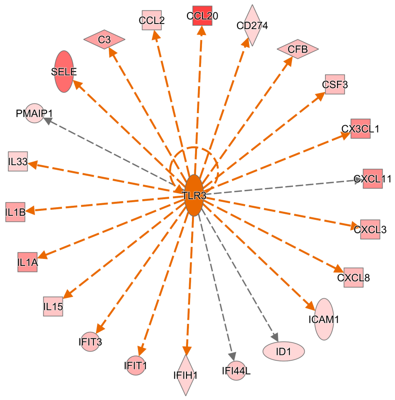
A

Diseases or Functions Annotation	p-Value
Cellular infiltration by leukocytes	2.32E-10
Adhesion of monocytes	2.42E-10
Recruitment of leukocytes	4.45E-10
Attraction of leukocytes	1.86E-09
Infiltration by neutrophils	1.99E-09
Cell movement of neutrophils	2.4E-09
Cellular infiltration	2.8E-09
Cell movement of granulocytes	3.83E-09
Cellular infiltration by phagocytes	3.94E-09

B

Upstream regulator	Predicted State	*P* value
ERK1/2	Activated	9.04E-13
IRF1	Activated	4.21E-11
IL1RN	Inhibited	4.61E-11
TLR3	Activated	4.94E-11
IL10	Inhibited	9.04E-11
RELA	Activated	1.2E-10
TICAM1	Activated	2.44E-10
STAT3	Activated	2.77E-10
Vegf	Activated	4.3E-10

C



Supplemental Figure 1. **Ingenuity Pathway Analysis of LPC-induced genes in HAECs**. A. Top 10 disease or function pathways upregulated by LPI determined by Ingenuity Pathway Analysis (IPA). B. Top 10 predicated upstream regulators of LPI in ECs determined by IPA. C. The 20 TLR3-regulated genes that are significantly induced by LPI in HAECs.

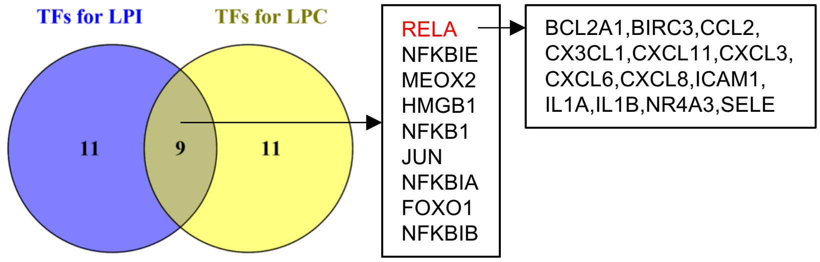
A

Upstream TFs	Predicted State	*P* value
IRF1	Activated	4.2E-11
RELA	Activated	1.2E-10
STAT3	Activated	2.8E-10
NFKBIE		4.1E-09
STAT1	Activated	4.1E-09
MEOX2	Inhibited	1.2E-08
HMGB1	Activated	1.3E-08
NFKB1		1.4E-07
JUN	Activated	2.2E-06
WWTR1		3.9E-06
NFKBIA		4.6E-06
IRF3	Activated	6.0E-06
SMAD3	Activated	9.8E-06
FOXO1	Activated	1.2E-05
ZFP36	Inhibited	1.5E-05
SP1	Activated	2.1E-05
NFKBIB		3.0E-05
SMAD4		3.4E-05
RCAN1		6.2E-05
BCL3		6.5E-05

B

Upstream TFs	Predicted State	*P* value
SREBF2	Activated	6.3E-25
SREBF1	Activated	9.5E-15
SIRT2	Activated	6.6E-09
TP53		5.9E-08
MEOX2	Inhibited	6.2E-08
PPARGC1B		3.2E-07
NFKBIE		1.4E-06
CREB1		2.3E-06
JUN	Activated	7.3E-06
NFKBIB	Activated	8.2E-06
TWIST1		9.9E-06
CREM		9.9E-06
TSC22D3	Inhibited	1.4E-05
RELA	Activated	3.8E-05
NFYB		3.9E-05
CTNNB1		5.1E-05
NFKBIA		5.1E-05
FOXO1		5.3E-05
NFKB1		6.3E-05
HMGB1	Activated	6.3E-05

C



RELA
NFKBIE
MEOX2
HMGB1
NFKB1
JUN
NFKBIA
FOXO1
NFKBIB

BCL2A1,BIRC3,CCL2,
CX3CL1,CXCL11,CXCL3,
CXCL6,CXCL8,ICAM1,
IL1A,IL1B,NR4A3,SELE

Supplemental Figure 2. Upstream transcription factor analysis of the genes induced by LPI and LPC in HAECs. A. Top 20 predicted upstream transcription regulators of LPI in HAECs as determined by Ingenuity Pathway Analysis (IPA). B. Top 20 predicted upstream transcription factors (TFs) of LPC in HAECs as determined by IPA. C. Left & Middle: Venn diagram showing 9 predicted co-upregulated transcription regulators by LPI and LPC using IPA. Right, The 13 RELA-regulated genes that are significantly induced by LPI and LPC in HAECs were shown.

Supplemental Table 1. Gene expression changes of cytokines after LPC/LPI stimulation in HAECs. Red-colored numbers indicate gene expression fold changes that are more than 1.4 folds. FC, fold change.

Gene ID	Symbol	Entrez Gene Name	LPC FC	LPI FC
970	CD70	CD70 molecule	2.92	1.27
1435	CSF1	colony stimulating factor 1	-1.07	-1.10
1437	CSF2	colony stimulating factor 2	1	2.11
1440	CSF3	colony stimulating factor 3	-1.28	1.78
3458	IFNG	interferon gamma	1.00	1.00
3586	IL10	interleukin 10	1	1
3592	IL12A	interleukin 12A	1.40	1.26
3593	IL12B	interleukin 12B	1	1.02
3600	IL15	interleukin 15	-2.08	1.65
3603	IL16	interleukin 16	1.20	1.98
3605	IL17A	interleukin 17A	1	1
3552	IL1A	interleukin 1 alpha	1.43	2.57
3553	IL1B	interleukin 1 beta	1.85	2.21
11009	IL24	interleukin 24	1	1.66
246778	IL27	interleukin 27	1	1
9235	IL32	interleukin 32	2.70	1.02
90865	IL33	interleukin 33	-1.84	1.47
27178	IL37	interleukin 37	-∞	1.54
3565	IL4	interleukin 4	1	1
3569	IL6	interleukin 6	1.12	-1.28
3574	IL7	interleukin 7	1.43	-1.39
4049	LTA	lymphotoxin alpha	1	-1.61
4050	LTB	lymphotoxin beta	1	2.39
7124	TNF	tumor necrosis factor	1	1
8741	TNFSF13	TNF superfamily member 13	1.54	-1.15
10673	TNFSF13B	TNF superfamily member 13b	∞	-2.67
9966	TNFSF15	TNF superfamily member 15	1.79	2.64

Supplemental Table 2. Gene expression changes of chemokines after LPC/LPI stimulation in HAECs. Red-colored numbers indicate gene expression fold changes that are more than 1.4 folds. FC, fold change.

Gene ID	Symbol	Class	Entrez Gene Name	LPC FC	LPI FC
6346	CCL1	Beta	C-C motif chemokine ligand 1	1	1
6347	CCL2	Beta	C-C motif chemokine ligand 2	1.78	1.60
6348	CCL3	Beta	C-C motif chemokine ligand 3	1	1
6351	CCL4	Beta	C-C motif chemokine ligand 4	1	1
6352	CCL5	Beta	C-C motif chemokine ligand 5	1	-1.12
6354	CCL7	Beta	C-C motif chemokine ligand 7	∞	1
6355	CCL8	Beta	C-C motif chemokine ligand 8	1	1
6356	CCL11	Beta	C-C motif chemokine ligand 11	1	1
6357	CCL13	Beta	C-C motif chemokine ligand 13	1	1
6358	CCL14	Beta	C-C motif chemokine ligand 14	-1.13	1.06
6359	CCL15	Beta	C-C motif chemokine ligand 15	1	1.72
6360	CCL16	Beta	C-C motif chemokine ligand 16	1.09	1.42
6361	CCL17	Beta	C-C motif chemokine ligand 17	1	1
6362	CCL18	Beta	C-C motif chemokine ligand 18	1	1
6363	CCL19	Beta	C-C motif chemokine ligand 19	1	1
6364	CCL20	Beta	C-C motif chemokine ligand 20	-1.03	5.46
6366	CCL21	Beta	C-C motif chemokine ligand 21	-∞	1
6367	CCL22	Beta	C-C motif chemokine ligand 22	1	1.06
6368	CCL23	Beta	C-C motif chemokine ligand 23	-1.54	-2.70
6369	CCL24	Beta	C-C motif chemokine ligand 24	∞	-1.46
6370	CCL25	Beta	C-C motif chemokine ligand 25	1	1
10344	CCL26	Beta	C-C motif chemokine ligand 26	1	3.08
10850	CCL27	Beta	C-C motif chemokine ligand 27	1	1
56477	CCL28	Beta	C-C motif chemokine ligand 28	1.95	1.34
6376	CX3CL1	Delta	C-X3-C motif chemokine ligand 1	2.03	2.85
2919	CXCL1	Alpha	C-X-C motif chemokine ligand 1	1.59	1.29
2920	CXCL2	Alpha	C-X-C motif chemokine ligand 2	1.26	1.17
2921	CXCL3	Alpha	C-X-C motif chemokine ligand 3	1.46	2.18
6374	CXCL5	Alpha	C-X-C motif chemokine ligand 5	-∞	3.29
6372	CXCL6	Alpha	C-X-C motif chemokine ligand 6	1.95	2.54
3576	CXCL8	Alpha	C-X-C motif chemokine ligand 8	1.43	1.86
4283	CXCL9	Alpha	C-X-C motif chemokine ligand 9	1	1
3627	CXCL10	Alpha	C-X-C motif chemokine ligand 10	1	1
6373	CXCL11	Alpha	C-X-C motif chemokine ligand 11	1.78	2.80
6387	CXCL12	Alpha	C-X-C motif chemokine ligand 12	1.77	-1.40
10563	CXCL13	Alpha	C-X-C motif chemokine ligand 13	1	1
9547	CXCL14	Alpha	C-X-C motif chemokine ligand 14	∞	-1.96
58191	CXCL16	Alpha	C-X-C motif chemokine ligand 16	-1.72	-1.07
284340	CXCL17	Alpha	C-X-C motif chemokine ligand 17	1	1
6375	XCL1	Gamma	X-C motif chemokine ligand 1	1	1
6846	XCL2	Gamma	X-C motif chemokine ligand 2	1	1

Supplemental Table 3. Gene expression changes of T cell co-stimulation and co-inhibition receptors after LPC/LPI stimulation in HAECs. Red-colored numbers indicate gene expression fold changes that are more than 1.4 folds. FC, fold change.

Gene ID	Symbol	Alias	Entrez Gene Name	LPC FC	LPI FC
940	CD28		CD28 molecule	∞	1.70
29851	ICOS		inducible T-cell co-stimulator	1	1
1493	CTLA4		cytotoxic T-lymphocyte-associated protein 4	-∞	-3.02
5133	PDCD1	PD1	programmed cell death 1	1	1
151888	BTLA		B and T lymphocyte associated	1	2.75
8764	TNFRSF14	HVEM	tumor necrosis factor receptor superfamily, member 14	1.11	-1.35
939	CD27		CD27 molecule	1	-1.24
3604	TNFRSF9	41-BB	tumor necrosis factor receptor superfamily, member 9	4.38	1
7293	TNFRSF4	OX40	tumor necrosis factor receptor superfamily, member 4	1.17	1.73
8718	TNFRSF25	DR3	tumor necrosis factor receptor superfamily, member 25	1.12	-1.21
8784	TNFRSF18	GITR	tumor necrosis factor receptor superfamily, member 18	∞	1
943	TNFRSF8	CD30	tumor necrosis factor receptor superfamily, member 8	-∞	1.14
6504	SLAMF1	SLAM	signaling lymphocytic activation molecule family member 1	1	1
914	CD2		CD2 molecule	1	1
51744	CD244	2B4	CD244 molecule, natural killer cell receptor 2B4	1	1
26762	HAVCR1	TIM1	hepatitis A virus cellular receptor 1	1	2.26
84868	HAVCR2	TIM3	hepatitis A virus cellular receptor 2	1	-1.85
201633	TIGIT		T cell immunoreceptor with Ig and ITIM domains	1	1.04
10666	CD226		CD226 molecule	1	1.18
11126	CD160		CD160 molecule	1	1.36
3902	LAG3		lymphocyte-activation gene 3	-1.54	1.09
3903	LAIR1		leukocyte-associated immunoglobulin-like receptor 1	1	1.62
941	CD80	B7-1	CD80 molecule	1	1
29126	CD274	B7-H1	CD274 molecule	1.39	1.43

Supplemental Table 4. Gene expression changes of key regulators in endothelial-mesenchymal transition after LPC/LPI stimulation in HAECs. Red-colored numbers indicate gene expression fold changes that are more than 1.4 folds. FC, fold change.

Gene ID	Symbol	Alias	Entrez Gene Name	LPC FC	LPI FC
3678	ITGA5	CD49e	integrin subunit alpha 5	1.05	-1.04
800	CALD1		caldesmon 1	1.44	1.22
4478	MSN		moesin	1.19	-1.08
6695	SPOCK1	Testican	SPARC/osteonectin, cwcv and kazal like domains proteoglycan 1	-1.07	-1.01
6678	SPARC	Osteonectin	secreted protein acidic and cysteine rich	1.04	-1.06
3685	ITGAV	CD51	integrin subunit alpha V	1.12	1
79026	AHNAK	Desmoyokin	AHNAK nucleoprotein	-1.41	-1.14
4851	NOTCH1		notch 1	-1.17	-1.15
182	JAG1	CD339	jagged 1	1.01	-1.04
6583	SLC22A4		solute carrier family 22 member 4	-1.31	1.13
9839	ZEB2	Sip1	zinc finger E-box binding homeobox 2	1	1.07
7852	CXCR4	CD184	C-X-C motif chemokine receptor 4	1.09	-1.03
6935	ZEB1		zinc finger E-box binding homeobox 1	1.01	1.04
23493	HEY2	CHF1	hes related family bHLH transcription factor with YRPW motif 2	1.04	1
6615	SNAI1	SNAIL	snail family transcriptional repressor 1	-1.24	1.06
6591	SNAI2	SLUG	snail family transcriptional repressor 2	1.75	-1.03
23462	HEY1		hes related family bHLH transcription factor with YRPW motif 1	1.22	1.33
7291	TWIST1	TWIST	twist family bHLH transcription factor 1	-1.03	1.21
81029	WNT5B		Wnt family member 5B	-1.03	1.03
7481	WNT11		Wnt family member 11	∞	-1.23
26508	HEYL		hes related family bHLH transcription factor with YRPW motif-like	1	1
23230	VPS13A		vacuolar protein sorting 13 homolog A	-1.35	-1.15

Supplemental Table 5. Gene expression changes of mesenchymal markers after LPC/LPI stimulation in HAECs. Red-colored numbers indicate gene expression fold changes that are more than 1.4 folds. FC, fold change.

Gene ID	Symbol	Alias	Entrez Gene Name	LPC FC	LPI FC
59	ACTA2	aSMA	actin, alpha 2, smooth muscle, aorta	-1.16	-1.13
8038	ADAM12		ADAM metallopeptidase domain 12	1.58	1.35
57124	CD248	Endosialin	CD248 molecule	1.00	1.12
960	CD44		CD44 molecule (Indian blood group)	-1.04	-1.13
1009	CDH11	CAD11	cadherin 11	1.12	-1.03
1000	CDH2	NCAD	cadherin 2	1.04	1
1264	CNN1		calponin 1	1.75	-1.61
1277	COL1A1		collagen type I alpha 1 chain	-3.08	1.14
1278	COL1A2		collagen type I alpha 2 chain	1.11	1
1281	COL3A1		collagen type III alpha 1 chain	1.19	1
1289	COL5A1		collagen type V alpha 1 chain	1.02	-1.17
1290	COL5A2		collagen type V alpha 2 chain	1.10	-1.02
1291	COL6A1		collagen type VI alpha 1 chain	1.01	-1.09
1490	CTGF	CCN2	connective tissue growth factor	-1.05	-1.06
4921	DDR2		discoidin domain receptor tyrosine kinase 2	-1.20	1.10
10395	DLC1	STARD12	DLC1 Rho GTPase activating protein	-1.07	1.05
2191	FAP	DPPIV	fibroblast activation protein alpha	-1.06	1.08
2192	FBLN1		fibulin 1	1.00	1.14
10516	FBLN5		fibulin 5	-1.08	-1.43
2335	FN1		fibronectin 1	-1.22	-1.04
3486	IGFBP3		insulin like growth factor binding protein 3	-1.75	-1.22
4323	MMP14		matrix metallopeptidase 14	1.01	-1.13
4313	MMP2		matrix metallopeptidase 2	-1.05	-1.16
4318	MMP9		matrix metallopeptidase 9	∞	-4.03
4627	MYH9	NMHC-IIA	myosin heavy chain 9	1.05	-1.12
91624	NEXN		nexilin F-actin binding protein	1.38	-1.13
22795	NID2		nidogen 2	1.06	1.56
4854	NOTCH3	CADASIL	notch 3	-2.51	1.44
4907	NT5E	CD73	5'-nucleotidase ecto	1.17	1.12
5033	P4HA1	P4HA	prolyl 4-hydroxylase subunit alpha 1	1.06	1.15
5327	PLAT	tPA	plasminogen activator, tissue type	1.28	1.05
5328	PLAU		plasminogen activator, urokinase	1.05	1.20
5329	PLAUR	CD87	plasminogen activator, urokinase receptor	1	-1.15
26499	PLEK2		pleckstrin 2	1.29	-1.20
10631	POSTN		periostin	-1.12	-1.07
5578	PRKCA	PKCa	protein kinase C alpha	-1.01	1.02
5806	PTX3		pentraxin 3	1.06	1.14
8434	RECK		reversion inducing cysteine rich protein with kazal motifs	-1.07	1.13
6275	S100A4		S100 calcium binding protein A4	2.73	1.08
5054	SERPINE1		serpin family E member 1	1.27	-1.11
5270	SERPINE2		serpin family E member 2	1.11	-1.15
6696	SPP1	Osteopontin	secreted phosphoprotein 1	1.00	-3.70
6722	SRF		serum response factor	1.26	-1.07
5552	SRGN	PPG	serglycin	1.06	1.14
6876	TAGLN	SM22	transgelin	1.32	-1.22
7168	TPM1		tropomyosin 1 (alpha)	1.27	-1.06
7846	TUBA1A		tubulin alpha 1a	1.15	-1.17
1462	VCAN		versican	-1.27	-1.34
7431	VIM		vimentin	-1.06	1