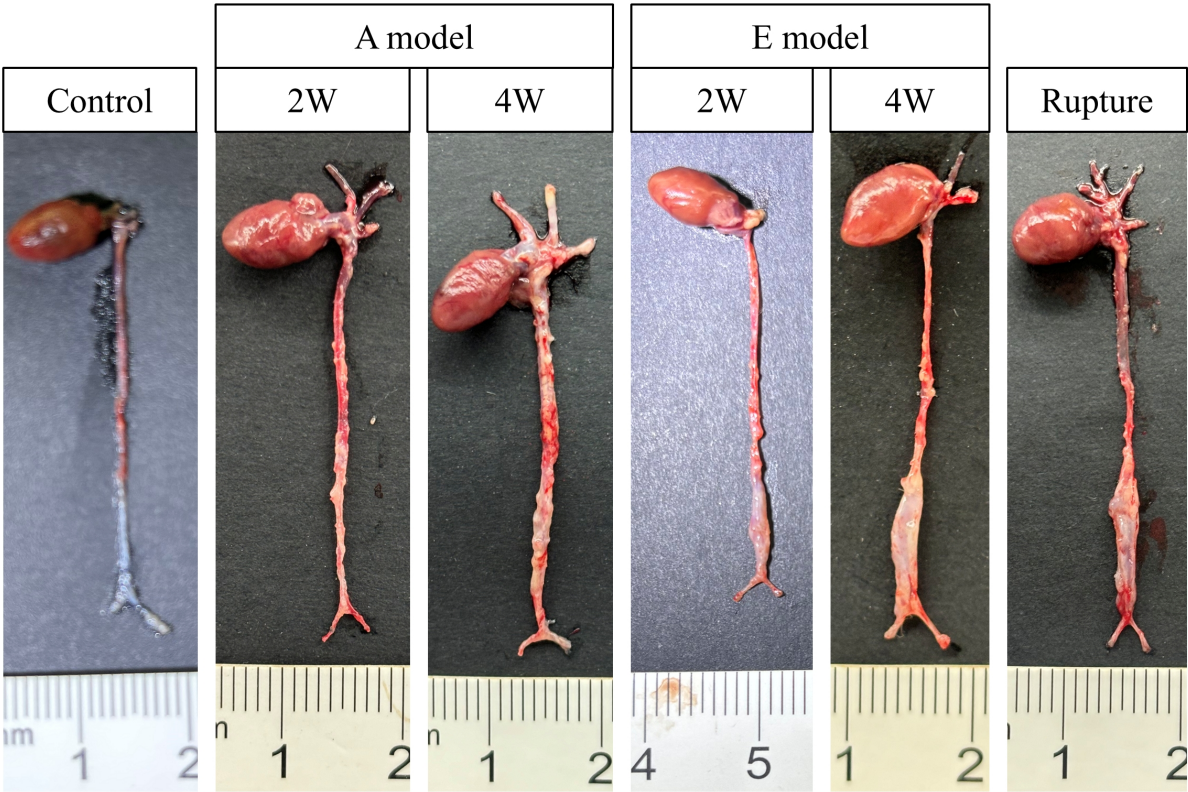
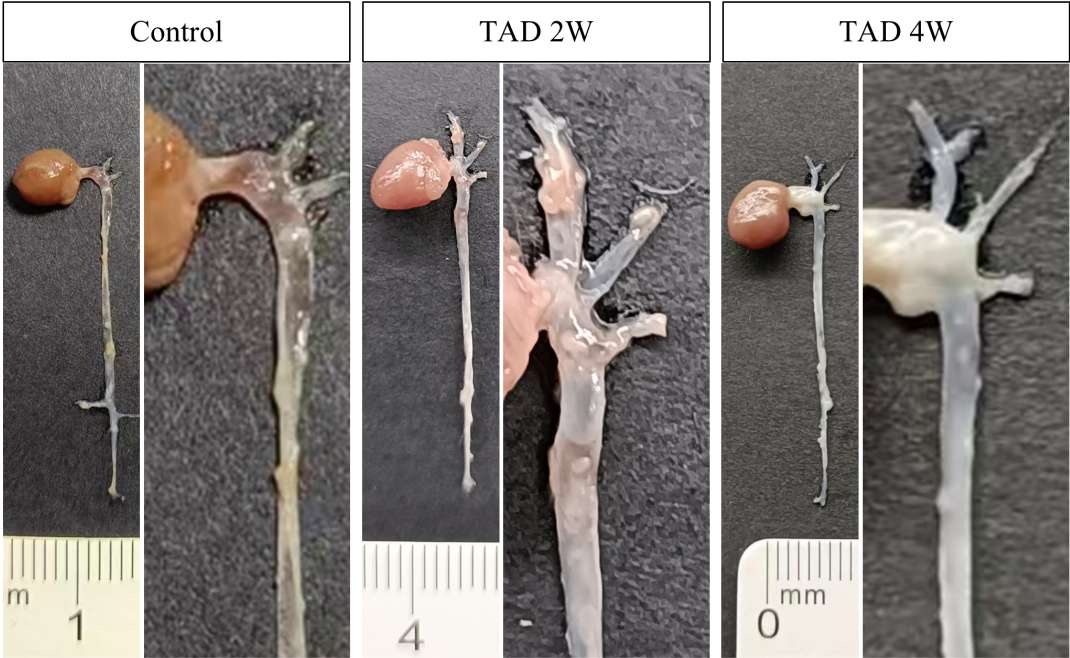


1 **Supplementary Figures**

A



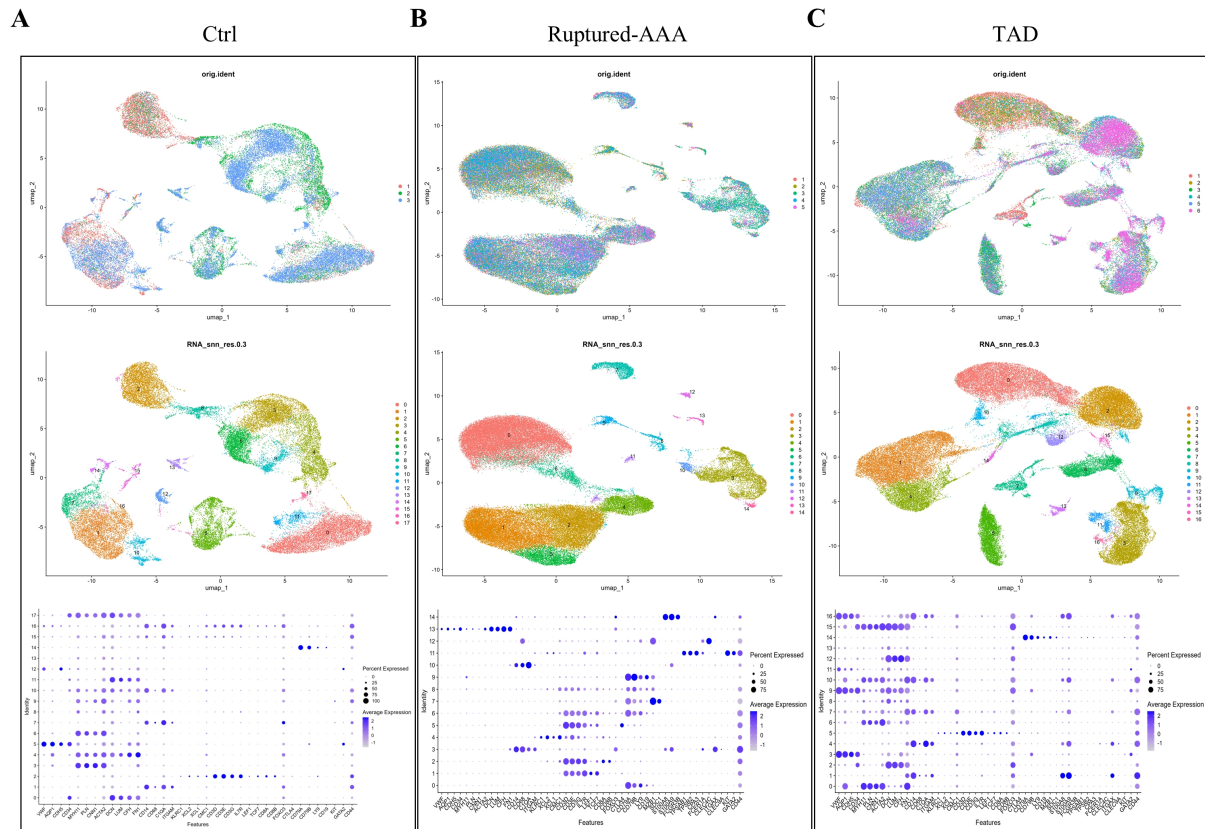
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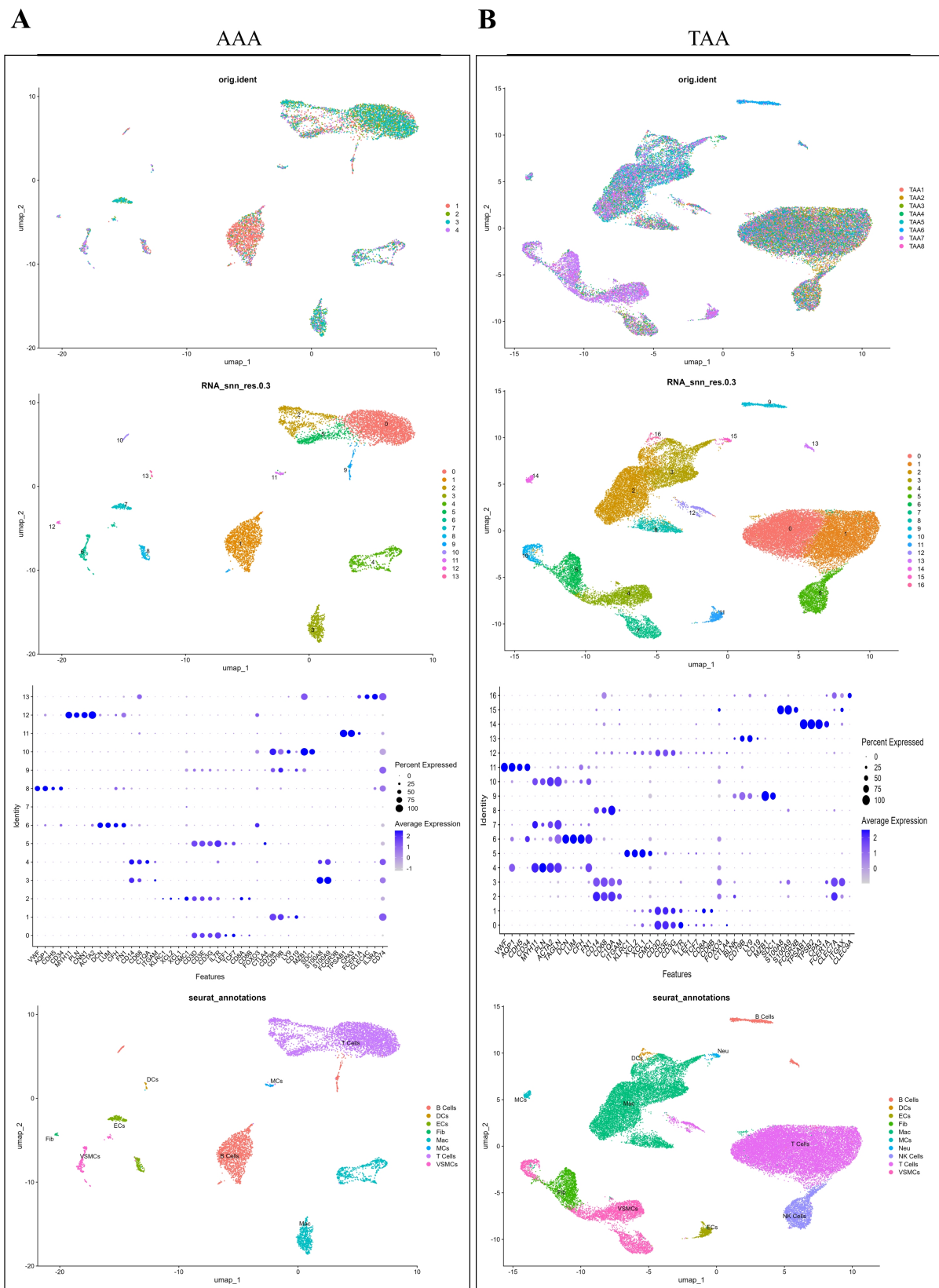
2
3 **Supplementary Fig. 1. Gross morphology of mouse aortas in experimental aortic aneurysm**
4 **and thoracic aortic dissection models. (A)** Representative gross images of aortas from mouse
5 abdominal aortic aneurysm (AA) models. A model indicates the angiotensin II (AngII)

6 infusion-induced aneurysm model, while E model indicates the elastase perfusion-induced
7 aneurysm model. Aortas were harvested at 2 and 4 weeks after induction and compared with control
8 aortas. A representative ruptured aneurysm is also shown. **(B)** Representative gross images of aortas
9 from the mouse thoracic aortic dissection (TAD) model at 2 and 4 weeks after induction, compared
10 with control aortas. Rulers indicate millimeter scale.

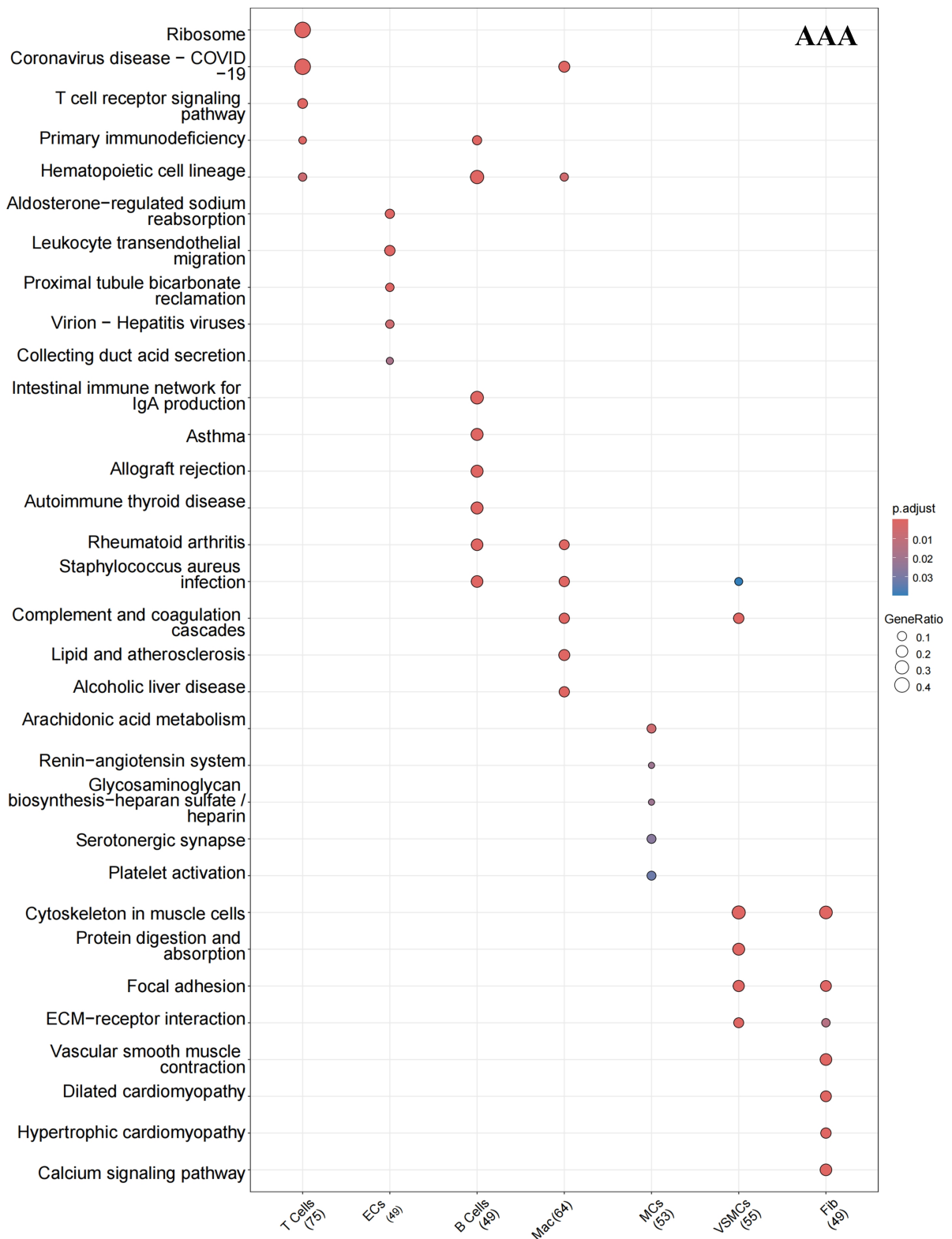
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Supplementary Fig. 2. Single-cell clustering and marker gene annotation of human aortic tissues. (A) UMAP visualization of single-cell transcriptomic profiles from normal control aortic tissue (Ctrl). The upper panel shows cell clustering, and the middle panel shows annotated cell populations based on canonical marker genes. The lower panel displays a dot plot of representative marker genes used for cell-type identification. (B) UMAP visualization of single-cell transcriptomic profiles from ruptured abdominal aortic aneurysm (AAA) tissue. The upper panel shows unsupervised clustering, and the middle panel shows annotated cell populations. The lower panel presents marker gene expression across identified cell clusters. (C) UMAP visualization of single-cell transcriptomic profiles from thoracic aortic dissection (TAD) tissue. The upper panel shows unsupervised clustering, the middle panel shows cell-type annotation based on marker genes, and the lower panel presents the dot plot of representative marker genes across clusters. Dot size represents the percentage of cells expressing the gene, and color intensity indicates the average expression level.



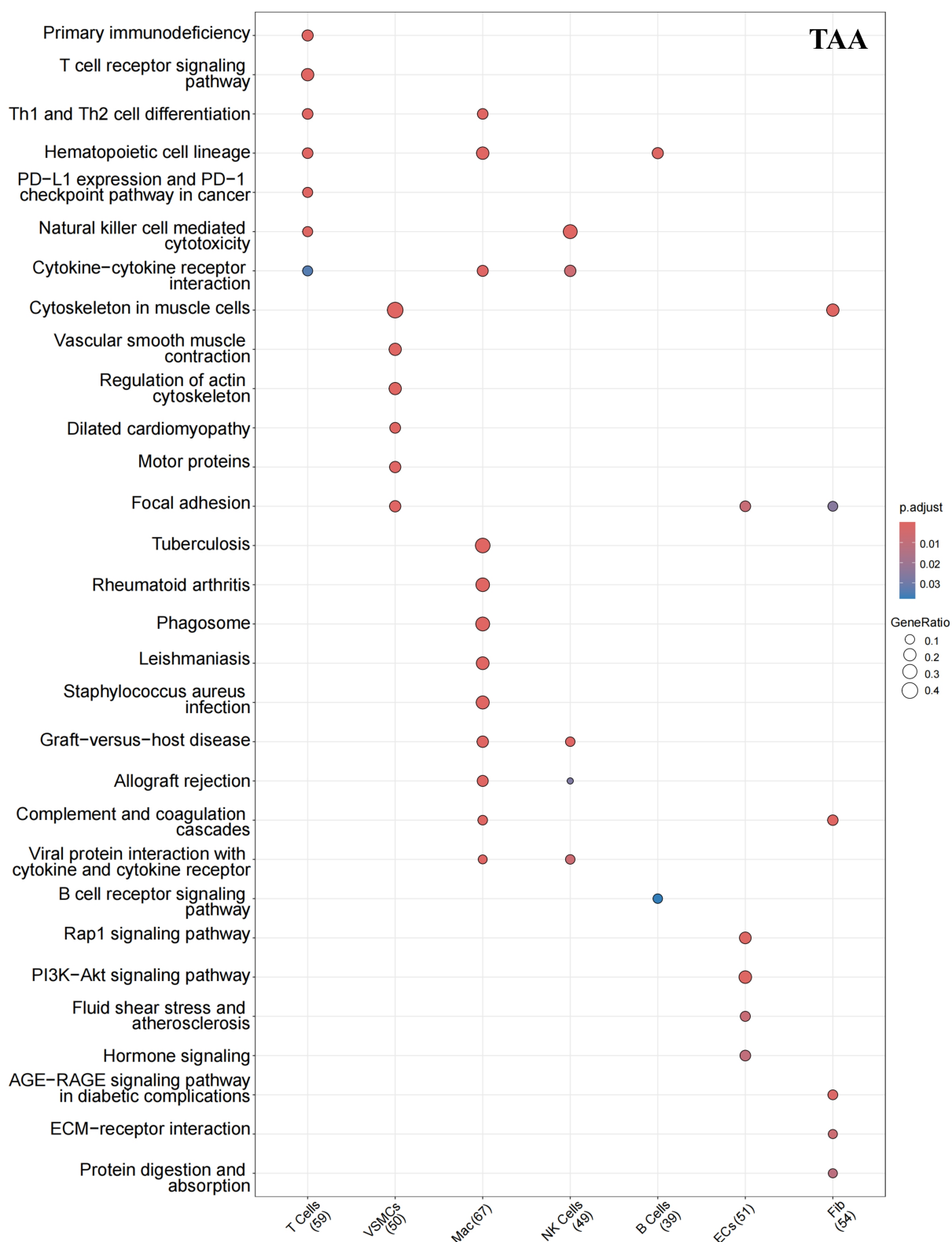
32 = 0.3). The third panel presents a dot plot of representative marker genes used for cell-type
33 identification. The bottom panel shows the annotated cell populations based on canonical marker
34 genes. **(B)** UMAP visualization of single-cell transcriptomic profiles from TAA tissue. The top
35 panel shows cells colored by sample identity. The second panel displays unsupervised clustering
36 results (resolution = 0.3). The third panel shows marker gene expression across clusters using a dot
37 plot. The bottom panel presents the final cell-type annotation. Dot size represents the percentage of
38 cells expressing each gene, and color intensity indicates the average expression level.
39



Supplementary Fig. 4. KEGG pathway enrichment analysis across major cell populations in abdominal aortic aneurysm (AAA). KEGG pathway enrichment analysis of differentially expressed genes in major cell populations identified in AAA tissue, including T cells, endothelial cells (ECs), B cells, macrophages (Mac), mast cells (MCs), vascular smooth muscle cells (VSMCs), and fibroblasts (Fib). Each dot represents a significantly enriched pathway. Dot size indicates the

46 gene ratio (GeneRatio), and color represents the adjusted p value (p.adjust).

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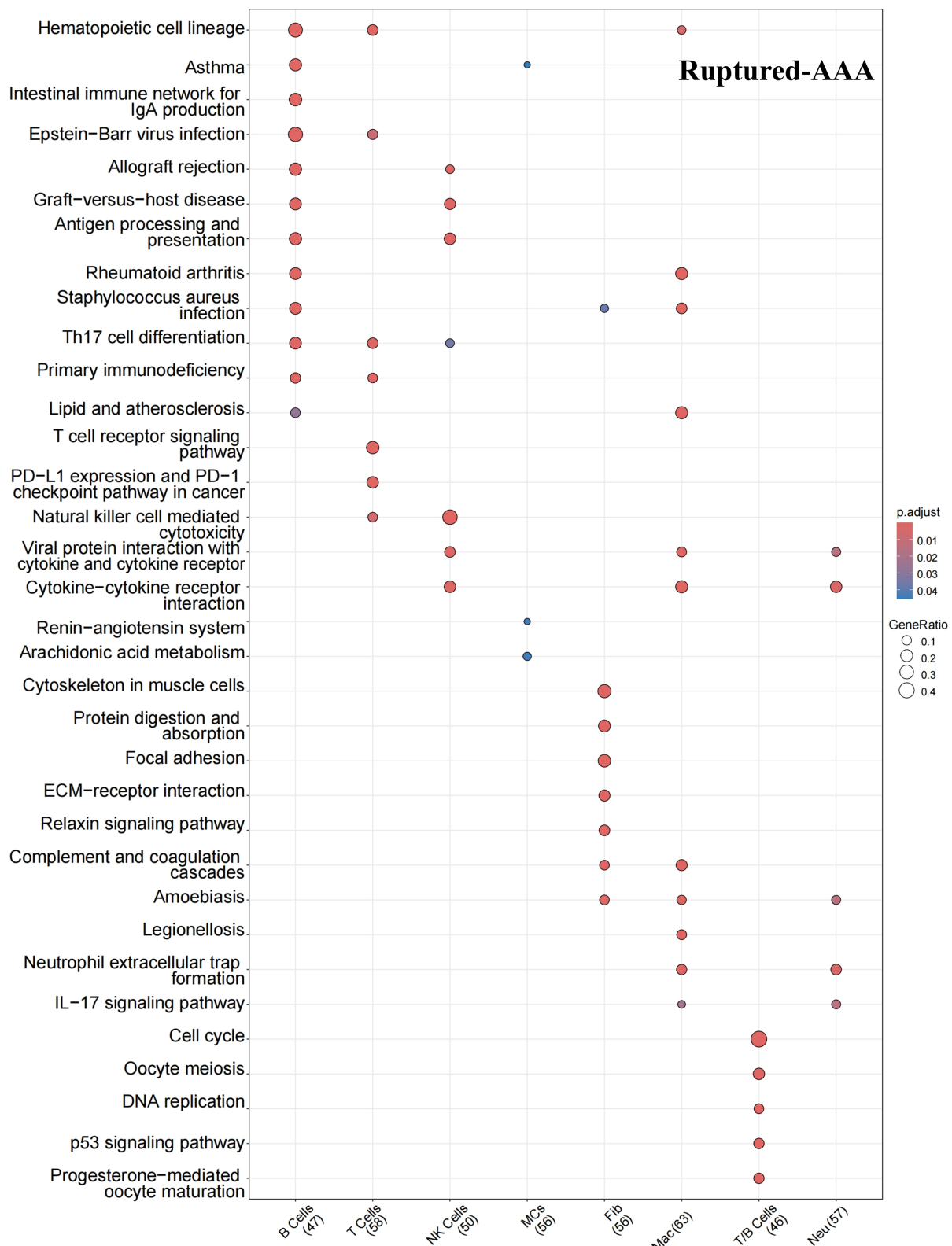


48

49 **Supplementary Fig. 5. KEGG pathway enrichment analysis across major cell populations in**
 50 **thoracic aortic aneurysm (TAA).** KEGG pathway enrichment analysis of differentially expressed
 51 genes in major cell populations identified in TAA tissue, including T cells, vascular smooth muscle
 52 cells (VSMCs), macrophages (Mac), natural killer (NK) cells, B cells, endothelial cells (ECs), and
 53 fibroblasts (Fib). Each dot represents a significantly enriched pathway. Dot size indicates the gene

54 ratio (GeneRatio), and color represents the adjusted p value (p.adjust).

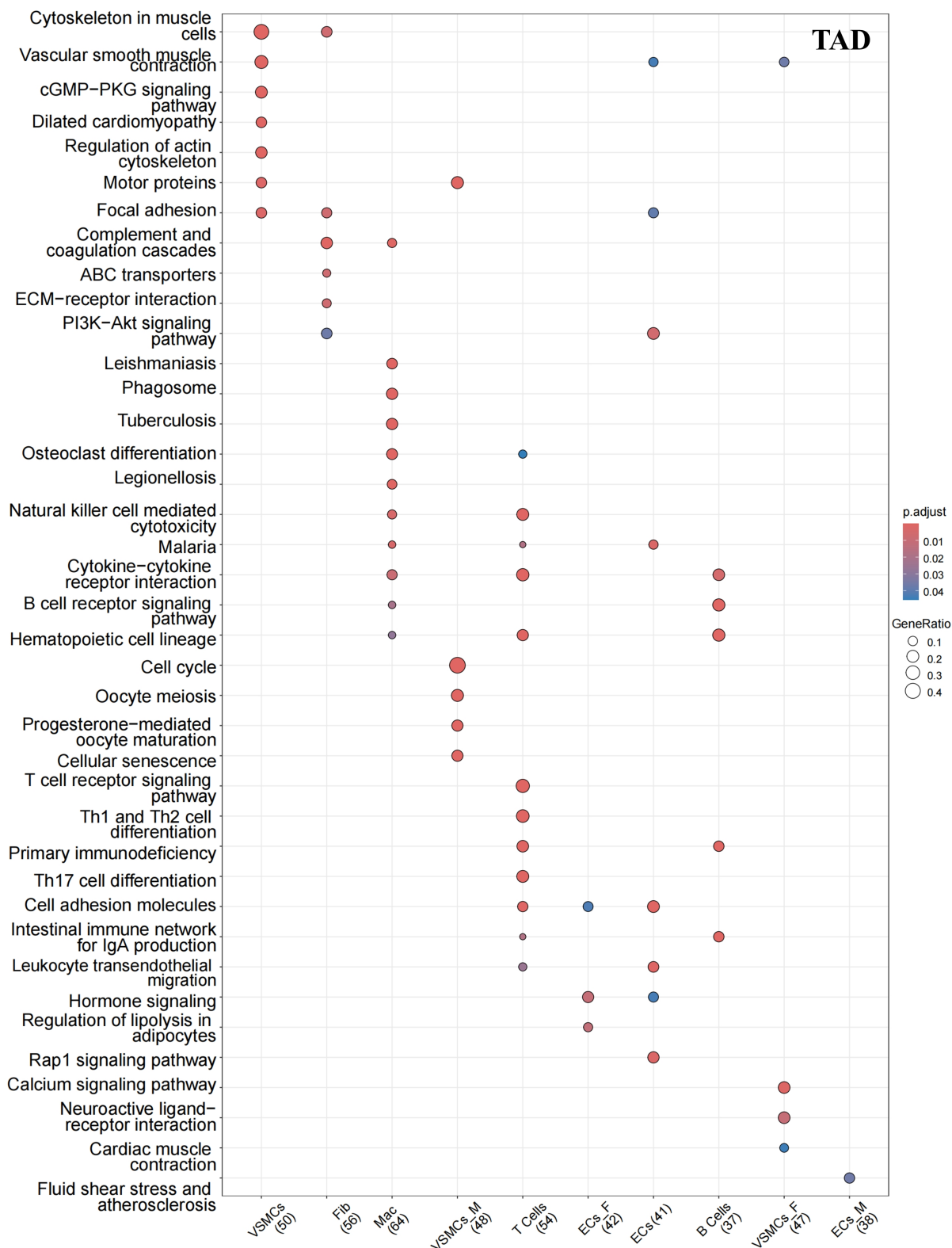
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56

57 **Supplementary Fig. 6. KEGG pathway enrichment analysis across major cell populations in**
 58 **ruptured abdominal aortic aneurysm (ruptured-AAA).** KEGG pathway enrichment analysis of
 59 differentially expressed genes in major cell populations identified in ruptured-AAA tissue, including
 60 B cells, T cells, natural killer (NK) cells, mast cells (MCs), fibroblasts (Fib), macrophages (Mac),
 61 T/B cells, and neutrophils (Neu). Each dot represents a significantly enriched pathway. Dot size

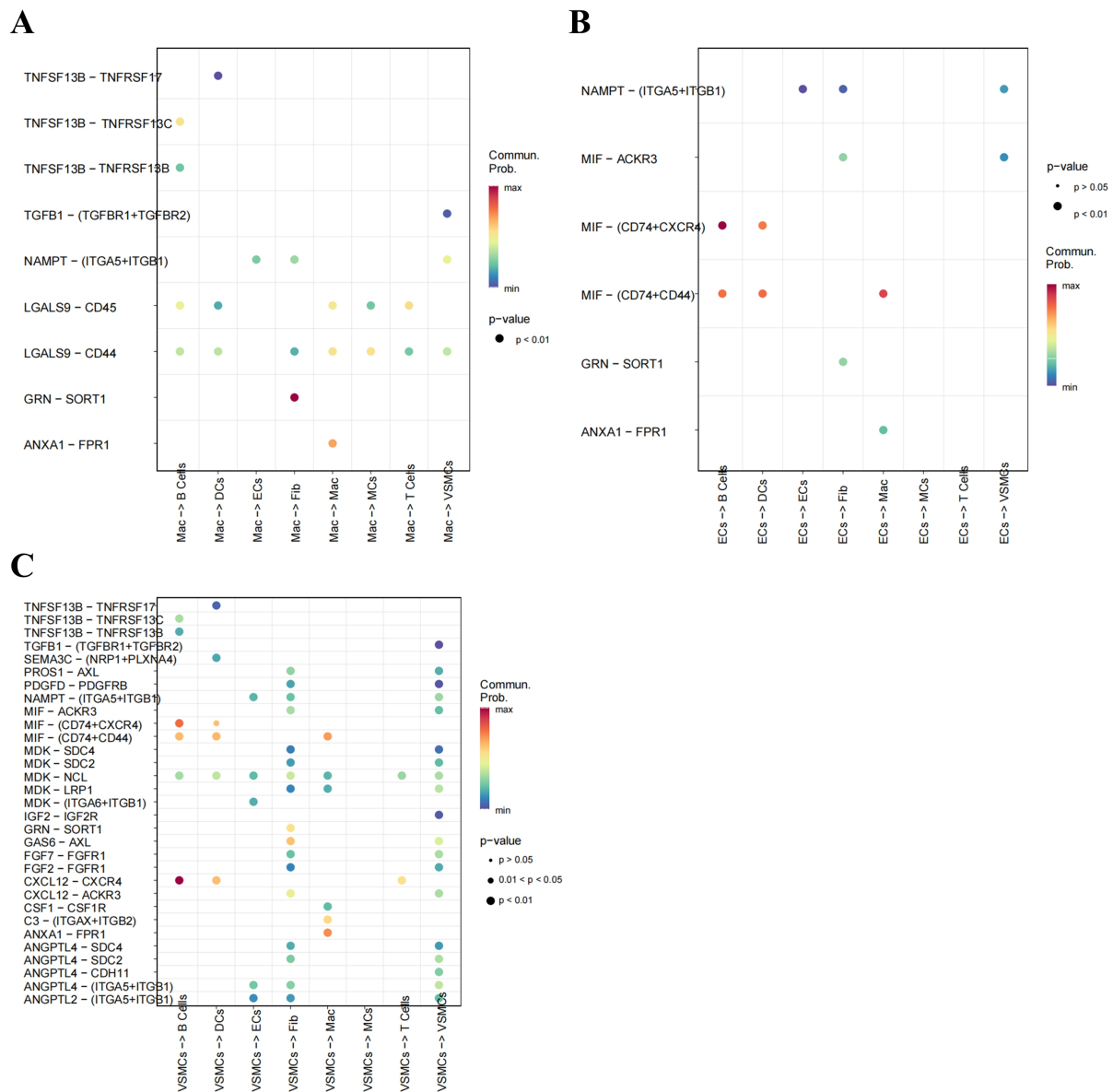
62 indicates the gene ratio (GeneRatio), and color represents the adjusted p value (p.adjust).
63



64

65 **Supplementary Fig. 7. KEGG pathway enrichment analysis across major cell populations in**
 66 **thoracic aortic dissection (TAD).** KEGG pathway enrichment analysis of differentially expressed
 67 genes in major cell populations identified in TAD tissue, including vascular smooth muscle cells
 68 (VSMCs), fibroblasts (Fib), macrophages (Mac), VSMC-M-like cells, T cells, endothelial cells
 69 (ECs), B cells, and neutrophils (Neu). Each dot represents a significantly enriched pathway. Dot

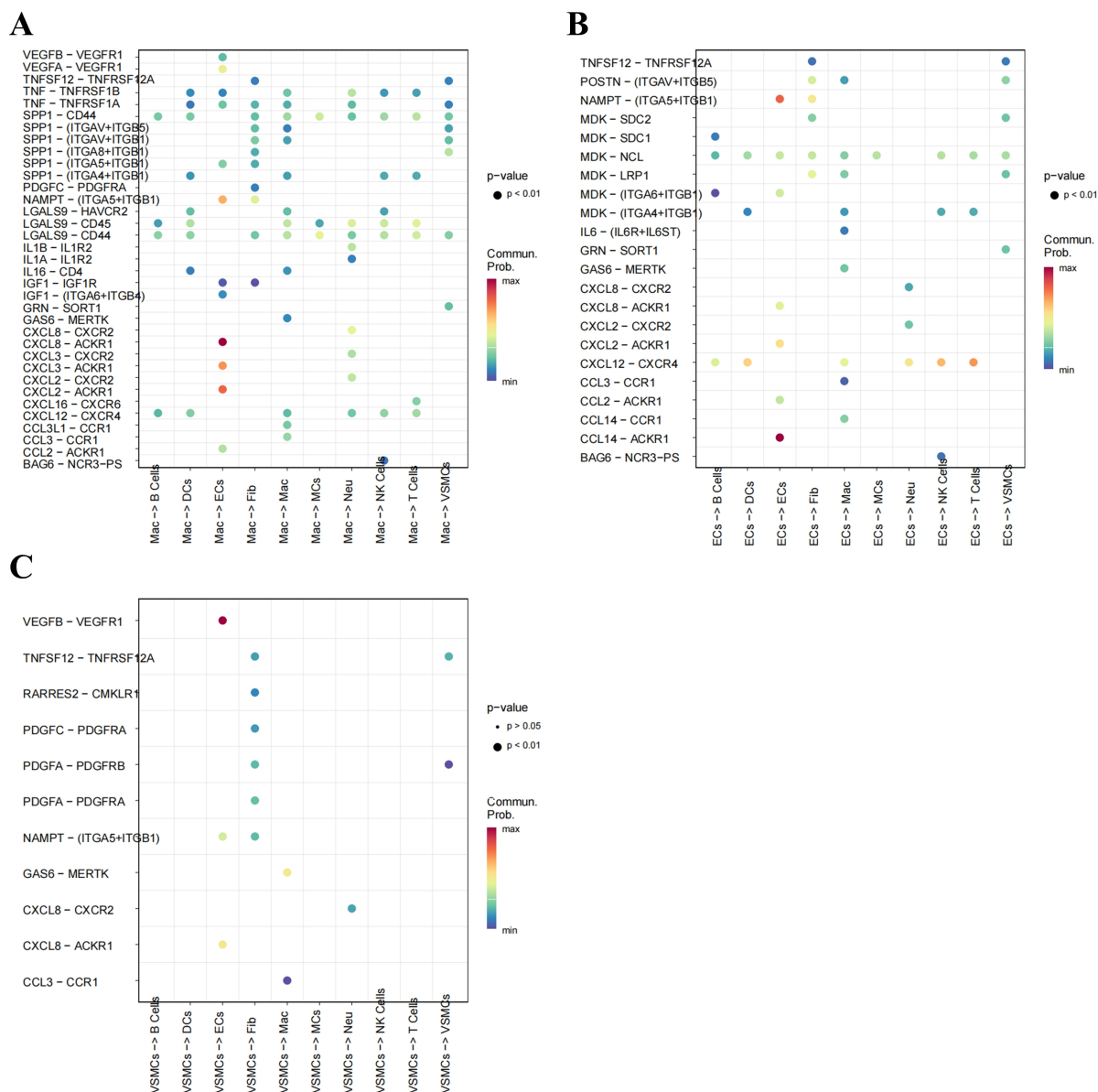
70 size indicates the gene ratio (GeneRatio), and color represents the adjusted p value (p.adjust).
71



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73 **Supplementary Fig. 8. Intercellular communication analysis among major cell populations in**
 74 **human abdominal aortic aneurysm (AAA) tissue. (A)** Predicted ligand–receptor interactions
 75 mediated by macrophages (Mac) with other cell populations in AAA tissue. **(B)** Predicted
 76 ligand–receptor interactions mediated by endothelial cells (ECs) with other cell populations. **(C)**
 77 Predicted ligand–receptor interactions mediated by vascular smooth muscle cells (VSMCs) with
 78 other cell populations. Each dot represents a ligand–receptor pair involved in intercellular
 79 communication between the indicated sender and receiver cell populations. Dot color indicates the
 80 communication probability, and dot size reflects the statistical significance of the interaction.

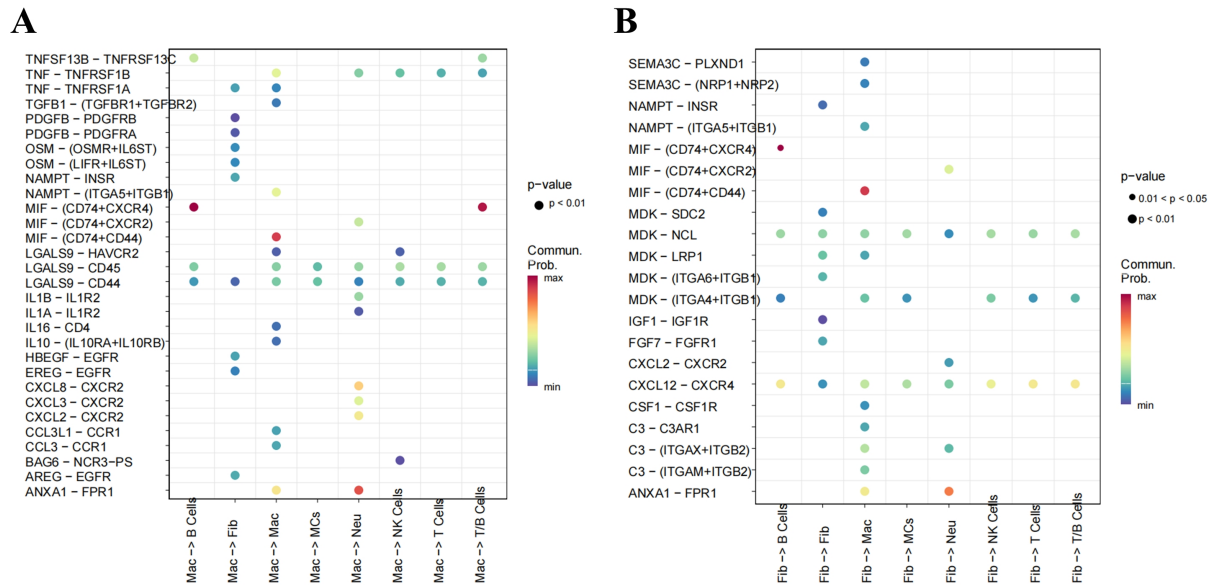
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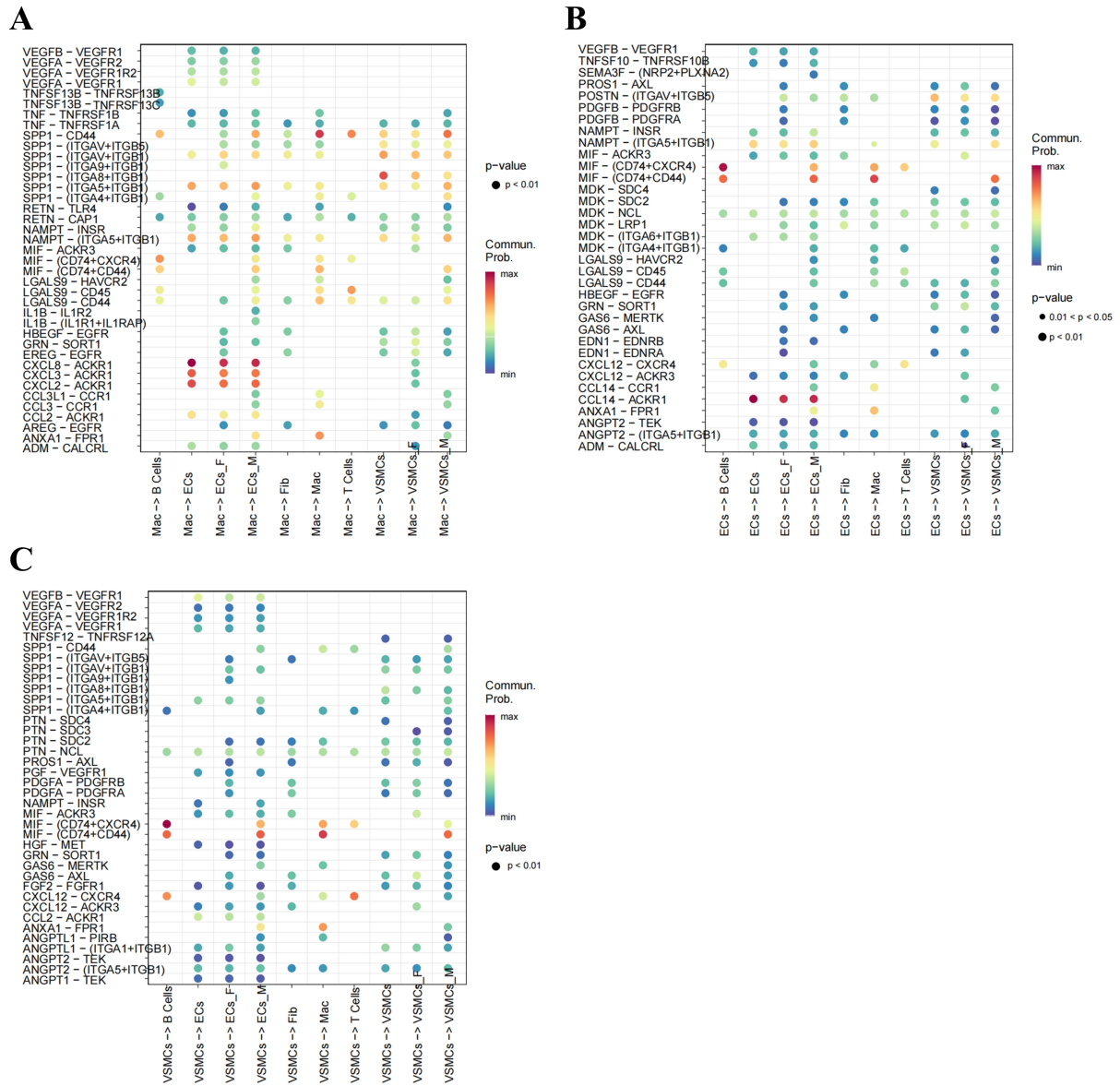
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83 **Supplementary Fig. 9. Intercellular communication networks among major cell populations in**
 84 **human thoracic aortic aneurysm (TAA) tissue. (A)** Predicted ligand–receptor interactions
 85 mediated by macrophages (Mac) with other cell populations in TAA tissue. **(B)** Predicted
 86 ligand–receptor interactions mediated by endothelial cells (ECs) with other cell populations. **(C)**
 87 Predicted ligand–receptor interactions mediated by vascular smooth muscle cells (VSMCs) with
 88 other cell populations. Ligand–receptor interactions were inferred using the CellChat algorithm.
 89 Each dot represents a ligand–receptor pair involved in intercellular communication between the
 90 indicated sender and receiver cell populations. Dot color indicates the communication probability,
 91 and dot size represents the statistical significance of the interaction.

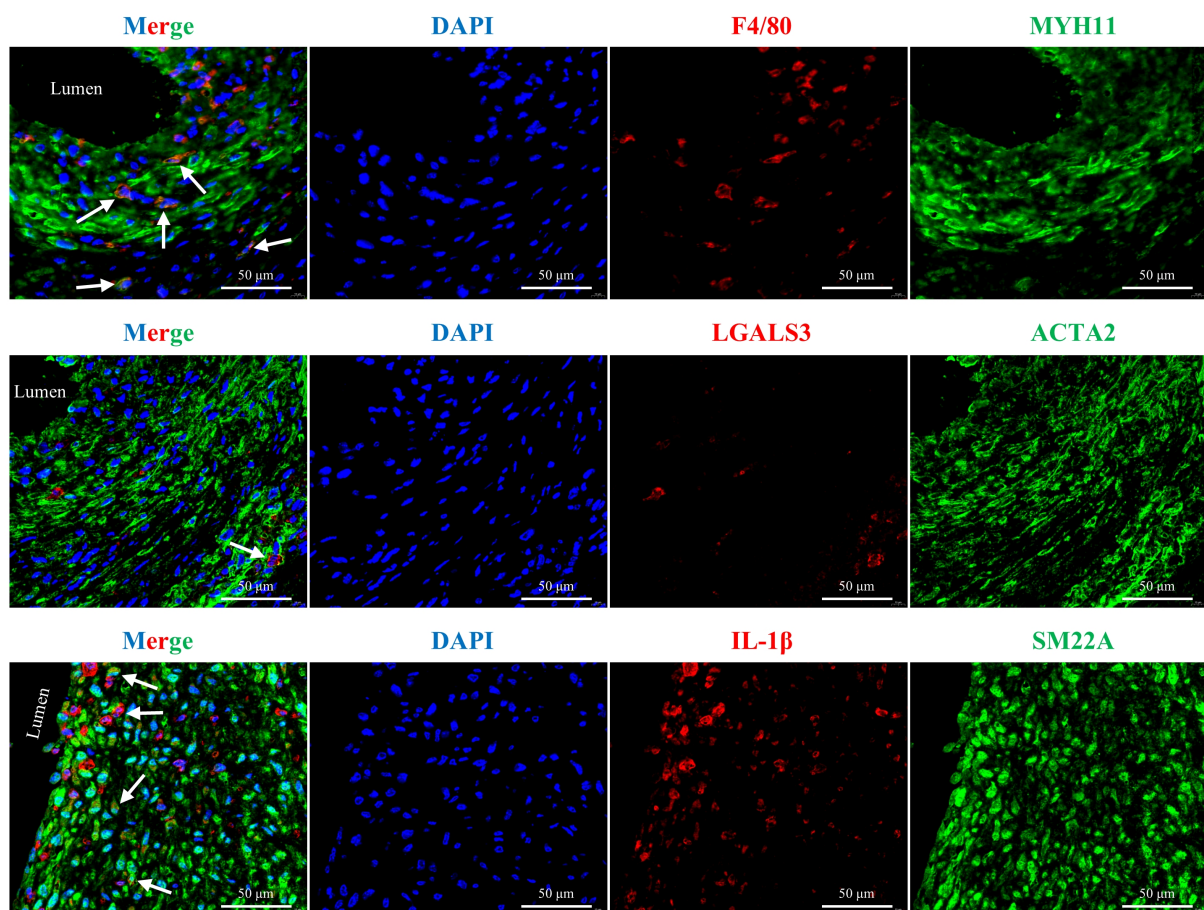
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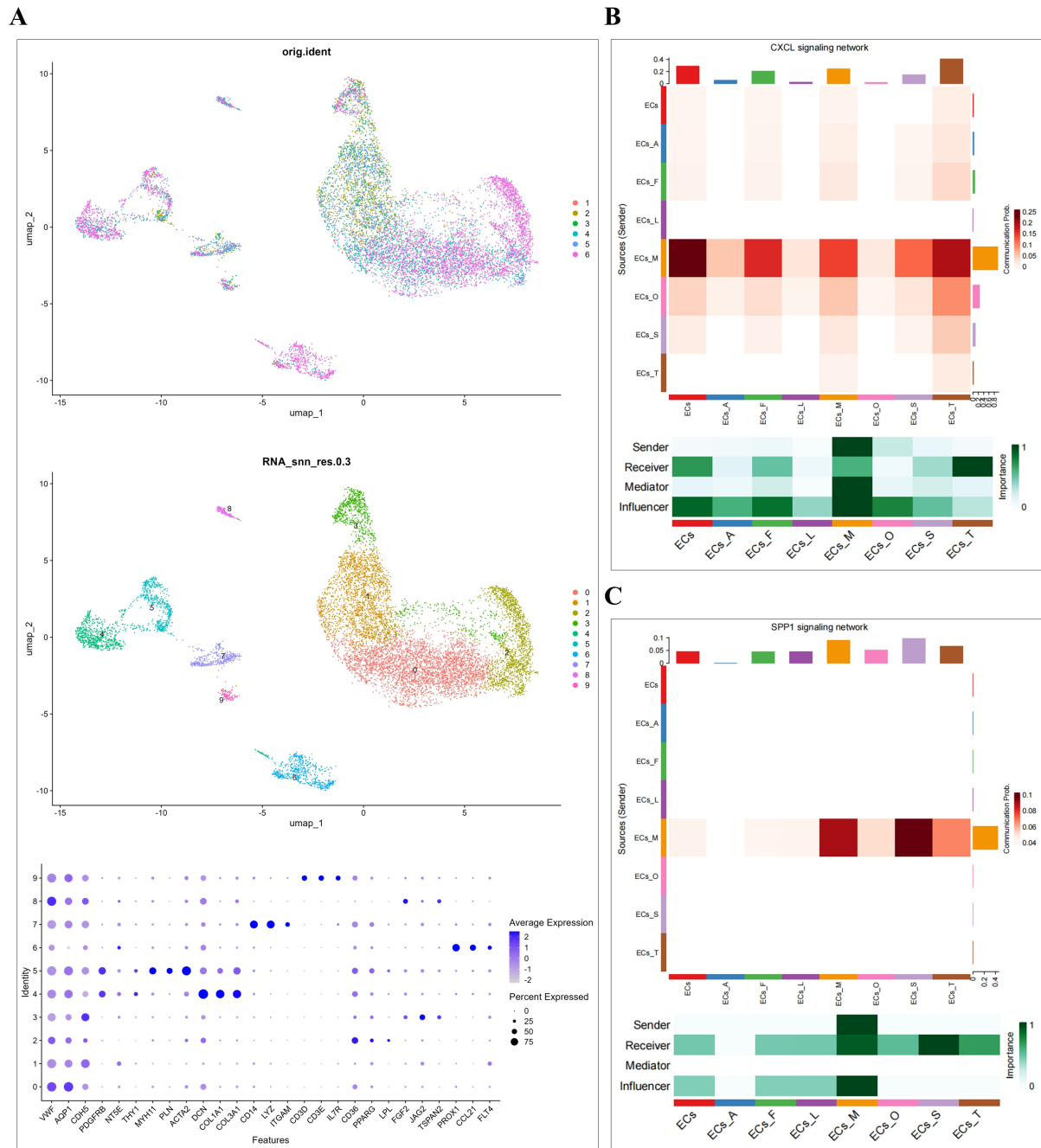
Supplementary Fig. 10. Intercellular communication networks among major cell populations in human ruptured abdominal aortic aneurysm (AAA) tissue. (A) Predicted ligand–receptor interactions mediated by macrophages (Mac) with other cell populations in ruptured AAA tissue. **(B)** Predicted ligand–receptor interactions mediated by fibroblasts (Fib) with other cell populations. Ligand–receptor interactions were inferred using the CellChat algorithm. Each dot represents a ligand–receptor pair involved in intercellular communication between the indicated sender and receiver cell populations. Dot color indicates the communication probability, and dot size represents the statistical significance of the interaction.



Supplementary Fig. 11. Intercellular communication networks among major cell populations in human thoracic aortic dissection (TAD) tissue. (A) Predicted ligand–receptor interactions mediated by macrophages (Mac) with other cell populations in TAD tissue. **(B)** Predicted ligand–receptor interactions mediated by endothelial cells (ECs) with other cell populations. **(C)** Predicted ligand–receptor interactions mediated by vascular smooth muscle cells (VSMCs) with other cell populations. Ligand–receptor interactions were inferred using the CellChat algorithm. Each dot represents a ligand–receptor pair involved in intercellular communication between the indicated sender and receiver cell populations. Dot color indicates the communication probability, and dot size represents the statistical significance of the interaction.



114
 115 **Supplementary Fig. 12. Immunofluorescence staining of macrophage and vascular smooth**
 116 **muscle cell markers in aortic tissues from the mouse abdominal aortic aneurysm (AAA)**
 117 **model.** Representative immunofluorescence images of aortic sections from AAA mice showing the
 118 expression of macrophage and vascular smooth muscle cell markers. The upper panel shows F4/80
 119 (red) and MYH11 (green) staining. The middle panel shows LGALS3 (red) and ACTA2 (green)
 120 staining. The lower panel shows IL-1 β (red) and SM22A (green) staining. Nuclei were
 121 counterstained with DAPI (blue). Arrows indicate cells co-expressing macrophage markers and
 122 smooth muscle cell markers in the aortic wall. Scale bars, 50 μ m.



124

125 **Supplementary Fig. 13. Endothelial cell (EC) subpopulation clustering and intercellular**
 126 **communication analysis in human thoracic aortic dissection (TAD) tissue. (A)** UMAP
 127 visualization of endothelial cell (EC) subpopulations identified in TAD tissue. The upper panel
 128 shows cells colored by sample identity (orig.ident), and the middle panel shows unsupervised
 129 clustering results (resolution = 0.3). The lower panel presents a dot plot of representative marker
 130 genes used for EC subpopulation annotation. **(B)** Predicted CXCL signaling network among EC
 131 subpopulations inferred using the CellChat algorithm. Heatmaps indicate the communication
 132 probability between sender and receiver EC subpopulations, and the relative signaling roles of each
 133 EC subpopulation are summarized below. **(C)** Predicted SPP1 signaling network among EC

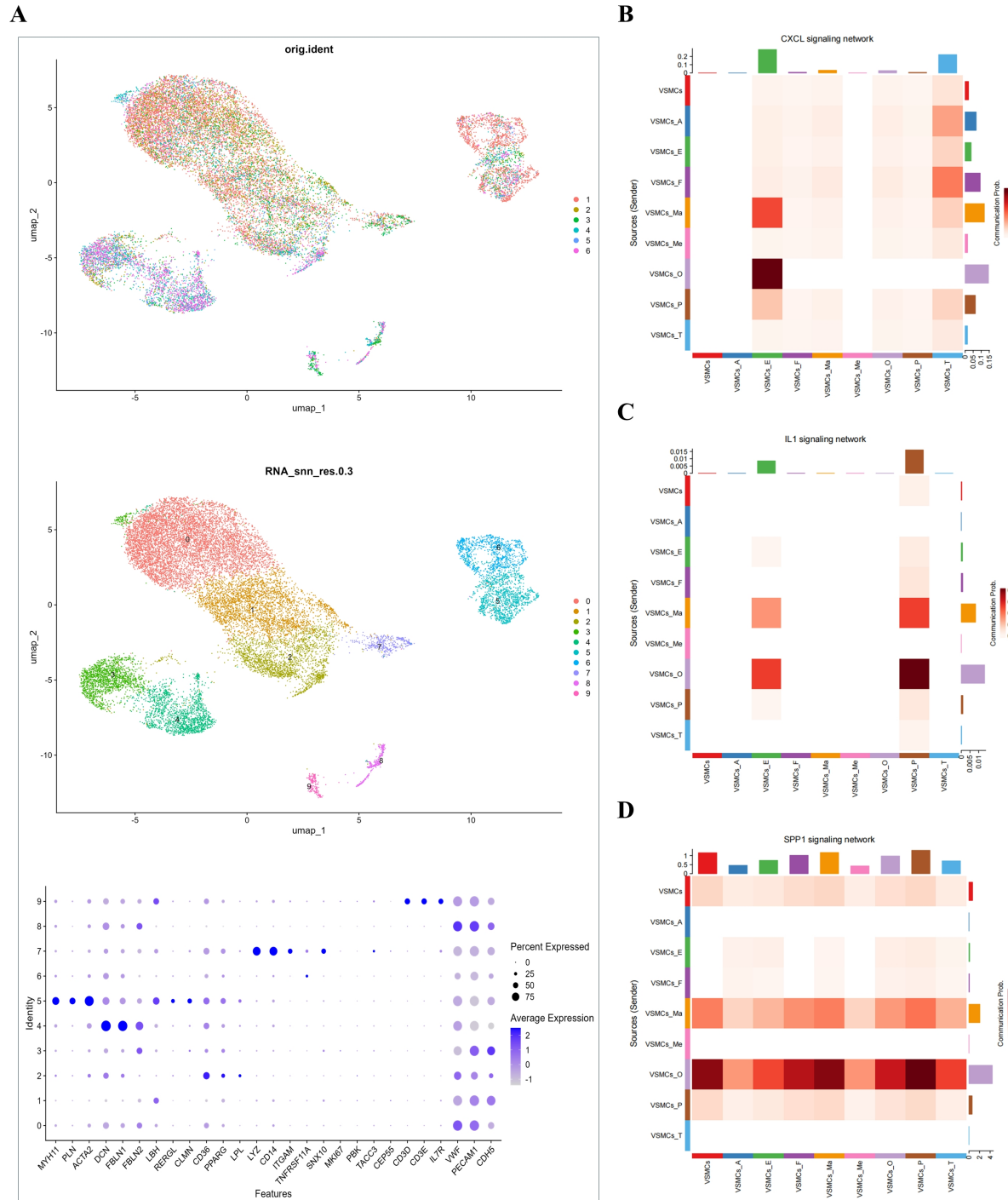
134 subpopulations inferred by CellChat. Heatmaps show the communication strength between EC
135 subpopulations, and the signaling roles of each EC subtype are summarized below.
136



137

138 **Supplementary Fig. 14. Reactome pathway enrichment analysis of endothelial cell (EC)**
 139 **subpopulations in human thoracic aortic dissection (TAD) tissue.** Reactome pathway
 140 enrichment analysis was performed using differentially expressed genes from EC subpopulations
 141 identified in TAD tissue. Each dot represents a significantly enriched pathway in the corresponding
 142 EC subpopulation. Dot size indicates the gene ratio (GeneRatio), and color represents the adjusted p

143 value (p.adjust). The boxed area highlights pathways enriched in the EC_M subpopulation,
144 including neutrophil degranulation, interleukin-10 signaling, and FCGR activation.
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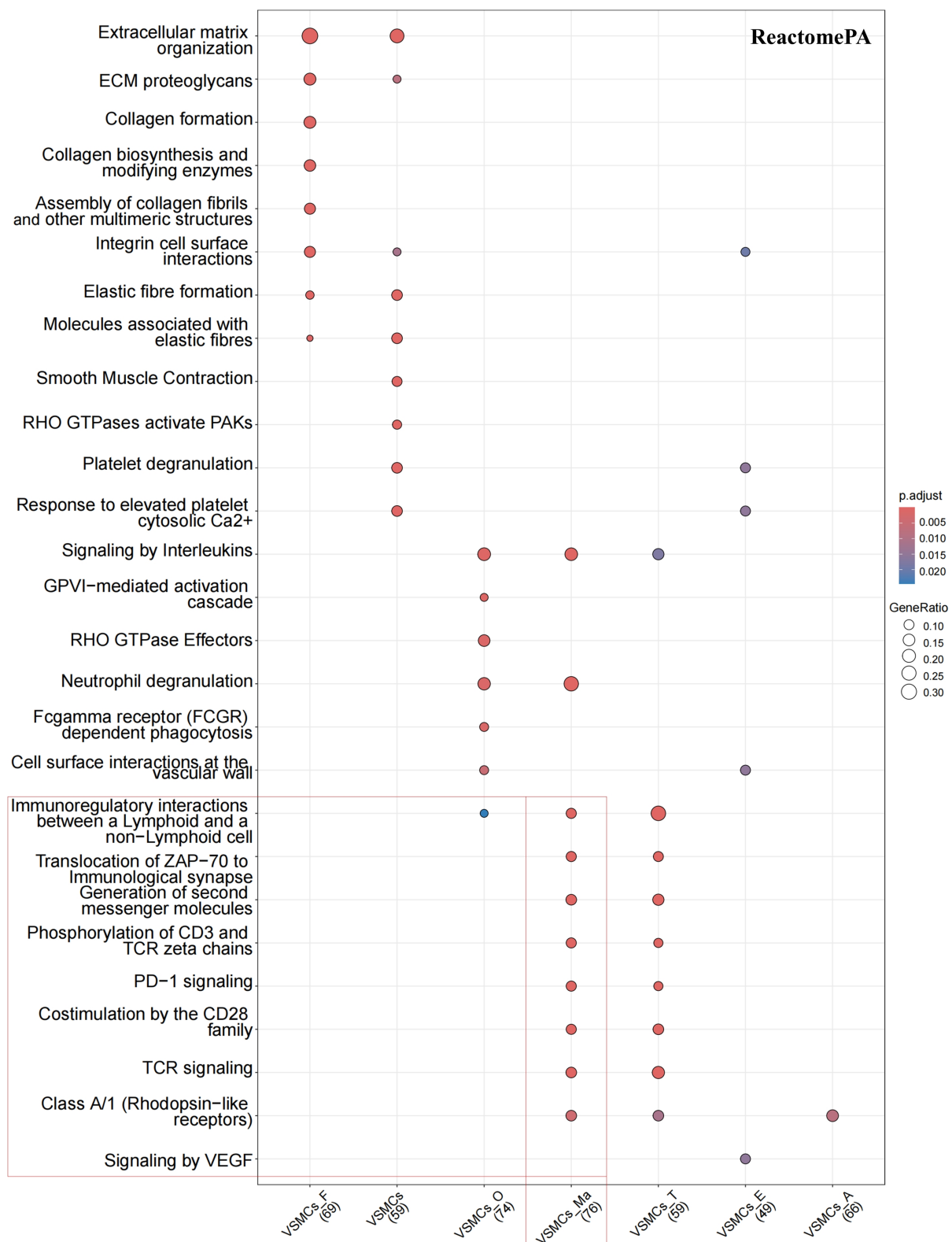
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Supplementary Fig. 15. Vascular smooth muscle cell (VSMC) subpopulation clustering and intercellular communication analysis in human thoracic aortic dissection (TAD) tissue. (A) UMAP visualization of VSMC subpopulations identified in TAD tissue. The upper panel shows cells colored by sample identity (orig.ident), and the middle panel shows unsupervised clustering results (resolution = 0.3). The lower panel presents a dot plot of representative marker genes used for VSMC subpopulation annotation. **(B)** Predicted CXCL signaling network among VSMC subpopulations inferred using the CellChat algorithm. **(C)** Predicted IL-1 signaling network among

154 VSMC subpopulations inferred using CellChat. **(D)** Predicted SPP1 signaling network among
155 VSMC subpopulations inferred using CellChat. Heatmaps indicate the communication probability
156 between sender and receiver VSMC subpopulations, and the relative signaling roles of each
157 subpopulation are summarized above the heatmaps.

158



159

160 **Supplementary Fig. 16. Reactome pathway enrichment analysis of vascular smooth muscle**
 161 **cell (VSMC) subpopulations in human thoracic aortic dissection (TAD) tissue.** Reactome
 162 pathway enrichment analysis was performed using differentially expressed genes from VSMC
 163 subpopulations identified in TAD tissue. Each dot represents a significantly enriched pathway in the
 164 corresponding VSMC subpopulation. Dot size indicates the gene ratio (GeneRatio), and color

165 represents the adjusted p value (p.adjust). The boxed region highlights immune-related pathways
166 enriched in the VSMC_Ma subpopulation, including T cell receptor (TCR) signaling, PD-1
167 signaling, and CD28 costimulation.