Resident and recruited macrophages differentially contribute to cardiac healing after

myocardial ischemia

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ABSTRACT

Cardiac macrophages are heterogenous in phenotype and functions, which has been associated

with differences in their ontogeny. Despite extensive research, our understanding of the precise

role of different subsets of macrophages in ischemia/reperfusion injury remains incomplete. We

here investigated macrophage lineages and ablated tissue macrophages in homeostasis and after

I/R injury in a CSF1R-dependent manner. Genomic deletion of a fms-intronic regulatory element

(FIRE) in the Csf1r locus resulted in specific absence of resident homeostatic and antigen-

presenting macrophages, without affecting the recruitment of monocyte-derived macrophages to

the infarcted heart. Specific absence of homeostatic, monocyte-independent macrophages altered

the immune cell crosstalk in response to injury and induced proinflammatory neutrophil

polarization, resulting in impaired cardiac remodelling without influencing infarct size. In contrast,

continuous CSF1R inhibition led to depletion of both resident and recruited macrophage

populations. This augmented adverse remodelling after I/R and led to an increased infarct size and

deterioration of cardiac function. In summary, resident macrophages orchestrate inflammatory

responses improving cardiac remodelling, while recruited macrophages determine infarct size after

I/R injury. These findings attribute distinct beneficial effects to different macrophage populations

in the context of myocardial infarction.

GRAPHICAL ABSTRACT

INTRODUCTION

Macrophages are important effectors of innate immunity. They are essential for host defense against infections but are also involved in different cardiovascular diseases. They represent the most abundant immune cell population in healthy cardiovascular tissues (Heidt *et al*, 2014; Weinberger *et al*, 2020), where they contribute to organ functions (Hulsmans *et al*, 2017) and maintenance of tissue homeostasis (Nicolas-Avila *et al*, 2020). In cardiovascular diseases such as atherosclerosis and its main sequelae, ischemic stroke and acute myocardial infarction (AMI), macrophage functions are central to both disease development and healing. AMI has remained a leading cause of mortality and morbidity worldwide (Ahmad & Anderson, 2021; Lozano *et al*, 2012). Although acute survival in this condition has improved through the broad availability of percutaneous coronary intervention, adverse myocardial remodeling and fibrosis frequently result in heart failure (Gerber *et al*, 2016). Pathophysiologically, the diminished blood supply to myocardial tissue during AMI leads to acute tissue necrosis, which induces a profound sterile inflammation and triggers complex cascade of immune processes and tissue remodeling (Hilgendorf *et al*, 2014; Honold & Nahrendorf, 2018; Nahrendorf *et al*, 2007). Consequently, uncontrolled immune reactions in the course of AMI are associated with impaired wound healing and adverse remodeling and can result in worsened cardiac outcome (Panizzi *et al*, 2010).

Macrophages play an essential role in cardiac injury, and thus represent a potential therapeutic target (Hilgendorf *et al.*, 2014; Nahrendorf *et al.*, 2007). However, they are an heterogeneous population (Kubota *et al*, 2019; Weinberger & Schulz, 2015; Zaman & Epelman, 2022), and a large body of work has shown that they can have both pro- and anti-inflammatory functions. The differential roles of macrophage populations in AMI have remained incompletely understood. Cardiac macrophages can derive from embryonic and adult hematopoietic progenitors

(Epelman *et al*, 2014). Fate mapping analyses have identified yolk sac (YS) erythro-myeloid

progenitors (EMPs) as a principal source of cardiac macrophages in adult life (Ginhoux *et al*,

2010). However, limited labeling in inducible cre reporter systems have not allowed for precisely

differentiating and quantifying developmental origins of cardiac macrophages. Further, targeting

of these macrophages has been challenging (Frieler *et al*, 2015; Ruedl & Jung, 2018).

In this study, we investigated the cellular identity of cardiac macrophages in association

with their developmental paths and their immune responses to ischemia/reperfusion (I/R) injury.

By combining lineage tracing with single cell RNA sequencing, we provide an in-depth analysis

of the differential functions of resident and recruited cardiac macrophages. We then harnessed

mice with genomic deletion of the fms-intronic regulatory element (FIRE) (Rojo *et al*, 2019), that

allowed us to specifically address populations of resident macrophages in the infarcted heart and

compared them to mice, in which both recruited as well as resident macrophages are depleted by

pharmacological inhibtion of the CSF1R-signalling pathway. Using these approaches of selective

macrophage depletion, we could attribute different beneficial functions to resident and also to

recruited macrophages which impact differently on cardiac remodeling, infarct size and cardiac

outcome.

RESULTS

Absence of resident cardiac macrophages in Csf1r$^{\Delta FIRE}$ mice

To quantify the contribution of YS EMPs to cardiac resident macrophages, we harnessed constitutive labeling in *Rank*^{Cre};*Rosa26*^{eYFP} mice (Jacome-Galarza *et al*, 2019; Mass *et al*, 2016; Percin *et al*, 2018). ~80% of cardiac macrophages expressed YFP in hearts of 12 week-old animals, whereas blood monocytes were not labeled (**Fig 1A; Fig S1**). EMP-derived microglia served as control confirming high efficiency of Cre-mediated recombination. In a comparative analysis, we traced fetal and adult definitive hematopoiesis in *Flt3*^{Cre}*Rosa26*^{eYFP} mice (Gomez Perdiguero *et al*, 2015; Schulz *et al*, 2012), indicating that ~20% of cardiac macrophages derived from definitive HSC **(Fig 1B)**. Thus, the majority of resident macrophages in the healthy heart is of early embryonic origin.

To determine the role of resident macrophages in the mouse heart, we generated *Rank*^{Cre}*Rosa26*^{DTR} mice that express the avian diphtheria toxin (DT) receptor in the EMP lineage, rendering them susceptible to DT-mediated ablation. Administration of a single DT dose, however, resulted in premature death of all mice (n=6) within 24 hours (**Fig S2**). The injected mice presented with a systemic inflammatory response syndrome (SIRS)-like phenotype, indicating that acute depletion of EMP-derived macrophages is not viable.

In *Csf1r*$^{\Delta FIRE}$ mice, genetic deletion of the fms-intronic regulatory element (FIRE) in the first intron of the *Csf1r* gene leads to a selective absence of tissue macrophages without the developmental defects observed in *Csf1r*$^{-/-}$ mice (Munro *et al*, 2020; Rojo *et al.*, 2019). We first confirmed that cardiac macrophages in *Csf1r*$^{\Delta FIRE/\Delta FIRE}$ *mice* (further termed ΔFIRE) mice were reduced by ~90% and the number of monocytes and neutrophils was not altered **(Fig 1C-G)**. We thus crossed the ΔFIRE animals with the YS EMP fate mapping line (*Rank*^{Cre}*Rosa26*^{eYFP} mice) and showed that

the macrophages absent in ΔFIRE animals were EMP-derived macrophages **(Fig 1E)**, thus offering

a new model to investigate the role of resident macrophages in cardiac injury.

Changes in the cardiac immune phenotype in Csf1r$^{\Delta FIRE}$ mice in baseline conditions

To further characterize the macrophage populations absent in healthy hearts of adult ΔFIRE mice,

we carried out single cell RNA-sequencing (scRNA-seq) of CD45$^+$ immune cells in wildtype,

ΔFIRE and *Rank^{Cre}Rosa26^{eYFP}* mice **(Fig 2A, Fig S3)**. We identified the presence of six

macrophage clusters in control mice **(Fig 2B, Fig S3)**. Two clusters of macrophages expressing

homeostatic (*e.g. Lyve-1, Gas6, Stab1*) and antigen presentation-related genes (*e.g. CD74, H2-*

Ab1) were specifically ablated in ΔFIRE mice **(Fig 2C)**, which largely represent YFP-expressing

macrophages in *Rank^{Cre}Rosa26^{eYFP}* mice **(Fig 2D).** Specifically, we mapped ~90% of *yfp*

transcripts to the two clusters of homeostatic and antigen presenting macrophages that were ablated

in ΔFIRE. Other clusters were not reduced in ΔFIRE, and also were not quantitatively represented

in the YS macrophage lineage tracing model, i.e. *Cx3cr1^{hi}* (2% *yfp*), *Ccr2^{low}Ly6c^{lo}* (5% *yfp*) and

Ccr2^{hi}Ly6c^{hi} (1% *yfp*) macrophages within respective clusters (**Fig 2D**). The specific impact of

ΔFIRE on resident macrophages is further supported by the observation, that no changes in gene

expression nor cell numbers were observed in *Ly6c^{hi}* monocytes and inflammatory *Ccr2^{hi}Ly6c^{hi}*

macrophages **(Fig 2C Fig S4)**. Together, ΔFIRE allows for investigating the role of resident

cardiac macrophages that are largely of YS origin.

Absence of resident macrophages in ΔFIRE was associated with changes in gene expression in

non-macrophage clusters such as *T- and B-cells* and *natural killer (NK)* cells (**Fig S5**). Further,

overall phagocytic capacity, as inferred by expression of phagocytosis related genes (Amorim *et*

al, 2022), was reduced (**Fig 2E**). This suggests that absence of resident macrophages is

accompanied by distinct changes in immune functions in the homeostatic heart.

Adverse cardiac remodeling in Csf1r^{ΔFIRE} mice after I/R injury

To assess the impact of the absence of resident macrophages in cardiac injury, we subjected

ΔFIRE mice to I/R injury and investigated remodeling and functional outcome by sequential

positron emission tomography (PET) imaging after 6 and 30 days **(Fig 3A)**. Function of the cardiac

left ventricle (LV), as determined by ejection fraction (LVEF) and stroke volume (SV), improved

in controls in the course of post-I/R remodeling **(Fig 3B-C)**. In contrast, LVEF and SV remained

unchanged or worsened in ΔFIRE mice, and longitudinal observations of mice indicated a negative

net effect on ejection fraction from day 6 to day 30 post I/R. Thus, absence of resident macrophages

negatively influenced cardiac remodeling in the course of infarct healing **(Fig 3D-G)**. Infarct size

as determined by viability defect (PET) and fibrotic area (histology) was not different after 30 days

(Fig 3E-H).

Recruitment of BM-derived macrophages into infarct zone of Csf1r^{ΔFIRE} mice

To gain a deeper understanding of the inflammatory processes taking place in the infarcted

heart, we quantified macrophage distribution by immunofluorescence and flow cytometry analysis

of ischemic and remote areas after I/R. In ΔFIRE mice, macrophages were largely absent in the

remote zone of infarcted hearts **(Fig 4A)**, indicating sustained depletion of resident macrophages.

However, macrophages strongly increased in the infarct area and their numbers were not different

in both infarct and border zones between ΔFIRE and control mice **(Fig 4A)**. This indicated

recruitment and differentiation of ΔFIRE-independent macrophages from the circulation into these

regions. Indeed, complementing lineage tracing of BM HSC in *Flt3^{Cre}* mice **(Fig 4B)** and YS EMP

in *Rank^{Cre}* mice **(Fig 4C)** proved the recruitment of macrophages from BM HSC (Flt3 GFP+ and

Rank RFP-, respectively) in the early phase of I/R injury. 30 days after I/R, BM-derived

macrophages remained overrepresented in the infarct zone (~75% HSC contribution), and

differential contribution of BM HSC declined from the border zone (~50%) to the remote zone

(~35%) **(Fig 4D)**. Taken together, recruited BM-derived macrophages represent the main

population in the infarct area and their recruitment was unaltered in ΔFIRE mice. This supports

the notion that resident macrophages influence cardiac remodeling but recruited macrophages

drive infarct size after I/R.

Transcriptional landscape of resident versus recruited macrophages in I/R injury

To address the differential responses of resident and recruited macrophages to I/R injury, we

generated BM chimeric mice. We applied an irradiation-independent model using conditional

deletion of c-myb to deplete BM hematopoietic cells in CD45.2 mice and replace them with

CD45.1 donor HSC. 2 days after I/R injury, we FACS-sorted recruited (CD45.1$^+$) and resident

(CD45.2$^+$) macrophages and carried out bulk RNA sequencing **(Fig 5A)**. The two macrophage

populations exhibited profound transcriptional differences after I/R injury. Expression of

homeostasis-related genes like *Timd4, Lyve-1, CD163* and *Retnla* was increased in resident

CD45.2$^+$ macrophages **(Fig 5B, C).** Substantiating the differential regulation of macrophage

programs, CD45.1$^+$ macrophages increased inflammatory- and host defense-related gene ontology

(GO) terms (e.g. myeloid leukocyte related immunity, killing of cells), whereas CD45.2$^+$

macrophages upregulated development- and homeostasis-related GO terms (e.g. extracellular

matrix organization, vasculature development, heart muscle development) **(Fig 5D)**. GO

enrichment analysis further predicted that processes involved in innate (e.g. leukocyte migration,

regulation of defense response, response to bacterium) as well as the adaptive immunity (e.g. T

cell selection, T cell activation, B cell proliferation) were increased in CD45.1$^+$ macrophages after

infarction **(Fig 5D)**. Thus, resident and recruited macrophages provide distinct transcriptional

changes and inferred functions in response to I/R.

Altered inflammatory patterns and immune cell communication in Csf1r$^{\Delta FIRE}$ mice

To evaluate the immune response of resident and recruited macrophages to I/R injury in ΔFIRE mice, we interrogated the transcription profile of CD45$^+$ cells from the infarct area **(Fig 6A)**. In contrast to the absence of homeostatic and antigen-presenting macrophage clusters in healthy hearts of ΔFIRE mice **(Fig 2B-C)**, there were less differences in immune cell clusters between ΔFIRE and control mice 2 days after I/R **(Fig 6B, C)**. Abundance of homeostatic macrophages was also reduced at this time point, however, other clusters including *Ccr2^{hi}Ly6c^{hi}* inflammatory macrophages were not altered, which is in line with our histological findings.

ΔFIRE was associated with some changes in gene expression in cardiac non-macrophage immune cells. Across different clusters, including lymphocyte and neutrophil clusters, expression of anti-inflammatory genes like *Chil3 (Ym1)* and *Lcn2* was reduced**.** Vice versa, expression of Bcl-family genes like *Blc2a1a* and *Bcl2a1d*, which are associated with apoptosis and inflammatory pathways, was higher in ΔFIRE mice **(Fig S6-8)**. Other upregulated genes were related to antigen presentation (e.g.*CD74, H2-Ab1*), as identified in the *Ccr2^{lo}Ly6c^{lo},* homeostatic and *Ccr2^{hi}Ly6c^{hi}* macrophage clusters **(Fig S6 and 7)**. Further, we interrogated inflammatory gene expression in neutrophils, which are abundant first responders to myocardial infarction. We found that a computed score summing up inflammasome activation (Amorim *et al.*, 2022) was increased in all neutrophil clusters in ΔFIRE mice **(Fig 6D)**. Thus, the absence of cardiac macrophages was associated with altered inflammatory properties of non-macrophage immune cells in the infarcted heart.

Altered intercellular crosstalk of macrophages is a hallmark of cardiac inflammation. We therefore assessed ligand-receptor (LR) interactions between immune cell populations after I/R injury. Indeed, the number of LR interactions with neutrophils and lymphocytes, as well as the strength of the macrophage-emitted communication signals was markedly reduced in homeostatic, antigen-

presenting and *Ccr2^{lo}Ly6c^{lo} Mø* macrophage clusters (**Fig 6E, F, Fig. S9**). In contrast, immune

cell communication in BM-derived macrophage clusters (e.g. *Ccr2^{hi}Ly6c^{hi} Mø cluster,* **Fig S10***)*

was not different to control mice. Taken together, deficiency in resident macrophages in I/R injury

altered the intercellular immune crosstalk and induced a pro-inflammatory signature in e.g. cardiac

neutrophils. However, transcriptional profiles of BM-derived inflammatory macrophages were

largely unaltered. Together with our histological analysis showing the dominance of recruited BM-

derived macrophages in the early phase of I/R, this potentially explained the limited impact of

ΔFIRE on functional outcome after I/R injury.

Ablation of resident and recruited macrophages severely impacts on cardiac healing after I/R

injury

To test this hypothesis, we determined the effect of combined ablation of resident and recruited

macrophages. We therefore exposed mice to continuous treatment with the CSF1R-inhibitor

PLX5622 (**Fig 7A**). In healthy hearts, inhibitor treatment resulted in the absence of cardiac

macrophages within 3 days (**Fig S11**). We then subjected mice to I/R injury and investigated

outcome by sequential PET imaging and histology **(Fig 7A)**. Treatment with PLX5622 diminished

macrophage numbers in both remote and infarct areas in the early phase (day 2) after injury.

Recruitment of other myeloid cells e.g. neutrophils was not altered in this context (**Fig 7B**). This

effect was pronounced in the chronic phase (day 30) after I/R injury, in which macrophages were

largely absent in remote, border and infarct zones (**Fig 7C,D**). Absence of resident and recruited

macrophages was associated increased infarct size, as determined by fibrosis area (WGA

histology) as well as viability defect (PET), and resulted in deterioration of cardiac function **(Fig**

7E-I). Specifically, LVEF was reduced 6 days after I/R, and remained strongly impaired at 30 days

(Fig 7E).

Taken together, sole absence of resident macrophages had limited negative impact on cardiac

remodeling. Absence of both resident and recruited macrophages resulted in a significant increase

in infarct size and deterioration of left ventricular function after I/R injury, highlighting a beneficial

effect of recruited macrophages in cardiac healing.

DISCUSSION

Macrophages are key players in cardiac homeostasis and disease (Bajpai *et al*, 2019; Bajpai *et al*, 2018; Dick *et al*, 2019; Epelman *et al.*, 2014; Hulsmans *et al.*, 2017; Nahrendorf *et al.*, 2007; Nicolas-Avila *et al.*, 2020; Panizzi *et al.*, 2010; Sager *et al*, 2016). The precise understanding of their developmental origin, their functions and their regulation could enable the identification of macrophage-targeted strategies to modify inflammation in the heart. In cardiac repair after myocardial infarction, macrophages have both positive and negative effects. They are critical for tissue repair, angiogenesis, and inflammation regulation, but their actions need to be carefully balanced to prevent excessive inflammation, scar tissue formation, and adverse remodeling. This study sheds light on the differential role of resident and recruited macrophages in cardiac remodeling and outcome after AMI.

BM-derived recruited macrophages represents a small population in the healthy heart but are recruited in vast numbers to the injured myocardium after I/R injury. These recruited cells exhibit substantially different transcriptional profiles in comparison to their resident counterpart, and show pro-inflammatory properties. Resident macrophages remain present in the remote and border zone and display a reparative gene expression profile after I/R injury. In comparison to recruited macrophages, resident macrophages expressed higher levels of genes related to homeostatic functions (e.g. *Lyve-1, Timd4, CD163, Stab1*). These markers have recently been associated with self-renewing tissue macrophages that are maintained independently of BM contribution (Dick *et al*, 2022). Biological processes associated with cardiac healing are upregulated in resident macrophages (e.g. regulation of vascular development, regulation of cardiomyocyte development, extracellular matrix organization). Transcriptional profiles of recruited macrophages show enhanced inflammatory biological processes also in macrophages

harvested from the remote area, underlining their potentially detrimental influence on remote

cardiac injury.

Two recent studies addressed the role of resident macrophages using DT-mediated

macrophage depletion and reported impaired cardiac remodeling in chronic myocardial infarction

(Dick *et al.*, 2019) and after I/R injury (Bajpai *et al.*, 2019). However, DT-mediated cell ablation

is known to induce neutrophil recruitment and tissue inflammation (Frieler *et al.*, 2015; Oh *et al*,

2017; Ruedl & Jung, 2018; Sivakumaran *et al*, 2016). This inflammatory preconditioning of

cardiac tissue after DT-depletion is likely to impact on cardiac remodeling and influence

assessment of tissue macrophage functions. Genomic deletion of FIRE in the *Csf1r* gene results in

the near-absence of resident cardiac macrophages but circumvents the inflammatory stimulus of

DT-induced depletion. ΔFIRE specifically diminished homeostatic and antigen-presenting

macrophages. Substantiating the specificity to resident cardiac macrophages in this genetic model,

the amount of macrophages recruited to the infarct area after I/R injury was not affected in ΔFIRE

mice. Further, scRNAseq analysis revealed that gene expression of monocytes as well as

Ccr2^{hi}Ly6c^{hi} and Cx3cr1^{hi} Mφ, representing mainly recruited immune cells*,* was mostly

unchanged in ΔFIRE compared to control mice. The specific targeting of the resident macrophage

population introduces an interesting in vivo model for studying their role in MI without the need

for inflammation-prone conditional deletion of macrophages (Frieler *et al.*, 2015).

Ablation of resident macrophages altered macrophage crosstalk to non-macrophage

immune cells, especially lymphocytes and neutrophils. This was characterized by a

proinflammatory gene signature, such as neutrophil expression of inflammasome-related genes

and a reduction in anti-inflammatory genes like *Chil3* and *Lcn2* (Gordon & Martinez, 2010; Guo

et al, 2014; Parmar *et al*, 2018). Interestingly, inflammatory polarization of neutrophils have also

been associated with poor outcome after ischemic brain injury (Cuartero *et al*, 2013). Clinical trials

in myocardial infarction patients show a correlation of inflammatory markers with extent of the

myocardial damage(Sanchez *et al*, 2006) and with short- and long-term mortality (Mueller *et al*,

2002).

Our study provides evidence that the absence of resident macrophages negatively

influences cardiac remodeling in the late postinfarction phase in ΔFIRE mice indicating their

biological role in myocardial healing. In the early phase after I/R injury, absence of resident

macrophages had no significant effect on infarct size or LV function. These observations

potentially indicate a protective role in the chronic phase after myocardial infarction by modulating

the inflammatory response, including adjacent immune cells like neutrophils or lymphocytes.

Deciphering in detail the specific functions of resident macrophages is of considerable

interest but requires both cell-specific and temporally-controlled depletion of respective immune

cells in injury, which to our knowledge is not available at present. These experiments could be

important to tailor immune-targeted treatments of myocardial inflammation and postinfarct

remodelling.

Depletion of macrophages by pharmacological inhibition of CSF1R induced the absence

of both resident and recruited macrophages, allowing us to determine cardiac outcome in

juxtaposition to the ΔFIRE mice. Continuous CSF1R inhibition induced the absence of

macrophages also in the infarcted area and had deleterious effect on infarct size and LV function.

In line with our findings, depletion of macrophages by anti-CSF1R treatment was associated with

worsened cardiac function in a model of pressure overload induced heart failure (Revelo *et al*,

2021). Controversially, a recent study in which monocytes were depleted using DT-injections in

Ccr2[DTR] mice reported beneficial effects on cardiac outcome after MI in mice (Bajpai *et al.*, 2019).

An explanation of this controversy might be the timing and duration of macrophage depletion.

Bajpai et al. depleted recruited macrophages only in the initial phase of myocardial infarction

which improved cardiac healing (Bajpai *et al.*, 2019), while depletion of macrophages over a

longer period of time, as shown in our study, is detrimental for cardiac repair. Furhter, other

immune cells including neutrophils express CCR2 and may therefore be affected directly (Talbot

et al, 2015; Xu *et al*, 2017). In line with this, Ccr2-deficient mice exhibit reduced acute recruitment

of neutrophils to the brain after I/R injury, which was associated with reduced infarct size and

brain edema (Dimitrijevic *et al*, 2007).

Taken together our study underlines the heterogeneity of cardiac macrophages and the

importance of ontogeny therein. Resident macrophages, which mainly derive from YS EMPs,

govern cardiac homeostasis in the healthy heart, and contribute positively to cardiac healing after

I/R injury by orchestrating anti-inflammatory programming of other cardiac immune cells.

However, recruited macrophages contribute to the healing phase after AMI and their absence

defines infarct size and cardiac outcome.

MATERIALS AND METHODS

Mice

Rank^{Cre} (Jacome-Galarza *et al.*, 2019; Percin *et al.*, 2018), *Flt3^{Cre}* (Benz *et al*, 2008), *Myb$^{fl/fl}$* (Emambokus *et al*, 2003), *Mx1^{Cre}* (Kuhn *et al*, 1995) (from The Jackson Laboratory (JAX), Stock No: 003556), *Csf1r^{ΔFIRE}* (Rojo *et al.*, 2019), *Rosa26^{DTR}* (Buch *et al*, 2005) (JAX Stock No: 007900), *Rosa26$^{mT/mG}$* (Muzumdar *et al*, 2007) (JAX Stock No: 007676), *Rosa26^{eYFP}* (Srinivas *et al*, 2001) (JAX Stock No: 006148), and *Rosa26^{RFP}* (JAX Stock No: 034720) mice have been previously described. PCR genotyping was performed according to protocols described previously. Animals were aged between 10-16 weeks. We have complied with all relevant ethical regulations. Animal studies were approved by the local regulatory agency (Regierung von Oberbayern, Munich, Germany, record numbers ROB-55.2-2532.Vet_02-19-17 and ROB-55.2-2532.Vet_02-19-1; Care and Use Committee of the Institut Pasteur (CETEA), dap190119).

FIRE mice were kept on a CBA/Ca background. Experiments in which reporter mice were necessary (*Csf1r^{ΔFIRE}Rank^{Cre}Rosa26^{eYFP}*) the background was mixed with a C57Bl6 background. All experiments evaluating cardiac function and outcome after infarction in FIRE mice were performed on mice kept with a CBA/Ca background.

For fate-mapping analysis of Flt3$^+$ precursors, *Flt3^{Cre}* males (the transgene is located on the Y chromosome) were crossed to *Rosa26^{eYFP}* or *Rosa26$^{mT/mG}$* female reporter mice and only the male progeny was used. For all other experiments, the offspring of both sexes was used for experiments.

BM transplantation was enabled by conditional deletion of the transcription factor *myb* as previously described (Stremmel *et al*, 2018). In brief, we induced BM ablation by 4 injections of

polyI:C into *CD45.2; Mx1^{Cre}Myb$^{flox/flox}$* every other day, and then transplanted BM from congenic

C57BL/6 CD45.1 (*Ly5.1*; JAX Stock No: 006584). We confirmed the success (chimerism of above

90%) of the BM-transplantation after 4 weeks**.**

To deplete macrophages, we used the selective CSF1R-inhibitor PLX5622. Control and

PLX5622 (300 ppm formulated in AIN-76A standard chow, Research Diets, Inc.) chows were

kindly provided by Plexxikon Inc (Berkeley, CA). For depletion of RANK-lineage macrophages,

Rank^{Cre}Rosa26^{DTR} mice were injected intraperitoneally with 0.02 mg/kg body weight diphtheria

toxin (DT; Sigma-Aldrich) at the timepoints mentioned in Fig ure and corresponding legend. Mice

were closely monitored by veterinarians and according to score sheets that were approved by the

regulatory agency. Single DT application in *Rank^{Cre}Rosa26^{DTR}* mice let to rapid deterioration of

their health (without infarction or other interventions), and consequently experiments needed to be

aborted according to regulations; experimental outcomes were then documented as premature

death as indicated.

Ischemia-reperfusion (I/R) injury

I/R injury was carried out as previously described (Novotny *et al*, 2018). In brief, mice

were anesthetized using 2% isoflurane and intraperitoneal injection of fentanyl (0.05 mg/kg),

midazolam (5.0 mg/kg) and medetomidine (0.5 mg/kg), and then intubated orally (MiniVent

Ventilator model nr. 845, Harvard Apparatus®) and ventilated (volume of 150 µL at 200/min).

After lateral thoracotomy, the left anterior descending artery (LAD) was ligated with an 8-0

prolene suture producing an ischemic area in the apical left ventricle (LV). To induce the

reperfusion injury, the suture was removed after 60 min and reperfusion was confirmed by

observing the recoloring of the LV. Postoperative analgesia was performed by injection of

Buprenorphin (0.1 mg/kg) twice per day for 3 days. After 2, 6 or 30 days after I/R injury organs

were harvested after cervical dislocation.

Organ harvest

Mice were anaesthetized using 2% isoflurane and organ harvest was performed after

cervical dislocation. Blood was harvested with a heparinized syringe (2mL) by cardiac puncture.

After perfusion with 20 mL of ice-cold PBS hearts were excised and kept in PBS on ice until

further tissue processing. For flow cytometry, hearts were divided into the ischemia (tissue distal

of the LAD ligation) and remote area (tissue proximal of the LAD ligation). For histological

examinations of tissues, hearts were incubated in 4% PFA for 30 min followed by an incubation

in 30% sucrose-solution (Sigma Aldrich®) for 24 h. Afterwards, hearts were mounted onto a heart

slicing device and cut transversally into 3 equal parts (termed level 1, 2 and 3) and stored in Tissue-

Tek® (Sakura Finetek Germany GmbH) at -80°C.

Immunohistology

Cryosections (10-12 µm) of heart tissue were fixed with 4% paraformaldehyde for 10 min.

Blocking and permeabilization were performed with 0.5% Saponin and 10% goat serum for 1h.

Primary antibodies were added and incubated for 2-18 h (see Supplemental Table 1). Slides were

washed with PBS and secondary antibodies were added and incubated for 1h (see Supplemental

Table 1). WGA-staining (Wheat Germ Agglutinin Alexa Fluor™ 647 conjugated antibody,

ThermoFisher Scientific®) was used to locate and measure the infarct area and nuclei were stained

with DAPI. Finally, slides were washed one more time and Fluorescence Mounting Medium was

used to cover the stained sample.

Heart samples were evaluated using an Axio Imager M2 (Carl Zeiss®) and blinded picture

analysis was performed using ZEN Imaging and Axiovision SE64 Rel. 4.9.1 (Carl Zeiss®). For

the evaluation of cell numbers, 6 individual high-resolution images from each respective

anatomical region (infarct area, border zone and remote zone) were analysed for each animal. To

measure infarct size the heart was cut into 3 parts and the infarcted area was measured as WGA$^+$

area in sections from each part.

Flow cytometry

100 µL of heparinized blood was used for FACS analysis. Erythrocytes were lysed with

1% ammonium chloride. After washing with PBS, the cell suspension was resuspended in purified

rat anti-mouse CD16/CD32 (BD Pharmingen®) and incubated for 15 min at 4°C. Following this,

cells were incubated with FACS-antibodies for 15 min at 4°C **(table S1)**.

Heart tissue was dissected into remote and ischemic tissue as described above and minced

into small pieces using forceps and a scalpel. When comparing baseline and I/R injury in FACS

analysis, basal heart tissue was used for comparison with remote tissue and apical heart tissue for

comparison with ischemia tissue. After enzymatic digestion (Collagenase XI 1200 U/mg,

Collagenase I 125 U/mg, Hyaluronidase 500 U/mg, DNase I 1836 U/mg; Sigma Aldrich®) for 30

min at 37°C cells were washed and incubated with purified anti-CD16/32 (FcγRIII/II; dilution

1/50) for 10 min. Thereafter, cells were incubated wit FACS-antibodies **(table S1)** for 30 min at

4°C. FACS-analysis was performed on a BD Fortessa® or a BeckmanCoulter Cytoflex® flow

cytometer and gating strategies are shown in Supplemental Fig ures 1 and 3. Data were analysed

using FlowJo® (version 10.0.8r1).

Cell Sorting

Cell sorting was performed on a MoFlo Astrios (Beckman Coulter) to obtain cardiac

macrophages from *CD45.2; Mx1^{Cre}Myb$^{flox/flox}$* after BM-transplantation of CD45.1 BM (n=3 for 2

days after I/R injury) for bulk sequencing, or all cardiac immune cells (CD45$^+$ cells) of *Csf1r^{ΔFIRE}*

and *Rank^{Cre}Rosa26^{eYFP}* mice (n=3 for *Csf1r$^{ΔFIRE/+}$* and *Csf1r$^{ΔFIRE/ΔFIRE}$* in baseline conditions, n=1

for *Rank^{Cre}Rosa26^{eYFP}* in baseline conditions; n=2 for *Csf1r$^{ΔFIRE/+}$* and *Csf1r$^{ΔFIRE/ΔFIRE}$* 2 days after

I/R injury) for single cell analysis. CD45$^+$ cells were enriched by using magnetic beads and MS

columns (CD45 MicroBeads; Miltenyi Biotec). Cells were then sorted as single/live/CD45$^+$ cells

for single cell sequencing from baseline hearts and from the ischemic myocardium 2 days after I/R

injury.   Bulk   sequencing   was   performed   on   single/live/CD45$^+$/lin$^-$

/CD11b$^+$/F4/80$^+$/CD64$^+$/CD45.1$^+$ or CD45.2$^+$ cells from the remote and the ischemic myocardium

2 days after I/R injury. Dead cells were identified with SYTOX Orange Dead Cell Stain.

Bulk sequencing and analysis

For each sample, ~1000 macrophages were sorted into 75µL of RLT buffer (Qiagen,

containing 1% beta-mercaptoethanol), vortexed for 1 min and immediately frozen (-80°C). RNA

extraction (RNeasy® Plus Micro Kit, Qiagen), cDNA generation (SMART®-Seq v4 Ultra Low

Input RNA Kit, Takara Bio) and library preparation (Nextera® XT DNA Library Prep Kit,

Illumina) were performed according to the manufacturer's specifications. Sequencing was

performed on a HiSeq4000 system (Ilumina).

The obtained reads were trimmed using bbduk from the BBMap

(https://sourceforge.net/projects/bbmap/) v38.87 collection using parameters "ktrim=r k=23

mink=11 hdist=1 tpe tbo". The trimmed reads were aligned with Hisat2 2.2.1 against the Ensembl

release 102 reference mouse genome (Yates *et al*, 2020).

Gene expression was quantified using the featureCounts (Liao *et al*, 2014) application from

the subread package (v2.0.1) and with parameters "--primary -O -C -B -p -T 8 --minOverlap 5".

Differential expression analysis was performed using DESeq2 (v1.30.0) (Love *et al*, 2014). A

Gene Ontology Set Enrichment analysis was performed using the ClusterProfiler R package

(v3.18.1). The visualization of the respective clustermaps was layouted using the ForceAtlas2

implementation of the python fa2 (https://pypi.org/project/fa2/) package for networkx (v2.5)

(https://networkx.org/).

On the library-size normalized count data, the pymRMR ((Peng *et al*, 2005),

https://pypi.org/project/pymrmr/) package was used to derive the top 100 discriminatory genes

(Mutual Information Quotient method) for subsequently calculating the UMAP 2D-embedding (

(McInnes *et al*, 2020), (https://pypi.org/project/umap-learn/)) for all samples (umap-learn package

v0.5.0rc1, 3 neighbors) ((McInnes *et al*, 2018), https://pypi.org/project/pymrmr/).

Single cell RNA sequencing and analysis

After sorting, cells were proceeded for single cell capture, barcoding and library

preparation using Chromium Next GEM single cell 3' (v3.1, 10x Genomics) according to

manufacturer's specifications. Pooled libraries were sequenced on an Illumina HiSeq1500

sequencer (Illumina, San Diego, USA) in paired-end mode with asymmetric read length of 28+91

bp and a single indexing read of 8bp.

The reads of heart1 sample ($Rank^{Cre}Rosa26^{eYFP}$) were demultiplexed using Je-

demultiplex-illu (Girardot *et al*, 2016) and mapped against a customized mouse reference genome

(GRCm38.p6, Gencode annotation M24) including eYfp sequence using CellRanger (v3.1.0, 10x

Genomics).

The six mouse samples 20133-0001 to 20133-0006 (baseline condition of $Csf1r^{\Delta FIRE/+}$ and

$Csf1r^{\Delta FIRE/\Delta FIRE}$), were processed using Cellranger 4.0.0 using the 2020A mm10 reference.

The 4 mouse samples (MUC13956-13959, infarct condition of $Csf1r^{\Delta FIRE/+}$ and

$Csf1r^{\Delta FIRE/\Delta FIRE}$), were sequenced with 4 technical sequencing replicates and pooled using the

cellranger (v4.0.0, 10x Genomics) pipeline. Cellranger 4.0.0 was called with default parameters

and the 2020A mm10 reference for gene expression.

Finally, all 11 samples were integrated using Seurat 4.0.0 (on R 4.0.1) (Stuart & Satija,

2019). The samples were processed, and cells were filtered to contain between 200 and 6000

features, have at least 1000 molecules detected (nCount_RNA > 1000), have below 15% mtRNA

content (^MT) and below 40% ribosomal RNA content (^Rps|^Rpl). After this filtering a total of

35759 cells remained.

After performing SCTransform (Hafemeister & Satija, 2019) on the samples, the SCTransform

vignette for integrating the datasets was followed (with 2000 integration features). For

dimensionality reduction, PCA was performed using default parameters, and UMAP and

Neighbour-Finding was run on 50 PCs. Clustering was performed at a resolution of 0.8. A total of

18 clusters was identified using this approach. Cluster markers were calculated using the t-test in

the FindMarkers function. Subsequently cell types were initially predicted using the cPred cell

type prediction (https://github.com/mjoppich/scrnaseq_celltype_prediction). Upon manual

curation, further fine-grained cell type annotations were made. Differential comparisons were

performed against several subgroups of the data set. These comparisons were performed using the

t-test in the FindMarkers function of Seurat. Differential results are visualized using the

EnhancedVolcano library (Blighe K, 2021).

For the analysis of cell-cell interactions we downloaded the ligand-receptor pairs from Jin

et al. (Jin *et al*, 2021) from the Lewis Lab GitHub repository

(https://github.com/LewisLabUCSD/Ligand-Receptor-Pairs). For each interaction (ligand-

receptor pair for a cluster-pair) the communication score is calculated as the expression product

(Armingol *et al*, 2021) of the mean normalized expressions exported from the Seurat object. This

ensures that little expression of either ligand or receptor in only one cluster results in a relatively

low communication score, and only good expression of ligand and receptor will result in a high

communication score. The direction of an interaction is fixed from ligand to receptor. The single

ligand-receptor-communication-scores were then aggregated (sum) such that only interactions

with a score greater six were taken into account.

Gene module scores for inflammasome, ROS and phagocytosis gene sets were calculated

using Seurat's AddModuleScore function. All scripts, including the ones for creating the

visualizations of bulk and scRNA-seq data, are available online through

https://github.com/mjoppich/myocardial_infarction .

In Vivo PET Imaging

ECG-gated positron emission tomography (PET) images were performed on day 6 and 30

after I/R injury of the LAD using a dedicated small-animal PET scanner (Inveon Dedicated PET,

Preclinical Solutions, Siemens Healthcare Molecular Imaging, Knoxville, TN, USA), as

previously described (Brunner *et al*, 2012). Anaesthesia was induced with isoflurane (2.5%),

delivered via a face mask in pure oxygen at a rate of 1.2 L/min and maintained with isoflurane

(1.5%). Approximately 15 MBq 2-deoxy-2-[18F]fluoro-D-glucose ([18F]-FDG) (~100 μL) were

administered through a teil vein catheter and slowly flushed immediately afterwards with 50 μL

saline solution. Body temperature was monitored using a rectal thermometer and maintained

within the normal range using a heating pad. After placing animals within the aperture of the PET

scanner ECG electrodes (3M, St. Paul, MN, USA) were placed on both forepaws and the left hind

paw and ECG was recorded using a dedicated physiological monitoring system (BioVet; Spin

Systems Pty Ltd., Brisbane, Australia) (Todica *et al*, 2018). The PET emission acquisition (list-

mode) was initiated 30 min after [18F]-FDG injection and lasted 15 min (Brunner *et al.*, 2012;

Gross *et al*, 2016). For scatter and attenuation correction and additional 7-min long transmission

scan was performed using a Co-57 source.

The accuracy of the ECG trigger signal was verified retrospectively using in-house

software programmed in MATLAB (The Mathworks, Natick, USA) and in C programming

language and erroneous trigger events were removed when needed, as previously described

(Boning *et al*, 2013). Further processing of the data was performed using the Inveon Acquisition

Workplace (Siemens Medical Solutions, Knoxville, TN). As previously described, data was

reconstructed as a static image or as a cardiac gated image with 16 bins in a 128 × 128 matrix with

a zoom of 211% using an OSEM 3D algorithm with 4 and a MAP 3D algorithm with 32 iterations

(Brunner *et al.*, 2012). The reconstructed data was normalized, corrected for randoms, dead time

and decay as well as attenuation and scatter.

PET images were analysed using the Inveon Research Workplace in a blinded manner (Siemens

Medical Solutions, Knoxville, TN). Infarct sizes were determined from static reconstructed images

using QPS® (Cedars-Sinai, Los Angeles, CA, USA). Hereby, datasets were compared to a

normative database and the viability defect was calculated as percentage of the left ventricular

volume, as described previously (Lehner *et al*, 2014; Todica *et al*, 2014). Left ventricular function

volumes (EDV, ESV, SV), as well as the LVEF, were determined from ECG-gated images using

QGS® (Cedars-Sinai, Los Angeles, CA, USA), as described previously (Brunner *et al.*, 2012;

Croteau *et al*, 2003).

Statistical analysis

Student's t-test or Fisher's LSD test was used (Prism GraphPad®). Welch's correction for

unequal variances was used when applicable. A p-value of $p < 0.05$ was considered significant.

The Shapiro-Wilk test was used to test normality. Data are presented as mean +/- standard

deviation (SD).

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The authors declare no conflict of interest.

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Figure 1. Absence of resident cardiac macrophages in *Csf1r*^{ΔFIRE} mice.

(A) Flow cytometry analysis of 3 month-old *Rank*^{Cre}*Rosa26*^{eYFP} mice, showing single/CD45$^+$/lin-(CD11c, Ter119, Tcrß, Nk1.1)/CD11b$^+$ cardiac cells, eYFP expression in macrophages (CD64$^+$/F4/80$^+$) and percentage of eYFP$^+$ blood monocytes, microglia and cardiac macrophages (n=3-5 each from an independent experiment). (B) Flow cytometry analysis of 3 month-old *Flt3*^{Cre}*Rosa26*^{eYFP} mice, showing macrophage expression of eYFP and percentage of eYFP$^+$ blood monocytes, microglia and cardiac macrophages (n=4 each from an independent experiment). **(C)** Representative flow cytometry analysis of cardiac macrophages in *control* and Δ*FIRE mice* **(D)** Quantification of myeloid cells by flow cytometry (CD45$^+$/lin$^-$/CD11b$^+$), macrophages (CD45$^+$/lin$^-$/CD11b$^+$/CD64$^+$/F4/80$^+$), neutrophils (CD45$^+$/lin$^-$/CD11b$^+$/CD64$^-$/F4/80$^-$/Ly6g$^+$) and Ly6c^{hi} monocytes (CD45$^+$/lin$^-$/CD11b$^+$/CD64$^-$/F4/80$^-$/Ly6g-/Ly6c^{hi}) (*n=6 for control* and n=5 for Δ*FIRE* mice, each single experiments). **(E)** Representative flow cytometry analysis of cardiac macrophages and their expression of eYFP in *Csf1r*$^{ΔFIRE/+}$*Rank*^{Cre}*Rosa26*^{eYFP} *and* *Csf1r*$^{ΔFIRE/ΔFIRE}$*Rank*^{Cre}*Rosa26*^{eYFP}. **(F)** Representative immunohistological images showing macrophages (CD68$^+$ cells in white and Hoechst in blue) in *control* and Δ*FIRE* hearts in 3 month-old mice at baseline conditions (scale bars represent 500μm). **(F)** Quantification of macrophages by histology ((*n=3 for control* and Δ*FIRE* mice). Either Fisher's LSD test or unpaired t-test were performed and mean ± SD is shown.

Figure 2

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Figure 2. **Changes in the cardiac immune phenotype in *Csf1r^ΔFIRE* mice in baseline conditions.**
(A) Experimental setup to analyze cardiac immune cells using scRNA-seq of sorted CD45⁺/live
cells. **(B)** UMAPs of control and ΔFIRE in baseline conditions (n=3 for *control* and Δ*FIRE)* **(C)**
Absolute difference (percentage points) in cluster abundance between *control* and Δ*FIRE*. **(D)**
Contribution of EMP-derived (*eYfp* expressing) macrophages to the different macrophage clusters
analysed by scRNA-seq analysis of immune cells harvested from a *Rank^CreRosa26^eYFP* mouse. **(E)**
Phagocytosis score projected on a UMAP displaying *control and* Δ*FIRE* immune cell subsets.
Violin and box plots show the computed phagocytosis score combined in all macrophage clusters
(n1/n2 represents number of cells from control/ Δ*FIRE* mice).
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Figure 3. Adverse cardiac remodeling in *Csf1r^ΔFIRE* mice after I/R injury
(**A**) Schematic of the sequential analysis of cardiac function, dimensions and viability using positron-emission tomography 6 and 30 days after I/R injury in *control* and *ΔFIRE* with (B and C) showing the intraindividual changes in each parameter from d6 to d30 and (D-G) the individual timepoints on d6 and d30 (d6: n=11 for *control and ΔFIRE*, d30: n=10 for *control and n=11 for ΔFIRE*). (**B and D**) left ventricular ejection fraction (LVEF), (**C and E**) percentage of the viability defect, (**F**) stroke volume and (**F**) left-ventricular end-diastolic volume. (**H**) Representative immunohistological images showing the fibrotic area (WGA⁺ area) in hearts from *control and ΔFIRE* mice 30 days after I/R injury. Right panel shows the percentage of fibrotic area in the respective groups (n= 6 for each group). Student's t-test was performed and mean ± SD is shown.

Figure 4. Recruitment of BM-derived macrophages into infarct zone of $Csf1r^{\Delta FIRE}$ mice.
(A) Representative immunohistology of hearts from $\Delta FIRE$ mice 30 days after I/R injury showing macrophages (CD68$^+$ cells in red and Hoechst in blue) in the infarct, border and remote zone. Right panel shows number of cardiac macrophages in the respective area (n=5 *control* and n=3 for $\Delta FIRE$). **(B)** Flow cytometry analysis of $Flt3^{Cre}Rosa26^{mT/mG}$ mice 2 days after I/R injury, (left) representative flow cytometry showing expression of tomato and GFP in macrophages in the remote and ischemic myocardium and (right) number of tomato$^+$ and GFP$^+$ cardiac macrophages in the respective area (n=3, each individual experiments). **(C)** Flow cytometry analysis of $Rank^{Cre}Rosa26^{RFP}$ mice 2 days after I/R injury, (left) representative flow cytometry showing expression of RFP in macrophages in the remote and ischemic myocardium and (right) number of RFP$^-$ and RFP$^+$ cardiac macrophages in the respective area (n=3, each individual experiments). **(D)** Histological analysis of $Flt3^{Cre}Rosa26^{mT/mG}$ mice 30 days after I/R injury in the infarct, border and remote zone, (left) representative immunohistology of the infarct and border zone and (right) number of GFP$^-$ and GFP$^+$ cardiac macrophages in the respective areas (n=4). Fishers LSD test was performed for all experiments and mean ± SD is shown.

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Figure 5. Transcriptional landscape of resident versus recruited macrophages in I/R injury
(A) Experimental setup to generate non-irradiation BM chimera using *CD45.2 Mx1^{Cre}Myb^{flox/flox}*
and transplantation of CD45.1 BM. I/R injury was induced 4 weeks after BM-transplantation and
CD45.1+ and CD45.2+ macrophages were sorted from the remote and ischemic myocardium 2 days
after I/R injury and RNA-sequencing was performed on bulk cells (n=3)**. (B and C)** Volcano plot
showing differential gene expression analysis results of recruited CD45.1 vs. resident CD45.2
macrophages in the **(B)** remote and **(C)** ischemic zone. **(D)** Gene ontology enrichment analysis
showing specific biological processes enriched in CD45.1 and CD45.2 macrophages in the
ischemic and remote zone.
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Figure 6. **Altered inflammatory patterns and immune cell communication in _Csf1r$^{\Delta FIRE}$_ mice.**
(**A**) Experimental setup to analyze transcriptional changes in cardiac immune cells on a single cell
level 2 days after I/R injury in _ΔFIRE_ mice. (**B**) UMAPs of control and ΔFIRE 2 days after I/R
injury (n=2 for _control_ and _ΔFIRE)_. (**C**) Absolute difference (percentage points) in cluster
abundance between _control_ and_ΔFIRE_. (**D**) Inflammasome score projected on a UMAP displaying
control and ΔFIRE immune cell subsets after I/R injury. Violin and box plots show the computed
inflammasome score in neutrophil clusters (n1/n2 represents number of cells from control/ _ΔFIRE_
mice). (**E**) Ligand–receptor interactions of _antigen-presenting, Ccr2^{lo} ly6c^{lo} and homeostatic
macrophages_ (highlighted) with other immune cell clusters. Shown are the aggregated
communication scores (width of interactions) for all cell types. Only communication scores larger
than 6 are considered. (**F**) Number of interactions (with communication score > 6) outgoing from
homeostatic, antigen presenting and Ccr2^{lo} macrophages to other immune cell clusters.

Figure 7. **Ablation of resident and recruited macrophages severely impacts on cardiac healing after I/R injury**

(A) Schematic of the analysis of cardiac function and infarct size in mice treated with PLX5622 7 days prior and 30 days after I/R injury. **(B)** Number of cardiac macrophages and neutrophils in the remote and ischemic myocardium 2 days after I/R injury in mice fed control chow (n=6) or PLX5622 (n=7). **(C)** Representative immunohistology of hearts 30 days after I/R injury showing macrophages (CD68^{+} cells in red and Hoechst in blue) in the infarct, border and remote zone and **(D)** number of cardiac macrophages in the respective area (n=4 for control chow and n=4 for PLX5622). **(E)** Left ventricular ejection fraction (LVEF), **(F)** viability deficit, **(G)** stroke volume and **(H)** end-diastolic volume measured using positron-emission tomography 6 and 30 days after I/R injury (n=6 for control chow, n=8 for PLX5622). **(I)** Representative immunohistological images showing the fibrotic area (WGA[+] area) in hearts 30 days after I/R injury from mice fed control chow or PLX5622. Percentage of fibrotic area in the respective groups (n= 4 for each group). Student's t-test or Fishers LSD test was performed and mean ± SD is shown.