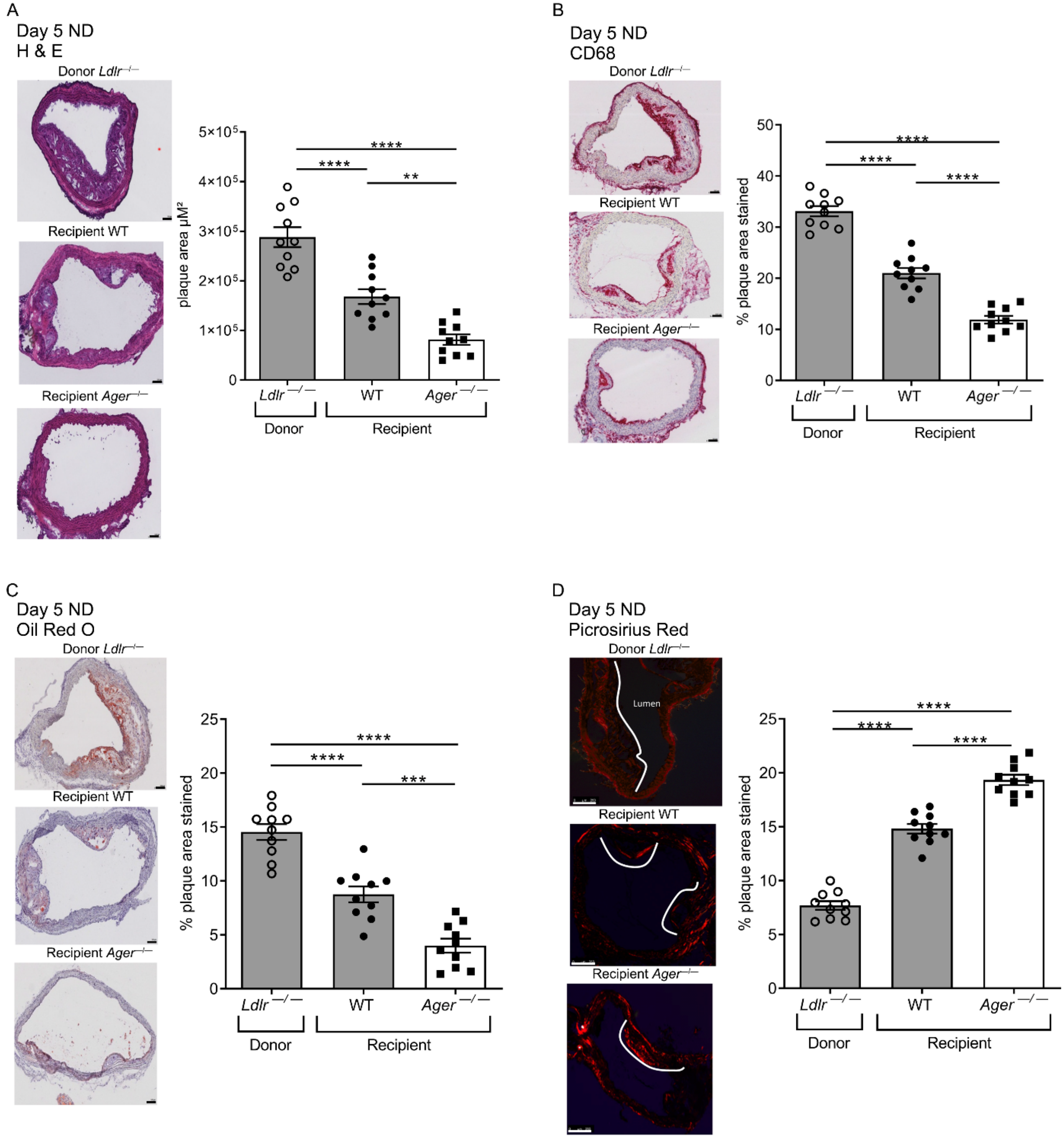
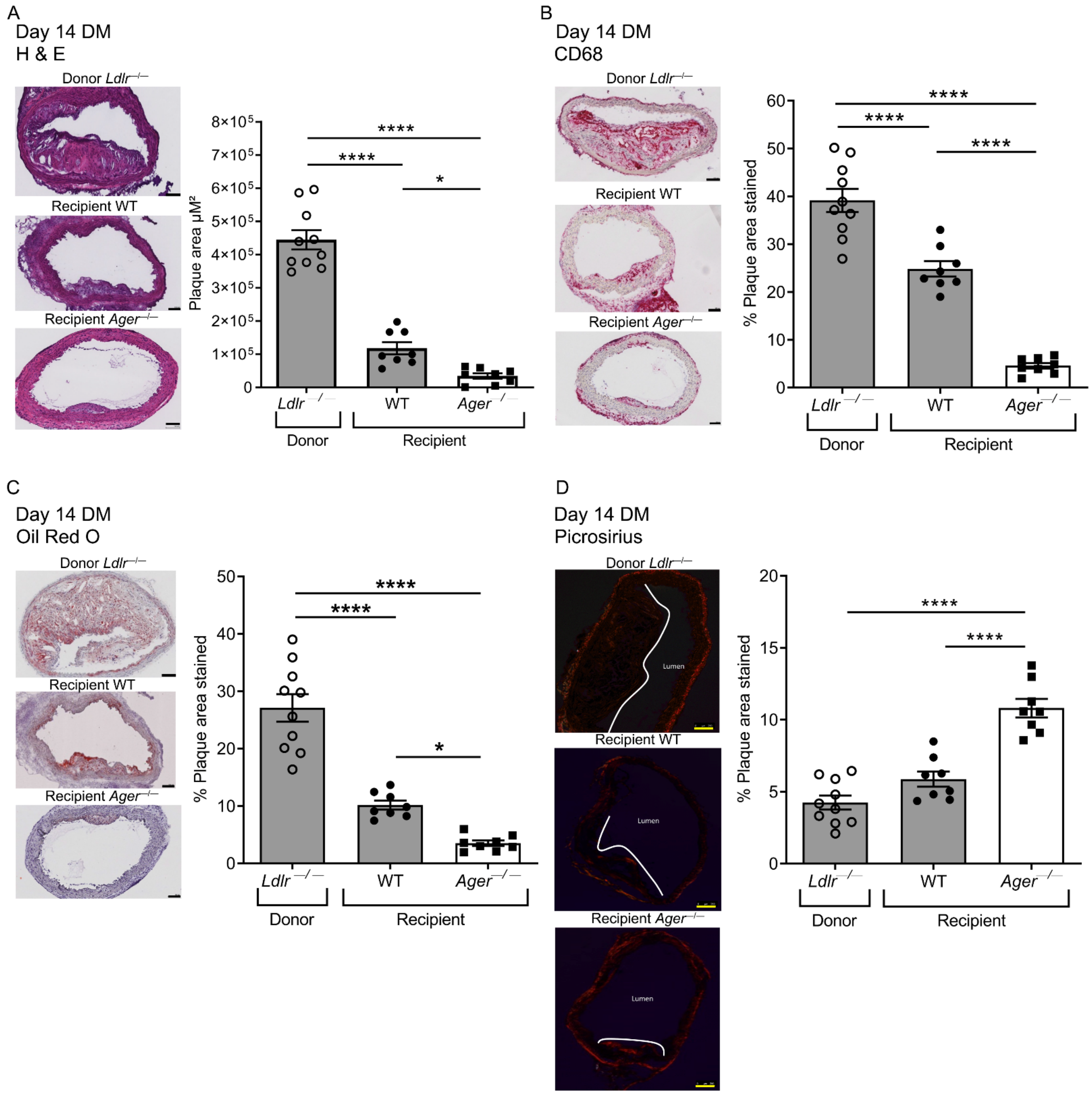
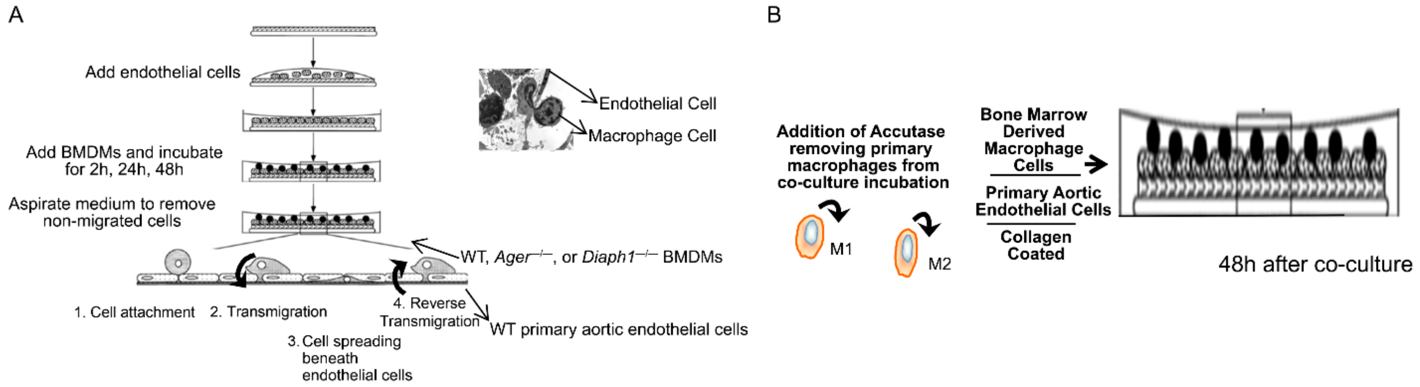


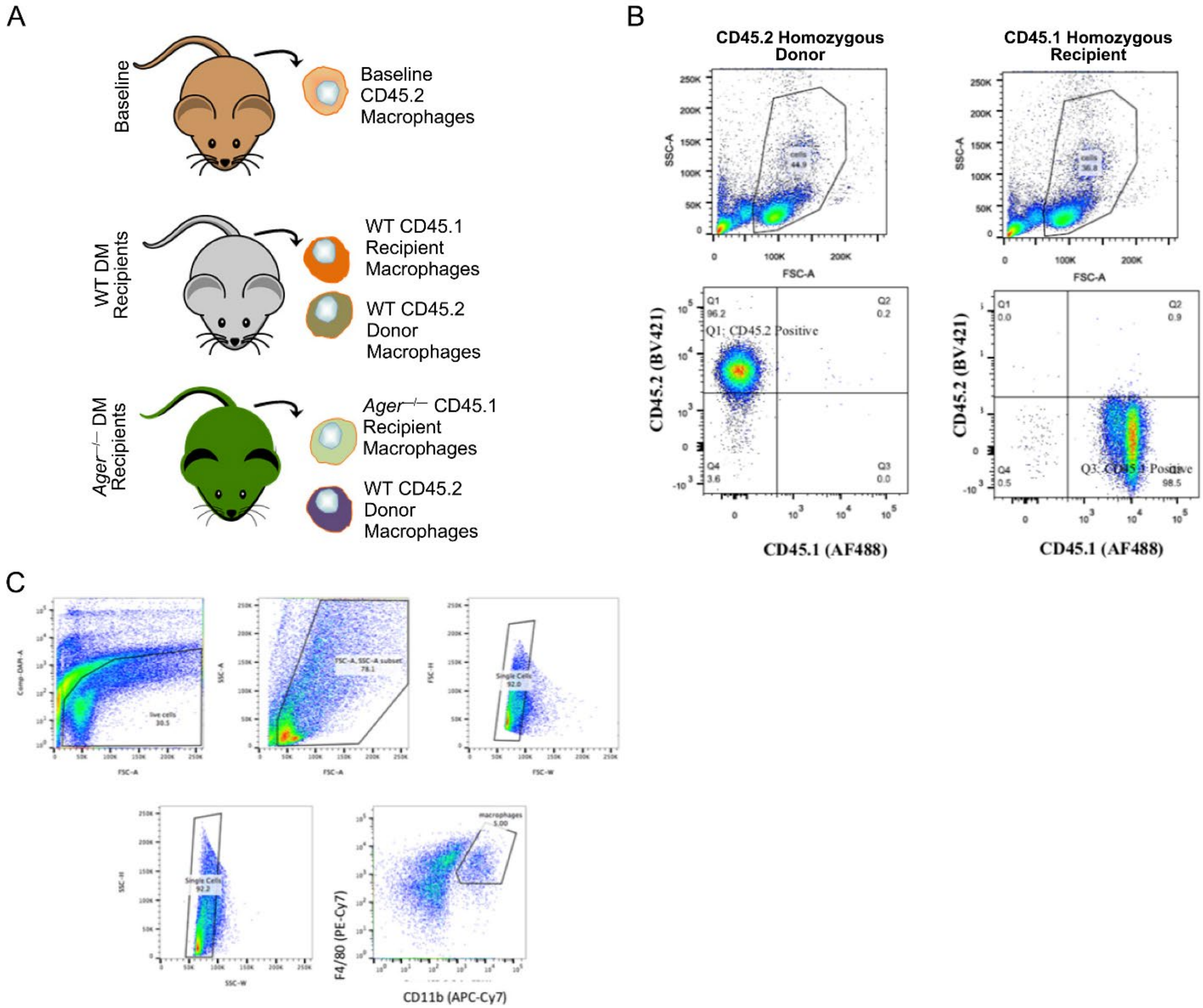
Supplement Figure 1. RAGE impairs regression of non-diabetic atherosclerosis. A-B-C-D) Aortic arch sections and quantification from non-diabetic *Ldlr*$^{-/-}$ donor/baseline mice, wild-type (WT), and *Ager*$^{-/-}$ recipient mice at day 5 post-transplantation were subjected to H&E (A), CD68 (B), Oil Red O (C) and Picrosirius Red staining (D) are shown. Scale bar: (A-C) 100 µm and (D) 250 µm. Representative images are shown and the mean ± SEM is reported from N=10 mice/group. One-way ANOVA with post hoc Tukey's multiple comparisons test was used to assess the group difference. $^{**}p < 0.01$, $^{***}p < 0.001$, $^{****}p < 0.0001$.



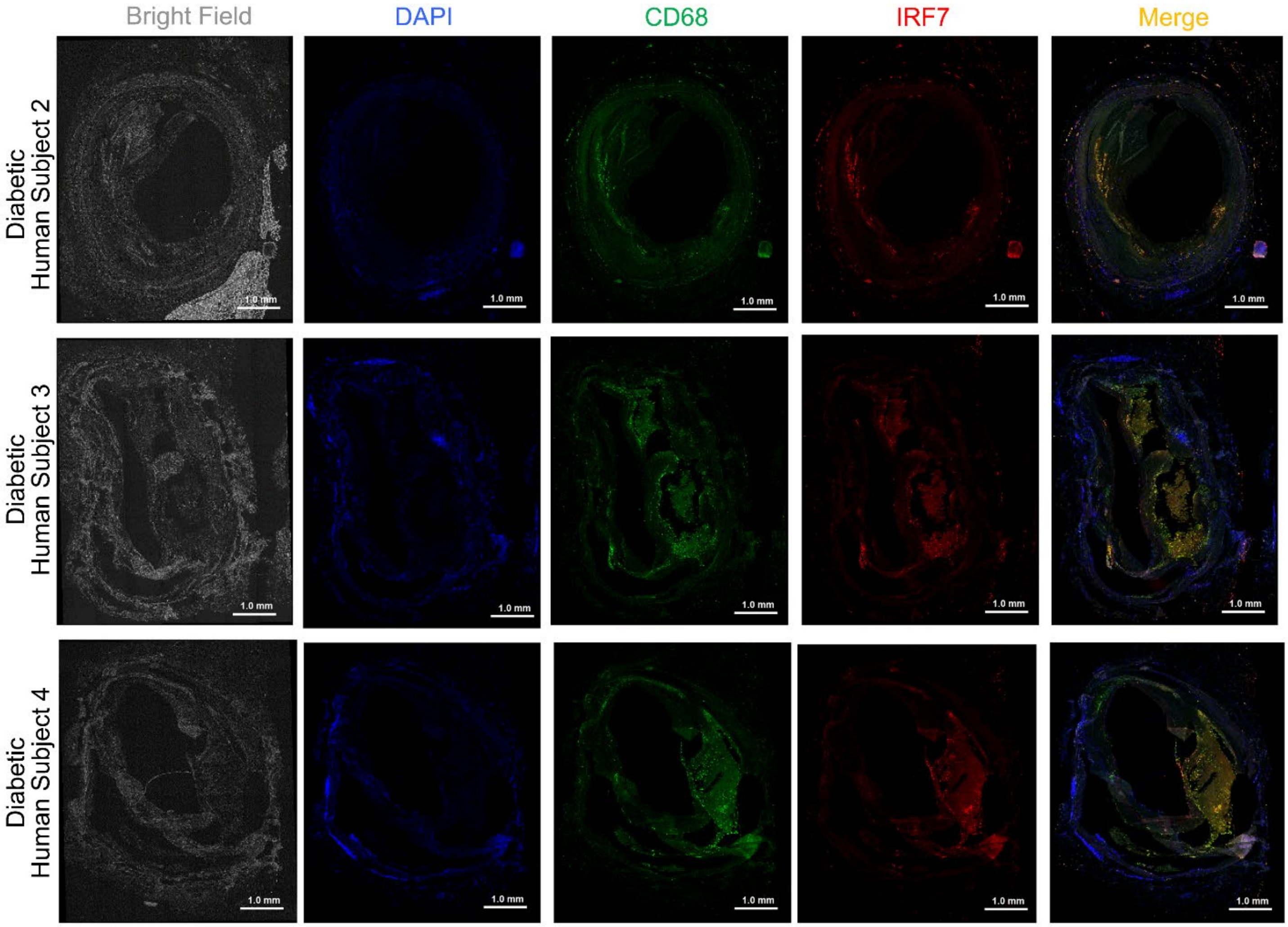
Supplement Figure 2. RAGE impairs diabetic atherosclerotic plaque regression at day 14 post-transplantation. A-B-C-D) H&E (A), CD68 (B), Oil Red O staining (C) and Picrosirius Red staining (D) of aortic arch transplant sections and their quantification were performed in diabetic *Ldlr*$^{-/-}$ non-transplanted mice, (donor, baseline), (WT), and *Ager*$^{-/-}$ diabetic recipient mice at day 14 post-transplantation. Scale bar: 100 μm. Representative images are shown and the mean ± SEM is reported from *Ldlr*$^{-/-}$ diabetic donors (N=10), WT diabetic recipients (N= 8), and *Ager*$^{-/-}$ diabetic recipients (N= 8). One-way ANOVA with post-hoc Tukey's multiple comparisons test was used to assess the group difference. *$p<0.05$, ****$p< 0.0001$.



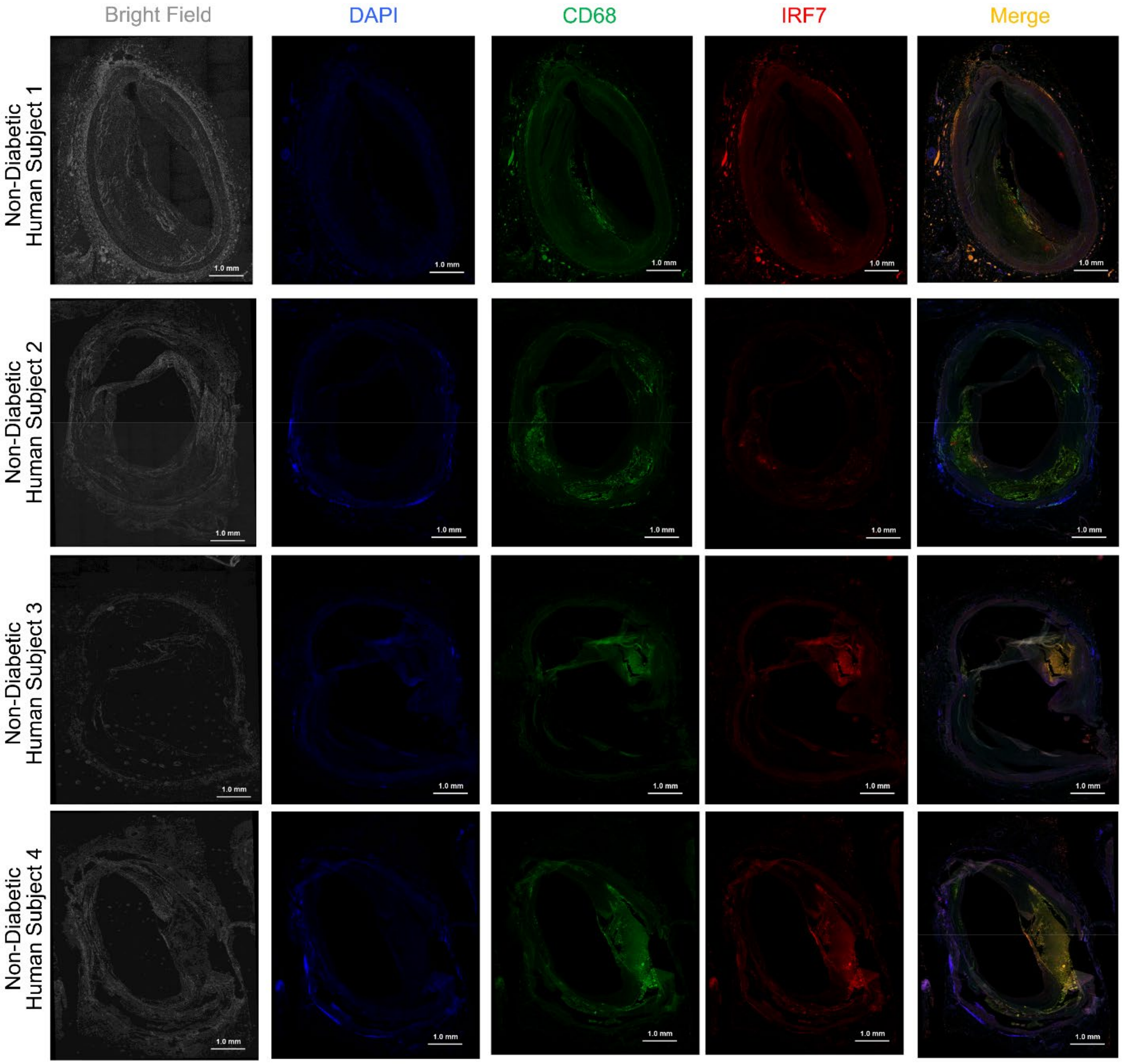
Supplement Figure 3. In vitro assays of reverse transendothelial migration. A) Schematic of macrophage reverse transendothelial migration assay using primary murine aortic endothelial cells (MAEC) and macrophages. Primary bone marrow derived macrophages (BMDMs) undergo (1) cell attachment, (2) transendothelial migration, (3) cell spreading beneath endothelial cells and (4) reverse transendothelial migration. **B)** Schematic of reverse transendothelial migration accutase macrophage removal assay.



Supplement Figure 4. Assessment of CD45.1 and CD45.2 macrophages in aortic arch transplanted atherosclerotic plaques. A) Schematic of CD45.1 recipients and CD45.2 donor. **B**) CD45.1 and CD45.2 population verification in peripheral blood samples from diabetic WT or *Ager*$^{-/-}$ recipients and diabetic *Ldlr*$^{-/-}$ donor mice, respectively. **C**) Gating strategy for the identification of donor CD45.2 and recipient CD45.1 macrophages.



Supplement Figure 5. IRF7 co-localizes with CD68 in diabetic human atherosclerotic plaques. Representative images from N=3 subjects are shown. Scale bar: 1.0 mm.



Supplement Figure 6. IRF7 co-localizes with CD68 in non-diabetic human atherosclerotic plaques. Representative images from N=4 non-diabetic subjects are shown Scale bar: 1.0 mm.

Table S1A. Biochemical Parameters: Non-Diabetic Donor / Non-Diabetic Recipient Mice

	Mouse Group		
Parameter	*Ldlr*$^{-/-}$ ND Donor$^{\#}$	WT ND Recipient	*Ager*$^{-/-}$ ND Recipient
Body Weight (g)	29±0.3	28±0.3	27±0.3*
Glucose (mg/dL)	168±2	162±3	146±4*^
Total Cholesterol (mg/dL)	1,012±16	110±6*	86±8*
Triglyceride (mg/dL)	62±2	27±2*	23±2*

\# receives Western Diet; all other groups receive standard chow diet
ND = Non-Diabetic
Values represent Mean±SEM

* Donor versus Recipient
^ WT recipient versus *Ager*$^{-/-}$ recipient
*, ^ $P<0.05$

Table S1B. Correlation between Atherosclerotic Lesion Area (H&E staining) and Total Cholesterol Levels in Non-diabetic Donor and Non-diabetic Recipient Mice.

Genotype/Condition	**Correlation Coefficient/P-value**
Ldlr$^{-/-}$ Donor	0.56/0.09
WT Recipient	0.66/0.04*
Ager$^{-/-}$ Recipient	0.61/0.058

* $P<0.05$

Table S2. Number of Reactome Gene Sets for each comparison with CAMERA (FDR≤0.05).

Comparison		Highly ranked Reactome Gene Sets	Detailed in
C1	WT Recipient **versus** *Ldlr*$^{-/-}$ Donor	12	Table S3
C2	*Ager*$^{-/-}$ Recipient **versus** *Ldlr*$^{-/-}$ Donor	16	Table S4
C3	*Ldlr*$^{-/-}$ Donor→ *Ager*$^{-/-}$ **versus** *Ldlr*$^{-/-}$ Donor→ WT	119	Table S5
C4	*Ager*$^{-/-}$ Recipient **versus** WT Recipient	4	Table 4

Table S3. Reactome Gene sets in a WT recipient environment vs. untransplanted *Ldlr*$^{-/-}$ donor using CAMERA with a FDR≤0.05 (Comparison 1, C1).

Gene set	Direction	P-value	FDR
Glucose Metabolism	↑	1.4E-07	8.0E-05
Complement Cascade	↓	1.8E-07	8.4E-05
Glycolysis	↑	9.1E-05	4.8E-05
Activation of Chaperone Genes by Atf6 Alpha	↓	2.2E-05	4.0E-03
Gluconeogenesis	↑	3.2E-05	5.0E-03
Activation of Chaperones by Atf6 Alpha	↓	6.7E-05	9.1E-03
Translocation of Zap 70 to Immunological Synapse	↓	1.4E-04	0.017
Perk Regulated Gene Expression	↓	1.7E-04	0.018
Regulation of Complement Cascade	↓	2.3E-04	0.021
Phosphorylation of Cd3 and TCR Zeta Chains	↓	3.5E-04	0.030
Interaction between L1 and Ankyrins	↓	4.2E-04	0.031
Chylomicron Mediated Lipid Transport	↑	8.0E-04	0.049

Table S4. Reactome Gene sets in recipient macrophages devoid of *Ager* environment vs. untransplanted *Ldlr*$^{-/-}$ donor using CAMERA with a FDR≤0.05 (Comparison 2, C2).

Gene set	Direction	P-Value	FDR
Glycolysis	↑	2.3E-11	1.8E-08
Glucose Metabolism	↑	4.6E-09	2.4E-06
Complement Cascade	↓	8.5E-07	2.2E-04
Translocation of Zap 70 To Immunological Synapse	↓	1.5E-06	3.6E-04
Gluconeogenesis	↑	7.2E-06	1.1E-03
Phosphorylation of Cd3 and Tcr Zeta Chains	↓	9.9E-06	1.3E-03
Interferon Gamma Signaling	↓	2.4E-05	2.5E-03
Activation of Chaperone Genes by Atf6 Alpha	↓	1.8E-04	0.012
Synthesis And Interconversion of Nucleotide Di and Triphosphates	↑	2.0E-04	0.012
Generation Of Second Messenger Molecules	↓	2.5E-04	0.014
Interferon Alpha Beta Signaling	↓	2.7E-04	0.015
Perk Regulated Gene Expression	↓	2.7E-04	0.015
Metabolism of Nucleotides	↑	2.9E-04	0.015
Activation of Chaperones by Atf6 Alpha	↓	3.0E-04	0.015
Regulation of Complement Cascade	↓	3.9E-04	0.019
Nef Mediated Downregulation of MHC Class I Complex Cell Surface Expression	↓	1.3E-03	0.045

Table S5. Reactome Gene sets in *Ager*$^{-/-}$ Donor macrophages vs. WT recipient environment using CAMERA with a FDR≤0.05 (Comparison 3, C3).

Gene set	Direction	P-value	FDR
Peptide Chain Elongation	↑	1.9E-15	9.0E-12
Influenza Viral RNA Transcription	↑	2.6E-14	3.0E-11
Srp dependent Cotranslational Protein Targeting to Membrane	↑	6.1E-13	5.7E-10
3'UTR Mediated Translational Regulation	↑	3.9E-12	3.1E-09
Respiratory Electron Transport ATP Synthesis by Chemiosmotic coupling And Heat Production by Uncoupling Proteins	↑	9.3E-12	6.3E-09
Respirator Electron Transport	↑	3.8E-11	2.3E-08
Nonsense-Mediated Decay Enhanced by the Exon Junction Complex	↑	4.4E-11	3.2E-08
Influenza Life Cycle	↑	1.8E-10	6.4E-08
Translation	↑	6.7E-10	1.7E-07
Collagen Formation	↓	8.3E-10	2.0E-07
Formation of the Ternary Complex and Subsequently the 43S Complex	↑	2.7E-09	4.6E-07
Extracellular Matrix Organization	↓	1.3E-08	1.7E-06
TCA Cycle and Respiratory Electron Transport	↑	2.9E-08	3.7E-06
Metabolism of mRNA	↑	1.8E-07	1.4E-05
Activation of the mRNA Binding of the Cap Binding Complex and Eifs and Subsequent Binding to 43S	↑	5.4E-07	3.1E-05
Metabolism of mRNA	↑	6.0E-07	3.3E-05
NCAM1 interactions	↓	1.0E-06	4.6E-05
M G1 Transition	↑	5.8E-06	1.8E-04
Assembly of the Pre Replicative Complex	↑	6.6E-06	2.0E-04
Yap1 and Wwtr1 Stimulated Gene Expression	↓	9.7E-06	2.7E-04
Cdt1 Association with the Cdc6 Orc Origin Complex	↑	1.5E-05	3.7E-04
Autodegradation of the E3 Ubiquitin Ligase Cop1	↑	1.7E-05	4.0E-04
Cdk Mediated Phosphorylation and Removal of Cdc6	↑	2.7E-05	6.0E-04
Synthesis of DNA	↑	3.1E-05	6.7E-04
Platelet Adhesion to Exposed Collagen	↓	3.8E-05	7.7E-04
Orc1 Removal from Chromatin	↑	4.1E-05	8.2E-04
Regulation of Mitotic Cell Cycle	↑	5.0E-05	9.6E-04
Scf Beta Trcp Mediated Degradation of Emi1	↑	6.3E-05	1.2E-03
Integrin Cell Surface Interactions Apc C Cdc20 Mediated	↓	6.4E-05	1.2E-03
Degradation of Mitotic Proteins	↑	6.6E-05	1.2E-03
Signaling by BMP	↓	6.9E-05	1.3E-03
Vif Mediated Degradation of Apobec3G	↑	7.2E-05	1.3E-03
S Phase	↑	7.4E-05	1.3E-03
Scfskp2 Mediated Degradation of P27P21	↑	8.5E-05	1.5E-03
Il6 Signaling	↓	1.1E-04	1.8E-03
ApcC Cdh1 Mediated Degradation of Cdc20 and Other Apc C Cdh1 targeted proteins in Late Mitosis Early G1	↑	1.2E-04	2.0E-03
RNA Pol1 Promoter Opening	↑	1.3E-04	2.0E-03
P53 Dependent G1 S DNA Damage Checkpoint	↑	1.5E-04	2.3E-03

Mitotic G1 S Phases	↑	1.6E-04	2.4E-03
NCAM signaling for neurite Outgrowth	↓	1.6E-04	2.5E-03
G1 S Transition	↑	1.8E-04	2.7E-03
Meiotic Recombination	↑	1.9E-04	2.7E-03
RNA Pol I Transcription	↑	2.0E-04	2.8E-03
Formation of ATP by Chemiosmotic Coupling	↑	2.0E-04	2.8E-03
RNA Pol 1 RNA Pol III and Mitochondrial Transcription	↑	2.0E-04	2.8E-03
Autodegradation of Cdh1 by Cdh1 Apc C	↑	2.2E-04	3.0E-03
P53 Dependent G1 DNA Damage Response	↑	2.2E-04	3.0E-03
Mitotic M M G1 Phases	↑	2.5E-04	3.3E-03
DNA Replication	↑	2.5E-04	3.4E-03
Packaging of Telomere Ends	↑	2.9E-04	3.8E-03
Rora Activates Circadian Expression	↓	3.0E-04	3.8E-03
Destabilization of mRNA by Auf1 Hnrnp D0	↑	3.2E-04	4.0E-03
Circadian Expression of Expression By Rev Erba	↓	3.5E-04	4.3E-03
DNA Repair	↑	3.6E-04	4.4E-03
Signaling by FGFR mutants	↓	3.9E-04	4.6E-03
Amyloids	↑	4.1E-04	4.8E-03
Cyclin E associated events during G1 S Transition	↑	5.0E-04	5.6E-03
Formation of the HIV1 Early Elongation Complex	↑	5.2E-04	5.8E-03
Regulation of Ornithine Decarboxylase Odc	↑	5.6E-04	6.0E-03
Fanconi Anemia pathway	↑	6.7E-04	6.8E-03
Telomere Maintenance	↑	7.8E-04	7.7E-03
Formation of RNA Poli II Elongation complex	↑	8.0E-04	7.9E-03
Apoptosis Induced DNA Fragmentation	↑	8.2E-04	8.1E-03
Signal Attenuation	↓	8.2E-04	8.1E-03
Transcription	↑	9.1E-04	8.7E-03
Signaling by PDGF	↓	9.2E-04	8.7E-03
Signaling by WNT	↑	9.6E-04	9.0E-03
Elongation Arrest and Recovery	↑	1.4E-03	0.01
BMAL1 Clock NPAS2 Activates Circadian Expression	↓	1.5E-03	0.01
Cross Presentation of Soluble Antigens Endosomes	↑	1.5E-03	0.01
Regulation of Insulin Like Growth Factor Igf activity by insulin like growth factor binding proteins Igfbps	↓	1.5E-03	0.01
Regulation of apoptosis	↑	1.6E-03	0.01
HIV Life Cycle	↑	2.1E-03	0.02
Terminatoin of O glycan Biosynthesis	↓	2.1E-03	0.02
Abortive Elongation of HIV1 Transcript in the absence of TAT	↑	2.1E-03	0.02
MRNA splicing minor pathway	↑	2.2E-03	0.02
Meiosis	↑	2.3E-03	0.02
Notch Hlh Transcription Pathway	↓	2.4E-03	0.02
Pre Notch Processing in Golgi	↓	2.4E-03	0.02
Formation of Transcription Coupled Ner Tc Ner Repair Complex	↑	2.4E-03	0.02
Signaling by FGFR1 mutants	↓	2.6E-03	0.02
RNA Pol Ii Pre Transcription Events	↑	2.7E-03	0.02

ER Phagosome Pathway	↑	2.8E-03	0.02
MRNA Capping	↑	2.8E-03	0.02
Viral Messenger RNA synthesis	↑	3.0E-03	0.02
Late Phase of HIV Life Cycle	↑	3.3E-03	0.02
Shc mediated cascade	↓	3.3E-03	0.02
Cell Surface Interactions at the Vascular Wall	↓	3.9E-03	0.03
Phase 1 functionalization of compounds	↓	4.1E-03	0.03
RNA Pol II Transcription Pre Initiation and Promoter Opening	↑	4.4E-03	0.03
Axon Guidance	↓	4.4E-03	0.03
Developmental Biology	↓	4.5E-03	0.03
Association of Licensing Factors with Pre Replicative Complex	↑	4.5E-03	0.03
Role of second messenger in Netrin 1 signaling	↓	4.5E-03	0.03
Nuclear Receptor Transcription Pathway	↓	4.8E-03	0.03
Gpvi Mediated Activation Cascade	↓	4.9E-03	0.03
Keratan sulfate biosynthesis	↓	5.4E-03	0.03
Meiotic synapsis	↑	5.5E-03	0.03
Activated point mutants of FGFR2	↓	5.7E-03	0.03
FGFR ligand binding and activation	↓	5.7E-03	0.03
O Linked glycosylation of mucins	↓	5.7E-03	0.03
Transcription coupled Ner Tc Ner	↑	5.9E-03	0.04
PI3K Events in Erbb2 signaling	↓	6.0E-03	0.04
Cell cycle checkpoints	↑	6.1E-03	0.04
A Tetrasaccharide Linker Sequence is Required for GAG synthesis	↓	6.1E-03	0.04
RNA Pol III Transcription from Type 3 promoter	↑	6.2E-03	0.04
Peptide ligand binding receptors	↓	6.3E-03	0.04
Regulation of MRNA Stability by Proteins that bind Au Rich elements	↑	6.5E-03	0.04
Cell Cycle Mitotic	↑	6.9E-03	0.04
Amino Acid and Oligopeptide Slc Transporters	↓	7.1E-03	0.04
Cell Cycle	↑	7.2E-03	0.04
PI3K Events in Erbb4 Signaling	↓	7.4E-03	0.04
Metabolism of Proteins	↑	7.5E-03	0.04
Traf6 Mediated IRF7 Activation	↓	7.9E-03	0.04
Nucleotide Excision Factor	↑	7.9E-03	0.04
Amino Acid Transport Across The Plasma Membrane	↓	8.1E-03	0.04
Deposition of new Cenpa Containing Nucleosomes at the centromere	↑	9.0E-03	0.05
Signaling by FGFR1 Fusion Mutants	↓	9.0E-03	0.05
TRAF3 Dependent IRF4 Activation Pathway	↓	9.5E-03	0.05

Table S6. Number of Differentially Expressed Genes by Distinct Criteria

Comparison	FDR≤0.05	p≤0.001, FDR≤0.2	Detail list in
C1 WT Recipient vs. *Ldlr*$^{-/-}$ Donor	219	268	Table S7
C2 *Ager*$^{-/-}$ Recipient vs. *Ldlr*$^{-/-}$ Donor	489	426	Table S8
C3 *Ager*$^{-/-}$ vs. WT on Donor	0	0	
C4 *Ager*$^{-/-}$ Recipient vs. WT Recipient	4	11	Table S9

Table S7. Differentially Expressed Genes on the WT Recipient macrophages vs. *Ldlr*$^{-/-}$ Not Transplanted macrophages. Comparison 1 (C1), p≤0.001 and FDR≤0.2.

SYMBOL	GENE NAME	log2FC	P.Value	fdr
Cd209b	CD209b antigen	-10.49	2.8E-08	2.5E-04
Mucl1	mucin-like 1	-8.86	2.9E-08	2.5E-04
C6	complement component 6	-10.26	5.7E-08	2.6E-04
Hspa1a	heat shock protein 1A	-2.62	6.2E-08	2.6E-04
Fgf9	fibroblast growth factor 9	-7.45	7.4E-08	2.6E-04
Hif1a	hypoxia inducible factor 1, alpha subunit	2.37	1.1E-07	3.0E-04
Enpep	glutamyl aminopeptidase	-9.28	1.2E-07	3.0E-04
Arg1	arginase, liver	7.85	2.6E-07	5.6E-04
Tmod1	tropomodulin 1	-9.16	3.6E-07	6.2E-04
Dnajb1	DnaJ heat shock protein family (Hsp40) member B1	-3.15	3.6E-07	6.2E-04
C2	complement component 2 (within H-2S)	-7.83	3.9E-07	6.2E-04
Gm45138	NA	-8.53	4.5E-07	6.5E-04
P3h2	prolyl 3-hydroxylase 2	-9.51	6.1E-07	7.5E-04
Vegfa	vascular endothelial growth factor A	3.65	6.2E-07	7.5E-04
Cd93	CD93 antigen	2.15	6.5E-07	7.5E-04
Gm4524	predicted gene 4524	-7.36	1.0E-06	1.1E-03
Thbs1	thrombospondin 1	3.48	1.2E-06	1.2E-03
Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)	-3.16	1.3E-06	1.2E-03
Jup	junction plakoglobin	-2.67	1.4E-06	1.3E-03
Themis	thymocyte selection associated	-7.62	1.7E-06	1.4E-03
Dnaja1	DnaJ heat shock protein family (Hsp40) member A1	-1.77	2.5E-06	2.0E-03
Gm26714	NA	-6.09	3.5E-06	2.6E-03
Hsph1	heat shock 105kDa/110kDa protein 1	-2.22	3.6E-06	2.6E-03
Ak4	adenylate kinase 4	6.86	3.7E-06	2.6E-03
Tox	thymocyte selection-associated high mobility group box	-6.52	3.7E-06	2.6E-03
Cdr2	cerebellar degeneration-related 2	-4.20	4.8E-06	3.2E-03
Tanc2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	-2.34	5.7E-06	3.7E-03
Spats2l	spermatogenesis associated, serine-rich 2-like	-6.70	7.4E-06	4.5E-03
Cd209f	CD209f antigen	-8.43	7.7E-06	4.5E-03
Aldoa	aldolase A, fructose-bisphosphate	1.85	7.8E-06	4.5E-03
Thrb	thyroid hormone receptor beta	-7.25	8.5E-06	4.8E-03
Cd209d	CD209d antigen	-6.70	9.4E-06	5.0E-03
Tshz3	teashirt zinc finger family member 3	-7.67	9.7E-06	5.0E-03
Cd209g	CD209g antigen	-8.85	1.0E-05	5.0E-03
Pmp22	peripheral myelin protein 22	-3.46	1.1E-05	5.0E-03
Hspa1b	heat shock protein 1B	-2.81	1.1E-05	5.0E-03
AC159502.1	NA	5.86	1.1E-05	5.0E-03
C4b	complement component 4B (Chido blood group)	-2.95	1.1E-05	5.0E-03
Cd209e	CD209e antigen	-6.51	1.2E-05	5.3E-03
Mgl2	macrophage galactose N-acetyl-galactosamine specific lectin 2	-3.91	1.2E-05	5.4E-03
Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A member 1	-1.62	1.4E-05	6.0E-03

Klhl13	kelch-like 13	-6.72	1.5E-05	6.2E-03
Micall2	MICAL-like 2	6.20	1.5E-05	6.2E-03
Bst1	bone marrow stromal cell antigen 1	1.77	1.7E-05	6.7E-03
Saa3	serum amyloid A 3	6.11	1.9E-05	7.5E-03
Cd81	CD81 antigen	-2.21	2.0E-05	7.5E-03
Lck	lymphocyte protein tyrosine kinase	-6.38	2.2E-05	7.7E-03
Ank2	ankyrin 2, brain	-5.99	2.2E-05	7.7E-03
Epor	erythropoietin receptor	-6.48	2.3E-05	7.7E-03
Wnk2	WNK lysine deficient protein kinase 2	5.94	2.3E-05	7.7E-03
Camk4	calcium/calmodulin-dependent protein kinase IV	-6.62	2.4E-05	7.7E-03
Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	-6.52	2.4E-05	7.7E-03
Creb5	cAMP responsive element binding protein 5	-1.33	2.4E-05	7.7E-03
Mb21d2	Mab-21 domain containing 2	-6.20	2.4E-05	7.7E-03
Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	-3.73	2.5E-05	7.7E-03
AC108401.1	NA	7.21	2.5E-05	7.7E-03
Ephx1	epoxide hydrolase 1, microsomal	-3.82	2.6E-05	7.7E-03
Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	2.13	2.6E-05	7.7E-03
Slamf9	SLAM family member 9	-2.11	2.6E-05	7.7E-03
Cd8a	CD8 antigen, alpha chain	-6.02	2.6E-05	7.7E-03
F830016B08Rik	RIKEN cDNA F830016B08 gene	-5.27	2.8E-05	8.0E-03
Lifr	leukemia inhibitory factor receptor	-1.98	2.8E-05	8.0E-03
Jun	jun proto-oncogene	-1.38	3.0E-05	8.2E-03
Dst	dystonin	-2.18	3.0E-05	8.2E-03
Rai14	retinoic acid induced 14	2.31	3.1E-05	8.2E-03
Ldlr	low density lipoprotein receptor	3.96	3.1E-05	8.2E-03
Lilra5	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	-4.33	3.2E-05	8.2E-03
Itgam	integrin alpha M	0.98	3.5E-05	8.8E-03
B430306N03Rik	RIKEN cDNA B430306N03 gene	1.93	3.5E-05	8.9E-03
Gm38340	NA	-6.36	3.6E-05	8.9E-03
Naip1	NLR family, apoptosis inhibitory protein 1	6.23	3.7E-05	9.1E-03
Diras2	DIRAS family, GTP-binding RAS-like 2	-6.14	3.9E-05	9.3E-03
Kcnn3	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	6.71	4.5E-05	0.01
Ust	uronyl-2-sulfotransferase	-3.00	5.1E-05	0.01
Zbtb10	zinc finger and BTB domain containing 10	-2.33	5.1E-05	0.01
Pla2g2d	phospholipase A2, group IID	-8.70	5.2E-05	0.01
Spp1	secreted phosphoprotein 1	3.10	5.5E-05	0.01
Gm42972	NA	-6.18	5.6E-05	0.01
Pkm	pyruvate kinase, muscle	1.54	5.7E-05	0.01
Tslp	thymic stromal lymphopoietin	-5.85	5.8E-05	0.01
Tns1	tensin 1	-2.51	5.8E-05	0.01
Lif	leukemia inhibitory factor	5.60	5.9E-05	0.01
Abcc1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	1.13	6.0E-05	0.01
Ankrd37	ankyrin repeat domain 37	6.00	6.2E-05	0.01

Gpr155	G protein-coupled receptor 155	-2.23	6.4E-05	0.01
AC122426.1	NA	-5.74	6.5E-05	0.01
Hs3st3a1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	-5.41	6.9E-05	0.01
Chp2	calcineurin-like EF hand protein 2	-5.76	6.9E-05	0.01
Igf2r	insulin-like growth factor 2 receptor	1.83	7.1E-05	0.01
Ctsd	cathepsin D	1.71	7.1E-05	0.01
Prtn3	proteinase 3	5.53	7.1E-05	0.01
A4galt	alpha 1,4-galactosyltransferase	-6.58	7.1E-05	0.01
Ldha	lactate dehydrogenase A	1.59	7.2E-05	0.01
Rspo1	R-spondin 1	5.16	7.4E-05	0.01
Lat	linker for activation of T cells	-7.68	7.6E-05	0.01
Slc16a10	solute carrier family 16 (monocarboxylic acid transporters), member 10	1.14	8.0E-05	0.01
Ctse	cathepsin E	3.55	8.1E-05	0.01
Dnm1	dynamin 1	-4.82	8.2E-05	0.01
Rtn4rl1	reticulon 4 receptor-like 1	-4.21	8.4E-05	0.01
Hilpda	hypoxia inducible lipid droplet associated	2.77	8.5E-05	0.01
Arhgef5	Rho guanine nucleotide exchange factor (GEF) 5	-6.54	8.5E-05	0.01
Ehd3	EH-domain containing 3	-6.07	8.7E-05	0.01
Adam8	a disintegrin and metallopeptidase domain 8	2.01	8.7E-05	0.01
Fxyd2	FXYD domain-containing ion transport regulator 2	-4.96	9.0E-05	0.02
Ighm	immunoglobulin heavy constant mu	-1.88	9.2E-05	0.02
Pfkl	phosphofructokinase, liver, B-type	2.17	1.0E-04	0.02
Raet1e	retinoic acid early transcript 1E	4.93	1.0E-04	0.02
Sulf2	sulfatase 2	-1.25	1.0E-04	0.02
Adamtsl5	ADAMTS-like 5	-5.28	1.0E-04	0.02
Ikbke	inhibitor of kappaB kinase epsilon	2.74	1.1E-04	0.02
Tppp	tubulin polymerization promoting protein	-6.22	1.2E-04	0.02
Il1rl1	interleukin 1 receptor-like 1	-4.03	1.2E-04	0.02
Epcam	epithelial cell adhesion molecule	-5.58	1.3E-04	0.02
Cd163	CD163 antigen	-3.38	1.3E-04	0.02
Slc39a4	solute carrier family 39 (zinc transporter), member 4	5.94	1.3E-04	0.02
Mat2a	methionine adenosyltransferase II, alpha	-1.21	1.3E-04	0.02
Siglech	sialic acid binding Ig-like lectin H	-6.21	1.4E-04	0.02
1810011O10Rik	RIKEN cDNA 1810011O10 gene	-7.32	1.5E-04	0.02
Cd6	CD6 antigen	-5.19	1.6E-04	0.02
Gm4951	predicted gene 4951	-4.99	1.6E-04	0.02
Prdx5	peroxiredoxin 5	2.21	1.7E-04	0.02
Snx18	sorting nexin 18	1.07	1.7E-04	0.02
Fam20c	family with sequence similarity 20, member C	2.56	1.8E-04	0.02
AF529169	cDNA sequence AF529169	-5.40	1.8E-04	0.03
Fabp7	fatty acid binding protein 7, brain	5.58	1.8E-04	0.03
Ablim3	actin binding LIM protein family, member 3	-5.81	1.8E-04	0.03
Mxi1	MAX interactor 1, dimerization protein	1.38	1.9E-04	0.03
Lyve1	lymphatic vessel endothelial hyaluronan receptor 1	-4.80	1.9E-04	0.03
Eno1	enolase 1, alpha non-neuron	1.46	1.9E-04	0.03

Gm26686	NA	5.30	2.0E-04	0.03
C230031I18Rik	RIKEN cDNA C230031I18 gene	-5.49	2.0E-04	0.03
Gm8995	predicted gene 8995	-1.04	2.0E-04	0.03
Lix1	limb and CNS expressed 1	-4.83	2.0E-04	0.03
Plin2	perilipin 2	1.19	2.0E-04	0.03
Plin2	perilipin 2	1.19	2.0E-04	0.03
Atf3	activating transcription factor 3	-1.11	2.1E-04	0.03
Negr1	neuronal growth regulator 1	-5.10	2.1E-04	0.03
Dpyd	dihydropyrimidine dehydrogenase	-4.51	2.1E-04	0.03
Psd3	pleckstrin and Sec7 domain containing 3	-2.15	2.1E-04	0.03
Vsig4	V-set and immunoglobulin domain containing 4	-6.44	2.1E-04	0.03
Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	2.46	2.2E-04	0.03
Kitl	kit ligand	-4.47	2.2E-04	0.03
Tgm2	transglutaminase 2, C polypeptide	1.70	2.2E-04	0.03
Egln3	egl-9 family hypoxia-inducible factor 3	6.93	2.2E-04	0.03
Ifi27l2a	interferon, alpha-inducible protein 27 like 2A	-1.99	2.2E-04	0.03
Gm15550	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase pseudogene	-5.98	2.3E-04	0.03
Tmem176a	transmembrane protein 176A	-1.32	2.3E-04	0.03
H2-Q6	histocompatibility 2, Q region locus 6	-2.83	2.3E-04	0.03
Zcchc14	zinc finger, CCHC domain containing 14	-2.62	2.4E-04	0.03
Gm6209	predicted gene 6209	5.36	2.4E-04	0.03
Gm20735	predicted gene, 20735	4.71	2.5E-04	0.03
Pygl	liver glycogen phosphorylase	2.24	2.6E-04	0.03
Adrb1	adrenergic receptor, beta 1	-6.00	2.7E-04	0.03
Pla2g7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	0.99	2.7E-04	0.03
Hsf2bp	heat shock transcription factor 2 binding protein	6.22	2.8E-04	0.03
Ctsl	cathepsin L	1.55	2.8E-04	0.03
Trpm1	transient receptor potential cation channel, subfamily M, member 1	-5.92	2.9E-04	0.03
Ptchd1	patched domain containing 1	-5.56	3.0E-04	0.03
Ric3	RIC3 acetylcholine receptor chaperone	-5.28	3.0E-04	0.03
Mast1	microtubule associated serine/threonine kinase 1	-5.46	3.0E-04	0.03
Gm38095	NA	-5.60	3.1E-04	0.03
Gm10441	predicted gene 10441	-5.62	3.1E-04	0.03
Gm45752	NA	5.41	3.1E-04	0.03
Slamf1	signaling lymphocytic activation molecule family member 1	-5.73	3.1E-04	0.03
Etv3	ets variant 3	-1.11	3.2E-04	0.03
Mill2	MHC I like leukocyte 2	-5.84	3.2E-04	0.03
St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	-2.77	3.2E-04	0.03
Klf4	Kruppel-like factor 4 (gut)	-1.46	3.3E-04	0.03
Stard13	StAR-related lipid transfer (START) domain containing 13	-5.80	3.3E-04	0.03
Gm16062	predicted gene 16062	-5.58	3.4E-04	0.03
Olr1	oxidized low density lipoprotein (lectin-like) receptor 1	3.43	3.4E-04	0.03
Gm42987	NA	6.18	3.6E-04	0.04

Hrh1	histamine receptor H1	-5.40	3.6E-04	0.04
Rem1	rad and gem related GTP binding protein 1	-5.76	3.6E-04	0.04
D730045B01Rik	RIKEN cDNA D730045B01 gene	-5.32	3.7E-04	0.04
Txn1	thioredoxin 1	1.58	3.7E-04	0.04
P4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	1.42	3.7E-04	0.04
AB124611	cDNA sequence AB124611	1.38	3.8E-04	0.04
Cd96	CD96 antigen	-4.63	3.8E-04	0.04
Nynrin	NYN domain and retroviral integrase containing	-4.54	3.8E-04	0.04
Slamf7	SLAM family member 7	-1.69	3.9E-04	0.04
Ccl12	chemokine (C-C motif) ligand 12	-2.40	4.0E-04	0.04
Cfh	complement component factor h	-1.88	4.1E-04	0.04
Mtus1	mitochondrial tumor suppressor 1	1.20	4.1E-04	0.04
Plekhg5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	-6.85	4.1E-04	0.04
Thsd4	thrombospondin, type I, domain containing 4	-5.94	4.2E-04	0.04
Creb3l4	cAMP responsive element binding protein 3-like 4	5.28	4.3E-04	0.04
Utp14b	UTP14B small subunit processome component	-1.70	4.3E-04	0.04
Tnfsf13b	tumor necrosis factor (ligand) superfamily, member 13b	-4.40	4.3E-04	0.04
Helz2	helicase with zinc finger 2, transcriptional coactivator	1.69	4.4E-04	0.04
Ddit4	DNA-damage-inducible transcript 4	3.20	4.4E-04	0.04
Pgd	phosphogluconate dehydrogenase	1.21	4.5E-04	0.04
Kcnt2	potassium channel, subfamily T, member 2	-5.99	4.5E-04	0.04
Uck2	uridine-cytidine kinase 2	2.12	4.5E-04	0.04
Gm45774	NA	-5.09	4.6E-04	0.04
2510039O18Rik	RIKEN cDNA 2510039O18 gene	1.18	4.6E-04	0.04
Gucy1a3	guanylate cyclase 1, soluble, alpha 3	-5.59	4.7E-04	0.04
Gm37354	NA	-5.66	4.8E-04	0.04
Crnde	colorectal neoplasia differentially expressed (non-protein coding)	-5.43	4.8E-04	0.04
Rfx2	regulatory factor X, 2 (influences HLA class II expression)	-3.19	4.8E-04	0.04
Plxna4	plexin A4	-2.43	4.9E-04	0.04
Mamdc2	MAM domain containing 2	-5.54	4.9E-04	0.04
Barx2	BarH-like homeobox 2	-5.07	5.0E-04	0.04
Hk2	hexokinase 2	1.42	5.0E-04	0.04
Soat1	sterol O-acyltransferase 1	1.00	5.1E-04	0.04
Osm	oncostatin M	1.99	5.1E-04	0.04
Hspb1	heat shock protein 1	-4.10	5.1E-04	0.04
Gm15326	predicted gene 15326	5.08	5.2E-04	0.04
Adam33	a disintegrin and metallopeptidase domain 33	-4.82	5.2E-04	0.04
Gclm	glutamate-cysteine ligase, modifier subunit	2.29	5.3E-04	0.04
Tcaf1	TRPM8 channel-associated factor 1	-5.97	5.4E-04	0.04
E430014B02Rik	RIKEN cDNA E430014B02 gene	-4.66	5.4E-04	0.04
Fn1	fibronectin 1	1.85	5.4E-04	0.04
N4bp1	NEDD4 binding protein 1	1.13	5.4E-04	0.04
Car11	carbonic anhydrase 11	-5.06	5.6E-04	0.05
CT009713.10	NA	5.59	5.7E-04	0.05

Gm37372	NA	5.19	5.8E-04	0.05
Retnla	resistin like alpha	-6.32	5.8E-04	0.05
Fgd2	FYVE, RhoGEF and PH domain containing 2	-1.40	6.0E-04	0.05
Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1	-1.49	6.3E-04	0.05
Tpi1	triosephosphate isomerase 1	1.71	6.3E-04	0.05
Nostrin	nitric oxide synthase trafficker	-1.92	6.4E-04	0.05
Cd74	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	-1.67	6.4E-04	0.05
Gm15270	predicted gene 15270	-4.73	6.4E-04	0.05
Ighd	immunoglobulin heavy constant delta	-4.21	6.6E-04	0.05
Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1	2.46	6.6E-04	0.05
Clec4d	C-type lectin domain family 4, member d	2.22	6.6E-04	0.05
Msr1	macrophage scavenger receptor 1	1.08	6.6E-04	0.05
Cd226	CD226 antigen	-5.36	6.6E-04	0.05
Arid5b	AT rich interactive domain 5B (MRF1-like)	1.16	6.7E-04	0.05
Slc11a1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	1.01	6.7E-04	0.05
Adam10	a disintegrin and metallopeptidase domain 10	0.92	6.9E-04	0.05
mt-Cytb	NA	-1.73	7.0E-04	0.05
Ank1	ankyrin 1, erythroid	-4.07	7.2E-04	0.05
Gm43112	NA	-4.86	7.3E-04	0.05
Hspa8	heat shock protein 8	-0.81	7.3E-04	0.05
Cadm1	cell adhesion molecule 1	-2.97	7.4E-04	0.05
Gm18646	adaptor protein complex AP-2, mu1 pseudogene	-4.72	7.4E-04	0.05
Emilin2	elastin microfibril interfacer 2	1.27	7.5E-04	0.05
Egln1	egl-9 family hypoxia-inducible factor 1	1.21	7.6E-04	0.06
Mylip	myosin regulatory light chain interacting protein	-1.53	7.7E-04	0.06
Pgk1	phosphoglycerate kinase 1	2.57	7.7E-04	0.06
Grap	GRB2-related adaptor protein	-3.28	7.8E-04	0.06
Nav3	neuron navigator 3	-5.29	8.0E-04	0.06
AC152827.1	NA	-4.34	8.0E-04	0.06
Fosb	FBJ osteosarcoma oncogene B	-1.22	8.2E-04	0.06
Rag1	recombination activating gene 1	-5.94	8.2E-04	0.06
Ptpn13	protein tyrosine phosphatase, non-receptor type 13	-5.44	8.3E-04	0.06
Cobll1	Cobl-like 1	-4.76	8.4E-04	0.06
H2-Eb1	histocompatibility 2, class II antigen E beta	-1.56	8.4E-04	0.06
Hlcs	holocarboxylase synthetase (biotin- [propriony-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)	-1.76	8.5E-04	0.06
Gm37215	NA	-4.58	8.5E-04	0.06
Cmah	cytidine monophospho-N-acetylneuraminic acid hydroxylase	-3.38	8.6E-04	0.06
Hepacam2	HEPACAM family member 2	-4.12	8.7E-04	0.06
Elavl4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	-4.71	8.8E-04	0.06
Rab6b	RAB6B, member RAS oncogene family	-2.02	8.8E-04	0.06
Oas2	2'-5' oligoadenylate synthetase 2	-1.18	8.8E-04	0.06
Spam1	sperm adhesion molecule 1	-4.30	9.1E-04	0.06
Slco2b1	solute carrier organic anion transporter family, member 2b1	-2.49	9.2E-04	0.06

mt-Co1	NA	-1.57	9.2E-04	0.06
2610203C22Rik	RIKEN cDNA 2610203C22 gene	-3.79	9.5E-04	0.06
Pgam1	phosphoglycerate mutase 1	3.63	9.5E-04	0.06
Ifi207	interferon activated gene 207	-1.00	9.6E-04	0.06
Marchf9	membrane-associated ring finger (C3HC4) 9	4.90	9.6E-04	0.06
Bank1	B cell scaffold protein with ankyrin repeats 1	-2.42	9.6E-04	0.06
Adssl1	adenylosuccinate synthetase like 1	2.05	9.6E-04	0.06
Frk	fyn-related kinase	-4.83	9.7E-04	0.06
Fsd2	fibronectin type III and SPRY domain containing 2	-4.59	9.9E-04	0.06

Table S8. Differentially Expressed Genes on the *Ager null* Recipient macrophages vs. *Ldlr*$^{-/-}$ not Transplanted macrophages. Comparison 2 (C2), $p \leq 0.001$ and FDR$\leq$0.2.

SYMBOL	GENE NAME	log2FC	P.Value	fdr
Cd209d	CD209d antigen	-10.53	2.8E-09	4.9E-05
Mucl1	mucin-like 1	-8.76	1.3E-08	8.1E-05
C6	complement component 6	-10.38	1.4E-08	8.1E-05
Hif1a	hypoxia inducible factor 1, alpha subunit	2.55	2.1E-08	9.1E-05
Arg1	arginase, liver	8.82	2.9E-08	1.0E-04
Ak4	adenylate kinase 4	8.27	4.0E-08	1.0E-04
Cd209f	CD209f antigen	-10.83	4.1E-08	1.0E-04
Cd209b	CD209b antigen	-9.57	5.0E-08	1.1E-04
Fgf9	fibroblast growth factor 9	-7.20	5.8E-08	1.1E-04
Pla2g7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	1.67	7.1E-08	1.2E-04
Tmem176a	transmembrane protein 176A	-2.39	8.3E-08	1.2E-04
Chp2	calcineurin-like EF hand protein 2	-9.13	8.3E-08	1.2E-04
Rtn4rl1	reticulon 4 receptor-like 1	-7.15	1.1E-07	1.4E-04
Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)	-4.40	1.2E-07	1.4E-04
F830016B08Rik	RIKEN cDNA F830016B08 gene	-7.33	1.4E-07	1.6E-04
Tanc2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	-2.95	2.0E-07	2.2E-04
Naip1	NLR family, apoptosis inhibitory protein 1	8.01	2.6E-07	2.6E-04
Gm20735	predicted gene, 20735	6.79	3.0E-07	2.6E-04
Thbs1	thrombospondin 1	3.73	3.0E-07	2.6E-04
Vegfa	vascular endothelial growth factor A	3.76	3.0E-07	2.6E-04
Enpep	glutamyl aminopeptidase	-8.22	3.7E-07	3.1E-04
Tmod1	tropomodulin 1	-8.46	4.6E-07	3.6E-04
Aldoa	aldolase A, fructose-bisphosphate	2.15	4.8E-07	3.6E-04
B430306N03Rik	RIKEN cDNA B430306N03 gene	2.48	5.3E-07	3.9E-04
Gm4524	predicted gene 4524	-7.25	6.1E-07	4.3E-04
Gm15487	NA	5.12	7.3E-07	4.7E-04
Hspa1a	heat shock protein 1A	-2.13	7.3E-07	4.7E-04
Gm26686	NA	7.18	8.0E-07	4.9E-04
Cdr2	cerebellar degeneration-related 2	-6.13	8.4E-07	5.0E-04
C4b	complement component 4B (Chido blood group)	-3.69	8.7E-07	5.1E-04
Lifr	leukemia inhibitory factor receptor	-2.53	9.4E-07	5.3E-04
AC154742.1	NA	7.87	1.0E-06	5.3E-04
Pkm	pyruvate kinase, muscle	1.97	1.0E-06	5.3E-04
Eno1	enolase 1, alpha non-neuron	2.05	1.1E-06	5.6E-04
Klhl13	kelch-like 13	-7.55	1.1E-06	5.7E-04
Sulf2	sulfatase 2	-1.73	1.2E-06	5.9E-04
Saa3	serum amyloid A 3	7.24	1.3E-06	6.2E-04
Tmem176b	transmembrane protein 176B	-1.89	1.4E-06	6.2E-04
Hmga1-rs1	high mobility group AT-hook I, related sequence 1	5.68	1.7E-06	7.4E-04
Dnajb1	DnaJ heat shock protein family (Hsp40) member B1	-2.64	1.8E-06	7.9E-04

Thrb	thyroid hormone receptor beta	-7.58	1.9E-06	7.9E-04
AC159502.1	NA	6.36	1.9E-06	8.0E-04
Ifi207	interferon activated gene 207	-1.67	2.0E-06	8.0E-04
Gpr155	G protein-coupled receptor 155	-3.54	2.4E-06	9.5E-04
Jup	junction plakoglobin	-2.41	2.5E-06	9.5E-04
C2	complement component 2 (within H-2S)	-6.65	2.5E-06	9.5E-04
Gm26714	NA	-5.99	2.6E-06	9.5E-04
Spats2l	spermatogenesis associated, serine-rich 2-like	-6.90	2.6E-06	9.5E-04
P3h2	prolyl 3-hydroxylase 2	-8.14	2.7E-06	9.5E-04
Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	2.43	2.8E-06	9.8E-04
Creb5	cAMP responsive element binding protein 5	-1.52	2.9E-06	1.0E-03
Adam8	a disintegrin and metallopeptidase domain 8	2.50	3.0E-06	1.0E-03
Gpi1	glucose phosphate isomerase 1	1.70	3.1E-06	1.0E-03
Rai14	retinoic acid induced 14	2.65	3.2E-06	1.0E-03
Igf2r	insulin-like growth factor 2 receptor	2.22	3.3E-06	1.0E-03
Pmp22	peripheral myelin protein 22	-3.67	3.4E-06	1.1E-03
Negr1	neuronal growth regulator 1	-6.62	3.4E-06	1.1E-03
Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	3.23	4.0E-06	1.2E-03
Itgam	integrin alpha M	1.11	4.1E-06	1.2E-03
Bst1	bone marrow stromal cell antigen 1	1.91	4.2E-06	1.2E-03
Gm45138	NA	-7.01	4.5E-06	1.3E-03
Etv3	ets variant 3	-1.56	4.6E-06	1.3E-03
Mgl2	macrophage galactose N-acetyl-galactosamine specific lectin 2	-5.19	4.7E-06	1.3E-03
Cd93	CD93 antigen	1.87	5.0E-06	1.4E-03
Tox	thymocyte selection-associated high mobility group box	-6.05	5.1E-06	1.4E-03
Lilra5	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	-5.61	5.2E-06	1.4E-03
Slamf9	SLAM family member 9	-2.35	5.7E-06	1.5E-03
Wnk2	WNK lysine deficient protein kinase 2	6.42	5.8E-06	1.5E-03
Oas2	2'-5' oligoadenylate synthetase 2	-1.83	5.9E-06	1.5E-03
Trbc2	T cell receptor beta, constant 2	-7.64	6.2E-06	1.5E-03
H2-Eb1	histocompatibility 2, class II antigen E beta	-2.41	6.2E-06	1.5E-03
Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	-7.41	6.3E-06	1.5E-03
Kcnn3	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	7.45	6.3E-06	1.5E-03
Rgs7bp	regulator of G-protein signalling 7 binding protein	-7.31	6.4E-06	1.5E-03
Cd74	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	-2.51	6.6E-06	1.5E-03
Ephx1	epoxide hydrolase 1, microsomal	-4.77	6.6E-06	1.5E-03
Pfkl	phosphofructokinase, liver, B-type	2.59	7.1E-06	1.6E-03
AC122426.1	NA	-6.45	7.1E-06	1.6E-03
Themis	thymocyte selection associated	-6.57	7.5E-06	1.6E-03
Cd209g	CD209g antigen	-8.52	7.6E-06	1.6E-03
Ighm	immunoglobulin heavy constant mu	-2.25	8.1E-06	1.7E-03
Fam20c	family with sequence similarity 20, member C	3.16	8.1E-06	1.7E-03

Micall2	MICAL-like 2	6.40	8.1E-06	1.7E-03
Cd209e	CD209e antigen	-6.41	8.6E-06	1.8E-03
Nwd1	NACHT and WD repeat domain containing 1	-7.00	8.9E-06	1.8E-03
Lck	lymphocyte protein tyrosine kinase	-6.47	9.0E-06	1.8E-03
Rab6b	RAB6B, member RAS oncogene family	-4.44	9.2E-06	1.8E-03
Cd81	CD81 antigen	-2.27	9.2E-06	1.8E-03
Cd209c	CD209c antigen	-6.31	9.3E-06	1.8E-03
Ldha	lactate dehydrogenase A	1.81	9.7E-06	1.9E-03
Zfhx3	zinc finger homeobox 3	-1.32	9.9E-06	1.9E-03
Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	-4.20	1.1E-05	2.1E-03
Epor	erythropoietin receptor	-6.46	1.2E-05	2.2E-03
Ctsl	cathepsin L	1.93	1.2E-05	2.3E-03
Sgpp1	sphingosine-1-phosphate phosphatase 1	-1.57	1.4E-05	2.5E-03
Zbtb10	zinc finger and BTB domain containing 10	-2.73	1.4E-05	2.6E-03
Reps2	RALBP1 associated Eps domain containing protein 2	-2.93	1.4E-05	2.6E-03
Cd8a	CD8 antigen, alpha chain	-6.01	1.5E-05	2.6E-03
Anxa3	annexin A3	1.73	1.5E-05	2.6E-03
Dst	dystonin	-2.24	1.5E-05	2.7E-03
Slamf7	SLAM family member 7	-2.23	1.6E-05	2.7E-03
Spp1	secreted phosphoprotein 1	3.33	1.6E-05	2.7E-03
Tgm2	transglutaminase 2, C polypeptide	2.04	1.6E-05	2.7E-03
Klf4	Kruppel-like factor 4 (gut)	-1.86	1.7E-05	2.8E-03
Fgd2	FYVE, RhoGEF and PH domain containing 2	-1.98	1.7E-05	2.8E-03
Mb21d2	Mab-21 domain containing 2	-6.05	1.8E-05	3.0E-03
Galnt12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12	-5.90	1.9E-05	3.1E-03
Gm45752	NA	6.37	1.9E-05	3.1E-03
Ifi27l2a	interferon, alpha-inducible protein 27 like 2A	-2.51	2.1E-05	3.3E-03
Patj	PATJ, crumbs cell polarity complex component	-5.94	2.1E-05	3.3E-03
Fn1	fibronectin 1	2.34	2.1E-05	3.3E-03
Cd6	CD6 antigen	-5.82	2.1E-05	3.3E-03
Kbtbd11	kelch repeat and BTB (POZ) domain containing 11	-3.21	2.2E-05	3.4E-03
Plin2	perilipin 2	1.39	2.2E-05	3.4E-03
Plin2	perilipin 2	1.39	2.2E-05	3.4E-03
Kcnt2	potassium channel, subfamily T, member 2	-7.31	2.2E-05	3.4E-03
Ikbke	inhibitor of kappaB kinase epsilon	3.04	2.3E-05	3.4E-03
Soat1	sterol O-acyltransferase 1	1.25	2.5E-05	3.7E-03
Ctsd	cathepsin D	1.81	2.6E-05	3.8E-03
Gm38340	NA	-6.26	2.7E-05	3.9E-03
Egln3	egl-9 family hypoxia-inducible factor 3	8.14	2.7E-05	3.9E-03
Tns1	tensin 1	-2.60	2.7E-05	3.9E-03
Abcc1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	1.18	2.8E-05	4.0E-03
Hilpda	hypoxia inducible lipid droplet associated	2.98	2.8E-05	4.0E-03
Vsig4	V-set and immunoglobulin domain containing 4	-7.29	2.9E-05	4.1E-03
Bcl11b	B cell leukemia/lymphoma 11B	-6.73	3.0E-05	4.2E-03

H2-Ab1	histocompatibility 2, class II antigen A, beta 1	-2.29	3.1E-05	4.3E-03
Gm9825	ribonucleic acid binding protein S1 pseudogene	4.28	3.1E-05	4.3E-03
Hspa1b	heat shock protein 1B	-2.49	3.2E-05	4.4E-03
Gm37844	NA	-6.18	3.2E-05	4.4E-03
Kitl	kit ligand	-5.38	3.3E-05	4.4E-03
Rpl10a-ps2	ribosomal protein L10A, pseudogene 2	5.24	3.4E-05	4.5E-03
Tppp	tubulin polymerization promoting protein	-6.58	3.4E-05	4.5E-03
Mtmr12	myotubularin related protein 12	-1.39	3.4E-05	4.5E-03
Axl	AXL receptor tyrosine kinase	-1.51	3.5E-05	4.5E-03
Gm37873	NA	-5.46	3.7E-05	4.8E-03
Pip4k2a	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	-1.07	3.9E-05	4.9E-03
Zfp383	zinc finger protein 383	-5.20	3.9E-05	4.9E-03
Aff3	AF4/FMR2 family, member 3	-6.14	3.9E-05	4.9E-03
Ctse	cathepsin E	3.73	3.9E-05	4.9E-03
Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	3.91	3.9E-05	4.9E-03
Plxna4	plexin A4	-3.77	4.0E-05	4.9E-03
Ank2	ankyrin 2, brain	-4.66	4.1E-05	5.0E-03
Adssl1	adenylosuccinate synthetase like 1	2.65	4.2E-05	5.1E-03
Stard8	START domain containing 8	-2.37	4.3E-05	5.1E-03
Pygl	liver glycogen phosphorylase	2.56	4.3E-05	5.1E-03
Ldlr	low density lipoprotein receptor	3.85	4.3E-05	5.1E-03
Rtn1	reticulon 1	-4.33	4.3E-05	5.1E-03
Tnxb	tenascin XB	-7.09	4.3E-05	5.1E-03
Prdx5	peroxiredoxin 5	2.41	4.4E-05	5.1E-03
Ust	uronyl-2-sulfotransferase	-2.87	4.4E-05	5.1E-03
Cd163	CD163 antigen	-3.64	4.5E-05	5.2E-03
Msr1	macrophage scavenger receptor 1	1.33	4.5E-05	5.2E-03
Gm26584	predicted gene, 26584	6.61	4.9E-05	5.5E-03
Gpr34	G protein-coupled receptor 34	-3.27	4.9E-05	5.5E-03
AF529169	cDNA sequence AF529169	-5.74	4.9E-05	5.5E-03
Gm43751	NA	-5.59	5.1E-05	5.6E-03
Slc39a4	solute carrier family 39 (zinc transporter), member 4	6.29	5.2E-05	5.7E-03
Gm45540	NA	-5.85	5.2E-05	5.8E-03
Ptchd1	patched domain containing 1	-6.12	5.3E-05	5.8E-03
Tpi1	triosephosphate isomerase 1	2.07	5.4E-05	5.8E-03
Hlcs	holocarboxylase synthetase (biotin- [propriony-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)	-2.46	5.5E-05	5.9E-03
Gm28096	NA	5.30	5.5E-05	6.0E-03
Fosb	FBJ osteosarcoma oncogene B	-1.53	5.7E-05	6.1E-03
Hs3st3a1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	-5.31	5.8E-05	6.1E-03
Ric3	RIC3 acetylcholine receptor chaperone	-5.84	5.9E-05	6.2E-03
Hsph1	heat shock 105kDa/110kDa protein 1	-1.70	5.9E-05	6.2E-03
Rag1	recombination activating gene 1	-7.11	6.1E-05	6.4E-03
A430106G13Rik	RIKEN cDNA A430106G13 gene	-5.50	6.2E-05	6.5E-03
Cxxc5	CXXC finger 5	-5.38	6.4E-05	6.6E-03

Serinc3	serine incorporator 3	-1.09	6.5E-05	6.6E-03
Cadm1	cell adhesion molecule 1	-4.85	6.6E-05	6.8E-03
Txn1	thioredoxin 1	1.79	6.8E-05	6.8E-03
Siglech	sialic acid binding Ig-like lectin H	-6.28	6.8E-05	6.8E-03
Faah	fatty acid amide hydrolase	-5.80	6.8E-05	6.8E-03
Clec10a	C-type lectin domain family 10, member A	-3.06	7.0E-05	6.9E-03
2610203C22Rik	RIKEN cDNA 2610203C22 gene	-4.75	7.1E-05	7.0E-03
Nfatc2	nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 2	-1.70	7.2E-05	7.0E-03
Prtn3	proteinase 3	5.47	7.3E-05	7.2E-03
Rfx2	regulatory factor X, 2 (influences HLA class II expression)	-4.57	7.4E-05	7.2E-03
Gm42994	NA	-5.26	7.5E-05	7.2E-03
Cd83	CD83 antigen	-1.93	7.5E-05	7.2E-03
Psd3	pleckstrin and Sec7 domain containing 3	-2.29	7.7E-05	7.3E-03
Mgarp	mitochondria localized glutamic acid rich protein	6.14	7.7E-05	7.3E-03
Prdx6	peroxiredoxin 6	1.82	7.7E-05	7.3E-03
Atf3	activating transcription factor 3	-1.18	7.8E-05	7.3E-03
Clec4d	C-type lectin domain family 4, member d	2.62	7.9E-05	7.4E-03
Pgd	phosphogluconate dehydrogenase	1.37	7.9E-05	7.4E-03
Gm6209	predicted gene 6209	5.71	8.1E-05	7.5E-03
Nynrin	NYN domain and retroviral integrase containing	-4.97	8.1E-05	7.5E-03
Slc16a10	solute carrier family 16 (monocarboxylic acid transporters), member 10	1.11	8.4E-05	7.7E-03
Skap1	src family associated phosphoprotein 1	-5.73	8.5E-05	7.7E-03
Gm37354	NA	-6.29	8.5E-05	7.7E-03
Dpyd	dihydropyrimidine dehydrogenase	-4.70	8.8E-05	8.0E-03
Car4	carbonic anhydrase 4	5.51	9.0E-05	8.0E-03
Lyve1	lymphatic vessel endothelial hyaluronan receptor 1	-5.79	9.3E-05	8.3E-03
Slc5a3	solute carrier family 5 (inositol transporters), member 3	-2.63	9.6E-05	8.6E-03
Pla2g2d	phospholipase A2, group IID	-7.77	9.8E-05	8.6E-03
Ccl12	chemokine (C-C motif) ligand 12	-2.73	9.8E-05	8.6E-03
Naaa	N-acylethanolamine acid amidase	-1.48	9.9E-05	8.7E-03
Slco2b1	solute carrier organic anion transporter family, member 2b1	-3.24	9.9E-05	8.7E-03
Pgk1	phosphoglycerate kinase 1	3.04	1.0E-04	8.7E-03
C230031I18Rik	RIKEN cDNA C230031I18 gene	-5.61	1.0E-04	8.7E-03
Slc11a2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	-1.81	1.0E-04	8.7E-03
Coro6	coronin 6	-5.93	1.0E-04	8.8E-03
Gm9655	heat shock protein 1 (chaperonin) pseudogene 5	-5.38	1.0E-04	8.8E-03
Utp14b	UTP14B small subunit processome component	-1.94	1.1E-04	9.4E-03
Slc16a14	solute carrier family 16 (monocarboxylic acid transporters), member 14	-5.41	1.1E-04	9.4E-03
Hsf3	heat shock transcription factor 3	-5.14	1.1E-04	9.4E-03
Gm42972	NA	-5.60	1.1E-04	9.5E-03
Hspb1	heat shock protein 1	-4.52	1.1E-04	9.5E-03
Ninl	ninein-like	-5.37	1.2E-04	9.6E-03
Xlr	X-linked lymphocyte-regulated	-4.57	1.2E-04	9.6E-03

Gm4951	predicted gene 4951	-4.86	1.2E-04	9.8E-03
Il1rl1	interleukin 1 receptor-like 1	-4.07	1.2E-04	9.9E-03
Pea15a	phosphoprotein enriched in astrocytes 15A	-1.75	1.2E-04	0.01
Epcam	epithelial cell adhesion molecule	-5.37	1.2E-04	0.01
Hepacam2	HEPACAM family member 2	-4.81	1.3E-04	0.01
Blnk	B cell linker	-2.07	1.3E-04	0.01
Mef2c	myocyte enhancer factor 2C	-1.54	1.3E-04	0.01
Hrh1	histamine receptor H1	-5.65	1.3E-04	0.01
Fabp7	fatty acid binding protein 7, brain	5.67	1.3E-04	0.01
Pgam1	phosphoglycerate mutase 1	4.20	1.3E-04	0.01
Thsd4	thrombospondin, type I, domain containing 4	-6.26	1.3E-04	0.01
Emilin2	elastin microfibril interfacer 2	1.46	1.3E-04	0.01
Gm15270	predicted gene 15270	-5.28	1.4E-04	0.01
Trbc1	T cell receptor beta, constant region 1	-6.20	1.5E-04	0.01
Itk	IL2 inducible T cell kinase	-6.92	1.5E-04	0.01
Raet1e	retinoic acid early transcript 1E	4.77	1.5E-04	0.01
Grap	GRB2-related adaptor protein	-3.94	1.5E-04	0.01
Clec4n	C-type lectin domain family 4, member n	2.18	1.6E-04	0.01
Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	-1.87	1.6E-04	0.01
Zfp248	zinc finger protein 248	-5.15	1.6E-04	0.01
Snx18	sorting nexin 18	1.06	1.6E-04	0.01
Adam33	a disintegrin and metallopeptidase domain 33	-5.52	1.6E-04	0.01
Mlph	melanophilin	-5.26	1.6E-04	0.01
Arhgef6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	-0.99	1.7E-04	0.01
Pld4	phospholipase D family, member 4	-1.02	1.8E-04	0.01
Capg	capping protein (actin filament), gelsolin-like	1.20	1.8E-04	0.01
F7	coagulation factor VII	4.68	1.8E-04	0.01
H2-M3	histocompatibility 2, M region locus 3	-2.17	1.8E-04	0.01
Lix1	limb and CNS expressed 1	-4.72	1.8E-04	0.01
Fat3	FAT atypical cadherin 3	-7.16	1.9E-04	0.01
Ajuba	ajuba LIM protein	-5.30	1.9E-04	0.01
Cbr2	carbonyl reductase 2	-3.30	1.9E-04	0.01
Dnaja1	DnaJ heat shock protein family (Hsp40) member A1	-1.19	1.9E-04	0.01
F10	coagulation factor X	2.83	2.0E-04	0.01
Retnla	resistin like alpha	-4.97	2.0E-04	0.01
Kmo	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	-3.40	2.0E-04	0.01
1700025G04Rik	RIKEN cDNA 1700025G04 gene	-1.79	2.0E-04	0.01
Frrs1	ferric-chelate reductase 1	1.16	2.1E-04	0.01
Gas6	growth arrest specific 6	-3.19	2.1E-04	0.01
Fxyd2	FXYD domain-containing ion transport regulator 2	-4.08	2.1E-04	0.01
A4galt	alpha 1,4-galactosyltransferase	-5.75	2.2E-04	0.01
Tslp	thymic stromal lymphopoietin	-5.03	2.2E-04	0.02
Dnm1	dynamin 1	-3.41	2.3E-04	0.02
Ppfia4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	-5.92	2.3E-04	0.02

Olr1	oxidized low density lipoprotein (lectin-like) receptor 1	3.51	2.3E-04	0.02
Rem1	rad and gem related GTP binding protein 1	-5.76	2.3E-04	0.02
Pxdc1	PX domain containing 1	-4.17	2.4E-04	0.02
Kcnj10	potassium inwardly-rectifying channel, subfamily J, member 10	-4.78	2.4E-04	0.02
Notch4	notch 4	5.64	2.4E-04	0.02
Cfh	complement component factor h	-1.91	2.5E-04	0.02
Mbnl1	muscleblind-like 1 (Drosophila)	-0.77	2.5E-04	0.02
Gm38228	NA	4.83	2.5E-04	0.02
Slc6a12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12	6.09	2.5E-04	0.02
Gm38095	NA	-5.50	2.6E-04	0.02
4930556M19Rik	RIKEN cDNA 4930556M19 gene	5.29	2.6E-04	0.02
Jag1	jagged 1	2.01	2.6E-04	0.02
Plcb1	phospholipase C, beta 1	3.54	2.7E-04	0.02
D730045B01Rik	RIKEN cDNA D730045B01 gene	-5.29	2.7E-04	0.02
Nr1d1	nuclear receptor subfamily 1, group D, member 1	-2.64	2.7E-04	0.02
Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A member 1	-1.20	2.9E-04	0.02
Adrb1	adrenergic receptor, beta 1	-5.71	2.9E-04	0.02
Igsf9	immunoglobulin superfamily, member 9	-3.26	3.0E-04	0.02
Bank1	B cell scaffold protein with ankyrin repeats 1	-2.67	3.0E-04	0.02
Gm10441	predicted gene 10441	-5.26	3.0E-04	0.02
Ifi203	interferon activated gene 203	-1.29	3.1E-04	0.02
AC124346.3	NA	-4.72	3.1E-04	0.02
Fam129a	family with sequence similarity 129, member A	-1.13	3.2E-04	0.02
Mtus1	mitochondrial tumor suppressor 1	1.20	3.2E-04	0.02
Mat2a	methionine adenosyltransferase II, alpha	-1.08	3.2E-04	0.02
Spry1	sprouty homolog 1 (Drosophila)	-4.81	3.3E-04	0.02
Ttc28	tetratricopeptide repeat domain 28	-3.31	3.3E-04	0.02
Gm24727	NA	4.53	3.4E-04	0.02
Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	-5.59	3.4E-04	0.02
Trac	T cell receptor alpha constant	-5.96	3.4E-04	0.02
Mill2	MHC I like leukocyte 2	-5.52	3.4E-04	0.02
Abca9	ATP-binding cassette, sub-family A (ABC1), member 9	-1.64	3.4E-04	0.02
Cd96	CD96 antigen	-4.52	3.4E-04	0.02
AC159283.2	NA	-4.79	3.5E-04	0.02
Slc16a3	solute carrier family 16 (monocarboxylic acid transporters), member 3	2.47	3.5E-04	0.02
Nav3	neuron navigator 3	-5.49	3.5E-04	0.02
Camk4	calcium/calmodulin-dependent protein kinase IV	-4.94	3.5E-04	0.02
Gm8995	predicted gene 8995	-0.96	3.6E-04	0.02
Trpm1	transient receptor potential cation channel, subfamily M, member 1	-5.60	3.6E-04	0.02
Mamdc2	MAM domain containing 2	-5.40	3.6E-04	0.02
Plxna4os2	plexin A4, opposite strand 2	-4.97	3.6E-04	0.02
Spam1	sperm adhesion molecule 1	-4.56	3.6E-04	0.02
Stard13	StAR-related lipid transfer (START) domain containing 13	-5.31	3.7E-04	0.02

Irf4	interferon regulatory factor 4	-2.95	3.7E-04	0.02
Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1	2.56	3.7E-04	0.02
Hspa8	heat shock protein 8	-0.84	3.7E-04	0.02
Lif	leukemia inhibitory factor	4.80	3.7E-04	0.02
Colgalt2	collagen beta(1-O)galactosyltransferase 2	-5.55	3.7E-04	0.02
E430014B02Rik	RIKEN cDNA E430014B02 gene	-4.63	3.8E-04	0.02
Wbp1l	WW domain binding protein 1 like	1.01	3.8E-04	0.02
Hectd2	HECT domain containing 2	-3.79	3.8E-04	0.02
Espn	espin	-5.64	3.8E-04	0.02
Gm36963	NA	-4.24	3.9E-04	0.02
Nsg2	neuron specific gene family member 2	-5.11	3.9E-04	0.02
Dmxl2	Dmx-like 2	2.18	3.9E-04	0.02
Neurl1a	neuralized E3 ubiquitin protein ligase 1A	-4.44	4.0E-04	0.02
Trerf1	transcriptional regulating factor 1	-1.75	4.0E-04	0.02
9930111J21Rik2	RIKEN cDNA 9930111J21 gene 2	-1.78	4.0E-04	0.02
Cd209a	CD209a antigen	-6.35	4.0E-04	0.02
Ptger4	prostaglandin E receptor 4 (subtype EP4)	-1.26	4.1E-04	0.02
Gys1	glycogen synthase 1, muscle	2.22	4.1E-04	0.02
Agmo	alkylglycerol monooxygenase	-3.76	4.2E-04	0.02
Cd3g	CD3 antigen, gamma polypeptide	-5.64	4.2E-04	0.02
Jun	jun proto-oncogene	-1.06	4.3E-04	0.02
Slc14a1	solute carrier family 14 (urea transporter), member 1	-4.97	4.3E-04	0.02
P4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	1.38	4.4E-04	0.02
Fgl2	fibrinogen-like protein 2	-1.63	4.4E-04	0.02
Barx2	BarH-like homeobox 2	-4.96	4.4E-04	0.02
Lag3	lymphocyte-activation gene 3	-4.52	4.4E-04	0.02
Chil1	chitinase-like 1	6.60	4.5E-04	0.02
Cmah	cytidine monophospho-N-acetylneuraminic acid hydroxylase	-4.56	4.6E-04	0.02
Gm6377	predicted gene 6377	-1.48	4.6E-04	0.02
Dcaf12	DDB1 and CUL4 associated factor 12	1.28	4.6E-04	0.02
Sytl2	synaptotagmin-like 2	-4.92	4.7E-04	0.02
2010005H15Rik	RIKEN cDNA 2010005H15 gene	6.86	4.7E-04	0.02
Ccl8	chemokine (C-C motif) ligand 8	-5.04	4.7E-04	0.02
Gm42793	NA	3.68	4.8E-04	0.02
Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	-5.70	4.8E-04	0.03
Nt5e	5' nucleotidase, ecto	3.98	4.9E-04	0.03
Dntt	deoxynucleotidyltransferase, terminal	-5.30	4.9E-04	0.03
Frmd4b	FERM domain containing 4B	-1.63	4.9E-04	0.03
Pltp	phospholipid transfer protein	-1.60	5.0E-04	0.03
Slc45a1	solute carrier family 45, member 1	-4.91	5.0E-04	0.03
Ric1	RAB6A GEF complex partner 1	1.27	5.1E-04	0.03
Gkap1	G kinase anchoring protein 1	-2.73	5.2E-04	0.03
Arid5a	AT rich interactive domain 5A (MRF1-like)	-1.26	5.2E-04	0.03
Timd4	T cell immunoglobulin and mucin domain containing 4	-6.10	5.2E-04	0.03

Fmnl2	formin-like 2	1.30	5.2E-04	0.03
Usp24	ubiquitin specific peptidase 24	-0.90	5.2E-04	0.03
Ighd	immunoglobulin heavy constant delta	-4.10	5.2E-04	0.03
Gm15713	predicted gene 15713	-4.92	5.2E-04	0.03
Gspt2	G1 to S phase transition 2	5.39	5.3E-04	0.03
Xcl1	chemokine (C motif) ligand 1	-5.16	5.3E-04	0.03
Nostrin	nitric oxide synthase trafficker	-1.99	5.4E-04	0.03
Arhgef10	Rho guanine nucleotide exchange factor (GEF) 10	-4.37	5.4E-04	0.03
Mif	macrophage migration inhibitory factor	2.95	5.4E-04	0.03
9930111J21Rik1	RIKEN cDNA 9930111J21 gene 1	-2.06	5.5E-04	0.03
Stxbp6	syntaxin binding protein 6 (amisyn)	-2.36	5.6E-04	0.03
Ada	adenosine deaminase	-2.55	5.6E-04	0.03
AC160637.1	NA	2.63	5.6E-04	0.03
Slc27a3	solute carrier family 27 (fatty acid transporter), member 3	-5.60	5.7E-04	0.03
Etv1	ets variant 1	-2.80	5.7E-04	0.03
Gm12117	glyceraldehyde-3-phosphate dehydrogenase pseudogene	3.95	5.8E-04	0.03
Ildr2	immunoglobulin-like domain containing receptor 2	-6.71	5.9E-04	0.03
Dzip1	DAZ interacting protein 1	-4.92	5.9E-04	0.03
Npepps	aminopeptidase puromycin sensitive	1.35	5.9E-04	0.03
Gm28913	NA	4.51	6.0E-04	0.03
Myh6	myosin, heavy polypeptide 6, cardiac muscle, alpha	-5.63	6.0E-04	0.03
Rhbdf1	rhomboid 5 homolog 1	-4.77	6.0E-04	0.03
Ly6e	lymphocyte antigen 6 complex, locus E	-1.21	6.2E-04	0.03
Vash1	vasohibin 1	-4.93	6.3E-04	0.03
Anks1b	ankyrin repeat and sterile alpha motif domain containing 1B	-4.42	6.3E-04	0.03
Sort1	sortilin 1	1.52	6.3E-04	0.03
Gclm	glutamate-cysteine ligase, modifier subunit	2.23	6.4E-04	0.03
Gm29480	predicted gene 29480	5.30	6.4E-04	0.03
Pepd	peptidase D	-1.49	6.7E-04	0.03
Sox7	SRY (sex determining region Y)-box 7	-5.27	6.8E-04	0.03
1700047M11Rik	RIKEN cDNA 1700047M11 gene	5.47	6.8E-04	0.03
Vcan	versican	2.74	6.9E-04	0.03
Mylip	myosin regulatory light chain interacting protein	-1.51	6.9E-04	0.03
Gpr160	G protein-coupled receptor 160	-1.41	7.0E-04	0.03
Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1	-5.64	7.1E-04	0.03
Chn2	chimerin 2	-3.21	7.2E-04	0.03
Ankrd37	ankyrin repeat domain 37	5.06	7.2E-04	0.03
Slc11a1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	0.99	7.3E-04	0.03
Tgfbr2	transforming growth factor, beta receptor II	-1.06	7.3E-04	0.03
Plekhg5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	-5.29	7.4E-04	0.03
Cfap157	cilia and flagella associated protein 157	4.98	7.6E-04	0.03
Fbxl5	F-box and leucine-rich repeat protein 5	2.13	7.7E-04	0.03
Syt3	synaptotagmin III	-5.57	7.8E-04	0.04

Hpgds	hematopoietic prostaglandin D synthase	-1.98	7.8E-04	0.04
Sgk1	serum/glucocorticoid regulated kinase 1	1.41	7.8E-04	0.04
Tnfrsf9	tumor necrosis factor receptor superfamily, member 9	4.32	7.8E-04	0.04
Homer2	homer scaffolding protein 2	-5.11	7.9E-04	0.04
Elavl4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	-4.60	8.1E-04	0.04
Gm20658	predicted gene 20658	5.46	8.1E-04	0.04
Tarm1	T cell-interacting, activating receptor on myeloid cells 1	5.62	8.1E-04	0.04
Vill	villin-like	3.95	8.1E-04	0.04
Glrx	glutaredoxin	1.70	8.1E-04	0.04
Gm17228	actin, gamma, cytoplasmic 1 pseudogene	-3.19	8.2E-04	0.04
2610306O10Rik	RIKEN cDNA 2610306O10 gene	-4.39	8.3E-04	0.04
Ogn	osteoglycin	-5.37	8.4E-04	0.04
Ablim3	actin binding LIM protein family, member 3	-4.83	8.4E-04	0.04
Fsd2	fibronectin type III and SPRY domain containing 2	-4.52	8.4E-04	0.04
Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1	-1.39	8.4E-04	0.04
Scara5	scavenger receptor class A, member 5	-5.94	8.5E-04	0.04
Pros1	protein S (alpha)	-1.85	8.8E-04	0.04
Ero1l	ERO1-like (S. cerevisiae)	2.86	8.8E-04	0.04
Adam10	a disintegrin and metallopeptidase domain 10	0.88	8.9E-04	0.04
Clec4b1	C-type lectin domain family 4, member b1	-4.54	8.9E-04	0.04
H2-Aa	histocompatibility 2, class II antigen A, alpha	-2.05	8.9E-04	0.04
Gm10364	glyceraldehyde-3-phosphate dehydrogenase pseudogene	3.88	8.9E-04	0.04
Cfap126	cilia and flagella associated protein 126	-4.86	8.9E-04	0.04
Pou2f2	POU domain, class 2, transcription factor 2	-1.47	9.0E-04	0.04
Tnnt2	troponin T2, cardiac	-5.45	9.2E-04	0.04
Gm16486	predicted gene 16486	-3.21	9.3E-04	0.04
Alas1	aminolevulinic acid synthase 1	1.52	9.4E-04	0.04
Tlr3	toll-like receptor 3	-1.96	9.4E-04	0.04
Gm19931	protein LLP homolog	-4.77	9.4E-04	0.04
Tcaf1	TRPM8 channel-associated factor 1	-5.32	9.5E-04	0.04
H2-DMb1	histocompatibility 2, class II, locus Mb1	-1.93	9.5E-04	0.04
E230020A03Rik	RIKEN cDNA E230020A03 gene	-4.63	9.5E-04	0.04
Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	-2.56	9.7E-04	0.04
Ccnd1	cyclin D1	-1.38	9.8E-04	0.04
Ampd2	adenosine monophosphate deaminase 2	1.72	9.8E-04	0.04
Sult1a1	sulfotransferase family 1A, phenol-preferring, member 1	-3.16	9.8E-04	0.04
Por	P450 (cytochrome) oxidoreductase	1.07	9.9E-04	0.04
mt-Nd2	NA	-1.94	9.9E-04	0.04
Gm20544	predicted gene 20544	4.84	1.0E-03	0.04

Table S9. Differentially Expressed Genes in Recipient Macrophages Devoid of *Ager* vs. WT. Comparison 4 (C4), p≤0.001 and FDR≤0.2.

SYMBOL	GENE NAME	log2FC	P_Value	FDR
Gm15487	NA	4.63	1.8E-07	3.1E-03
Rspo1	R-spondin 1	-6.43	3.9E-07	3.4E-03
Hmga1-rs1	high mobility group AT-hook I, related sequence 1	5.18	9.1E-07	4.3E-03
Gm9825	ribonucleic acid binding protein S1 pseudogene	4.89	9.9E-07	4.3E-03
Rpl10a-ps2	ribosomal protein L10A, pseudogene 2	5.00	1.9E-05	0.07
Zfp383	zinc finger protein 383	-4.85	4.0E-05	0.11
Gdf9	growth differentiation factor 9	-5.88	5.4E-05	0.13
Oas3	2'-5' oligoadenylate synthetase 3	-1.53	6.4E-05	0.14
Mir7027	microRNA 7027	-4.60	8.4E-05	0.16
Irf7	interferon regulatory factor 7	-1.68	9.8E-05	0.16
Bag2	BCL2-associated athanogene 2	-5.39	1.0E-04	0.16

Table S10. TaqMan premade primers.

RT-PCR primers	Thermofisher Catalog #
Abca1	Mm00442646_m1
Abcg1	Mm00437390_m1
Ager	Mm00545815_m1
Arg1	Mm00475988_m1
Ccl2	Mm00441242_m1
Cd36	Mm00432403_m1
Hmgcr	Mm01282499_m1
Hprt	Mm03024075_m1
Il6	Mm00446190_m1
Il10	Mm01288386_m1
Irf7	Mm00516793_g1
Nr1lh3 (Lxrα)	Mm00443451_m1
Nr1h2 (Lxrβ)	Mm00437265_m1
Nos2	Mm00440502_m1
Tnfa	Mm00443258_m1
Scap	Mm01250176_m1
Srebp1	Mm00550338_m1
18S	Hs99999901_s1