SUPPLEMENTARY INFORMATION

Extended Experimental Procedures

Cell isolation and purification

Hind limb muscles were carefully dissected to remove attached tendons and connective tissue. Muscles were minced with a razor blade and digested in 0.2% Collagenase Type 2 (Invitrogen) in Ham's F-10 media with gentle agitation for one hour at 37°C. After washing and pelleting the digested tissue, a second digestion was performed in 0.05% Collagenase Type 2 and 0.1% Dispase 1 (Invitrogen) in Ham's F-10 for 25 minutes at 37°C. Cells were liberated from digested tissue by five passages through a syringe attached to an 18-gauge needle. The resulting cellular suspension was filtered through a 40 μM cell strainer, pelleted at 1500 rpm, and washed once with PBS.

The Miltenyi MACS purification system was used to isolate FAPs from injured muscles. Briefly, cells isolated from digested muscles were incubated with anti-CD16/32 antibody (Biolegend) for 5 minutes to block Fc receptors followed by incubation with biotin conjugated anti-CD31 (Biolegend), anti-CD45 (Biolegend), and anti-α7 integrin for 15 minutes. Subsequently, cells were pelleted, washed once with MACS buffer, and incubated with anti-biotin microbeads (Miltenyi). Antibody-microbead cellular complexes were passed through magnetic LD column and the flow through fraction was collected for FAPs.

Cell Culture

FAPs were cultured in non-coated plastic plates in DMEM supplemented with 20% FBS (Lonza) and penicillin/streptomycin. To induce adipogenic differentiation, insulin (1 μg/ml) was added to culture media for 5 days. For gene expression studies, FAPs were cultured in serum free DMEM supplemented with 2% BSA (U.S. Biological) and stimulated with vehicle (PBS) or IL-4 (10

nM) for 24 hours. To examine the activation of signaling pathways by IL-4 in FAPs, cells were cultured in serum free DMEM supplemented with 2% BSA for 16 hours prior to treatment with PBS or IL-4 (10 nM) for 20 minutes. Inhibitors of MEK1 (PD98059 30 μM, Cell Signaling) or PI3K (LY294002 30 μM, Cell Signaling) were added to cells one hour prior to stimulation with IL-4.

Flow Cytometry

Single cell suspensions obtained after muscle digestion were stained with LIVE/DEAD (Invitrogen) in PBS at a 1:100 dilution for 20 minutes, washed, resuspended in FACS buffer (PBS + 5 mM EDTA + 2.5% FBS), and stained with the appropriate primary antibody. Concentrations and source of antibodies that were used are listed in Table S5.

For analysis of BrdU incorporation, cells were first stained for surface markers, resuspended in Cytofix/Cytoperm (BD) for 20 min, permeabilized with saponin using perm wash buffer (BD), treated with DNase 1 (Roche) in PBS for 1 hour at 37ºC, and stained with anti-BrdU antibody for 30 min at RT.

Western Blotting

Cells were lysed in Trition X-100 lysis buffer (10mM Tris pH 7.4, 150mM NaCl, 1mM NaF, 1mM Na3VO4, 1mM NaPO4, 10% Glycerol, 1% Triton X-100, and cocktail protease inhibitors). 30 μg of total lysate was separated on SDS-PAGE gels, transferred to nitrocellulose membranes, and incubated with primary and secondary antibodies in 5% fat free milk (Bio-Rad).

RNA Extraction and Quantitative PCR

RNA was isolated from plated FAPs using RNeasy purification columns (Qiagen), whereas TRIzol Reagent (Invitrogen) was used to extract RNA from homogenized TA muscles. RNA purity was quantified with NanoDrop 2000 (Thermo). After DNAse I treatment of purified RNA,

1 μg of RNA was used for first strand cDNA synthesis (Origene). As described previously(Nguyen et al., 2011), quantitative real time-PCR analyses were carried out with cDNA templates using SensiFast SYBR green (Bioline) on the CFX384 Real Time PCR system (BioRAD). All primer sequences that were used are available upon request.

Microarray Analysis

25μg of total RNA was hybridized to Illumina MouseRef-8 v2.0 Expression BeadChip. Microarrays were variance stabilized and normalized using the robust spline algorithm in the *lumi* R package (Du et al., 2008). Differentially expressed transcripts were identified with the *limma* R package, which uses a model-based approach for variance estimation and is thus particularly effective for small sample sizes (Smyth, 2005). A conservative Benjamini-Hochberg correction was applied to estimate false discovery rates (FDR) (Benjamini and Hochberg, 1995). For pathway enrichment analysis, transcripts that were at least 1.5 fold changed in expression and significant at a false discovery rate of 5% were analyzed for GO term enrichment using the Funcassociate web-based software tool, which employs a Fisher's Exact Test for significance and Monte Carlo simulations to adjust for multiple hypothesis testing (Berriz et al., 2003). Up- and down-regulated transcripts were analyzed separately.

Hierarchical clustering was carried out using the *seriation* package, which performs optimal leaf reordering so that neighboring samples within a cluster are "closer together" than those that are spatially separated (Hahsler et al., 2008). Probe sets for clustering were selected by taking all 6 pairwise comparisons from 4 possible conditions (WT + Vehicle, WT+ IL-4, IL-4R$\alpha^{-/-}$ + Vehicle, IL-4R$\alpha^{-/-}$ + IL-4) and identifying all (297) differentially expressed probe sets (0.1% FDR, ≥1.7 fold change). All statistical analyses were performed using R 2.12. The matrix of intensity values was row-centered and scaled to a standard deviation of 1 prior to clustering.

Histology and Imaging

For Oil Red O, perilipin and GFP staining (4get and YARG mice), TA muscles were fixed in paraformaldehyde (4%) at RT for 4 hours at 4ºC followed by overnight incubation at 4ºC in PBS solution containing 30% sucrose. Subsequently, muscles were embedded in OCT, sectioned, and stained with respective antibodies. GFP was detected using rabbit anti-GFP antibody (Novus Biologicals) followed by the amplification of secondary signal (Perkin-Elmer). For immunostaining, injured muscles were embedded in OCT, sectioned, fixed in paraformaldehyde (3.7%) for 15 minutes, washed, and permeabilized in PBS containing TritonX-100 (0.3%) for 20 minutes. After blocking in 15% goat serum for 1 hour, slides were incubated with primary antibodies in blocking buffer overnight at 4°C. Slides were then washed, incubated with fluorophore conjugated goat anti-rabbit or goat anti-mouse antibodies (Invitrogen) for 1 hour and finally incubated in solution containing DAPI (1 μg/ml, Invitrogen). Concentrations and source of antibodies that were used are listed in Table S5. Mounted slides were visualized using Zeiss LSM 510 confocal, Zeiss Observer inverted tissue culture, Zeiss AxioImager M1 upright, and and AMG EVOS-fl microscopes.

Oil Red O and Alizarin Red S Staining

Triglyceride accumulation in cultured FAPs was examined by Oil Red O staining. Briefly, cells were washed with PBS, fixed in 4% paraformaldehyde for 30 minutes, rinsed in dH_2O and then 60% isopropanol, and subsequently stained with Oil Red O solution in 60% isopropanol. Free dye was removed by dH_2O washes. For Oil Red O staining of muscle sections, 10 μM thick sections of TA muscles were fixed 4% PFA for 1 hour, washed 3 times in dH_2O (5 mins each), and then stained with Oil Red O solution in triethly-pentane for 30 minutes. Excess stain was

removed by dH_2O washes and glass cover slips were mounted with 10% glycerol solution prior to imaging.

Calcified necrotic muscle fibers were visualized by Alizarin Red S stain(American Mastertech Scientific). Briefly, tissue sections were stained with Alizarin Red S stain for 3 minutes, and washed sequentially in acetone, acetone-xylene (1:1), and xylene prior to mounting for visualization.

Phagocytosis studies.

Generation of phagocytic targets

Necrotic cells: Thymus of 4-week-old WT mice were dissociated into single cells using the Miltenyi Gentle Macs system, and labeled with CFSE (5 μM) for 30 min. After extensive washing in PBS, primary thymocytes were subjected to 2-3 cycles of freeze/thaw in liquid nitrogen to obtain necrotic cells (99% labeled by trypan blue). Necrotic cells were counted and filtered through a 40 μM filter prior to use *in vitro* or *in vivo*.

Apoptotic cells: To induce apoptosis, primary thymocytes were cultured in serum free RPMI for 18 hours and labeled with CFSE.

Opsonized cells: Primary thymocytes were opsonized with anti CD3 (1 μg) for 30 minutes at 37°C, and cells were washed to remove unbound antibodies.

In vitro phagocytosis assay

FAPs were plated in a 12 well plate and fed CFSE-labeled thymocytes (ratio of 1:5-1:10) for 1h. Subsequently, FAPs were washed in PBS with EDTA (5 mM) to remove any unbound thymocytes, stained with CD140a (PDGFRα) and Sca-1 antibodies, and analyzed by Flow Cytometry. To visualize FAPs by confocal microscopy, cells were plated on 15 mm round coverslips in a 12-well plate, incubated with CFSE-labeled thymocytes or FluoSpheres, washed

to remove unbound cells or beads, stained with CD140a antibody, and visualized using a confocal microscope.

In vivo phagocytosis assays

Three days after injury with CTX, CFSE-labeled necrotic thymocytes (50 µl volume, 1.5-3.5x10^6 cells) were injected into the belly of the TA muscle. At indicated time points, single cell suspensions were prepared from TA muscles and analyzed by Flow Cytometry.

Supplemental References

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Table S1. Immune cell infiltrate of CTX-injured muscle, Related to Figure 1. Mononuclear cells were isolated from WT and IL-4/IL-13$^{-/-}$ mice on day 1 of CTX-induced muscle injury. Isolated cells were gated for side- and forward-scatter (SSC/FSC), singlets, and live cells prior to the analysis for cell surface markers of innate or adaptive immune cells. The following antibodies were used for identification: neutrophils (Ly6G and CD11b), macrophages (F4/80 and CD11b), eosinophils (Siglec F), T cells (CD3), hematopoietic cells (CD45), and NK cells (CD49b). Data is presented as mean +/- SEM.

Figure S1. Analysis of IL-4 expressing/GFP^{+} cells in regenerating muscles, Related to Figure 2.

(A) Detection of IL-4 expressing cells in regenerating muscle. TA muscles from 4get mice were stained for GFP on various days after injury with CTX (magnification, X100). Note that expression of IL-4 is not detected in regenerating myofibers but rather in mononuclear cells.

(B) Presence of GFP+ cells in uninjured and injured muscles of 4get mice. CTX-injured muscles were digested on various days and mononuclear cells were isolated for flow cytometric analysis. Note that all GFP+ cells are of hematopoietic origin (CD45^{+}).

(C) Expression of various chemokines and cytokines that have been implicated in the recruitment of eosinophils and macrophages in regenerating muscle, n=4-6 per time point. *P<0.05, **P<0.01, ***P<0.001.

(D) GFP^{+} cells were enumerated in CTX-injured muscles of 4get and ΔdblGATA/4get mice on day 1.

(E) Intracellular staining for IL-4 in WT, ΔdblGATA, and IL4/IL13$^{-/-}$ mice. Mononuclear cells were isolated from injured muscle on day 2 and cultured in the presence of Brefeldin A for 18 hours prior to staining for IL-4.

Data presented as mean±SEM.

Figure S2. Analysis of macrophages in regenerating muscles, Related to Figure 3.

(A) Isolated mononuclear cells were gated for live/dead and doublets prior to analysis of myeloid cells, FAPs and MPs. FAPs were defined as $SCA1^{+}\alpha7\ inegrin^{-}CD45^{-}CD31^{-}$; MPs as $SCA1^{-}\alpha7\ inegrin^{+}CD45^{-}CD31^{-}$; and myeloid cells as $CD45^{+}CD11b^{+}$.

(B) Quantitative RT-PCR analysis for expression of IL-4 mRNA in regenerating WT and IL-4/IL-$13^{-/-}$ muscles, n=3 per genotype and time point. *P<0.05.

(C-F) Quantitative RT-PCR analysis for macrophage markers during the time course of muscle regeneration, n=4 per time point. Chi3l3 is a marker of alternatively activated (M2) macrophages; Emr1 encodes the pan macrophage marker F4/80; IL-6 and Tnfα are markers of classically activated (M1) macrophages. *P<0.05, **P<0.01, ***P<0.001.

(G) Localization of Arg1 positive cells in day 2 regenerating muscle. TA muscle sections were stained for Arg1, a marker of alternative activation, and CD68, a pan-marker of macrophages (magnification, X400). Note, nearly all of the $Arg1^{+}$ cells co-localize with cells staining positively for $CD68^{+}$.

(H) Flow cytometric analysis of IL-4Rα expression on macrophages infiltrating injured muscle. Mononuclear cells were isolated on day 3 after injury from the TA muscles of IL-$4R\alpha^{f/f}$, IL-$4R\alpha^{f/f}LysM^{Cre}$, and IL-$4R\alpha^{-/-}$ mice, and IL-4Rα expression was analyzed on infiltrating macrophages.

Data presented as mean±SEM.

Figure S3. Analysis of FAPs, MPs, and IL-4Rα expression in regenerating muscles, Related to Figure 4.

(A) Representative flow plots demonstrating BrdU incorporation in FAPs isolated from WT and IL-4/IL-13$^{-/-}$ mice.

(B) Representative flow plots demonstrating BrdU incorporation in MPs isolated from WT and IL-4/IL-13$^{-/-}$ mice.

(C) Quantification of FAPs on day 3 of regenerating muscles of WT, IL-4Rα$^{-/-}$, and IL-4/IL-13$^{-/-}$, mice, n=5-8 per genotype. ***P<0.001.

(D, E) Quantification of BrdU incorporation in FAPs (C) and MPs (D) of IL-4Rα$^{f/f}$ and IL-4Rα$^{f/f}$LysM^{Cre} mice 24 hours after muscle injury, n=4 per genotype.

(F) Immunoblot analysis for IL-4Rα in FAPs, myogenic progenitors (MP), and differentiated myotubes (MT). FAPs express PDGFRα, whereas MP and MT express Myo D and Desmin.

(G) Quantitative PCR analysis of recombination efficiency in satellite cells. Primers spanning the excised exons (7-9) were used amplify the IL-4Rα gene in sorted satellite cells. **P<0.01.

(H) Immunostaining for IL-4Rα in regenerating muscle. Sections of WT and IL-4Rα$^{-/-}$ TA muscles were stained for IL-4Rα. Note expression of IL-4Rα is primarily detected in mononuclear cells 8 days after injury with CTX (magnification, X200).

Data presented as mean±SEM.

Figure S4. Analysis of IL-4 signaling in FAPs, Related to Figure 5.

(A) Flow cytometric analysis of FAPs before and after purification with Miltenyi MACS purification system. FAPs were negatively selected using CD31, CD45, and α7 integrin antibodies. Purified FAPs are $SCA1^{+}$ and $CD45^{-}CD31^{-}$.

(B) Quantification of cell number after stimulation of WT FAPs with vehicle or IL-4 (10nM) for 48 or 72 hours, n=4 per treatment and time point.

(C) Activation of signaling pathways by IL-4 in WT FAPs. Cells were stimulated with IL-4 (10nM) for 15 minutes, and cell lysates were analyzed for the indicated proteins by immunoblotting. PI3K was inhibited by LY294002 (30 μM) and PD98059 (30 μM) was used to inhibit MEK1.

(D) BrdU incorporation in WT FAPs after inhibition of PI3K or MEK1. FAPs were stimulated PBS or IL-4 (10nM) for 24 hours in the presence or absence of inhibitors for PI3K (LY294002 (30 μM)) or MEK1 (PD98059 (30 μM)). Cells were pulsed with BrdU for 30 minutes prior to harvest for analysis, n=3 per treatment. Data is normalized to the PBS sample in each treatment group.

(E) Quantitative RT-PCR analysis of myogenic genes. Wild type MPs were cultured with conditioned media from WT or IL-4R$\alpha^{-/-}$ FAPs for 5 days, and gene expression was quantified in differentiating MPs, n=3/genotype and treatment. *$P<0.05$.

(F) Quantification of satellite cells in single fibers exposed to FAPs conditioned media. Wild type muscle single fibers were cultured with conditioned media from WT or IL-4R$\alpha^{-/-}$ FAPs for 3 days, and $MyoD^{+}$ satellite cells were enumerated.

Data presented as mean±SEM.

Figure S5. IL-4 inhibits adipogenic differentiation of FAPs, Related to Figure 6.

(A) Oil Red O staining of WT FAPs cultured in growth medium supplemented with vehicle (veh) or IL-4 (10 nM) for 7 days.

(B) Phase contrast images of WT FAPs differentiated into adipocytes with insulin in the absence or presence of IL-4.

(C) Quantitative RT-PCR analysis of adipogenic mRNAs in WT and IL-4R$\alpha^{-/-}$ FAPs treated with insulin or insulin plus IL-4, n=3 per genotype and treatment.

(D) Sections of TA muscles were stained for perilipin, a marker of mature adipocytes (20x).

*P<0.05, **P<0.01, and ***P<0.001.

Data presented as mean±SEM.

Figure S6. FAPs efficiently phagocytize necrotic cells, Related to Figure 7.

(A) Efficiency of FAPs to phagocytize live (LTs), necrotic (NTs), apoptotic (ATs), and opsonized (OTs) thymocytes *in vitro*. Mean fluorescence intensity (MFI) of $CSFE^{+}$ FAPs is plotted for the various targets, n=3 per treatment.

(B) Representative flow cytometry plots for phagocytosis of live (LTs), necrotic (NTs), apoptotic (ATs), and opsonized (OTs) thymocytes by FAPs.

(C) 3-D reconstruction from confocal z-stacks. PDGFRα staining (red) identifies FAPs, whereas CFSE (green) represents necrotic thymocytes. Blue is DAPI.

(D-G) Representative flow plots demonstrating phagocytosis of necrotic thymocytes (NTs) by various cell populations in present in regenerating muscles.

(H) Flow cytometric analysis of cells that phagocytose CSFE-labeled necrotic thymocytes in injured muscle on day 3.

Data presented as mean±SEM.

Figure S7. Type 2 innate signals regulate clearance of necrotic debris in FAPs, Related to Figure 7.

(A) Flow cytometric analysis of GFP^+ cells from regenerating muscles of Pdgfrα-GFP mice.

(B) Representative flow plots demonstrating the deletion of IL-4Rα in FAPs but not MPs, $CD45^+$ or $CD31^+$ cells isolated from regenerating muscles of IL-4R$\alpha^{f/f}$ and IL-4R$\alpha^{f/f}$Pdgfrα^{Cre} mice 3 days after injury with CTX.

(C) Kinetics of clearance of $CSFE^+$-labeled necrotic thymocytes by FAPs in WT mice, n=4-6 per time point. *P<0.05, ***P <0.001.

(D) Representative flow plots demonstrating persistence of CSFE-labeled necrotic thymocytes in FAPs of mice lacking type 2 innate immune signals.

Data presented as mean±SEM.

Table S2. Analysis of genes regulated by IL-4 in FAPs, Related to Figure 5.

Please see attached Table S2 excel file.

Table S3. GO term enrichment analysis for genes induced by IL-4 in FAPs, Related to Figure 5.

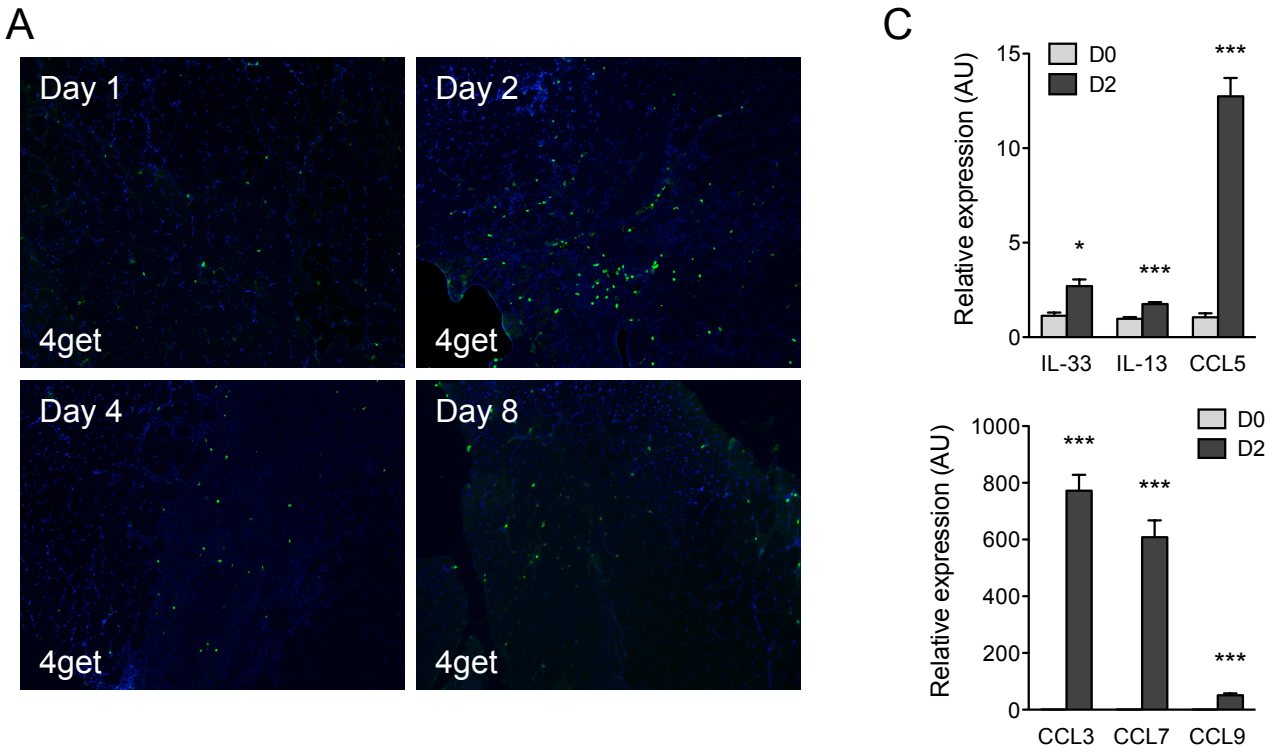
Please see attached Table S3 excel file.

Table S4. GO term enrichment analysis for genes suppressed by IL-4 in FAPs, Related to Figure 5.

Please see attached Table S4 excel file.

Table S5. List of antibodies that were used in the reported studies. Related to Extended Experimental Procedures.

Antibody	Source	Application
Anti-Desmin	Novacastra	IB/IF
Anti-MyoD1	Dako	IB
Anti-GFP	Novus Biologicals	IF
Anti-IL4Rα	Novus Biologicals	IF
Anti-Arg1 (V-20)	Santa Cruz	IF
Anti-CD68	Biolegend	IF
Anti-NOS2	Santa Cruz	IF
Anti-Perilipin A	Sigma-Aldrich	IF
Donkey anti-rabbit-488	Invitrogen	IF
Donkey anti-goat-488	Invitrogen	IF
Donkey anti-goat-594	Invitrogen	IF
Donkey anti-rat-594	Invitrogen	IF
Anti-IL4Rα (E-1)	Santa Cruz	IB
Anti-STAT6 (M-20)	Santa Cruz	IB
Anti-phospho-STAT6 (pY641)	BD Pharmingen	IB
Anti-Akt (9272)	Cell Signaling	IB
Anti-phopho-Akt (4058)	Cell Signaling	IB
Anti-ERK1/2 (4695)	Cell Signaling	IB
Anti-phopho-ERK1/2 (4377)	Cell Signaling	IB
Anti-ACC1 (3676)	Cell Signaling	IB
Anti-HSL (4107)	Cell Signaling	IB
Anti-PDGFRa (3174)	Cell Signaling	IB/IF
Anti-PPARγ (E-8)	Santa Cruz	IB
Anti-HSP90	Santa Cruz	IB
Anti-CD45 (30-F11)	Biolegend	FC
Anti-CD31 (390)	Biolegend	FC
Anti-Sca 1 (D7)	Biolegend	FC
Anti-α7 Integrin	Antibody Company	FC
Anti-CD124 (mIL4R-M1)	BD	FC
Anti-CD11b (M1/70)	Biolegend	FC
Anti-F480 (BM8)	Biolegend	FC
Anti-Ly6G (IA8)	Biolegend	FC
Anti-Siglec F (E50-2440)	BD Pharmingen	FC
Anti-FcεR1 (MAR-1)	E bioscience	FC
Anti-c-kit (2B8)	Biolegend	FC
Anti-CD3e (145-2C11)	Biolegend	FC
Anti-CD4 (GK1.5)	Biolegend	FC
Anti-CD8 (53-6.7)	Biolegend	FC
Anti-YM1	R&D	FC
Anti-BrdU (3D4)	BD Pharmingen	FC
Anti-BrdU (MoBU-1)	Invitrogen	FC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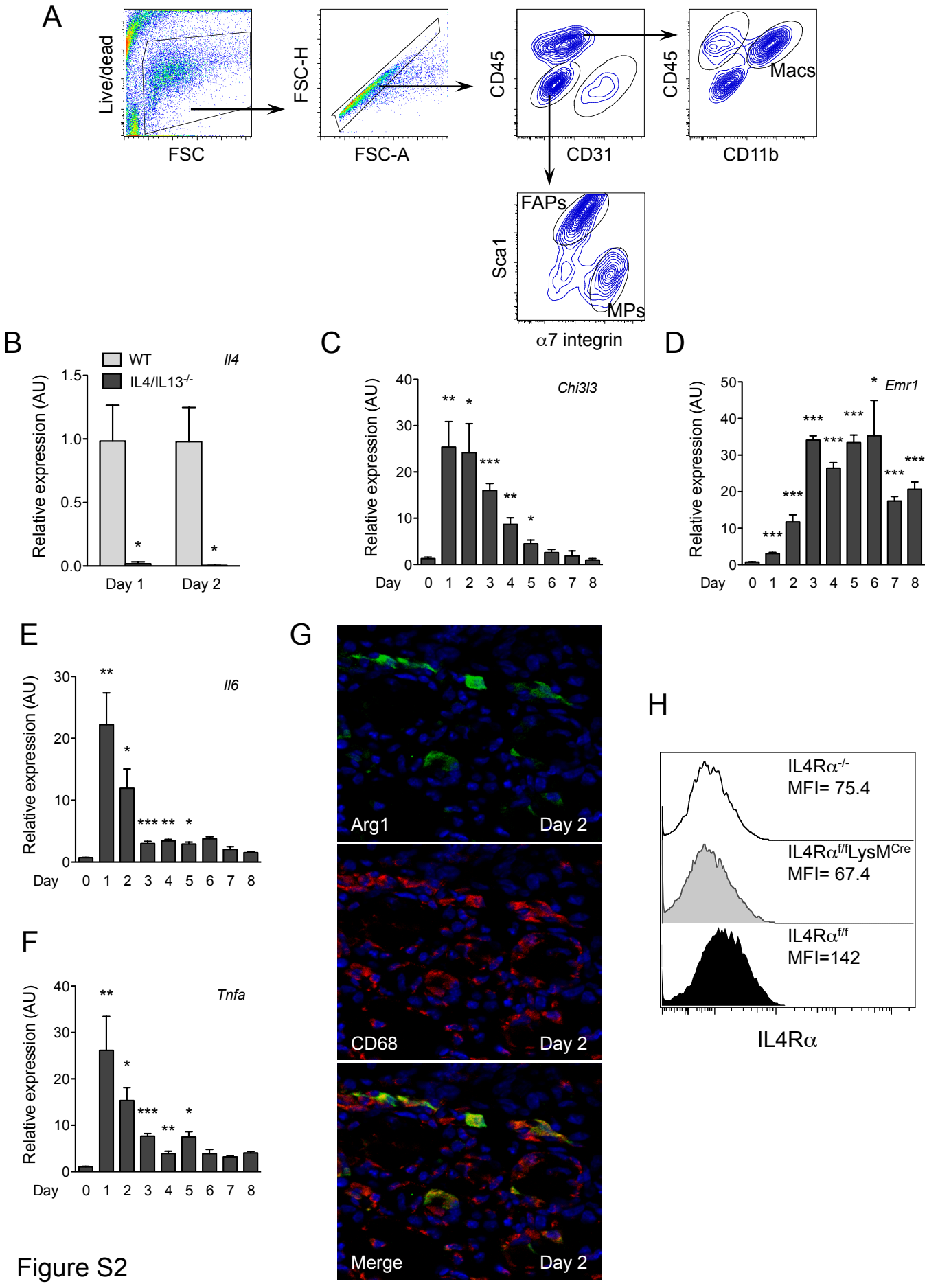
Day 1
4get
Day 2
4get
Day 4
4get
Day 8
4get
C
Relative expression (AU)
D0
D2
IL-33
IL-13
CCL5
CCL3
CCL7
CCL9
B
Empty channel
WT-GFP
0.037
D0
0.39
D1
1.73
D2
1.38
4get-GFP
SSC
CD45
D
WT
4get
4get-ΔdblGATA
Empty channel
GFP
0
0.22
0.06
E
MFI: 147
WT
MFI: 95
ΔdblGATA
MFI: 89
IL4/IL13-/-
IL-4

Figure S1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Live/dead
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FSC-H
FSC-A
CD45
CD31
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Macs
CD11b
FAPs
Sca1
MPs
α7 integrin
B
WT
IL4/IL13-/-
Il4
Relative expression (AU)
Day 1
Day 2
C
Chi3l3
Relative expression (AU)
Day
D
Emr1
Relative expression (AU)
Day
E
Il6
Relative expression (AU)
Day
F
Tnfa
Relative expression (AU)
Day
G
Arg1
Day 2
CD68
Day 2
Merge
Day 2
H
IL4Rα-/-
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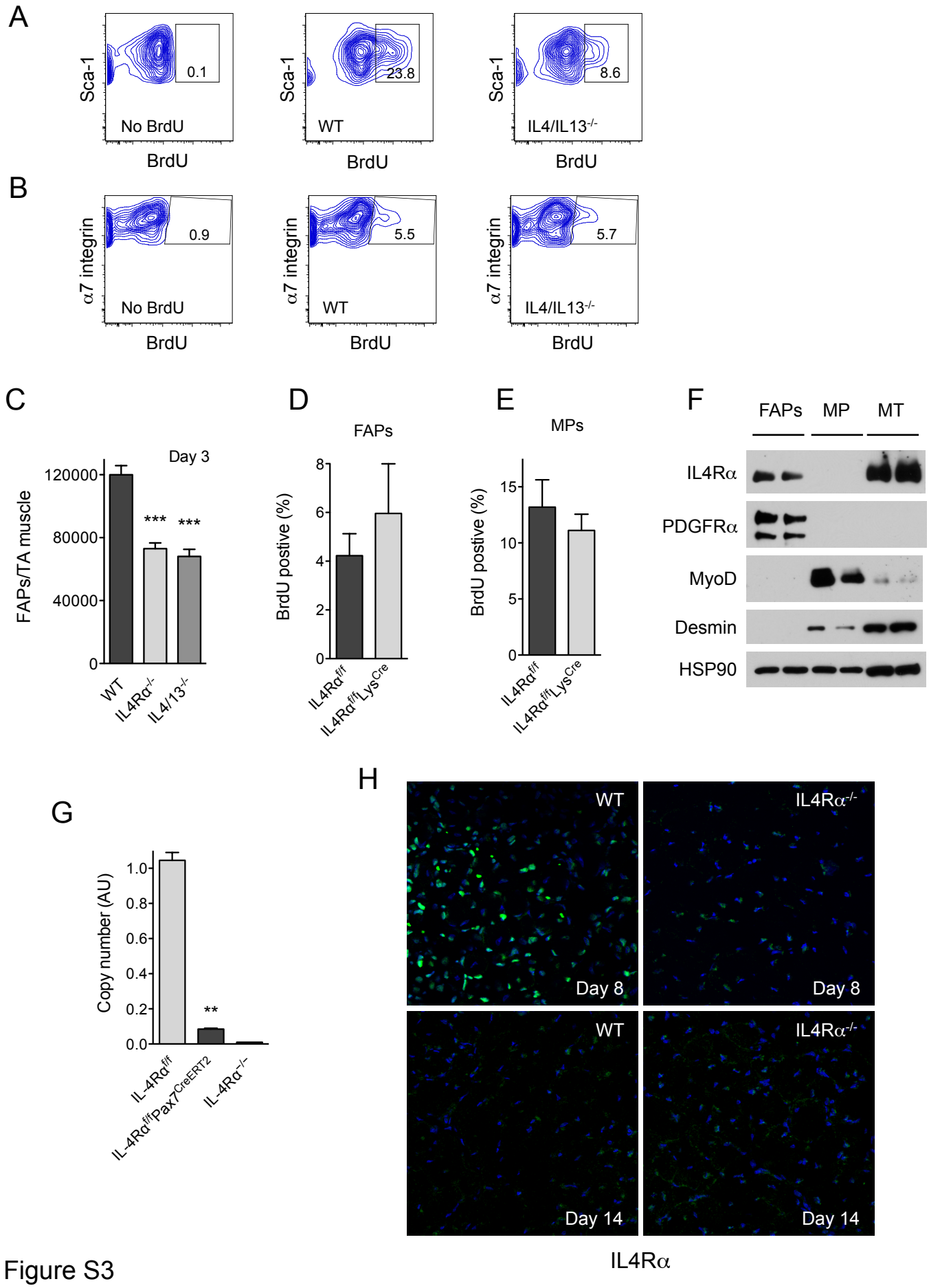
IL4Rαf/fLysMCre
MFI= 67.4
IL4Rαf/f
MFI=142
IL4Rα

Figure S2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8.6
IL4/IL13-/-
B
α7 integrin
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5.5
5.7
C
Day 3
FAPs/TA muscle
120000
80000
40000
0
***
WT
IL4Rα-/-
IL4/13-/-
D
FAPs
BrdU postive (%)
8
6
4
2
IL4Rαf/f
IL4Rαf/fLysCre
E
MPs
15
10
5
F
FAPs
MP
MT
IL4Rα
PDGFRα
MyoD
Desmin
HSP90
G
Copy number (AU)
1.0
0.8
0.6
0.4
0.2
0.0
**
IL-4Rαf/f
IL-4Rαf/fPax7CreERT2
IL-4Rα-/-
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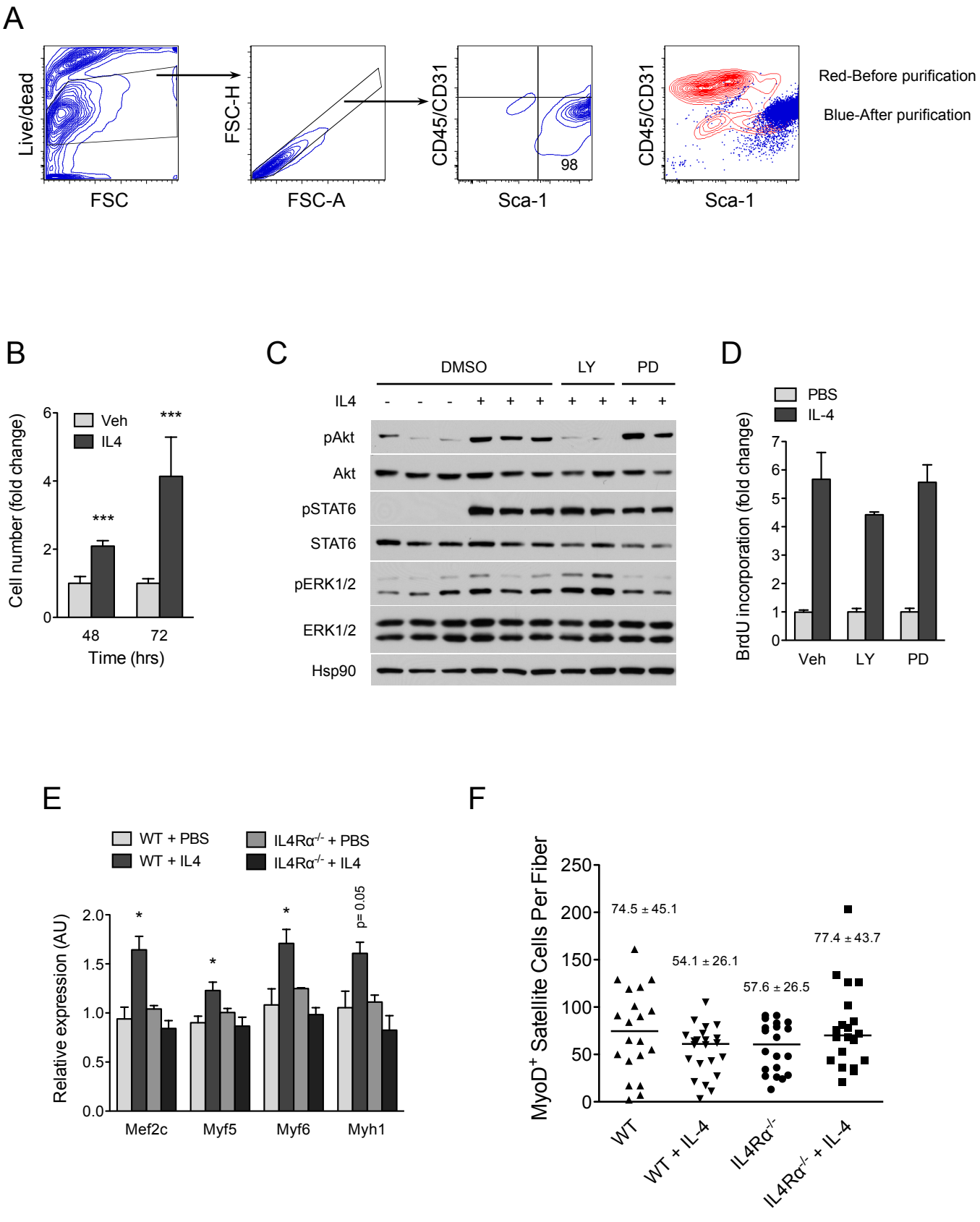
WT
IL4Rα-/-
Day 8
Day 14
IL4Rα

Figure S3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Live/dead
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FSC-A
CD45/CD31
Sca-1
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CD45/CD31
Sca-1
Red-Before purification
Blue-After purification
B
Cell number (fold change)
Veh
IL4
***
***
48
72
Time (hrs)
C
DMSO
LY
PD
IL4
pAkt
Akt
pSTAT6
STAT6
pERK1/2
ERK1/2
Hsp90
D
PBS
IL-4
BrdU incorporation (fold change)
Veh
LY
PD
E
WT + PBS
WT + IL4
IL4Rα-/- + PBS
IL4Rα-/- + IL4
Relative expression (AU)
p= 0.05
Mef2c
Myf5
Myf6
Myh1
F
MyoD+ Satellite Cells Per Fiber
74.5 ± 45.1
54.1 ± 26.1
57.6 ± 26.5
77.4 ± 43.7
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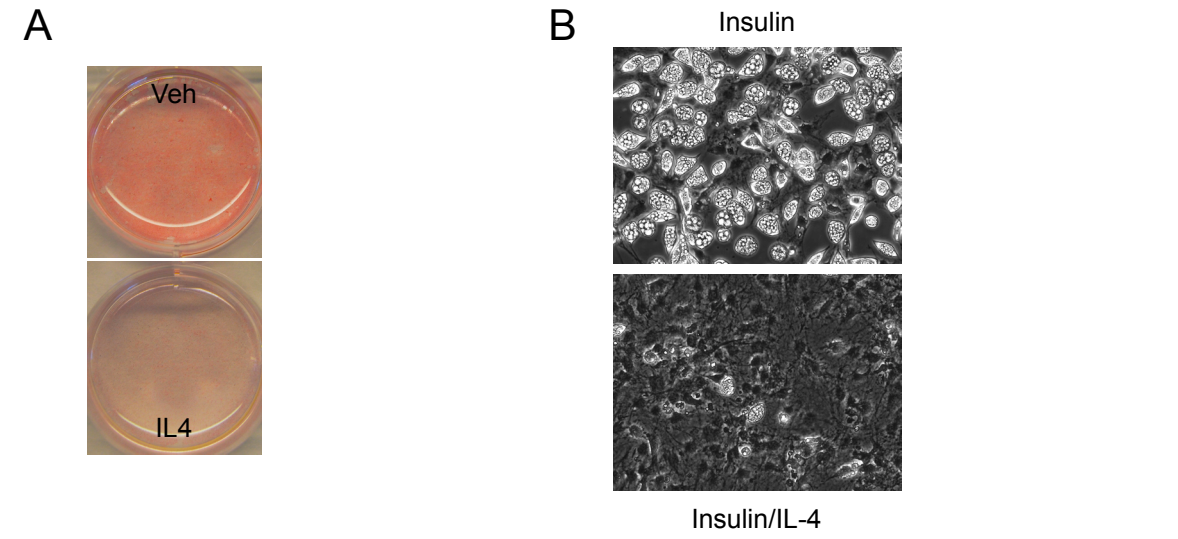
WT + IL-4
IL4Rα-/-
IL4Rα-/- + IL-4

Figure S4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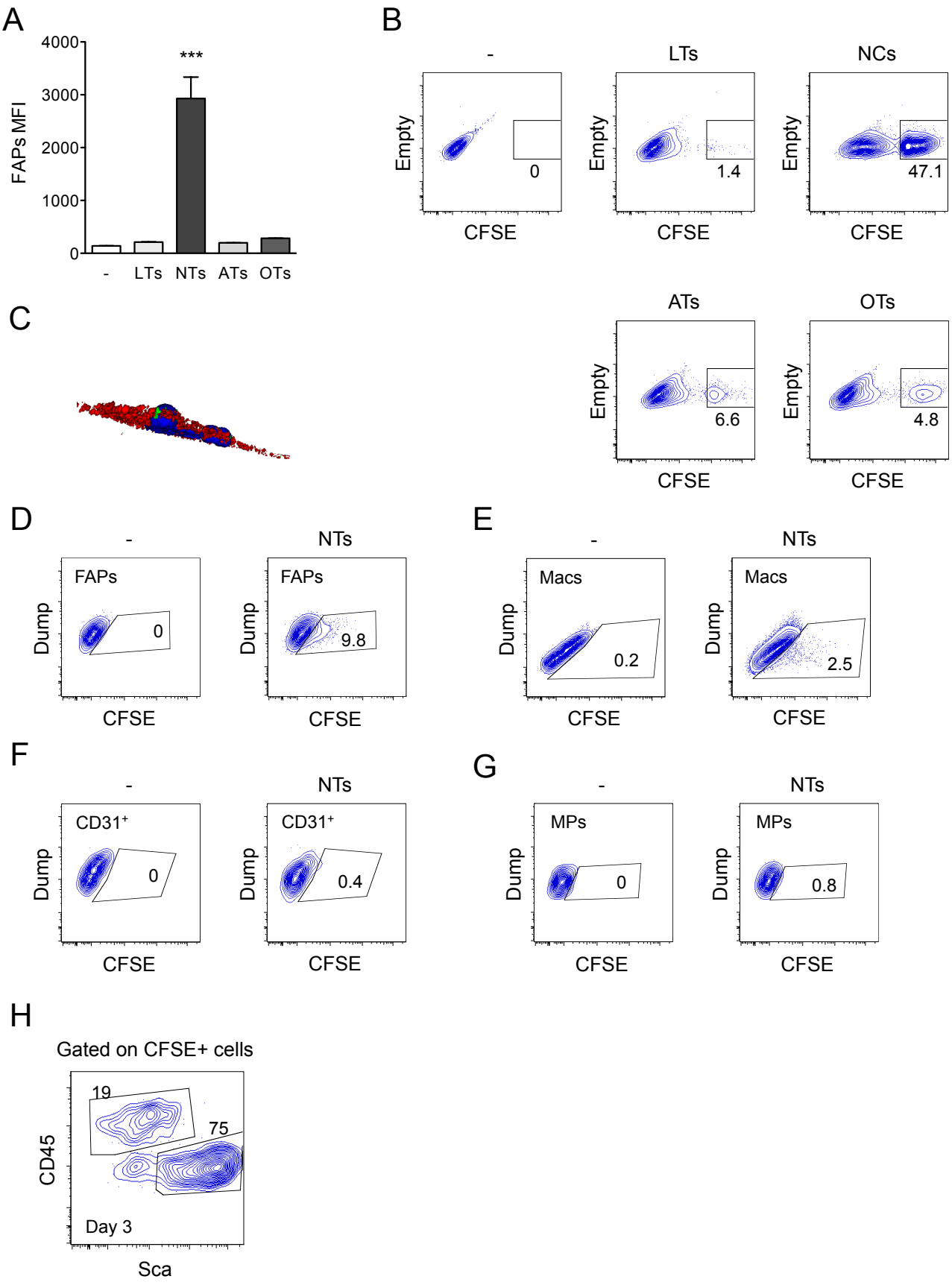
IL4
B
Insulin
Insulin/IL-4
C
WT + Insulin
WT + Insulin/IL4
IL4Rα-/- + Insulin
IL4Rα-/- + Insulin/IL4
Relative expression (AU)
1.5
1.0
0.5
0.0
**
***
***
**
**
***
Acaca
Fabp4
Fasn
Srebf1
Lep
Adipoq
D
Veh
IL4
Perilipin

Figure S5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2000
1000
0
***
-
LTs
NTs
ATs
OTs
B
-
LTs
NCs
Empty
CFSE
0
1.4
47.1
ATs
OTs
6.6
4.8
C
D
FAPs
Dump
0
9.8
E
Macs
0.2
2.5
F
CD31+
0.4
G
MPs
0.8
H
Gated on CFSE+ cells
CD45
Sca
19
75
Day 3

Figure S6

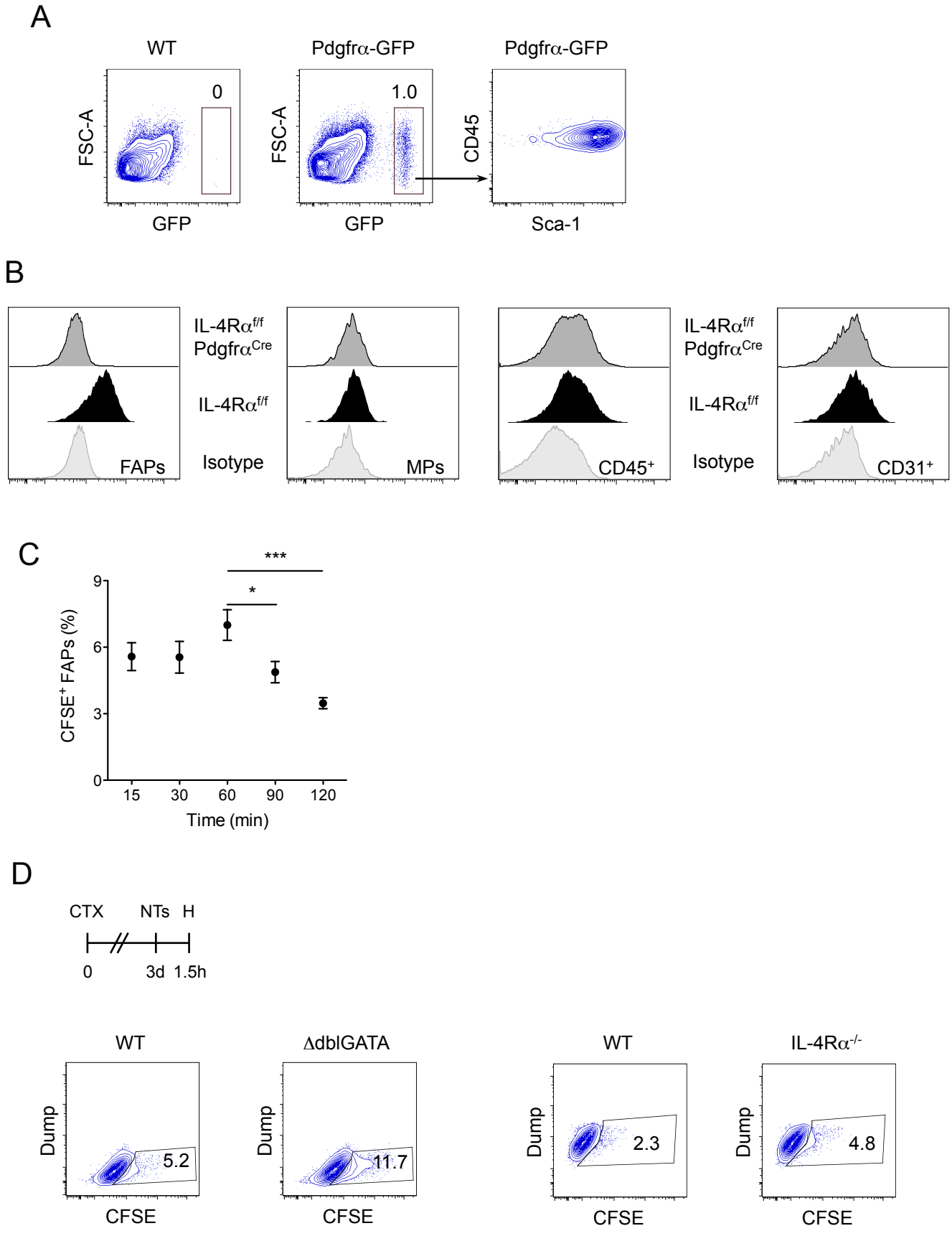
A
WT
Pdgfrα-GFP
Pdgfrα-GFP
0
1.0
FSC-A
GFP
FSC-A
GFP
CD45
Sca-1
B
IL-4Rα f/f Pdgfrα Cre
IL-4Rα f/f
Isotype
FAPs
MPs
CD45+
CD31+
C
***
*
CFSE+ FAPs (%)
Time (min)
D
CTX
NTs
H
0
3d
1.5h
WT
ΔdblGATA
WT
IL-4Rα-/-
Dump
CFSE
5.2
11.7
2.3
4.8

Figure S7