

Supplementary Information

Figure Legends

Figure S1. Direct reprogramming of human fibroblasts to functional iECs. (A) FACs plot data (obtained using CD31+ antibody) of iECs derived from fibroblasts (*left panel*) compared to HMVECs (*right panel*). (B) Representative bright field image of iECs depicting a typical “cobblestone” monolayer. (C-F) Real-Time RT-PCR of iECs for endothelial markers CD144, KDR, vWF and eNOS. (G) Immunofluorescent staining of the iECs for endothelial markers CD144 and vWF. (H) iECs incorporate acetylated LDL compared to fibroblasts. (I) iECs form capillary-like network compared to fibroblasts when seeded on matrigel (J) L-NAME inhibits the NO production in iECs. (K) iECs formed vascular structures in matrigel which contained red blood cells; a larger vessel is shown in this view. (L) Capillary density in the matrigel plug, normalized to total number of cells in the field.

Figure S2. iECs are heterogeneous. (A) Quantitative gene expression analysis of arterial, venous and lymphatic markers in iECs when compared to parental fibroblasts. Data represented as mean \pm S.E.M., n = 3. (B) *Gene expression data* of cells that have undergone the transdifferentiation protocol at day 28 immediately prior to FAC sorting. At this time point, there is no increase in endodermal and ectodermal markers, nor is there expression of pluripotency markers such as Nanog and Oct4. Only the mesodermal (endothelial) markers PECAM1 and DES are increased.

Figure S3. Histone modifications during direct reprogramming to iECs.

ChIP analysis to assess H3K4me3 and H3K27me3 of the CD31 promoters on iECs and HMVEC. Quantitative RT-PCR showed an (A) increase in histone H3K4 and (B) decrease in

histone H3K27 trimethylation levels in iECs as also observed in HMVEC. Data represented as mean \pm S.D, n = 2.

Figure S4. Improvement in blood perfusion in the ischemic hindlimb after iEC transplantation. (A) Perfusion ratios of ischemic limbs at day 0, 4, 7, 11, 14 and 18 after iEC treatment. The perfusion ratio (value of the ischemic limb divided by that of the nonischemic limb) was greater in mice that received iEC transplantation compared to those that received control EGM-2 medium on day 7 and 14 (n=5 each group, *P<0.05). (B) Effect of injection of fibroblasts on blood perfusion in the ischemic hindlimb is similar to that obtained with injection of EGM2 media.

Figure S5. Characterization of iECs derived from TLR3-KD cells. (A-E) Quantitative RT-PCR of iECs derived from Scramble and TLR3-KD fibroblasts for endothelial markers CD31, CD144, KDR, vWF and eNOS. (F) Immunofluorescent staining of the iECs derived from Scramble and TLR3-KD fibroblasts for endothelial markers CD31, CD144 and vWF. (G&H) Heat map of genes differentially expressed in iECs generated from scramble or TLR3KD fibroblasts. RNA-seq data shows that most of upregulated genes observed in scramble-iECs associated with endothelial biology are reversed in the TLR3KD-iECs. A variety of genes whose expression was activated in iEC was prevented by anti-TLR3 but unaffected by the scrambled vector. For example, angiogenesis essential genes GJA4, HOXA1, HOXA3, HOXB3, HEY2, GBX2, and SEMA3A were all prevented from being activated in iEC treated with TLR3 KD but not so in the scrambled-treated iEC. For the assessment gene expression similarities between iEC and HMVEC, we identified genes from the ANOVA performed in Figure 3 that were more strongly expressed in both iEC and HMVEC as compared to parental fibroblasts. Subsequently, using Toppgene (<http://toppgene.cchmc.org/>), we used its Fisher's Exact test function to assess the

enrichment of that set of genes for its enrichment for genes known to be associated with endothelial and angiogenic biology.

Figure S6. Direct reprogramming of TLR3 knockout tail-tip fibroblasts to iECs. FACS plot data obtained using CD144+ antibody to quantify iECs. (*left panel*) - WT tail-tip fibroblasts treated with vehicle control, then transdifferentiation medium; (*middle panel*) - WT tail-tip fibroblasts treated with Poly I:C then transdifferentiation medium; and (*right panel*) – TLR3KO tail-tip fibroblasts treated with Poly I:C then transdifferentiation medium.

Fig S7. No changes in gene expression of markers for mesoderm, endoderm and ectoderm; nor endothelial progenitor markers including c-kit and CD34 during transdifferentiation of fibroblasts to iECs.

Fig. S8. Changes in gene expression of KDR, CD144, CD31 and eNOS during the transdifferentiation of fibroblasts to iECs.

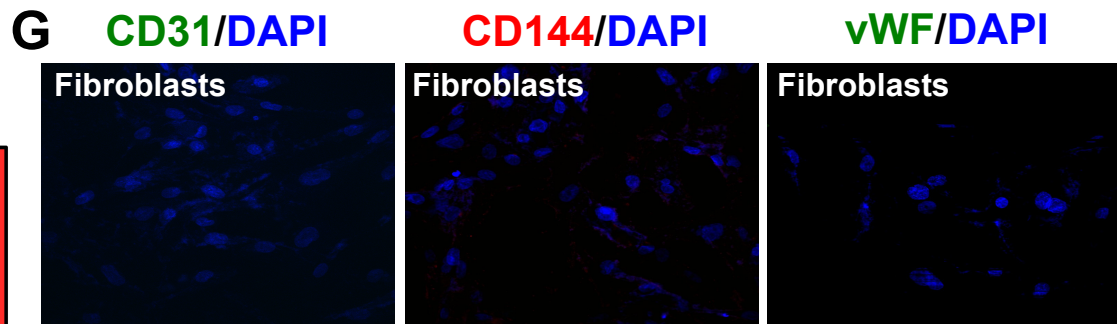
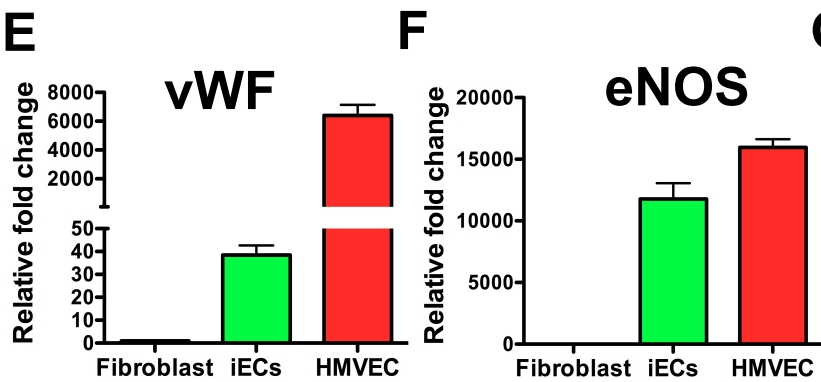
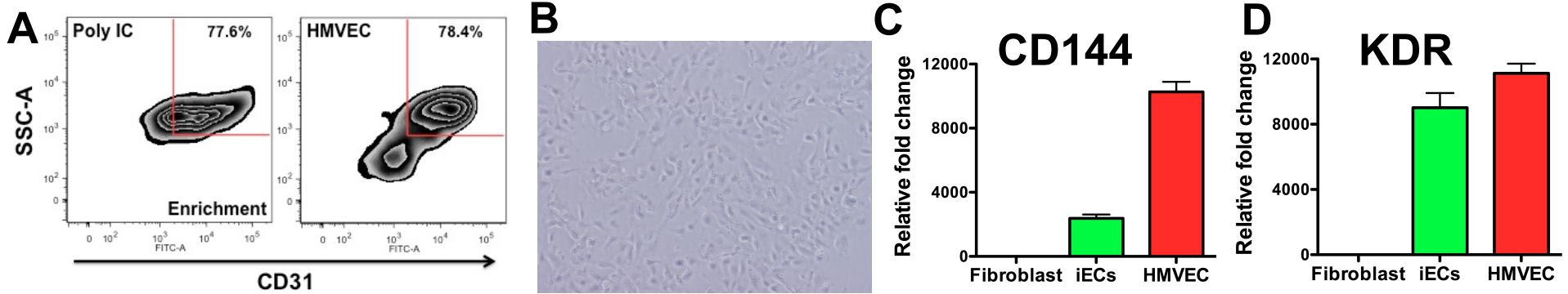


Fig. S1

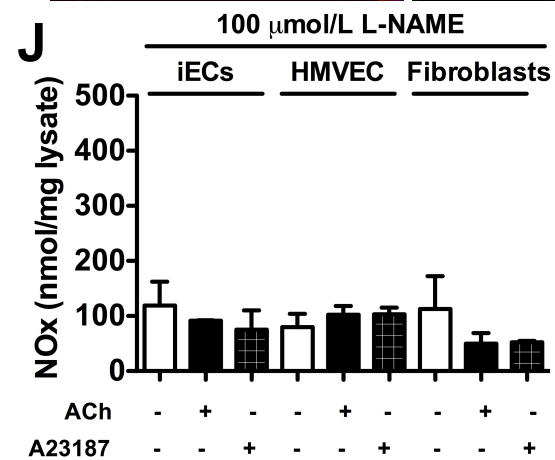
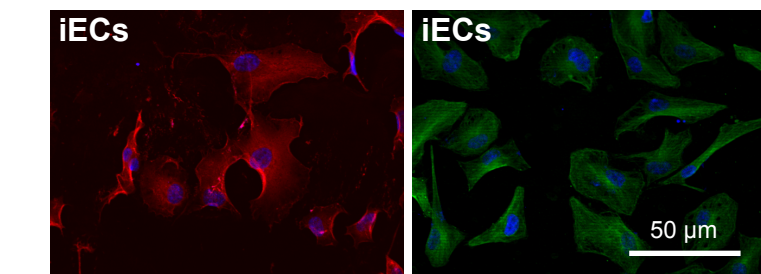
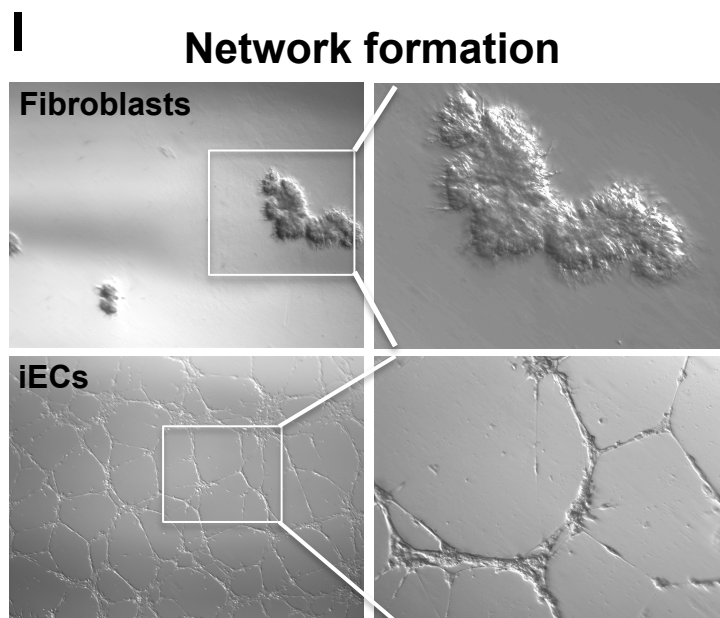
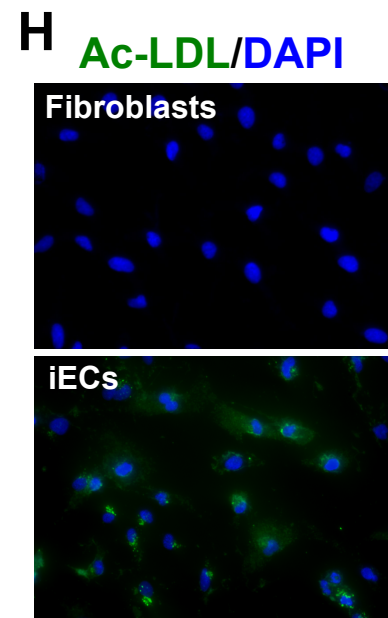
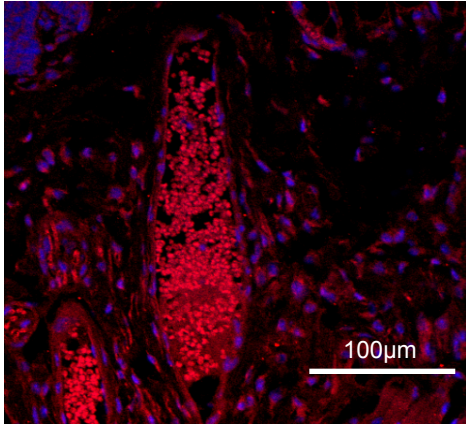


Fig. S1

K



L

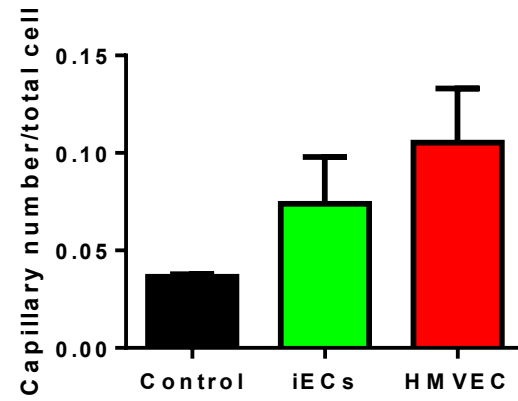


Fig. S2

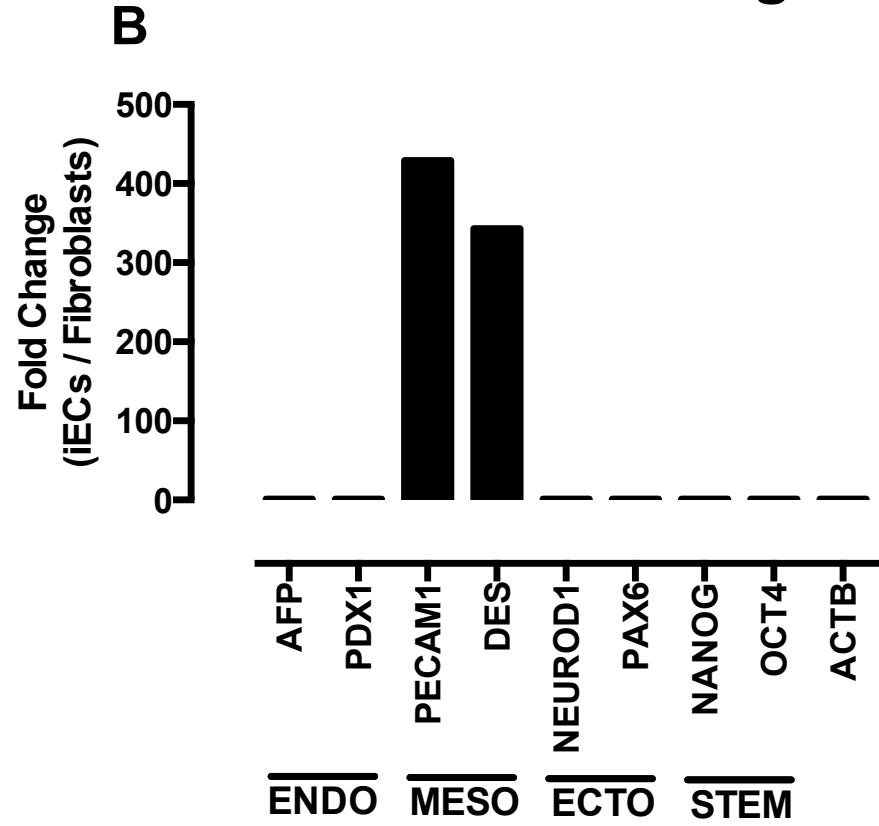
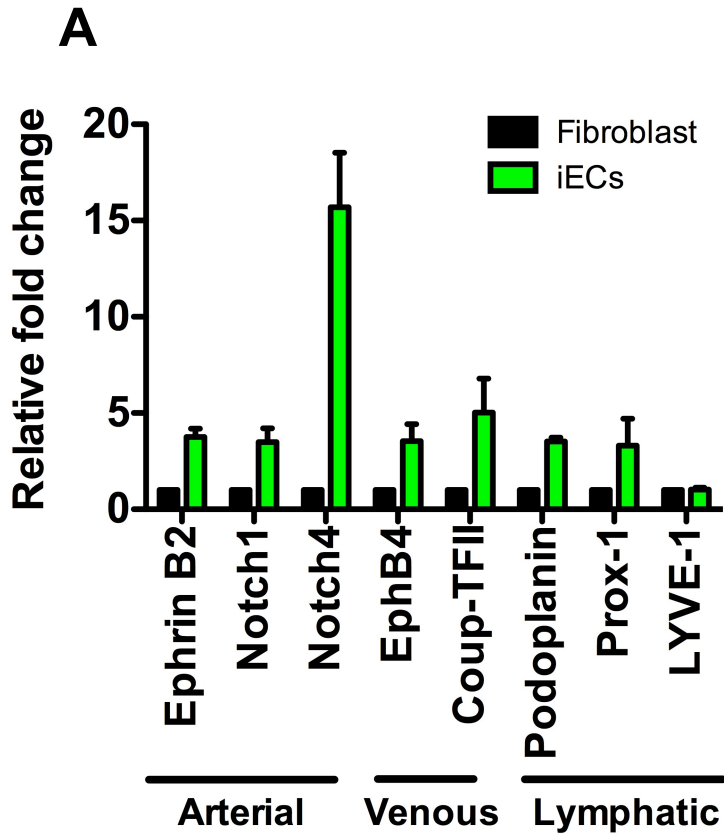


Fig. S3

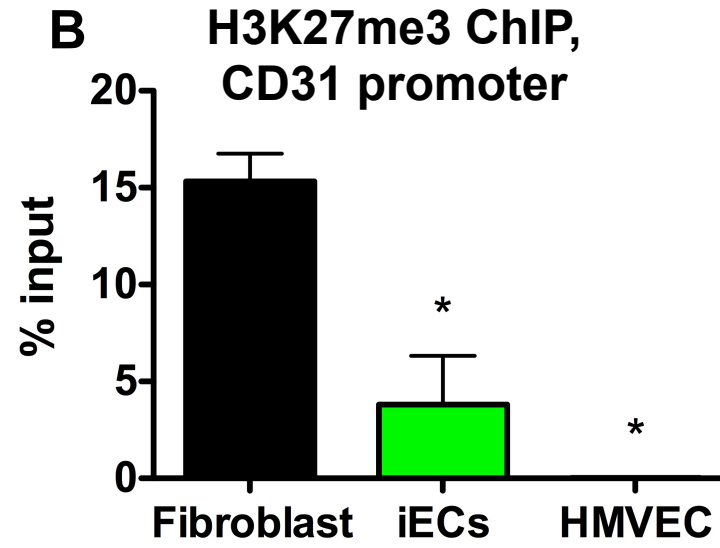
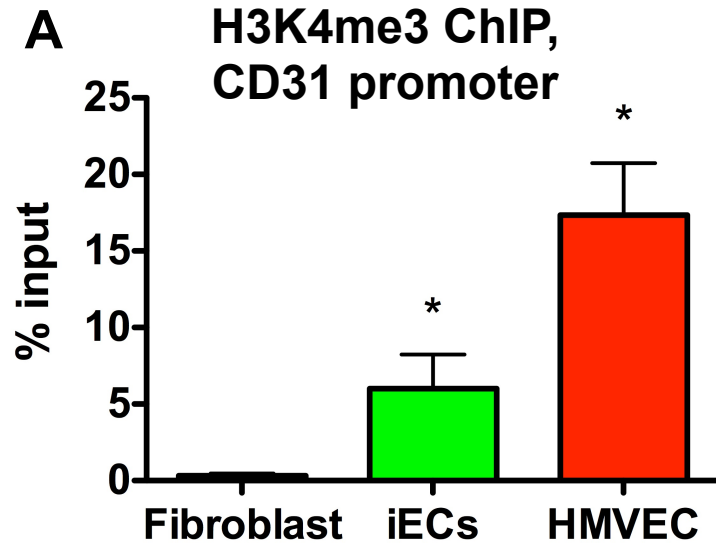


Fig. S4

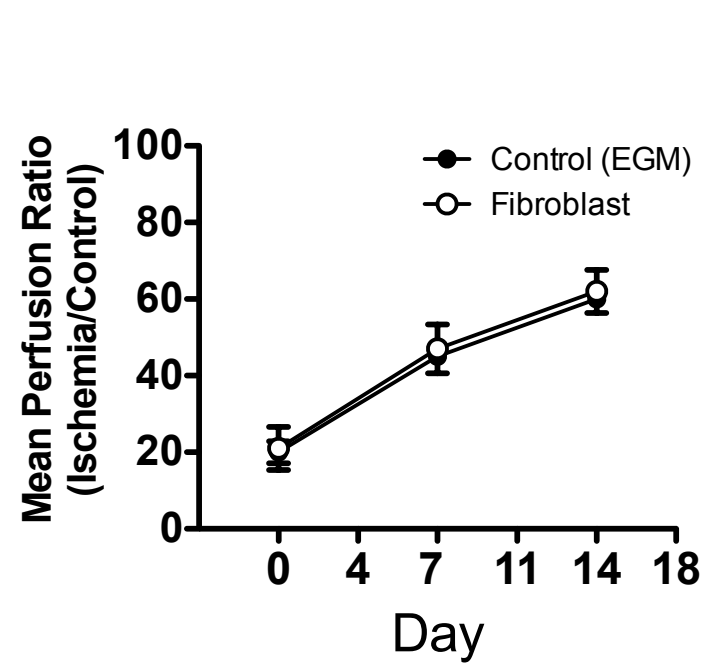
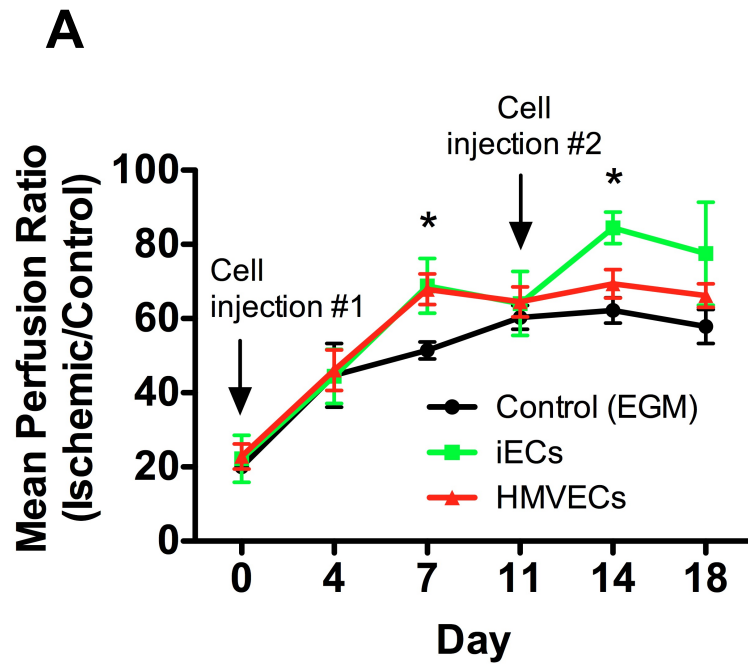
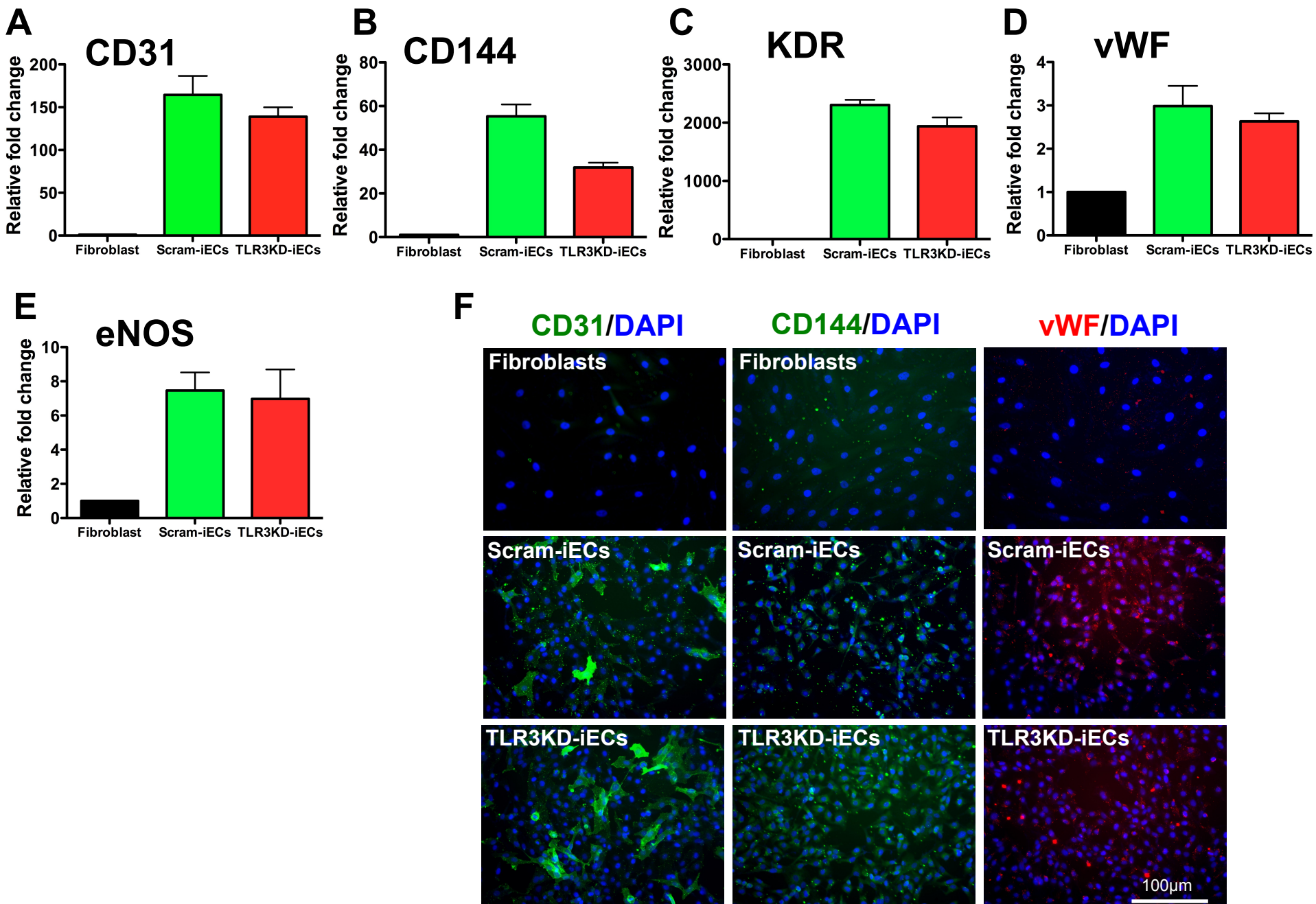


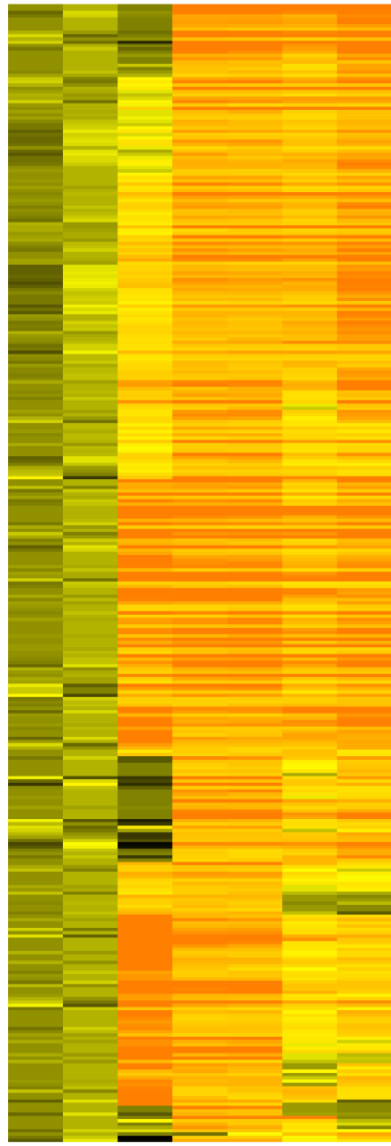
Fig. S5



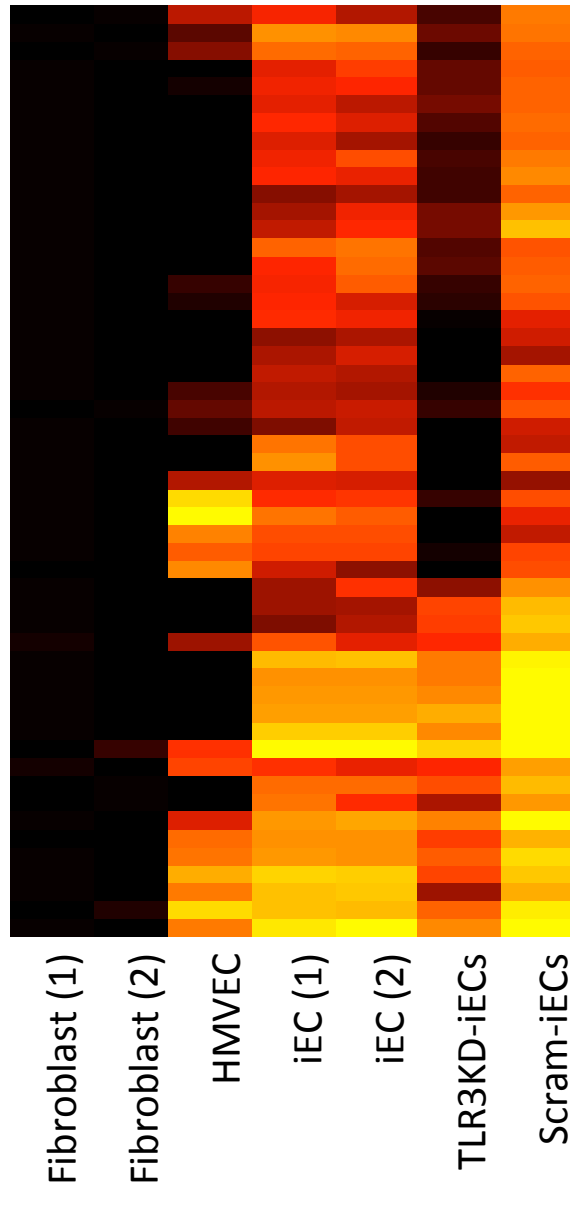
G

FPKM

Fibroblasts (1)
Fibroblasts (2)
HMVEC
iECs (1)
iECs (2)
TLR3KD - iECs
Scram - iECs



385 up-regulated iECs
& endothelial - associated

Fig. S5**H**

HOXA-AS2
HOXA1
HOXA3
PNMT
HOXB4
SHISA3
TCL1B
WFIKKN1
WDR86
TPPP3
DNAH11
GADD45G
SEMA3E
PRKCO-AS1
ZNF423
ADM5
HOXA2
C14orf39
HEY2
PTPRZ1
RHBDL3
RP11-5N23.2
ARHGDI6
RP11-126K1.6
MLLT4-AS1
RNU1-39P
SUGT1P3
GJA4
MMRN2
PLVAP
GBX2
SKP1P1
SSUH2
TMEM215
CNTFR
CCDC150
ARC
FXVD6
SYT6
TTYH1
LAMP5
RBP1
RBM38
BVES
HOTAIRM1
ANK3
ADAMTS9
HOXB3
HAGLR
HOXD1
SNCG
TMEM88

Expression

FPKM

Fig. S6

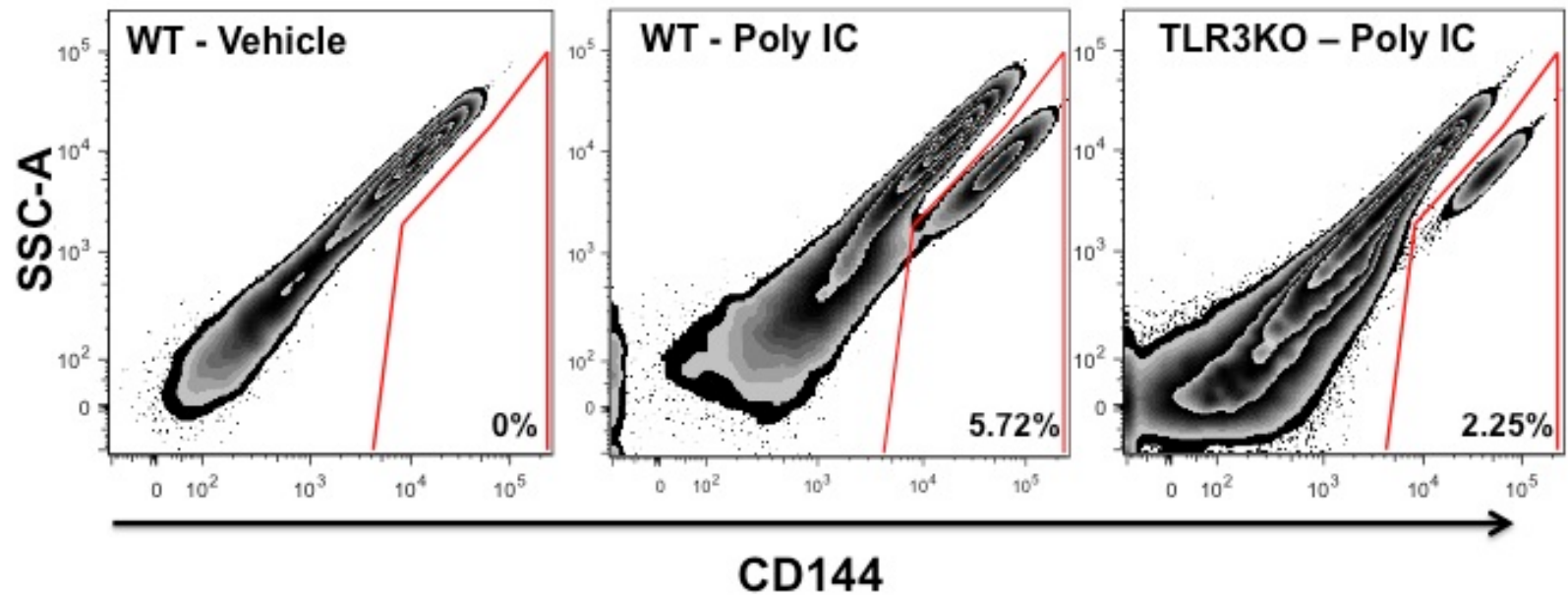
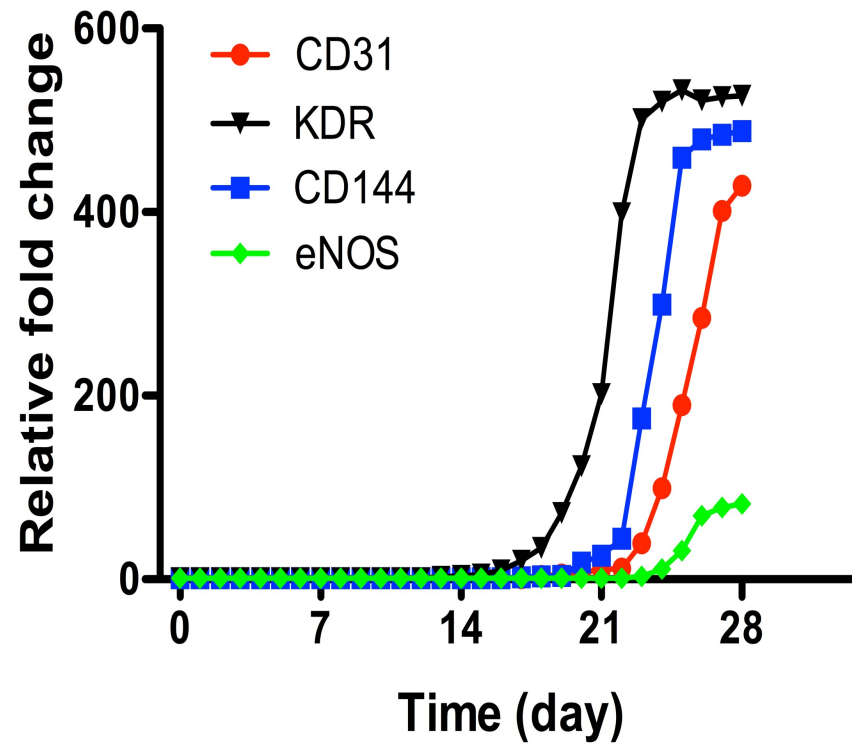


Fig. S8



Supplemental Table 1: List of 172 upregulated genes with known endothelial biology

Symbol	Description	FPKM_fibroblast	FPKM_IEC (1)	FPKM_IEC (2)	FPKM_HMVEC
ECSCR	endothelial cell surface expressed chemotaxis and apoptosis regulator	0.0	47.9	37.9	1082.8
ARHGGEF15	Rho guanine nucleotide exchange factor (GEF) 15	0.1	40.2	57.7	52.2
LMO2	LIM domain only 2 (rhombotin-like 1)	0.0	10.7	11.4	8.6
EFNA5	ephrin-A5	0.0	8.8	3.1	4.4
FABP5P1	fatty acid binding protein 5 pseudogene 1	0.0	8.3	8.2	7.5
SHE	Src homology 2 domain containing E	0.1	8.9	6.9	14.5
C20orf160	chromosome 20 open reading frame 160	0.0	4.9	4.7	9.5
APLN	apelin	1.0	120.0	111.9	173.9
FLT4	fms-related tyrosine kinase 4	0.0	4.9	6.1	46.2
EMCN	endomucin	0.7	81.3	80.3	59.6
KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	1.0	120.2	118.5	79.0
CLDN5	claudin 5	0.0	3.5	5.6	38.2
ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	0.5	41.5	37.6	92.3
HOXB3	homeobox B3	0.2	18.7	20.9	11.7
CXADR	coxsackie virus and adenovirus receptor	0.1	6.5	4.5	3.8
FGF12	fibroblast growth factor 12	0.3	20.5	23.9	3.1
NRARP	NOTCH-regulated ankyrin repeat protein	0.1	10.4	10.7	22.8
ESAM	endothelial cell adhesion molecule	0.4	32.6	43.6	100.8
TIE1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	2.0	149.3	147.1	392.5
INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	0.1	6.4	4.4	30.6
LIPG	lipase, endothelial	0.1	9.2	7.6	83.9
HOXD3	homeobox D3	0.2	12.3	11.7	6.0
CHD7	chromodomain helicase DNA binding protein 7	0.8	48.2	47.7	6.8
NOS3	nitric oxide synthase 3 (endothelial cell)	1.3	70.1	55.9	45.1
PLVAP	plasmalemma vesicle associated protein	0.2	8.8	8.8	14.1
THBD	thrombomodulin	0.5	23.1	20.5	41.1
THSD7A	thrombospondin, type I, domain containing 7A	0.1	5.4	5.5	3.8
GJA4	gap junction protein, alpha 4, 37kDa	0.2	7.7	7.1	35.4
AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	0.6	28.4	28.8	22.3
GRB14	growth factor receptor-bound protein 14	0.8	36.7	25.4	4.7
RASIP1	Ras interacting protein 1	0.5	21.7	18.8	44.6
TEK	TEK tyrosine kinase, endothelial	1.1	45.6	45.6	58.8
BMP6	bone morphogenetic protein 6	0.4	16.3	15.8	72.3
GBX2	gastrulation brain homeobox 2	0.2	8.7	8.5	9.2
SOX18	SRY (sex determining region Y)-box 18	0.2	6.6	7.2	47.3
TBX1	T-box 1	0.3	10.9	9.9	49.6
PDE4D	phosphodiesterase 4D, cAMP-specific	0.5	18.5	21.8	3.1
PKP2	plakophilin 2	0.3	9.0	8.3	12.3
PNP	purine nucleoside phosphorylase	3.6	119.4	119.7	202.3
SOX7	SRY (sex determining region Y)-box 7	0.3	8.8	7.6	40.3
CALCRL	calcitonin receptor-like	1.9	53.0	62.5	159.3
MMRN2	multimerin 2	0.4	10.9	13.0	60.5
E2F8	E2F transcription factor 8	0.3	7.7	9.1	3.7
ROBO4	roundabout, axon guidance receptor, homolog 4 (Drosophila)	1.0	24.6	21.3	187.7
PODXL	podocalyxin-like	14.5	351.6	363.6	270.7
CDH5	cadherin 5, type 2 (vascular endothelium)	0.8	19.1	20.8	315.8
ALPL	alkaline phosphatase, liver/bone/kidney	0.4	9.5	7.2	5.7
PDGFB	platelet-derived growth factor beta polypeptide	0.4	8.4	9.1	163.9
ANGPT2	angiopoietin 2	0.2	5.8	4.0	83.3
ANKRD1	ankyrin repeat domain 1 (cardiac muscle)	2.5	56.5	53.8	581.3
FGFR3	fibroblast growth factor receptor 3	1.5	35.3	32.6	5.6
HES1	hairy and enhancer of split 1, (Drosophila)	1.1	25.1	21.2	27.7
FABP5	fatty acid binding protein 5 (psoriasis-associated)	5.1	109.9	115.4	183.9
GRAP	GRB2-related adaptor protein	0.2	4.0	4.6	47.9
CASP10	caspase 10, apoptosis-related cysteine peptidase	0.8	15.9	17.0	15.1
LYL1	lymphoblastic leukemia derived sequence 1	0.4	7.4	7.6	31.0
EXOC3L1	exocyst complex component 3-like 1	1.1	20.2	16.1	11.1
JAG1	jagged 1	2.2	38.2	41.2	93.8
NRCAM	neuronal cell adhesion molecule	6.8	116.7	116.8	18.6
MDK	midkine (neurite growth-promoting factor 2)	37.0	620.2	603.2	333.2
PTPRB	protein tyrosine phosphatase, receptor type, B	2.5	41.5	41.3	43.5
TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	0.5	7.6	8.7	8.3
CCNB1	cyclin B1	10.5	168.0	179.1	67.1
NOTCH4	notch 4	0.5	7.3	3.7	22.1
F11R	F11 receptor	1.2	18.6	18.3	94.2
CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	0.3	4.3	4.2	47.2
CENPA	centromere protein A	1.4	19.2	17.9	8.4
SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	2.0	27.1	26.7	63.0
ICAM2	intercellular adhesion molecule 2	1.2	15.5	20.1	212.2
RAMP2	receptor (G protein-coupled) activity modifying protein 2	1.7	21.8	20.2	32.5
ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	1.5	18.6	19.1	6.2
ITGA6	integrin, alpha 6	14.0	173.8	167.9	115.4
TNFRSF21	tumor necrosis factor receptor superfamily, member 21	3.4	40.8	37.0	23.6
HEY1	hairy/enhancer-of-split related with YRPW motif 1	0.5	5.4	4.2	5.4

Symbol	Description	FPKM_fibroblast	FPKM_iEC (1)	FPKM_iEC (2)	FPKM_HMVEC
EZH2	enhancer of zeste homolog 2 (Drosophila)	2.4	28.5	23.0	6.9
LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	2.5	29.2	30.4	8.1
RAPGEF3	Rap guanine nucleotide exchange factor (GEF) 3	2.3	25.9	22.4	17.0
CD34	CD34 molecule	1.0	11.3	9.0	23.0
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	0.9	10.0	12.1	10.5
TBXA2R	thromboxane A2 receptor	1.1	11.6	10.6	3.7
BIRC5	baculoviral IAP repeat containing 5	3.3	36.1	32.8	13.9
CCNE2	cyclin E2	1.7	17.9	12.6	7.0
JAG2	jagged 2	0.3	3.3	5.6	43.7
HOXA3	homeobox A3	1.3	13.7	14.1	3.9
CCNF	cyclin F	1.1	10.9	11.4	5.7
STIL	SCL/TAL1 interrupting locus	1.1	10.5	11.0	4.0
EGFL7	EGF-like-domain, multiple 7	14.1	134.6	126.1	599.7
KDM8	lysine (K)-specific demethylase 8	0.8	6.7	4.4	3.9
ZFPM2	zinc finger protein, multitype 2	1.6	13.8	11.1	6.1
S1PR1	sphingosine-1-phosphate receptor 1	4.5	39.5	32.8	110.5
MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	10.7	90.3	86.3	34.7
KIF11	kinesin family member 11	2.2	18.6	18.3	5.9
NRP2	neuropilin 2	18.2	152.8	172.2	96.3
MKI67	antigen identified by monoclonal antibody Ki-67	3.7	31.2	36.8	17.1
FLI1	Friend leukemia virus integration 1	3.5	28.6	28.5	68.1
PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	0.8	6.6	6.4	22.8
EHD4	EH-domain containing 4	8.8	71.4	70.4	99.2
CLU	clusterin	40.0	321.9	299.9	246.2
RECQL4	RecQ protein-like 4	4.0	31.7	35.9	13.3
PLXNA2	plexin A2	1.5	11.7	7.3	74.8
HHEX	hematopoietically expressed homeobox	1.2	9.2	8.0	28.5
ARID3B	AT rich interactive domain 3B (BRIGHT-like)	1.4	10.3	9.8	3.4
JUP	junction plakoglobin	8.3	61.3	58.3	65.7
HIPK2	homeodomain interacting protein kinase 2	1.6	11.5	12.8	5.3
DUSP6	dual specificity phosphatase 6	29.1	213.9	195.9	108.7
PLAU	plasminogen activator, urokinase	14.4	103.0	103.6	62.0
FOXM1	forkhead box M1	4.7	33.5	33.1	12.6
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	21.8	150.7	147.8	70.7
MCAM	melanoma cell adhesion molecule	9.5	64.8	65.2	786.2
FES	feline sarcoma oncogene	3.0	20.0	22.9	20.4
NES	nestin	27.7	184.1	179.3	64.4
PLEKHG5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	5.0	33.1	32.1	21.7
LDLR	low density lipoprotein receptor	10.2	66.7	50.5	47.2
GIT1	G protein-coupled receptor kinase interacting ArfGAP 1	17.5	111.6	99.8	76.7
TK1	thymidine kinase 1, soluble	7.6	48.2	48.7	27.4
STEAP3	STEAP family member 3, metalloredutase	0.9	5.4	5.5	13.6
FURIN	furin (paired basic amino acid cleaving enzyme)	21.5	135.2	123.2	70.7
EPHB2	EPH receptor B2	1.1	7.0	4.8	19.1
MERTK	c-mer proto-oncogene tyrosine kinase	0.5	3.0	4.1	4.3
EPHB4	EPH receptor B4	14.6	88.3	80.8	106.3
FDPS	farnesyl diphosphate synthase	47.7	277.8	290.3	384.1
DCHS1	dachsous 1 (Drosophila)	3.2	18.4	17.9	17.5
TMEM231	transmembrane protein 231	2.4	13.9	12.1	5.5
ARAP3	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	5.0	27.8	26.4	28.9
HMGB2	high mobility group box 2	29.6	162.3	186.7	101.1
VASH1	vasohibin 1	4.7	25.5	29.0	14.1
PRKCH	protein kinase C, eta	0.9	5.0	6.4	46.2
FLNB	filamin B, beta	33.2	172.9	171.7	163.0
NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	1.1	5.4	4.8	7.0
SGK1	serum/glucocorticoid regulated kinase 1	32.9	155.8	187.5	203.7
SH3PXD2B	SH3 and PX domains 2B	4.9	23.0	31.2	15.1
NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase	1.5	6.9	7.3	8.4
HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	216.7	961.2	926.6	542.4
GOLM1	golgi membrane protein 1	19.5	85.9	82.0	69.8
RAC3	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	4.6	20.3	19.7	14.4
DHCR7	7-dehydrocholesterol reductase	16.3	71.7	74.0	69.9
ACVRL1	activin A receptor type II-like 1	6.5	28.6	26.9	153.2
HMGA1	high mobility group AT-hook 1	97.1	411.6	401.9	567.9
ADAM15	ADAM metallopeptidase domain 15	36.2	153.0	117.1	208.1
HOXA5	homeobox A5	3.0	12.6	11.6	13.4
SNAI1	snail homolog 1 (Drosophila)	3.4	14.1	14.4	17.9
RCE1	RCE1 homolog, prenyl protein protease (S. cerevisiae)	4.5	18.5	19.5	13.4
RGCC	regulator of cell cycle	4.3	17.5	15.4	101.1
TEAD2	TEA domain family member 2	10.6	43.4	43.3	26.2
PIK3CB	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit beta	4.7	18.7	13.6	17.0
DHCR24	24-dehydrocholesterol reductase	14.0	55.9	58.5	54.9
AKAP12	A kinase (PRKA) anchor protein 12	16.5	65.2	64.6	118.7
CD36	CD36 molecule (thrombospondin receptor)	3.9	15.3	15.5	49.8
MVK	mevalonate kinase	3.4	13.0	11.8	11.7
NOTCH1	notch 1	2.6	10.0	9.7	25.3

Symbol	Description	FPKM_fibroblast	FPKM_iEC (1)	FPKM_iEC (2)	FPKM_HMVEC
PLCG1	phospholipase C, gamma 1	25.5	92.5	87.5	80.0
TNFAIP3	tumor necrosis factor, alpha-induced protein 3	3.4	12.1	14.5	17.3
ABCA3	ATP-binding cassette, sub-family A (ABC1), member 3	1.9	6.6	7.7	12.4
LAMA5	laminin, alpha 5	9.1	31.8	26.7	86.4
E2F7	E2F transcription factor 7	1.7	5.9	5.3	9.3
POLG	polymerase (DNA directed), gamma	18.2	61.9	62.2	45.7
NSDHL	NAD(P) dependent steroid dehydrogenase-like	7.1	24.2	27.1	23.1
MKS1	Meckel syndrome, type 1	4.2	14.3	18.3	13.1
NTSE	5'-nucleotidase, ecto (CD73)	34.4	112.3	112.5	262.4
CSK	c-src tyrosine kinase	17.4	56.0	56.7	51.3
MAP1S	microtubule-associated protein 1S	6.0	19.1	19.1	20.9
SPTBN1	spectrin, beta, non-erythrocytic 1	26.6	85.3	86.7	78.5
WRN	Werner syndrome, RecQ helicase-like	4.2	13.3	12.5	11.6
EPHA2	EPH receptor A2	16.1	50.7	51.3	77.4
PGF	placental growth factor	4.7	14.4	17.1	59.9
EFNB1	ephrin-B1	13.8	41.5	40.4	44.3
PDE2A	phosphodiesterase 2A, cGMP-stimulated	1.5	4.6	6.2	45.1
USF1	upstream transcription factor 1	13.4	38.6	48.8	50.9
GATAD2A	GATA zinc finger domain containing 2A	19.2	54.8	57.8	46.3
PLD1	phospholipase D1, phosphatidylcholine-specific	4.6	12.6	15.3	36.0
COL4A5	collagen, type IV, alpha 5	5.4	14.3	14.9	51.6
CBFB	core-binding factor, beta subunit	24.4	64.0	78.9	57.2

Supplemental Table 2: Bioinformatic and Pathway Analysis of iECs

1085 iEC and HMVEC- high, EC up-regulated

Category	Name	P-value	# Genes in 1085
GO: Biological Process	mitotic cell cycle	1.65E-50	154
GO: Biological Process	M phase	4.38E-37	110
Coexpression Atlas	DevelopingKidney_e15.5_Endothelial cells_top1000	8.63E-32	139
GO: Cellular Component	chromosome	1.11E-23	98
GO: Cellular Component	microtubule cytoskeleton	2.27E-20	110
GO: Biological Process	blood vessel development	8.62E-11	63
GO: Biological Process	angiogenesis	1.21E-10	51
GO: Biological Process	S phase of mitotic cell cycle	1.44E-09	27
GO: Biological Process	circulatory system development	6.05E-08	76
GO: Biological Process	cholesterol biosynthetic process	1.04E-07	13
Mouse Phenotype	abnormal vascular development	1.37E-07	57
GO: Biological Process	sprouting angiogenesis	2.32E-06	12
GO: Biological Process	chromatin remodeling	3.01E-06	18
GO: Biological Process	hemopoiesis	3.07E-06	55
Mouse Phenotype	abnormal blood vessel morphology	3.57E-06	88
GO: Biological Process	endothelium development	6.06E-06	13
GO: Biological Process	cell junction organization	4.41E-05	24
Mouse Phenotype	abnormal artery development	6.45E-05	19
GO: Molecular Function	cytoskeletal protein binding	7.87E-05	56
Mouse Phenotype	abnormal vein development	3.37E-04	8
GO: Cellular Component	cell junction	3.94E-04	59
Mouse Phenotype	decreased angiogenesis	4.35E-04	13
Pathway	Angiogenesis	5.29E-04	21

1270 fibroblasts-high, EC down-regulated

Category	Name	P-value	# Genes in 1270
GO: Cellular Component	extracellular matrix	6.37E-27	87
GO: Biological Process	muscle structure development	3.05E-20	87
GO: Biological Process	extracellular structure organization	1.31E-16	48
GO: Biological Process	vasculature development	4.76E-16	80
GO: Biological Process	cell adhesion	1.80E-13	110
GO: Biological Process	biological adhesion	2.67E-13	110
Mouse Phenotype	muscle phenotype	4.61E-13	140
GO: Molecular Function	extracellular matrix structural constituent	7.45E-11	22
GO: Biological Process	angiogenesis	8.01E-10	52
GO: Molecular Function	growth factor binding	1.13E-09	25
GO: Molecular Function	fibronectin binding	5.68E-09	11
Human Phenotype	Aneurysm	1.10E-07	12
Pubmed	Transforming growth factor-fl signaling in myogenic cells regulates vascular morphogenesis, differentiation.	1.48E-07	12
Mouse Phenotype	abnormal blood vessel morphology	7.17E-07	107
Pathway	Focal Adhesion	1.36E-06	29
Pubmed	GPR124, an orphan G protein-coupled receptor, is required for CNS-specific vascularization and establishment of	1.91E-06	17
Pathway	Genes involved in Regulation of Insulin-like Growth Factor (IGF) Activity by Insulin-like Growth Factor Binding Pro	2.11E-06	8
Pathway	HIF-1-alpha transcription factor network	1.94E-05	14
Pathway	Genes involved in Smooth Muscle Contraction	4.42E-05	8
GO: Cellular Component	Golgi apparatus	1.02E-04	94
Pathway	Angiogenesis	2.87E-04	21
GO: Cellular Component	anchoring junction	7.34E-04	24