

1 **SUPPLEMENTAL MATERIALS**

2 **For**

3 **Single-Cell Spatial Transcriptomics Unravels the Cellular Landscape of**
4 **Abdominal Aortic Aneurysm**

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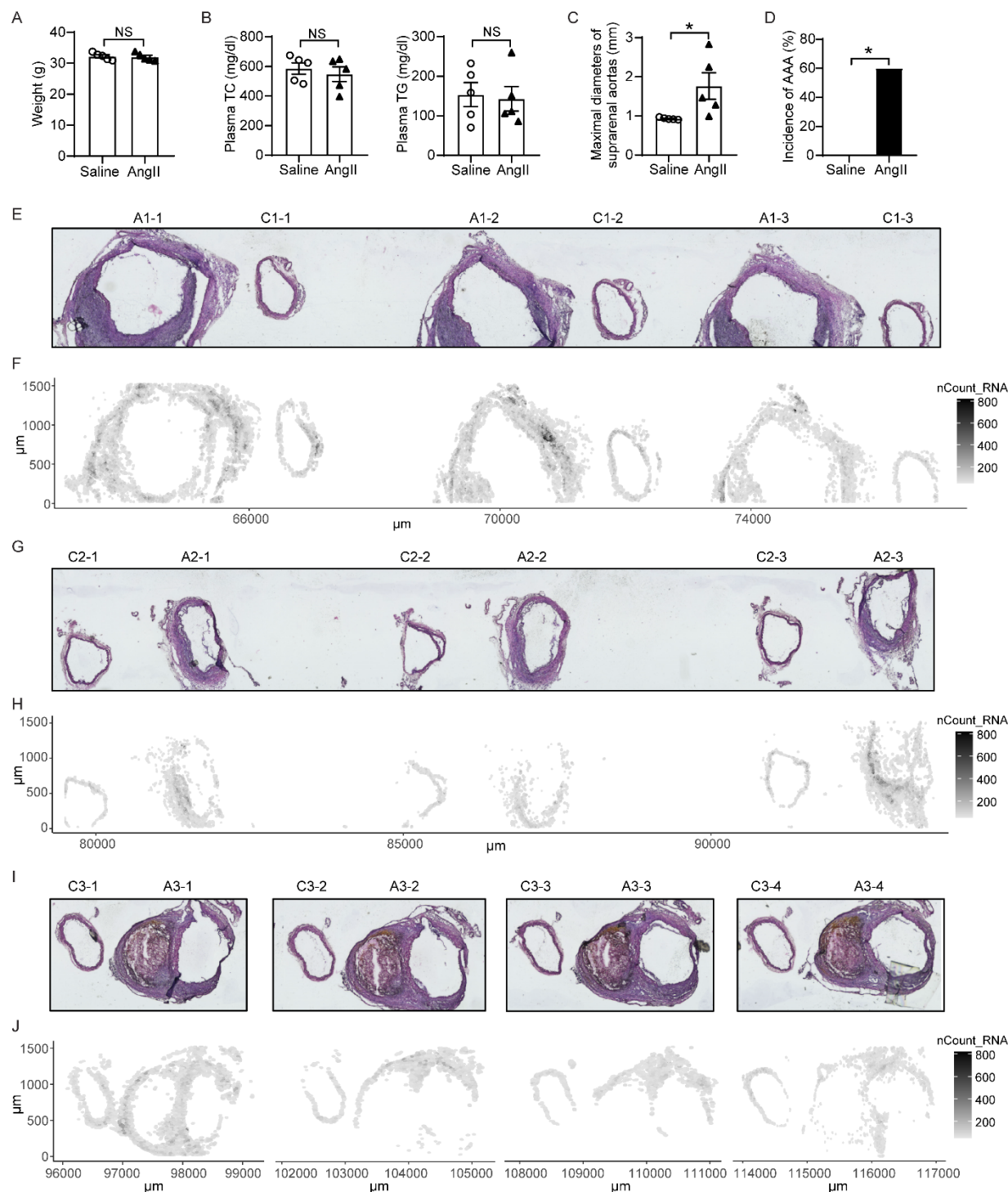
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11 Supplemental Figures 1 through 8 and Figure Legends.

12 Supplemental Tables 1 through 4.

13 Major Resource Table

14 **Supplemental Figures and Legends**

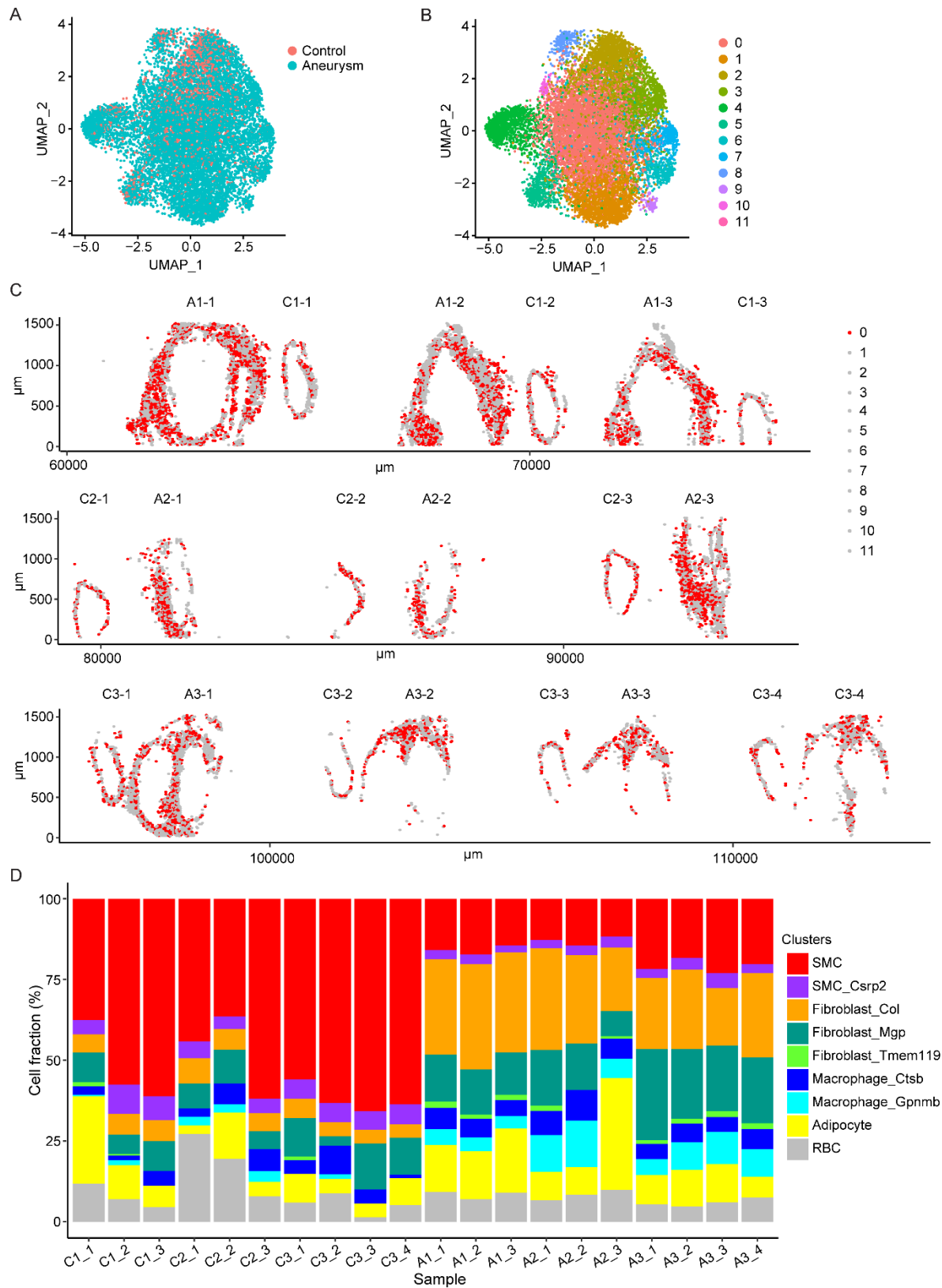


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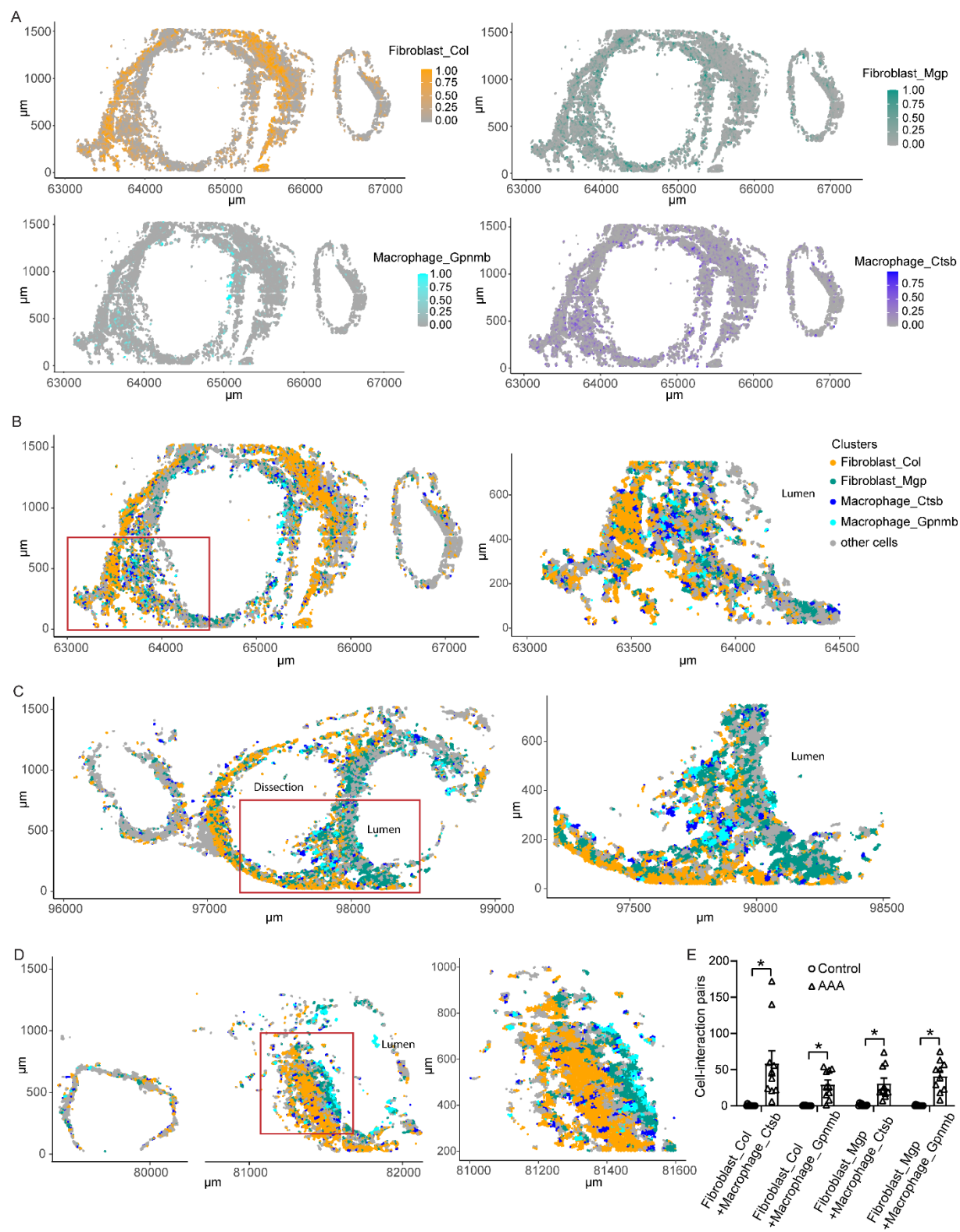
16 **Supplemental Figure 1. AngII infusion induction of abdominal aortic aneurysm in**

17 **mouse and Seq-Scope analysis of suprarenal abdominal aorta. 16-week-old male**

18 Apoe^{-/-} mice were infused AngII (1,000 ng/kg/min) or saline with minipumps for 4 weeks.
19 n=5/group. **A-B**, Body weight, plasms total cholesterol (TC) and triglycerides (TG) levels
20 after 4 weeks AngII infusion. **C**, Quantification of the maximum external diameters of
21 suprarenal abdominal aortas. **D**, AAA incidence. **E, G** and **I**, Representative hematoxylin
22 and eosin (H&E) staining of mouse suprarenal abdominal aortas from normal controls
23 and AAAs. **F, H** and **J**, Hexagons with gene expression information corresponded to the
24 areas under aortic sections in E, G and I were analyzed by spatial transcriptomics (Seq-
25 Scope). Data are represented as mean±SEM. Student's t test for A-C. Chi-squared test
26 for D. NS, no significance. **P*<0.05.



Supplemental Figure 2. Spatial transcriptomics analysis of mouse normal and aneurysmal suprarenal abdominal aortas. **A**, UMAP of all spatial transcriptomics spots from normal control and aneurysm groups, which include 10 sections from 3 normal aortas and 10 sections from 3 aneurysmal aortas. **B**, UMAP visualization of spatial transcriptomics spots based on cell-type clusters. **C**, Spatial plots of indicated cell-type clusters. Cluster 0, red. Cluster 1-11, grey. **D**, Cell cluster (excluding clusters 0, 10 and 11) percentages in each aortic section. SMC, smooth muscle cells. *Csrp2*, SMC_ *Csrp2*, SMC highly expressing cysteine and glycine-rich protein 2. Fibroblast_ *Col*, fibroblast highly expressing collagen. Fibroblast_ *Mgp*, fibroblast highly expressing matrix Gla protein. Fibroblast_ *Tmem119*, fibroblast highly expressing transmembrane protein 119. Macrophage_ *Ctsb*, macrophage highly expressing cathepsin B. Macrophage_ *Gpnmb*, macrophage highly expressing glycoprotein Nmb. RBC, red blood cell. In all spatial plots, the axis units are in μm .



Supplemental Figure 3. Spatial mapping of macrophages and fibroblasts in

normal aorta and AAA. A, Spatial plot showing the spatial prediction score of

Fibroblast_Col, Fibroblast_Mgp, Macrophage_Gpnmb, and Macrophage_Ctsb in the

aortic tissues. **B-D,** Spatial plot visualizing locations of Fibroblast_Col, Fibroblast_Mgp,

Macrophage_Gpnmb, and Macrophage_Ctsb in the tissue sections. The boxed areas

(red boxes) are magnified on the right. In all spatial plots, the axis units are in μm . **E,**

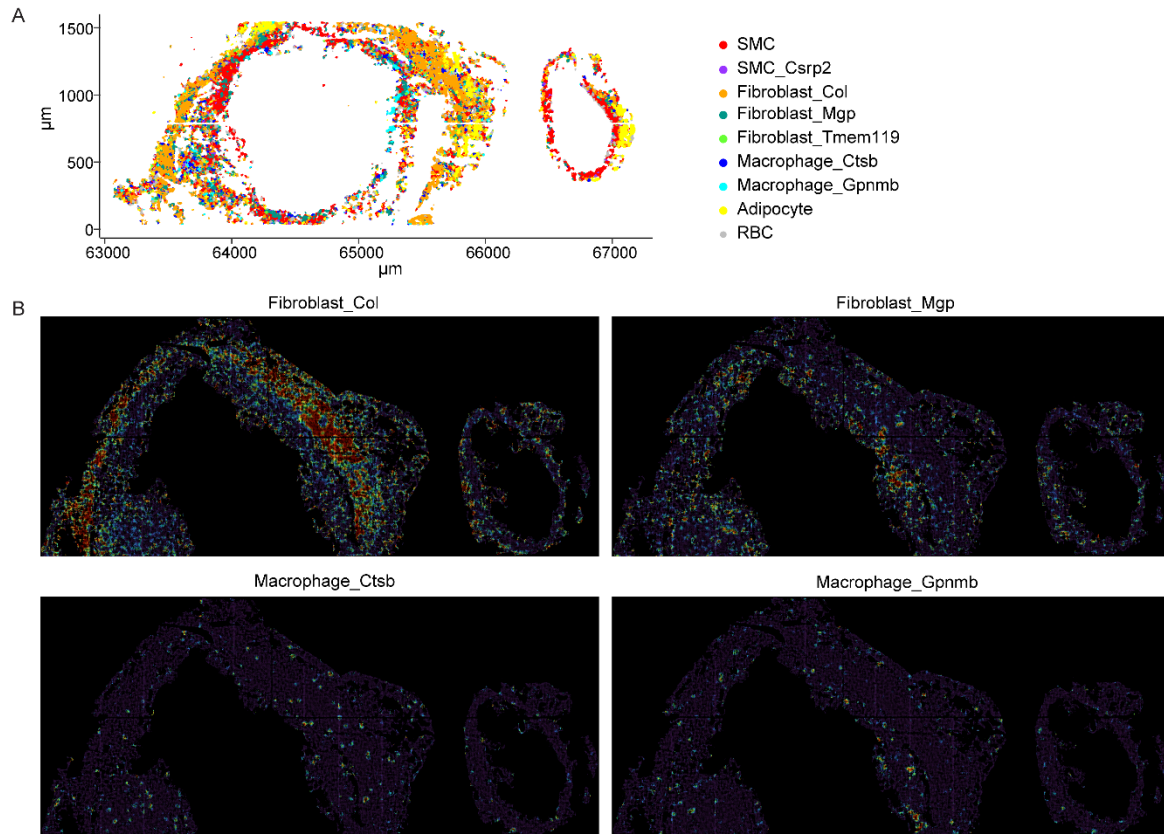
Quantification of cell-interaction pairs between Fibroblast_Col, Fibroblast_Mgp and

Macrophage_Gpnmb, Macrophage_Ctsb in the tissue sections from normal control and

aneurysm groups (10 sections for each group). Cell-cell interaction pairs were quantified

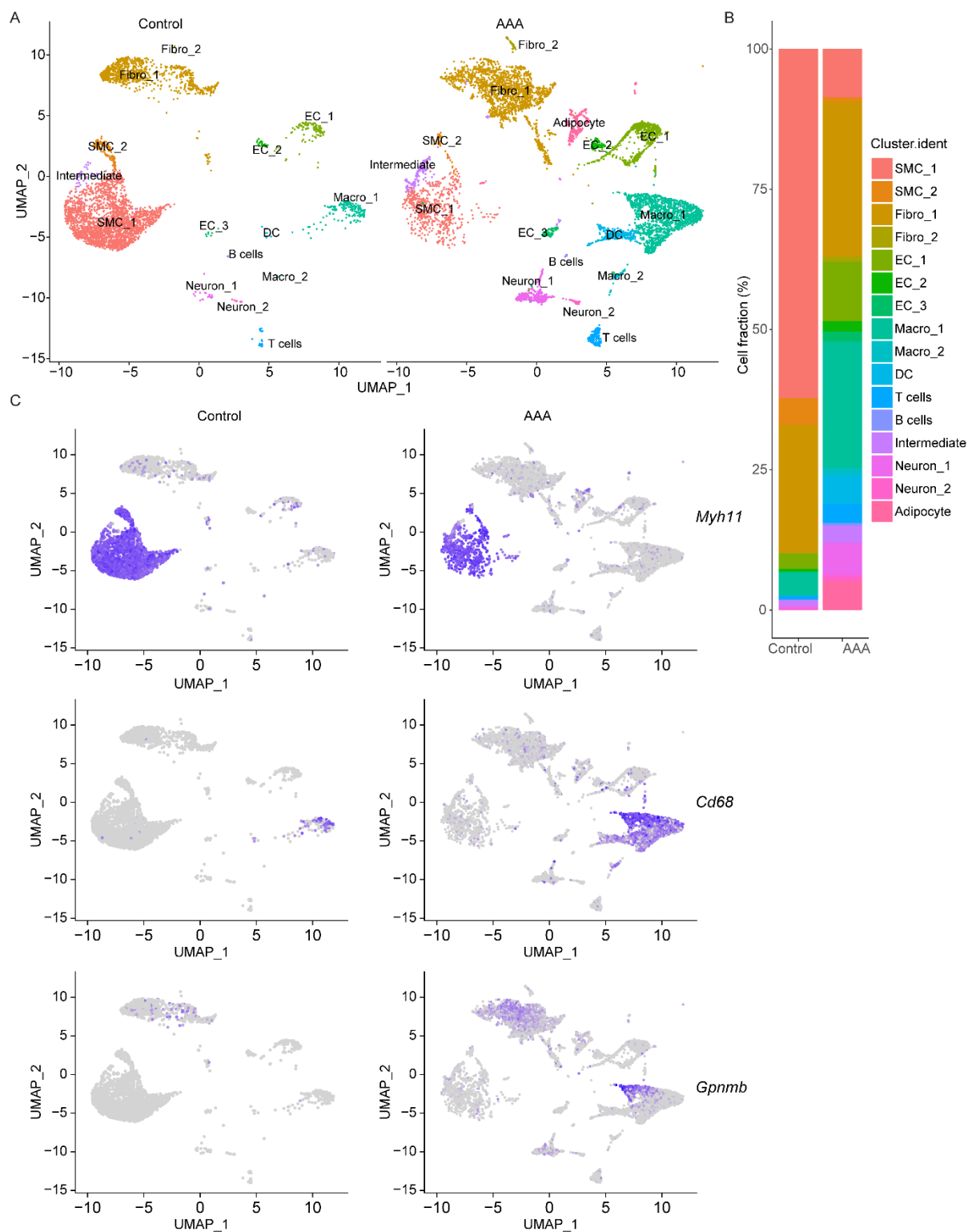
using a Euclidean distance threshold of 45 μm . Data are represented as mean $\pm$ SEM.

Student's t test for E. * $P < 0.05$.

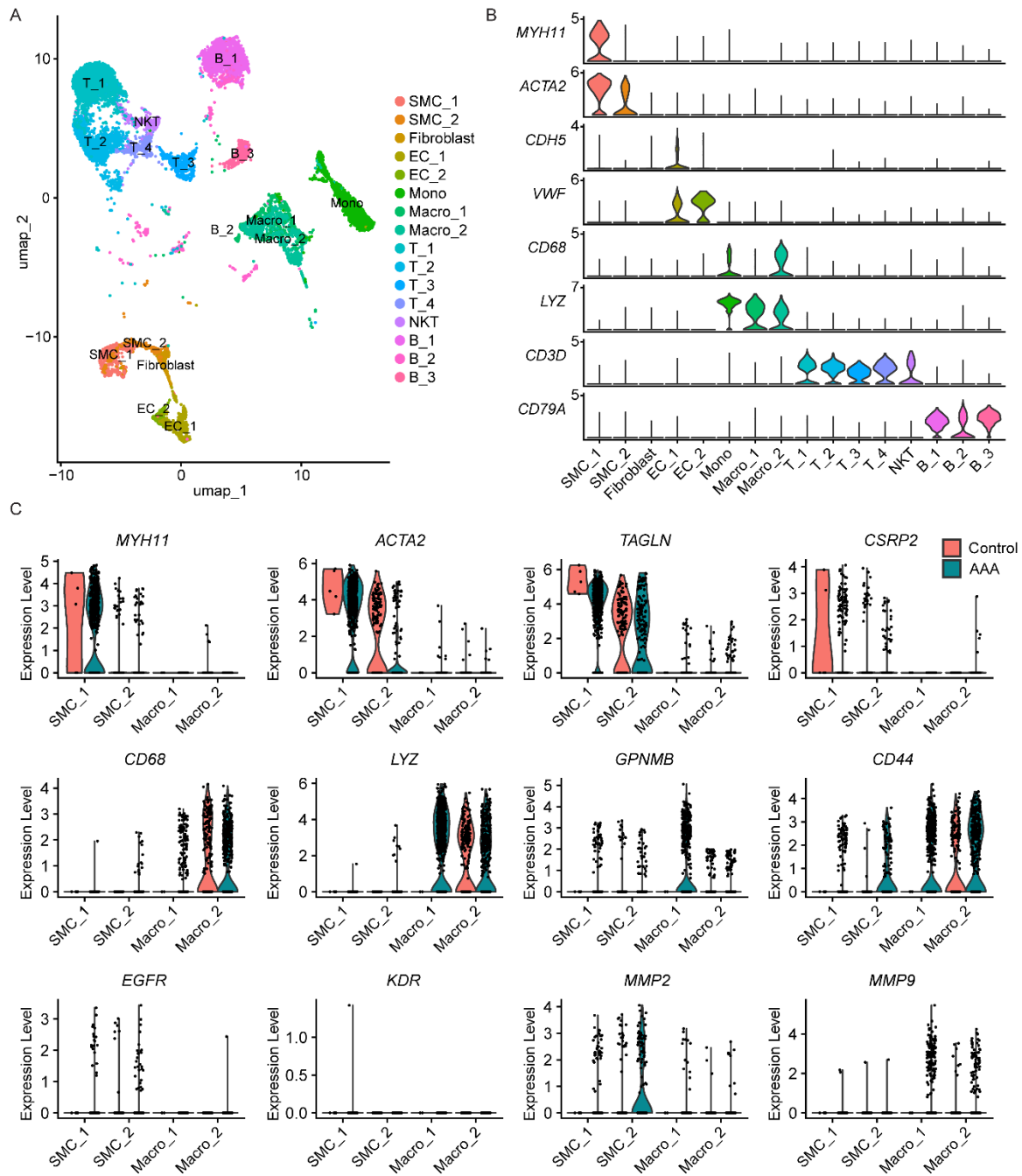


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55 **Supplemental Figure 4. Spatial probability distribution of fibroblast and**
 56 **macrophage subpopulations using FICTURE. A**, Spatial plots of cell-type clusters
 57 identified through Seurat. **B**, Spatial probability distribution of Fibroblast_Col,
 58 Fibroblast_Mgp, Macrophage_Ctsb and Macrophage_Gpnmb subpopulations using
 59 FICTURE (Factor Inference of Cartographic Transcriptome at Ultra-high Resolution).



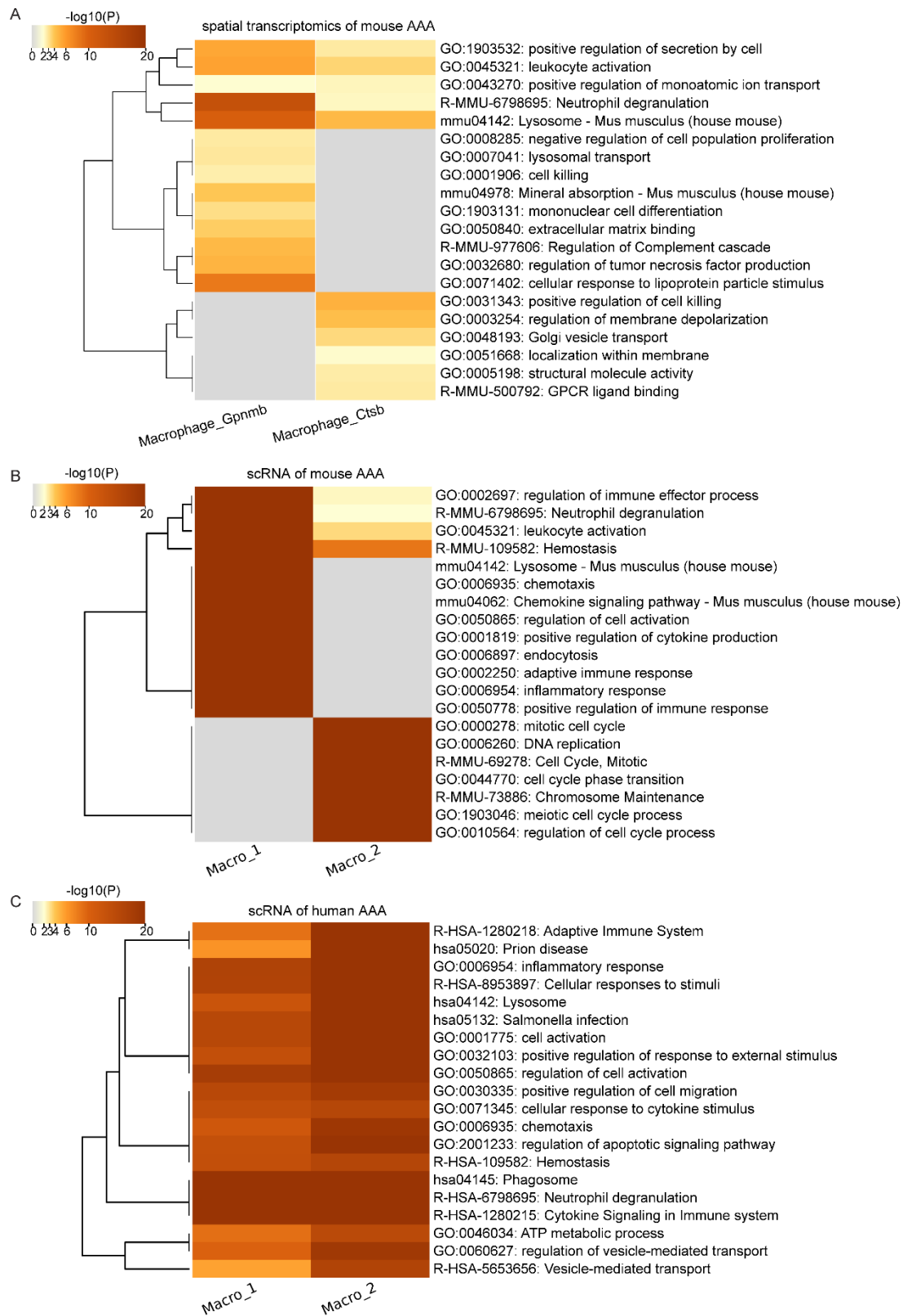
61 **Supplemental Figure 5. Single-cell RNA-sequencing analysis of healthy**
62 **suprarenal abdominal aorta and AngII-induced aneurysmal abdominal aorta.** The
63 data were reanalyzed from the datasets GSE193265 and GSE191226. Eight-week-old
64 male ApoE^{-/-} mice were implanted with minipumps to infuse AngII (1,000 ng/kg/min) for
65 4 weeks. The suprarenal abdominal aorta from AngII-infused mice or control mice were
66 dissociated into single cells for scRNA-seq. **A**, UMAP plot of cell clusters in abdominal
67 aortas of control and AAA groups. **B**, Cell population percentages in abdominal aortas
68 across control and AAA groups. **C**, Feature plots showing the expression of Myh11,
69 Cd68 and Gpnmb in abdominal aortic cells from control and AAA groups.



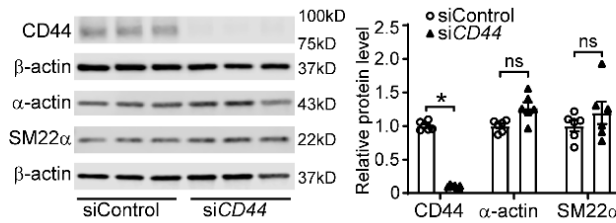
Supplemental Figure 6. Single-cell RNA-sequencing analysis of human abdominal aortic tissues from patients with AAA or control aorta. The data were reanalyzed from the dataset GSE166676 and GSE237230. Fresh human aortic tissue from patients with AAA (4 samples in GSE166676, 4 samples in GSE237230) or nonaneurysmal

75 control aorta (2 samples in GSE166676). **A**, UMAP plot of cell clusters in human
76 abdominal aortas. **B**, StackedVlnPlot showing the representative marker genes for each
77 cell type. **C**, Violin plot showing the expression of *MYH11*, *ACTA2*, *TAGLN*, *CSRP2*,
78 *CD68*, *LYZ*, *GPNMB*, *CD44*, *EGFR*, *KDR*, *MMP2* and *MMP9* in SMC and macrophage
79 subpopulations across the control and AAA conditions.

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Supplemental Figure 7. Functional and pathway enrichment analysis of macrophage subpopulations. Heatmap showing the Gene Ontology (GO) and KEGG-terms enrichment of the cluster-specific genes for the macrophage subpopulations in the spatial transcriptomic data (**A**), reanalyzed scRNA-seq mouse aortic data (GSE193265 and GSE191226, **B**) and human aortic data (GSE166676 and GSE237230, C).



Supplemental Figure 8. CD44 knockdown did not affect the basal expression of SMC marker proteins. Human aortic smooth muscle cells were transfected with nontargeting control siRNA (siControl) or siCD44, following by serum-starved for 24h. The protein abundance of smooth muscle α -actin, calponin and SM22 α was determined by Western blot. Data are represented as mean $\pm$ SEM. Student's t test. * P <0.05. ns, not significant.

96 **Supplemental Table 1. The overall quality of Seq-Scope**

Number of Reads	778045214
Reads With Valid Barcodes	0.481664
Sequencing Saturation	0.81113
Q30 Bases in CB+UMI	0.960287
Q30 Bases in RNA read	0.84374
Reads Mapped to Genome: Unique+Multiple	0.916232
Reads Mapped to Genome: Unique	0.73462
Reads Mapped to GeneFull: Unique+Multiple GeneFull	0.142683
Reads Mapped to GeneFull: Unique GeneFull	0.126213

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gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	cluster	Annotated cell type
Col1a2	3.05E-199	0.505552	0.491	0.195	4.58E-195	1	Fibroblast_Col
Igfbp4	5.44E-181	0.417270	0.39	0.133	8.17E-177	1	
Fbln1	6.61E-166	0.267426	0.223	0.048	9.91E-162	1	
Col3a1	3.04E-165	0.518699	0.591	0.31	4.57E-161	1	
Cst3	5.71E-163	0.525356	0.535	0.259	8.57E-159	1	
Dcn	1.05E-124	0.265829	0.259	0.08	1.57E-120	1	
Col1a1	4.21E-82	0.256998	0.281	0.119	6.32E-78	1	
C3	1.81E-79	0.270583	0.294	0.13	2.71E-75	1	
Gpx3	3.74E-55	0.164125	0.159	0.059	5.61E-51	1	
Lum	1.66E-35	0.104086	0.119	0.048	2.49E-31	1	
Loxl1	9.54E-28	0.089558	0.101	0.042	1.43E-23	1	
Sparc	2.13E-19	0.122058	0.237	0.155	3.20E-15	1	
Grn	6.11E-16	0.093362	0.141	0.084	9.16E-12	1	
Rps21	1.77E-13	0.087817	0.189	0.127	2.65E-09	1	
Rps19	3.35E-13	0.078896	0.146	0.092	5.03E-09	1	
Tpt1	2.15E-12	0.095272	0.357	0.278	3.22E-08	1	
Rpl37	4.23E-12	0.083434	0.161	0.107	6.34E-08	1	
Rps27a	1.24E-11	0.079982	0.16	0.107	1.86E-07	1	
H2-D1	9.15E-11	0.065377	0.128	0.083	1.37E-06	1	
Rps28	6.98E-10	0.074533	0.168	0.119	1.05E-05	1	
Rps12	1.95E-09	0.070280	0.158	0.111	2.92E-05	1	
Mgp	4.16E-09	0.036372	0.664	0.577	6.24E-05	1	
Lamp1	4.96E-09	0.061073	0.137	0.094	7.44E-05	1	
Ubc	5.75E-09	0.066101	0.131	0.089	8.63E-05	1	
Rps9	1.05E-08	0.065952	0.176	0.128	0.000158	1	
Rps13	1.83E-08	0.066430	0.192	0.143	0.000275	1	
Bgn	2.61E-08	0.079005	0.288	0.23	0.000391	1	
Rpl13	6.21E-08	0.056240	0.158	0.115	0.000931	1	
Selenop	1.72E-07	0.067882	0.21	0.162	0.002580	1	
Rack1	1.76E-07	0.060291	0.151	0.11	0.002642	1	
Rps20	5.97E-07	0.062540	0.173	0.131	0.008951	1	
Rps14	9.16E-07	0.050174	0.114	0.081	0.013738	1	
Rps29	2.74E-06	0.069478	0.271	0.224	0.041119	1	
Rps24	7.54E-06	0.052833	0.193	0.152	0.113126	1	
Serinc3	1.29E-05	0.040663	0.136	0.102	0.193181	1	
Rpl32	1.56E-05	0.046111	0.124	0.092	0.233726	1	
Rps3	2.93E-05	0.040949	0.118	0.088	0.439015	1	
Rpl35a	0.000238	0.037973	0.12	0.093	1	1	
Bsg	0.000292	0.037983	0.115	0.089	1	1	
Rpl13a	0.000343	0.051320	0.24	0.205	1	1	

Rplp1	0.000641	0.046427	0.241	0.207	1	1	
Rpl31	0.000770	0.036812	0.134	0.108	1	1	
Rps15	0.000993	0.036479	0.102	0.08	1	1	
Rps23	0.001188	0.037648	0.153	0.126	1	1	
Rps4x	0.001380	0.033985	0.109	0.087	1	1	
Rps26	0.001910	0.032471	0.117	0.095	1	1	
Anxa5	0.002073	0.028137	0.103	0.082	1	1	
Itm2b	0.005314	0.024463	0.103	0.084	1	1	
Eef2	0.008276	0.039619	0.208	0.183	1	1	
Atp5e	0.008873	0.029657	0.1	0.082	1	1	
Acta2	0	0.711127	0.696	0.276	0	2	SMC
Tagln	1.00E-270	0.518067	0.464	0.133	1.50E-266	2	
Myl9	2.48E-223	0.492624	0.438	0.139	3.72E-219	2	
Cpe	2.46E-116	0.326293	0.316	0.116	3.69E-112	2	
Ptgis	4.11E-72	0.179505	0.147	0.042	6.16E-68	2	
Flna	8.45E-69	0.236445	0.236	0.097	1.27E-64	2	
Col18a1	5.13E-51	0.120147	0.118	0.037	7.70E-47	2	
Tpm2	1.61E-49	0.140590	0.144	0.052	2.41E-45	2	
Ccn2	2.13E-49	0.145494	0.144	0.052	3.20E-45	2	
Myl6	7.61E-32	0.184169	0.284	0.173	1.14E-27	2	
Csrp1	4.65E-31	0.120677	0.125	0.054	6.97E-27	2	
Mfge8	1.08E-29	0.132616	0.132	0.06	1.62E-25	2	
Serpine2	2.41E-24	0.092178	0.107	0.048	3.61E-20	2	
Fn1	5.43E-22	0.162890	0.296	0.2	8.15E-18	2	
Dstn	5.02E-20	0.109785	0.152	0.085	7.53E-16	2	
Bgn	5.27E-15	0.135319	0.308	0.228	7.90E-11	2	
Sod3	7.22E-15	0.073578	0.1	0.053	1.08E-10	2	
S100a6	4.92E-12	0.086120	0.199	0.137	7.39E-08	2	
Igfbp7	9.87E-12	0.068106	0.114	0.069	1.48E-07	2	
Tmsb4x	2.09E-11	0.096161	0.237	0.173	3.14E-07	2	
Lgals1	8.03E-09	0.070349	0.115	0.075	0.000120	2	
Cavin1	9.08E-09	0.082661	0.128	0.087	0.000136	2	
Actb	1.91E-07	0.105085	0.478	0.423	0.002864	2	
Clu	2.09E-07	0.057032	0.112	0.076	0.003129	2	
Hspa8	0.00142254	0.047402	0.14	0.114	1	2	
Mgp	0	1.195987	0.919	0.555	0	3	Fibroblast_Mgp
Elfn	1.92E-191	0.437159	0.326	0.072	2.88E-187	3	
Fn1	8.69E-61	0.329205	0.385	0.195	1.30E-56	3	
Tm4sf1	7.18E-31	0.116639	0.101	0.034	1.08E-26	3	
Ccn2	1.65E-19	0.099416	0.124	0.058	2.48E-15	3	
Cpe	5.28E-17	0.124323	0.222	0.135	7.93E-13	3	
Bgn	1.48E-16	0.173185	0.328	0.229	2.22E-12	3	
Ltbp2	1.59E-13	0.084004	0.109	0.057	2.38E-09	3	
Lgals1	2.09E-06	0.050007	0.115	0.077	0.031396	3	

Col1a1	2.38E-06	0.082714	0.186	0.138	0.035668	3	
Myl6	1.51E-05	0.075171	0.232	0.183	0.226630	3	
Psap	4.40E-05	0.052505	0.26	0.208	0.659637	3	
Actb	5.41E-05	0.081546	0.483	0.425	0.812210	3	
Igfbp7	0.000336	0.036075	0.1	0.072	1	3	
Acta2	0.000449	0.040646	0.382	0.328	1	3	
S100a6	0.000555	0.061759	0.178	0.143	1	3	
Sparc	0.001665	0.054078	0.198	0.164	1	3	
Cst3	0.002838	0.059054	0.334	0.296	1	3	
Tagln	0.003225	0.037334	0.209	0.175	1	3	
Fstl1	0.003721	0.038010	0.105	0.081	1	3	
Dstn	0.008491	0.032778	0.115	0.092	1	3	
Cfd	0.000000	1.469763	0.898	0.139	0	4	Adipose
Hp	2.08E-235	0.536368	0.406	0.091	3.11E-231	4	
Fabp4	4.57E-220	0.427232	0.325	0.061	6.86E-216	4	
Ifi27l2a	3.31E-130	0.232514	0.157	0.022	4.97E-126	4	
Car3	8.60E-112	0.245458	0.186	0.037	1.29E-107	4	
Lpl	3.04E-110	0.265555	0.209	0.047	4.56E-106	4	
Glul	9.93E-63	0.181558	0.16	0.044	1.49E-58	4	
Dbi	5.17E-58	0.232586	0.236	0.09	7.76E-54	4	
Scd1	3.92E-57	0.306435	0.366	0.182	5.88E-53	4	
Cyp2e1	1.85E-38	0.135311	0.122	0.039	2.78E-34	4	
Cox6a1	1.10E-26	0.122913	0.134	0.056	1.64E-22	4	
Cdo1	8.86E-25	0.110677	0.125	0.052	1.33E-20	4	
C4b	8.66E-19	0.099726	0.11	0.049	1.30E-14	4	
Cox8a	1.75E-15	0.109684	0.15	0.083	2.63E-11	4	
Scp2	1.07E-08	0.086017	0.164	0.109	0.000160	4	
Gpx3	5.61E-08	0.061996	0.113	0.07	0.000842	4	
Atp5g3	7.89E-08	0.076758	0.13	0.085	0.001184	4	
H2-D1	1.34E-06	0.069358	0.127	0.086	0.020040	4	
Cox4i1	1.79E-06	0.057016	0.107	0.07	0.026917	4	
Rps28	9.09E-06	0.059511	0.167	0.122	0.136324	4	
C3	1.24E-05	0.075282	0.197	0.15	0.186262	4	
H2-K1	4.05E-05	0.057888	0.135	0.098	0.608271	4	
Mgst1	4.33E-05	0.059257	0.106	0.073	0.649680	4	
Atp5e	0.000797	0.048148	0.11	0.082	1	4	
B2m	0.001293	0.042868	0.134	0.103	1	4	
Atp5a1	0.001727	0.052299	0.128	0.101	1	4	
Chchd2	0.003322	0.056636	0.166	0.137	1	4	
Gpx1	0.009413	0.028515	0.118	0.095	1	4	
Hba-a2	0	0.893265	0.59	0.053	0	5	RBC
Hbb-bs	0	0.596711	0.399	0.018	0	5	
Hbb-bt	2.36E-285	0.224316	0.138	0.002	3.55E-281	5	
Ctsb	0	1.148723	0.916	0.053	0	6	Macrophage_Ctsb

Lamp1	2.68E-07	0.113074	0.171	0.098	0.004014	6	
Psap	0.000147	0.127768	0.282	0.21	1	6	
Ltbp2	0.000724	0.047561	0.1	0.06	1	6	
Rpl34	0.002838	0.059558	0.115	0.077	1	6	
Rpl37	0.007154	0.049507	0.155	0.114	1	6	
Lyz2	0.007804	0.042549	0.102	0.069	1	6	
Gpnmb	0	0.800627	0.569	0.041	0	7	Macrophage_Gpnmb
Cd5l	4.01E-208	0.335780	0.218	0.012	6.02E-204	7	
Ctsd	4.70E-129	0.723536	0.486	0.115	7.05E-125	7	
Psap	1.74E-74	0.667877	0.53	0.202	2.61E-70	7	
Lyz2	2.39E-56	0.313845	0.259	0.064	3.59E-52	7	
Ctsb	2.13E-32	0.232991	0.236	0.077	3.20E-28	7	
Ctsl	7.32E-32	0.230012	0.183	0.052	1.10E-27	7	
Lgals3	9.70E-28	0.127856	0.12	0.028	1.46E-23	7	
Ctss	2.14E-27	0.141128	0.118	0.027	3.21E-23	7	
Ftl1	5.41E-23	0.158043	0.144	0.043	8.11E-19	7	
Atp6v0c	8.72E-14	0.140617	0.157	0.066	1.31E-09	7	
C1qc	5.56E-08	0.083995	0.104	0.047	0.000835	7	
Actb	9.14E-08	0.194078	0.539	0.427	0.001371	7	
Lpl	2.77E-07	0.088255	0.12	0.06	0.004158	7	
Fth1	5.57E-07	0.154109	0.236	0.15	0.008364	7	
Mfge8	5.15E-05	0.084246	0.118	0.068	0.773394	7	
Eln	0.001702	0.056486	0.141	0.095	1	7	
Clu	0.003578	0.075733	0.118	0.08	1	7	
Prdx1	0.004731	0.054021	0.104	0.069	1	7	
Lamp1	0.008037	0.073890	0.137	0.099	1	7	
Csrp2	0	1.129600	0.935	0.022	0	8	SMC_Csrp2
Acta2	1.15E-15	0.384232	0.418	0.208	1.73E-11	8	
Rbp4	0.001208	0.189439	0.169	0.054	0.001525	8	
Tmem119	0	1.144419	0.867	0.004	0	9	Fibroblast_Tmem119
Cst3	5.22E-04	0.542094	0.419	0.125	1.00E+00	9	
Rps29	1.03E-02	0.251539	0.39	0.15	1.00E+00	9	
Eef1a1	2.69E-02	0.332823	0.4	0.225	1.00E+00	9	
Mgp	3.59E-11	0.601679	0.648	0.365	5.38E-07	9	
Col3a1	9.25E-07	0.319955	0.486	0.276	1.39E-02	9	
Col1a2	6.00E-05	0.259455	0.286	0.144	9.00E-01	9	
Rpl28	0	1.342801	0.904	0.03	0	10	Unknown
Ddx17	2.77E-06	0.253954	0.123	0.011	4.16E-02	10	
Ttn	0	0.937618	0.7	0.005	0	11	
Tmcc1	1.44E-91	0.345019	0.225	0.004	2.16E-87	11	

102 **Supplemental Table 3. The differentially expressed markerd for all cell clusters**

103 **across two conditions**

gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	cluster	group
Acta2	1.15E-57	0.435266736	0.592	0.373	1.73E-53	SMC	Normal
Myl9	1.45E-28	0.256125267	0.348	0.204	2.17E-24	SMC	Normal
Tagln	4.53E-16	0.180662304	0.312	0.205	6.80E-12	SMC	Normal
Myl6	4.18E-12	0.137594252	0.277	0.189	6.27E-08	SMC	Normal
Ptgis	5.29E-10	0.092291694	0.117	0.064	7.94E-06	SMC	Normal
Cpe	7.26E-09	0.124130489	0.222	0.154	0.0001088 63	SMC	Normal
Flna	1.34E-08	0.116511459	0.189	0.127	0.0002006 52	SMC	Normal
Tpm2	1.67E-05	0.056199557	0.113	0.075	0.2498560 58	SMC	Normal
Csrp1	5.03E-05	0.054796498	0.103	0.068	0.7543633 84	SMC	Normal
Dstn	0.0004876 56	0.064815079	0.131	0.097	1	SMC	Normal
Bc1	1.03E-08	0.087727299	0.112	0.056	0.0001547 57	SMC	AAA
Col3a1	3.58E-08	0.11945377	0.324	0.245	0.0005367 07	SMC	AAA
Rps24	3.54E-06	0.085730098	0.168	0.114	0.0530726 55	SMC	AAA
Rplp1	1.25E-05	0.086314252	0.216	0.159	0.1874857 98	SMC	AAA
Igfbp4	1.67E-05	0.06891686	0.141	0.093	0.2510985 82	SMC	AAA
Mptx1	3.01E-05	0.088528539	0.424	0.36	0.4512177 66	SMC	AAA
Rpl13a	3.13E-05	0.089895002	0.219	0.167	0.4697345 7	SMC	AAA
Col1a1	3.15E-05	0.062793657	0.116	0.074	0.4732794 93	SMC	AAA
C3	8.05E-05	0.066397556	0.131	0.089	1	SMC	AAA
Actb	0.0003160 86	0.080457752	0.453	0.397	1	SMC	AAA
Rps20	0.0004397 18	0.050518676	0.133	0.095	1	SMC	AAA
Ctsd	0.0009312 95	0.051565575	0.11	0.078	1	SMC	AAA
Rps9	0.0021989 78	0.051489789	0.138	0.105	1	SMC	AAA
Rps28	0.0030828 31	0.050915377	0.116	0.086	1	SMC	AAA
Apoe	0.0035358 91	0.059748784	0.387	0.343	1	SMC	AAA
Serinc3	0.0041971 99	0.040419355	0.104	0.076	1	SMC	AAA

Rpl23	0.0053047 12	0.044020064	0.133	0.103	1	SMC	AAA
Atp5a1	0.0099265 21	0.032951493	0.11	0.084	1	SMC	AAA

Acta2	0.0002746 79	0.371736324	0.563	0.363	1	SMC_Csrp2	Normal
Flna	0.0026555 54	0.210087992	0.268	0.118	1	SMC_Csrp2	Normal
Csrp2	0.0030883 78	0.17445883	0.986	0.922	1	SMC_Csrp2	Normal
Serf2	0.0070489 34	0.142830152	0.155	0.054	1	SMC_Csrp2	Normal

Mpc2	1.57E-06	0.125428761	0.116	0.022	0.0234890 85	Fibroblast_Col	Normal
Col3a1	7.12E-05	0.41033719	0.606	0.391	1	Fibroblast_Col	AAA
C3	0.0021423 91	0.294526498	0.294	0.13	1	Fibroblast_Col	AAA
Gpx3	0.0031477 29	0.21616518	0.159	0.029	1	Fibroblast_Col	AAA
Actb	0.0048084 24	0.246988497	0.424	0.246	1	Fibroblast_Col	AAA
Fbln1	0.0052434 44	0.220149349	0.227	0.087	1	Fibroblast_Col	AAA
Mup20	0.0073030 23	0.19046607	0.243	0.101	1	Fibroblast_Col	AAA
Rpl31	0.0087206 01	0.159103817	0.139	0.029	1	Fibroblast_Col	AAA
Col1a1	0.0089561 86	0.180292639	0.292	0.145	1	Fibroblast_Col	AAA
Rpl27a	0.0051786 7	0.151616881	0.102	0	1	Fibroblast_Col	AAA
H2-D1	0.0095502 03	0.145153379	0.114	0.014	1	Fibroblast_Col	AAA
Lum	0.0071355 52	0.139985472	0.123	0.014	1	Fibroblast_Col	AAA

Mylk	1.98E-05	0.156949946	0.139	0.044	0.2968982 85	Fibroblast_Mgp	Normal
Tns1	0.0007091 79	0.112399374	0.102	0.035	1	Fibroblast_Mgp	Normal
Cyp3a11	0.0002853 35	0.095661737	0.105	0.033	1	Fibroblast_Mgp	Normal
Mgp	3.29E-05	0.313225643	0.926	0.852	0.4930433 65	Fibroblast_Mgp	AAA
Fn1	0.0008445 04	0.261322508	0.398	0.238	1	Fibroblast_Mgp	AAA
Ctsd	0.0022084 25	0.16615981	0.158	0.048	1	Fibroblast_Mgp	AAA
Actb	0.0023029 47	0.213951908	0.496	0.343	1	Fibroblast_Mgp	AAA
Col1a2	0.0042755 64	0.197103517	0.256	0.133	1	Fibroblast_Mgp	AAA

Col3a1	0.0076664 26	0.198512694	0.369	0.248	1	Fibroblast_Mgp	AAA
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Ndufs6	1.57E-09	0.570462931	0.5	0.01	2.35E-05	Fibroblast_Tmem119	Normal
Tcp1	9.29E-09	0.415037499	0.333	0	0.0001393 7	Fibroblast_Tmem119	Normal
D130017N 08Rik	5.80E-05	0.415037499	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Liph	5.80E-05	0.415037499	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Tnfrsf23	5.80E-05	0.415037499	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Tnrc6c	5.80E-05	0.415037499	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Vmn2r50	5.80E-05	0.415037499	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Al427809	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Abcg2	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Adra2a	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Aldh18a1	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Anapc5	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Aox1	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Apaf1	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Apc	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Appl1	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Armc1	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Ascc3	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Ate1	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Aup1	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Avpr1a	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
B130024G 19Rik	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Birc3	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Boc	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
C1qbp	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Cabin1	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal

Calm2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Camsap2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Cd151	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Cdc14b	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Cdc5l	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Cdh18	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Cdh2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Ciart	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Clptm1	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Col5a2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Ctdnep1	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Dazap1	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Ddx54	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Desi2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Dhx29	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Dhx33	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Dld	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Ebp	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Enah	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Evi5	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Faf2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Fam193a	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Fam222b	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Fbxw5	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Fibin	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Foxk2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Foxn3	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal

Fundc2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Glyr1	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Gria2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Grpel1	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Hao1	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Hdx	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Hes6	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Hoxa2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Hpn	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Hsd17b4	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Hsd17b6	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Itga8	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Kit	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Lamb2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Lcat	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Leng8	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Lratd2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Lsm2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Mettl9	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Mfsd5	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Mrpl12	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Mrpl48	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Myom1	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Mysm1	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Oard1	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Ociad1	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Olf1238	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal

Otud4	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
P4hb	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Pafah2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Pcyt2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Pdia6	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Pgpep1	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Pim3	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Plcb3	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Plxdc2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Pot1a	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Prkag2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Prxl2c	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Purb	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Rab22a	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Rabl2	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Rapgef1	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Rev1	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Rfx7	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Rhog	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Riok3	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Rnf213	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Rpgrip1l	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Rrp15	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Sccpdh	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Senp7	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Serpina10	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal
Sh2d3c	5.80E-05	0.222392421	0.167	0	0.869547578	Fibroblast_Tmem119	Normal

Slc16a1	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Slc16a7	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Slc35e4	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Smim4	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Smpdl3a	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Sptssb	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Synpo2	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Tbc1d9b	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Tgfr3	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Thbs4	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Thrsp	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Tmbim1	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Tmem29	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Tmem47	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Tpp2	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Trmt1l	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Ttc13	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Txn1	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Ugt2b5	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Unc13d	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Unc93b1	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Vamp1	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Vps52	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Wdr18	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Zfp809	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Zfp869	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal
Zmym6	5.80E-05	0.222392421	0.167	0	0.8695475 78	Fibroblast_Tmem119	Normal

Manf	6.46E-05	0.513879403	0.5	0.051	0.9685099 26	Fibroblast_Tmem119	Normal
Malat1	0.0002551 64	0.486398666	0.5	0.061	1	Fibroblast_Tmem119	Normal
Nedd8	0.0009278 65	0.343954401	0.333	0.03	1	Fibroblast_Tmem119	Normal
Cyp3a11	0.0029766 8	0.357893592	0.333	0.04	1	Fibroblast_Tmem119	Normal
Rps25	0.0033344 74	0.343954401	0.333	0.04	1	Fibroblast_Tmem119	Normal
Rpl24	0.0061015 96	0.406964199	0.5	0.101	1	Fibroblast_Tmem119	Normal
Cldnd1	0.0067051 34	0.722466024	0.167	0.01	1	Fibroblast_Tmem119	Normal
Ddx1	0.0067051 34	0.40053793	0.167	0.01	1	Fibroblast_Tmem119	Normal
Kctd10	0.0067051 34	0.40053793	0.167	0.01	1	Fibroblast_Tmem119	Normal
Eef1a1	0.0069375 85	0.75161237	0.833	0.374	1	Fibroblast_Tmem119	Normal
Ahnak	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Amotl2	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Arf3	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Atp6v1g1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Bub3	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Ccnd2	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Cd200	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Col5a3	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Cox6b1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Crp	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Cyhr1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Fam160b2	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Gpn1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Gps1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Hdac1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Iqgap2	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Irf9	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal

Kansl2	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Mars	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Mrps16	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Mrps6	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Mtpap	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Ndufa2	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Ndufb2	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Net1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Nfx1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Nox4	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Npepps	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Npr2	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Prdm2	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Psmc3	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Ptch1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Ptpn14	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Pum1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Rad21	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Rgs19	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Rnf167	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Sec61b	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Serpina1e	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Slc16a2	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Slc24a3	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Slc25a36	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Socs7	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Ssb	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal

Szrd1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Tank	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Timm8b	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Tm6sf2	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Tmem127	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Tpp1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Tra2b	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Tram1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Tyms	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Uba1	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Uqcrc2	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Vmn2r102	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Ybx3	0.0073157 94	0.207892852	0.167	0.01	1	Fibroblast_Tmem119	Normal
Hmgn1	0.0076315 37	0.343954401	0.333	0.051	1	Fibroblast_Tmem119	Normal
Muc2	0.0076315 37	0.343954401	0.333	0.051	1	Fibroblast_Tmem119	Normal
Cbx7	0.0079817 56	0.193537559	0.167	0.01	1	Fibroblast_Tmem119	Normal
Cul1	0.0079817 56	0.193537559	0.167	0.01	1	Fibroblast_Tmem119	Normal
Dnpep	0.0079817 56	0.193537559	0.167	0.01	1	Fibroblast_Tmem119	Normal
Rab5b	0.0079817 56	0.193537559	0.167	0.01	1	Fibroblast_Tmem119	Normal
Tex264	0.0079817 56	0.193537559	0.167	0.01	1	Fibroblast_Tmem119	Normal
Tmem132 b	0.0079817 56	0.193537559	0.167	0.01	1	Fibroblast_Tmem119	Normal
Pdia3	0.0079817 56	0.179323699	0.167	0.01	1	Fibroblast_Tmem119	Normal
Myl6	0.0080070 99	0.663572335	0.667	0.202	1	Fibroblast_Tmem119	Normal

Naa10	5.94E-17	0.222392421	0.167	0	8.92E-13	Macrophage_Gpnmb	Normal
Fnta	1.57E-11	0.218961516	0.167	0.002	2.36E-07	Macrophage_Gpnmb	Normal
Gramd1a	1.57E-11	0.218961516	0.167	0.002	2.36E-07	Macrophage_Gpnmb	Normal
Ugt2b35	8.41E-09	0.21553875	0.167	0.005	0.0001261 39	Macrophage_Gpnmb	Normal
Ergic1	1.03E-07	0.391190757	0.25	0.017	0.0015504 09	Macrophage_Gpnmb	Normal

Gja1	1.23E-07	0.298081353	0.25	0.017	0.0018414 37	Macrophage_Gpnmb	Normal
Pcna	6.21E-07	0.291339775	0.25	0.019	0.0093150 55	Macrophage_Gpnmb	Normal
Bad	2.96E-05	0.205318908	0.167	0.012	0.4440704 33	Macrophage_Gpnmb	Normal
Elf3i	2.96E-05	0.205318908	0.167	0.012	0.4440704 33	Macrophage_Gpnmb	Normal
Aoc3	0.0001175 63	0.201928319	0.167	0.014	1	Macrophage_Gpnmb	Normal
Emp3	0.0001175 63	0.201928319	0.167	0.014	1	Macrophage_Gpnmb	Normal
Hmgcs2	0.0003458 13	0.198545679	0.167	0.017	1	Macrophage_Gpnmb	Normal
Flna	0.0003487 76	0.368122918	0.417	0.095	1	Macrophage_Gpnmb	Normal
Ddb1	0.0008237 44	0.195170953	0.167	0.019	1	Macrophage_Gpnmb	Normal
F2	0.0008237 44	0.195170953	0.167	0.019	1	Macrophage_Gpnmb	Normal
Arcn1	0.0016822 48	0.191804102	0.167	0.021	1	Macrophage_Gpnmb	Normal
Sri	0.0017327 98	0.188445089	0.167	0.021	1	Macrophage_Gpnmb	Normal
Cyp3a11	0.0030597 33	0.188445089	0.167	0.024	1	Macrophage_Gpnmb	Normal
Aldh1a1	0.0031435 11	0.18509388	0.167	0.024	1	Macrophage_Gpnmb	Normal
Map1lc3a	0.0050892 63	0.18509388	0.167	0.026	1	Macrophage_Gpnmb	Normal
Psmb4	0.0050892 63	0.18509388	0.167	0.026	1	Macrophage_Gpnmb	Normal
Rps27	0.0050892 63	0.18509388	0.167	0.026	1	Macrophage_Gpnmb	Normal
Ugt2b34	0.0050892 63	0.18509388	0.167	0.026	1	Macrophage_Gpnmb	Normal
Rpl36	0.0078890 31	0.181750437	0.167	0.029	1	Macrophage_Gpnmb	Normal
Alb	0.0081070 96	0.410464769	0.833	0.526	1	Macrophage_Gpnmb	Normal

Mt1	0.0004101 61	0.127195684	0.114	0.02	1	Macrophage_Ctsb	Normal
Ctsb	0.0008049 31	0.266466376	0.929	0.795	1	Macrophage_Ctsb	AAA

Hadh	1.49E-08	0.138871656	0.125	0.027	0.0002240 79	Adipose	Normal
Ndufb8	3.57E-08	0.145569638	0.14	0.034	0.0005354 62	Adipose	Normal
Aco2	1.35E-07	0.227484811	0.199	0.068	0.0020309 44	Adipose	Normal
Acadl	5.84E-06	0.16658805	0.118	0.034	0.0876541 08	Adipose	Normal

Ech1	8.80E-06	0.12748823	0.162	0.058	0.1319819 96	Adipose	Normal
Pnpla2	1.39E-05	0.219437868	0.191	0.079	0.2092558 41	Adipose	Normal
Atp5b	5.64E-05	0.163462826	0.162	0.065	0.8455972 94	Adipose	Normal
Ifi27	9.73E-05	0.121858193	0.118	0.041	1	Adipose	Normal
Pck1	0.0001240 1	0.140404118	0.132	0.05	1	Adipose	Normal
Cox6a1	0.0003225 42	0.132534451	0.235	0.121	1	Adipose	Normal
Glul	0.0014964 48	0.169084893	0.25	0.148	1	Adipose	Normal
Cs	0.0018025 19	0.082407462	0.103	0.042	1	Adipose	Normal
Cyb5a	0.0035018 12	0.096937513	0.118	0.054	1	Adipose	Normal
Cox4i1	0.0048202 12	0.125764374	0.176	0.099	1	Adipose	Normal
Car3	0.0073534 08	0.172795159	0.265	0.176	1	Adipose	Normal
Hp	8.61E-08	0.396772871	0.432	0.199	0.0012914 91	Adipose	AAA
Cfd	7.62E-05	0.377741765	0.901	0.868	1	Adipose	AAA
Col3a1	0.0011624 23	0.186031836	0.291	0.162	1	Adipose	AAA
Rpl13a	0.0028981 13	0.14459972	0.212	0.103	1	Adipose	AAA
C4b	0.0034961 56	0.137305132	0.119	0.037	1	Adipose	AAA

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Supplemental Table 4. Sequences of the primers used for real-time PCR

	Primer Sequence	
mouse <i>Gpnmb</i>	Forward	ACGGCAGGTGGAAGGACT
	Reverse	CGGTGAGTCACTGGTCAGG
mouse <i>Actb</i>	Forward	GTGACGTTGACATCCGTAAAGA
	Reverse	GCCGGACTCATCGTACTCC
human <i>GPNUMB</i>	Forward	TAAACCTTGAGTGCCTGCGTC
	Reverse	GTCTTTCATTGCCCAGCACA
human <i>CD44</i>	Forward	TCTACCCCAGCAACCCTACT
	Reverse	TTGGTTGCTGTCTCAGTTGCT
human <i>EGFR</i>	Forward	TCCAGTATTGATCGGGAGAGCC
	Reverse	TGAGCTTGTTACTCGTGCCTT
human <i>KDR</i>	Forward	CAAGTGGCTAAGGGCATGGA
	Reverse	ATTTCAAAGGGAGGCGAGCA
human <i>MYH11</i>	Forward	CATCTACTCGGAGAAGATCGTCG
	Reverse	CGCCTGTGCATAGAATGGACT
human <i>ACTA2</i>	Forward	CTTGAGAAGAGTTACGAGTTG
	Reverse	GATGCTGTTGTAGGTGGTT
human <i>TAGLN</i>	Forward	AGTGCAGTCCAAAATCGAGAAG
	Reverse	CTTGCTCAGAATCACGCCAT
human <i>CCL2</i>	Forward	CAGCCAGATGCAATCAATGCC
	Reverse	TGGAATCCTGAACCCACTTCT
human <i>IL6</i>	Forward	ACTCACCTCTTCAGAACGAATTG
	Reverse	CCATCTTTGGAAGGTTCAAGTTG
human <i>CXCL3</i>	Forward	CGCCCAAACCGAAGTCATAG
	Reverse	GCTCCCCTTGTTCAAGTATCTTTT
human <i>CXCL5</i>	Forward	AGCTGCGTTGCGTTTGTTTAC
	Reverse	TGGCGAACACTTGCAGATTAC
human <i>MMP2</i>	Forward	TACAGGATCATTGGCTACACACC
	Reverse	GGTCACATCGCTCCAGACT
human <i>MMP9</i>	Forward	AGACCTGGGCAGATTCCAAAC
	Reverse	CGGCAAGTCTTCCGAGTAGT
human <i>ADAM10</i>	Forward	AGCAACATCTGGGGACAAAC
	Reverse	CCCAGGTTTCAGTTTGCATT
human <i>ACTB</i>	Forward	CATGTACGTTGCTATCCAGGC
	Reverse	CTCCTTAATGTCACGCACGAT

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Major Resource Table

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Animals

Species (Mouse)	Source	Stock No.	Sex
Apoe ^{-/-}	The Jackson Lab	002052	male
C57BL/6J	The Jackson Lab	000664	male

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Antibodies

Target antigen	Source	Catalog No.	Applications	Working concentration
GPNMB	Fisher Scientific	AF2330	IF	2µg/ml
Mac2	Thermo Fisher Scientific	14-5301-85	IF	5µg/ml
α-actin	Abcam	Ab5694	IF	1µg/ml
CD44	Fisher Scientific	5012580	IF	5µg/ml
SM22 α	Abcam	ab10135	IF&WB	IF, 2.5µg/ml; WB, 0.5µg/ml
α-actin	Abcam	ab119952	WB	0.5µg/ml

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IF, immunofluorescence staining; WB, western blot.