Supplemental tables

Table S I. Top ranked genes for single-cell RNA sequencing analysis cluster.

genes	logfoldchanges	score	*P*-value	cluster
Ms4a2	32,17730713	4,885575771	1,03127E-06	*Basophil*
Mcpt8	30,8923893	3,053484917	0,002262	*Basophil*
Fcer1a	14,95272446	4,885575771	1,03127E-06	*Basophil*
Cpa3	12,7094593	4,883338928	1,04304E-06	*Basophil*
Cyp11a1	10,95959663	3,661199331	0,000251037	*Basophil*
Cd200r3	10,23174095	4,270777702	1,94792E-05	*Basophil*
Gata2	9,726697922	4,266676903	1,98406E-05	*Basophil*
Il6	9,017007828	3,037453175	0,002385864	*Basophil*
Rab44	8,831991196	3,041927099	0,002350687	*Basophil*
Hdc	8,333846092	4,85425806	1,20838E-06	*Basophil*
Ifitm1	6,255457401	3,474038124	0,000512688	*Basophil*
Ccl3	5,630964279	3,196651936	0,001390325	*Basophil*
Ccl4	5,249568462	3,131033897	0,001741921	*Basophil*
Cd7	5,219405651	3,473292589	0,000514115	*Basophil*
Ccl6	4,417239666	3,572465658	0,000353636	*Basophil*
Cd79a	7,740267754	26,43621254	5,2566E-154	*B cell*
Ly6d	7,35939455	24,84671783	2,806E-136	*B cell*
Ms4a1	7,12919569	24,83703995	3,57E-136	*B cell*
Ebf1	6,799319744	25,2107811	3,0511E-140	*B cell*
Fcmr	6,702617168	20,79995346	4,33232E-96	*B cell*
Mzb1	6,31575489	18,88094521	1,63631E-79	*B cell*
Cd79b	6,153306961	26,15522385	8,5949E-151	*B cell*
Gm43603	5,92986393	20,7942276	4,88141E-96	*B cell*
Bank1	5,764195442	20,46655655	4,27803E-93	*B cell*
Fcrla	5,708143234	16,42088318	1,35579E-60	*B cell*
H2-DMb2	5,518703461	23,5134697	2,97E-122	*B cell*
Siglecg	4,954312801	16,98919868	9,87303E-65	*B cell*
H2-Ob	4,809836388	18,07178307	5,31671E-73	*B cell*
Ralgps2	4,658328533	16,62799454	4,36973E-62	*B cell*
H2-Oa	4,252504349	17,28592873	6,0046E-67	*B cell*
Tcf7	4,513453007	13,56557465	6,40755E-42	*CD4 T cell*
Lef1	4,489587307	12,69128132	6,60956E-37	*CD4 T cell*
Cd3g	4,359367371	15,48692513	4,25144E-54	*CD4 T cell*
Cd3d	4,275510311	15,30279732	7,32393E-53	*CD4 T cell*
Lat	4,019424438	13,23984528	5,16551E-40	*CD4 T cell*
Ms4a4b	3,832198143	14,97555923	1,06072E-50	*CD4 T cell*
Tmsb10	1,814377427	13,13952541	1,95449E-39	*CD4 T cell*
Rpl12	1,558308005	15,21677113	2,7371E-52	*CD4 T cell*
Rpl5	1,164606333	14,22511196	6,40016E-46	*CD4 T cell*
Rpl13a	1,108007312	13,73043728	6,673E-43	*CD4 T cell*
Rps27	1,076374292	12,76496792	2,57258E-37	*CD4 T cell*
Rps7	1,060416102	14,07960415	5,06932E-45	*CD4 T cell*
Rps15a	1,060255647	14,03175163	9,96588E-45	*CD4 T cell*
Gm10073	1,059884548	12,80953503	1,45002E-37	*CD4 T cell*

Rps24	1,041148901	14,16500854	1,50848E-45	*CD4 T cell*
Cd8b1	6,919670105	14,25400352	4,23304E-46	*CD8 T cell*
Nkg7	5,828896523	14,91225433	2,74331E-50	*CD8 T cell*
Cd3g	5,196243286	16,40915108	1,64488E-60	*CD8 T cell*
Cd3d	5,186452866	16,85204124	1,01355E-63	*CD8 T cell*
Thy1	4,906655312	15,2247591	2,42251E-52	*CD8 T cell*
Ms4a4b	4,83349371	16,36470032	3,41709E-60	*CD8 T cell*
Lck	4,134778976	13,33833313	1,38522E-40	*CD8 T cell*
Lat	4,000152111	12,48033619	9,55824E-36	*CD8 T cell*
AW112010	2,761917591	12,46634865	1,13927E-35	*CD8 T cell*
Saraf	2,309516191	13,27491283	3,23647E-40	*CD8 T cell*
Tmsb10	2,153654337	14,93543816	1,93795E-50	*CD8 T cell*
Rpl22l1	1,552589536	12,63016987	1,43968E-36	*CD8 T cell*
Rpl12	1,524740815	14,1247673	2,67282E-45	*CD8 T cell*
Rpl13a	1,315062165	14,8501749	6,9387E-50	*CD8 T cell*
Rpsa	1,281026483	14,58432674	3,53393E-48	*CD8 T cell*
Cd209a	7,084644	9,428524	4,16E-21	*Dendritic cells*
Ffar2	6,474395	7,935768	2,09E-15	*Dendritic cells*
Flt3	5,387873	8,287161	1,16E-16	*Dendritic cells*
Klrb1b	5,320319	7,995071	1,29E-15	*Dendritic cells*
Ifitm1	4,323915	7,725995	1,11E-14	*Dendritic cells*
Clec10a	3,970304	8,628596	6,21E-18	*Dendritic cells*
H2-Eb1	3,815535	12,81378	1,37E-37	*Dendritic cells*
H2-Aa	3,774281	13,03738	7,5E-39	*Dendritic cells*
Klrd1	3,760131	9,432617	4E-21	*Dendritic cells*
H2-Ab1	3,758918	13,04911	6,43E-39	*Dendritic cells*
Cd74	3,682577	12,35097	4,81E-35	*Dendritic cells*
Cbfa2t3	3,473026	11,21492	3,45E-29	*Dendritic cells*
Olfm1	3,329613	10,15454	3,16E-24	*Dendritic cells*
Bhlhe40	3,171868	8,661235	4,67E-18	*Dendritic cells*
Plscr1	3,15024	8,928431	4,32E-19	*Dendritic cells*
Lyz2	5,86966	31,52023	4,60E-218	*Mono_macs*
C1qb	5,293979	24,27806	3,30E-130	*Mono_macs*
Ms4a7	5,277662	23,96194	6,90E-127	*Mono_macs*
Apoe	4,955027	30,22719	1,00E-200	*Mono_macs*
C5ar1	4,909602	24,92502	4,00E-137	*Mono_macs*
Trem2	4,87865	24,98375	9,20E-138	*Mono_macs*
Adgre1	4,743454	25,82356	4,80E-147	*Mono_macs*
C3ar1	4,596313	24,15751	6,20E-129	*Mono_macs*
Fcgr3	4,574409	29,45475	1,10E-190	*Mono_macs*
Mafb	4,560227	25,82833	4,30E-147	*Mono_macs*
Ctsb	4,493658	31,3882	2,90E-216	*Mono_macs*
Fcer1g	4,40872	31,15072	5,00E-213	*Mono_macs*
Cd14	4,285527	25,41162	1,90E-142	*Mono_macs*
Aif1	4,197026	26,54554	2,90E-155	*Mono_macs*
Csf1r	4,193206	28,82995	9,00E-183	*Mono_macs*
Ncr1	11,20700359	8,590027809	8,69482E-18	*NK cells*
Klra8	10,77591133	5,938164711	2,8823E-09	*NK cells*
Gzma	10,68203545	7,235824108	4,6271E-13	*NK cells*
Klrb1a	9,677329063	4,947109699	7,53235E-07	*NK cells*

Klrb1c	9,55841732	8,900306702	5,56926E-19	*NK cells*
Klre1	8,628218651	8,564511299	1,08535E-17	*NK cells*
Ccl5	8,304552078	8,601051331	7,89894E-18	*NK cells*
Gzmb	7,445357323	6,201085091	5,60751E-10	*NK cells*
Nkg7	7,269181728	8,809672356	1,25512E-18	*NK cells*
Klrb1f	7,001911163	5,556236267	2,75654E-08	*NK cells*
Fasl	6,977669239	5,54847908	2,88165E-08	*NK cells*
Xcl1	6,944013596	6,153522968	7,57805E-10	*NK cells*
Klrk1	6,69391346	8,400798798	4,43452E-17	*NK cells*
Car2	6,611712933	5,838140488	5,27866E-09	*NK cells*
Il2rb	6,242600441	6,46196413	1,03352E-10	*NK cells*

Table S II. Description of patients enrolled in leukocyte kinetics study.

Baseline characteristics	**Control** (*n* = 9)	**STEMI** (*n* = 11)	***P*-value**
Female sex	2 (22.2 %)	1 (9.1 %)	*P* = 0.43
Age (mean ± SD)	70.2 (± 9.1)	65.6 (± 13.9)	*P* = 0.46
CV risk			
Diabetes mellitus	2 (22.2 %)	1 (9.1 %)	*P* = 0.43
Smoker	2 (22.2 %)	3 (27.3 %)	*P* = 0.80
Hypertension	7 (77.8 %)	8 (72.7 %)	*P* = 0.80
Hypercholesterolemia	5 (55.6 %)	7 (63.6 %)	*P* = 0.72
Family history	2 (22.2 %)	6 (54.5 %)	*P* = 0.15
Obesity	2 (22.2 %)	5 (45.5 %)	*P* = 0.29
Infarct-related artery			
Left anterior descending	n/a	4 (36.4 %)	n/a
Circumflex	n/a	3 (27.3 %)	n/a
Right coronary artery	n/a	4 (36.4 %)	n/a

Table S III. Description of STEMI patients enrolled in the prospective outcome study.

Baseline characteristics	*n* = 82
Female sex	11 (13.4 %)
Age (mean, range)	59.1 (40 - 79)
CV risk	
Diabetes mellitus	23 (28.0 %)
Smoker	26 (31.7 %)
Hypertension	42 (51.2 %)
Hypercholesterolemia	36 (43.9 %)
Family history	19 (23.2 %)
Obesity	29 (35.4 %)
Infarct-related artery	
Left anterior descending	37 (45.1 %)
Circumflex	11 (13.4 %)
Right coronary artery	34 (41.5 %)
Laboratory parameters	
Basophils max – cells/nl (mean ± SD)	0.03 (± 0.02)
cTnT 24h – pg/ml (mean ± SD)	2178.1 (± 2672.9)
CRP max – mg/l (mean ± SD)	43.0 (± 55.7)
Leukocytes max – cells/nl (mean ± SD)	12.0 (± 4.0)

Table S IV. Univariate regression analysis for the prospective outcome study.

Covariate	**R square**	***P*-value**
Sex	0.0295	0.1231
Age	0.0025	0.6548
CV risk		
Diabetes mellitus	0.0259	0.1484
Smoker	0.0185	0.2225
Hypertension	0.0078	0.4302
Hypercholesterolemia	0.0181	0.2278
Family history	0.0014	0.9704
Obesity	0.0032	0.6137
Laboratory parameters		
Basophils max	0.1224	0.0013*
cTnT 24h (log)	0.1467	0.0004*
CRP max	0.1623	0.0002*
Leukocytes max	0.0999	0.0038*

Table S V. Multivariate regression analysis for the prospective outcome study.

Covariate	Coefficient	Confidence interval	*P*-value
Intercept	0.083	[-0.059; 0.226]	0.247
Basophils max	-0.017	[-0.030; -0.005]	0.007*
cTnT 24h (log)	0.065	[0.025; 0.104]	0.002*
CRP max	0.0007	[0.0003; 0.0012]	0.002*
Sex	-0.073	[-0.147; -0.0001]	0.049*

Supplemental methods

TTC staining

For the detection of infarction area 24 hours after MI with TTC staining, hearts were removed and rinsed quickly in PBS. Hearts were frozen with dry ice and sliced into parallel transverse sections (thickness 1 mm). The slices were incubated in freshly prepared 2 % TTC (Sigma-Aldrich) at 37°C for 15 minutes. Each heart was recorded with a microscope and a digital camera. TTC-negative staining area (white area) was defined as infarction area.

Plasma and serum measurements

For the measurement of cardiac Troponin T (cTnT), peripheral blood was collected from facial vein puncture in a heparinized tube at indicated time points. Plasma obtained after centrifugation (4°C, 2000g, 10 minutes) was 40 times diluted in PBS and cTnT was detected using an automated Cobas Troponin T hs STAT Elecsys (Roche). For measurements of IgE, peripheral blood was collected, kept at room temperature for 30 minutes and centrifugated (2000g, 10 minutes) in order to obtain serum. Serum levels of IgE were obtained using murine IgE ELISA kits (Abcam) following the manufacturer's instructions.

Isolation, Cell Culture and Stimulation of human basophils and monocytes

For isolation of basophils and monocytes from peripheral blood of healthy donors, ethylene diamine tetra-acetic acid (EDTA)-blood was separated via density gradient centrifugation with Ficoll / Percoll (100/6, density 1.080 g/l) followed by counter flow elutriation. Basophils were further purified by magnetic cell sorting (MACS) using the basophil isolation kit II for negative selection of basophils (Miltenyi). Across the samples, ≥98% purity was achieved. After isolation, cell culture was performed in

Iscove's Modified Dulbecco's Media (IMDM; Capricorn) containing 2 mM glutamine (Capricorn), 5 µg/ml insulin (Gibco), 50 µg/ml apo-transferrin (Sigma-Aldrich), 100 µg/ml Pen/Strep (Capricorn), 10% heat-inactivated Fetal Calf Serum (GE Healthcare) and 2.5 ng/ml IL-3 (gift from Kirin Brewery, Japan) as a basophil survival factor. Basophils were stimulated overnight with a final concentration of 100 ng/ml recombinant IPSE/alpha-1, 2.5 ng/ml IL-33 (Biolegend) or both. Basophil culture supernatants were kept at -80°C until either analyzed for cytokine production by the respective cytokine-specific ELISA (IL-4 and IL-13 (Diaclone)) or further used for culture of monocytes. Therefore, 0.25 x 10^6 monocytes were stimulated with 10 ng/ml LPS (Salmonella friedenau, kind gift of Prof. H. Brade, RCB) and cultured in 1 ml basophil culture supernatant per well in 24-well flat-bottom culture plates for 24 h. Monocytes were harvested and analyzed at the flow cytometer LSR II (BD Biosciences) for expression of CD206 and CD209 after staining with anti-human CD206-FITC (BD Biosciences, clone 19.2) and anti-human CD209-PE (BD Biosciences, clone DCN46).

Fluorescent antibodies and gating strategies

The following antibodies were used: anti-CD45-PerCP-Cy5.5 (BD Biosciences, clone 30-F11), anti-CD45-BV510 (Biolegend, clone 30-F11), anti-CD45-FITC (BD Biosciences, clone 30-F11), anti-Ter119-PE (BD Biosciences, clone TER-119), anti-CD4-PE (Biolegend, clone RM4-5), anti-CD19-PE (BD Biosciences, clone 1D3), anti-Ly6G-PE (BD Biosciences, clone 1A8), anti-CD11c-PE (BD Biosciences, clone HL3), anti-CD117-PE-Cy7 (BD Biosciences, clone 2B8), anti-CD49b-APC (Biolegend, clone DX5), anti-FcεRI-FITC (Biolegend, clone MAR-1), anti-IgE-BV421 (BD Biosciences, clone R35-72), anti-CD90.2-PE (BD Biosciences, clone 53-2.1), anti-B220-PE (BD Biosciences, clone RA3-6B2), anti-CD49b-PE (BD Biosciences, clone DX5), anti-

NK1.1-PE (BD Biosciences, clone PK136), anti-CD11b-APC-Cy7 (BD Biosciences, clone M1/70), anti-F4/80-PE-Cy7 (Biolegend, clone BM8), anti-Ly6C-APC (BD Biosciences, clone AL-21), anti-CD64-BV421 (Biolegend, clone X54-5/7.1), anti-CD206-APC (Biolegend, clone C068C2), anti-CD11c-BV510 (Biolegend, clone N418), anti-CD3-BV421 (Biolegend, clone 17A2), anti-CD4-FITC (Biolegend, clone RM4-5), anti-CD4-PE-Cy5 (Biolegend, clone RM4-5), anti-CD8-PE (Biolegend, clone 53-6.7), anti-B220-PE-Cy7 (BD Biosciences, clone RA3-6B2), anti-Ly6G-PerCP (Biolegend, clone 1A8), anti-GFP-APC (Biolegend, clone FM264G).

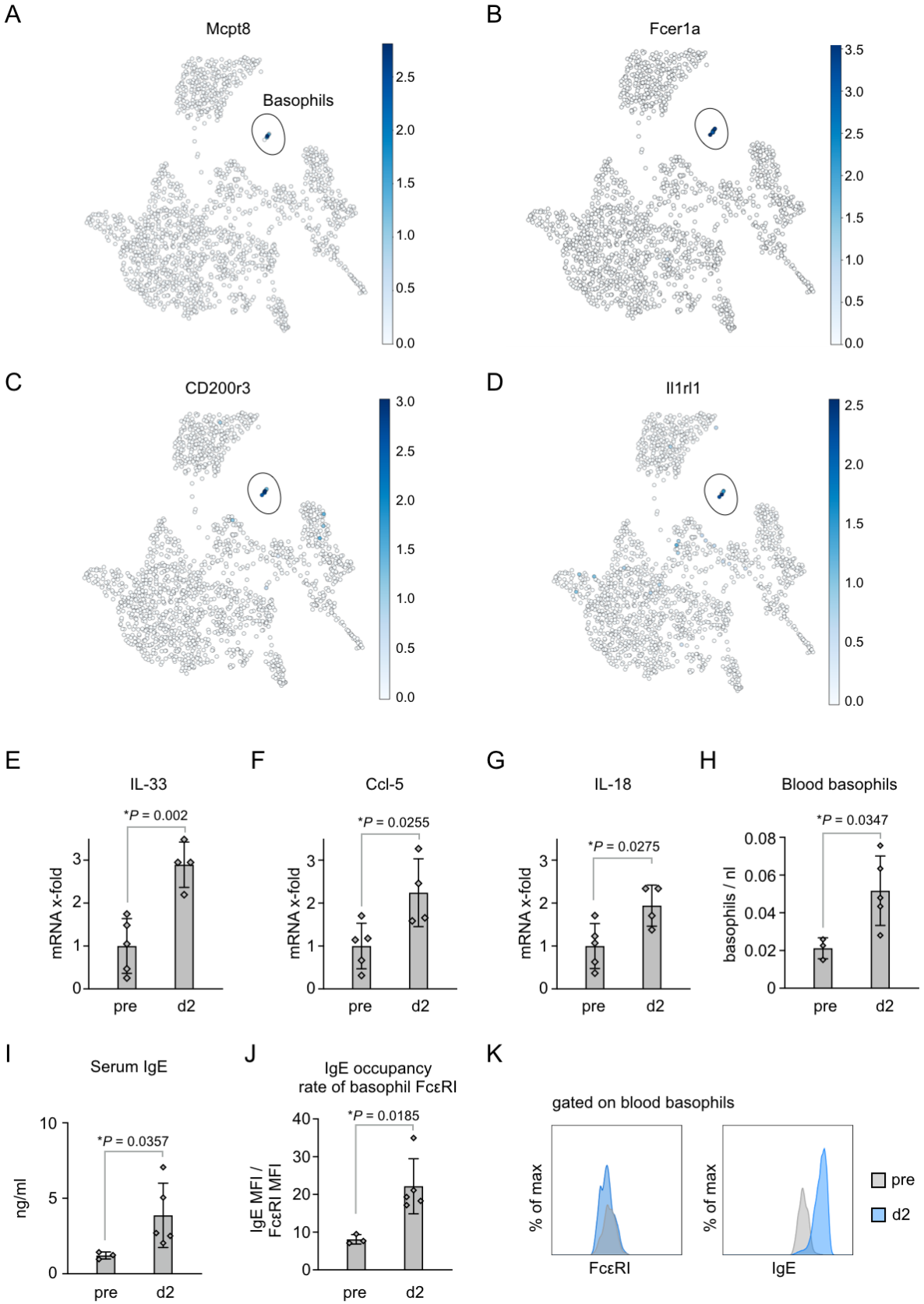
Basophils were identified as $CD45^{int/high}$, $Lin1^{-}$(Ter119;CD4;CD19;Ly6G;CD11c), $CD117^{-}$, $CD49b^{+}$, IgE^{+}. Mast cells were gated as $CD45^{+}$, $Lin1^{-}$, $CD117^{+}$, IgE^{+} cells. Inflammatory monocytes were identified as $CD45^{+}$, $Lin2^{-}$ (CD90;B220;CD49b;NK1.1;Ly6G;Ter119), $CD11b^{+}$, $F4/80^{-}$, $Ly6C^{high}$. Anti-inflammatory macrophages were identified as $CD45^{+}$, $Lin2^{-}$, $CD11b^{+}$, $F4/80^{+}$, $Ly6C^{low}$ $CD64^{+}$. Dendritic cells were identified as $CD45^{+}$, $CD11b^{+}$, $Ly6G^{-}$, $CD11c^{+}$. $CD4^{+}$ T cells were gated as $CD45^{+}$, $CD3^{+}$, $CD4^{+}$ cells. $CD8^{+}$ T cells were identified as $CD45^{+}$, $CD3^{+}$, $CD8^{+}$ cells. B cells were gated as $CD45^{+}$, $CD3^{-}$, $B220^{+}$ cells. Neutrophils were identified as $CD45^{+}$, $CD11b^{+}$, $Ly6G^{+}$.

Quantitative real-time PCR

The following primers were used: 18s: GCAATTATTCCCCATGAACG (fwd), GGCCTCACTAAACCATCCAA (rev); Tnfa: CCCTCACACTCAGATCATCTTCT (fwd), GCTACGACGTGGGCTACAG (rev); IL6: GATGCTACCAAACTGGATATAATC (fwd), GGTCCTTAGCCACTCCTTCTG (rev); IL13: GACTGCAGTCCTGGCTCTTGC (fwd), TGAGTCCACAGCTGAGATGCC (rev); Ifng: AGGAACTGGCAAAAGGATGGT (fwd),

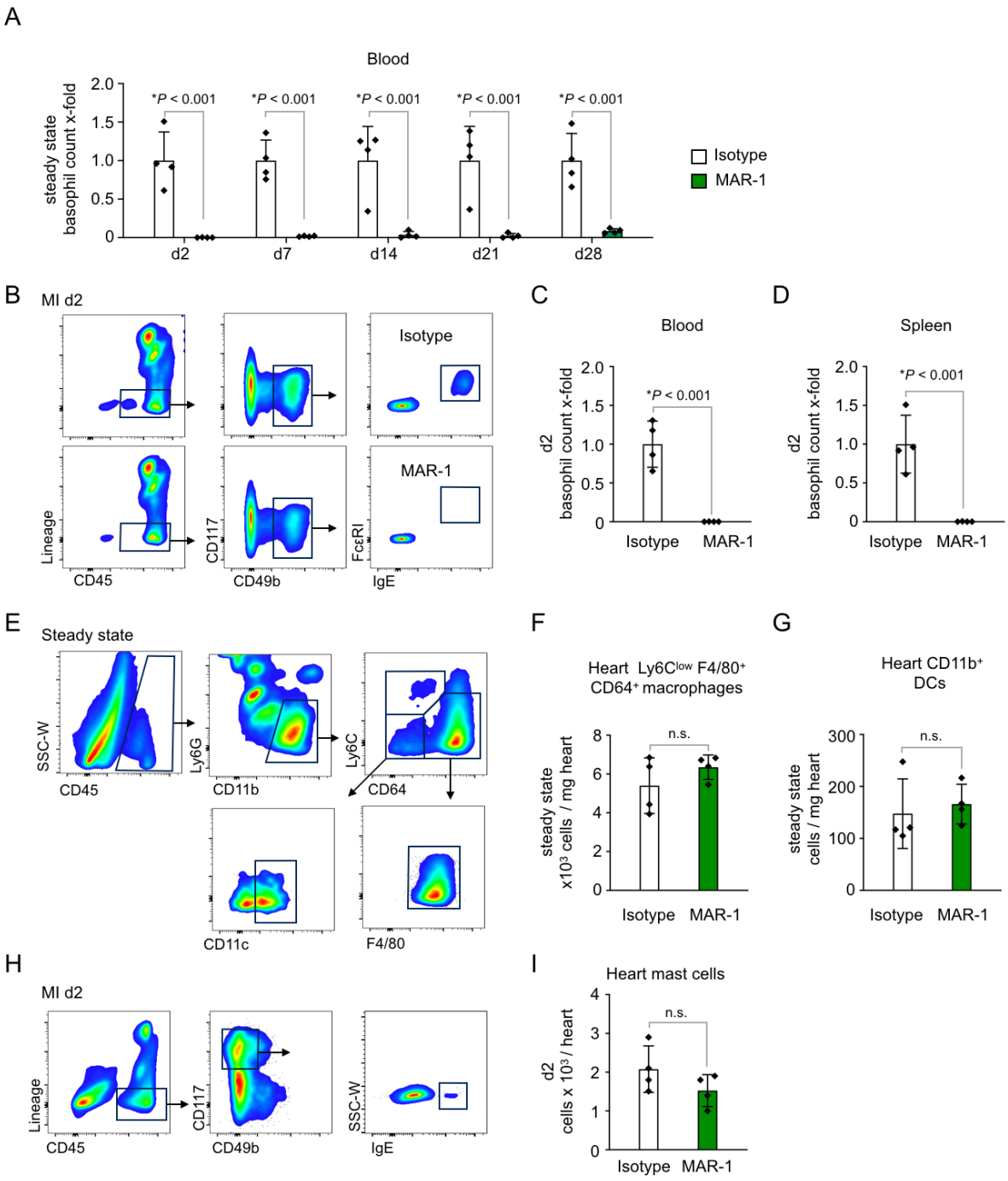
TCATTGAATGCTTGGCGCTG (rev); Il12b: TGGGAGTACCCTGACTCCTG (fwd), GAGGAACGCACCTTTCTGGT (rev); Arg1: TTTTAGGGTTACGGCCGGTG (fwd), CCTCGAGGCTGTCCTTTTGA (rev); Hdc: GATCAGATTTCTACCTGTGG (fwd), GTGTACCATCATCCACTTGG (rev); Vcam1: TCTTACCTGTGCGCTGTGAC (fwd), ACTGGATCTTCAGGGAATGAGT (rev); Ccl5: TGCAGAGGACTCTGAGACAGC (fwd), GAGTGGTGTCCGAGCCATA (rev); IL18: CAAACCTTCCAAATCACTTCCT (fwd), TCCTTGAAGTTGACGCAAGA (rev); IL33: GGTGAACATGAGTCCCATCA (fwd), CGTCACCCCTTTGAAGCTC (rev); IL4: ATCCTGCTCTTCTTTCTCGAATGT (fwd), GCCGATGATCTCTCTCAAGTGATT (rev).

Supplemental figures



Supplemental figure 1. Basophil markers and potential upstream mediators for basophil activation after MI.

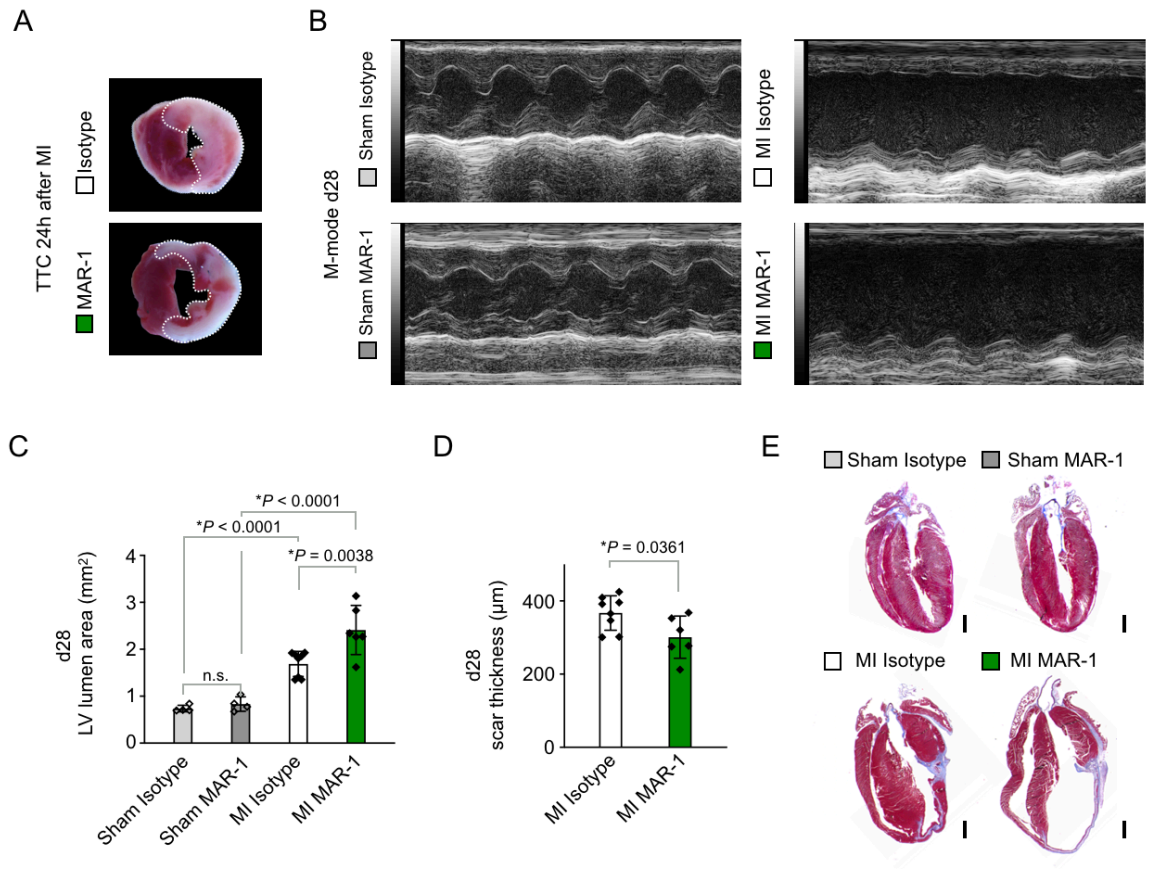
(**A**-**D**) Gene expression plot of basophil-specific markers (Mcpt8, Fcer1a, CD200r3 and IL-33-receptor Il1rl1) in leukocyte subpopulations on d7 after MI in the UMAP embedding. (**E**-**G**) mRNA expression of basophil chemoattractants IL-33, Ccl-5 and IL-18 in either healthy hearts or infarct tissue 2 days after MI (*n* = 4-5). Error bars show mean ± SD. Asterisks signify significant differences using two-tailed Student's t test. (**H** and **I**) Levels of blood basophils based on flow cytometric analysis and serum IgE levels under steady state and 2 days after MI in mice. (**J** and **K**) Representative histograms of FcεRI and IgE expression on blood basophils obtained from both healthy and infarcted mice based on flow cytometry. IgE occupancy was defined as IgE mean fluorescence intensity (MFI) normalized to FcεRI MFI (*n* = 3-5). Error bars show mean ± SD. Asterisks signifies significant difference using two-tailed Student's t test



Supplemental figure 2. Effect of MAR-1 administration under both steady state and post-MI conditions.

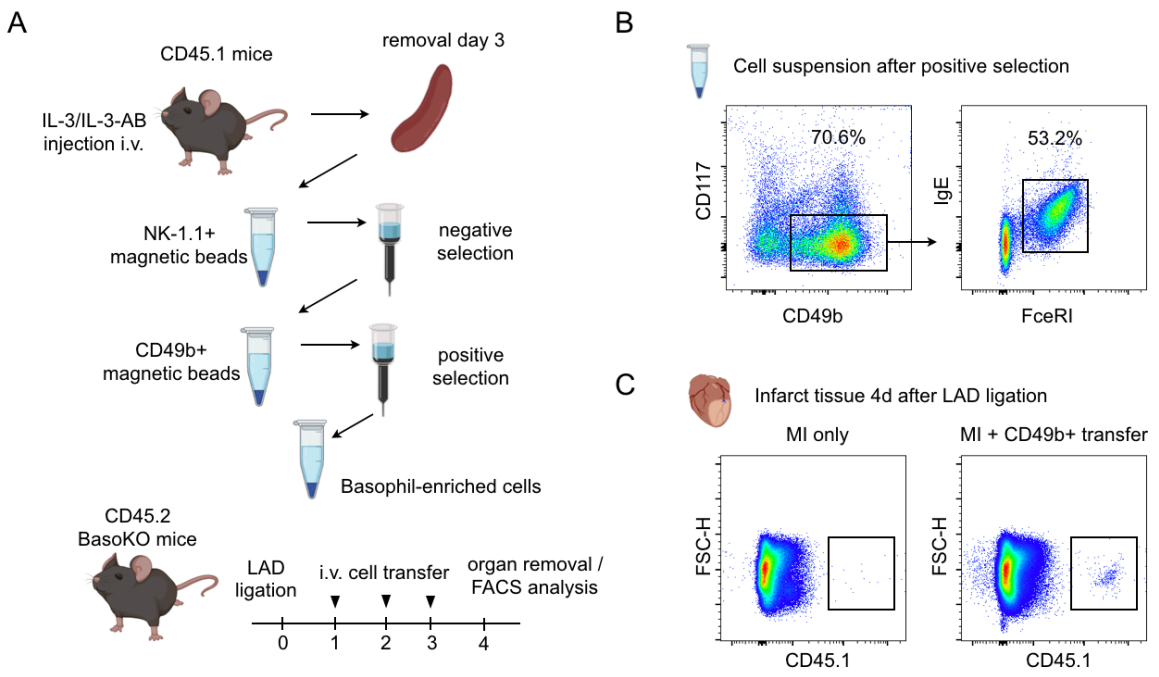
(**A**-**D**) Validation of basophil depletion via MAR-1 antibody treatment in blood under steady state (A), in blood 2d post-MI (B and C) and spleen 2d post-MI (D) (*n* = 4). Statistics was performed by using two-tailed Student's t test. (**E**) Gating strategy for identification of cardiac macrophages and dendritic cells under baseline conditions. ~~after both, IgG and MAR-1 treatment.~~ (**F** and **G**) Absolute cell numbers of cardiac

$Ly6C^{low}F4/80^{+}CD64^{+}$ macrophages and cardiac $CD11b^{+}CD11c^{+}$ dendritic cells (DCs). (**H)** Gating strategy for identification of cardiac mast cells 2 days post-MI. (**I**) Mast cell levels assessed 2 days after MI (*n* = 4). Statistics was performed by using two-tailed Student's t test. Error bars show mean ± SD.



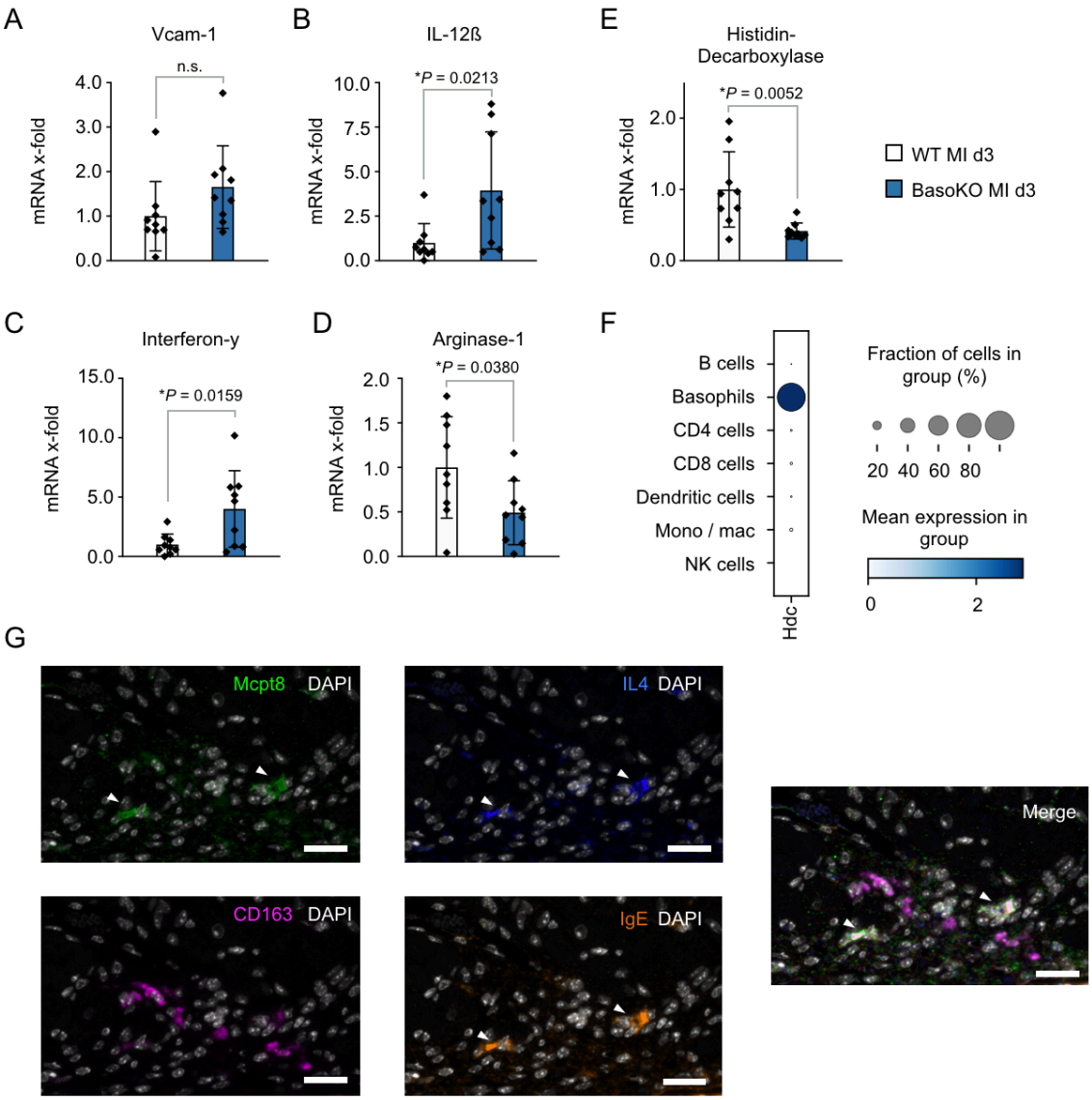
Supplemental figure 3. Histopathological and echocardiographic evaluation of basophil-depleted mice after acute MI in mice.

(**A**) Representative TTC stainings of hearts from IgG-treated and MAR-1-treated mice 24h after LAD ligation. The dotted line indicates the infarcted area. (**B**) Representative M-mode echocardiographic images of IgG-treated and MAR-1-treated mice 4 weeks after MI induction or sham intervention. (**C** and **D**) Quantification of left ventricular (LV) lumen area and scar thickness 4 weeks after MI (*n* = 4-8). Error bars show mean ± SD. Asterisks signify significant differences using two-way ANOVA (C) or two-tailed Student's t test (D). (**E**) Representative histological sections stained with Masson's trichrome 4 weeks after MI. The scale bar indicates 500 µm.



Supplemental figure 4. Reconstitution of basophils in BasoKO mice by adoptive transfer of basophil-enriched CD49b$^+$ splenocytes.

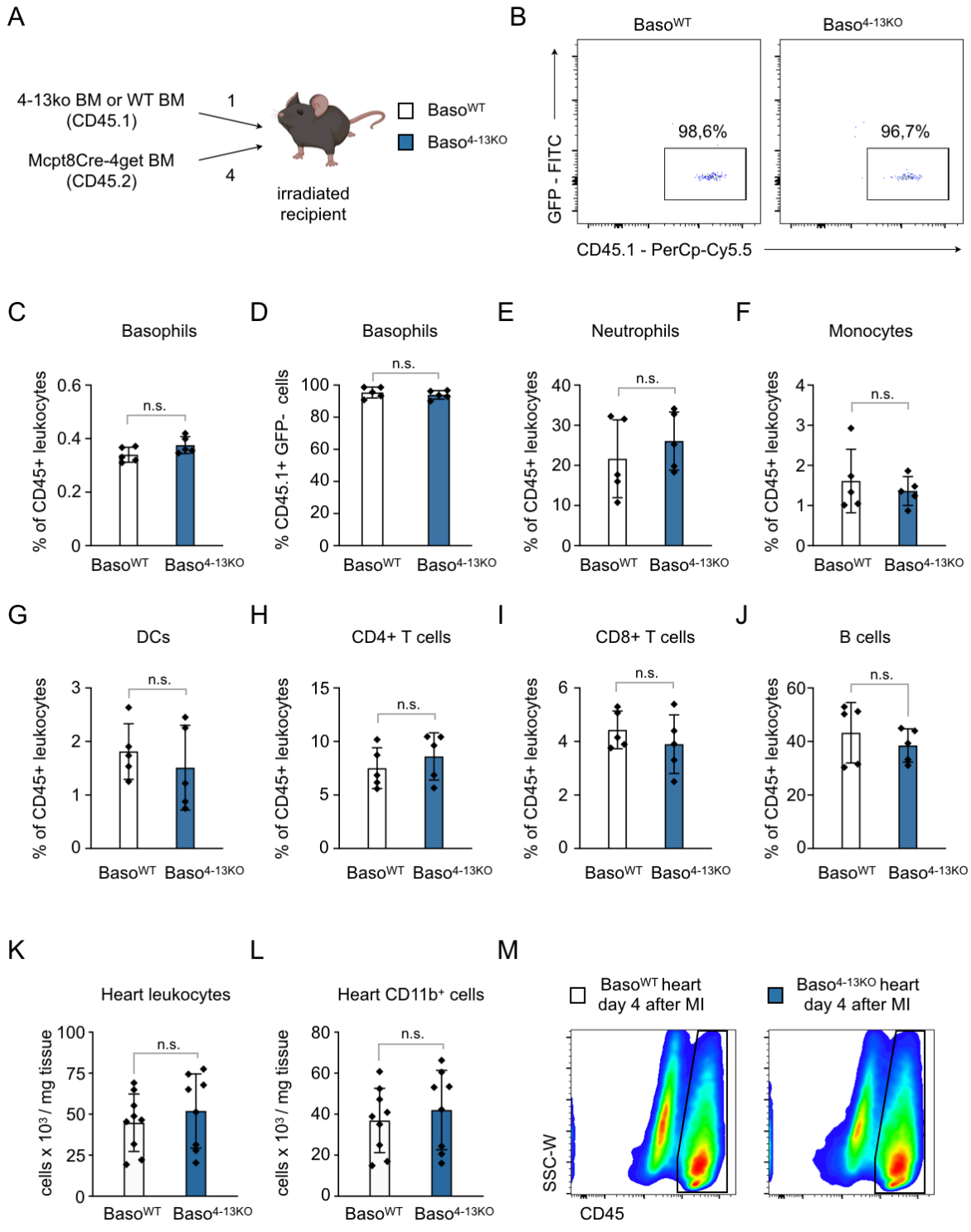
(**A**) Schematic and validation of the basophil transfer model. IL-3/IL-3-antibody-treated CD45.1 mice served as donors. Following negative selection of Nk1.1$^-$ cells from splenic single cell suspensions, basophils were enriched by using CD49b$^+$ magnetic beads. Basophil-enriched cells were adoptively transferred into CD45.2 BasoKO mice on day 1-3 after experimental MI. The scheme was created with BioRender. (**B**) Representative images of flow cytometric analysis of cell suspensions after positive selection step. Approximately 30-40% of all cells were found to be CD117$^-$ CD49b$^+$FcεRI$^+$IgE$^+$ basophils. (**C**) Frequencies of CD45.1+ cells were assessed 4 days after MI via flow cytometric analysis of hearts from CD45.2 BasoKO mice after transfer of basophil-enriched cells or MI only.



Supplemental figure 5. Basophils can be localized in close proximity to macrophages and influence macrophage polarization after MI.

(**A**-**D**) mRNA expression of Vcam-1, M1 markers IL-12β and Interferon-γ, and M2 marker/mediator Arginase I, in infarct tissue homogenates of WT and BasoKO mice 3 days after LAD ligation (*n* = 8-9). Error bars show mean ± SD. Asterisks signify significant differences using two-tailed Student's t test. (**E**) mRNA expression of Histidin-Decarboxylase (Hdc) in infarct tissue homogenates of WT and BasoKO mice 3 days after LAD ligation. (**F**) Gene expression dot plot of Hdc gene based on single-cell RNA sequencing analysis. Mean expression is depicted as color intensity, while

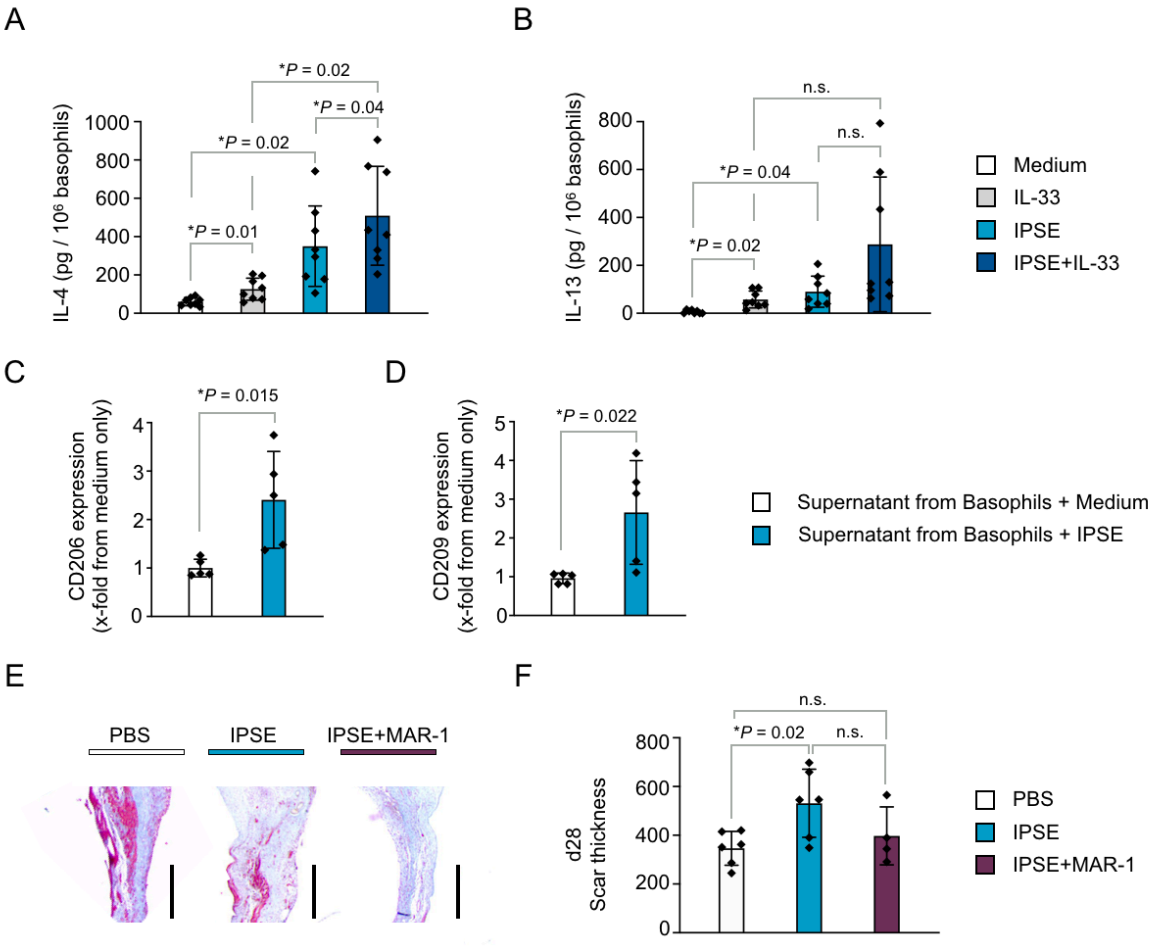
dot size represents fraction of cells expressing Hdc. **(G)** Multiplex immunohistochemistry of murine infarct tissue with staining of Mcpt8 (green), IL-4 (blue), IgE (orange), CD163 (violet), and DAPI (white). Arrowheads mark $Mcpt8^{+}$ cells. Scale bar indicates 20 μm.



Supplemental figure 6. Generation and characterization of mice with basophil-specific IL-4/IL-13 deficiency.

(**A**) Schematic of the generation of mixed bone marrow chimeras. Mcpt8Cre-4get BM was mixed at a 4:1 ratio with BM from either WT mice (CD45.1) or 4-13KO mice and injected intravenously into lethally irradiated recipient mice. (**B**-**D**) Number of basophils

in blood from Baso^{WT} or Baso$^{4\text{-}13KO}$ mice and percentage of CD45.1+ GFP- cells within basophils. (**E-J**) Number of neutrophils, monocytes, DCs, CD4^{+} T cells, CD8^{+} T cells, and B cells in blood from Baso^{WT} or Baso$^{4\text{-}13KO}$ mice under steady state (*n* = 5). Error bars show mean ± SD. For statistics, two-tailed Student's t test was performed. (**K** and **L**) Quantification of total cell numbers per mg heart tissue of CD45^{+} cells or CD45^{+}CD11b^{+} cells 4 days post-MI in Baso^{WT} and Baso$^{4\text{-}13Ko}$ mice (*n* = 8-9). (**M**) Representative images of flow cytometric analysis of heart tissue of indicated groups 4 days post-MI.



Supplemental figure 7. Effect of IPSE/α-1 on monocyte/macrophage polarization and cardiac remodeling.

(**A** and **B**) Release of IL-4 (A) and IL-13 (B) of basophils after in vitro stimulation with IL-33, IPSE/alpha-1 and IL-33+IPSE/alpha-1 (*n* = 8). Error bars show mean ± SD. Asterisks signify significant differences using repeated-measures one-way ANOVA with Sidak's multiple comparisons test. (**C** and **D**) Expression of CD206 and CD209 on LPS-activated monocytes cultured with supernatant obtained from either control basophils (cultured with medium only) or basophils stimulated with IPSE/alpha-1. Quantification was based on flow cytometric analysis. Error bars show mean ± SD. Asterisks indicate significant differences using two-tailed Student's t test. (**E**) Representative histological sections depicting scar area 4 weeks after MI. The scale

bar indicates 500 μm. (**F**) Quantification of scar thickness 4 weeks after MI (*n* = 4-6). Error bars show mean ± SD. Asterisks signify significant differences using one-way ANOVA with Tukey's multiple comparisons test.