a

0	Forebrain/Midbrain/Hindbrain
1	Paraxial mesoderm A
2	Somatic Mesoderm/Splanchnic mesoderm/Intermediate mesoderm/Second heart field
3	Neuromesodermal progenitors
4	Pre-epidermal keratinocytes/Gut/Placodal Area/Primordial Germ Cells
5	Spinal cord
6	Paraxial mesoderm B
7	Extraembryonic mesoderm B/Allantois
8	Forebrain/Midbrain
9	Neural crest
10	Hematoendothelial progenitors/Endothelium/Blood progenitors
11	Allantois/Amniochorionic mesoderm A/Amniochorionic mesoderm B
12	Forebrain/Midbrain/Spinal cord
13	Primitive erythroid cells
14	First heart field/Second heart field
15	Anterior floor plate/Posterior floor plate
16	Extraembryonic visceral endoderm
17	Fusing epithelium
18	Notochord/Definitive endoderm

b

Figure S1.

The expression patten of *Exoc3l2* at E8.5 mouse embryos from sc-RNA-seq data (GSE186069). (**a**) UMAP was generated using a part of E8.5 mouse embryo sc-RNA-seq dataset from GSE186069. Cluster 10 was composed of 51.0% of endothelium. (**b**) The expression levels of endothelial cell markers and *Exoc3l2*. The same UMAPs as in **a**, colored by the expression value of typical endothelial cell markers, *Pecam1* and *Cdh5*, and *Exoc3l2*.

Supplemental Table S1: Primers for mouse genotyping PCR

Strain	Allele	Primer name	Primer seqnce	Amplicon length
Exoc3l2 eGFP KI	WT	161_Exoc3l2_3'arm_Target_Forward	5'– ATAGGATCCTTGTCTTCCCGTCCTCTCCCAACAG –3'	415 bp
		197_Exoc3l2_3'arm_Reverse2	5'– AACCTCCTATCCCAGAAGTCGGTGTC –3'	
	KI	070_GFP-S2	5'– TTCAAGGACGACGGCAACTACAAGAC –3'	517 bp
		197_Exoc3l2_3'arm_Reverse2	5'– AACCTCCTATCCCAGAAGTCGGTGTC –3'	
	Δ	159_Exoc3l2_5'arm_Target_Forward	5'– ATAGGATCCGAAGCCTCTAATGTTTCTAAGAGTGGGACCTG –3'	275 bp
		197_Exoc3l2_3'arm_Reverse2	5'– AACCTCCTATCCCAGAAGTCGGTGTC –3'	
Exoc3l2 flox (*)	WT	218_Exoc3l2_flox_Cent-F	5'– TGCGTCTTGGCTAATTATCTAACTCAGGACC –3'	940 bp (Not digested by EcoRV)
		219_Exoc3l2_flox_3arm-R	5'– TTGCTCTCTCCTTCCACCCTTCCAC –3'	
	flox	218_Exoc3l2_flox_Cent-F	5'– TGCGTCTTGGCTAATTATCTAACTCAGGACC –3'	980 bp (EcoRV produces 334bp + 646 bp fragments)
		219_Exoc3l2_flox_3arm-R	5'– TTGCTCTCTCCTTCCACCCTTCCAC –3'	
	Exon3 Δ	216_Exoc3l2_flox_5arm-F	5'– CTCTCAAACCTATGCCTCCCCTTTCTACAG –3'	875 bp
		219_Exoc3l2_flox_3arm-R	5'– TTGCTCTCTCCTTCCACCCTTCCAC –3'	

* As for Exoc3l2 flox strain, PCR products from WT and flox alleles were distinguished by EcoRV restriction enzyme digestion.

Supplemental Table S2: Primers for qPCR

Target gene	Strand	Primer seqnce
Hprt	Forward	5'– TTGTTGTTGGATATGCCCTTGACTA –3'
Hprt	Reverse	5'– AGGCAGATGGCCACAGGACTA –3'
Cdh5	Forward	5'– CCTCTGCATCCTCACCATCACAG –3'
Cdh5	Reverse	5'– ACCAACTGCTCGTGAATCTCCAG –3'
Pecam1	Forward	5'– GCTGCTCCACTTCTGAACTCCAA –3'
Pecam1	Reverse	5'– TGGGTTTTACTGCATCATTTCCAGA –3'
Exoc1	Forward	5'– GGAGGAGAACTTACTGCAGGTGG –3'
Exoc1	Reverse	5'– CGTAACTCCAGATCCAGGGTAGC –3'
Exoc2	Forward	5'– GCATGCAGAGGTATTCACTATTTCC –3'
Exoc2	Reverse	5'– TTCTGCTGAAGGATGAGACGCAC –3'
Exoc3	Forward	5'– CAGACGTGTGGTGGTGGAATAC –3'
Exoc3	Reverse	5'– AGCCTCTCTGACCATCTTCTCGG –3'
Exoc3l1	Forward	5'– ATTGAGTTCTGAGTTGCTAGATGGT –3'
Exoc3l1	Reverse	5'– CTTAGGTATTGTAACACCACGGTTC –3'
Exoc3l2	Forward	5'– AGATCCTACAGTTGGAGGACACTC –3'
Exoc3l2	Reverse	5'– ACCACTTTCAGATAGTTCCAGGTC –3'
Exoc3l3	Forward	5'– CCATTAAGATCGAGGTGGCCACA –3'
Exoc3l3	Reverse	5'– ATGCTCCTGACTTCACTGCTTGG –3'
Exoc3l4	Forward	5'– GACACACTTCGTCCCCTCATGG –3'
Exoc3l4	Reverse	5'– GTATTCGCGGACCACAAAACGG –3'
Exoc4	Forward	5'– CGGGAGGCAGACTTGGACTTTG –3'
Exoc4	Reverse	5'– GTACTTCACACCCTGGTCCACC –3'
Exoc5	Forward	5'– CGGGAGAACAACTTGCCAATCTG –3'
Exoc5	Reverse	5'– TGCCTTTGTAAATTCAGCTCAGC –3'
Exoc6	Forward	5'– ACATATTCGCCCAGTTCCGGAAG –3'
Exoc6	Reverse	5'– ACATACCAGTCACCAAGCCTCTG –3'
Exoc6b	Forward	5'– GAACCCTGTGACAGCTCTGACC –3'
Exoc6b	Reverse	5'– GCCACGGTGTCAATCAATTTCTGC –3'
Exoc7	Forward	5'– GCGGCAGATGATTAAGGAACGTTTC –3'
Exoc7	Reverse	5'– TCTCTGCTCTGTGTCTGGAATAGC –3'
Exoc8	Forward	5'– AGGAGATGAAAAGTTGCGGGGTC –3'
Exoc8	Reverse	5'– CCCATAGTCTGCTTGGTGAAGGC –3'