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Reporting Summary

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Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☒	☐	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	data collection was performed manually
Data analysis	GraphPad Prism 7 and SAS for all statistical analyses. FlowJo v7.6.5. for FACS and Partek Genome Suite was used for microarray analysis

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
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Provide your data availability statement here.

Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences

Study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Sample sizes were chosen based on specimen availability. We targeted a sample size of n>10 to account for sample variability.
Data exclusions	We did not exclude any data.
Replication	All experiments were reproduced at least 3 times. All attempts at replication were successful.
Randomization	When comparing between groups, samples were randomly assigned.
Blinding	Investigators quantifying data were blinded to group allocation during the analysis and measurement procedures.

Materials & experimental systems

Policy information about availability of materials

n/a	Involved in the study
☒	☐ Unique materials
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Research animals
☐	☒ Human research participants

Antibodies

Antibodies used	Flow cytometery antibodies are listed in Supplemental Figure 3. Immunostaining antibodies: CD68 (KP1 eBiosceince 1:2000), CCR2 (7A7 Abcam 1:2000), CD34 (Q/bend1 Abcam 1:2000), Collagen 1 (COL-1 Abcam 1:2000), IL-1β (NB600-633 NOVUS 1:2000), Ki67 (ab15580 Abcam 1:1000), CD14 (ab183322 Abcam 1:2000), CD64 (ab119843 Abcam 1:4000), iNOS (ab76198 Abcam 1:1000), HLA-DR (clone L243 Biolegend 1:1000).
Validation	All antibodies were commercially available and validated in our laboratory using isotype controls.

Human research participants

Policy information about studies involving human research participants

Population characteristics	Recruitment of human research participants, covariate data collection, and analysis is described in the methods section. Relevant covariates (age, sex, race, heart failure etiology, diabetes, hypertension, echocardiographic parameters) are displayed in Supplemental Tables 1 and 2.

Method-specific reporting

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ Magnetic resonance imaging

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Sample preparation is described in detail in the methods section. To generate single cell suspensions, saline perfused cardiac tissue specimens were finely minced, and digested in DMEM with Collagenase type 1 (450 U/ml) Hyaluronidase (60 U/ml) and DNase I (60 U/ml) for 1 hour at 37°C. All enzymes were sourced from Sigma. Digested samples were then filtered through 40 µM cell strainers and washed with cold HBSS that was supplemented with 2% FBS and 0.2% BSA. Red blood cell lysis was performed with ACK lysis buffer (Thermo Fisher Scientific). Cells were washed with HBSS and resuspended in 100 µL of FACS buffer (DPBS containing 2% FBS and 2 mM EDTA).
Instrument	BD Lsr II and BD Aria III
Software	FlowJo
Cell population abundance	The relevant cell populations represent 40-50% of CD45+ immune cells within the heart.
Gating strategy	Gating strategy is displayed in Figure 1c

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.