## Supplementary figures and legends



Figure S1. Endothelial cell sorting, quality control, and data integration.

(A) Gating logic to sort live CD31<sup>+</sup> CD45<sup>-</sup> cells via flow cytometry. (B) PCA plot showing highquality cells (blue) and low-quality cells (orange). Each circle represents a cell. Circle size indicate total features in the cell. (C-F) Violin plots showing the numbers of counts and features, percentages of mitochondrial and ribosomal genes after quality control. (G) PCA and UMAP plot of cells before and after batch effect removing, respectively. Cells are colored by batch. (H) Cell composition of each dermal EC cluster in four batches.

Cluster A: arteriole ECs; Cluster C1, C2: capillary ECs; Cluster P: post-capillary ECs; Cluster V: venule ECs; Cluster L1, L2: lymphatic endothelial cells.

PCA: principal component analysis; UMAP: uniform manifold approximation and projection.



## Figure S2. Distinguishing and filtering out non-endothelial cells.

(A) Expressions of markers of smooth muscle cells (*ACTA2*, *RGS5*), fibroblasts (*COL1A1*), pericytes (*PDGFRA*, *PDGFRB*), red blood cells (*HBA1*, *HBA2*, *HBB*), immune cells (*PTPRC*), and endothelial cells (*PECAM1*, *CDH5*) in single cell data. (B) UMAP plot showing endothelial cells and non-endothelial cells.

UMAP: uniform manifold approximation and projection.



Figure S3. Validation of potential arteriovenous markers in femoral artery and vein.

(A-D) Immunofluorescence of IGFBP3, RBP7, SELE, MT2A, and CD31 in murine femoral artery and vein. A stands for artery, and V stands for vein. Original magnification  $200\times$ ; scale bar:  $20 \mu m$ ; n = 3. White arrowheads point out positive co-staining of marker genes and CD31.



Figure S4. Pathways and transcriptional factors enriched in ECs from 10 different

tissues/organs.

(A) Heatmap of the enriched GO pathways in ECs from 10 different tissues/organs. the color represents the  $-\log p$  value. (B) Heatmap of the single-cell regulatory network inference and clustering in ECs from different tissues/organs. Numbers in brackets indicate the regulons for transcription factors.

ECs: vascular endothelial cells; GI: gastrointestinal; GO: gene ontology; SAT: subcutaneous adipose tissue.



Figure S5. Expressions of NR2F2 in dermal endothelial cells at mRNA and protein levels.

(A) mRNA levels of *NR2F2* in dermal endothelial cell clusters in single-cell RNA sequencing data. (B) Protein levels of NR2F2 in dermal vasculature via tissue immunofluorescence. Images of CD31<sup>+</sup> ECs in the superficial, intermediate, and deep plexus are zoomed in. The image is representative of 3 biological replicates. The white dotted line marks the interface between epidermis and dermis. Scale bars represent 20  $\mu$ m.

Cluster A: arteriole ECs; Cluster C1, C2: capillary ECs; Cluster P: post-capillary ECs; Cluster V: venule ECs.

A.U.: arbitrary unit.



Figure S6. Composition of dermal ECs derived from different anatomical locations.

(A) The cell proportions of dermal ECs from different anatomical locations in each dermal EC cluster. (B) UMAP plot of dermal endothelial cells colored by anatomical location. (C) Pathway analysis of DEGs of dermal ECs derived from limbs, trunk, and foreskin. y axis represents the rich factor. The circle size represents the -log p value, and the color represents the anatomical location.

Cluster A: arteriole ECs; Cluster C1, C2: capillary ECs; Cluster P: post-capillary ECs; Cluster V: venule ECs.

DEGs: differentially expressed genes; ECs: vascular endothelial cells; UMAP: uniform manifold approximation and projection.

## Supplementary tables

Genes:				
GO_ANTIGEN	PROCESSING_AND_PRESENTATION_OF_PEPTIDE_OR_POLYSACCHA			
RIDE_ANTIGEN_VIA_MHC_CLASS_II				
AC027237.1				
ACTR10				
ACTRIA				
ACTR1B				
AP1B1				
AP1G1				
AP1M1				
AP1M2				
AP1S1				
AP1S2				
AP1S3				
AP2A1				
AP2A2				
AP2B1				
AP2M1				
AP2S1				
ARF1				
CANX				
CAPZA1				
CAPZA2				
CAPZA3				
CAPZB				
<i>CD74</i>				
CENPE				
CLTA				
CLTC				
CTSD				
CTSE				
CTSF				
CTSL				
CTSS				
CTSV				
DCTN1				
DCTN2				
DCTN3				
DCTN4				
DCTN5				
DCTN6				

DNM2
DYNC1H1
DYNC111
DYNC112
DYNC1L11
DYNC1LI2
DYNLL1
DYNLL2
FCER1G
FCGR2B
HLA-DMA
HLA-DMB
HLA-DOA
HLA-DOB
HLA-DPA1
HLA <b>-</b> DPB1
HLA <b>-</b> DQA1
HLA-DQA2
HLA-DQB1
HLA-DQB2
HLA <b>-</b> DRA
HLA-DRB1
HLA-DRB3
HLA-DRB4
HLA-DRB5
IFI30
<i>KIF11</i>
KIF15
KIF18A
KIF22
KIF26A
KIF2A
KIF2B
KIF2C
KIF3A
KIF3B
KIF3C
KIF4A
KIF4B
KIF JA VIEAD2
NIFAF3
KLC1
NLC2
LGMN

MARCH1
OSBPL1A
PYCARD
RAB7A
RACGAP1
RILP
SAR1B
SEC13
SEC23A
SEC24A
SEC24B
SEC24C
SEC24D
SEC31A
SH3GL2
SPTBN2
THBS1
TRAF6
TREM2

## Table S2. Genes for measuring adhesion score.

Genes:

GO\_LEUKOCYTE\_ADHESION\_TO\_VASCULAR\_ENDOTHELIAL\_CELL

—	—	 —	_
ADD2			
CCL21			
<i>CCL25</i>			
<i>CCL28</i>			
CCR2			
CX3CR1			
CXCL12			
ELANE			
ETS1			
GCNT1			
GOLPH3			
ICAM1			
IRAK1			
ITGA4			
ITGB1			
ITGB7			
KLF4			
LEP			
MADCAMI			
<i>MIR141</i>			
MIR146A			
MIR155			
MIR21			
<i>MIR221</i>			
MIR222			
MIR31			
MIR92A1			
MIR92A2			
MIRLET7G			
NFAT5			
PODXL2			
PTAFR			
RELA			
RHOA			
ROCKI			
SELE			
SELL			
SELP			
SELPLG			
SPN			
INF			

TRAF6			
VCAMI			

Donor	Age	Gender	Tissue site	Surgery	Batch
II.a.14har Janan 1	10		limba (fanaama)		h a t a h 1
Healthy donor I	18	male	limbs (forearm)	nevus removal	batch I
XX 1.1 1 0	<u> </u>	0 1	1. 1 /		1.1.1
Healthy donor 2	25	female	limbs (upper arm)	nevus removal	batch I
	• •				
Healthy donor 3	20	female	limbs (upper arm)	nevus removal	batch 1
Healthy donor 4	32	male	limbs (forearm)	nevus removal	batch 1
Healthy donor 5	38	male	limbs (upper arm)	skin flap transplantation	batch 1
Healthy donor 6	25	female	trunk (back)	nevus removal	batch 2
•					
Healthy donor 7	45	female	trunk (breast)	reduction mammoplasty	batch 2
2				1 2	
Healthy donor 8	23	male	foreskin	circumcision	batch 3, 4
·					
Healthy donor 9	27	male	foreskin	circumcision	batch 3 4
ficating denot y	21	mure			Saton 5, 1
Healthy donor 10	28	male	foreskin	circumcision	batch 3 4
ficantity donor 10	20	maic		encumersion	баюн Э, т

Table S3. Clinical information of skin donors for scRNAseq.

Donor	Age	Gender	Tissue site	Surgery
Healthy donor 1	33	male	limbs (forearm)	nevus removal
Healthy donor 2	24	female	limbs (thigh)	plastic surgery
Healthy donor 3	30	female	trunk (breast)	reduction mammoplasty
Healthy donor 4	31	male	trunk (abdominal)	skin flap transplantation
Healthy donor 5	43	female	trunk (breast)	reduction mammoplasty
Healthy donor 6	37	female	limbs (upper arm)	skin flap transplantation
Healthy donor 7	25	femal	trunk (back)	nevus removal
Healthy donor 8	29	male	limbs (upper arm)	skin flap transplantation
Healthy donor 9	20	male	foreskin	circumcision
Healthy donor 10	22	male	foreskin	circumcision
Healthy donor 11	27	male	foreskin	circumcision

 Table S4. Clinical information of skin donors for immunofluorescence.