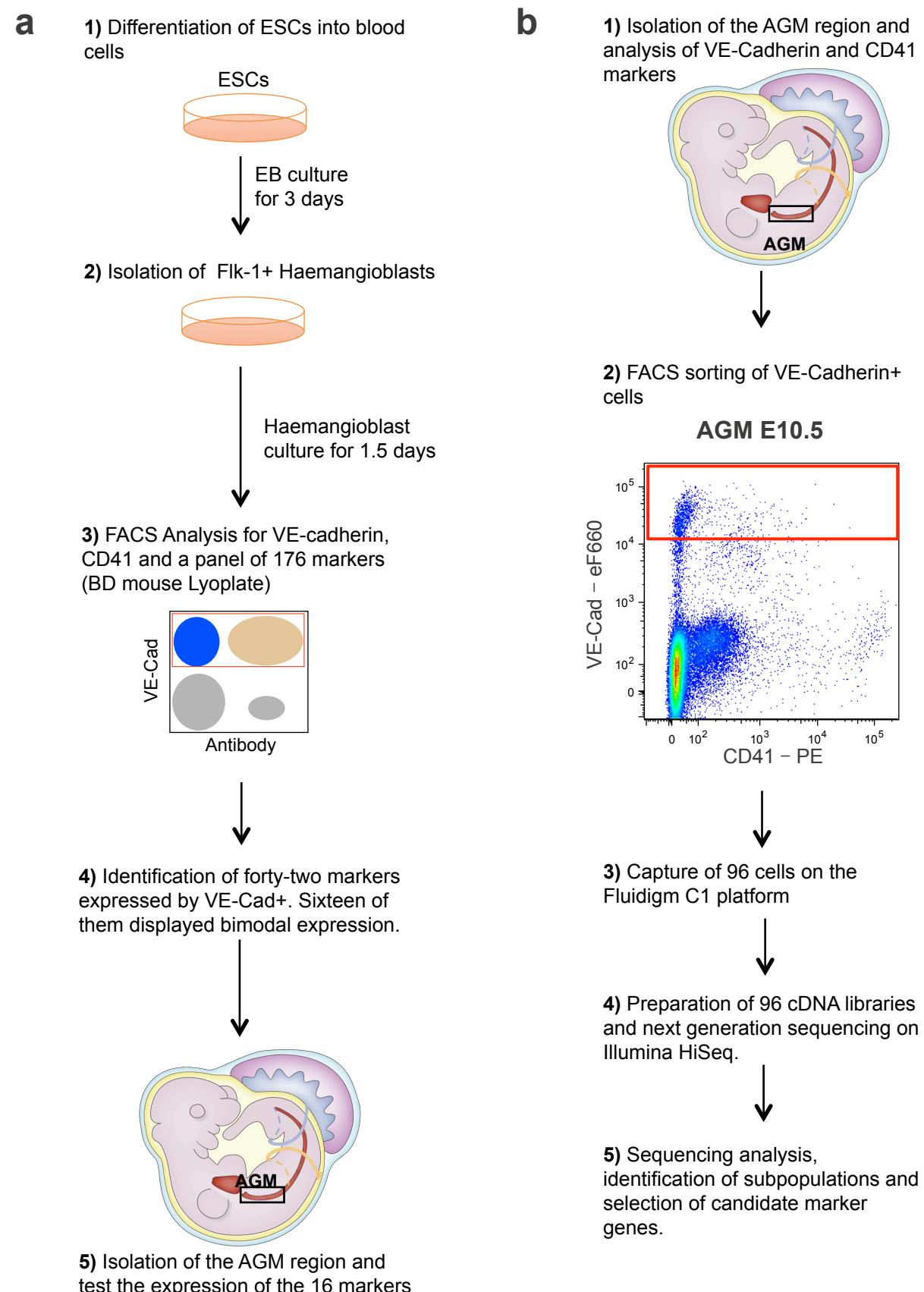


**Supplementary Information for:**

**Single-cell transcriptomics identifies CD44 as a new marker and regulator  
of endothelial to haematopoietic transition**

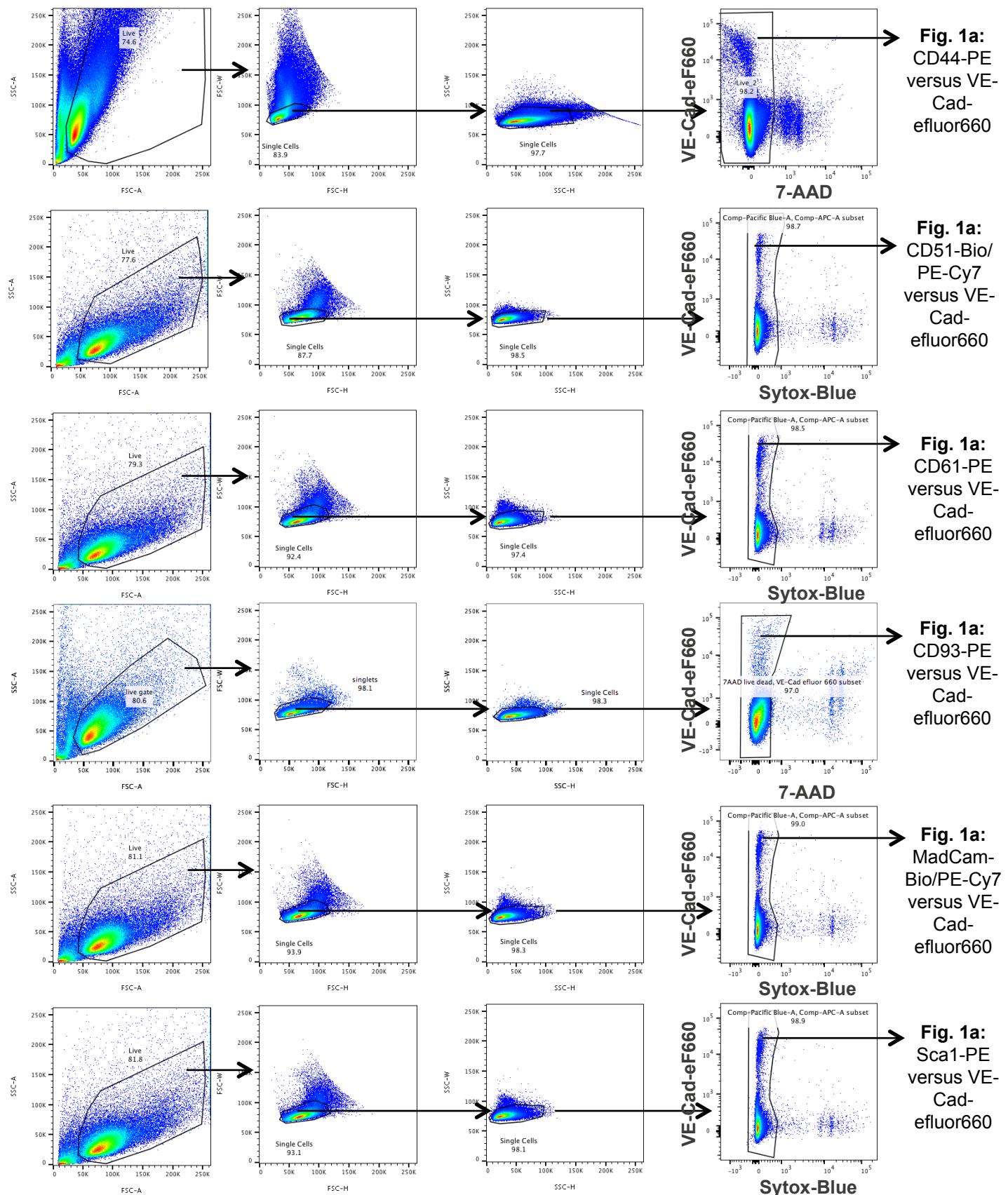
Oatley *et al.*

# Supplementary Figure 1



**Supplementary Figure 1: Experimental layout for the experiments for antibody screen and single-cell RNA sequencing.** (a) Strategy used for the antibody screen. (b) Description of the different steps following for the single cell RNA sequencing analysis in the AGM. See also Figure 1 and Supplementary Table 1.

## Supplementary Figure 2

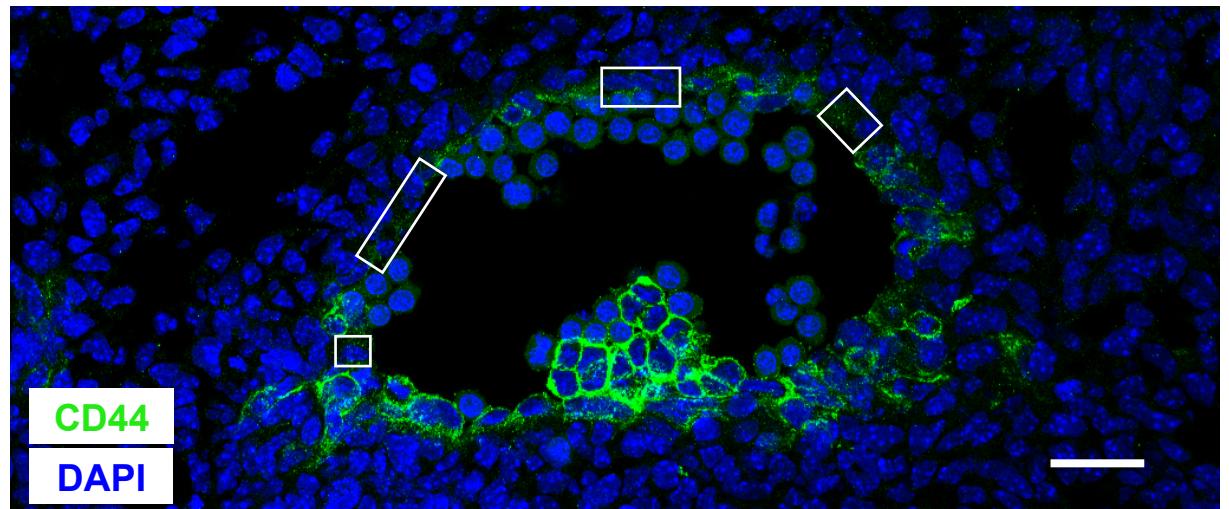


**Supplementary Figure 2: Gating strategies using for FACS analysis shown in Figure 1a.**

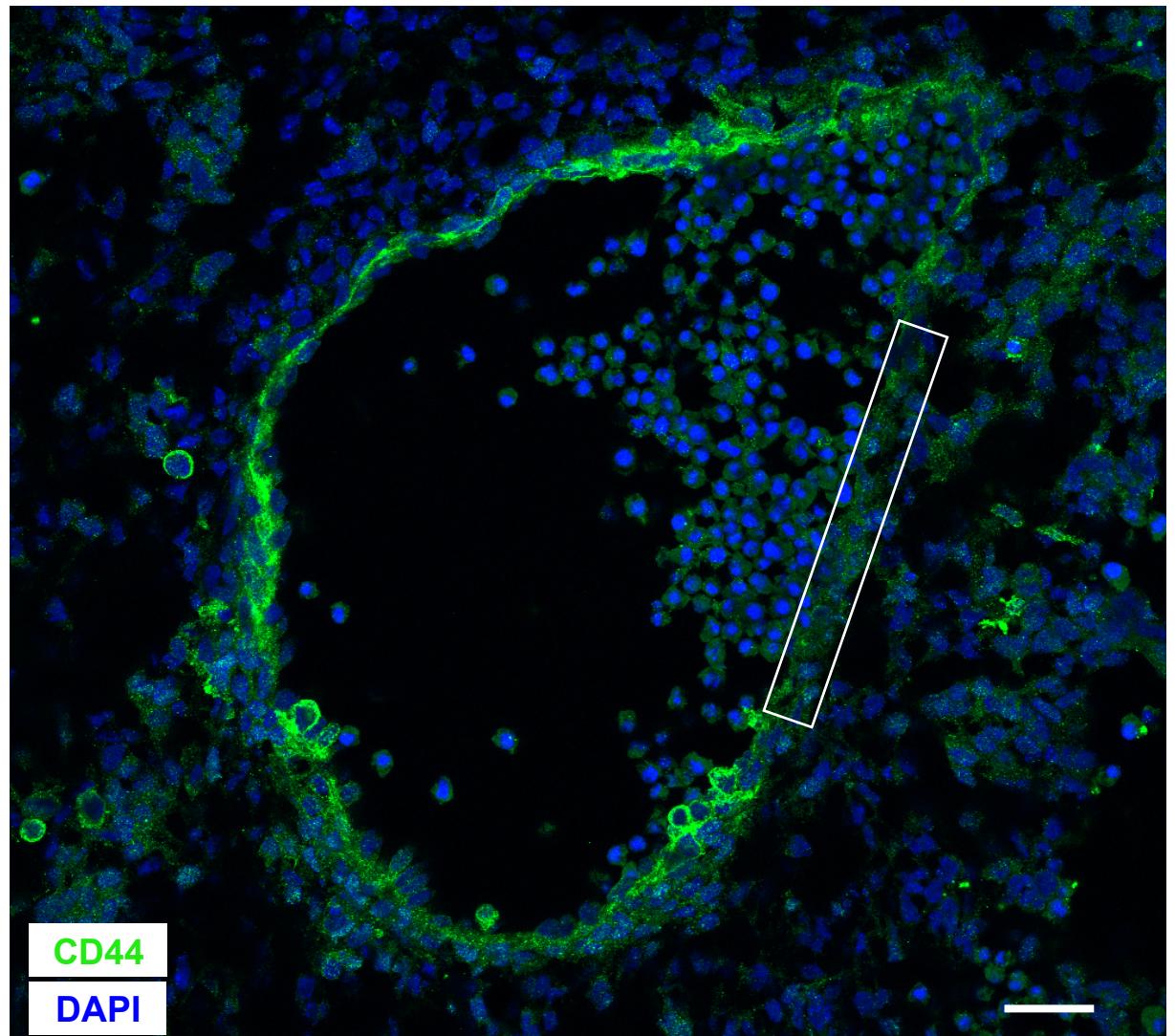
From left to right: FSC-A versus SSC-A, FSC-H versus FSC-W, SSC-H versus SSC-W and VE-Cad-eFluor660 versus dead cell dye 7-AAD or Sytox Blue. The arrows indicate the cells selected from one plot to the next.

### Supplementary Figure 3

a

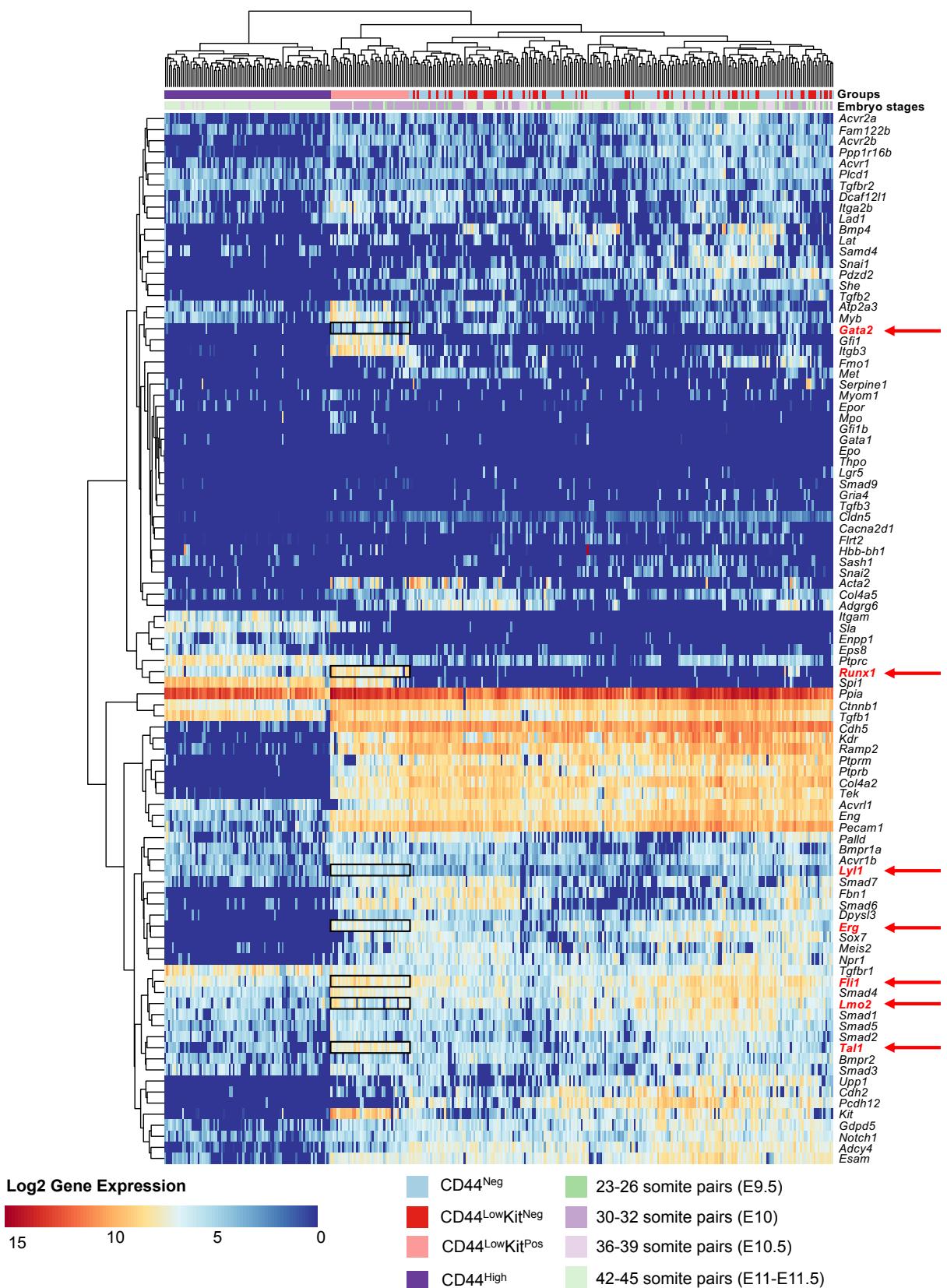


b



**Supplementary Figure 3: Immunofluorescence analysis of CD44 in the AGM region at E10 and E11.**  
**(a)** CD44 expression in the dorsal aorta at E10. Boxes indicate CD44 Negative areas. **(b)** CD44 expression in the dorsal aorta at E11. Boxes indicate CD44 Negative areas. Scale bars correspond to 30  $\mu$ m. See also Figure 2a.

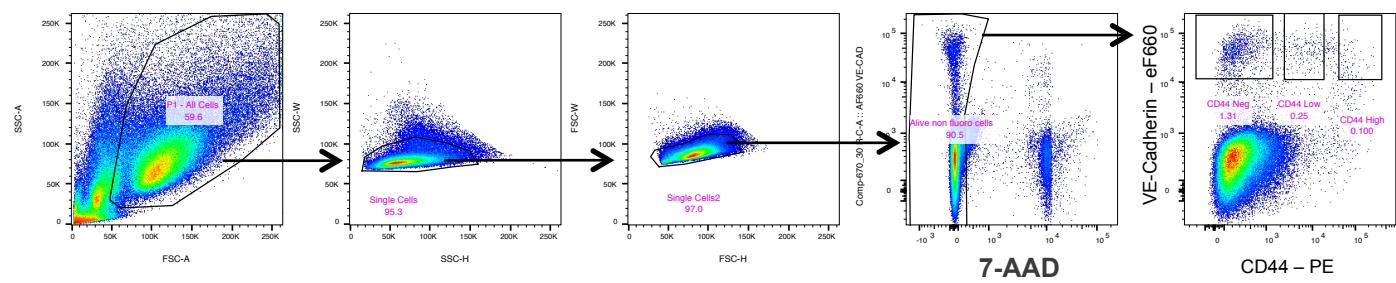
## Supplementary Figure 4



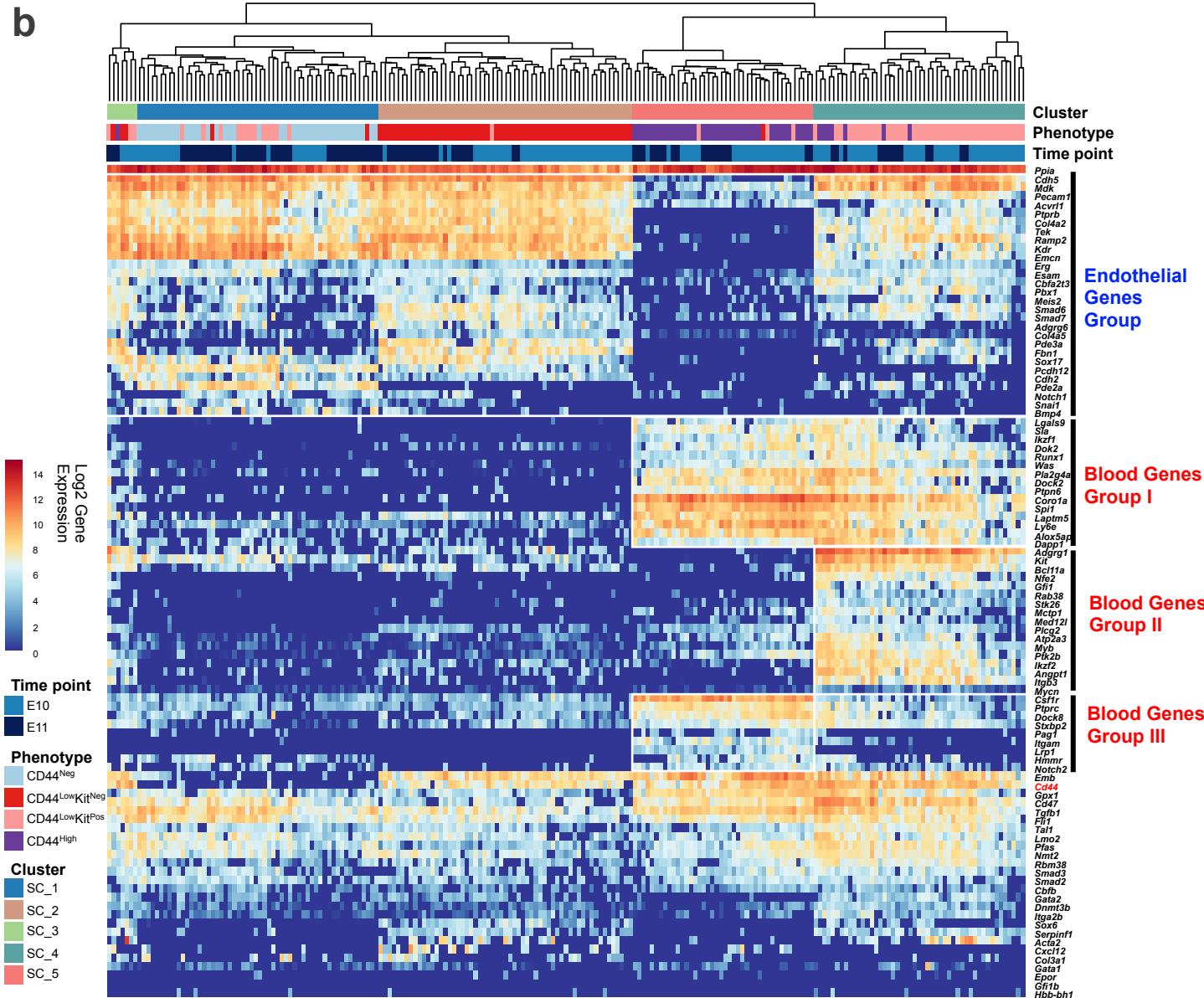
**Supplementary Figure 4: Single-cell q-RT-PCR analysis of the four populations defined by CD44, VE-Cad and Kit.** Single cells from indicated populations were isolated and tested for the expression of 95 genes by single-cell q-RT-PCR. The heatmap shows the result of the hierarchical clustering analysis (cells were clustered by Euclidian distance and the genes by Pearson correlation). Genes coding for *Gata2*, *Runx1*, *Lyl1*, *Lmo2*, *Tal1*, *Fli1* and *Erg* transcription factors are specifically co-expressed in the CD44<sup>LowKitPos</sup> population but not in the other two (see genes indicated by red arrows). See also Figure 3 and Supplementary Data 2.

# Supplementary Figure 5

**a**



**b**

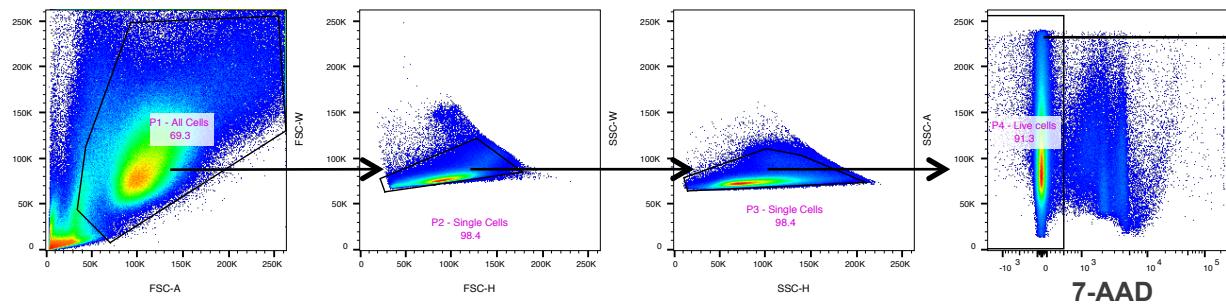


**Supplementary Figure 5: Expression of VE-Cad, CD44 and Kit defines transcriptionally distinct cell populations.**

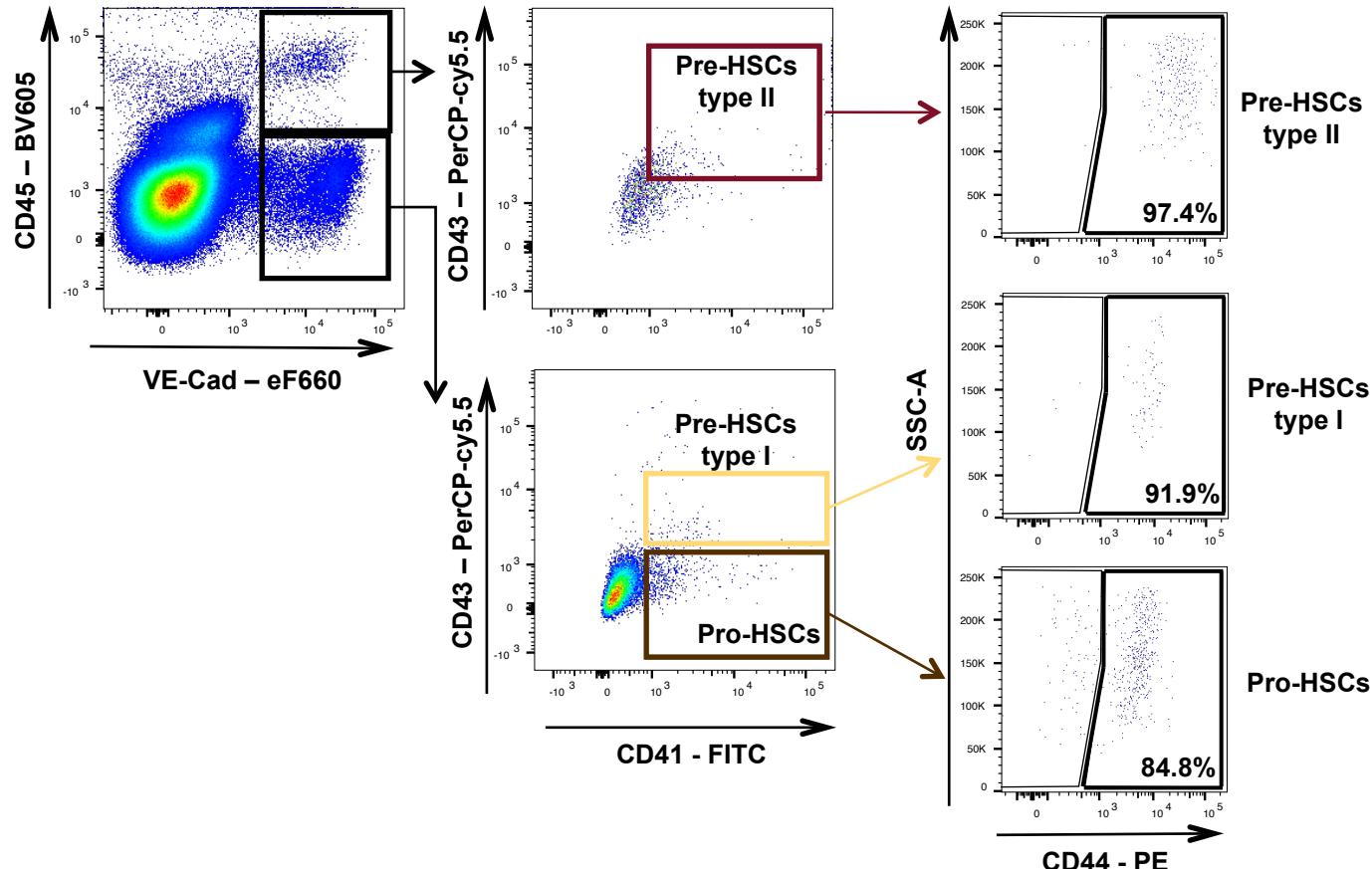
(a) FACS gating strategy for the CD44 populations shown in Fig. 2. (b) Single cells from each VE-Cad+ population were isolated and tested for the expression of 96 genes by single-cell q-RT-PCR. The heatmap shows the result of the hierarchical clustering analysis (cells were clustered by Euclidean distance). A selection of genes has been highlighted: endothelial genes group, blood genes groups I, II and III. See also Figure 3 and Supplementary Data 3.

## Supplementary Figure 6

**a**



**b**

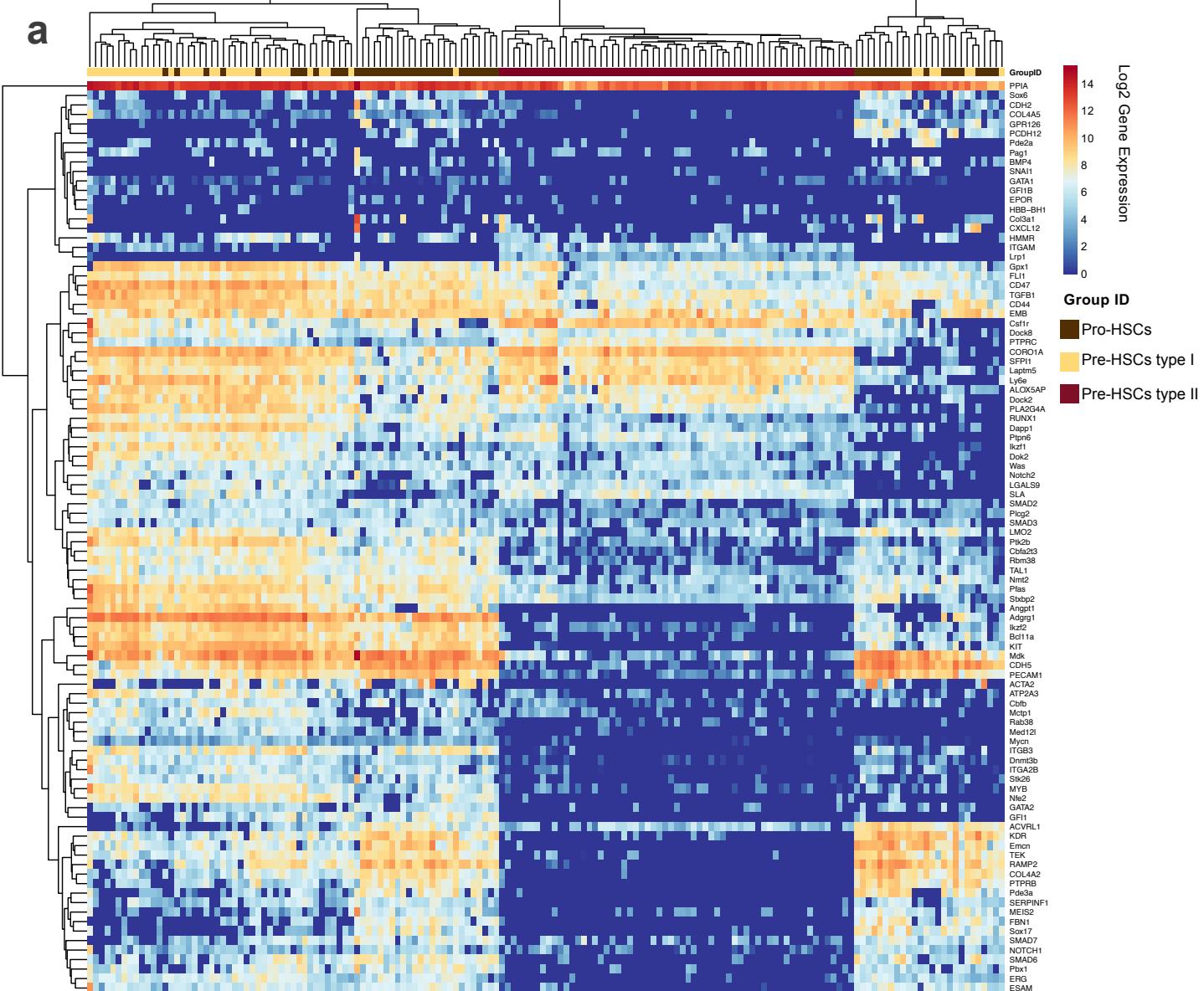


**Supplementary Figure 6: Pro-HSC, Pre-HSC-I and Pre-HSC-II are expressing CD44 protein.**

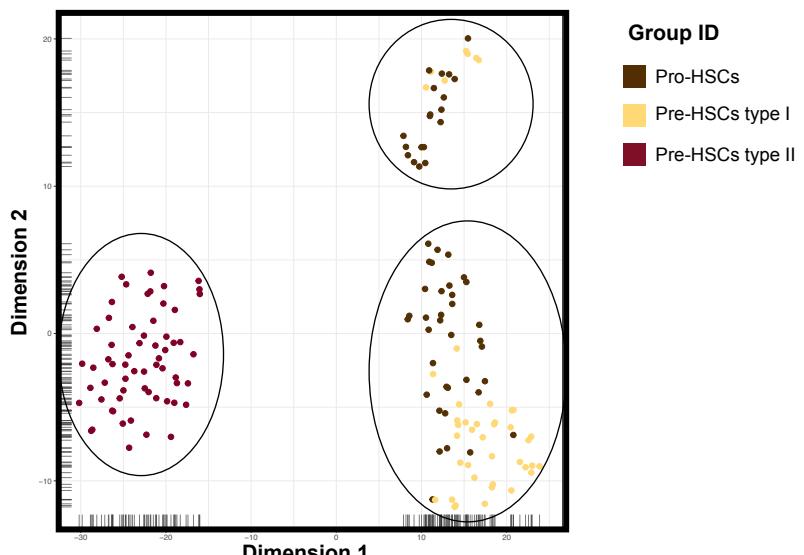
(a) FACS gating strategy for pro-HSC, pre-HSC type I and pre-HSC type II. (b) Pro-HSCs (VE-Cad<sup>+</sup> CD41<sup>+</sup> CD45<sup>-</sup> CD43<sup>+</sup>), Pre-HSC-I (VE-Cad<sup>+</sup> CD41<sup>+</sup> CD45<sup>-</sup> CD43<sup>+</sup>), Pre-HSC-II (VE-Cad<sup>+</sup> CD45<sup>+</sup>) populations were analysed by FACS analysis to assess the expression of CD44 protein. See also Figure 4b.

## Supplementary Figure 7

a



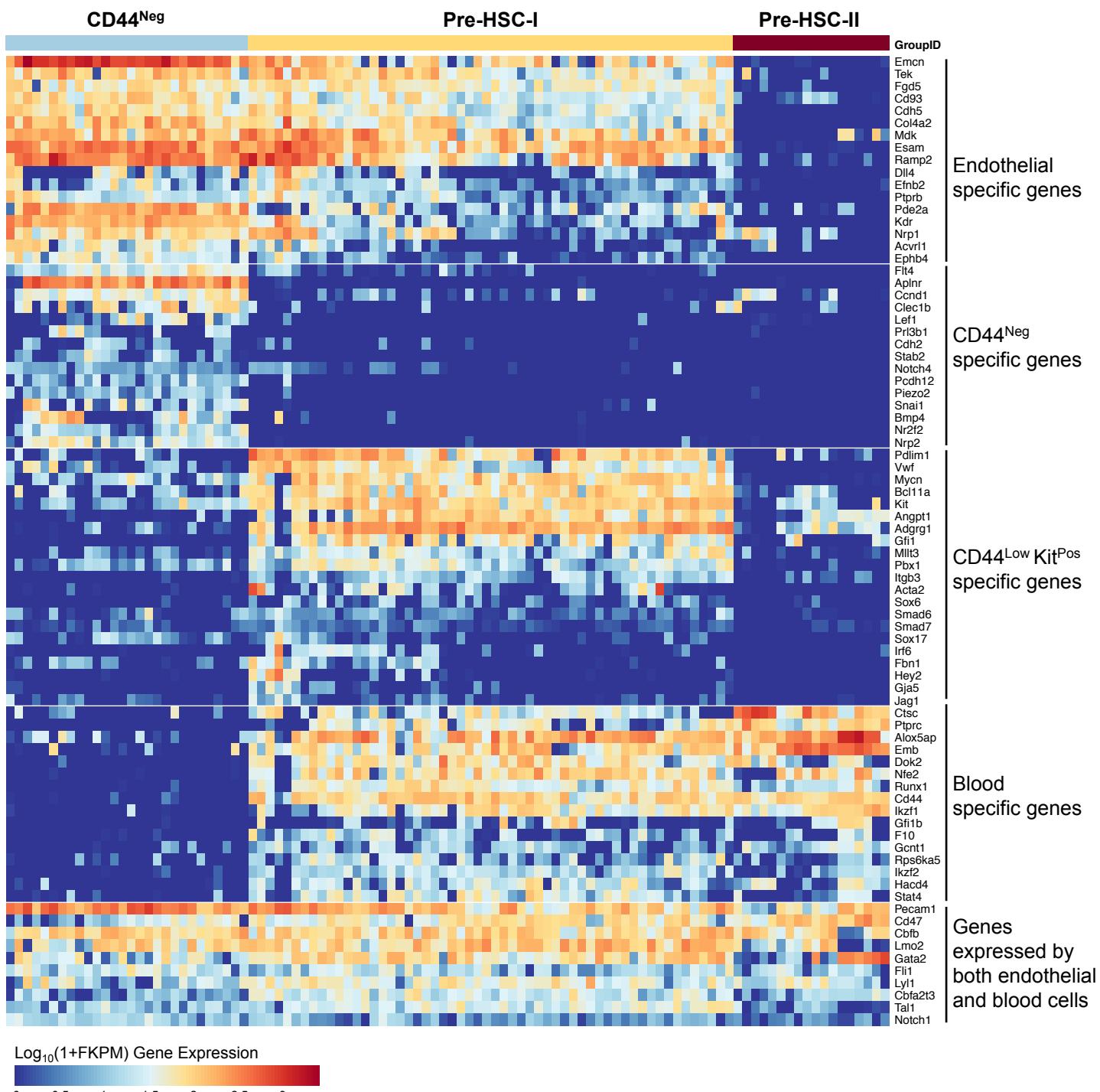
b



**Supplementary Figure 7: Results of single cell q-RT-PCR analysis of Pro-HSC, Pre-HSC-I and Pre-HSC-II.**

(a) Single cells from Pro-HSCs (VE-Cad<sup>+</sup> CD41<sup>+</sup> CD45<sup>-</sup>CD43<sup>-</sup>), Pre-HSC-I (VE-Cad<sup>+</sup> CD41<sup>+</sup> CD45<sup>-</sup> CD43<sup>+</sup>), Pre-HSC-II (VE-Cad<sup>+</sup> CD45<sup>+</sup>) populations were isolated and tested by single-cell q-RT-PCR. The heatmap shows the result of the hierarchical clustering analysis (cells were clustered by Euclidian distance and the genes by Pearson correlation). (b) tSNE plot from single cell q-RT-PCR data shown in (a). See also Figure 4 and Supplementary Data 4.

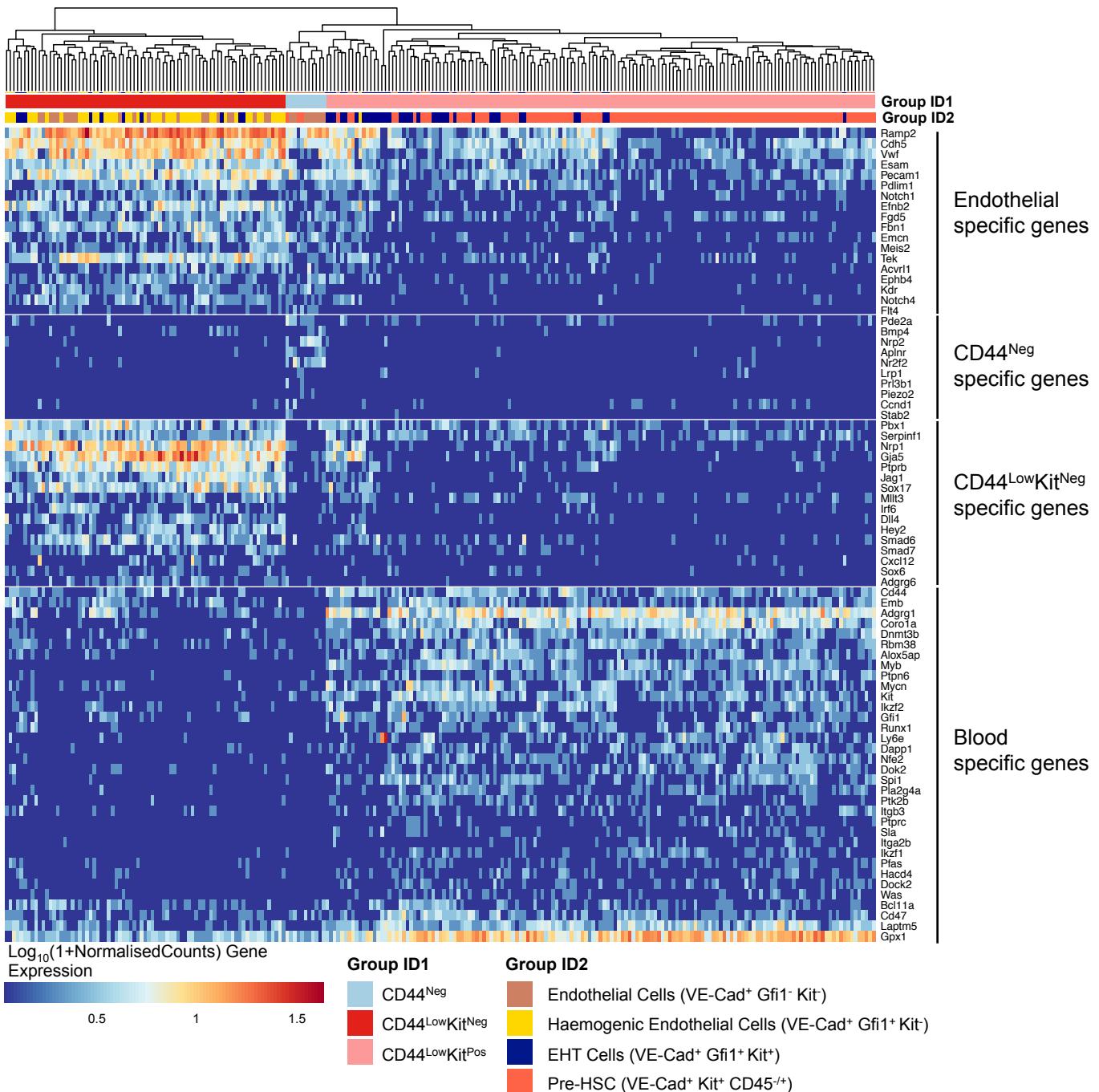
## Supplementary Figure 8



**Supplementary Figure 8: Analysis of the Zhou et al. sc-RNA-seq dataset.**

The heatmap shows the expression pattern of genes selected from Fig. 3 and Fig. 5 in the single cells studied by Zhou et al.<sup>14</sup> using sc-RNA-seq. These cells were isolated from E11 mouse embryos and included endothelial cells (CD44 Neg), Pre-HSC-I and Pre-HSC-II. The genes were grouped in the five indicated categories. See also Supplementary Data 6.

## Supplementary Figure 9

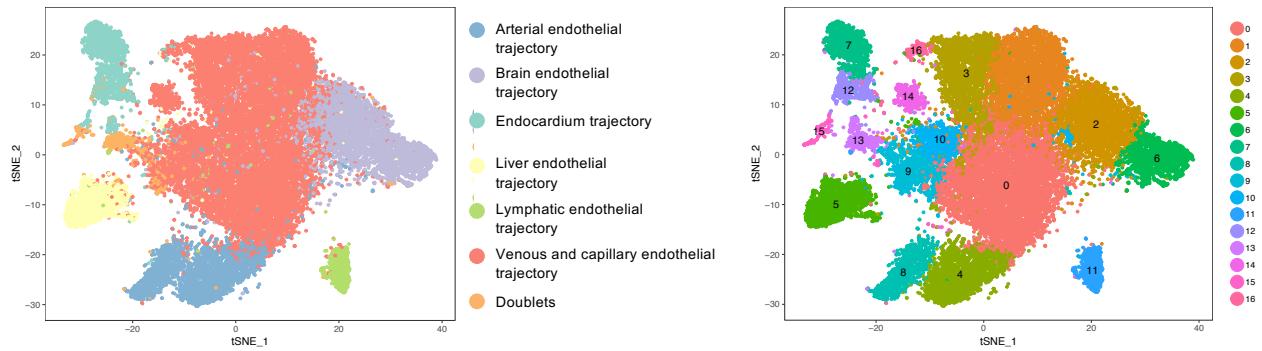


**Supplementary Figure 9: Analysis of the Baron, Kester et al. sc-RNA-seq dataset .**

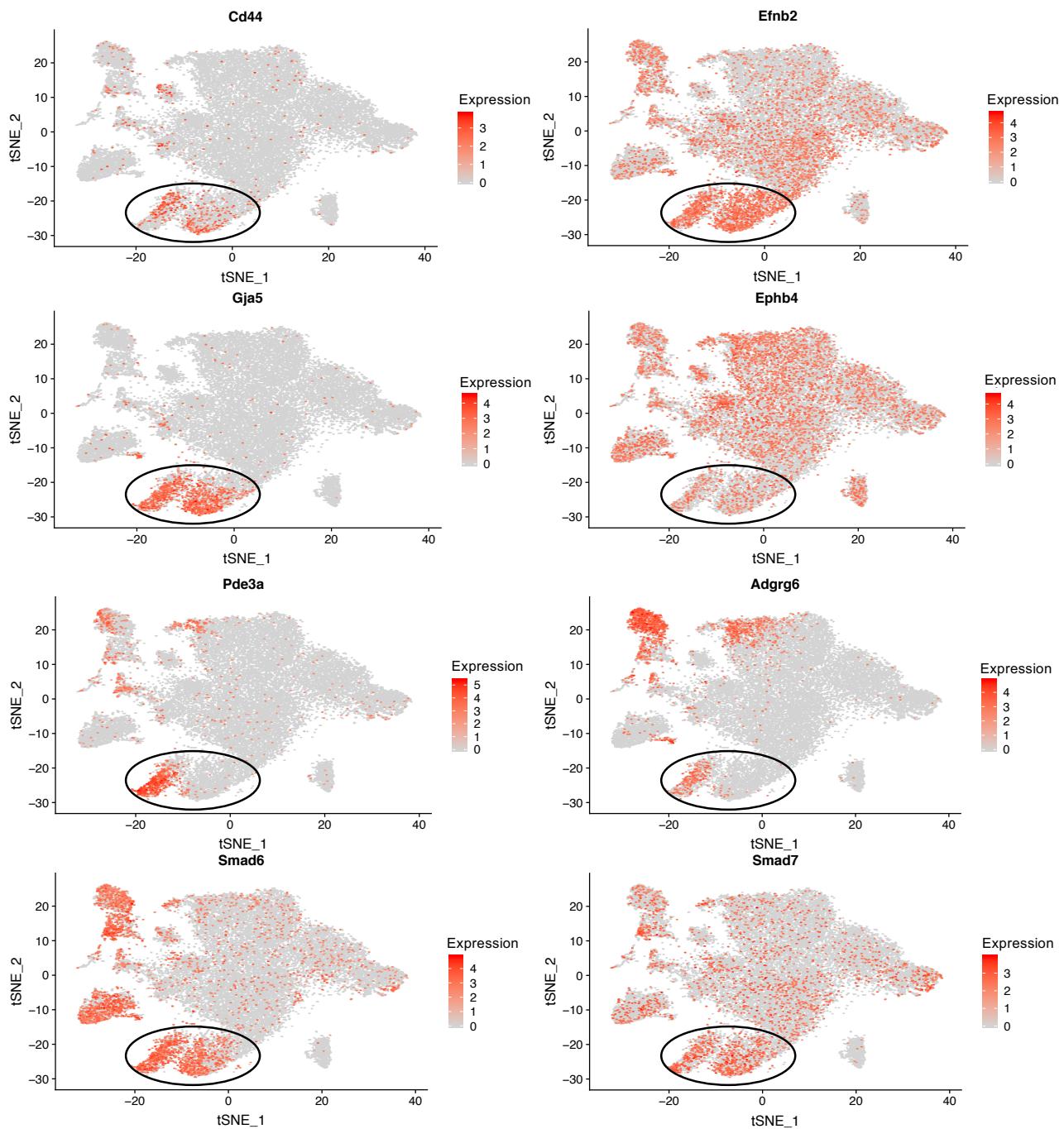
The heatmap shows the expression pattern of genes selected from Fig. 3 and Fig. 5 in the single cells studied by Baron, Kester et al.<sup>25</sup> using sc-RNA-seq. These cells were isolated from E11 mouse AGM and included endothelial cells (VE-Cad<sup>+</sup> Gfi1<sup>-</sup> Kit<sup>-</sup>), haemogenic endothelial cells (VE-Cad<sup>+</sup> Gfi1<sup>+</sup> Kit<sup>-</sup>), EHT cells (VE-Cad<sup>+</sup> Gfi1<sup>+</sup> Kit<sup>+</sup>), Pre-HSC (VE-Cad<sup>+</sup> CD45<sup>-/+</sup>). Based on hierarchical clustering (Euclidian distance), most of endothelial and haemogenic endothelial cells clustered together and correspond to CD44<sup>LowKit</sup><sup>Neg</sup> cells, some endothelial cells formed a cluster of CD44<sup>Neg</sup> cells while EHT cells and Pre-HSC formed a cluster of CD44<sup>LowKit</sup><sup>Pos</sup>. The genes were grouped in the 4 indicated categories. See also Supplementary Data 7.

# Supplementary Figure 10

**a**



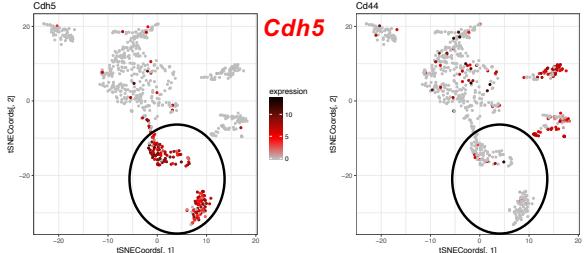
**b**



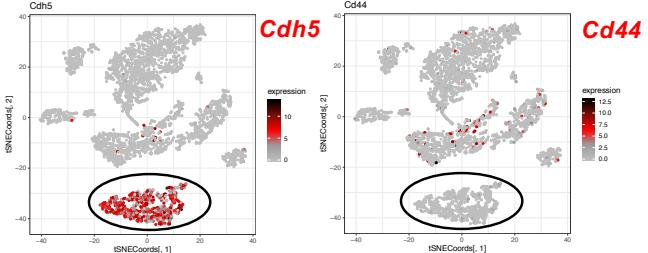
**Supplementary Figure 10: Expression of Cd44 is restricted to arterial endothelial cells between E9.5 and E13.5.** (a) The t-SNE plots show the 26,107 endothelial cells from the Cao et al. mouse organogenesis atlas according to specific trajectories (left panel) and based on their belonging to distinct clusters (right panel). (b) The t-SNE plots show the expression of the indicated genes. The black ellipse highlights the cells with arterial features (co-expression of *Efnb2* and *Gja5*). The scale of gene expression is indicated next to each plot.

## Supplementary Figure 11

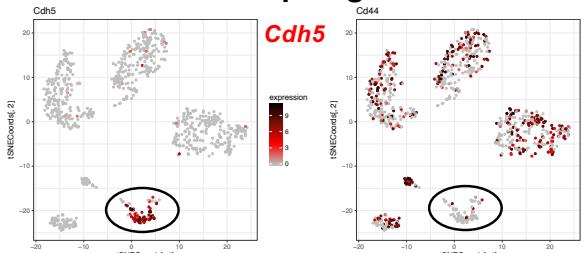
### Aorta



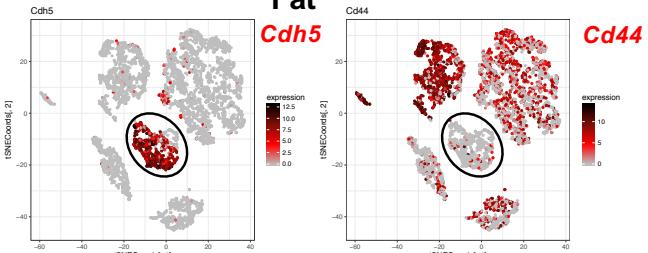
### Brain



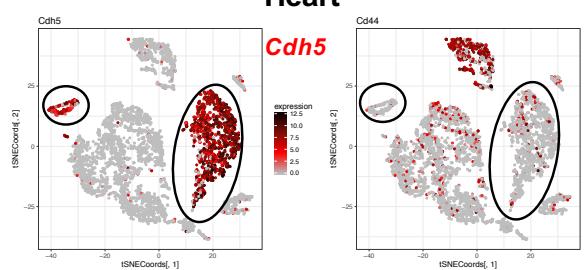
### Diaphragm



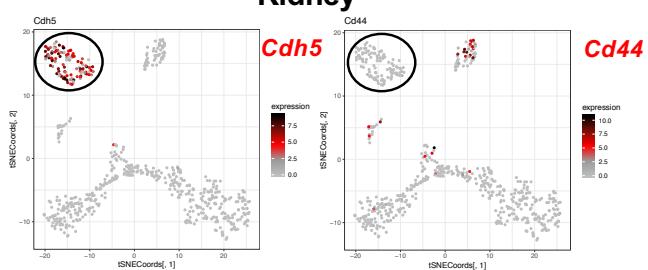
### Fat



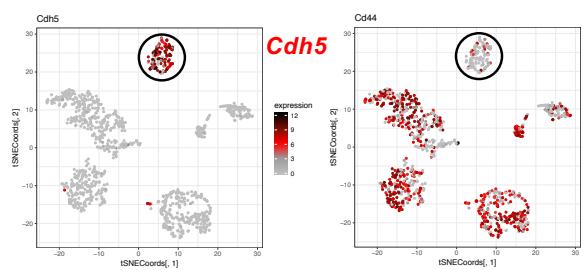
### Heart



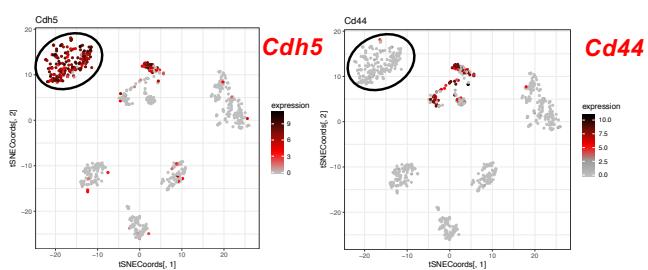
### Kidney



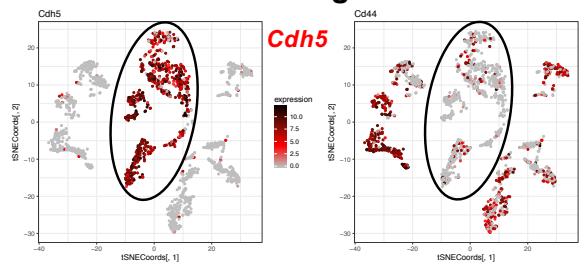
### Limb Muscle



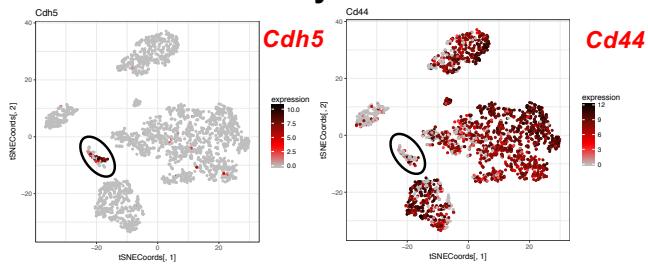
### Liver



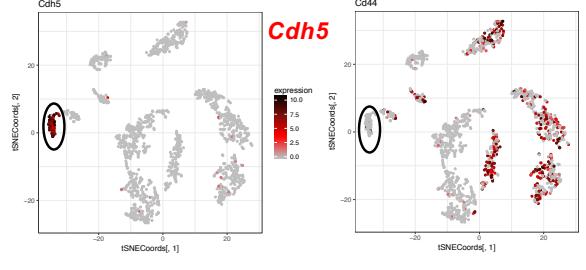
### Lung



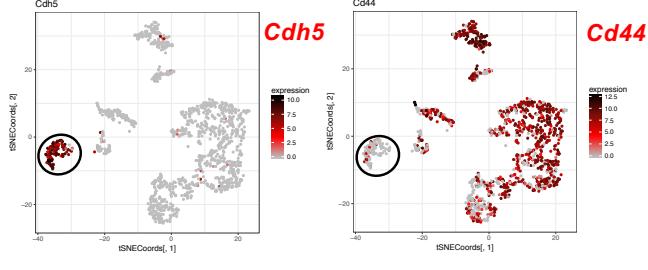
### Mammary Glands



### Pancreas



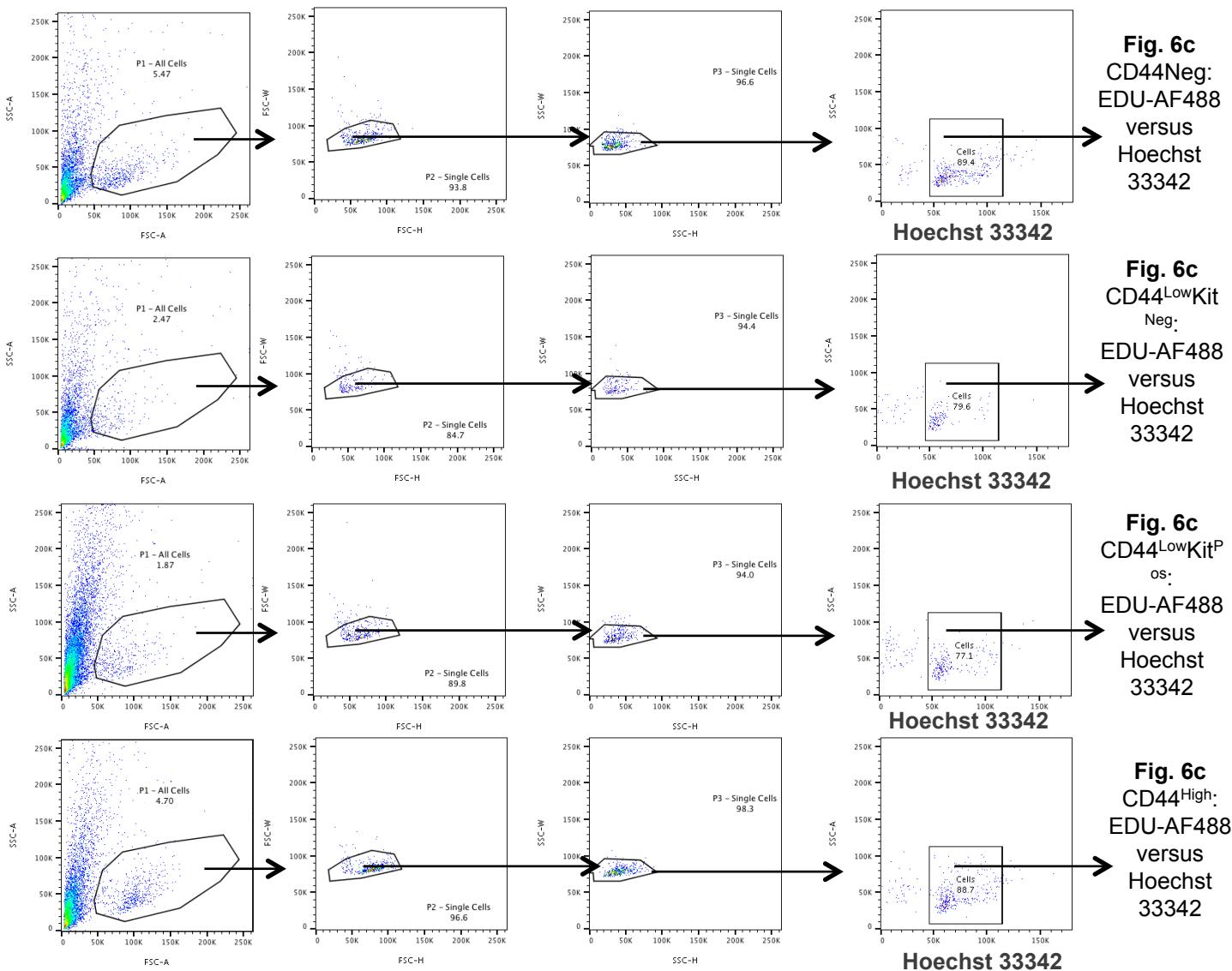
### Trachea



**Supplementary Figure 11: Expression of *Cd44* is absent from most of adult mouse endothelial cell populations.**

The t-SNE plots show the expression pattern of the *Cdh5* and *Cd44* genes in endothelial cells of twelve different mouse adult organs from the Tabula Muris dataset (Single FACS-sorted cells were analysed with the Smart-Seq2 full-length transcriptome method). The scale of gene expression is indicated next to each plot.

# Supplementary Figure 12

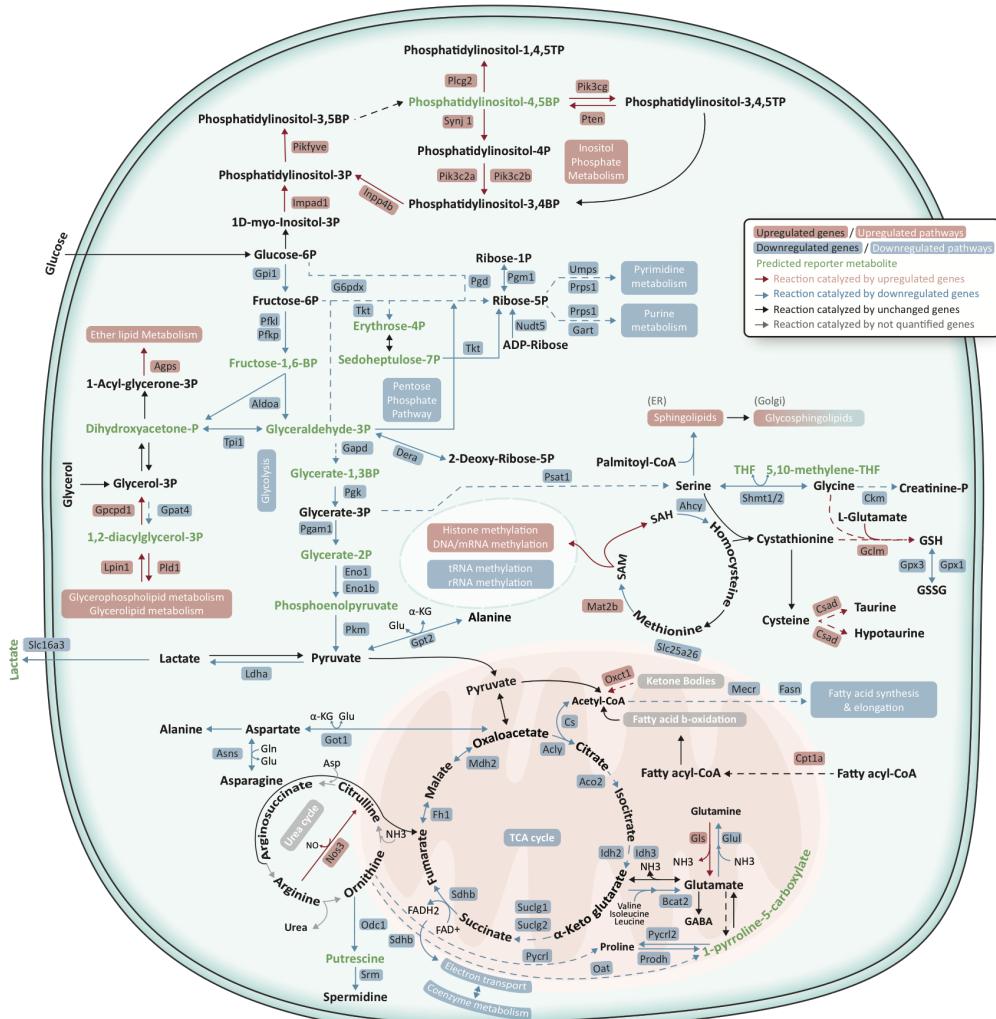


**Supplementary Figure 12: Gating strategies using for FACS analysis shown in Figure 6c.**

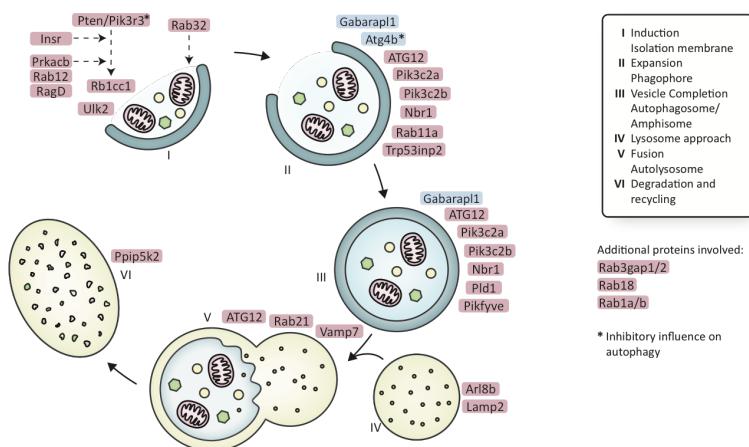
From left to right: FSC-A versus SSC-A, FSC-H versus FSC-W, SSC-H versus SSC-W and SSC-A versus Hoechst 33342. The arrows indicate the cells selected from one plot to the next.

# Supplementary Figure 13

a

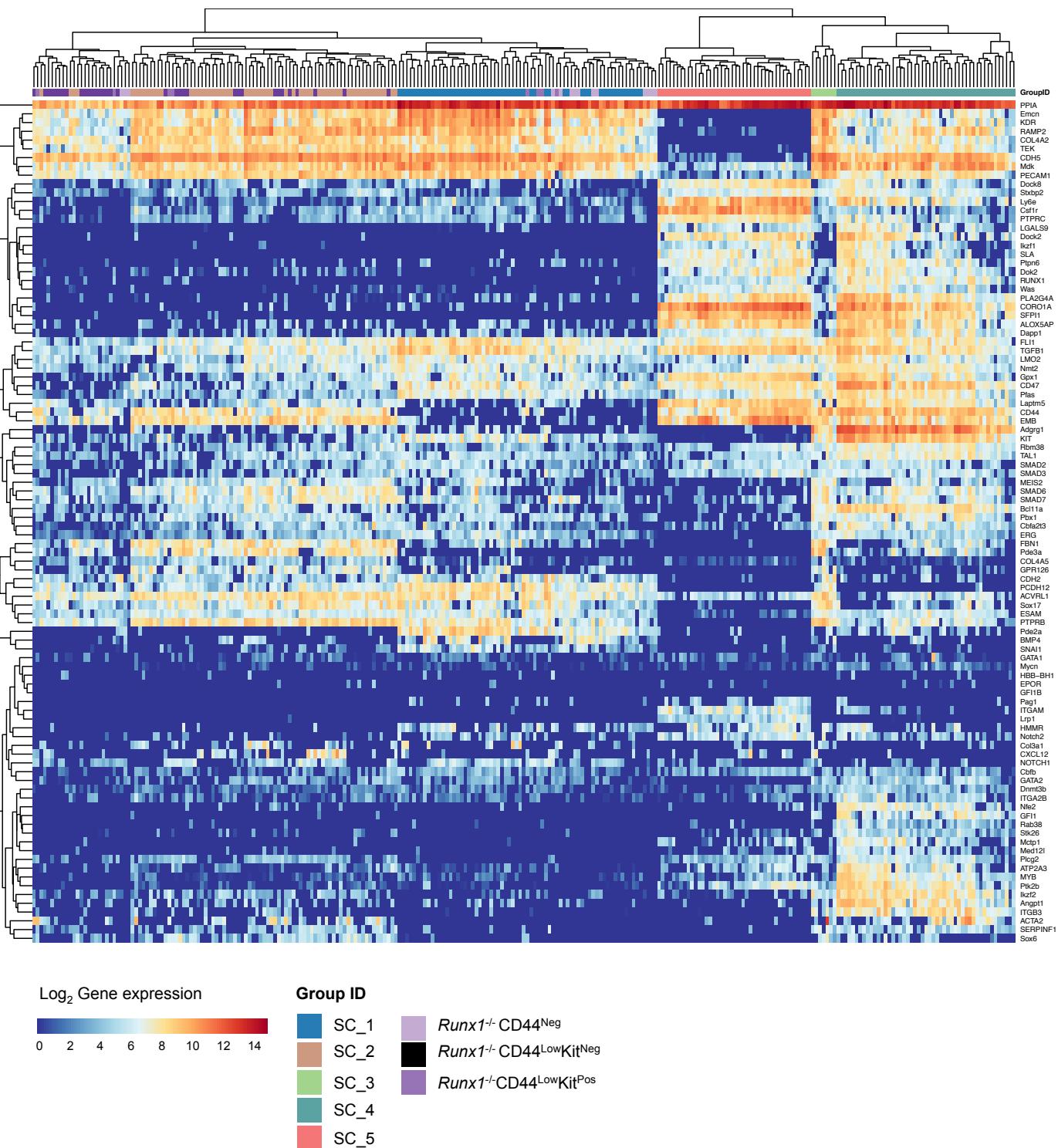


b



**Supplementary Figure 13: CD44<sup>Low</sup>Kit<sup>Neg</sup> endothelial cells feature altered expression of genes involved in metabolism and autophagy.** (a) Overview of key metabolic nodes and pathways enriched in differentially expressed genes when comparing the CD44<sup>Low</sup>Kit<sup>Neg</sup> and CD44<sup>Neg</sup> endothelial populations. These were selected based on reporter metabolite analysis. Pathway boxes summarize multiple genes / reporter metabolites (Supplementary Table 3). The mentioned upregulated and downregulated genes refer to the expression in the CD44<sup>Low</sup>Kit<sup>Neg</sup> population compared to CD44<sup>Neg</sup>. (b) Schematic representation of the autophagy process marking differentially expressed genes. Included are genes coding for structural as well as regulatory aspects of autophagy. The colour code is the same as in (a). See also Figure 6.

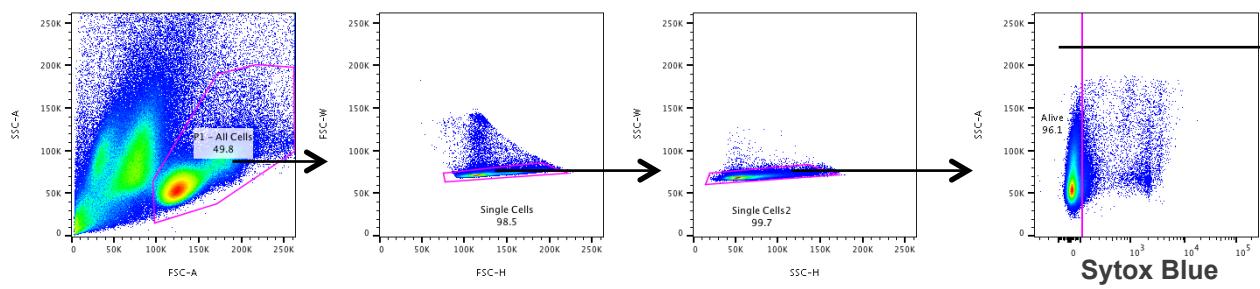
## Supplementary Figure 14



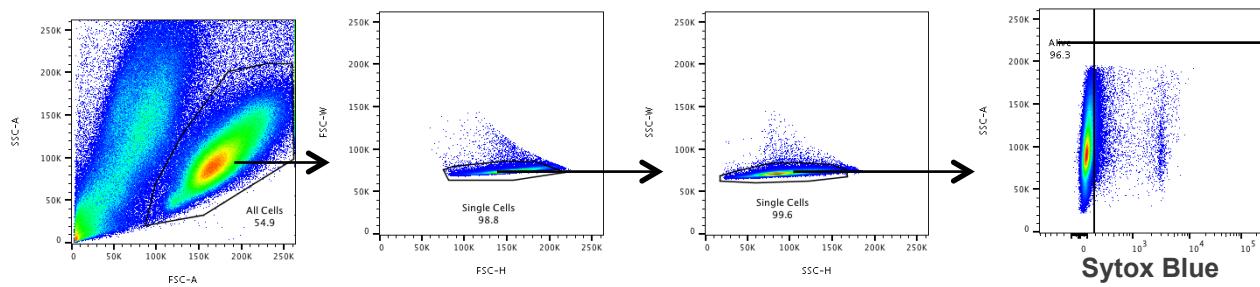
**Supplementary Figure 14: Results of single cell q-RT-PCR analysis in the wild type and *Runx1*<sup>-/-</sup> AGM.**

Single cells from *Runx1*<sup>-/-</sup> CD44<sup>Neg</sup>, *Runx1*<sup>-/-</sup> CD44<sup>Low</sup>Kit<sup>Neg</sup> and *Runx1*<sup>-/-</sup> CD44<sup>Low</sup>Kit<sup>Pos</sup> populations were isolated and tested by single-cell q-RT-PCR. The heatmap shows the result of the hierarchical clustering analysis in combination with the wild type single-cells from Figure 3a (cells were clustered by Euclidian distance and the genes by Pearson correlation). See also Figure 7 and Supplementary Data 9.

# Supplementary Figure 15



→ **Fig. 8g:**  
SSC-A  
versus  
CD19-PE

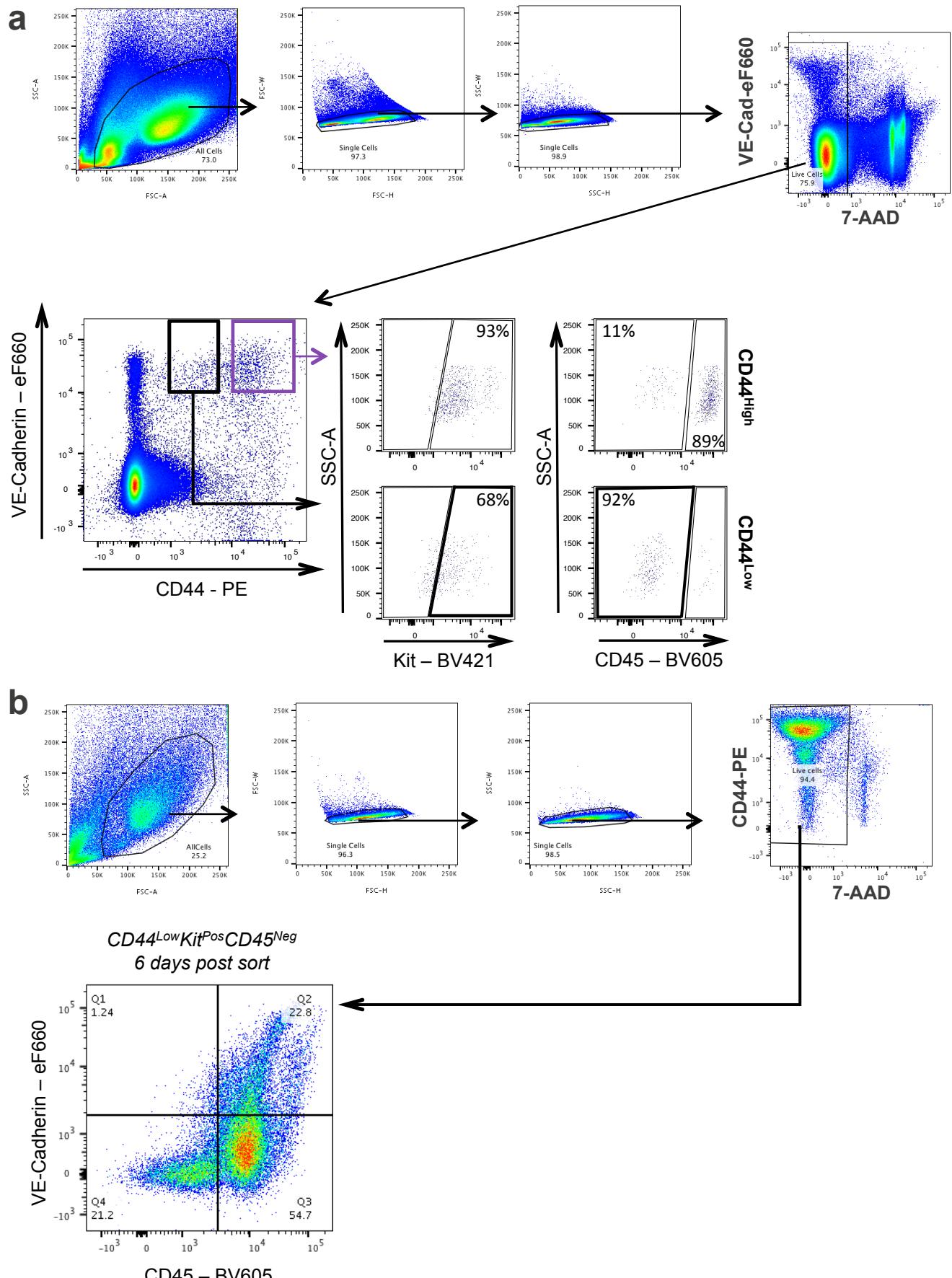


→ **Fig. 8g:**  
CD4-PE-  
Cy7 versus  
CD8a-FITC

## Supplementary Figure 15: Gating strategies used for FACS analysis shown in Figure 8g.

From left to right: FSC-A versus SSC-A, FSC-H versus FSC-W, SSC-H versus SSC-W and SSC-A versus dead cell dye Sytox Blue. The arrows indicate the cells selected from one plot to the next.

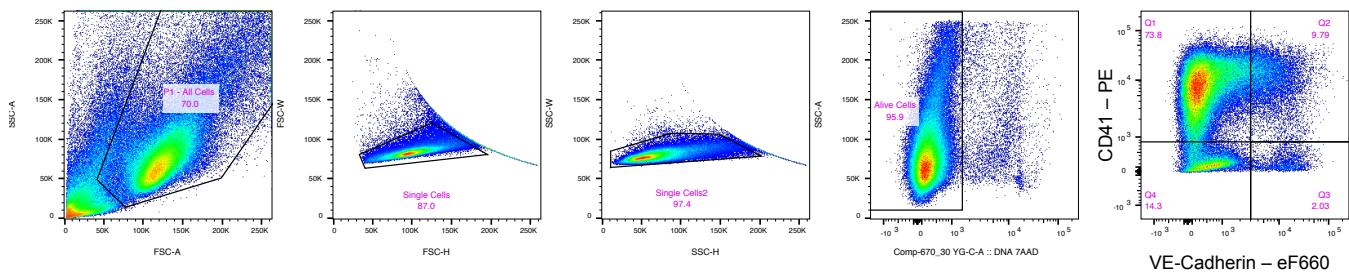
## Supplementary Figure 16



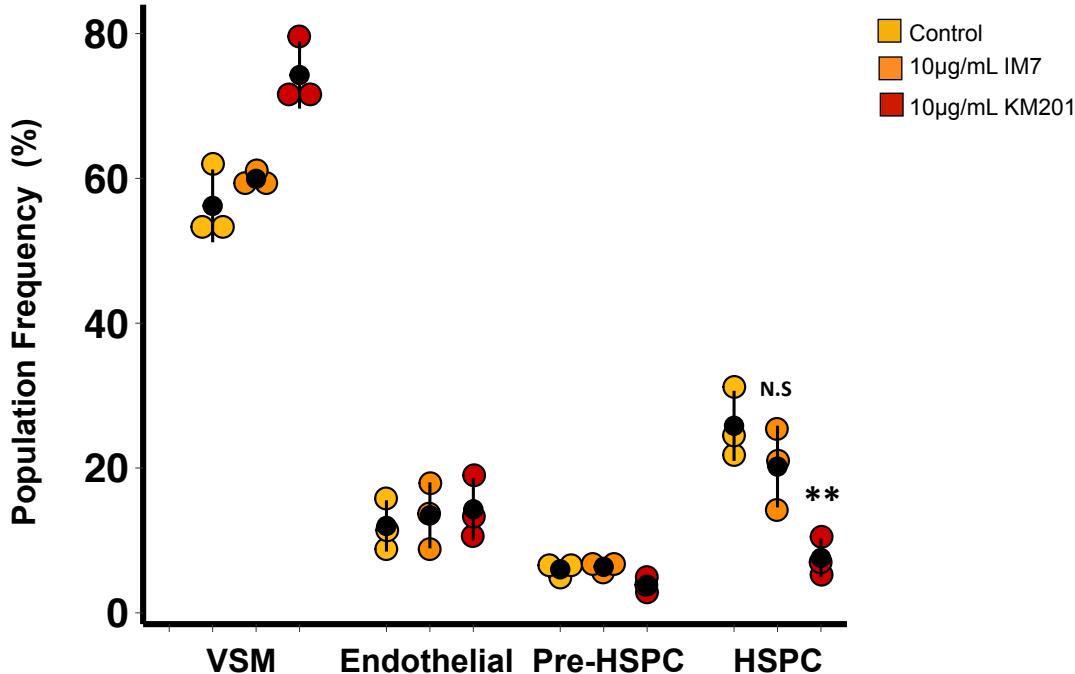
**Supplementary Figure 16: CD44<sup>Low</sup>Kit<sup>Pos</sup> cells give rise to VE-Cad<sup>Pos</sup> CD45<sup>Pos</sup> cells in OP9 co-culture.**  
**(a)** FACS plots indicating the gating strategy to isolate VE-Cad<sup>Pos</sup>CD44<sup>Low</sup> Kit<sup>Pos</sup>CD45<sup>Neg</sup> from E10.5 AGM for OP9 co-culture.  
**(b)** FACS plots indicating the gating strategy to analyse the expression of CD45 and VE-Cad following six days of OP9 co-culture.

## Supplementary Figure 17

a



b



**Supplementary Figure 17: Only an antibody binding close to the hyaluronan binding site on the extracellular domain of CD44 disrupts EHT in vitro.** (a) FACS gating strategy to analyse the expression of CD41 and VE-Cad in haemangioblast culture. (b) Dot plot showing the population percentage for vascular smooth muscle (VSM)(VE-Cad-CD41-), endothelial cells (VE-Cad+CD41-), Pre-HSPCs (VE-Cad+CD41+) and HSPCs (VE-Cad-CD41+) after two days of haemangioblast differentiation. Treatment with KM201 disrupted EHT while IM7, another CD44 antibody, did not. N=3. Significance was determined for HSPC population using a one-way ANOVA followed by Dunnett's post hoc tests (see supplementary material). Source data are provided as a Source Data file. See also Figure 9.

**Supplementary Table 1**

Target protein	Gene symbol	Gene name	Bimodal expression
CD9	<i>Cd9</i>	CD9 antigen	No
CD13	<i>Anpep</i>	alanyl (membrane) aminopeptidase	No
CD19	<i>Cd19</i>	CD19 antigen	No
<b>CD23</b>	<b><i>Fcer2a</i></b>	<b>Fc receptor, IgE, low affinity II, alpha polypeptide</b>	<b>Yes</b>
CD24	<i>Cd24a</i>	CD24a antigen	No
CD29	<i>Itgb1</i>	integrin beta 1 (fibronectin receptor beta)	No
CD31	<i>Pecam1</i>	platelet/endothelial cell adhesion molecule 1	No
<b>CD34</b>	<b><i>Cd34</i></b>	<b>CD34 antigen</b>	<b>Yes</b>
CD35	<i>Cr2</i>	complement receptor 2	No
CD38	<i>Cd38</i>	CD38 antigen	No
<b>CD41</b>	<b><i>Itga2b</i></b>	<b>integrin alpha 2b</b>	<b>Yes</b>
<b>CD44</b>	<b><i>Cd44</i></b>	<b>CD44 antigen</b>	<b>Yes</b>
CD47	<i>Cd47</i>	CD47 antigen	No
<b>CD49d</b>	<b><i>Itga4</i></b>	<b>integrin alpha 4</b>	<b>Yes</b>
CD49e	<i>Itga5</i>	integrin alpha 5 (fibronectin receptor alpha)	No
<b>CD51</b>	<b><i>Itgav</i></b>	<b>integrin alpha V</b>	<b>Yes</b>
<b>CD54</b>	<b><i>Icam1</i></b>	<b>intercellular adhesion molecule 1</b>	<b>Yes</b>
<b>CD55</b>	<b><i>Cd55</i></b>	<b>CD55 molecule, decay accelerating factor for complement</b>	<b>Yes</b>
<b>CD61</b>	<b><i>Itgb3</i></b>	<b>integrin beta 3</b>	<b>Yes</b>
CD62e	<i>Sele</i>	selectin, endothelial cell	No
<b>CD71</b>	<b><i>Tfrc</i></b>	<b>transferrin receptor</b>	<b>Yes</b>
CD81	<i>Cd81</i>	CD81 antigen	No
CD93	<i>Cd93</i>	CD93 antigen	No
CD94	<i>Klrd1</i>	killer cell lectin-like receptor, subfamily D, member 1	No
CD98	<i>Slc3a2</i>	solute carrier family, member 2	No
CD102	<i>Icam2</i>	intercellular adhesion molecule 2	No
CD104	<i>Itgb4</i>	integrin beta 4	No
<b>CD106</b>	<b><i>Vcam1</i></b>	<b>vascular cell adhesion molecule 1</b>	<b>Yes</b>
<b>CD117</b>	<b><i>Kit</i></b>	<b>KIT proto-oncogene receptor tyrosine kinase</b>	<b>Yes</b>
<b>CD119</b>	<b><i>Ifngr1</i></b>	<b>interferon gamma receptor 1</b>	<b>Yes</b>
CD137	<i>Tnfrsf9</i>	tumor necrosis factor receptor superfamily, member 9	No
CD138	<i>Sdc1</i>	syndecan 1	No
CD144	<i>Cdh5</i>	cadherin 5	No
CD147	<i>Bsg</i>	basigin	No
CD200	<i>Cd200</i>	CD200 antigen	No
CD284	<i>Tlr4</i>	toll-like receptor 4	No
CD309	<i>Kdr</i>	kinase insert domain protein receptor	No
Crry/p65	<i>Cr1l</i>	complement component (3b/4b) receptor 1-like	No
<b>MadCam1</b>	<b><i>MadCam1</i></b>	<b>mucosal vascular addressin cell adhesion molecule 1</b>	<b>Yes</b>
Meca32	<i>Plvap</i>	plasmalemma vesicle associated protein	No
<b>PIR-A/B</b>	<b>NA</b>	<b>NA</b>	<b>Yes</b>
<b>Sca1</b>	<b><i>Ly6a/e</i></b>	<b>lymphocyte antigen 6 complex, locus A/E</b>	<b>Yes</b>

**Supplementary Table 1: Results of the antibody screen.** List of the forty-two antigens (out of 176) expressed by VE-Cad<sup>+</sup> cells from day 1.5 haemangioblast culture following the antibody screen. Sixteen of these markers have a bimodal expression (indicated in bold). See also Supplementary Figure 1.

## Supplementary Table 2

**Supplementary Table 2: List of primers for single-cell q-RT-PCR.** These primers were used to detect the genes shown in Fig. 3, Fig. 4, Supplementary Fig. 5, Supplementary Fig. 7 and Supplementary Fig. 14.

### Supplementary Table 3

Antibody	Reference	Final concentration
Anti-Mouse CD19 PE	eBiosciences 12-0191-81	1 µg/mL
Anti-Mouse CD4 PE-Cy7	BD Biosciences 561099	0.25 µg/mL
anti-Mouse CD41-PE	eBiosciences 12-0411-82	0.5 µg/mL
Anti-Mouse CD43 PerCP-Cy5-5	BD Biosciences 562865	4 µg/mL
Anti-Mouse CD44	Abcam ab157107	2 µg/mL
Anti-Mouse CD44	Abcam ab25340 (KM207)	5 µg/mL and 10 µg/mL
Anti-Mouse CD44	BD Biosciences 550538 (IM7)	10 µg/mL
anti-Mouse CD44-PE	BD Biosciences 553134	0.16 µg/mL
Anti-Mouse CD45 BV605	BD Biosciences 563053	2 µg/mL
Anti-Mouse CD45-FITC	BD Biosciences 553079	5 µg/mL
Anti-Mouse CD51-Biotin	BD Biosciences 551380	2.5 µg/mL
Anti-Mouse CD61-PE	BD Biosciences 553347	1 µg/mL
Anti-Mouse CD8a-Alexa Fluor 488	BD Biosciences 557668	5 µg/mL
Anti-Mouse CD93-PE	BD Biosciences 558039	1 µg/mL
Anti-Mouse Flk1-APC	eBiosciences 17-5821-81	6 µg/mL
Anti-Mouse Kit-BV421	BD Biosciences 562609	1 µg/mL
Anti-Mouse Ly-6A/E (Sca1)-PE	BD Biosciences 561076	1 µg/mL
Anti-Mouse MAdCAM-1-Biotin	BD Biosciences 553808	2.5 µg/mL
Anti-Mouse VE-Cadherin	eBiosciences 14-1441-81	2.5 µg/mL
anti-Mouse VE-Cadherin-eFluor660	eBiosciences 50-1441-82	1 µg/mL
Anti-Rabbit-Alexa Fluor 488	ThermoFisher Scientific A-21206	4 µg/mL
Anti-Rat-Alexa Fluor 568	ThermoFisher Scientific A-11077	4 µg/mL
Mouse Cell Surface Marker Screening Panel (176 antibodies)	BD Biosciences 562208	Concentrations of antibodies are specified in the product datasheet.
Streptavidin PE-Cy7	eBioscience 25-4317	0.66 µg/mL

**Supplementary Table 3: List of antibodies used in this study.** Name, product reference and final concentration of antibodies are indicated.

## Supplementary Table 4

Populations	E9.5	E10	E11
VE-Cad <sup>Pos</sup> CD44 <sup>Neg</sup> (CD44 <sup>Neg</sup> )	4 x 25-cells	3 x 25-cells	3 x 25-cells
VE-Cad <sup>Pos</sup> CD44 <sup>Low</sup> Kit <sup>Neg</sup> (CD44 <sup>Low</sup> Kit <sup>Neg</sup> )	1 x 25-cells	2 x 25-cells	3 x 25-cells
VE-Cad <sup>Pos</sup> CD44 <sup>Low</sup> Kit <sup>Pos</sup> (CD44 <sup>Low</sup> Kit <sup>Pos</sup> )	1 x 25-cells	2 x 25-cells	Not done
VE-Cad <sup>Neg</sup> CD44 <sup>High</sup> (CD44 <sup>High</sup> )	Not done	Not done	3 x 25-cells

**Supplementary Table 4: List of samples used for bulk RNA sequencing.** The phenotype of populations, time points, and number of samples are indicated.