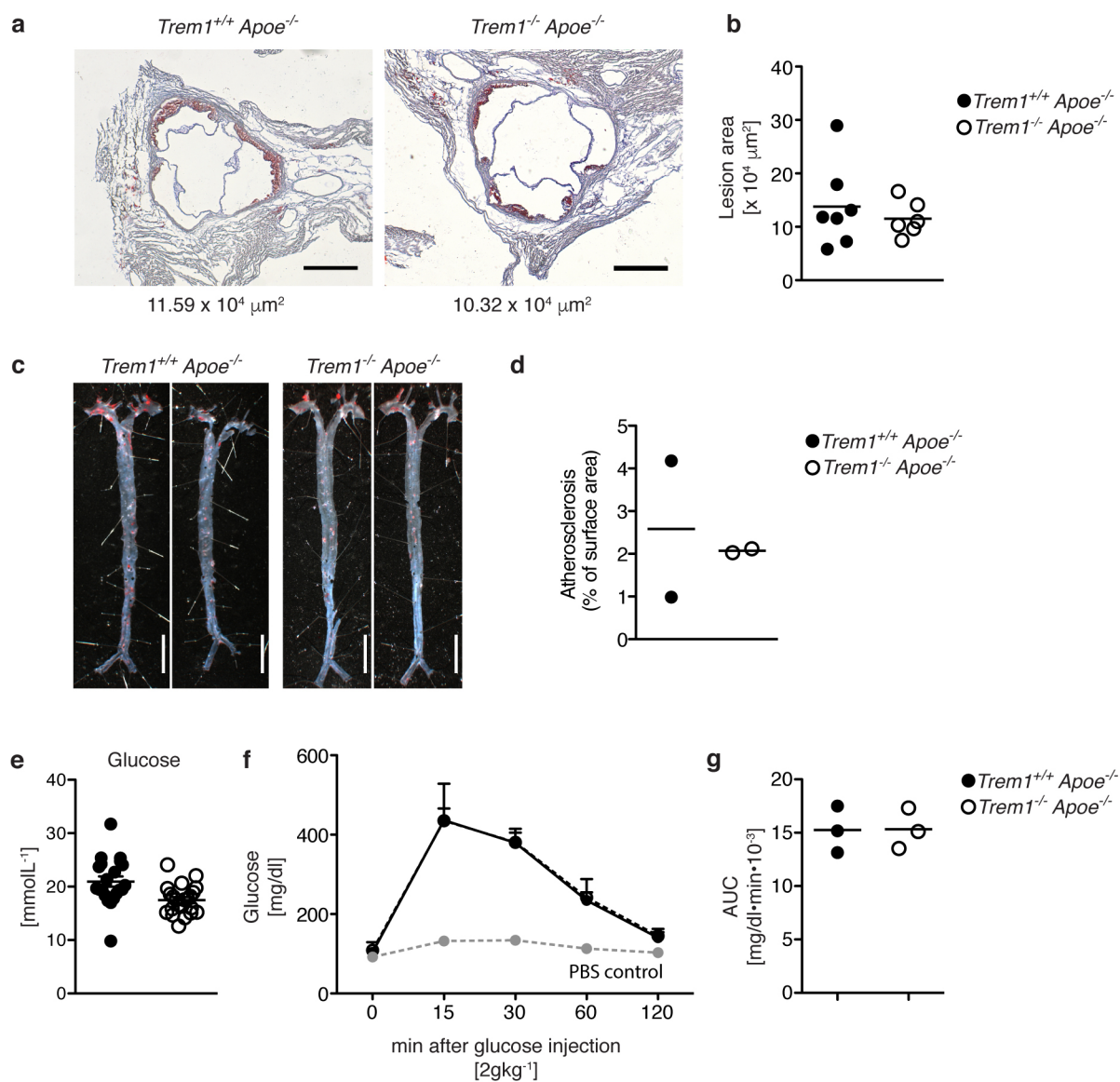


Supplementary Figure 1



Supplementary Figure 1

**(a-d) Analysis of aortic sinus sections at 4 weeks post HFCD or of aortas derived from 16 week chow-fed mice does not indicate a major impact of TREM-1 during early stages of atherogenesis. (a,b) Extent of atherosclerosis in the aortic root at 4 weeks post HFCD feeding. (a)** Representative examples of ORO stained sections of the aortic sinus. Scale bars indicate 500 μm. **(b)** The lesion area was calculated from 10 sequential ORO stained sections for each *Trem1<sup>+/+</sup> ApoE<sup>-/-</sup>* and *Trem1<sup>-/-</sup> ApoE<sup>-/-</sup>* mouse. Circles show data for individual mice. **(c,d) Extent of atherosclerotic lesions in aortas of 16 week chow-fed mice (n=2 per group). (c) en face** preparations of ORO-stained aortas. Scale bars indicate 10 mm. **(d)** Overall extent of atherosclerosis (aortic lesion surface area expressed as % of total aortic surface).

**(e-g) TREM-1 does not impact on serum glucose levels or glucose clearance in HFCD-fed mice.**

(e) Fasting serum glucose concentrations in *Trem1<sup>+/+</sup> ApoE<sup>-/-</sup>* (n=13) and *Trem1<sup>-/-</sup> ApoE<sup>-/-</sup>* (n=12) mice at 16 weeks post HFCD-feeding were determined on a cobas 8000 clinical chemistry analyzer (Roche diagnostics). (f,g) Intraperitoneal glucose tolerance test (IPGTT). 16 week HFCD-fed *Trem1<sup>+/+</sup> ApoE<sup>-/-</sup>* and *Trem1<sup>-/-</sup> ApoE<sup>-/-</sup>* mice were fasted o/n and challenged i.p. with 2 mg/kg glucose. (f) Blood glucose levels were calculated from blood samples obtained at the indicated intervals from the lateral tail vein using an Accu Chek blood glucose meter (Roche diagnostics). Mean values for n=3 mice per group are shown with error bars indicating the SD. (g) Area under the curve (AUC) of IPGTT as shown in (f). Statistical testing employed the two-tailed t-test. Statistically not significant differences with  $p > 0.05$  are not indicated.

Supplementary Figure 2



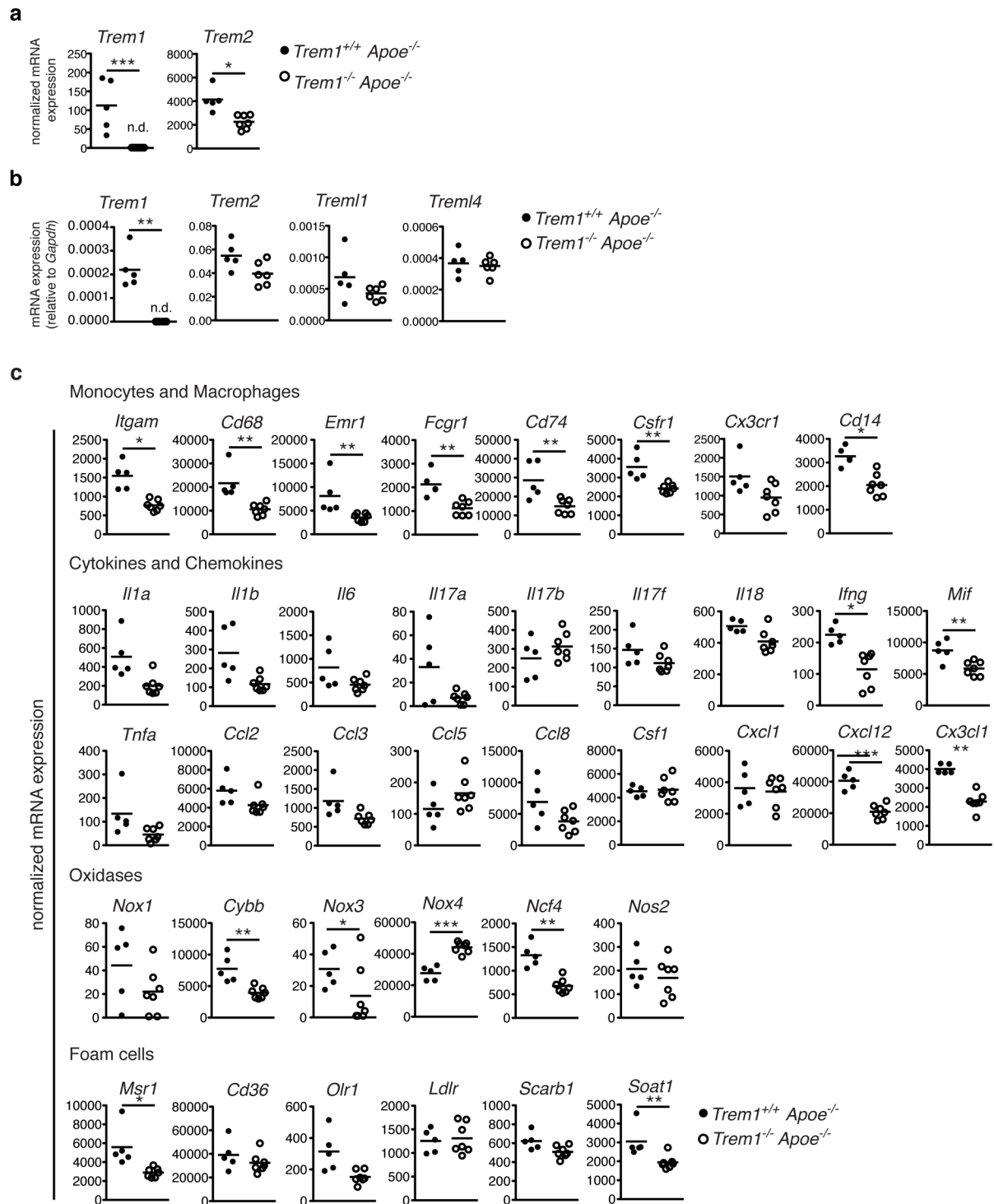
## Supplementary Figure 2

**(a-c) Gating strategies and representative staining panels for peripheral blood myeloid cell subsets and bone marrow hematopoietic stem and progenitor cells.**

**(a)** Gating strategy and representative dot plots for peripheral blood myeloid cell subsets in 16 week HFCD-fed *Trem1<sup>+/+</sup> Apoe<sup>-/-</sup>* and *Trem1<sup>-/-</sup> Apoe<sup>-/-</sup>* mice. **(b)** Gating strategy and representative dot plots for identification of hematopoietic stem cell-enriched LSK cells and myeloid progenitor cells in lineage marker negative (lin<sup>-</sup>) CD127<sup>-</sup> bone marrow (BM) cells of 16 week HFCD-fed *Trem1<sup>+/+</sup> Apoe<sup>-/-</sup>* and *Trem1<sup>-/-</sup> Apoe<sup>-/-</sup>* mice. LSK cells were identified by their Sca1<sup>+</sup>ckit<sup>hi</sup> phenotype while GMP and CMP were discriminated among the Sca1<sup>-</sup>ckit<sup>hi</sup> population based on their expression levels of FcγR and CD34. **(c)** Representative histogram overlays showing TREM-1 surface expression (bold line) in LSK cells, CMP and GMP as defined in **(b)** in 16 week HFCD-fed (red line) versus chow-fed (black line) *Trem1<sup>+/+</sup> Apoe<sup>-/-</sup>* mice. Filled histograms represent matched isotype control stained cells from HFCD-fed mice.

**(d,e) TREM-1-mediated stimulation of GMP isolated from 16 week HFCD-fed *Trem1<sup>+/+</sup> Apoe<sup>-/-</sup>* mice does not augment monocyte differentiation *in vitro*.** **(d,e)** GMP were FACS-sorted from 16 week HFCD-fed *Trem1<sup>+/+</sup> Apoe<sup>-/-</sup>* and *Trem1<sup>-/-</sup> Apoe<sup>-/-</sup>* mice and cultured in 96-well U-bottom plates in IMDM 10% FCS supplemented with IL-11 and TPO (10 ng/ml) as well as SCF and FLT3L (50 ng/ml) in the presence of plate-bound anti-TREM-1 or isotype control mAb (10 μg/ml). Where indicated, the medium was additionally supplemented with 5% HFCD serum. After 72 h of culture, cells were analyzed by flow cytometry for the expression of monocytic and granulocytic lineage markers. **(d)** Relative frequency of Ly6C<sup>hi</sup> monocytes. **(e)** Relative frequency of Ly6G<sup>+</sup> neutrophils. Columns show mean values of n=6 mice per group from two independent experiments with error bars indicating the SD. (Conditions with 5% HFCD serum: mean of n=2 mice from one experiment with error bars indicating the range).

Supplementary Figure 3

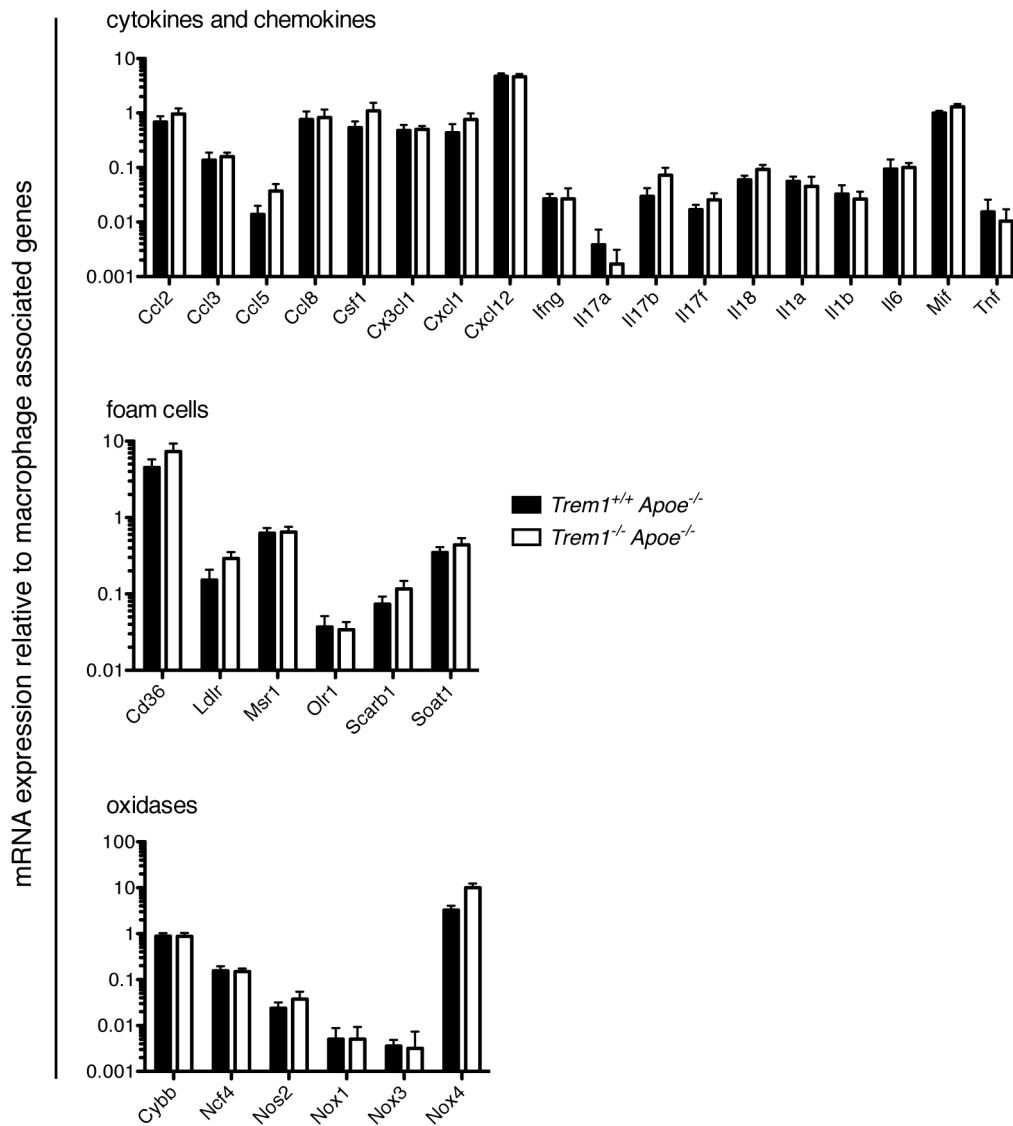


### Supplementary Figure 3

#### Expression of TREM family members and selected genes of interest in the aortic root of 16 week HFCD-fed *Trem1*<sup>+/+</sup> *ApoE*<sup>-/-</sup> versus *Trem1*<sup>-/-</sup> *ApoE*<sup>-/-</sup> mice.

(a) Nanostring nCounter-based quantification of *Trem1* and *Trem2* mRNA expression, nd: not detected. (b) qRT-PCR-based quantification of *Trem1*, *Trem2*, *Trem11* and *Trem41* mRNA. (c) Nanostring nCounter-based mRNA counts of selected genes of interest. Symbols show individual values for 16 week HFCD-fed *Trem1*<sup>+/+</sup> *ApoE*<sup>-/-</sup> (n=5) and *Trem1*<sup>-/-</sup> *ApoE*<sup>-/-</sup> (n=7) mice. \* p < 0.05, \*\* p < 0.01, \*\*\* p < 0.001. Significant differences in gene expression were calculated as described in the Methods section. Statistically not significant differences with p > 0.05 are not indicated.

Supplementary Figure 4

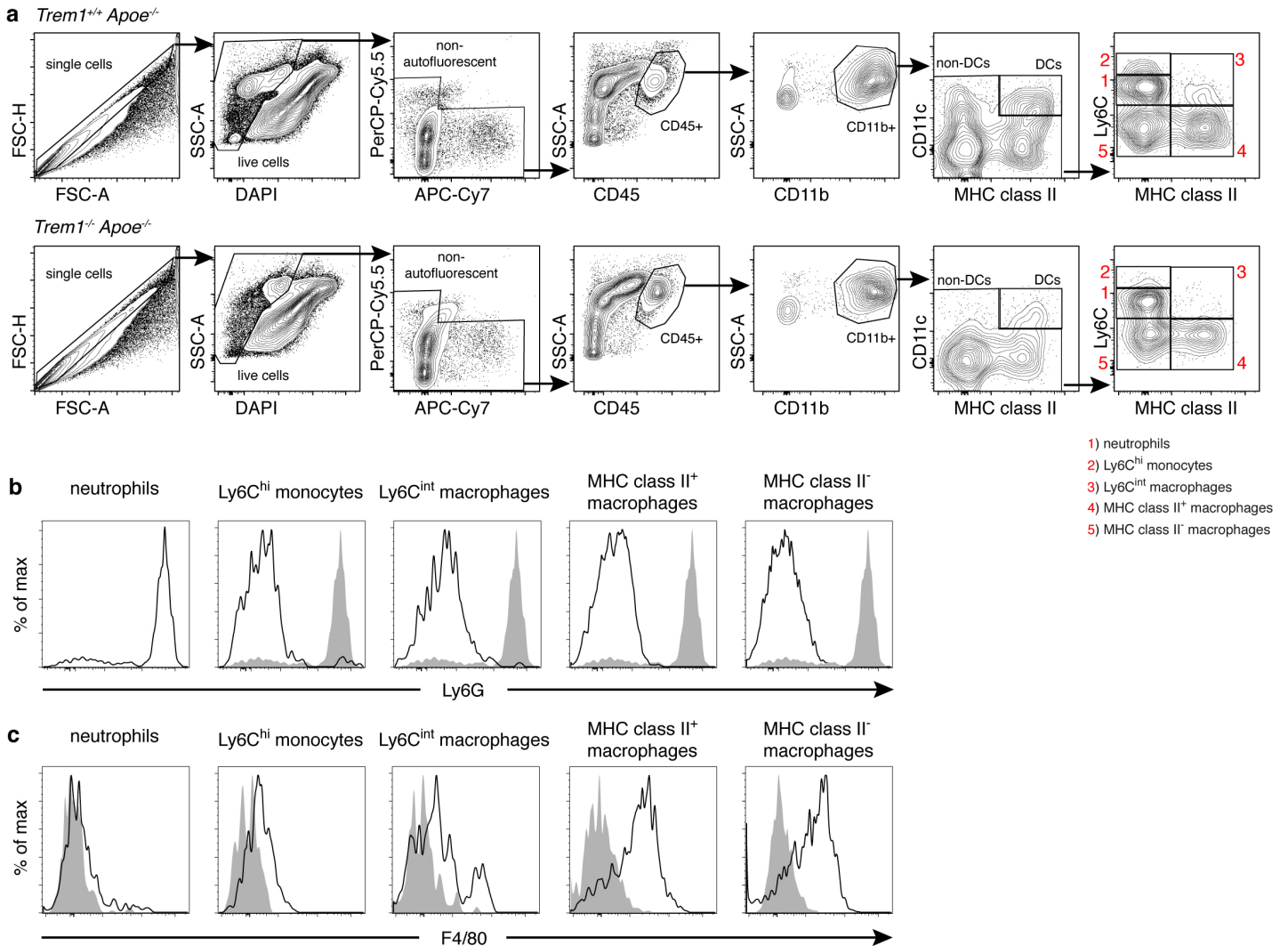


Supplementary Figure 4

**Nanostring-based gene expression data after normalization to combined macrophage markers.**

Expression levels of *Cd14*, *Cd68*, *Cd74*, *Csflr*, *Cx3cr1*, *Emr1*, *Fcgr1* and *Itgam* were used to calculate a mean combined macrophage marker expression level. For each sample, the expression of a candidate gene was calculated relative to the mean macrophage marker expression level. Column graphs show mean mRNA expression levels of genes of interest relative to macrophage-associated gene expression for each group of *Trem1*<sup>+/+</sup> *ApoE*<sup>-/-</sup> (n=5) and *Trem1*<sup>-/-</sup> *ApoE*<sup>-/-</sup> (n=7) mice. Bars indicate mean + SD.

Supplementary Figure 5



**Supplementary Figure 5**

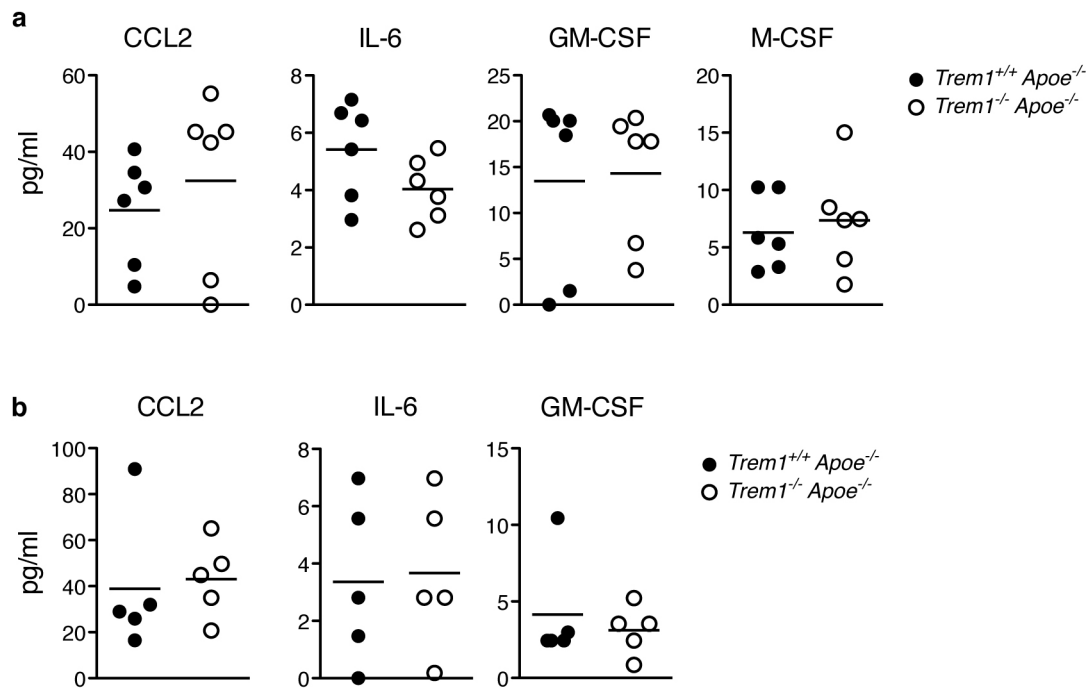
**Gating strategy for identification of aortic wall-infiltrating myeloid cell subsets.**

**(a)** Gating strategy for identification of aortic wall-infiltrating myeloid cell subsets and representative contour plots for cells retrieved from the digested aortas of 16 week HFCD-fed *Trem1<sup>+/+</sup> Apoe<sup>-/-</sup>* and *Trem1<sup>-/-</sup> Apoe<sup>-/-</sup>* mice. Initial gating comprised the exclusion of doublets, dead (DAPI<sup>+</sup>) and autofluorescent cells. Autofluorescence was defined based on double-positive expression of Ly6G (PerCP-Cy5.5) and MHC class II (APC-Cy7). Among single, live and non-autofluorescent cells leukocytes were subsequently discriminated from endothelial and stromal cells by gating on CD45<sup>+</sup> cells. CD45<sup>+</sup> leukocytes were further subgated into CD11b<sup>+</sup> cells. Among CD11b<sup>+</sup> cells, we gated out MHC class II<sup>+</sup> CD11c<sup>+</sup> cells as these were reported to represent dendritic cells (DC) <sup>1,2</sup>. The remaining CD11b<sup>+</sup> cells were finally separated according to their expression levels of Ly6C and MHC class II to



distinguish five myeloid cell subsets: 1. Neutrophils ( $\text{Ly6C}^{\text{int}}$ ,  $\text{MHCII}^-$ ), 2.  $\text{Ly6C}^{\text{hi}}$  monocytes ( $\text{Ly6C}^{\text{hi}}$ ,  $\text{MHCII}^-$ ) 3.  $\text{Ly6C}^{\text{int}}$  macrophages ( $\text{Ly6C}^{\text{int}}$   $\text{MHCII}^+$ ) 4.  $\text{MHCII}^+$  macrophages ( $\text{Ly6C}^{\text{lo}}$   $\text{MHCII}^+$ ) and 5.  $\text{MHCII}^-$  macrophages ( $\text{Ly6C}^{\text{lo}}$ ,  $\text{MHCII}^-$ ). **(b)** Ly6G surface expression of aortic wall infiltrating myeloid cell subsets. Black lines show Ly6G expression of the indicated subsets while gray filled histograms indicate Ly6G expression of neutrophils in comparison. **(c)** F4/80 expression of aortic wall-infiltrating myeloid cell subsets. Black lines show F4/80 expression of the indicated subsets with gray filled histograms representing isotype controls.

Supplementary Figure 6

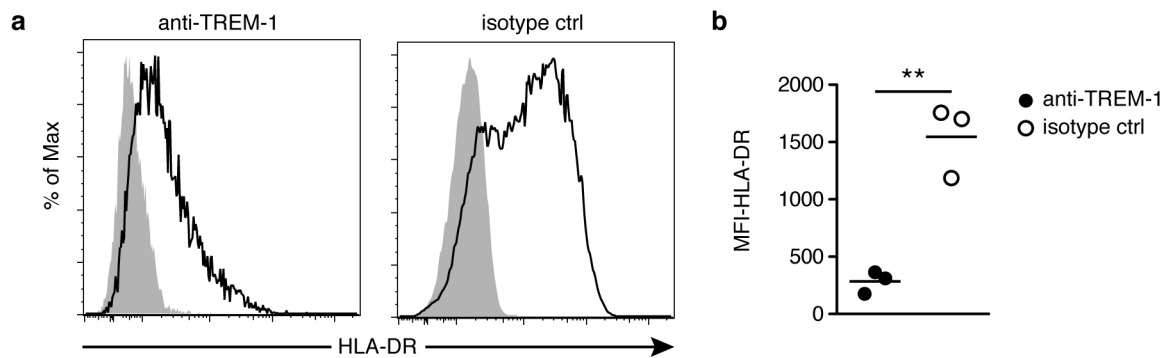


Supplementary Figure 6

**TREM-1 has no appreciable impact on the level of distinct cytokines and chemokines.**

(a) Bone flushes and (b) sera derived from *Trem1*<sup>+/+</sup> *Apoe*<sup>-/-</sup> and *Trem1*<sup>-/-</sup> *Apoe*<sup>-/-</sup> mice at 16 weeks post HFCD feeding were analyzed using either (a) the mouse discovery cytokine and chemokine 31-plex assay (Eve Technologies, Canada) or (b) a Luminex-based mouse cytokine 20-plex assay (LMC0006, Thermo Fisher Scientific) (M-CSF not included in assay). Symbols show individual values for 16 weeks HFCD-fed *Trem1*<sup>+/+</sup> *Apoe*<sup>-/-</sup> (n=5) and *Trem1*<sup>-/-</sup> *Apoe*<sup>-/-</sup> (n=5) mice with lines indicating mean values per group. Statistically not significant differences with  $p > 0.05$  are not indicated.

Supplementary Figure 7



Supplementary Figure 7

**TREM-1-mediated signaling reduces HLA-DR expression during macrophage differentiation *in vitro*.**

Primary human monocytes were differentiated to macrophages with recombinant human M-CSF (50 ng/ml) in the presence of a plate-bound agonistic anti-TREM-1 antibody or an isotype control antibody. After 4 days of culture, macrophages were detached, stained for HLA-DR and analyzed by flow cytometry by gating on single live cells. **(a)** Representative histograms of HLA-DR expression. Black lines represent the HLA-DR-stained cells and gray area show matched isotype control-stained cells. **(b)** MFI values for HLA-DR surface expression (with subtracted MFI values of matched isotype control-stained cells). Circles represent data for individual blood donors, lines indicate mean values of three independent experiments. \*\*  $p < 0.01$  as determined by the two-tailed t test.

**Supplementary Table 1**

List of genes added to the NanoString mouse immunology panel

<b>RefSeqID</b>	<b>symbol</b>	<b>logFC</b>	<b>adj.P.Val</b>
NM_013454.3	<i>Abca1</i>	-0.548182	0.020914
NM_009593.1	<i>Abcg1</i>	-0.903426	0.007975
NM_007482.3	<i>Arg1</i>	-1.605327	0.483673
NM_009754.3	<i>Bcl2l11</i>	-0.656498	0.032398
NM_009853.1	<i>Cd68</i>	-1.021322	0.008107
NM_009141.2	<i>Cxcl5</i>	-0.516252	0.733208
NM_007837.3	<i>Ddit3</i>	-0.098331	0.513715
NM_010439.3	<i>Hmgbl</i>	0.084819	0.668339
NM_010637.3	<i>Klf4</i>	-0.103353	0.738274
NM_010700.2	<i>Ldlr</i>	0.047427	0.913072
XM_909927.2	<i>Ly6g</i>	-1.953349	0.250607
NM_008562.3	<i>Mcl1</i>	-0.083424	0.716881
NM_008587.1	<i>Mertk</i>	-0.022212	0.922680
NM_008605.3	<i>Mmp12</i>	-0.599649	0.238986
NM_010902.3	<i>Nfe2l2</i>	-0.108595	0.573927
NM_145827.3	<i>Nlrp3</i>	-0.803574	0.284296
NM_009473.2	<i>Nr1h2</i>	-0.003419	0.993634
NM_013839.2	<i>Nr1h3</i>	-0.361939	0.088568
NM_011851.3	<i>Nt5e</i>	-0.057942	0.909367
NM_008744.2	<i>Ntn1</i>	-0.133649	0.519637
NM_138648.1	<i>Olr1</i>	-0.996517	0.470639
NM_008920.4	<i>Prg2</i>	-0.046406	0.887030
NM_016741.1	<i>Scarb1</i>	-0.287325	0.093439
NM_011355.1	<i>Sfp1</i>	-0.809824	0.010667
NM_145581.1	<i>Siglec5</i>	-1.569313	0.189712
NM_009230.3	<i>Soat1</i>	-0.629950	0.006853
NM_146064.1	<i>Soat2</i>	-0.994748	0.496803
NM_011480.1	<i>Srebf1</i>	-0.402164	0.063383
NM_011604.3	<i>Tlr6</i>	-0.710518	0.012207
NM_001025250.3	<i>Vegfa</i>	-0.577743	0.007533

**Supplementary Table 2**

List of genes that were significantly differentially expressed (adj. p. val < 0.05) between 16 weeks HFCD-fed *Trem1*<sup>+/+</sup> *Apoe*<sup>-/-</sup> vs. *Trem1*<sup>-/-</sup> *Apoe*<sup>-/-</sup> mice

RefSeqID	symbol	logFC	adj.P.Val	RefSeqID	symbol	logFC	adj.P.Val
NM_021406.3	<i>Trem1</i>	-6.548570	0.000589	NM_009914.4	<i>Ccr3</i>	-3.754729	0.026021
NM_013545.2	<i>Ptpn6</i>	-1.315980	0.000903	NM_010188.5	<i>Fcgr3</i>	-0.712803	0.026021
NM_021704.3	<i>Cxcl12</i>	-0.970956	0.000903	NM_009911.3	<i>Cxcr4</i>	-0.992579	0.027832
NM_007572.2	<i>C1qa</i>	-0.912202	0.001407	NM_001113326.1	<i>Msr1</i>	-0.901083	0.028592
NM_001110323.1	<i>Klra7</i>	-3.782532	0.001423	NM_011827.3	<i>Hcst</i>	-1.752307	0.029092
NM_009851.2	<i>Cd44</i>	-0.766548	0.001423	NM_010576.3	<i>Itga4</i>	-0.628088	0.029092
NM_008528.4	<i>Blnk</i>	-1.140291	0.002526	NM_198958.2	<i>Nox3</i>	-2.618617	0.030037
NM_008397.3	<i>Itga6</i>	-0.993086	0.003698	NM_011905.2	<i>Tlr2</i>	-0.608692	0.030770
NM_008677.2	<i>Ncf4</i>	-0.979928	0.003698	NM_019494.1	<i>Cxcl11</i>	-2.505075	0.032061
NM_007807.2	<i>Cybb</i>	-0.962905	0.003698	NM_011095.2	<i>Lilrb3</i>	-0.968129	0.032061
NM_010233.1	<i>Fnl1</i>	-0.749615	0.003698	NM_009754.3	<i>Bcl2l1l</i>	-0.656498	0.032398
NM_007486.4	<i>Arhgd1b</i>	-0.730459	0.003698	NM_008337.1	<i>Ifng</i>	-1.147221	0.032478
NM_010130.1	<i>Emr1</i>	-1.094794	0.004017	NM_011693.2	<i>Vcam1</i>	-0.779884	0.032783
NM_009777.2	<i>C1qb</i>	-0.943235	0.004017	NM_009910.2	<i>Cxcr3</i>	-3.309227	0.036463
NM_009230.3	<i>Soat1</i>	-0.629950	0.006853	NM_019732.2	<i>Runx3</i>	-3.035197	0.040985
NM_031178.2	<i>Tlr9</i>	-1.117207	0.007283	NM_016960.1	<i>Ccl20</i>	-3.135620	0.041094
NM_010186.5	<i>Fcgr1</i>	-0.947866	0.007283	NM_011518.2	<i>Syk</i>	-0.654921	0.044742
NM_001042605.1	<i>Cd74</i>	-0.926043	0.007283	NM_013532.2	<i>Lilrb4</i>	-0.822303	0.047020
NM_011577.1	<i>Tgfb1</i>	-0.601625	0.007283	NM_008355.2	<i>Il13</i>	-2.196345	0.049654
NM_011610.3	<i>Tnfrsf1b</i>	-0.932845	0.007533	NM_008349.5	<i>Il10rb</i>	-0.493404	0.005406
NM_009369.4	<i>Tgfb1</i>	-0.644661	0.007533	NM_001037859.1	<i>Csflr</i>	-0.542986	0.007283
NM_008404.4	<i>Itgb2</i>	-1.002995	0.007630	NM_001025250.3	<i>Vegfa</i>	-0.577743	0.007533
NM_010185.4	<i>Fcer1g</i>	-1.104990	0.007717	NM_010798.2	<i>Mif</i>	-0.574122	0.008491
NM_009142.3	<i>Cx3cl1</i>	-0.841099	0.007717	NM_010508.1	<i>Ifnar1</i>	-0.366953	0.009241
NM_009593.1	<i>Abcg1</i>	-0.903426	0.007975	NM_009812.2	<i>Casp8</i>	-0.343917	0.009241
NM_009853.1	<i>Cd68</i>	-1.021322	0.008107	NM_007544.3	<i>Bid</i>	-0.583093	0.011645
NM_001113474.1	<i>Lair1</i>	-1.077760	0.008895	NM_009982.2	<i>Ctsc</i>	-0.410117	0.011920
NM_011662.2	<i>Tyrobp</i>	-0.987466	0.008895	NM_009371.2	<i>Tgfb2</i>	-0.395849	0.015089
NM_001111021.1	<i>Runx1</i>	-0.895071	0.008895	NM_016923.1	<i>Ly96</i>	-0.477177	0.016295
NM_010378.2	<i>H2-Aa</i>	-0.806005	0.009241	NM_001113553.1	<i>Irak2</i>	-0.305006	0.018486
NM_001170632.1	<i>Fcamr</i>	-3.296913	0.009272	NM_008720.2	<i>Npc1</i>	-0.377297	0.018592
NM_001033122.3	<i>Cd69</i>	-3.300441	0.009388	NM_008823.3	<i>Cfp</i>	-0.577043	0.020476
NM_008604.3	<i>Mme</i>	-0.884249	0.009915	NM_013454.3	<i>Abca1</i>	-0.548182	0.020914
NM_010382.2	<i>H2-Eb1</i>	-1.015780	0.010136	NM_011113.3	<i>Plaur</i>	-0.542416	0.022895
NM_011355.1	<i>Sfp1</i>	-0.809824	0.010667	NM_011640.1	<i>Trp53</i>	-0.382943	0.028214
NM_021281.2	<i>Ctss</i>	-1.030240	0.011031	NM_009807.2	<i>Casp1</i>	-0.590112	0.029092
NM_013640.3	<i>Psmb10</i>	-0.688050	0.011031	NM_009046.2	<i>Relb</i>	-0.365291	0.030723
NM_001082960.1	<i>Itgam</i>	-1.004610	0.011920	NM_001163554.1	<i>Pou2f2</i>	-0.597801	0.035774
NM_011604.3	<i>Tlr6</i>	-0.710518	0.012207	NM_001164735.1	<i>Crlf2</i>	-0.419599	0.036463
NM_001271430.1	<i>Cd82</i>	-0.607500	0.012303	NM_009778.2	<i>C3</i>	-0.418029	0.036463
NM_010745.2	<i>Ly86</i>	-0.762518	0.015393	NM_010515.1	<i>Igf2r</i>	-0.284202	0.036463
NM_011638.3	<i>Tfrc</i>	-1.094356	0.016295	NM_010549.3	<i>Il11ra1</i>	-0.512377	0.038363
NM_001038604.1	<i>Clec5a</i>	-1.069723	0.016295	NM_153098.3	<i>Cd109</i>	-0.402790	0.041094
NM_008348.2	<i>Il10ra</i>	-1.138435	0.016696	NM_133990.4	<i>Il13ra1</i>	-0.419770	0.046369
NM_012057.3	<i>Irf5</i>	-0.666845	0.018486	NM_019777.3	<i>Ikbke</i>	-0.345539	0.047020
NM_031254.2	<i>Trem2</i>	-0.895160	0.019268	NM_001048177.1	<i>Jak2</i>	0.347616	0.032061
NM_007649.4	<i>Cd48</i>	-1.118095	0.019909	NM_011633.1	<i>Traf5</i>	0.360299	0.025435
NM_001043317.2	<i>Cd22</i>	-1.316593	0.020476	NM_007987.2	<i>Fas</i>	0.341247	0.020486
NM_011210.3	<i>Ptprc</i>	-0.843256	0.020486	NM_010578.1	<i>Itgb1</i>	0.385154	0.011645
NM_207105.2	<i>H2-Ab1</i>	-0.812375	0.020486	NM_009848.3	<i>Entpd1</i>	0.388919	0.009241
NM_001037177.1	<i>Nfate2</i>	-0.849600	0.022073	XM_356827.6	<i>C7</i>	0.634353	0.009241
NM_008873.2	<i>Plau</i>	-0.791118	0.022073	NM_008332.2	<i>Ifi2</i>	0.575927	0.007283
NM_001077189.1	<i>Fcgr2b</i>	-0.733583	0.022895	NM_011364.3	<i>Sh2d1a</i>	4.016440	0.006853
NM_009856.2	<i>Cd83</i>	-0.622932	0.022895	NM_008816.2	<i>Pecam1</i>	0.621827	0.003698
NM_013482.2	<i>Btk</i>	-0.921450	0.023260	NM_015760.4	<i>Nox4</i>	0.682014	0.000903
NM_008250.2	<i>Hlx</i>	-0.778719	0.023930				

**Supplementary Table 3**

**Maximum values of carotid intima-media thickness (IMT) according to the *TREMI* SNP rs2234237 genotype in the 421 CoLaus substudy participants.**

	<b>AA</b>	<b>AT</b>	<b>TT</b>	<b>p-value ANOVA</b>	<b>p-value additive effect</b>
N (% total)	340 (80.8)	75 (17.8)	6 (1.4)		
Left carotid					
Unadjusted	0.90±0.14	0.88±0.13	0.74±0.07	0.02	0.007
Adjusted <sup>§</sup>	0.90±0.01	0.89±0.02	0.75±0.05	0.02	0.006
Right carotid					
Unadjusted	0.85±0.15	0.82±0.12	0.77±0.05	0.14	0.14
Adjusted <sup>§</sup>	0.85±0.01	0.83±0.02	0.77±0.05	0.20	0.12

Results are expressed in mm and as mean ± standard deviation for unadjusted data or as adjusted mean ± standard error for multivariable-adjusted data. Statistical analysis by ANOVA and by linear regression supposing an additive genetic effect (qtl SNP command of Stata). <sup>§</sup> adjusted for gender, smoking status (never, former, current), age (continuous) and body mass index (continuous).

**Supplementary Table 4****Clinical characteristics of the 421 CoLaus substudy participants according to their *TREMI* SNP rs2234237 genotype.**

	<b>AA</b>	<b>AT</b>	<b>TT</b>	<b>P-value</b>
Sample size	340	75	6	
Women (%)	209 (61.5)	42 (56.0)	2 (33.3)	0.260
Age (years)	61.5 ± 5.3	60.6 ± 5.6	59.0 ± 5.2	0.253
BMI (kg/m <sup>2</sup> )	26.2 ± 4.4	25.9 ± 4.0	27.2 ± 5.5	0.718
BMI categories (%)				0.776
Normal	145 (42.7)	34 (45.3)	3 (50.0)	
Overweight	132 (38.8)	28 (37.3)	1 (16.7)	
Obese	63 (18.5)	13 (17.3)	2 (33.3)	
Smoking (%)				0.602
Never	144 (42.4)	31 (41.3)	2 (33.3)	
Former	127 (37.4)	33 (44.0)	2 (33.3)	
Current	69 (20.3)	11 (14.7)	2 (33.3)	
Blood pressure (mm Hg)				
Systolic	142 ± 21	144 ± 19	148 ± 27	0.592
Diastolic	85 ± 12	87 ± 12	89 ± 13	0.260

BMI, body mass index. Results are expressed as number of participants (or percentage) or as average ± standard deviation. Between-group comparisons using Fisher's exact test for categorical variables or analysis of variance for continuous variables.

## References

1. Choi, J.-H. *et al.* Flt3 signaling-dependent dendritic cells protect against atherosclerosis. *Immunity* **35**, 819–831 (2011).
2. Ensan, S. *et al.* Self-renewing resident arterial macrophages arise from embryonic CX3CR1+ precursors and circulating monocytes immediately after birth. *Nat Immunol* **17**, 159–168 (2015).