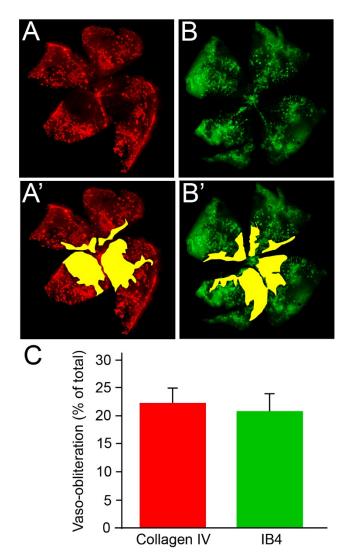
925 Supplemental Data



Supplemental Figure 1: Comparison between Collagen IV and Isolectin B4 Staining for the Detection of Vaso-obliteration. A: Representative image of retinal flatmount stained with Collagen IV (red). **A':** The retina in panel A with areas of vaso-obliteration highlighted (yellow). **B:** Representative image of retinal flatmount stained with Isolectin B4 (green). **B':** The retina in panel B with areas of vaso-obliteration highlighted (yellow). **C:** Summary of quantification of vaso-obliteration areas. Values are expressed as percentage of total retina ± SEM, n = 3 retinas for each data set.

Table S1. Genes differentially regulated in the OIR model as compared to normoxia.

Gene ID	Description	Fold change	p value
	Up-regulated		
	esis, proliferation and endothelial physioogy	04.00	0.705.00
Esm1 Igfbp3	endothelial cell-specific molecule 1 insulin-like growth factor binding protein 3	21.23 5.76	3.73E-08 1.10E-05
Angpt2	angiopoietin 2	3.76	6.21E-06
Vwf	Von Willebrand factor homolog	3.86	2.94E-08
lgfbp5	insulin-like growth factor binding protein 5	3.55	6.87E-05
Ednra	endothelin receptor type A	3.18	1.93E-08
Pecam1	platelet/endothelial cell adhesion molecule 1	2.76	6.58E-08
Procr	protein C receptor, endothelial	2.42 2.40	1.28E-05
Vegfa Vwa1	vascular endothelial growth factor A von Willebrand factor A domain containing 1	2.40	9.47E-07 3.99E-04
Angptl2	angiopoietin-like 2	2.24	2.34E-03
Eng	endoglin	1.91	5.43E-06
Kit	kit oncogene	1.84	7.10E-05
Ephb4	Eph receptor B4	1.77	3.27E-05
Efna1	ephrin A1	1.68	5.29E-06
Ece1	endothelin converting enzyme 1	1.51	6.43E-04
Inflammat		6 88	2.23E-09
Tgfbi Egln3	transforming growth factor, beta induced egl-9 family hypoxia-inducible factor 3	6.88 6.24	2.23E-09 1.27E-04
Cxcr4	chemokine (C-X-C motif) receptor 4	2.97	2.25E-07
Ctla2b	cytotoxic T lymphocyte-associated protein 2 beta	2.93	1.90E-05
lfitm3	interferon induced transmembrane protein 3	2.79	2.97E-04
Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	2.34	9.42E-05
Lyn	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	2.26	1.77E-04
Tgfb1	transforming growth factor, beta 1	2.13	7.63E-05
Tgfbr2	transforming growth factor, beta receptor II	2.02	1.23E-05
Ets2 Ets1	E26 avian leukemia oncogene 2, 3' domain E26 avian leukemia oncogene 1, 5' domain	1.94 1.88	3.60E-04 2.29E-05
Egln1	egl-9 family hypoxia-inducible factor 1	1.88	2.29E-05 4.68E-05
Tgif1	TGFB-induced factor homeobox 1	1.74	5.21E-05
ECM remo			J.L
Col1a1	collagen, type I, alpha 1	4.63	2.22E-03
Col4a1	collagen, type IV, alpha 1	4.21	2.84E-07
Col3a1	collagen, type III, alpha 1	3.54	3.79E-04
Col4a2	collagen, type IV, alpha 2	3.54	9.82E-06
Lama4	laminin, alpha 4	3.41	5.39E-08 2.84E-05
Fn1 Nid1	fibronectin 1 nidogen 1	3.30 3.29	2.84E-05 4.47E-04
Nid2	nidogen 2	3.02	2.19E-06
Col5a2	collagen, type V, alpha 2	2.60	3.54E-05
Col5a3	collagen, type V, alpha 3	2.39	7.29E-05
Lamb1	laminin B1	2.38	1.06E-04
Lamc1	laminin, gamma 1	2.29	9.52E-08
Col15a1	collagen, type XV, alpha 1	2.00	3.99E-04
Coll montri	collagen, type II, alpha 1	1.89	5.24E-07
	x interaction	2.30	4 225 05
Itga6 Icam1	integrin alpha 6 intercellular adhesion molecule 1	2.39 2.09	1.23E-05 3.77E-04
Itga9	integrin alpha 9	1.98	5.74E-04
ltgb1	integrin beta 1 (fibronectin receptor beta)	1.98	1.80E-05
lcam2	intercellular adhesion molecule 2	1.70	1.01E-04
Gene ID	Description	Fold	p value
Gelle 15		change	p valide
	Down-regulated Company of the Compan		
	and retina-specific pathways	2.00	= 00E 0E
	thyrotropin releasing hormone receptor	-2.66 -2.17	7.90E-05
Tacr3 Grik1	tachykinin receptor 3	-2.17 -1.78	1.22E-03 8.13E-04
Grik1 Arr3	glutamate receptor, ionotropic, kainate 1 arrestin 3, retinal	-1.78 -1.74	8.13E-04 1.10E-04
Nova1	neuro-oncological ventral antigen 1	-1.7 4 -1.62	4.20E-04
Syt2	synaptotagmin II	-1.59	9.79E-04
Cadps	Ca2+-dependent secretion activator	-1.59	2.11E-03
Transport	ers and channels		
Slc22a29	solute carrier family 22. member 29	-2.57	2.20E-03
	solute carrier organic anion transporter family, member 1a4	-2.56	2.26E-04
Slc22a8	solute carrier family 22 (organic anion transporter), member 8	-1.99	1.74E-05
	calcium channel, voltage-dependent, alpha2/delta subunit 3	-1.90 1.93	
Aqp4	aquaporin 4	-1.83	5.42E-05
	ATP-binding cassette, sub-family A (ABC1), member 8a	-1.80 1.55	2.65E-04
Atxn7l1 Slc2a3*	ataxin 7-like 1 solute carrier family 2 (facilitated glucose transporter), member 3	-1.55 1.54	1.47E-04 2.13E-03
Slc2a3* Slc39a8	solute carrier family 2 (facilitated glucose transporter), member 3 solute carrier family 39 (metal ion transporter), member 8	1.54 1.72	2.13E-03 8.61E-04
Slc39a8 Slc7a1	solute carrier family 39 (metal ion transporter), member 8 solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	1.72 1.85	8.61E-04 2.63E-06
Slc16a3	solute carrier family 16 (monocarboxylic acid transporters), member 3	2.11	1.10E-04
	solute carrier family 12, member 4	2.35	1.77E-04

Table S2. Genes differentially regulated in the combination treatment as compared to the individual cellular treatments, in the P5/P17 model

Gene ID	Description	Fold change	p value
	CD34 ⁺ /ECFCs vs. CD34 ⁺ Up-regulated		
	al structure and function		
Mbp* Mobp*	myelin basic protein myelin-associated oligodendrocytic basic protein	8.60 7.05	8.20E-03 2.36E-02
Slc17a6	solute carrier family 17 (Na-dependent inorganic phosphate cotransporter)	6.56	3.61E-04
Cldn11* Tspan2	claudin 11 tetraspanin 2	4.65 4.09	1.42E-02 1.94E-03
Sncg	synuclein, gamma	3.53	2.95E-03
Olig1*	oligodendrocyte transcription factor 1	3.42 3.27	2.61E-02 3.13E-03
Apod Kcnd2	apolipoprotein D potassium voltage-gated channel, Shal-related family, member 2	3.27	3.13E-03 5.82E-04
Gng4	guanine nucleotide binding protein (G protein), gamma 4	3.07	1.27E-03
Chrna6 Scn2a1	cholinergic receptor, nicotinic, alpha polypeptide 6 sodium channel, voltage-gated, type II, alpha 1	2.88 2.70	5.49E-04 2.33E-03
Tacr3	tachykinin receptor 3	2.68	1.13E-04
Scn1a Nefl	sodium channel, voltage-gated, type l, alpha neurofilament, light polypeptide	2.67 2.67	5.32E-04 1.51E-03
Cplx1	complexin 1	2.62	2.07E-03
Cacng5	calcium channel, voltage-dependent, gamma subunit 5	2.62	1.90E-04 2.42E-03
Chrnb3 Cacnb4	cholinergic receptor, nicotinic, beta polypeptide 3 calcium channel, voltage-dependent, beta 4 subunit	2.37 2.35	2.42E-03 2.16E-04
Gabra1	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 1	2.21	1.50E-05
Caln1 Syn2	calneuron 1 synapsin II	2.13 2.02	3.44E-04 3.30E-03
-	stem genes	2.02	0.002
Vsnl1	visinin-like 1	2.28	7.31E-04
Vsx1 Plcb1	visual system homeobox 1 homolog (zebrafish) phospholipase C, beta 1	2.17 1.94	5.92E-04 2.10E-03
Gucy1b3	guanylate cyclase 1, soluble, beta 3	1.94	1.32E-04
Cabp2	calcium binding protein 2	1.84	1.37E-04
Gnao1 Prkcg	guanine nucleotide binding protein, alpha O protein kinase C, gamma	1.71 1.71	3.33E-06 3.18E-03
Gucy1a3	guanylate cyclase 1, soluble, alpha 3	1.69	1.81E-06
Vsx2 Slc24a3	visual system homeobox 2 solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	1.68 1.64	2.35E-06 7.87E-04
Cabp5	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3 calcium binding protein 5	1.64	7.87E-04 3.91E-04
Calm1	calmodulin 1	1.59	5.46E-06
Gnai1	guanine nucleotide binding protein (G protein), alpha inhibiting 1 Down-regulated	1.51	2.64E-04
Extracell	ular matrix, WNT pathway		
Sfrp1	secreted frizzled-related protein 1	-10.49	1.52E-06
Sdc1 Wnt7b	syndecan 1 wingless-type MMTV integration site family, member 7B	-4.70 -4.28	7.46E-07 3.15E-03
Plau	plasminogen activator, urokinase	-3.91	3.21E-03
Col4a6 Col4a3	collagen, type IV, alpha 3	-3.79 -3.29	1.86E-05 7.09E-05
Col4a3 Col8a1	collagen, type IV, alpha 3 collagen, type VIII, alpha 1	-3.29 -3.27	7.09E-05 2.14E-03
Gene ID		Fold	p value
WIs	wntless homolog (Drosophila)	change -2.93	4.95E-06
Nid1	nidogen 1	-2.93 -2.57	3.38E-03
Col4a5	collagen, type IV, alpha 5	-2.50	3.69E-04
LoxI1 Wnt5b	lysyl oxidase-like 1 wingless-type MMTV integration site family, member 5B	-2.50 -2.47	2.15E-04 5.89E-07
Col4a4	collagen, type IV, alpha 4	-2.44	7.47E-06
Bgn Emid1**	biglycan EMI domain containing 1	-2.43 -2.10	3.03E-04 1.60E-05
Timp3	tissue inhibitor of metalloproteinase 3	-2.01	1.55E-04
Col4a1	collagen, type IV, alpha 1	-1.94	1.32E-03
Fmod P4ha2	fibromodulin proline 4-hydroxylase, alpha II polypeptide	-1.88 -1.72	2.39E-03 7.04E-04
P4ha1	proline 4-hydroxylase, alpha 1 polypeptide	-1.69	3.83E-05
Lama5 Stress re	laminin, alpha 5	-1.57	3.25E-03
Nupr1	nuclear protein transcription regulator 1	-9.48	1.91E-04
Gsta2	glutathione S-transferase, alpha 2 (Yc2)	-3.30	1.02E-04
Pon3 Gsta3	paraoxonase 3 glutathione S-transferase, alpha 3	-3.06 -2.55	1.48E-04 7.00E-05
Gsta3 Gpx3	glutathione beroxidase 3	-2.55 -2.52	3.27E-03
Gss	glutathione synthetase	-2.50	8.49E-04
Ggct Gstm2	gamma-glutamyl cyclotransferase glutathione S-transferase, mu 2	-2.47 -2.46	9.07E-04 6.67E-04
Mgst1	microsomal glutathione S-transferase 1	-2.45	1.61E-03
Gstm1	glutathione S-transferase, mu 1	-2.44 -2.26	1.85E-05
Rrm2 Prdx4	ribonucleotide reductase M2 peroxiredoxin 4	-2.26 -1.61	1.61E-03 3.81E-03
Pon2	paraoxonase 2	-1.57	1.87E-04
	CD34 ⁺ /ECFCs vs. ECFCs		
Myelin st	Up-regulated ructure and function		
Mbp*	myelin basic protein	9.87	5.37E-03
Mobp*	myelin-associated oligodendrocytic basic protein	6.86	2.53E-02
Plp1 Olig1*	proteolipid protein (myelin) 1 oligodendrocyte transcription factor 1	5.42 3.57	9.65E-03 2.18E-02
Mal	myelin and lymphocyte protein, T cell differentiation protein	2.99	3.60E-02
Slc15a2 Cldn11*	solute carrier family 15 (H+/peptide transporter), member 2 claudin 11	2.47 3.80	3.94E-02 3.02E-02
Cldn11* Scd1	claudin 11 stearoyl-Coenzyme A desaturase 1	3.80 2.10	3.02E-02 7.60E-03
	Down-regulated		1.0
Immune r	-	-3.51	1.26E-02
Tgtp1 H2-Q6	T cell specific GTPase 1 histocompatibility 2, Q region locus 6	-3.51 -2.77	1.26E-02 2.12E-02
Ccl5	chemokine (C-C motif) ligand 5	-2.62	3.62E-02
H2-Q7	histocompatibility 2, Q region locus 7	-2.50	1.05E-02
H2-K1 H2-T10	histocompatibility 2, K1, K region histocompatibility 2, T region locus 10	-2.14 -1.74	3.64E-02 1.57E-02
H2-D1	histocompatibility 2, D region locus 1	-1.74	1.79E-02
	ularization	4 70	225 03
Crispld1 Ptger4	cysteine-rich secretory protein LCCL domain containing 1 prostaglandin E receptor 4 (subtype EP4)	-1.78 -1.68	3.29E-03 1.05E-02
ECM	prostagianant in receptor in (easily point)		1.00_
Emid1**	EMI domain containing 1	-1.61	1.64E-03

Table S3. Proteomic analysis in the OIR model with the various treatments								
Pathway	Score	Proteins						
		vs. Normoxia						
Up-regulated								
Growth factors signaling pathways		ABL1, NFKB1, MAP2K1, MAPK3, PTPN11, STAT3, RAF1,						
Development HGF Signaling Pathway	51.42	BRAF, EIF4E, ERBB2, RPS6KA1, CDK1						
Development IGF-1 Receptor Signaling	46.34	NFKB1, MAP2K1, MAPK3, GYS1, PTPN11, BCL2L11, STAT3, RAF1, RPS6, RPS6KA1						
PI3K-Akt Signaling Pathway	40.84	NFKB1, MAP2K1, MAPK3, MCL1, GYS1, BCL2L11, RAF1, EIF4E, PDGFRA, ERBB2, RPS6, FN1, KDR						
Development VEGF Signaling Via VEGFR2 - Generic Cascades	33.52	NFKB1, MAP2K1, MAPK3, PTPN11, STAT3, RAF1, BRAF, KDR						
Development EGFR Signaling Via Small GTPases	33.42	MAP2K1, MAPK3, PTPN11, STAT3, RAF1, PDGFRA, ERBB2						
EGF/EGFR Signaling Pathway	32.29	ABL1, MAP2K1, PTPN11, STAT3, RAF1, BRAF, ERBB2, RPS6KA1						
Angiopoietin Like Protein 8 Regulatory Pathway	25.28	MAP2K1, MAPK3, GYS1, PTPN11, RAF1, EIF4E, RPS6KA1						
Inflammation and immune response								
Interleukin-11 Signaling Pathway	40.12	MAP2K1, MAPK3, PTPN11, STAT3, RAF1, RPS6, RPS6KA1						
Cytokine Signaling in Immune System	37.96	NFKB1, LCK, MAP2K1, MAPK3, MCL1, PTPN11, HIST1H3A, STAT3, RAF1, BRAF, EIF4E, PDGFRA, ERBB2, FN1						
HIF-1 Signaling Pathway	37.90	NFKB1, MAP2K1, MAPK3, STAT3, HK2, EIF4E, ERBB2, RPS6						
TGF-Beta Pathway	36.49	NFKB1, MAP2K1, MAPK3, HIST1H3A, STAT3, RAF1, BRAF, EIF4E, PDGFRA, ERBB2, RPS6, RPS6KA1, KDR						
B Cell Receptor Signaling Pathway (KEGG)	33.92	NFKB1, LCK, MAP2K1, MAPK3, PTPN11, RAF1, BRAF, RPS6KA1						
IL-2 Pathway	33.76	ABL1, NFKB1, LCK, MAP2K1, MAPK3, STAT3, RAF1, BRAF, ERBB2, RPS6KA1						
Immune Response IL-23 Signaling Pathway	32.50	NFKB1, MAPK3, YAP1, PTPN11, STAT3, PDGFRA, ERBB2, FN1						
IL6-mediated Signaling Events	24.00	MAP2K1, MAPK3, MCL1, PTPN11, STAT3						
Cell-Matrix interaction								
Focal Adhesion	30.87	MAP2K1, MAPK3, STAT3, RAF1, BRAF, PDGFRA, ERBB2, FN1, KDR						
	Do	wn-regulated						
ErbB Signaling Pathway	25.36	MAPK9, PRKCA, STAT5A, PAK4, PDK1, CCND1						
Autophagy - Animal	20.79	MAPK9, ATG3, PTEN, BCL2L1, BECN1						
The manufactural	CD34 ⁺ /	/ECFCs vs. CD34 ⁺						
Up-regulated	21.00	MDM2 STATEA BAE1 DAKA						
ErbB Signaling Pathway Autophagy	21.00 15.93	MDM2, STAT5A, RAF1, PAK4 MDM2, BECN1, RAF1, IRS1						
Down-regulated	13.33	WDWZ, DEONI, IVALI, IKOI						
Class I MHC Mediated Antigen Processing	a = :	UDAGA TARTA ORUM						
and Presentation	9.74	UBAC1, ZAP70, CDH1						
Cytoskeletal Signaling	8.27	STMN1, CDH1, MYH11						
Un an and And	CD34 ⁺	/ECFCs vs. ECFC						
Up-regulated	15 11	DLCC2 DOLISE1 DDKAA2 SOV2 DAE4						
Nanog in Mammalian ESC Pluripotency Retinoblastoma (RB) in Cancer	15.11 14.83	PLCG2, POU5F1, PRKAA2, SOX2, RAF1 RAF1, MSH6, CHEK1						
Down-regulated	17.00	TO G. 1, MOI IO, OFILIXI						
Donniegaratea								

14.25

COL6A1, SMAD3, ZAP70, CDK1

ERK Signaling