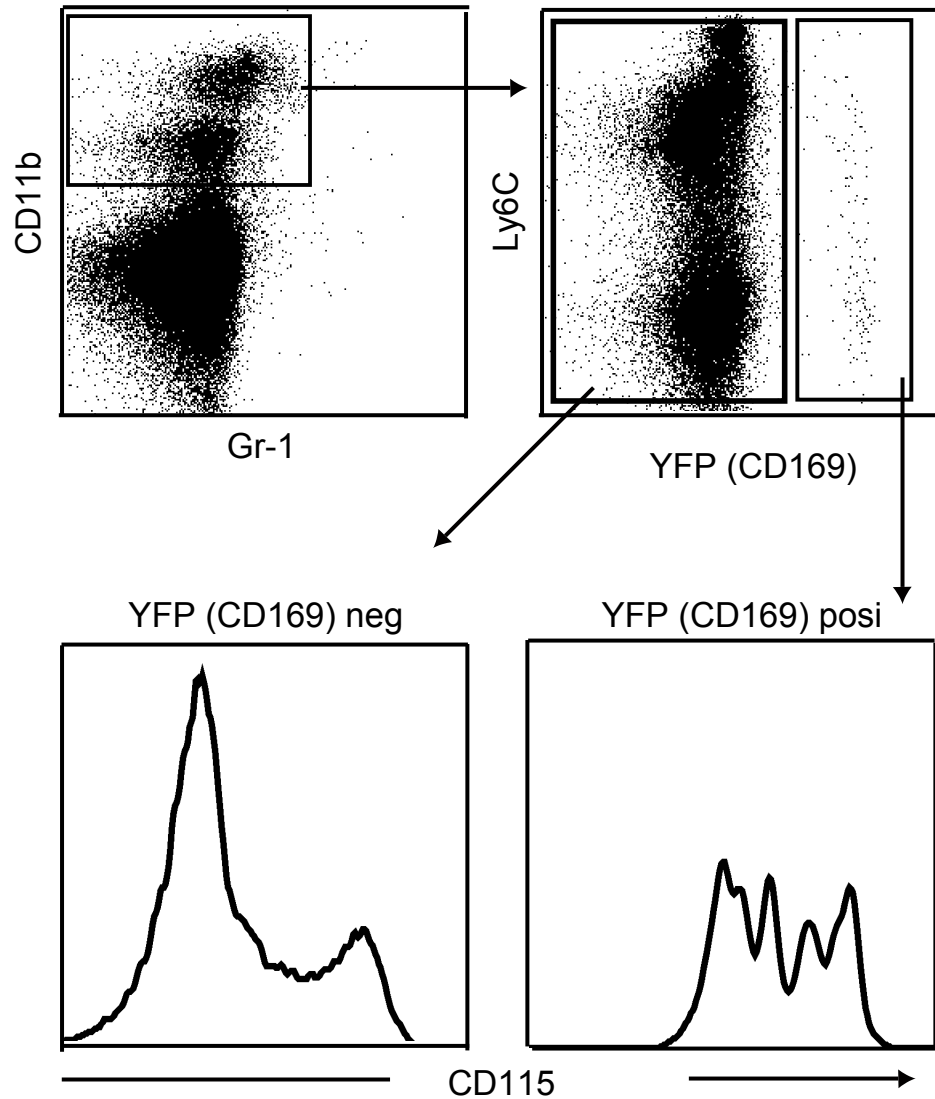
GM- CSF



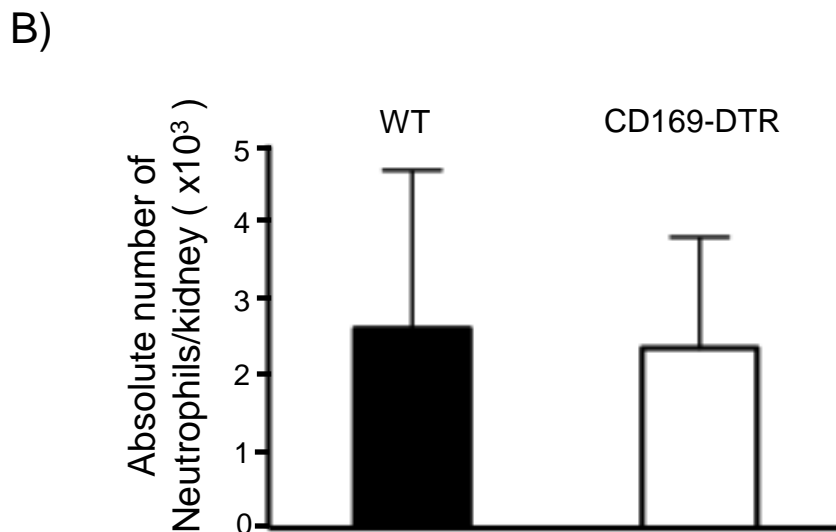
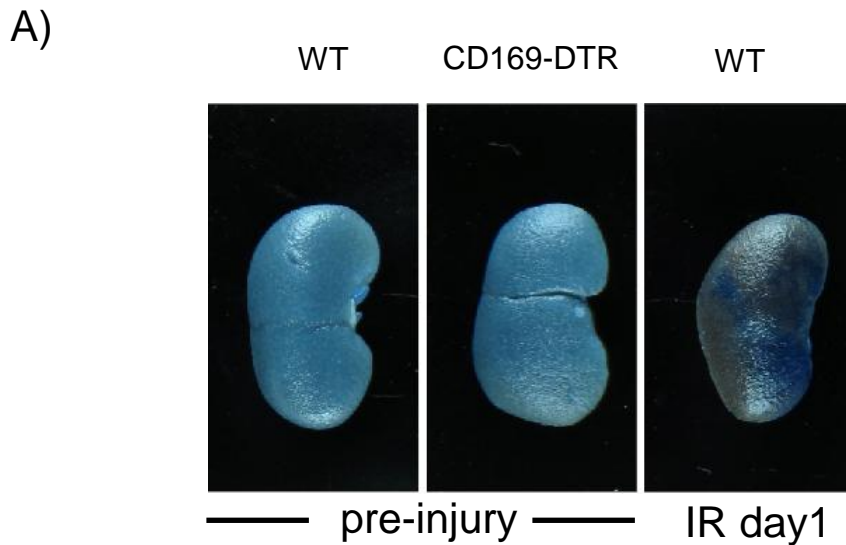
Supplementary Fig S3. YFP expression in bone marrow-derived macrophages and dendritic cells from CD169-Cre-YFP mice

Bone marrow cells from CD169-Cre-YFP mice were cultured either in DMEM/10% FCS supplemented with M-CSF (CMG 14-12 culture medium) or RPMI/10% FCS supplemented with GM-CSF (MGM-5 culture medium). YFP expression levels in CD11b⁺, F4/80⁺ fraction (M-CSF) or CD11b⁺, CD11c⁺ fraction (GM-CSF) were detected by a flowcytometer every 3 days up to 9 days after the culture. CD169 expression levels of those cells were detected with anti-CD169 antibody (clone M7). Shadow indicates unstained control for CD169 or YFP intensity of cells prepared from ROSA26-YFP mice. Data is representative of 2 independent experiments.

Karasawa et al. Fig.S4.

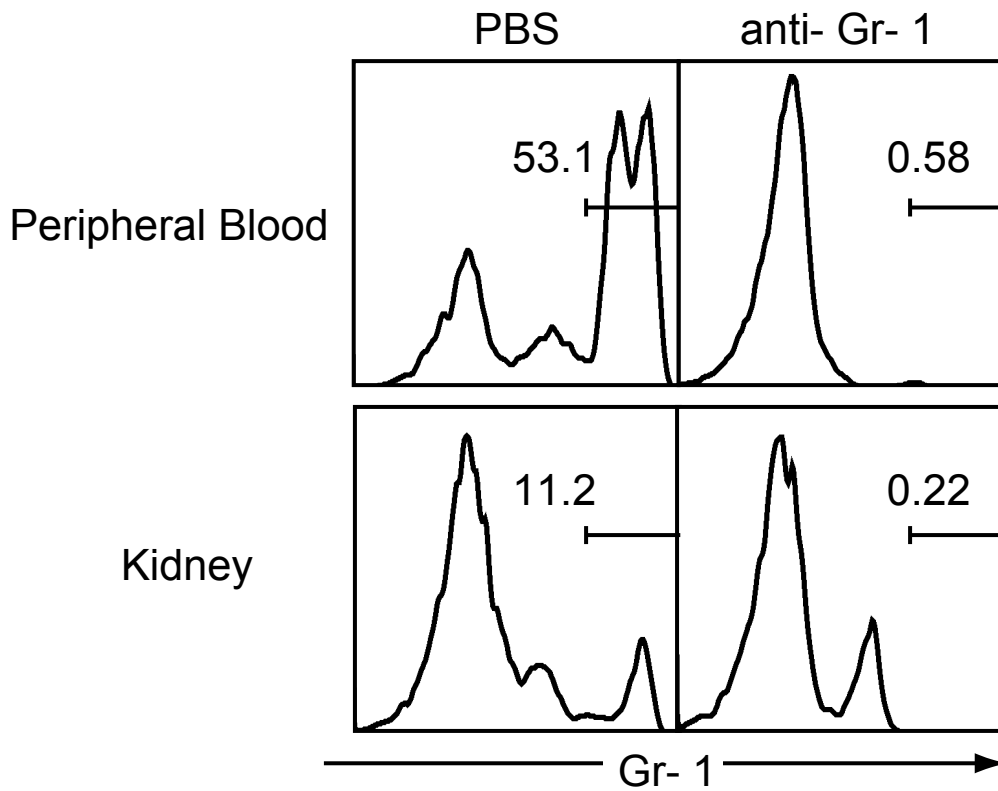


Supplementary Fig S4. YFP-positive cells in peripheral blood express CD115
Peripheral blood was obtained from CD169-Cre-YFP mice treated with anti-Gr-1 (Clone RB6-8C5) antibody. RBCs were lysed and residual leukocytes were stained for CD11b, Gr-1, Ly6C, and CD115, and analyzed with a flowcytometer. Data is representative of 3 independent experiments.



Supplementary Fig S5. A) Vascular permeability assay. Left and middle: DT was injected intraperitoneally into WT or CD169-DTR mice. Thirty-six hours later, Evans blue (200 μ l of 25mg/dl) was injected intravenously into WT or CD169-DTR mice. **Right:** DT was injected intraperitoneally into WT mice. Thirty-six hours later, unilateral IR was performed, followed by the i.v. injection of Evans blue. **B) The numbers of neutrophils in kidneys of WT and CD169-DTR mice in the pre-injury state.** DT was injected intraperitoneally into WT or CD169-DTR mice. Thirty-six hours later, absolute numbers of CD11b⁺, F4/80^{lo}, Gr-1^{high} neutrophils were quantitated by a flowcytometer.

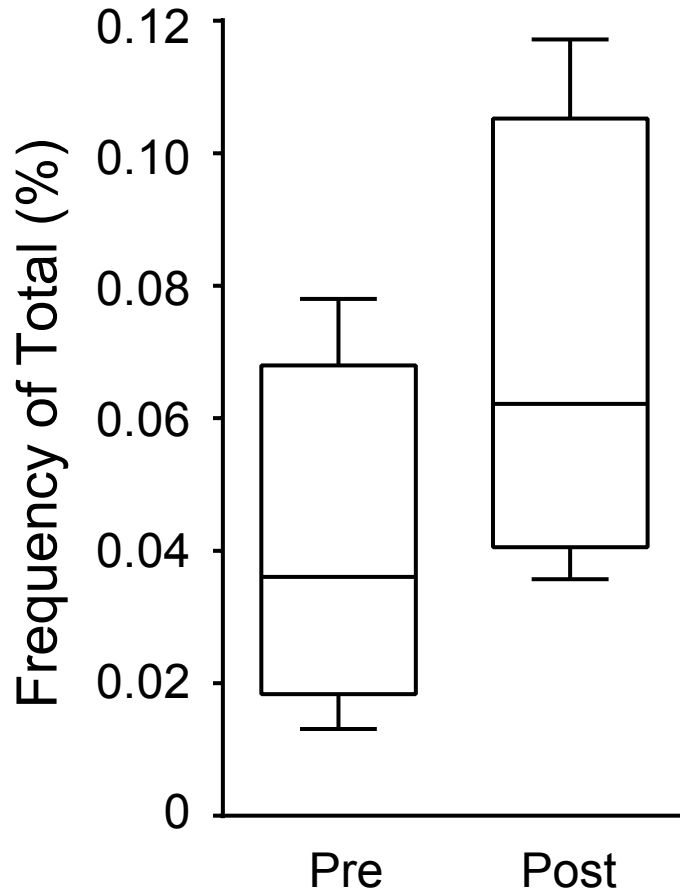
Karasawa et al. Fig.S6.



Supplementary Fig S6. Injection of anti-Gr-1 antibody selectively depletes neutrophils

One hundred μg of anti-Gr-1 (Clone RB6-8C5) antibody was injected intraperitoneally into WT mice. One day after the antibody injection, blood was collected and kidneys were resected, stained with anti-CD11b and anti-Gr-1 antibodies, and analyzed with a flowcytometer.

Karasawa et al. Fig.S7.



Supplementary Fig S7.

CD169⁺ monocytes adhere to vascular surface in a CD11b-dependent manner.

Anti-Gr-1 antibody was injected into CD169-Cre-YFP mice in order to deplete neutrophils. Fifteen hours after the anti-Gr-1 injection, 100 μ g of anti-CD11b antibody (clone 5C6) was injected intravenously into the mice. The frequency of YFP⁺ cells in Gr-1⁻, CD11b⁺, CD115⁺ fraction of peripheral blood monocytes was quantitated by a flowcytometer 3h before and 1 h after anti-CD11b antibody injection. Each symbol represents data from an individual animal. n = 4 mice/ group. Lines indicate the minimum, average \pm SD, and maximum values of each group.

Sequences of quantitative RT-PCR primers

Genes	Sequence (5' →3')	Position	Length (bp)
<i>icam1</i> (NM_010493.2)			
Fwd	ATCTCAGGCCCGCAAGGG	653-669	66
Rev	CGAAAGTCCGGAGGCTCC	701-718	
<i>icam2</i> (NM_010494.1)			
Fwd	TATGAGCCGATGCAGGACAAC	800-820	108
Rev	GTGCTGGCCAAAGATAAAGCATAG	884-907	
<i>tnf</i> (NM_013693.2)			
Fwd	ACCCTCACACTCAGATCATC	385-404	188
Rev	GAGTAGACAAGGTACAACCC	553-572	
<i>il1β</i> (NM_008361.3)			
Fwd	GGATGAGGACATGAGCACCT	323-342	174
Rev	AGCTCATATGGGTCCGACAG	477-496	
<i>cxcl1</i> (NM_008176.3)			
Fwd	ACTGCACCCAAACCGAAGTC	239-258	114
Rev	TGGGGACACCTTTTAGCATCTT	331-352	
<i>cxcl2</i> (NM_009140.2)			
Fwd	ACAGAAGTCATAGCCACTCTC	239-259	103
Rev	CCTTGCCTTTGTTTCAGTATC	322-341	
<i>ccl2</i> (NM_011333.3)			
Fwd	TGTTGGCTCAGCCAGATGCA	147-166	82
Rev	AGCCTACTCATTGGGATCATCTTG	205-228	

The positions of the primers are annotated according to the sequences derived from GenBank (accession numbers are given in parenthesis). Fwd, forward; Rev, reverse.