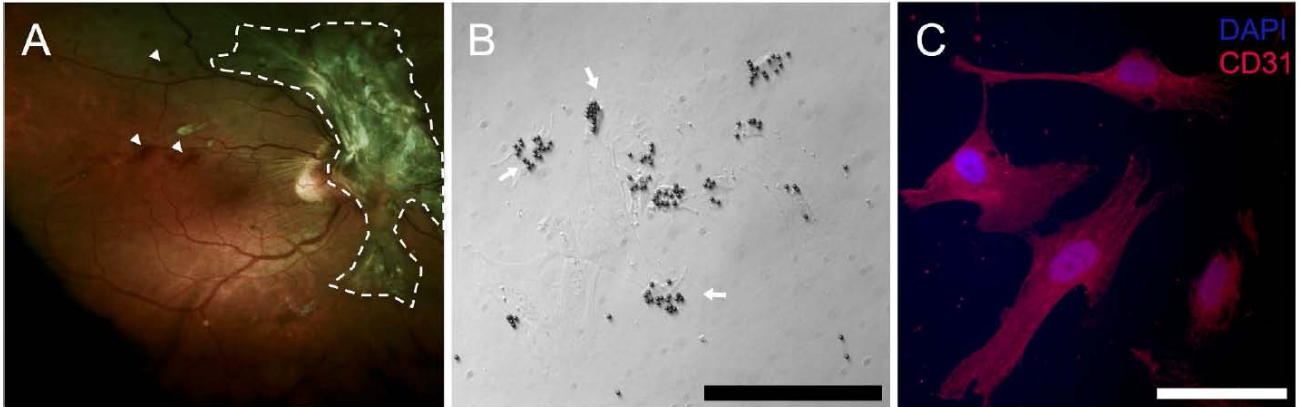


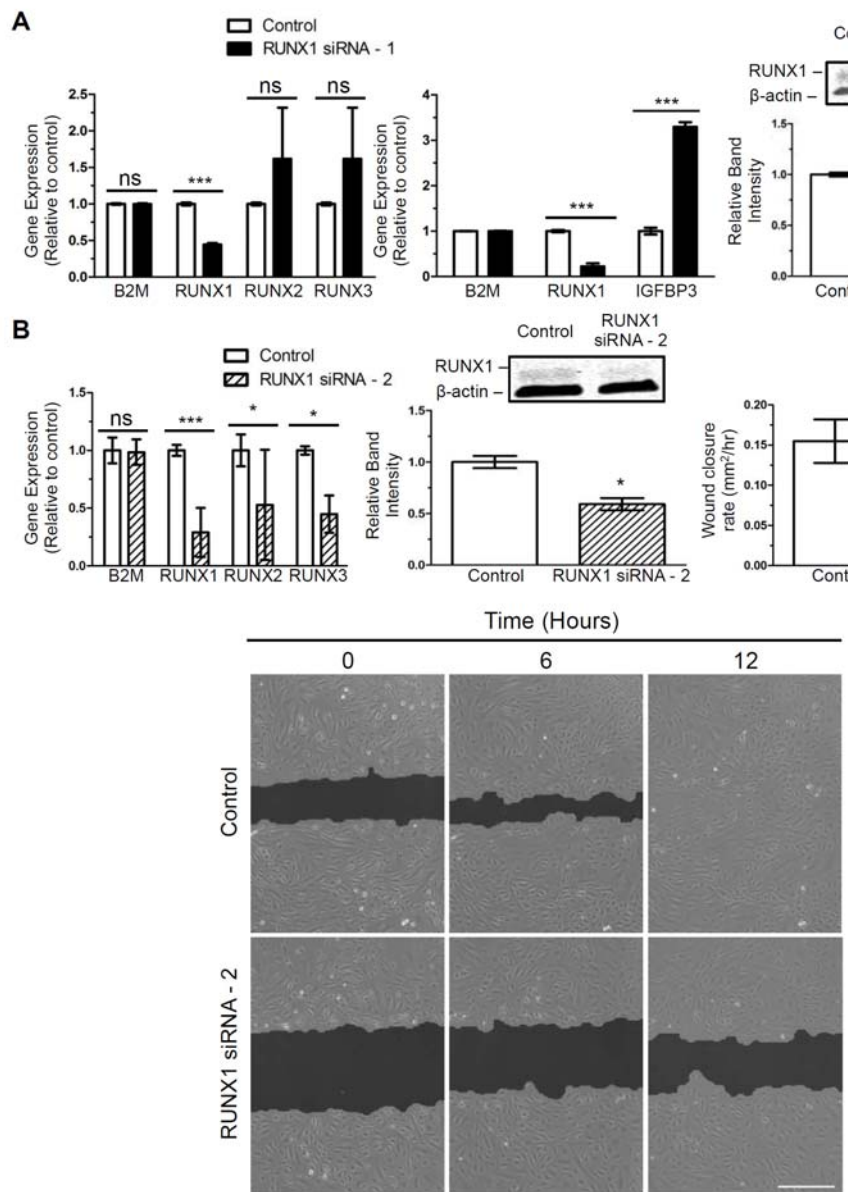
SUPPLEMENTARY DATA

Supplementary Figure 1. Isolation and culture of endothelial cells from surgical specimens of FVM. **(A)** Representative pre-surgical fundus photograph of a right eye exhibiting a FVM encroaching on the optic nerve (dashed line) causing tractional retinal detachment with blot hemorrhages throughout retina (arrow heads). **(B)** Magnetic beads (arrows) allow for separation and culturing of enriched cell populations from surgical specimens (scale bar = 100 μm). **(C)** Cultures of isolated cells stained positively for CD31 representing a successfully isolated enriched population (scale bar = 40 μm).



SUPPLEMENTARY DATA

Supplementary Figure 2. Efficient siRNA knockdown of RUNX1 expression and function demonstrated by qRT-PCR, Western Blot, and scratch assay. **(A)** RUNX1 siRNA induced a 60% reduction of RUNX1 expression measured by qRT-PCR 48 hrs post-transfection whereas expression of RUNX2 and RUNX3, the two other mammalian RUNX orthologues, showed no significant changes, indicating specificity of our siRNA. Functional inhibition of Runx1 signaling was demonstrated by a 330% increase in insulin-like growth factor binding protein-3 (IGFBP3) RNA expression level, a known target of RUNX1 inhibition. Western blot demonstrated similar reduction in protein levels. **(B)** siRNA-2's effect on RUNX1 was validated by qRT-PCR and western blot, demonstrating a similar reduction in both RNA and protein. Scratch assay demonstrates functional inhibition of RUNX1 by siRNA-2. ns: not significant, * $p < 0.05$, *** $p < 0.001$



SUPPLEMENTARY DATA

Supplementary Table 1. Demographic data for control post-mortem retina and FVM from PDR patients used for RNA-sequencing. VH: vitreous hemorrhage, TRD: tractional retinal detachment, RRD: rhegmatogenous retinal detachment.

Control Retina Samples				
Age	Sex	Last known HbA1c % (mmol/mol)		Cause of death
25	M	Unknown		Metastatic melanoma
54	M	5.3 (34)		Colectomy c/b sepsis
77	M	Unknown		Respiratory failure
87	F	5.8 (40)		Right temporoparietal hemorrhage
Fibrovascular Membrane Samples				
Age	Sex	Type of Diabetes Mellitus	Last known HbA1c % (mmol/mol)	Surgical Indication
29	F	1	Unknown	VH/TRD
51	F	2	6.5 (48)	VH/TRD/RRD
44	M	1	7.9 (63)	TRD/RRD
71	M	1	Unknown	TRD/RRD
38	F	2	6.3 (45)	TRD
40	F	2	14 (130)	VH/TRD
49	M	2	8.0 (64)	TRD/RRD
48	F	2	7.2 (55)	TRD/RRD

SUPPLEMENTARY DATA

Supplementary Table 2. Primer sequences used for qRT-PCR analysis. siRNA sequences are listed at the bottom. Previously published sequences are denoted by an asterisk (*).

SUPPLEMENTARY DATA

Gene/Symbol	Array	Alias (GeneCards.org)	Forward Primer Sequence	Reverse primer Sequence
AIF1*	Signal, Wound, Inflammation, Proliferation, Phosphoprotein	Allograft Inflammatory Factor 1	GATGATGCTGGGCAAGAGAT	CCTTCAATAGGGCAACTC
AMPD3	Phosphoprotein	Adenosine Monophosphate Deaminase 3	AAAGGAAGCCAGGAGGAGG	GGGACCAATCATCTTGA
AP02*	Signal, Apoptosis, Proliferation, Phosphoprotein	Apolipoprotein E	TTCTGTGGGCTGGCTGTG	TACACTGGAGGCGCTGTG
ARLAC	Metabolism	ADP-Ribosylation Factor-Like 4C	CGCTCCCTGCATATGCTCAT	TTACAGCACTGTTGAAGTTGA
ATPBAP2*	Signal, Phosphoprotein	ATPase, H+ Transporting, Lysosomal Accessory Protein 2	AGGGATGGAAACAATCGGCTTA	TACCATATCACTTATCTCCAAAGGGTA
AXL	Signal, Phosphoprotein	AXL Receptor Tyrosine Kinase	CCGTGGCCTACTGGCT	CCTTGGGTTATGGGCTC
B2M	Signal	Beta-2-Microglobulin	ACTGAATCCCCCCTACTGA	CCTCATGATGCTCTTACA
BASP1*	Phosphoprotein	Brain Abundant, Membrane Attached Signal Protein 1	CGAGCCCACTAGTGTGCT	GAGAGAATGTTGCTACTCCCAA
BGN*	Signal	Biglycan	CTGGCATCCCCAAGACCTC	GCTCCGTTCTGATCATCC
BMF*	Apoptosis	Bcl2 Modifying Factor	GACCAACCCGGGAGCTTG	GAAAGCCAGGGCCACAGCAG
CD10r10	Signal	Chromosome 10 Open Reading Frame 10	TGCCCAATCTGGGAGAC	AGACTCAGTAGTCTCCAG
CLL2	Signal, Wound, Apoptosis, Inflammation	Chemokine (C-C Motif) Ligand 2	GCCTCCAGATGAAAGTCTC	AGSTGACTGGGATTGAT
CLL20	Signal, Wound, Inflammation	Chemokine (C-C Motif) Ligand 20	GTGCTGCTACTCCACTGTG	CGTGTGAAGCCCAAAATA
CNND1	Proliferation, Phosphoprotein	Cyclin D1	GCTGGAAGTGGAAACATC	CCTCTCTGACACATTGAA
CD14	Signal, Wound, Inflammation	CD14 Molecule	ACGCCAGAACCTGTGAGC	GATGGATCTCCACTCTACTG
CD300LF	Signal, Phosphoprotein	CD300 Molecule-Like Family Member F	GAAACCCACTACTGCACAT	CTGATGGTGCTGATTCGGTG
CD44*	Signal, Wound, Apoptosis, Inflammation, Phosphoprotein	CD44 Molecule (Indian Blood Group)	CGAACCTCTGAGCAAGTTT	CGAACCTCTGAGCAAGTTT
CD83	Signal	CD83 Molecule	CTCCGAAGATGGGACTGTC	TCCATCTCTCTCAACC
CDPC1	Signal, Phosphoprotein	CUB Domain Containing Protein 1	CTGAAGTGGGGTCTCTAT	GGCAGAGCAATCTCAAAGC
CDH13	Signal, Apoptosis, Angiogenesis, Proliferation, Phosphoprotein	Cadherin 13	AGTGTTCATATCAATCAGCAG	CGAGACTCATAGGTAGCTT
CECR1	Signal	Cat Eye Syndrome Chromosome Region, Candidate 1	CAGAGAGCATCTGGCTTCAA	TCATGGTGTCTCCACTGAG
CHMP1B	Cell Cycle	Charged Multivesicular Body Protein 1B	AAAGACTGTAGTAGGAGTCCCA	TCATCTCTGCACTCATCT
CHST11	Apoptosis, Proliferation	Carbohydrate (Chondroitin 4) Sulfotransferase 11	TCCTTTGGTGTGGACTCT	CGAGGACAGCAAGTGTGAG
COLEC12	Phosphoprotein	Collectin Sub-Family Member 12	AGAGGAGGAGGAGGTGCAAT	TGATAGAAACTCAGTCCCA
CREG1	Cell Cycle	Cellular Repressor Of E1A-Induced Genes 1	GGGCTGCCATTTTCTACTGC	CAAAGTCATGCTCAGTGTGAT
CST3	Signal	Cystatin C	CGAGCAACGACATGTACCAC	CAGCTCCAGTCCAGAGAT
CTS8	Signal, Wound, Apoptosis	Cathepsin B	ACAACGTGGACATGAGTACT	TGGTAAACATAACTCTGGGG
CTS5	Signal	Cathepsin D	AGCCCTCAGCTCTCTG	CGATGGCACTGAACTTGT
CTL	Metabolism	Cathepsin L	GGCGTGACTGGTGTGAG	AAAGCGAGCAAGGTGAGTG
CTSS	Signal	Cathepsin S	CTTGTGGTGGCTATGGTGAT	CCTTATTTCTGCTCACCG
CXCL16	Signal	Chemokine (C-X-C Motif) Ligand 16	GTGTGGGAGGCAACAGG	CAATCCCCCGAGTAGGAT
CXCL2	Signal, Wound, Inflammation	Chemokine (C-X-C Motif) Ligand 2	GGCGAGAAGCTTGTCTCAA	GCTCTCTCTCTTGGT
CXCR4*	Wound, Angiogenesis, Inflammation, Phosphoprotein	Chemokine (C-X-C Motif) Receptor 4	CCAGTACCAGCCGACT	ATAGTCCCTGAGCCATTT
DBI	Phosphoprotein	Diazepam Binding Inhibitor (GABA Receptor Modulator, Acyl-CoA Binding Protein)	TGGCCACTAAACAAGCA	TCCCTTCAGCTTACTCAG
DHR83	Stress response	Dehydrogenase/Reductase (SDR Family) Member 3	TTTCTGACCATGTGCTGG	TTTGGATGTGACAGTGTGATG
EGR2	Phosphoprotein	Early Growth Response 2	TTGACCAAGTGAAGCGAGTG	AGCAAACTGTGGGATATG
EPB41L3	Cell Structure	Erythrocyte Membrane Protein Band 4.1-Like 3	GAGCTAGTCCCCAGC	CCTTGGATCCGAGTCTGAT
EZR	Phosphoprotein	Ezrin	ACCAATCAATGTCGAGATACC	GCCATGATCTTACCACTGTA
FAM49A	Signal	Family With Sequence Similarity 49, Member A	AGCTAAGCTGGTCTATCCCA	GACTTGGAGAGTGTTC
FAT1	Signal, Phosphoprotein	FAT Atypical Cadherin 1	CATCTGTCAAGATGGTGTGT	TCGAGAGATGTACTCTTCAAGTT
FSCN1	Phosphoprotein	Fascin Actin-Bundling Protein 1	CAAGGAGAGCTCTTGTGCT	TGATGTGGCAAGAGGTCAT
G0S2	Phosphoprotein	G0/G1 Switch 2	CTGACCGTCCCAACTG	GCTGACAGCTTTCATCT
GAL3ST4	Signal	Galactose-3-O-Sulfotransferase 4	TCCACATCTCTGTCCACC	GGTCTGGACATGAGAAA
GPR183	Phosphoprotein	G Protein-Coupled Receptor 183	ACTGGAAGATCGAGATGECT	AAATGAGCGGTAATCACTCAGG
GPX1*	Wound, Apoptosis, Angiogenesis, Proliferation	Glutathione Peroxidase 1	CAACAGT1GGGCACTAGR	GTTCACCTGCACATCTCG
GRN	Signal, Proliferation	Granulin	AGGAGAAGCTACCCAGGA	GGCAGAGCATAGCCACTGCT
GTF2B	Phosphoprotein	General Transcription Factor IIB	GCCGGTATGATGATCTGCC	GTCTAGTGGTAAAGTCCGC
HES1	Signal	Hes Family BHLH Transcription Factor 1	ACGTCGAGGGCGTAAATAC	GGGATAGCTGAGGCAITTA
HIF3A	Stress response	Hypoxia Inducible Factor 3, Alpha Subunit	CCAGTCCGGAGATATGCTC	GAATGGTCTGCGAGAGTGT
HPR1	Metabolism	Hypoxanthine Phosphoribosyltransferase 1	CTGGCTCTGGTATGATGAT	AGAGCTCTGCTGCTCCATA
HTRA1*	Signal	HTRA Serine Peptidase 1	TGGATCTCTTGTGATCTC	TTCTTGG TGATGGCTTTC
IDH1	Metabolism	Isocitrate Dehydrogenase 1 (NADP+ Soluble)	GTCTCATGCTATGGGGAT	CTTTTGGTTCCTGCACTTG
IF130	Signal, Proliferation, Phosphoprotein	Interferon, Gamma-Inducible Protein 30	GCTAGCTTCTGACCATTG	CACTGATAGTGTGGCCAC
IRAK2	Wound, Inflammation	Interleukin-1 Receptor-Associated Kinase 2	CTGCCACCCAATGCTTACC	AGGGAACCAATGCACTGATG
IRS2	Proliferation, Phosphoprotein	Insulin Receptor Substrate 2	ACCTACGCGAGCATGACT	CATCTGGTATAAGCCAGGA
LAPTM5	Hematopoiesis	Lysosomal Protein Transmembrane 5	AGACTGCTGCTGCTCAAT	CATCGGCCACTCTACTAGG
LGAL51	Signal	Lectin, Galactoside-Binding, Soluble, 1	TCCCGAGCAACTGAATCTC	GACGAGAGCTTACAGGCTCA
LGAL51BP	Signal, Apoptosis, Phosphoprotein	Lectin, Galactoside-Binding, Soluble, 3 Binding Protein	GAGGAGGCTCCACAGG	AGCAGCCACCCACAGAG
LGMIN	Signal	Ligumain	TGAAAGATGGAGCAACAGC	TTGCGGTGATGATCTGGTA
LIFPL2	Signal	Lipoma HMGIC Fusion Partner-Like 2	TCTCATGCTCTGTGGGCTG	GTCTATGGCTCTTGGGAC
LST1	Proliferation, Phosphoprotein	Leukocyte Specific Transcript 1	CTGCGCAGTTTGGAGTCTGT	TCCTTGGCTTTTATGGGAA
LTBP2	Signal, Phosphoprotein	Latent Transforming Growth Factor Beta Binding Protein 2	ACCTTGGCCAGAGCACAG	TGGAAAGGCGGGGCTGCT
LYN	Wound, Inflammation, Proliferation, Phosphoprotein	LYN Proto-Oncogene, Src Family Tyrosine Kinase	CTGAATCAAGTCAAGCTGG	TCCATGCTCAACTCAAGTGT
MAFB	Hematopoiesis	V-Maf Avian Musculoaponeurotic Fibrosarcoma Oncogene Homolog B	CATAGAGAAGCTGGCCAGCA	ATGCCCAGCAATTTTCTT
MMP19	Signal, Angiogenesis	Matrix Metalloproteinase 19	GCCTGTTGTGGCTAGAG	ATGCGAAAGTCAAGTGTCT
MMP2*	Signal, Phosphoprotein	Matrix Metalloproteinase 2	CAGACTGCTGGAATGCCATC	GAGCTGACTCCAGTGGATT
NEK6	Phosphoprotein	NIMA-Related Kinase 6	CAGACTGTGTCAAGGAGTGC	ATGTTCAAGTGTGTTCTTCC
NFKB2	Wound, Inflammation	Nuclear Factor Of Kappa Light Polypeptide Gene Enhancer In B-Cells Inhibitor, Zeta	ACACCCCAACCACTCTGG	CGCAAAACTGTGATCTTGAGCC
NIN1	Wound	Ninjuria 1	ACCGAGATGAGTACAGCA	GGCTCTCTGCTGGGTAT
NPC2	Signal	Niemann-Pick Disease, Type 2	AGCTACATCTGCTGCTGG	TGGGCTCAATCACTTCT
NRA2*	Apoptosis, Phosphoprotein	Nuclear Receptor Subfamily 4, Group A, Member 2	GCATATTTCTGCTTCTC	GGTAAGTGTCCAGAAAG
ODC1	Proliferation, Phosphoprotein	Ornithine Decarboxylase 1	GGCTGCACTCAGGCTC	CCTTGGAAACAGCATGAC
OLFML2B	Signal	Olfactomedin-Like 2B	CCCCAAGAAGAAGATGACA	CCATATGTTCTGGGTGTC
PDGFA*	Signal, Wound, Angiogenesis, Proliferation	Platelet-Derived Growth Factor Alpha Polypeptide	TCCACGCCTCAAGCATGTG	CGTAATGACCCCTCGGCTCT
PHLDA1	Apoptosis	Pleckstrin Homology-Like Domain, Family A, Member 1	CTCAACTCTGCTGAAAGG	TGTTTGGTCTTATGCTTCA
PIM3	Apoptosis, Phosphoprotein	Pim-3 Proto-Oncogene, Serine/Threonine Kinase	AAGGACGAAATCTGCTGTGG	CGAAGTGGTGTAGCCCTG
PLAU	Signal, Wound, Angiogenesis, Proliferation, Phosphoprotein	Plasminogen Activator, Urokinase	GGGAATGGTCACTTTTACCAG	GGGATGGTGTAGTGTGCTG
PLAUR	Signal, Wound	Plasminogen Activator, Urokinase Receptor	AGCTTACCGAGTGTGTG	AAATGATCTGAGTAAAGG
PLD3	Signal	Phospholipase D Family, Member 3	GGAGATGCTGCTCAAGTGA	CCACTTGGATAGACTCTCA
PMP22	Proliferation	Peripheral Myelin Protein 22	TCAAGAAATGCCACACTG	GCTGAAGATGTGCACAGGA
PIB	Signal	Peptidylprolyl Isomerase B (Cyclophilin B)	AGGACTCATGATCAGGG	TGAAGTCTCATCGGGAGG
PIPF	Apoptosis	Peptidylprolyl Isomerase F	ACAGGGTATCCCTTCTCTC	AAAGTCTCTGCAAGAAAG
PRNP	Signal, Apoptosis, Phosphoprotein	Prion Protein	CAGACTGGTCAATACACA	CTCCATCTTAAGTCGGCTC
RCC2	Phosphoprotein	Regulator of Chromosome Condensation 2	AAGGAGCGGCTCAACTTGA	GCTTCTGTTIAGGCCTTCT
REL	Phosphoprotein	V-Rel Avian Reticuloendotheliosis Viral Oncogene Homolog	GGAGAGGGAAATCGGTTTAA	GAAGAGGATGTCTCGTGTGG
RGS1	Signal	Regulator of G-Protein Signaling 1	GGAAAACTTCTGCCAACC	TAGTCTTCAAGCCAGCCA
RHDG	Proliferation	Ras Homolog Family Member G	ACGATGCAAGATCAAGTG	TTTGGGAAAGCTTGTGTTG
RILP	Signal	Rab Interacting Lysosomal Protein-Like 2	AGCTGTATGATCTCTACTG	ACGGCAGCACTTGTGATG
RUNX1*	Phosphoprotein	Runt-Related Transcription Factor 1	TCCCAAAACCACCCGCAAGT	CGCTGGAAAAGGCAAGG
RUNX2	Phosphoprotein	Runt-Related Transcription Factor 2	ACCATGGTGGAGATCATCGCC	TCCCATGTGACTTCCGAGGG
RUNX3	Phosphoprotein	Runt-Related Transcription Factor 3	AGG CAA TGA CGA GAA CTA CTC	TGC GGG TTG GTG AAC ACA GT
SAMS1	Phosphoprotein	SAM Domain, SH3 Domain And Nuclear Localization Signals 1	TGCTCAAGAGAAGCACTCC	TTATTTGAAAACAGCATGAA
SCD	Phosphoprotein	Stearoyl-CoA Desaturase (Delta-9-Desaturase)	TTCTACTGCAAGTCTACTACC	CCGAGCTTGTAGAGCCGCT
SDC4	Signal, Phosphoprotein	Syndecan 4	TCCCAACGAACCAGAA	CTTGTGGACATCACTACC
SH2B3	Phosphoprotein	SH2B Adaptor Protein 3	CTGGAGCTCTCCAGCCA	GTGTGACGATCTTCAAGCC
SMS	Phosphoprotein	Spermine Synthase	CCTCACTATGGCAGCAGCA	TCTTGGAAAATGGACTGGG
THBS1	Signal, Wound, Apoptosis, Angiogenesis, Inflammation, Proliferation	Thrombospondin 1	CAATGCTCAAGTCTCTGATG	CACAGCTGTGAAACAGGAGG
THY1*	Signal, Angiogenesis	Thy-1 Cell Surface Antigen	TCAGAAATGGCTTTTCCA	TCTCAATGAGTCCATAGCT
TNFAIP2	Angiogenesis, Phosphoprotein	Tumor Necrosis Factor, Alpha-Induced Protein 2	CACCTACATGCTGCTGCT	CCCATCTCTGCACTCAGC
TNFAIP3	Apoptosis	Tumor Necrosis Factor, Alpha-Induced Protein 3	TTTCTCTAGTTCGGGAGAT	ACTTCTGACCACTTGTGATT
TTYH2	Phosphoprotein	Tweety Family Member 2	CCCTGCTCCGAGTACATGA	CTCCCGAATGAGGCACTG
UNC93B1	Phosphoprotein	Unc-93 Homolog B1 (C. Elegans)	TTTTTGAAGCAAGTGTGATGT	GGCAACAAGCTGTAGTAGC
VAMP8	Phosphoprotein	Vesicle-Associated Membrane Protein 8	ACTTGGAACTCTCCGAC	CTTCCCAAGAAATTCGAG
ZSWIM6	Signal	Zinc Finger, SWIM-Type Containing 6	AAGCGGCTGCTGAGACAC	GCTCCGATGTGATCTCAGGT
RUNX1				
siRNA1	small interfering RNA	hs.R1.RUNX1.13.3	CCUUUACUUGUUAUCAAACAAGUGA	UCACUUGUUGUUAUCAAACAAGGGA
RUNX1				
siRNA2	small interfering RNA	HSC.RNAI.N001001890.12.1	ACUAGAUGAUCAGACCAAGCCCGG	CCCGGUGUUGUGUUAUCAAACAAGGGA
Control siRNA	small interfering RNA	Negative Control 1: DS NC1		

SUPPLEMENTARY DATA

Supplementary Table 3. RNA-sequencing of isolated CD31+ cells. Both control human retinal endothelial cells and CD31+ C-FVM express characteristic vascular endothelial cell markers. Differences in expression levels do not meet criteria for significance.

	Gene Symbol				
	CD93	CD31	KLF4	ESAM	VEGFR1
Ctrl 1	0.75	0.41	0.07	0.14	1.36
Ctrl 2	2.17	3.26	1.09	1.41	32.83
Ctrl 3	59.7	47.37	2.93	20.18	257.23
Ctrl 4	6.28	5.58	0.93	3.95	39.75
FVM 1	2.37	4.92	0.24	1.46	2.61
FVM 2	203.57	52.74	44.98	51.23	91
FVM 3	78.48	15.94	30.78	0.58	88.99
FVM 4	103.42	156.32	31.79	36.96	38.15
FVM 5	304.64	93.71	73.43	59.36	189.6
FVM 6	164.94	50.44	33.49	19.27	63.13
FVM 7	423.9	116.12	57.25	101.58	298.19
FVM 8	313.39	76.8	27.15	55.27	136.05

SUPPLEMENTARY DATA

Supplementary Table 4. Gene set enrichment analysis of the 200 differentially expressed genes in FVMs. Pathways that met statistical significance are listed with the relevant genes. Both up- and downregulated genes are pooled for the analysis and percentages indicate the number of genes from the list of 200 that were associated with the ontology term.

Term	%	Genes	Fold Enrichment	PValue	Benjamini	FDR
GO:0009611 "response to wounding"	22.11	CSAR1, TNF, CCL2, AIF1, C3, PDGFA, FXA1, CXCL2, COL3A1, TLR2, NIN1, ITGB2, C1QC, IL10, CD97, GPX1, CD44, CCL20, CXCR4, HMOX1, IL1B, C2, THBS1, BAGALT1, IRAK2, PTPN6, NFKB1Z, CEBPB, LYN, OLR1, PDPN, IL1RN, LYZ, CCL41, CD163, C1QA, C1QB, NUPR1, VCAN, CTSS, VSG4, PLAU, CD14	6.06348502	1.66E-23	3.26E-20	2.85E-20
GO:0006954 "inflammatory response"	17.09	CSAR1, TNF, CCL2, AIF1, C3, CXCL2, TLR2, ITGB2, C1QC, IL10, CD97, CD44, CCL20, CXCR4, HMOX1, IL1B, C2, THBS1, BAGALT1, IRAK2, NFKB1Z, CEBPB, LYN, OLR1, PDPN, IL1RN, LYZ, CCL41, CD163, C1QA, C1QB, NUPR1, VCAN, CTSS, VSG4, PLAU, CD14	8.324923077	4.76E-21	4.67E-18	8.17E-18
GO:0006952 "defense response"	22.11	CSAR1, CCL2, TNF, AIF1, C3, CXCL2, TLR2, ITGB2, C1QC, CD74, IL10, CD97, LGALS3BP, CD44, CCL20, CXCR4, HMOX1, IL1B, C2, THBS1, TYROBP, BAGALT1, IRAK2, NFKB1Z, CSAR1, CEBPB, LYN, OLR1, PDPN, IL1RN, LYZ, CST3, CCL41, COLEC12, CD163, C1QA, C1QB, IL1R2, CD83, NUPR1, CXCL16, VSG4, CD14, HLA-DRA	5.693275945	5.57E-21	3.64E-18	9.55E-18
GO:0006955 "immune response"	21.61	GPR183, CCL2, TNF, HLA-DRA, C3, CXCL2, TLR2, C1QC, CD74, IL10, CD97, CCL20, CXCR4, FCER1G, IL1B, CD4, C2, HLA-DOA, THBS1, LAIR1, CSAR1, CEBPB, LYN, OLR1, CMKLR1, IL1RN, CCL41, COLEC12, GEM, CTSS, HLA-DQA2, C1QA, C1QB, IL1R2, CD83, RGS1, CXCL16, IRF8, CD300F, VSG4, LCP1, CD14, HLA-DRA	4.959113384	2.94E-18	1.44E-15	5.05E-15
GO:0002684 "positive regulation of immune system process"	10.55	IRAK2, CSAR1, LYN, C3, TLR2, C1QC, CD74, THY1, C1QA, CD83, C1QB, CD17, IL1B, FCER1G, CD4, C2, THBS1, VSG4, SASH3, SYK, HLA-DRA	7.021453287	1.64E-11	6.44E-09	2.82E-08
GO:0001944 "vasculature development"	10.55	BAGALT1, PDPN, PDGFA, COL3A1, TLR2, IL10, AXL1, CD44, APOE, HMOX1, IL1B, IDH1, CD4, THBS1, IRAK2, IRS2, EGR2, LYN, IL1RN, NRAA2, FBP1, TNFAIP2, PLAU	6.657792246	4.32E-11	1.41E-08	7.41E-08
GO:0006935 "chemotaxis"	8.54	CSAR1, CCL2, CSAR1, CMKLR1, PDGFA, CXCL2, CCL41, ITGB2, IL10, PLAU, CCL20, CXCR4, CXCL16, IL1B, CMTM3, PLAU, SYK	8.455	1.48E-10	4.14E-08	2.53E-07
GO:0042330 "taxis"	8.54	CSAR1, CCL2, CSAR1, CMKLR1, PDGFA, CXCL2, CCL41, ITGB2, IL10, PLAU, CCL20, CXCR4, CXCL16, IL1B, CMTM3, PLAU, SYK	8.455	1.48E-10	4.14E-08	2.53E-07
GO:0001568 "blood vessel development"	10.05	BAGALT1, PDGFA, COL3A1, MMP19, COL15A1, MMP2, THY1, CITED2, CDH13, GPX1, BGN, CD44, CXCR4, APOE, HMOX1, IL1B, COL1A1, THBS1, TNFAIP2, PLAU	6.496038415	2.17E-10	5.33E-08	3.73E-07
GO:0050778 "positive regulation of immune response"	8.04	IRAK2, CSAR1, LYN, C3, TLR2, C1QC, THY1, C1QA, C1QB, IL1B, FCER1G, CD4, VSG4, SASH3, SYK, HLA-DRA	8.780851927	3.52E-10	7.67E-08	6.04E-07
GO:0048584 "positive regulation of response to stimulus"	9.55	IRAK2, CSAR1, TNF, LYN, C3, TLR2, C1QC, THY1, C1QA, CDH13, C1QB, IL1B, FCER1G, CD4, THBS1, VSG4, SASH3, SYK, HLA-DRA	6.406580259	8.77E-10	1.72E-07	1.50E-06
GO:0010033 "response to organic substance"	15.38	TNF, CCL2, GPR2, PDGFA, COL3A1, TLR2, IL10, AXL1, CD44, APOE, HMOX1, IL1B, IDH1, CD4, THBS1, IRAK2, IRS2, EGR2, LYN, IL1RN, NRAA2, FBP1, COLEC12, NRAA3, C1QB, CDH13, CD83, CDND1, CXCL6, COL1A1, CD14	3.421457217	5.06E-09	9.02E-07	8.88E-06
GO:0001817 "regulation of cytokine production"	8.04	TNF, CEBPB, ATP6AP2, TLR2, IL10, CD83, REL, HMOX1, IL1B, FCER1G, CD4, VSG4, THBS1, CD14, SASH3, SYK	7.03438414	7.74E-09	1.27E-06	1.33E-05
GO:0002253 "activation of immune response"	6.03	C1QA, IRAK2, C1QB, CSAR1, LYN, C3, TLR2, C1QC, THY1, C1QA, CDH13, C1QB, IL1B, FCER1G, CD4, THBS1, VSG4, SASH3, SYK, HLA-DRA	10.15869837	2.35E-08	3.55E-06	4.04E-05
GO:0002326 "acute inflammatory response"	6.03	C1QA, BAGALT1, C1QB, CEBPB, NUPR1, LYN, C3, IL1B, C2, VSG4, C1QC, CD163	9.138576233	3.86E-08	5.13E-06	6.27E-05
GO:0050885 "regulation of cell activation"	7.54	PDPN, PDGFA, CD74, IL10, THY1, CD83, APOE, HMOX1, IL1B, CD4, VSG4, HLA-DOA, THBS1, SASH3, SYK	6.820840336	3.91E-08	5.12E-06	6.71E-05
GO:0007626 "locomotory behavior"	9.05	CSAR1, CCL2, CSAR1, CMKLR1, PDGFA, CXCL2, CCL41, ITGB2, IL10, PLAU, CCL20, CXCR4, CXCL16, IL1B, CMTM3, PLAU, SYK	5.227651353	5.75E-08	7.05E-06	9.86E-05
GO:0048514 "blood vessel morphogenesis"	8.04	BAGALT1, PDGFA, MMP19, COL15A1, THY1, CITED2, CDH13, GPX1, BGN, CXCR4, APOE, HMOX1, IL1B, THBS1, TNFAIP2, PLAU	6.034234737	6.10E-08	7.04E-06	1.05E-04
GO:0001525 "angiogenesis"	6.53	BAGALT1, GPR1, CDH13, CXCR4, PDGFA, HMOX1, MMP19, COL15A1, THBS1, TNFAIP2, PLAU, THY1	5.980825319	3.38E-07	3.57E-05	5.62E-04
GO:0043127 "regulation of cell proliferation"	14.57	TNF, CCL2, AIF1, PDGFA, IFI16, IL10, GPX1, APOE, HMOX1, CHST11, IL1B, THBS1, GPNMB, RHOG, SYK, BAGALT1, ODC1, PTPN6, IRS2, LYN, SPARC, CDH13, CCND1, NUPR1, GRN, VSG4, PMP22, SASH3, PLAU	2.932236883	4.64E-07	4.80E-05	7.97E-04
GO:0007155 "cell adhesion"	13.57	BAGALT1, CCL2, TNF, OLR1, PDPN, COL3A1, COL15A1, CCL41, NIN1, POSTN, ITGB2, SIRPA, THY1, CD97, CDH13, LGALS3BP, EZR, CD44, ITGAX, FAT1, TGFBI, CD4, VCAN, GPNMB, MFAP4, THBS1, SYK	3.069378151	5.61E-07	5.50E-05	9.62E-04
GO:0022610 "biological adhesion"	13.57	BAGALT1, CCL2, TNF, OLR1, PDPN, COL3A1, COL15A1, CCL41, NIN1, POSTN, ITGB2, SIRPA, THY1, CD97, CDH13, LGALS3BP, EZR, CD44, ITGAX, FAT1, TGFBI, CD4, VCAN, GPNMB, MFAP4, THBS1, SYK	3.06499958	5.76E-07	5.38E-05	9.89E-04
GO:0006959 "humoral immune response"	5.03	C1QA, CD83, C1QB, GPR183, TNF, CCL2, C3, C2, VSG4, C1QC	10.07297096	5.83E-07	5.20E-05	9.99E-04
GO:0042981 "regulation of apoptosis"	14.57	BID, TNF, CCL2, TLR2, AKAP13, IL10, CD74, CITED2, GPX1, CD44, APOE, HMOX1, CHST11, IL1B, THBS1, BMF, PHLDA1, BAGALT1, CEBPB, LGALS1, BCL2A1, NRAA2, PIM3, PPIF, CDH13, NUPR1, CSB, TNFAIP3, PRNP	2.870295561	7.13E-07	6.08E-05	0.001223367
GO:0009719 "response to endogenous stimulus"	10.05	IRS2, TNF, EGR2, CCL2, LYN, PDGFA, GPR2, IL1RN, NRAA2, FBP1, NRAA3, IL10, CDH13, C1QB, CCND1, HMOX1, IDH1, IL1B, COL1A1, THBS1	3.929720221	7.32E-07	5.98E-05	0.001255444
GO:0043067 "regulation of programmed cell death"	14.57	BID, TNF, CCL2, TLR2, AKAP13, IL10, CD74, CITED2, GPX1, CD44, APOE, HMOX1, CHST11, IL1B, THBS1, BMF, PHLDA1, BAGALT1, CEBPB, LGALS1, BCL2A1, NRAA2, PIM3, PPIF, CDH13, NUPR1, CSB, TNFAIP3, PRNP	2.842016807	8.69E-07	6.82E-05	0.001490175
GO:0010941 "regulation of cell death"	14.57	BID, TNF, CCL2, TLR2, AKAP13, IL10, CD74, CITED2, GPX1, CD44, APOE, HMOX1, CHST11, IL1B, THBS1, BMF, PHLDA1, BAGALT1, CEBPB, LGALS1, BCL2A1, NRAA2, PIM3, PPIF, CDH13, NUPR1, CSB, TNFAIP3, PRNP	2.831555395	9.35E-07	7.05E-05	0.001603421
GO:0019886 "antigen processing and presentation of exogenous peptide antigen via MHC class II"	2.51	IFI30, FCER1G, HLA-DOA, CD74, HLA-DRA	49.73529412	1.58E-06	1.15E-04	0.002714716
GO:0002495 "antigen processing and presentation of peptide antigen via MHC class II"	2.51	IFI30, FCER1G, HLA-DOA, CD74, HLA-DRA	49.73529412	1.58E-06	1.15E-04	0.002714716
GO:0006916 "anti-apoptosis"	7.04	CCL2, CEBPB, TNF, BCL2A1, IL10, CITED2, CDH13, GPX1, APOE, HMOX1, IL1B, TNFAIP3, THBS1, PRNP	5.408109652	1.86E-06	1.31E-04	0.001918421
GO:0016477 "cell migration"	8.04	BAGALT1, GPX1, C1QB, CCL2, CD44, CXCR4, CXCL16, NRAA2, IL1B, ITGB2, VCAN, THBS1, IL10, PLAU, SYK	4.61312873	1.92E-06	1.30E-04	0.00292614
GO:0006928 "cell motion"	10.55	BAGALT1, DNAP9, TNF, EGR2, CCL2, NRAA2, CCL41, ITGB2, IL10, PLAU, CD97, CCL20, CXCR4, CXCL16, IL1B, VCAN, THBS1, PLAU, SYK	3.518117647	1.97E-06	1.29E-04	0.003387397
GO:0043066 "negative regulation of apoptosis"	6.05	TNF, CCL2, CEBPB, BCL2A1, NRAA2, PIM3, IL10, CD74, CITED2, CDH13, GPX1, APOE, HMOX1, CHST11, IL1B, TNFAIP3, THBS1, PRNP	4.046261216	2.12E-06	1.34E-04	0.003639777
GO:0031099 "regeneration"	4.52	GPX1, CCND1, CCL2, AXL, NIN1, VCAN, NRAA3, PLAU, PLAU	10.37539864	2.20E-06	1.35E-04	0.00377086
GO:0043069 "negative regulation of programmed cell death"	9.05	TNF, CCL2, CEBPB, BCL2A1, NRAA2, PIM3, IL10, CD74, CITED2, CDH13, GPX1, APOE, HMOX1, CHST11, IL1B, TNFAIP3, THBS1, PRNP	3.989906603	2.57E-06	1.53E-04	0.004401468
GO:0006548 "negative regulation of cell death"	9.05	TNF, CCL2, CEBPB, BCL2A1, NRAA2, PIM3, IL10, CD74, CITED2, CDH13, GPX1, APOE, HMOX1, CHST11, IL1B, TNFAIP3, THBS1, PRNP	3.978823529	2.66E-06	1.54E-04	0.004570045
GO:0002504 "antigen processing and presentation of peptide or polysaccharide antigen via MHC class II"	3.52	IFI30, FCER1G, HLA-DOA, HLA-DOA, HLA-DOA2, CD74, HLA-DRA	16.8798574	2.91E-06	1.63E-04	0.004996137
GO:0009725 "response to hormone stimulus"	3.05	IRS2, TNF, EGR2, CCL2, LYN, PDGFA, GPR2, IL1RN, RBP1, NRAA3, IL10, C1QB, CCND1, HMOX1, IDH1, IL1B, COL1A1, THBS1	3.902831362	3.85E-06	1.88E-04	0.005923811
GO:0016064 "immunoglobulin mediated immune response"	4.02	C1QA, C1QB, C3, FCER1G, C2, C1QC, CD74, HLA-DRA	11.78910675	4.53E-06	2.40E-04	0.007712813
GO:0002250 "adaptive immune response"	4.52	C1QA, C1QB, C3, FCER1G, C2, C1QC, CD74, IL10, HLA-DRA	9.301145913	5.08E-06	2.62E-04	0.008718605
GO:0002460 "adaptive immune response based on somatic recombination of immune receptors but"	4.52	C1QA, C1QB, C3, FCER1G, C2, C1QC, CD74, IL10, HLA-DRA	9.301145913	5.08E-06	2.62E-04	0.008718605
GO:0051270 "regulation of cell motion"	6.53	BAGALT1, IRS2, LYN, PDGFA, PDPN, THY1, CITED2, CDH13, APOE, CXCR4, HMOX1, CXCL16, THBS1	5.360073148	5.44E-06	2.74E-04	0.009339329
GO:0019748 "cell mediated immunity"	4.02	C1QA, C1QB, C3, FCER1G, C2, C1QC, CD74, HLA-DRA	11.385896723	5.81E-06	2.85E-04	0.009967394
GO:0007610 "behavior"	10.05	CSAR1, EGR2, CCL2, CSAR1, CMKLR1, PDGFA, CXCL2, NRAA2, CCL41, ITGB2, NRAA3, IL10, PLAU, CCL20, CXCR4, CXCL16, IL1B, CMTM3, PLAU, SYK	3.39452904	6.33E-06	3.03E-04	0.010861559
GO:0050900 "leukocyte migration"	4.02	BAGALT1, TNF, CCL2, CXCL16, IL1B, ITGB2, IL10, SYK	11.16862745	6.55E-06	3.05E-04	0.011244287
GO:0051241 "negative regulation of multicellular organismal process"	6.03	CD83, TNF, PDGFA, APOE, HMOX1, LGMN, CST3, APOC1, VSG4, THBS1, IL10, PLAU	5.822686838	6.59E-06	3.01E-04	0.011303048
GO:0048370 "cell motility"	8.04	BAGALT1, GPX1, CDH13, TNF, CCL2, CD44, CXCR4, CXCL16, NRAA2, IL1B, ITGB2, VCAN, THBS1, IL10, PLAU, SYK	4.147370913	7.06E-06	3.15E-04	0.01210256
GO:0002478 "antigen processing and presentation of exogenous peptide antigen"	2.51	IFI30, FCER1G, HLA-DOA, CD74, HLA-DRA	36.17112299	7.24E-06	3.16E-04	0.01242693
GO:0002694 "regulation of leukocyte activation"	6.03	CD83, HMOX1, IL1B, CD4, HLA-DOA, VSG4, THBS1, CD74, SASH3, IL10, THY1, SYK	5.752515946	7.40E-06	3.16E-04	0.012696405
GO:0070482 "response to oxygen levels"	5.53	CCL2, PDPN, CXCR4, PDGFA, HMOX1, NRAA2, HIF1A, THY1, CD44, APOE, HMOX1, CHST11, IL1B, TNFAIP3, THBS1, PRNP	6.28093945	1.07E-05	4.47E-04	0.01391701
GO:0002443 "leukocyte mediated immunity"	4.52	C1QA, C1QB, LYN, C3, FCER1G, C2, C1QC, CD74, HLA-DRA	8.27770178	1.17E-05	4.76E-04	0.019987007
GO:0050863 "regulation of T cell activation"	5.03	CD83, IL1B, CD4, HLA-DOA, VSG4, CD74, SASH3, IL10, THY1, SYK	6.801407743	1.56E-05	6.24E-04	0.026744069
GO:0001819 "positive regulation of cytokine production"	4.52	CD83, TNF, ATP6AP2, TLR2, FCER1G, IL1B, THBS1, SASH3, CD14	7.957647059	1.63E-05	6.40E-04	0.027988484
GO:0019886 "antigen processing and presentation of exogenous antigen"	2.51	IFI30, FCER1G, HLA-DOA, CD74, HLA-DRA	28.42016807	2.31E-05	8.21E-04	0.036603887
GO:0002449 "lymphocyte mediated immunity"	4.02	C1QA, C1QB, C3, FCER1G, C2, C1QC, CD74, HLA-DRA	9.094453782	2.59E-05	9.78E-04	0.044487655
GO:0048545 "response to steroid hormone stimulus"	6.03	C1QB, CCND1, TNF, CCL2, PDGFA, HMOX1, IL1RN, IL1B, IDH1, COL1A1, THBS1, IL10	4.973529412	2.91E-05	0.00107648	0.048898956