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Supplementary Materials for

Macrophages of diverse phenotypes drive vascularization of engineered tissues

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Other Supplementary Material for this manuscript includes the following:

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Table S1. Panel of markers used to assess phenotype-induced changes in EC behavior. Genes were selected based on a literature search of various stages of angiogenesis.

Gene	Class Name	Accession Number	Gene	Class Name	Accession Number
ACKR1 (DARC)	Endogenous	NM_002036.3	KDR (VEGFR2, FLK1)	Endogenous	NM_002253
ACVR1 (ALK2)	Endogenous	NM_001105.4	LAMA4	Endogenous	NM_002290.4
ACVRL1 (ALK1)	Endogenous	NM_000020.2	LOXL2	Endogenous	NM_002318.2
ADAMTS-1	Endogenous	NM_006988.4	MAPK14 (p38/MAPK)	Endogenous	NM_139012.2
ADAMTS-9	Endogenous	NM_182920.1	MET (c-Met)	Endogenous	NM_001127500.2
AMOTL2	Endogenous	NM_016201.3	MMP2	Endogenous	NM_004530
ANG (Angiogenin)	Endogenous	NM_001145.4	MMP9	Endogenous	NM_004994
ANGPT1 (Ang1)	Endogenous	NM_001146	NAA15 (Tubedown-1)	Endogenous	NM_057175.4
ANGPT2 (Ang2)	Endogenous	NM_001147	NFE2L2 (NRF2)	Endogenous	NM_006164.4
Apelin (APLN)	Endogenous	NM_017413	NID1 (Nidogen-1)	Endogenous	NM_002508.2
APLNR (APJ)	Endogenous	NM_005161	NOS3 (eNOS)	Endogenous	NM_000603.4
BAX	Endogenous	NM_001291428	Notch1	Endogenous	NM_017617
BMPR1A (ALK3)	Endogenous	NM_004329.2	NOTCH3	Endogenous	NM_000435
CCL2 (MCP1)	Endogenous	NM_002982.3	NRARP	Endogenous	NM_001004354
CCL5 (RANTES)	Endogenous	NM_002985	NRCAM	Endogenous	NM_001193582
CD34	Endogenous	NM_001773	NRP1	Endogenous	NM_003873
CD36	Endogenous	NM_001001548	NTN1 (Netrin-1)	Endogenous	NM_004822.2
CDC42	Endogenous	NM_044472.2	PDGFA	Endogenous	NM_002607
CDH2 (N-Cadherin)	Endogenous	NM_001792	PDGFB	Endogenous	NM_002608
CDH5 (VE-cadherin)	Endogenous	NM_001795.4	PDGFR-beta	Endogenous	NM_001355017
Col IV	Endogenous	NM_001845	PECAM1 (CD31)	Endogenous	NM_000442
CTNNB1	Endogenous	NM_001904	PFKFB3	Endogenous	NM_004566.3
CTSS (Cathepsin S)	Endogenous	NM_004079.4	PLAT (t-PA)	Endogenous	NM_000930.4
CXCL12 (SDF-1A)	Endogenous	NM_199168.3	PLAUR (uPAR)	Endogenous	NM_002659.3
CXCR4	Endogenous	NM_001008540	PLXND1 (PlexinD1)	Endogenous	NM_015103.2
CYR61	Endogenous	NM_001554.4	RAMP2	Endogenous	NM_005854.2
DLL4	Endogenous	NM_019074	RGS5	Endogenous	NM_003617
EDNRB	Endogenous	NM_001201397.1	ROBO4	Endogenous	NM_019055.5
EGFL7	Endogenous	NM_201446.2	S1PR1 (S1P1, EDG11)	Endogenous	NM_001400.4
EGLN1 (PHD2)	Endogenous	NM_022051.2	SELP	Endogenous	NM_003005.3
Endoglin (CD105)	Endogenous	NM_001114753	SEMA3E	Endogenous	NM_012431.2
EPHB4	Endogenous	NM_004444.4	SERPINE1 (PAI-1)	Endogenous	NM_000602.4
ERG	Endogenous	NM_182918	SRF	Endogenous	NM_001292001.1
ESM1	Endogenous	NM_007036.4	TEK (TIE2)	Endogenous	NM_000459
ETS1	Endogenous	NM_005238	TGFB1	Endogenous	NM_000660
F3 (Tissue Factor)	Endogenous	NM_001993.4	TIE1	Endogenous	NM_005424
FGF2 (bFGF)	Endogenous	NM_002006.5	TJP1 (ZO-1)	Endogenous	NM_003257.4
FGFR1 (Flt-2)	Endogenous	NM_023110.2	TNFSF11 (RANKL)	Endogenous	NM_003701.3
FLT1 (VEGFR1)	Endogenous	NM_002019	TP53	Endogenous	NM_000546
FLT4 (VEGFR3)	Endogenous	NM_182925.4	UNC5B	Endogenous	NM_170744.4
HES1	Endogenous	NM_005524.3	VCAM1	Endogenous	NM_001078.3
HIF1a	Endogenous	NM_001530	VEGFA	Endogenous	NM_001171623
HSPB1 (HSP27)	Endogenous	NM_001540.4	VEGFC	Endogenous	NM_005429
ICAM2	Endogenous	NM_001099786	VEGFD	Endogenous	NM_004469
ID1	Endogenous	NM_002165.3	VWF	Endogenous	NM_000552.4
ID2 (Inhibitor of DNA binding 2)	Endogenous	NM_002166.4	WNT5A	Endogenous	NM_001256105.1
ITGAV (Integrin AlphaVbeta3)	Endogenous	NM_002210.4	WNT7B	Endogenous	NM_058238
ITGB1BP1 (ICAP1)	Endogenous	NM_004763.4	HPRT1	Reference	NM_000194.2
Jag1	Endogenous	NM_000214	YWHAZ	Reference	NM_003406.3
KCNE3	Endogenous	NM_005472.4	B2M	Reference	NM_004048.2

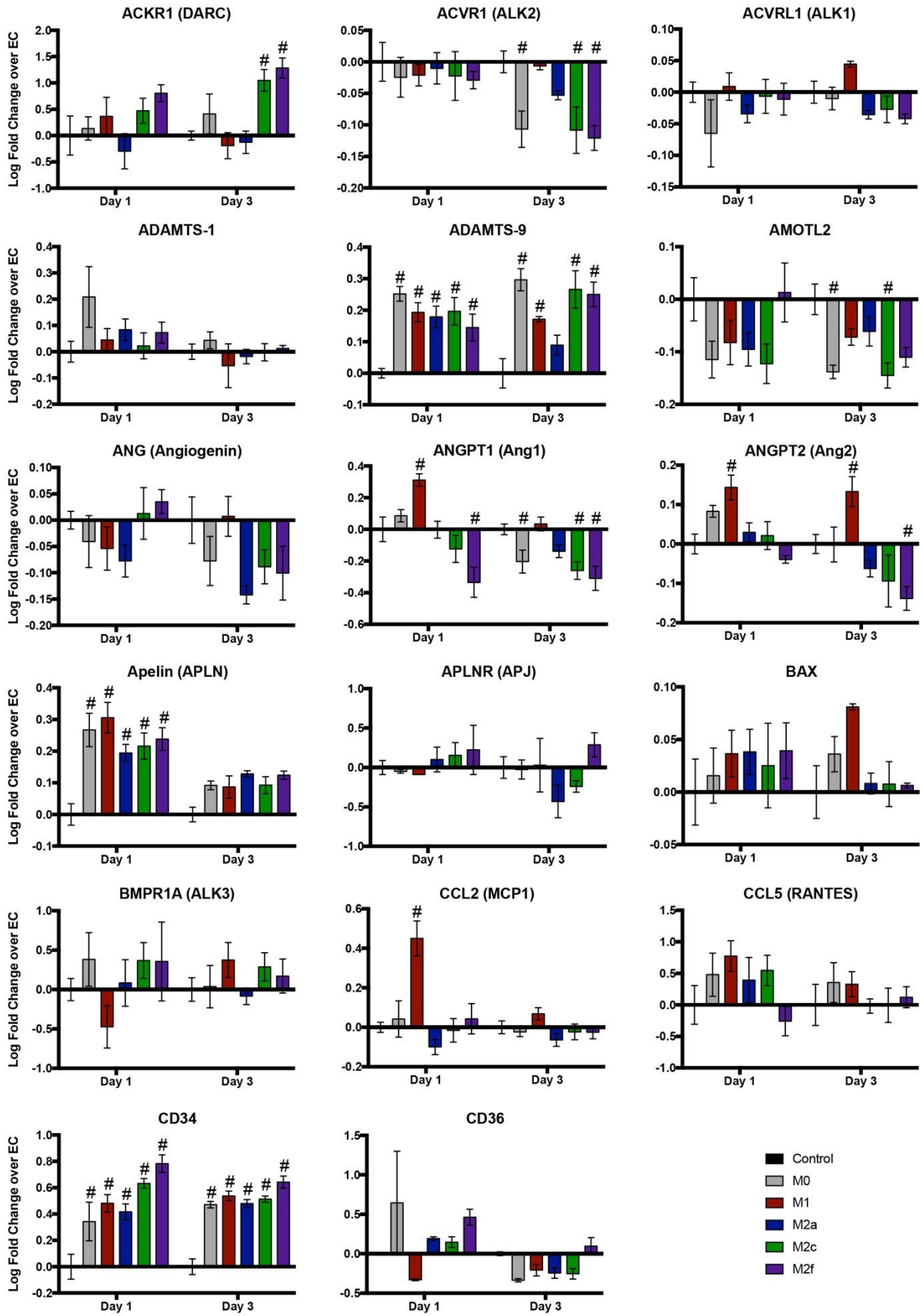


Figure S1. Individual gene plots of markers used to characterize phenotype-induced changes in EC behavior. Data analyzed using two-way ANOVA. Post-host analysis performed using the two-stage linear step-up method of Benjamini, Krieger and Yekutieli with Q=0.05. Data shown as mean ± SEM; n = 4 biological replicates per phenotype and # indicates significance relative to control.

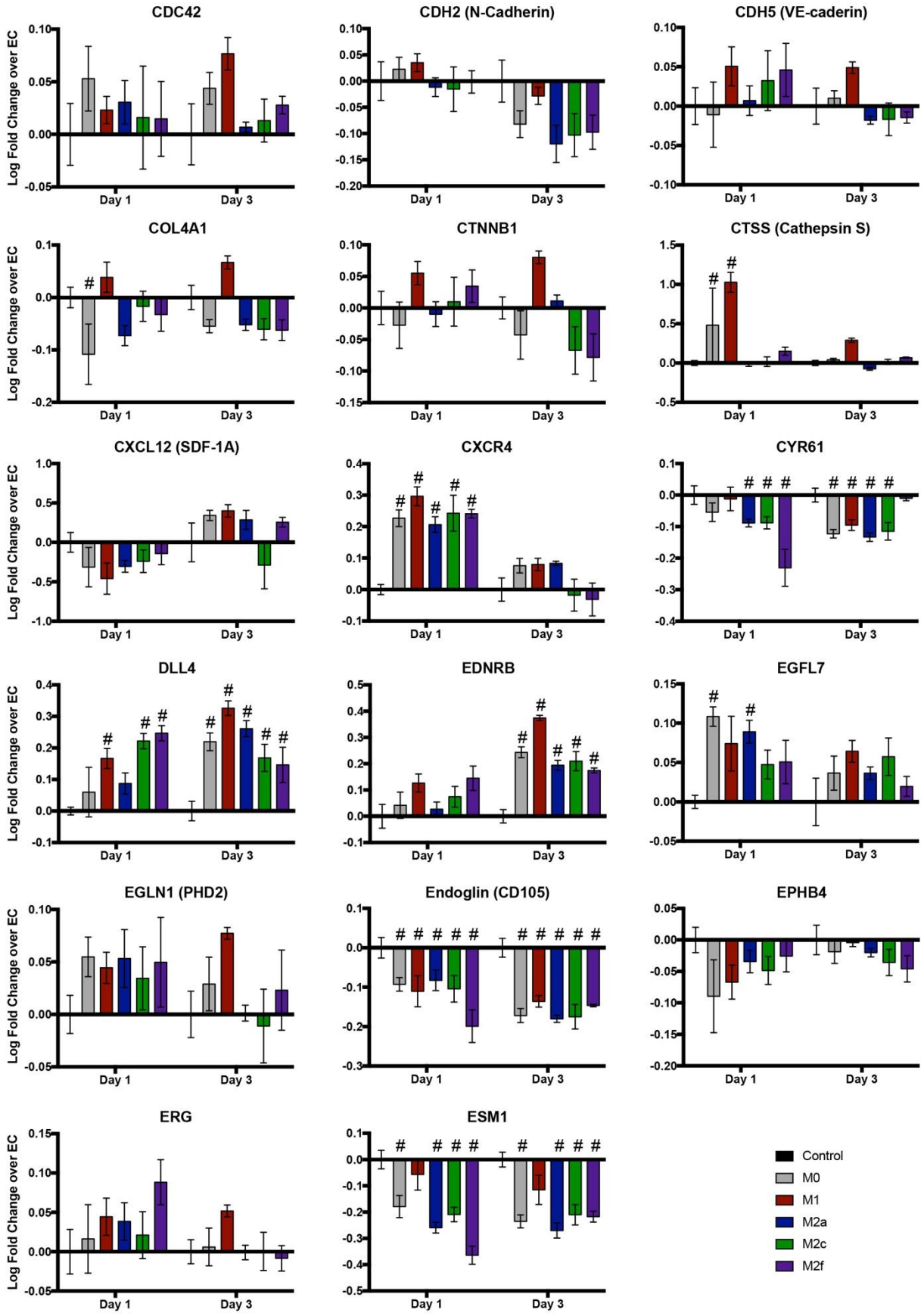


Figure S1. (continued) Data analyzed using two-way ANOVA. Post-host analysis performed using the two-stage linear step-up method of Benjamini, Krieger and Yekutieli with Q=0.05. Data shown as mean ± SEM; n = 4 biological replicates per phenotype and # indicates significance relative to control.

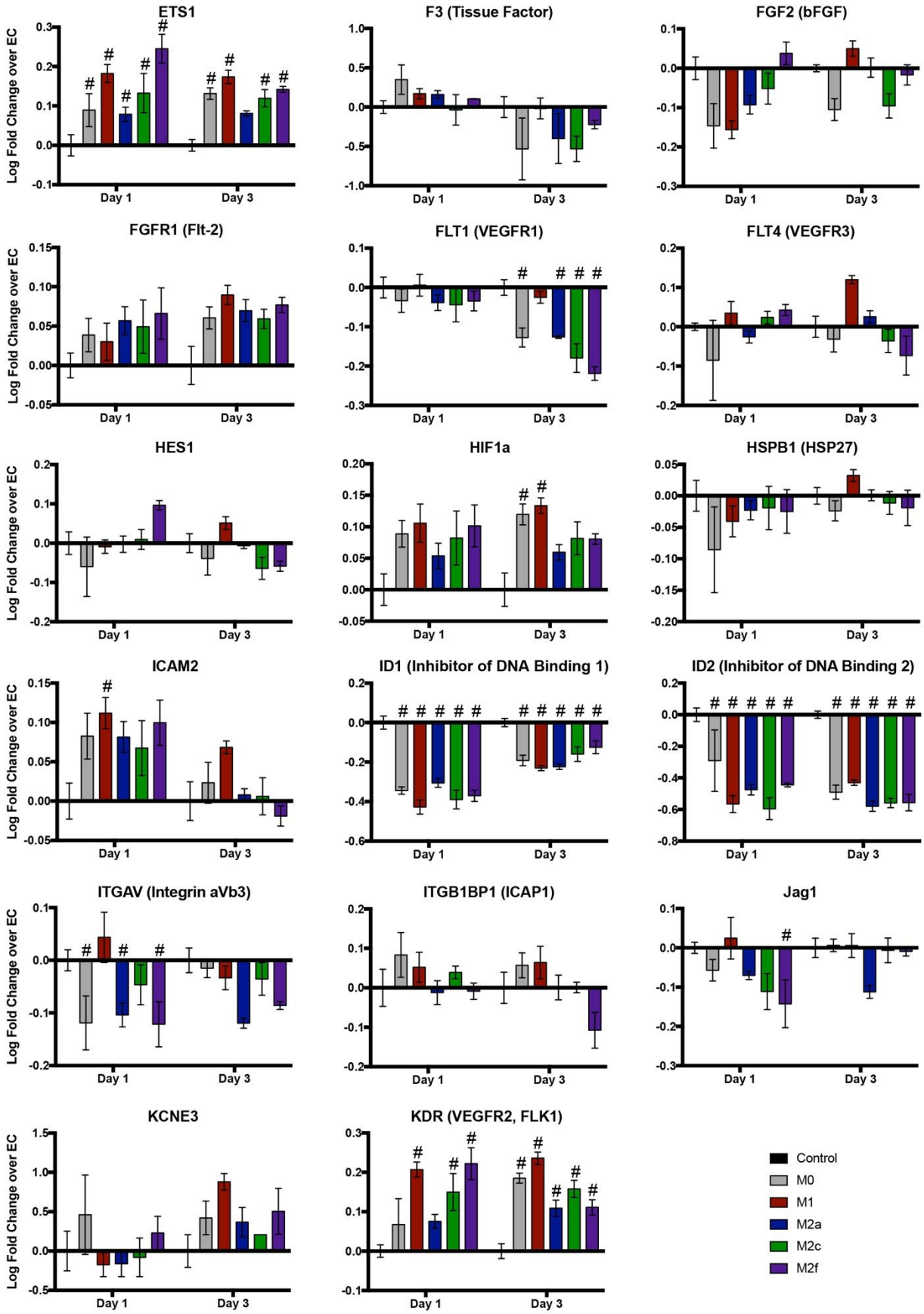


Figure S1. (continued) Data analyzed using two-way ANOVA. Post-host analysis performed using the two-stage linear step-up method of Benjamini, Krieger and Yekutieli with Q=0.05. Data shown as mean ± SEM; n = 4 biological replicates per phenotype and # indicates significance relative to control.

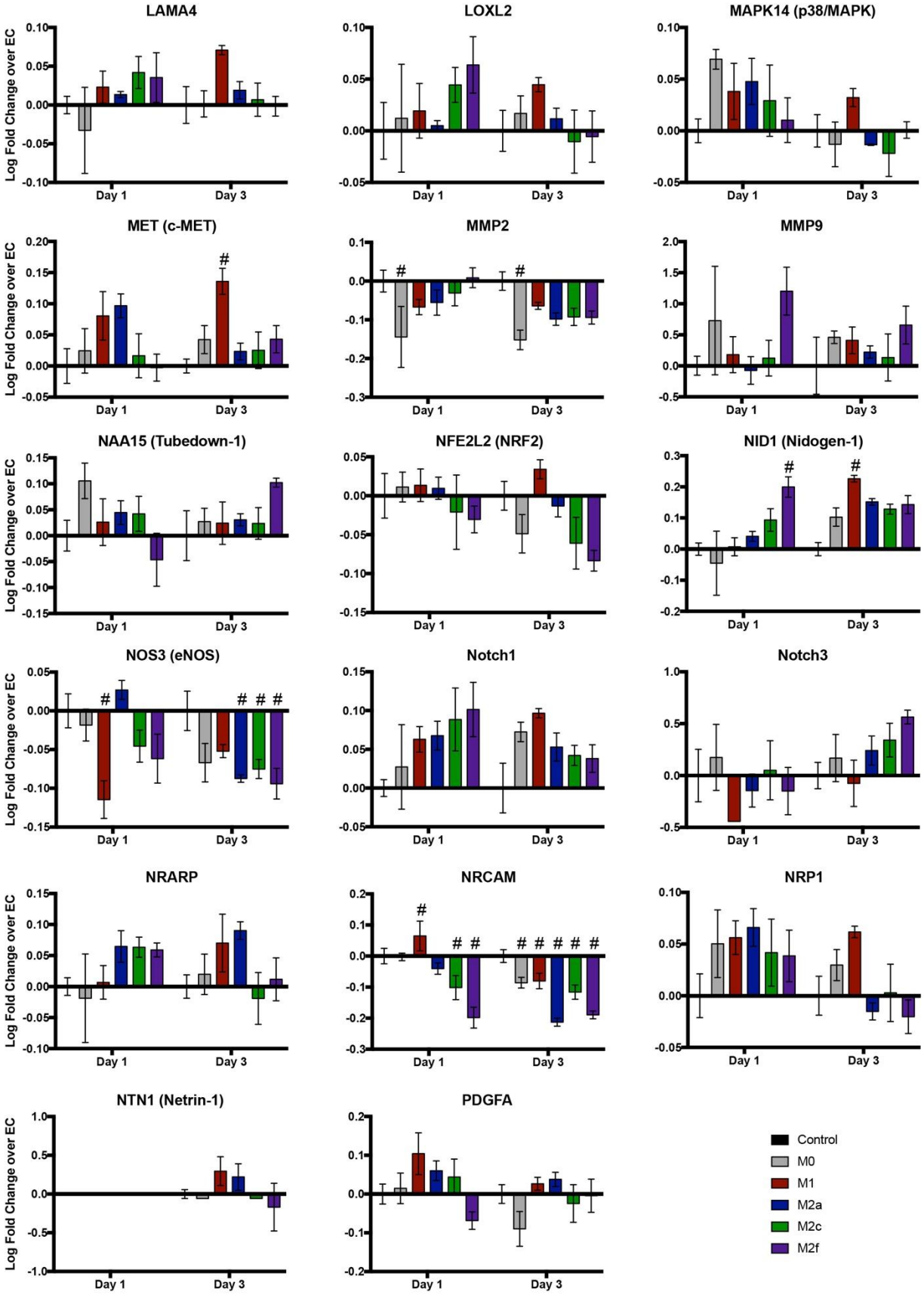


Figure S1. (continued) Data analyzed using two-way ANOVA. Post-host analysis performed using the two-stage linear step-up method of Benjamini, Krieger and Yekutieli with Q=0.05. Data shown as mean ± SEM; n = 4 biological replicates per phenotype and # indicates significance relative to control.

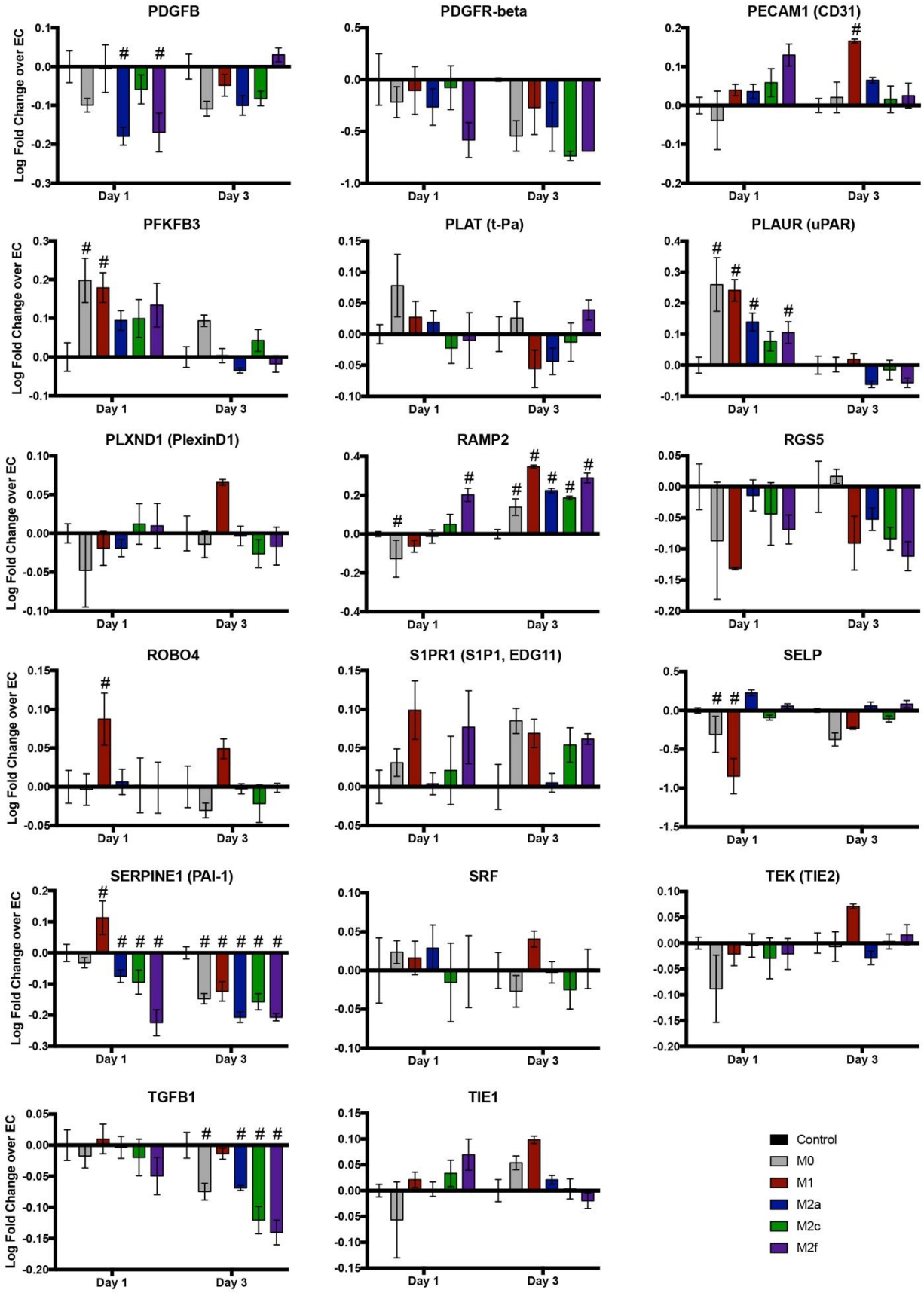


Figure S1. (continued) Data analyzed using two-way ANOVA. Post-host analysis performed using the two-stage linear step-up method of Benjamini, Krieger and Yekutieli with Q=0.05. Data shown as mean ± SEM; n = 4 biological replicates per phenotype and # indicates significance relative to control.

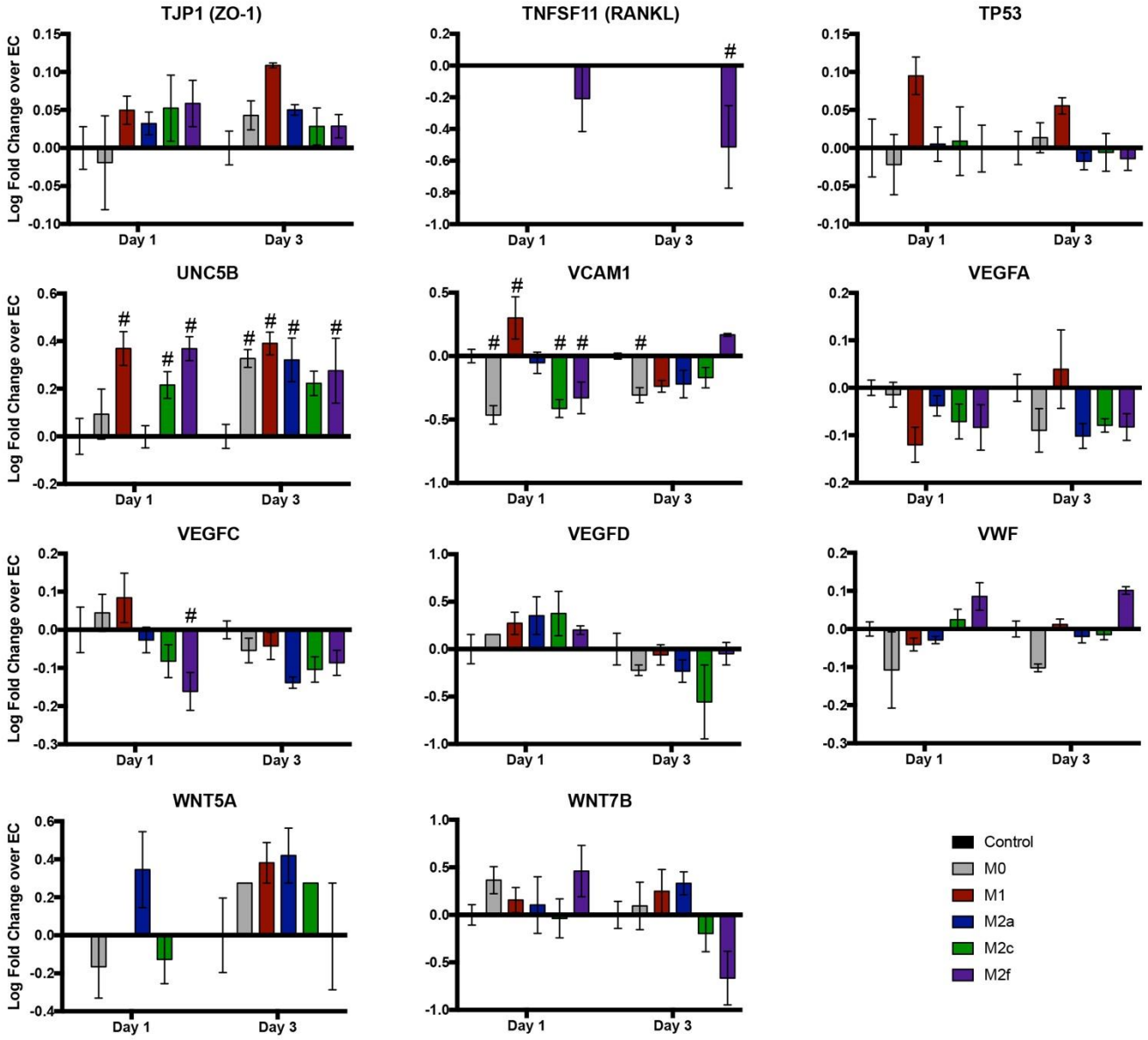


Figure S1. (continued) Data analyzed using two-way ANOVA. Post-host analysis performed using the two-stage linear step-up method of Benjamini, Krieger and Yekutieli with Q=0.05. Data shown as mean ± SEM; n = 4 biological replicates per phenotype and # indicates significance relative to control.

Table S2. Endothelial cell genes significantly up-regulated or down-regulated when co-cultured with macrophages of different phenotypes. Data were analyzed using two-way ANOVA. Post-host analysis was performed using the two-stage linear step-up method of Benjamini, Krieger and Yekutieli with Q=0.05 to control for the number of false positives resulting from multiple comparisons; (n = 4 donors).

UPREGULATED

DAY 1					DAY 3				
M0	**M1**	**M2a**	**M2c**	**M2f**	**M0**	**M1**	**M2a**	**M2c**	**M2f**
ADAMTS-9	ADAMTS-9	ADAMTS-9	ADAMTS-9	ADAMTS-9	ADAMTS-9	ADAMTS-9	CD34	ACKR1	ACKR1
Apelin	ANGPT1	Apelin	Apelin	Apelin	CD34	ANGPT2	DLL4	ADAMTS-9	ADAMTS-9
CD34	ANGPT2	CD34	CD34	CD34	DLL4	CD34	EDNRB	CD34	CD34
CTSS	CD34	CXCR4	CXCR4	CXCR4	EDNRB	DLL4	KDR	DLL4	DLL4
CXCR4	Apelin	EGFL7	DLL4	DLL4	ETS1	EDNRB	RAMP2	EDNRB	EDNRB
EGFL7	CCL2	ETS1	ETS1	ETS1	HIF1a	ETS1	UNC5B	ETS1	ETS1
ETS1	CTSS	PLAUR	KDR	KDR	KDR	HIF1a		KDR	KDR
PFKFB3	CXCR4		UNC5B	NID1	RAMP2	KDR		RAMP2	RAMP2
PLAUR	DLL4			PLAUR	UNC5B	MET			UNC5B
	ETS1			RAMP2		NID1			
	ICAM2			UNC5B		PECAM1			
	KDR					RAMP2			
	NRCAM					UNC5B			
	PFKFB3								
	PLAUR								
	ROBO4								
	SERPINE1								
	UNC5B								
	VCAM1								

DOWNREGULATED

DAY 1					DAY 3				
M0	**M1**	**M2a**	**M2c**	**M2f**	**M0**	**M1**	**M2a**	**M2c**	**M2f**
COL4A1	Endoglin	CYR61	CYR61	ANGPT1	ACVR1	CYR61	CYR61	ACVR1	ACVR1
Endoglin	FGF2	Endoglin	Endoglin	CYR61	AMOTL2	Endoglin	Endoglin	AMOTL2	ANGPT1
ESM1	ID1	ESM1	ESM1	Endoglin	ANGPT1	ID1	ESM1	ANGPT1	ANGPT2
FGF2	ID2	FGF2	ID1	ESM1	CYR61	ID2	FLT1	CYR61	Endoglin
ID1	NOS3	ID1	ID2	ID1	Endoglin	NRCAM	ID1	Endoglin	ESM1
ID2	SELP	ID2	NRCAM	ID2	ESM1	SERPINE1	ID2	ESM1	FLT1
ITGAV		ITGAV	SERPINE1	ITGAV	FLT1		NOS3	FLT1	ID1
MMP2		PDGFB	VCAM1	Jag1	ID1		NRCAM	ID1	ID2
RAMP2		SERPINE1		NRCAM	ID2		SERPINE1	ID2	NOS3
SELP				PDGFB	MMP2		TGFB1	NOS3	NRCAM
VCAM1				SERPINE1	NRCAM			NRCAM	SERPINE1
				VCAM1	SERPINE1			SERPINE1	TGFB1
				VEGFC	TGFB1			TGFB1	TNFSF11
					VCAM1				

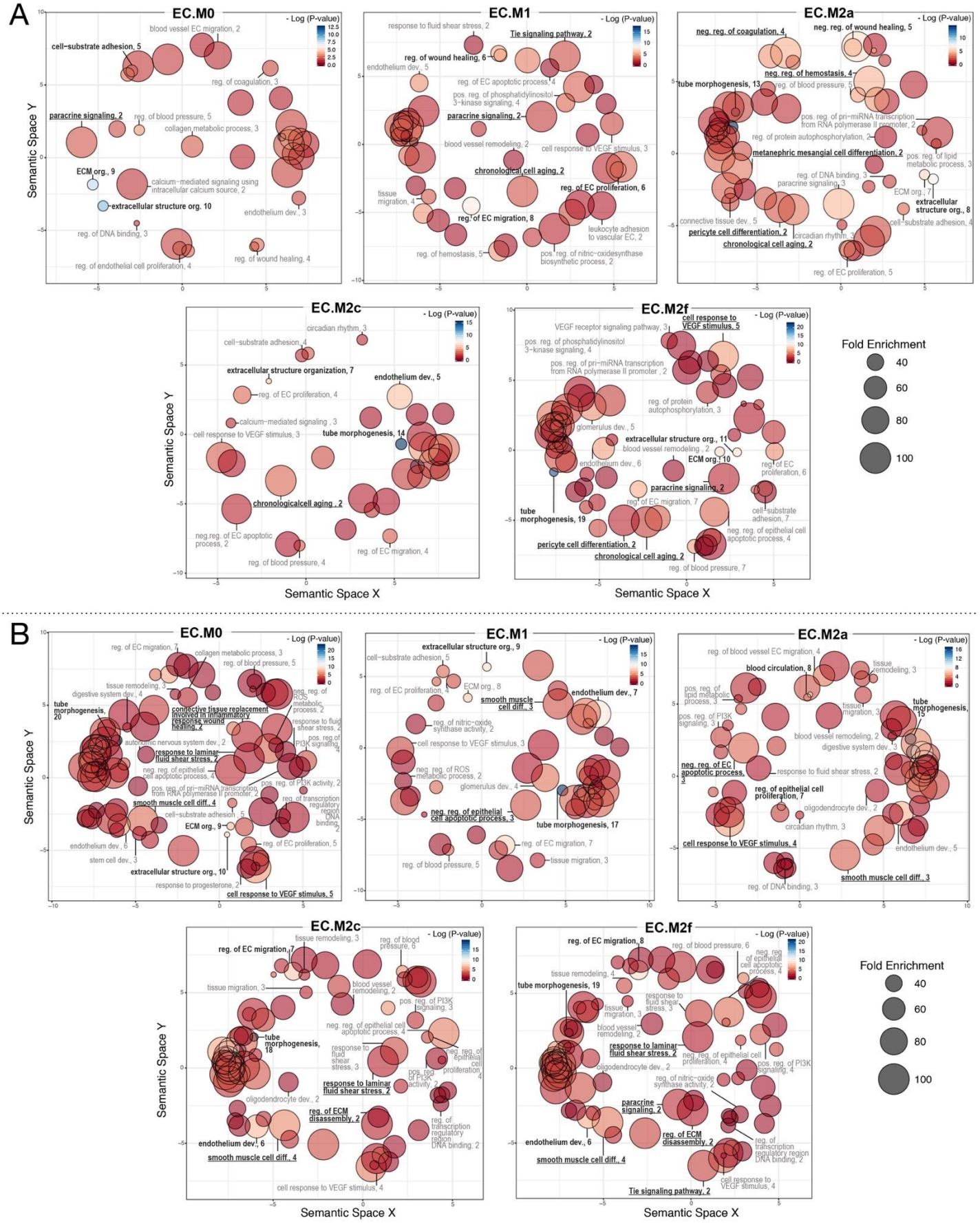


Figure S2. REVIGO analysis of biological processes altered in ECs by diverse macrophage phenotypes after transwell co-culture. REVIGO bubble plots indicating GO terms associated with genes differentially regulated in ECs in response to macrophage phenotype after **(A)** 1 and **(B)** 3 days. Ontologies are visualized

in semantic space such that overlapping terms have gene products with similar biological functions. Larger circles indicated greater enrichment. The top 3 terms for each phenotype with p-value < 0.001 are indicated in black, and all terms with fold enrichment ≥ 100 and p < 0.01 are indicated in black and underlined. All other non-dispensable terms are shown in gray; numbers correspond to the number of genes associated with each term.

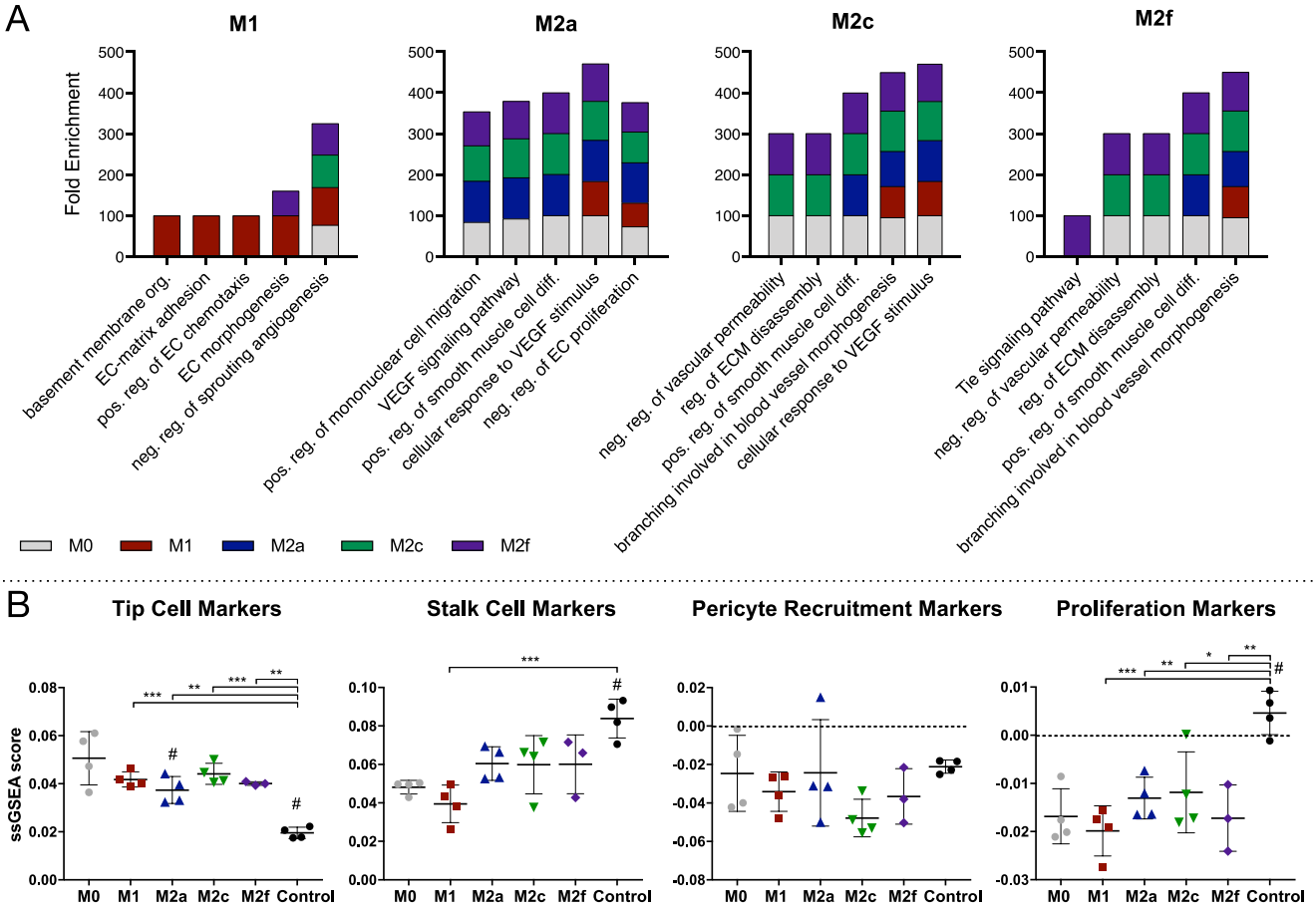


Figure S3. Effects of macrophage phenotype on biological processes in ECs after 3 days of transwell co-culture. Gene ontology enrichment analysis was performed on lists of genes differentially regulated in ECs in response to macrophage phenotype after 3 days of co-culture. **(A)** Top 5 most highly enriched, non-redundant GO terms for each phenotype. **(B)** Single-sample Gene Set Enrichment Analysis (ssGSEA) for gene sets related to specific processes of angiogenesis; analysis was not restricted to only differentially expressed genes. One-way ANOVA with Tukey's post-hoc analysis; *p<0.05, **p<0.01, ***p<0.001, # indicates p<0.05 relative to the M0 control.

Table S3. Lists of genes associated with angiogenic processes. Genes were selected and organized based on a literature search of various stages of angiogenesis.

Tip Cell	Stalk Cell	Migration	Proliferation
ADAMTS-1	ACKR1 (DARC)	AMOTL2	Apelin (APLN)
ADAMTS-9	ACVRL1 (ALK1)	ANGPT1 (Ang1)	AMOTL2
ANGPT2	APLNR (APJ)	CCL2	ANG
Apelin (APLN)	CD36	CCN1 (CYR61)	APLNR (APJ)
BMPR1A (ALK3)	ETS1	CDC42	CCL2
CD34	FLT1 (VEGFR1)	CDH2 (N-Cadherin)	CDC42
CDC42	HES1	CDH5 (VE-cadherin)	Endoglin (CD105)
COL4A1	ID1	Endoglin (CD105)	FGF2 (bFGF)
CTSS (Cathepsin S)	ID2	FGF2 (bFGF)	FLT4 (VEGFR3)
CXCR4	Jag1	FGFR1 (Flt-2)	ID1
DLL4	NOTCH1	FLT4 (VEGFR3)	Jag1
EDNRB	NRARP	HSPB1 (HSP27)	KDR (VEGFR2, FLK1)
ESM1	SELP	ICAM2	MMP9
FLT4 (VEGFR3)	TEK (TIE2)	ID1	NOS3 (eNOS)
KCNE3	VWF	ITGAV (Integrin $\alpha V\beta 3$)	NRARP
KDR (VEGFR2, FLK1)		ITGB1BP1	NTN1 (Netrin-1)
LAMA4		KDR (VEGFR2 FLK1)	PFKFB3
LOXL2		MAPK14 (p38/MAPK)	PLAUR (uPAR)
NID1		MMP2	SRF
NRP1		MMP9	TGFB1
PDGFB		NOS3 (eNOS)	VEGFA
PLAUR		NRP1	WNT5A
PLXND1 (PlexinD1)		NTN1 (Netrin-1)	
SRF		PECAM1 (CD31)	
TIE1		PFKFB3	
UNC5B		PLAUR (uPAR)	
		SERPINE1 (PAI-1)	
		SRF	
		TGFB1	
		TJP1 (ZO-1)	
		VCAM1	
		VEGFA	
		VEGFC	
		WNT5A	

Table S3. (continued) Lists of genes associated with angiogenic processes. Genes were selected and organized based on a literature search of various stages of angiogenesis.

Initiation	Initiation (cont.)	Prevents Leakage	Promotes Leakiness
ACKR1 (DARC)	SERPINE1 (PAI-1)	ACVRL1 (ALK1)	ANG2
ACVRL1 (ALK1)	SRF	AMOTL2	EGLN1 (PHD2)
ADAMTS-1	TEK (TIE2)	ANGPT1 (Ang1)	eNOS
ADAMTS-9	TGFB1	CDH2 (N-Cadherin)	PLAUR (uPAR)
AMOTL2	TIE1	CDH5 (VE-cadherin)	TNFSF11 (RANKL)
ANG	TJP1 (ZO-1)	CTNNB1	VEGFA
ANGPT1 (Ang1)	UNC5B	EGFL7 (VE statin)	VEGFC
ANGPT2	VCAM1	EPHB4	VEGFD
Apelin (APLN)	VEGFA	ERG	
APLNR (APJ)	VEGFC	ICAM2	
BMPR1A (ALK3)	VEGFR2	ITGAV (Integrin $\alpha V\beta 3$)	
CCL2	VWF	ITGB1BP1	
CCN1 (CYR61)	WNT5A	LAMA4	
CD34		NAA15 (Tubedown-1)	
CD36		NID1 (Nidogen-1)	
CDC42		NRARP	
CDH2 (N-Cadherin)		PDGFB	
CDH5 (VE-cadherin)		PECAM1 (CD31)	
Col IV		RAMP2	
CTSS (Cathepsin S)		ROBO4	
CXCR4		S1PR1 (S1P1 EDG11)	
DLL4		SERPINE1 (PAI-1)	
EDNRB		TEK (TIE2)	
Endoglin (CD105)		TGFB1	
ESM1		TJP1 (ZO-1)	
ETS1		UNC5B	
FGF2 (bFGF)			
FGFR1 (Flt-2)			
FLT1 (VEGFR1)			
FLT4 (VEGFR3)			
HES1			
HSPB1 (HSP27)			
ICAM2			
ID1			
ID2			
ITGAV (Integrin			
ITGB1BP1			
Jag1			
KCNE3			
KDR (VEGFR2			
LAMA4			
LOXL2			
MAPK14 (p38/MAPK)			
MMP2			
MMP9			
NID1			
NOS3 (eNOS)			
NOTCH1			
NRARP			
NRP1			
NTN1 (Netrin-1)			
PDGFB			
PECAM1 (CD31)			
PFKFB3			
PLAUR (uPAR)			
PLXND1 (PlexinD1)			
SELP			

Table S3. (continued) Lists of genes associated with angiogenic processes. Genes were selected and organized based on a literature search of various stages of angiogenesis.

Cell Junctions	Pericyte Adhesion/Interactions	Pericyte Recruitment	Monocyte Adhesion/Recruitment
CDC42	CDH2 (N-Cadherin)	ALK1	ACKR1 (DARC)
CDH2	Col IV	ANG1	CCL2
CDH5 (VE-cadherin)	ITGAV (Integrin $\alpha V\beta 3$)	CCL2	CCL5
CTNNB1	Jag1	F3 (Tissue Factor)	CCN1 (CYR61)
ERG	LAMA4	PDGFB	CDH5 (VE-cadherin)
ICAM2	NID1 (Nidogen-1)	S1PR1 (S1P1 EDG11)	CXCL12 (SDF-1A)
ITGAV (Integrin $\alpha V\beta 3$)	S1PR1 (S1P1 EDG11)	TGFB1	ICAM2
PECAM1 (CD31)	TEK (TIE2)		PECAM1 (CD31)
TJP1 (ZO-1)	VCAM1		SELP
	VWF		VCAM1
			VEGFA

Inhibits Angiogenesis	Response to Hypoxia	Anti-Apoptotic	Pro-Apoptotic
ACVR1 (ALK2)	CXCL12 (SDF-1A)	ANG1	BAX
ACVRL1 (ALK1)	CXCR4	CDH2 (N-Cadherin)	BMPR1A (ALK3)
ADAMTS1	HIF1A	CDH5 (VE-cadherin)	RGS5
ADAMTS9	LOXL2	ICAM2	TP53
EGFL7 (VE statin)	NFE2L2 (NRF2)	ITGB1BP1 (ICAP1)	UNC5B
EGLN1 (PHD2)		NTN1	
HSPB1 (HSP27)		TIE2	
ID1			
NAA15 (Tubedown-1)			
NID1 (Nidogen-1)			
Notch1			
PLXND1 (PlexinD1)			
ROBO4			
SEMA3E			
UNC5B			
VWF			

Podosome Formation	Proteases
CDC42	MMP2
CDH5 (VE-cadherin)	MMP9
SRF	PLAT
VEGFR2	PLAUR (uPAR)

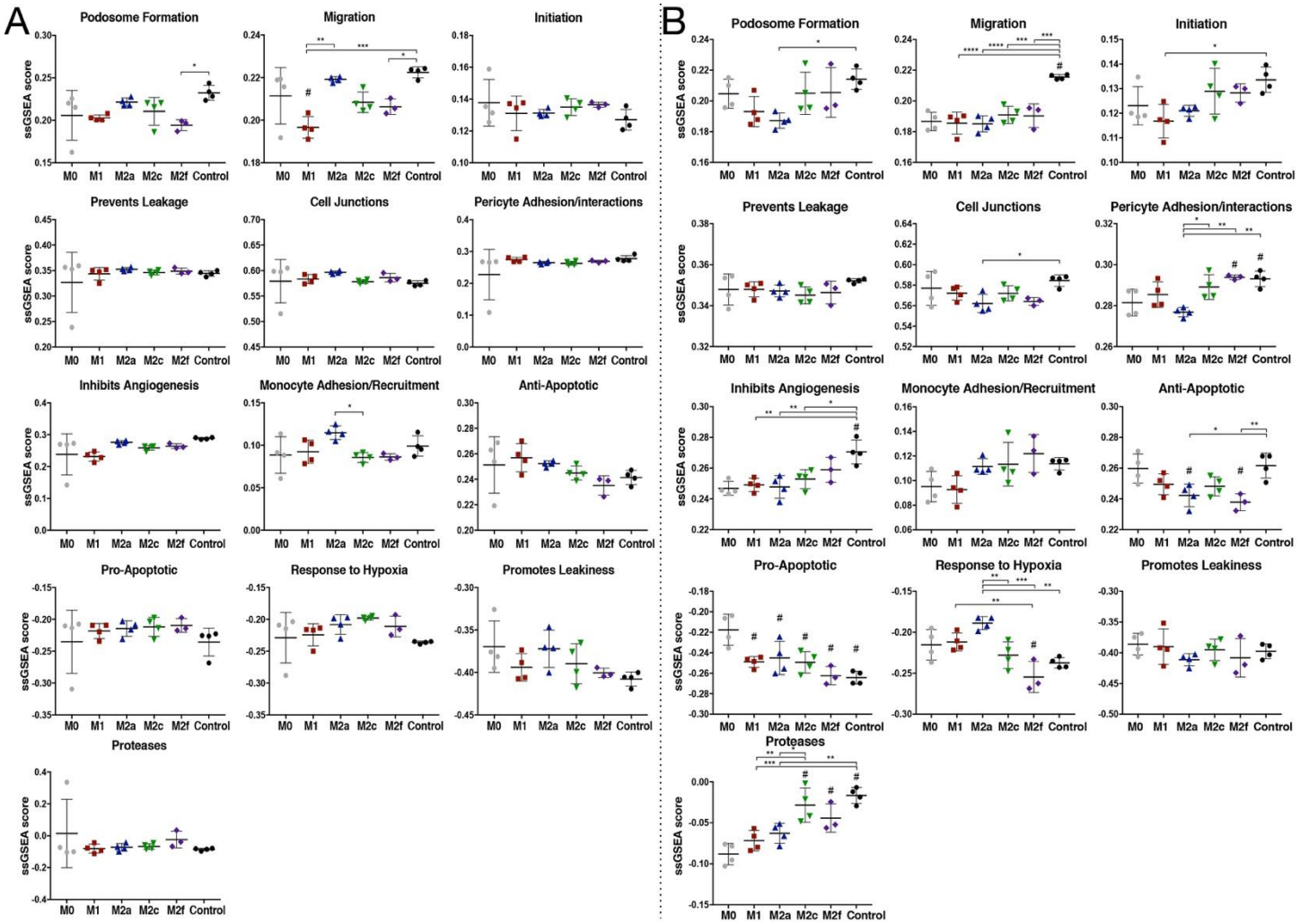


Figure S4. Single-sample Gene Set Enrichment Analysis (ssGSEA) for gene sets related to specific processes of angiogenesis after transwell co-culture. Macrophages were co-cultured with ECs for **(A)** 1 day and **(B)** 3 days. Analysis was not restricted to only differentially expressed genes. One-way ANOVA with Tukey's post-hoc analysis; *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001, # indicates p<0.05 relative to the M0 control.

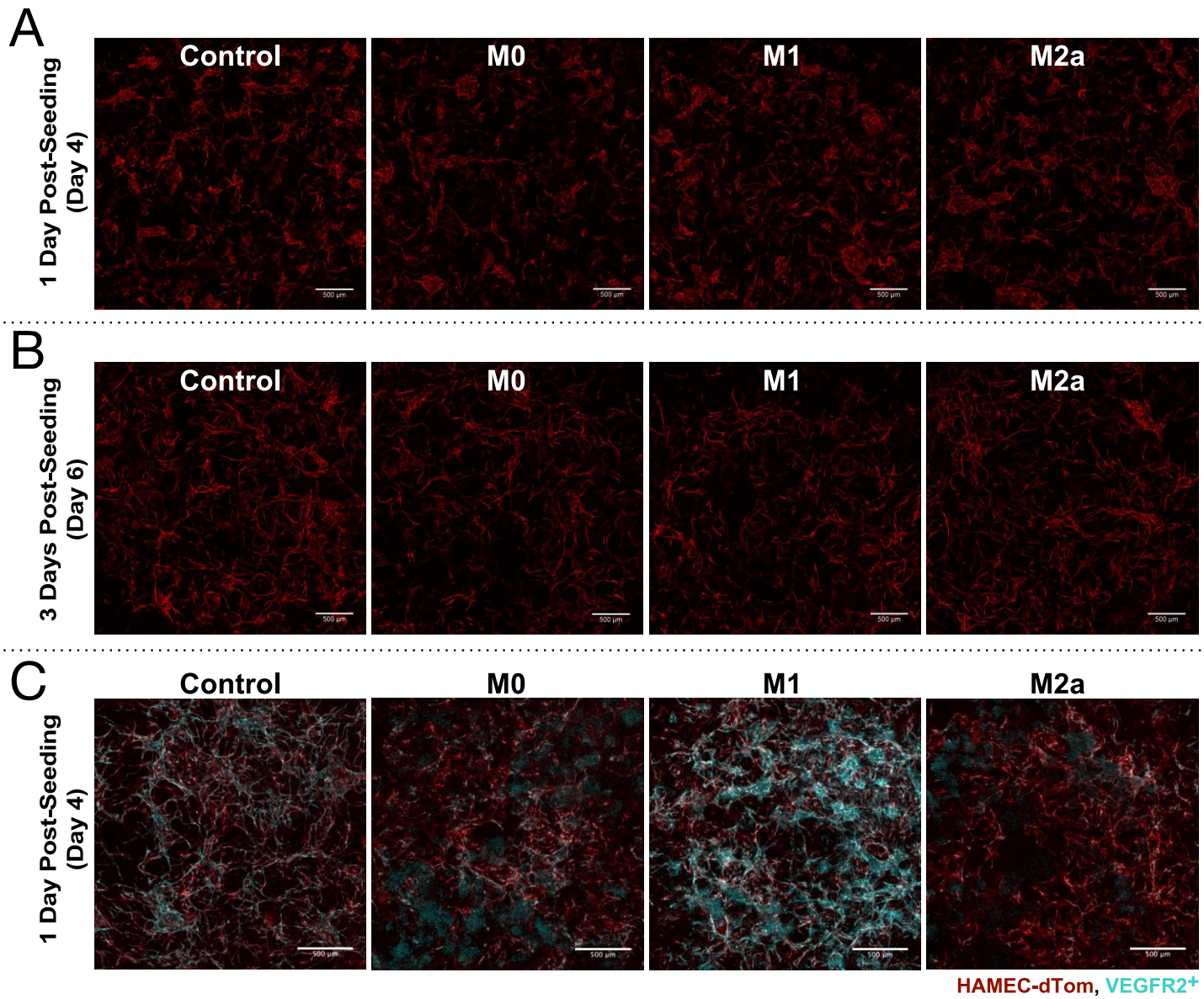


Figure S5. Effects of macrophage phenotype on *in vitro* tissue vascularization. Representative maximum intensity projections of engineered vascular grafts seeded for 1 **(A)** and 3 **(B)** days with M0, M1, or M2a macrophages on day 3 of vessel growth. Constructs without macrophages served as a control; n = 3 per group. Scale bar represents 500 µm. **(C)** Constructs were fixed and stained for the tip cell marker KDR (VEGFR2) via whole mount IHC, and 2x2 tiles were acquired using an LSM700 confocal microscope. Constructs without macrophages served as a control; n = 4-5 per group. Scale bar represents 500 µm.

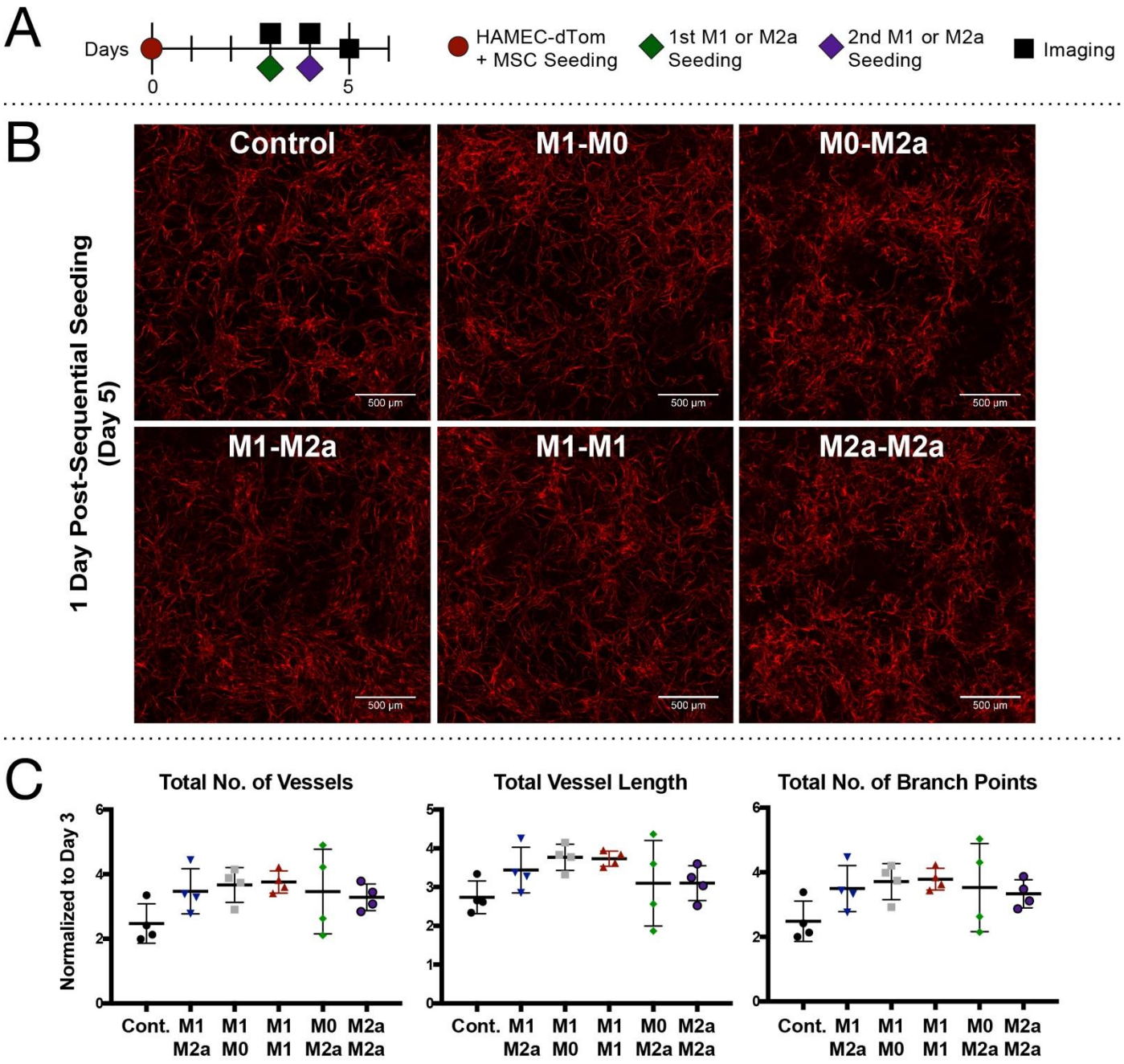


Figure S6. Impact of sequential control (24 h time interval) over macrophage activation on network development. (A) Engineered vascular grafts generated via co-culture of HAMEC-dTom and MSCs on Gelfoam scaffolds for self-assembly into blood vessels. M1 and M2a macrophages were sequentially added to the grafts on days 3 and 4 of vessel development and changes in network morphology were quantified on day 5 via live cell confocal microscopy. Controls included no macrophages, early M1, prolonged M1, late M2a, and prolonged M2a. **(B)** Representative maximum intensity projections of grafts on day 5. Scale bar = 500 µm. **(C)** Changes in network morphology were quantified in terms of number of vessels, vessel length, and number of branch points (junctions between two vessels) using a custom image analysis code in Matlab®. One-way ANOVA with Tukey's post-hoc analysis; n = 4 per group. All data normalized to day 3 baseline measurements and represent mean ± SD.

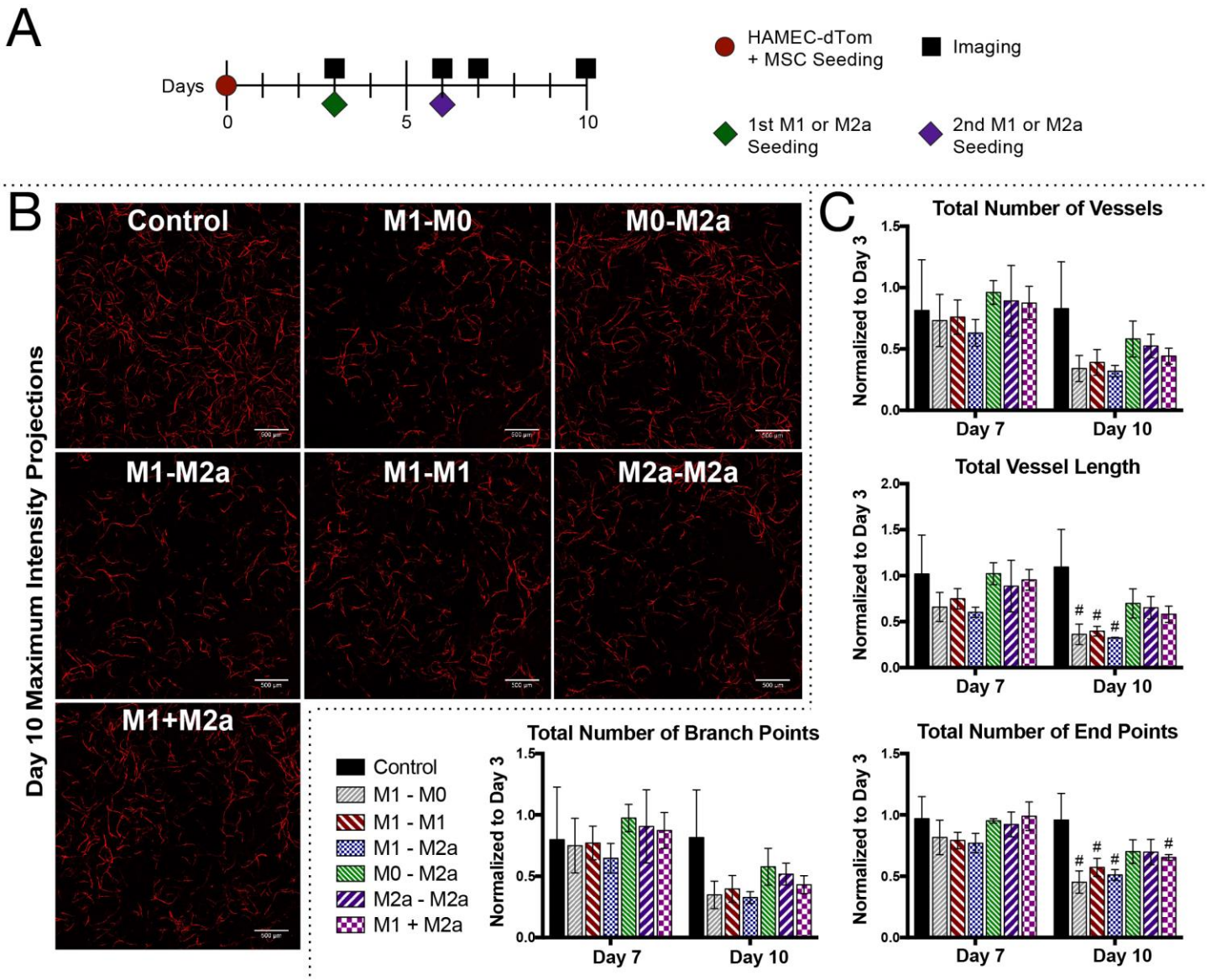
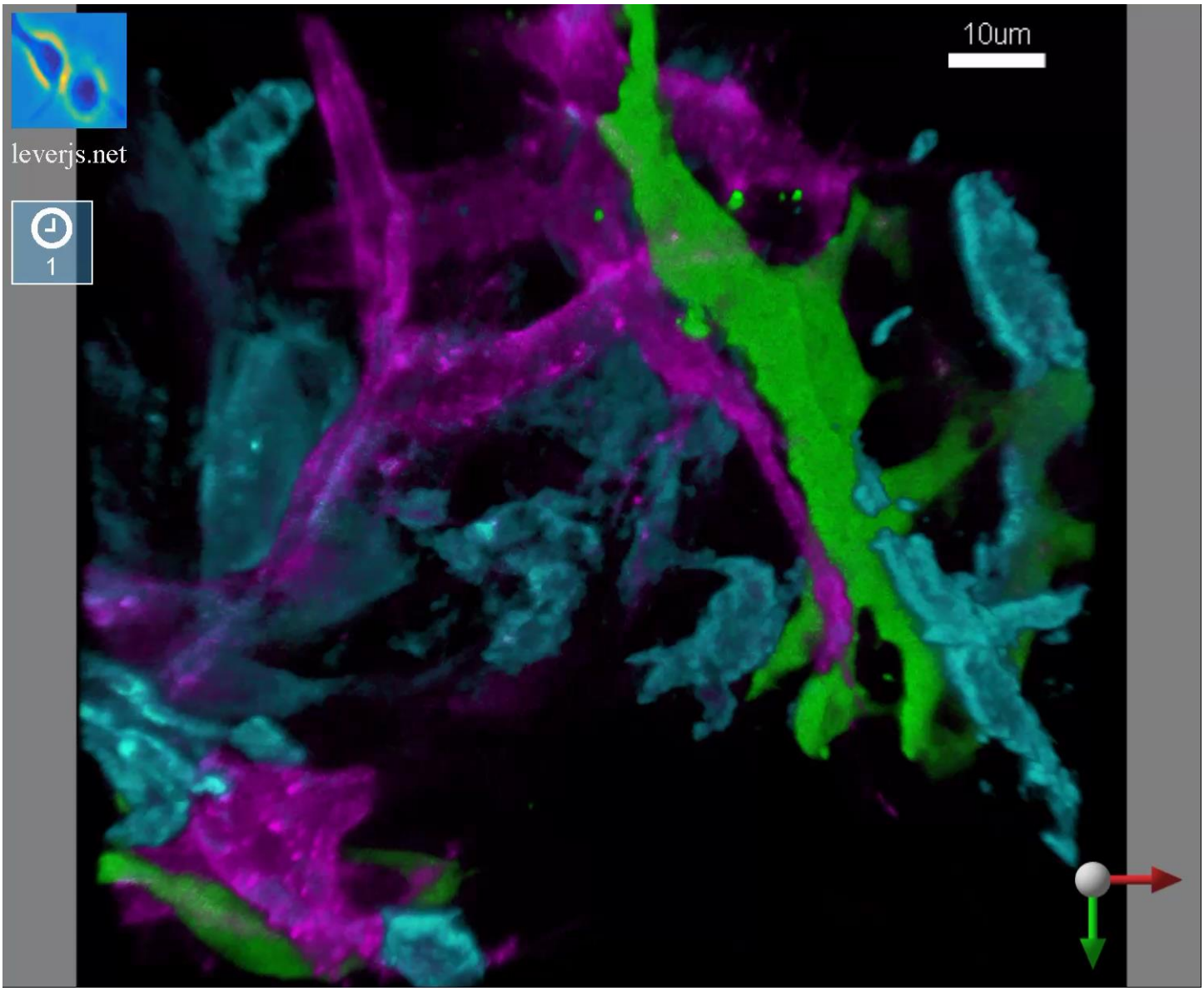
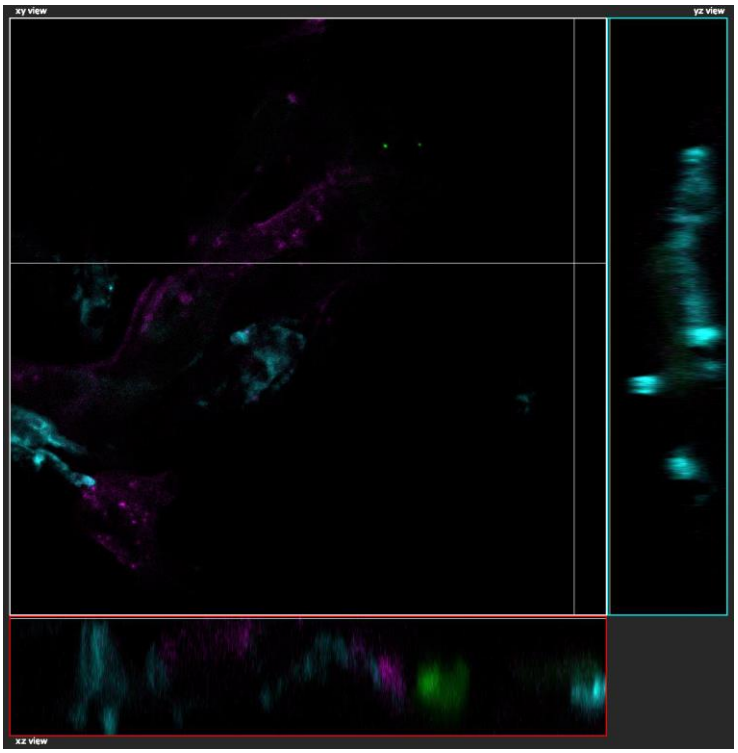


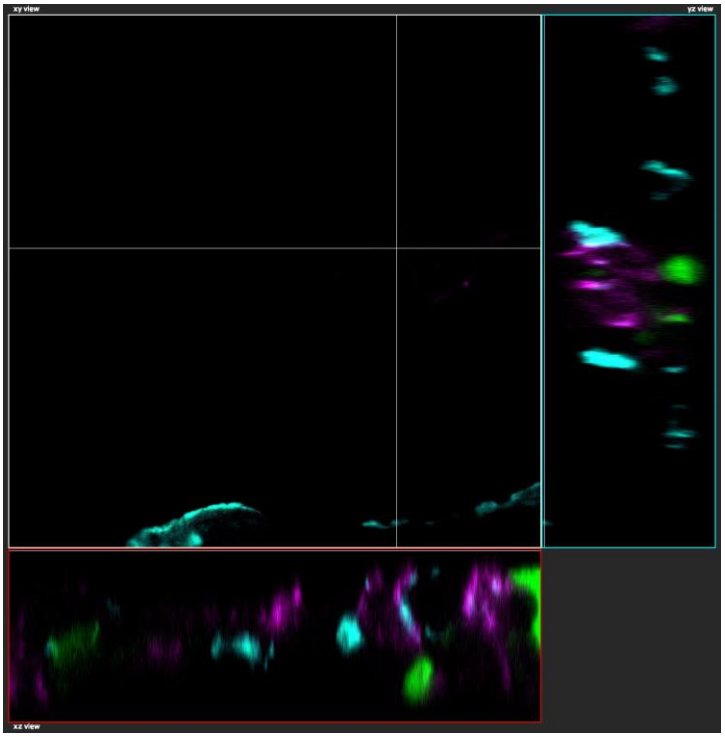
Figure S7. Impact of sequential control (72 h time interval) over macrophage activation on network development. (A) Engineered vascular grafts generated via co-culture of HAMEC-dTom and MSCs on Gelfoam scaffolds for self-assembly into blood vessels. M1 and M2a macrophages were sequentially added to the grafts on days 3 and 6 of vessel development and changes in network morphology were quantified on day 7 and 10 via live cell confocal microscopy. Controls included no macrophages, early M1, prolonged M1, late M2a, and prolonged M2a and simultaneous M1 and M2a. **(B)** Representative maximum intensity projections of grafts on day 10. Scale bar = 500 µm. **(C)** Changes in network morphology were quantified in terms of number of vessels, vessel length, and number of branch points (junctions between two vessels) using a custom image analysis code in Matlab®. Two-way ANOVA with Tukey's post-hoc analysis; n = 3 per group. All data normalized to day 3 baseline measurements and represent mean ± SD. # indicates significance relative to control.



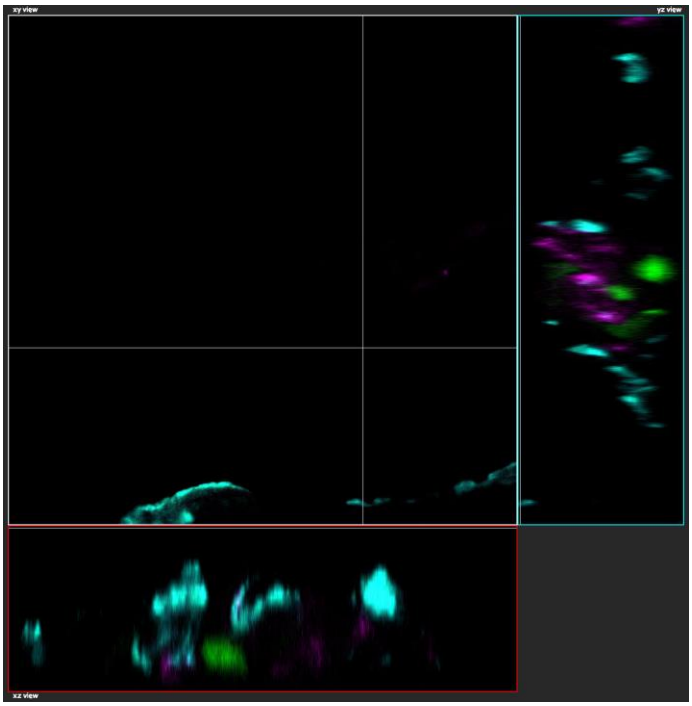
Movie S1: 3D reconstruction of z-stack depicting F4/80+ macrophages in graft tissue during revascularization and integration with host vessels. Z-stack image was acquired via confocal microscopy and processed and analyzed in Matlab® as described in the main text. F4/80+ macrophages shown in cyan; engineered vessels shown in green; host vessels shown in magenta. 3D reconstruction corresponds to maximum intensity projection shown in Fig. 4C.



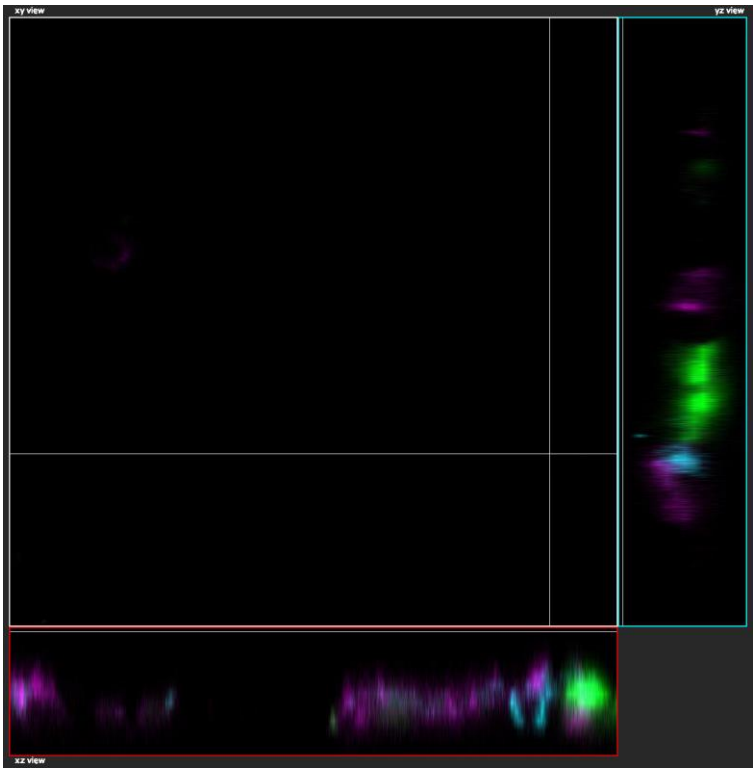
Movie S2: Orthogonal view depicting F4/80+ macrophages forming tube-like structures in graft tissue 14 days post-implantation. F4/80+ macrophages shown in cyan; engineered vessels shown in green; host vessels shown in magenta. Orthogonal views correspond to maximum intensity projection shown in Fig. 4C, and were prepared using ImageJ macro written by Martin Höhne.



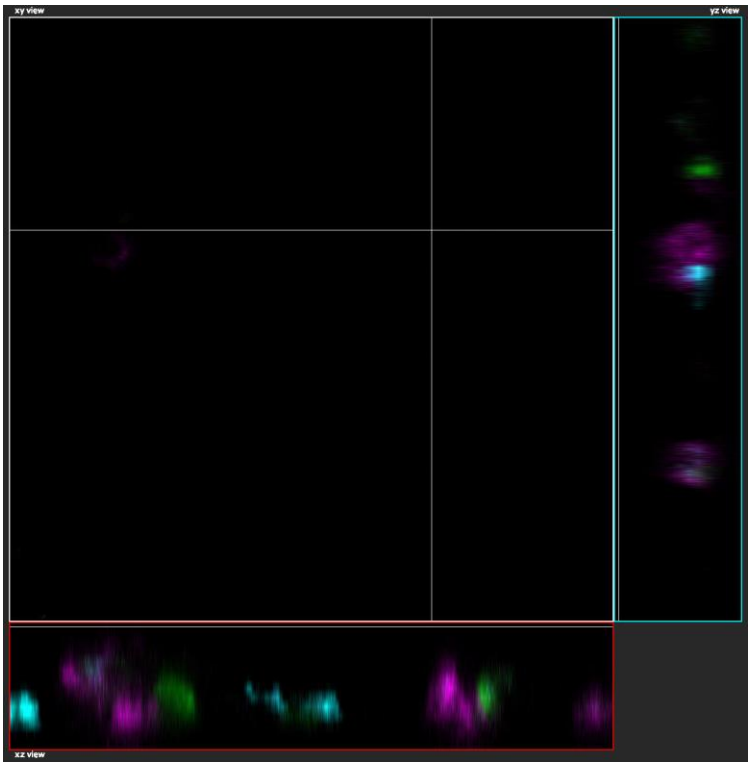
Movie S3: Orthogonal view depicting F4/80+ macrophage interacting with host vessels structures in graft tissue 14 days post-implantation. Host vessels shown in magenta; F4/80+ macrophages shown in cyan; engineered vessels shown in green. Orthogonal views correspond to maximum intensity projection shown in Fig. 4D, and were prepared using ImageJ macro written by Martin Höhne.



Movie S4: Orthogonal view depicting F4/80+ macrophages adjacent to both engineered and host vessels structures in graft tissue 14 days post-implantation. F4/80+ macrophages shown in cyan; engineered vessels shown in green; host vessels shown in magenta. Orthogonal views correspond to maximum intensity projection shown in Fig. 4D, and were prepared using ImageJ macro written by Martin Höhne.



Movie S5: Orthogonal view depicting F4/80+ macrophage wrapping around host vessels structures in graft tissue 14 days post-implantation. Host vessels shown in magenta; F4/80+ macrophages shown in cyan; engineered vessels shown in green. Orthogonal views correspond to maximum intensity projection shown in Fig. 4E, and were prepared using ImageJ macro written by Martin Höhne.



Movie S6: Orthogonal view depicting F4/80+ macrophage bridging vessel segments structures in graft tissue 14 days post-implantation. Host vessels shown in magenta; F4/80+ macrophages shown in cyan; engineered vessels shown in green. Orthogonal views correspond to maximum intensity projection shown in Fig. 4E, and were prepared using ImageJ macro written by Martin Höhne.

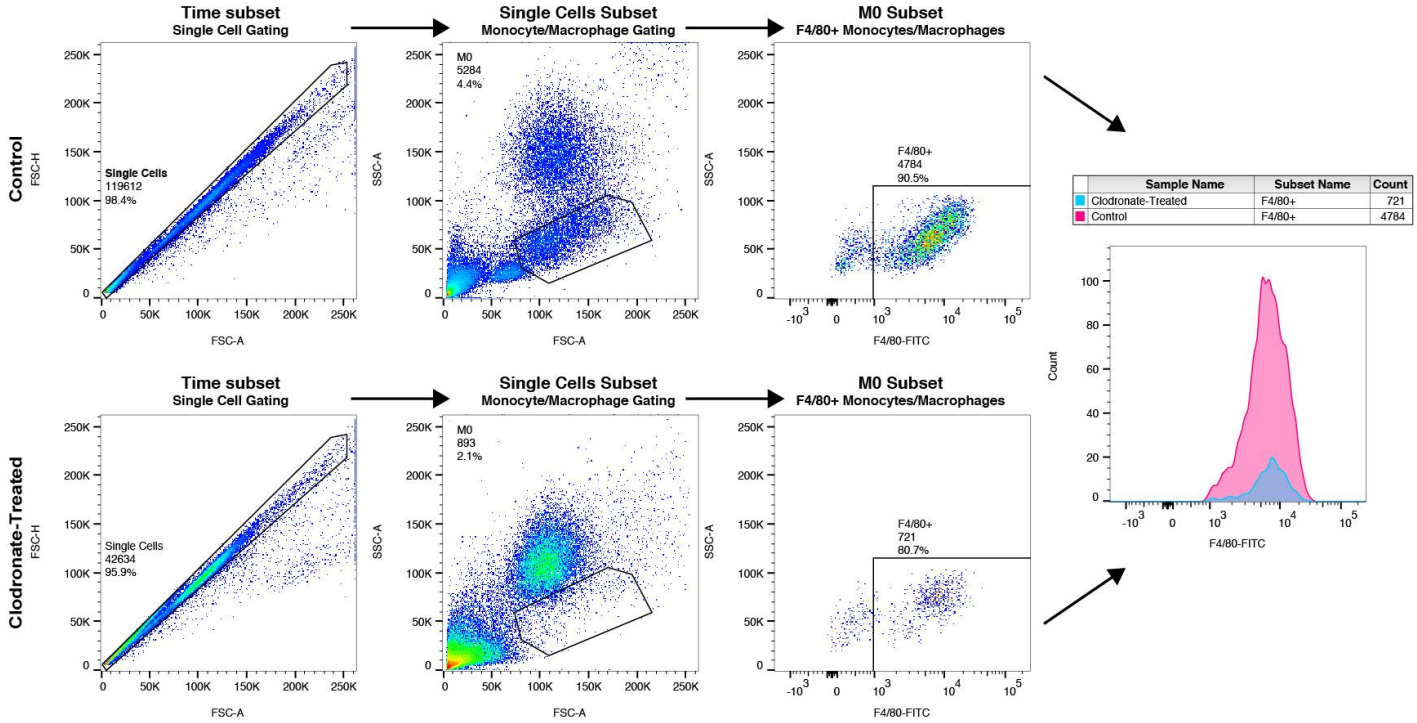


Figure S8. Sample gating of F4/80+ cells in murine whole blood. Pseudocolor dot plots show the scatter of cells collected from whole blood and gating scheme used to identify F4/80+ cells within the monocyte/macrophage population of single cells. Histogram illustrates F4/80+ cell population in murine whole blood after macrophage depletion via clodronate-loaded liposome administration (cyan) and in control mice treated with PBS-loaded liposomes (magenta).