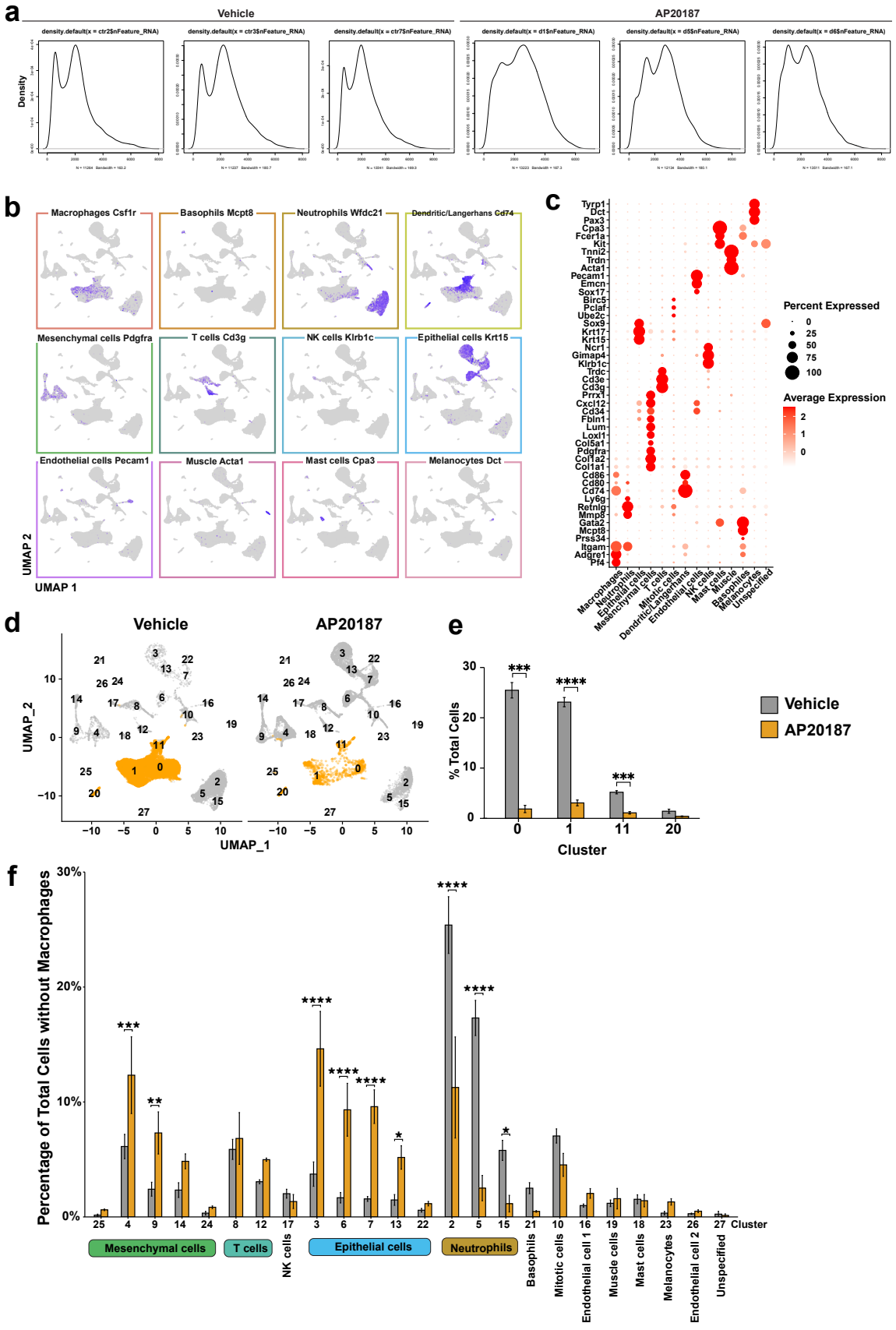
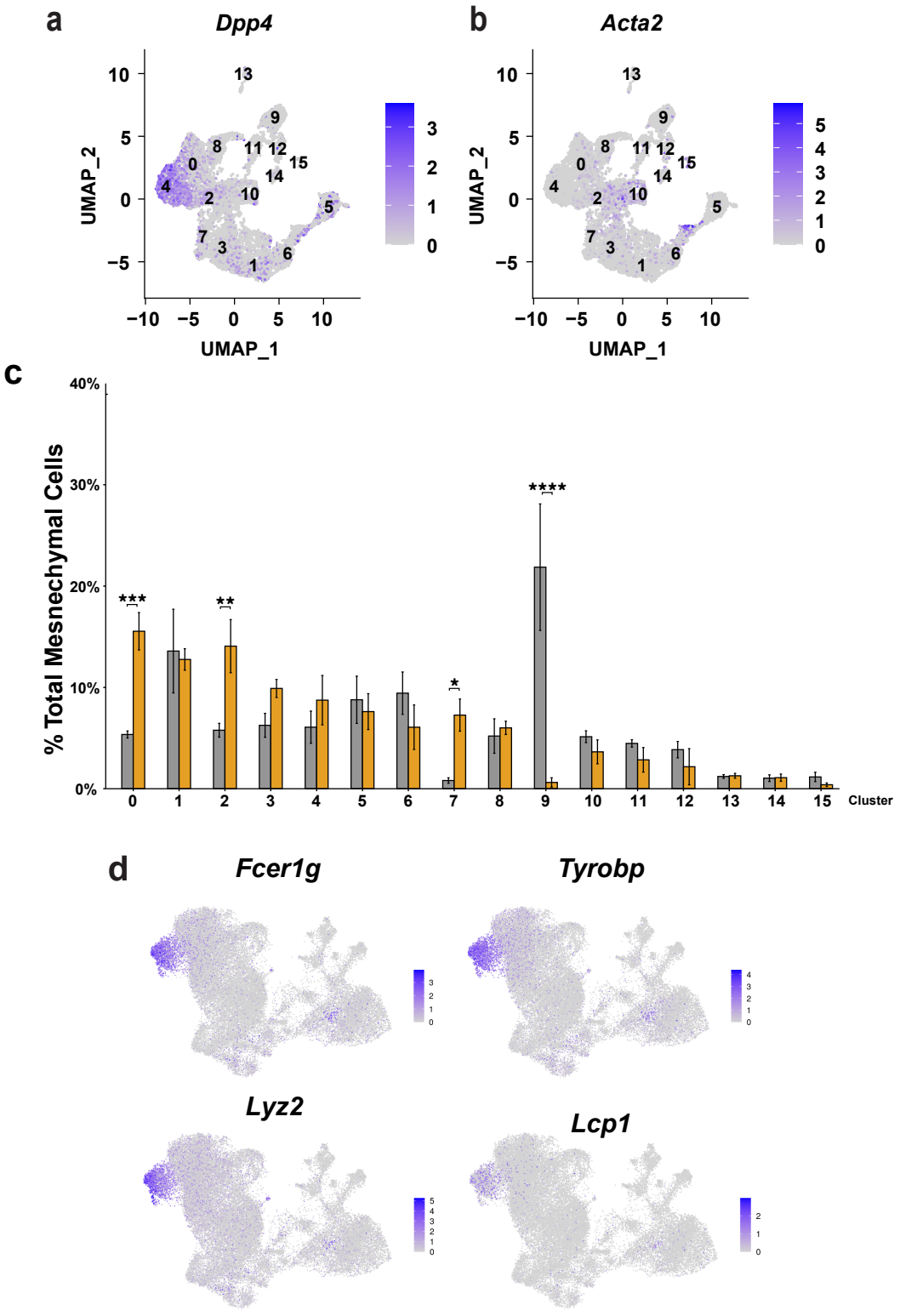
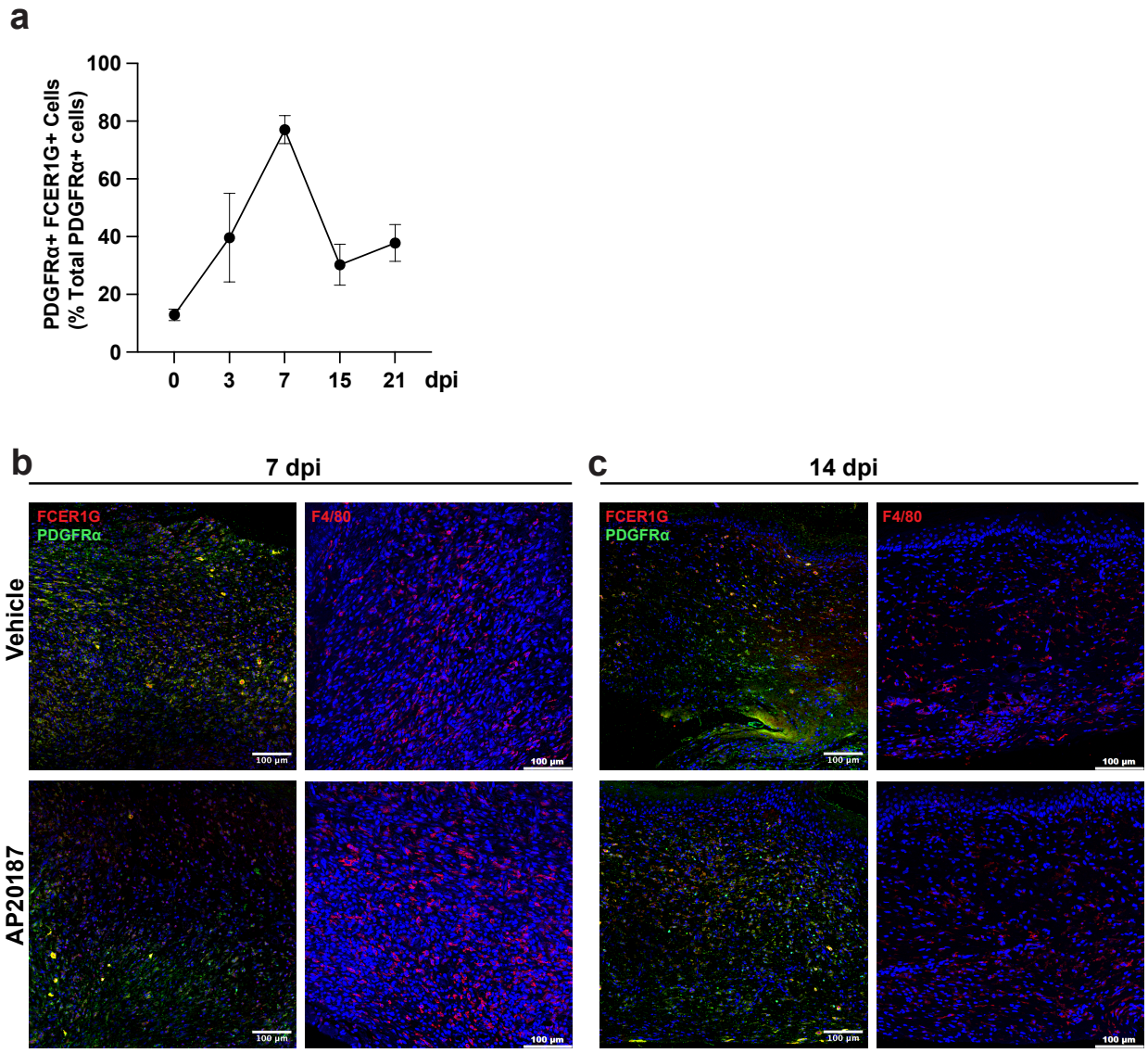

a
Vehicle
AP20187
density.default(x = ctr2$nFeature_RNA)
density.default(x = ctr3$nFeature_RNA)
density.default(x = ctr7$nFeature_RNA)
density.default(x = d1$nFeature_RNA)
density.default(x = d5$nFeature_RNA)
density.default(x = d6$nFeature_RNA)
Density
b
Macrophages Csf1r
Basophils Mcpt8
Neutrophils Wfdc21
Dendritic/Langerhans Cd74
Mesenchymal cells Pdgfra
T cells Cd3g
NK cells Klrb1c
Epithelial cells Krt15
Endothelial cells Pecam1
Muscle Acta1
Mast cells Cpa3
Melanocytes Dct
UMAP 2
UMAP 1
c
Tyrp1
Dct
Pax3
Cpa3
Fcer1a
Kit
Tnni2
Trdn
Acta1
Pecam1
Emcn
Sox17
Birc5
Pclaf
Ube2c
Sox9
Krt17
Krt15
Ncr1
Gimap4
Klrb1c
Trdc
Cd3e
Cd3g
Prrx1
Cxcl12
Cd34
Fbln1
Lum
Loxl1
Col5a1
Pdgfra
Col1a2
Col1a1
Cd86
Cd80
Cd74
Ly6g
Retnlg
Mmp8
Gata2
Mcpt8
Prss34
Itgam
Adgre1
Ptprc
Macrophages
Neutrophils
Epithelial cells
Mesenchymal cells
Mitotic cells
Dendritic/Langerhans
Endothelial cells
NK cells
Mast cells
Muscle
Basophils
Melanocytes
Unspecified
Percent Expressed
0
25
50
75
100
Average Expression
2
1
0
d
Vehicle
AP20187
UMAP_2
UMAP_1
e
% Total Cells
Cluster
0
1
11
20
***
****
***
Vehicle
AP20187
f
Percentage of Total Cells without Macrophages
30%
20%
10%
0%
Cluster
25
4
9
14
24
8
12
17
3
6
7
13
22
2
5
15
21
10
16
19
18
23
26
27
Mesenchymal cells
T cells
NK cells
Epithelial cells
Neutrophils
Basophils
Mitotic cells
Endothelial cell 1
Muscle cells
Mast cells
Melanocytes
Endothelial cell 2
Unspecified

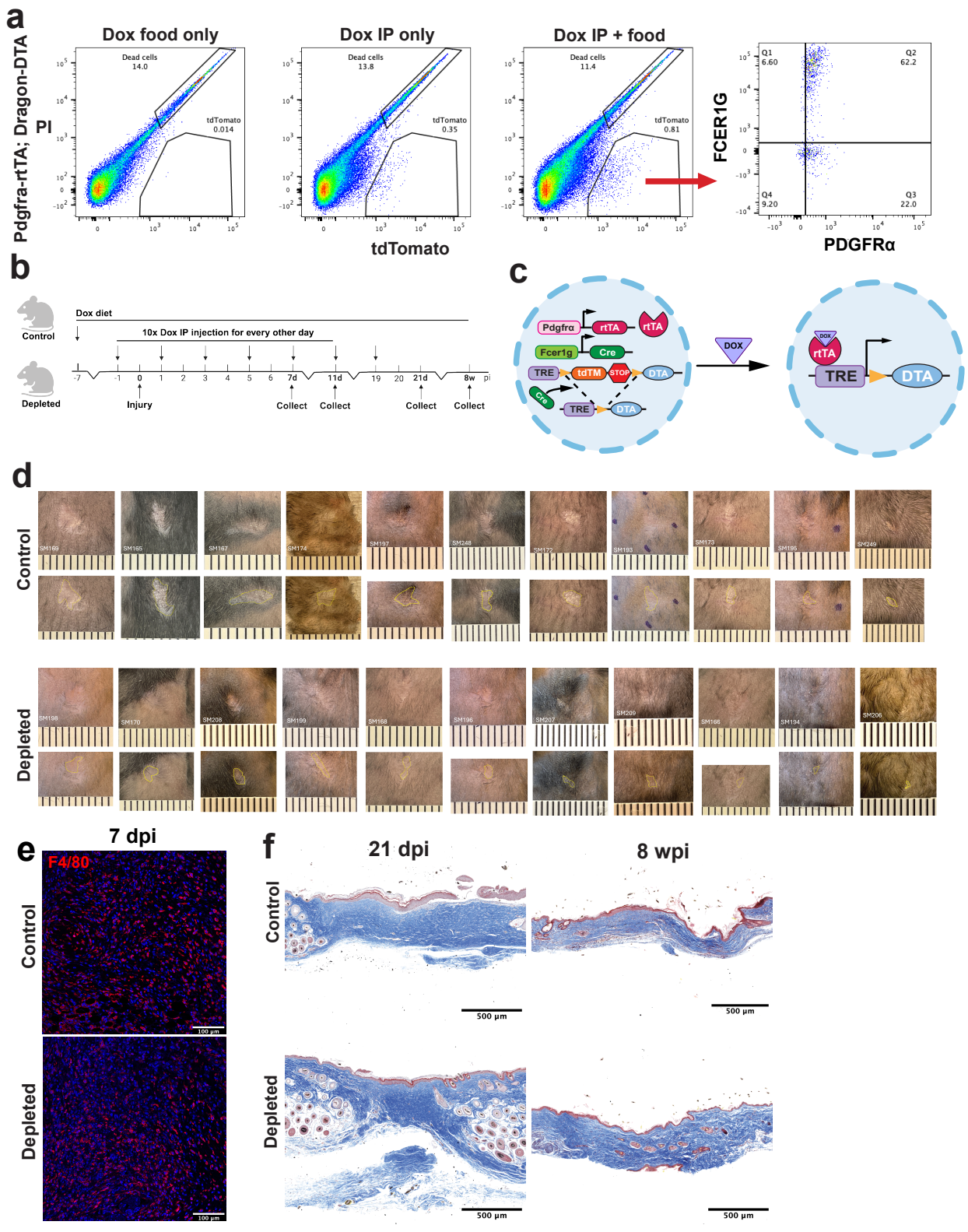
Supplementary Figure 1.
a, Density plots of Cell Ranger outputs for 3 dpi MaFIA wound cells treated with vehicle or AP20187.
b, Expression of key marker genes used to annotate all cell types in the MaFIA wound.
c, Expression of the key marker genes recovered by differential expression analysis for all cell types in the MaFIA wound.
d, Split UMAP of wounds treated with vehicle and AP20187 (n = 3 per condition); macrophage population highlighted in yellow.
e, Quantitative analysis of macrophage percentage over total cells (2-way repeated measures ANOVA).
f, Quantitative analysis of the percentage of each cell type over total cells (excluding macrophages) in the wounds treated with vehicle and AP20187 (2-way repeated measures ANOVA).
*P < 0.05, **P < 0.01, ***P < 0.001, ****P < 0.0001. Data are presented as mean ± s.d.


a
Dpp4
b
Acta2
UMAP_1
UMAP_2
c
% Total Mesnechymal Cells
40%
30%
20%
10%
0%
***
**
*
****
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
Cluster
d
Fcer1g
Tyrobp
Lyz2
Lcp1

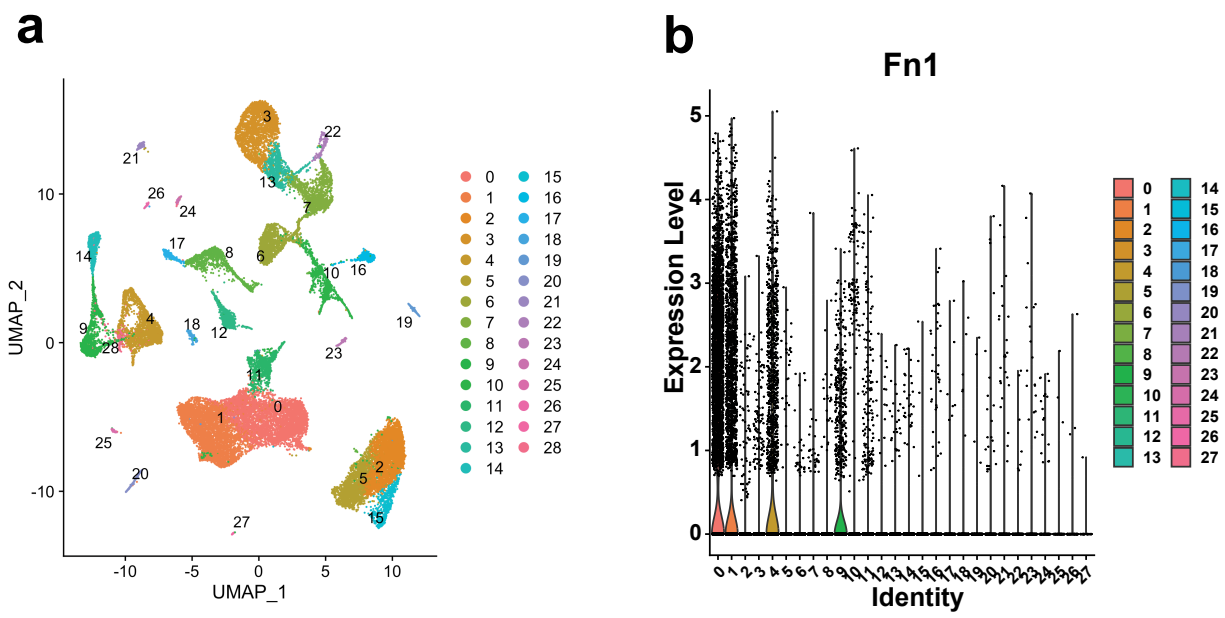
Supplementary Figure 2.
a, Expression of *Dpp4* in mesenchymal subclusters.
b, Expression of *Acta2* in mesenchymal subclusters.
c, Quantitative analysis of the percentage of each mesenchymal cell subtype over total mesenchymal cells (2-way repeated measures ANOVA).
d, Expression of *Fcer1g*, *Tyrobp*, *Lyz2* and *Lcp1* in a published time-course scRNA-seq data on wound healing.



Supplementary Figure 3.
a, Percentage of FCER1G^{+} PDGFRα^{+} cells over PDGFRα^{+} cells over time during wound healing (n = 2 for unwounded, 15 dpi and 21 dpi; n = 3 for 3 dpi and 7 dpi). **b-c,** Representative immunofluorescence images of FCER1G, PDGFRα, F4/80 staining of 7 dpi (**b**) and 14 dpi (**c**) wounds from MaFIA treated with vehicle and AP20187 (n=3 per condition for 7 dpi wounds; n=3 for 14 dpi vehicle-treated wounds; n=2 for 14 dpi AP20187-treated wounds).


a
Dox food only
Dox IP only
Dox IP + food
Pdgfra-rtTA; Dragon-DTA
PI
tdTomato
Dead cells
14.0
tdTomato
0.014
Dead cells
13.8
tdTomato
0.35
Dead cells
11.4
tdTomato
0.81
FCER1G
PDGFRα
Q1
6.60
Q2
62.2
Q4
9.20
Q3
22.0
b
Control
Depleted
Dox diet
10x Dox IP injection for every other day
-7
-1
0
1
2
3
4
5
6
7d
11d
19
20
21d
8w
pi
Injury
Collect
Collect
Collect
Collect
c
Pdgfrα
rtTA
rtTA
Fcer1g
Cre
TRE
tdTM
STOP
DTA
Cre
TRE
DTA
DOX
DOX
rtTA
TRE
DTA
d
Control
Depleted
e
7 dpi
F4/80
Control
Depleted
100 μm
100 μm
f
21 dpi
8 wpi
Control
Depleted
500 μm
500 μm
500 μm
500 μm

Supplementary Figure 4.
a, Left: FACS analysis of PI and tdTomato expression in skin cells collected from 7dpi Pdgfra-rtTA; Dragon-DTA mice treated with Dox food only, or Dox IP only, or Dox food and IP; Right: FACS analysis of FCER1G and PDGFRα expression of $tdTomato^{+}$ PI^{-} skin cells from Pdgfra-rtTA; Dragon-DTA mice treated with Dox food and IP.
b, Schematic of experiment design.
c, Schematic of the Pdgfra-rtTA; Fcer1gCre; Dragon-DTA mouse, which allows DTA-mediated ablation of *Fcer1g*-and *Pdgfrα*-expressing cells upon Dox administration.
d, Macroscopic appearance of scars in control and depleted groups at 8wpi. Top row: raw photo; Botton row: scars contoured for measurement.
e, Representative immunofluorescent images of 7 dpi wounds stained with F4/80 in control and depleted groups (control: n = 3, depleted: n = 4).
f, Masson's trichrome-stained sections from control and depleted groups at 21 dpi and 8 wpi (n=11 per time point).



Supplementary Figure 5.
a, UMAP of cell clusters in MaFIA wounds at 3 dpi with *Fcer1g*-expressing population mapped back as cluster 28.
b, Violin plot showing *Fn1* expression across all clusters.

Cell type	Cluster	Markers
Basophil	21	Prss34, Mcpt8, Gata2
Dendritic/Langerhans cell	11,20	Cd74, Cd80, Cd86,
Endothelial cell 1	16	Sox17, Emcn, Pecam1
Endothelial cell 2	26	Prox1, Ccl21a, Pecam1
Epithelial cell	3,6,7,13,22	Krt15, Krt17, Sox9
Macrophage	0,1	Pf4, Adgre1, Itgam
Mast cell	18	Kit, Fcer1a, Cpa3
Melanocyte	23	Pax3, Dct, Tyrp1
Mesenchymal cell	4,9,14,24,25	Col1a1, Col1a2, Pdgfra, Col5a1, Loxl1, Lum, Fbln1, Cd34
Mitotic cell	10	Ube2c, Pclaf, Birc5
Muscle	19	Acta1, Trdn, Tnni2
Natural killer cell	17	Klrb1c, Gimap4, Ncr1
Neutrophil	2,5,15	Mmp8, Retnlg, Ly6g
T cell	8,12	Cd3g, Cd3e, Trdc

Supplementary Table 1. Markers used to annotate cell types in 3 dpi MaFIA wound single-cell data.