Supplementary Table 2: List of Regulators identified by Ingenuity Pathway Analysis (IPA). IPA of the genes shown to be significantly (FDR corrected P value < 0.01) up-regulated or down-regulated >2-fold at 24 h vs basal was performed. To ensure gene annotations were current, Illumina probe IDs were used to interrogate the Ensembl BioMart database (www.ensembl.org/biomart/martview), and the Ensembl gene lists used in pathway and functional analyses (Ingenuity Systems): the Regulators identified are presented. The Consistency Score is an heuristic measure used to rank networks within the same global analysis setting, with higher values indicating greater interconnectivity with the highlighted Regulator. Node Total refers to the number of genes identified by IPA for a given Regulator, whilst Target Total refers to the actual number of genes identified from the differential expression test which are listed as Target Molecules (listed by gene name). Diseases and Functions lists the likely involvement for each identified Regulator, where a 100% Relationship indicates the literature strongly supports such an association and 0% reflects a possible indirect association.

Regulators	Consistency Score	Node Total	Target Total	Target Molecules	Diseases & Functions	Known Regulator-Disease/Function Relationship
ERK1/2	3.474	16	14	CCL2,CCL8,CD44,CXCL8,F3,FGF2,ICAM1,IL1B,IL6,NOS2,PTGS2, SERPINE1,TREM1,VEGFA	cell movement of blood cells	100% (1/1)
ERK1/2	3.474	16	14	CCL2,CCL8,CD44,CXCL8,F3,FGF2,ICAM1,IL1B,IL6,NOS2,PTGS2, SERPINE1,TREM1,VEGFA	leukocyte migration	100% (1/1)
PTGS2	3.333	11	9	CCL2,CXCL5,CXCL8,ICAM1,IL1B,IL6,NOS2,TGM2,VEGFA	leukocyte migration	100% (1/1)
IL18	3.328	15	13	CCL2,CD44,CXCL8,ICAM1,IL1B,IL6,MMP1,MMP13,NFKBIZ,NOS2,PTGS2,TGFBR2,VEGFA	activation of cells	100% (1/1)
IL1B	3.317	13	11	CCL2,CCL7,CXCL1,CXCL2,CXCL5,CXCL6,CXCL8,LBP,NGF,SAA1, SERPINE1	chemotaxis of myeloid cells	100% (1/1)
MYD88	3.317	13	11	CCL2,CD44,CXCL1,CXCL2,CXCL6,CXCL8,ICAM1,IL1B,IL6,NOS2,SAA1	migration of granulocytes	100% (1/1)
TLR7	3.317	13	11	CCL2,CCL20,CD38,CD44,CXCL1,CXCL2,CXCL8,FGF2,IL1B,IL6,SOCS1	chemotaxis	0% (0/1)
TLR7	3.317	13	11	CCL2,CCL20,CD38,CD44,CXCL1,CXCL2,CXCL8,FGF2,IL1B,IL6,SOCS1	homing of cells	0% (0/1)
IL1B	3.182	10	8	CCL2,CCL7,CXCL1,CXCL2,CXCL5,CXCL6,CXCL8,LBP	chemotaxis of granulocytes	100% (1/1)
IL1B	3.182	10	8	CCL2,CCL7,CXCL1,CXCL2,CXCL5,CXCL6,CXCL8,LBP	chemotaxis of neutrophils	100% (1/1)
HIF1A	3.162	12	10	CD44,CXCL2,CXCL8,FYN,IL1B,IL6,NOS2,PTGS2,SERPINE1,VEGFA	cell movement of phagocytes	100% (1/1)
MYD88	3.162	12	10	CD44,CXCL1,CXCL2,CXCL6,CXCL8,ICAM1,IL1B,IL6,NOS2,SAA1	migration of neutrophils	100% (1/1)
TICAM1	3.162	12	10	CCL2,CD38,CXCL2,CXCL6,CXCL8,IL1B,IL6,PTGS2,SERPINE1,SOCS1	chemotaxis	0% (0/1)
PTGS2	3.024	9	7	CCL2,CXCL8,ICAM1,IL1B,IL6,NOS2,VEGFA	activation of blood cells	100% (1/1)

Regulators	Consistency Score	Node Total	Target Total	Target Molecules	Diseases & Functions	Known Regulator-Disease/Function Relationship
PTGS2	3.024	9	7	CCL2,CXCL8,ICAM1,IL1B,IL6,NOS2,VEGFA	activation of leukocytes	100% (1/1)
PTGS2	3.024	9	7	CCL2,CXCL8,IL1B,IL6,MMP1,NOS2,VEGFA	invasion of cells	100% (1/1)
AGER	3	11	9	CCL2,F3,ICAM1,IL1B,IL6,PTGS2,S100A9,SERPINE1,VEGFA	cell movement	100% (1/1)
AGER	3	11	9	CCL2,F3,ICAM1,IL1B,IL6,PTGS2,S100A9,SERPINE1,VEGFA	leukocyte migration	100% (1/1)
PTGS2	3	11	9	CCL2,CXCL5,CXCL8,ICAM1,IL1B,IL6,NOS2,TGM2,VEGFA	cell movement of myeloid cells	100% (1/1)
PTGS2	3	11	9	CCL2,CXCL5,CXCL8,IL1B,IL6,MMP1,NOS2,TGM2,VEGFA	cell movement of tumor cell lines	100% (1/1)
PTGS2	3	11	9	CCL2,CXCL5,CXCL8,IL1B,IL6,MMP1,NOS2,TGM2,VEGFA	migration of tumor cell lines	100% (1/1)
TLR4	3	11	9	CCL2,CD44,CXCL2,CXCL6,CXCL8,ICAM1,IL1B,IL6,NOS2	migration of granulocytes	0% (0/1)
TNFRSF1A	3	11	9	CCL2,CD44,CXCL1,CXCL2,CXCL8,ICAM1,IL1B,IL6,SAA1	migration of granulocytes	100% (1/1)
IL18	2.887	14	12	CCL2,CCL20,CD44,CXCL8,ICAM1,IL1B,IL6,NFKBIZ,NOS2,PTGS2, TGFBR2,VEGFA	cell movement of leukocytes	100% (1/1)
IL1B	2.858	8	6	CCL2,FGF2,LIF,NGF,PLD1,VEGFA	activation of protein	100% (1/1)
PGF	2.858	8	6	CCL2,CCL20,CXCL8,IL1B,IL6,SERPINE1	chemotaxis	100% (1/1)
PTGS2	2.858	8	6	CCL2,CXCL8,IL1B,IL6,NOS2,VEGFA	activation of phagocytes	100% (1/1)
PTGS2	2.858	8	6	CCL2,CXCL8,IL6,MMP1,NOS2,VEGFA	invasion of tumor cell lines	100% (1/1)
ERK1/2	2.846	12	10	CCL2,CD44,CXCL8,F3,FGF2,ICAM1,IL1B,IL6,SERPINE1,VEGFA	recruitment of cells	0% (0/1)
Jnk	2.846	12	10	CCL2,CXCL6,CXCL8,ICAM1,IL1B,IL6,NOS2,PTGS2,SERPINE1,TGM2	leukocyte migration	100% (1/1)
NFkB (complex)	2.846	12	10	CCL2,CD44,CXCL1,CXCL2,CXCL6,CXCL8,ICAM1,IL1B,IL6,NOS2	migration of granulocytes	0% (0/1)
P38 MAPK	2.846	12	10	CCL2,CD82,CEBPB,CXCL8,IL1B,IL6,NGF,NOS2,PTGS2,VEGFA	synthesis of lipid	100% (1/1)
TLR4	2.846	12	10	CCL2,CCL20,CD44,CXCL2,CXCL8,ICAM1,IL1B,IL6,NFKBIA,NOD2	recruitment of blood cells	100% (1/1)

Regulators	Consistency Score	Node Total	Target Total	Target Molecules	Diseases & Functions	Known Regulator-Disease/Function Relationship
TLR4	2.846	12	10	CCL2,CCL20,CD44,CXCL2,CXCL8,ICAM1,IL1B,IL6,NFKBIA,NOD2	recruitment of cells	100% (1/1)
TLR4	2.846	12	10	CCL2,CCL20,CD44,CXCL2,CXCL8,ICAM1,IL1B,IL6,NFKBIA,NOD2	recruitment of leukocytes	100% (1/1)
TNFRSF1A	2.846	12	10	CCL2,CD44,CXCL1,CXCL2,CXCL8,ICAM1,IL1B,IL6,LBP,SAA1	cell movement of granulocytes	100% (1/1)
TNFRSF1A	2.846	12	10	CCL2,CD44,CXCL1,CXCL2,CXCL8,ICAM1,IL1B,IL6,LBP,SAA1	cell movement of neutrophils	100% (1/1)
TNFRSF1A	2.846	12	10	CCL2,CCL20,CD44,CXCL1,CXCL2,CXCL8,ICAM1,IL1B,IL6,SERPINE1	recruitment of leukocytes	100% (1/1)
CCL5	2.828	10	8	C5AR1,CCL2,CD44,CXCL2,CXCL8,IL1B,IL6,PLAUR	cell movement of leukocytes	100% (1/1)
CCL5	2.828	10	8	C5AR1,CCL2,CD44,CXCL2,CXCL8,IL1B,IL6,PLAUR	chemotaxis	100% (1/1)
ECSIT	2.828	10	8	CD44,CXCL8,IER3,IL1B,IL6,NFKBIA,PLAUR,PTGS2	invasion of cells	0% (0/1)
IL17A	2.828	10	8	CCL2,CXCL1,CXCL2,CXCL5,CXCL6,CXCL8,IL1B,S100A9	chemotaxis of neutrophils	0% (0/1)
IL1R1	2.828	10	8	CXCL8,ICAM1,IL1B,IL6,LBP,NOS2,PTGS2,SAA1	activation of leukocytes	0% (0/1)
MIF	2.828	10	8	CD44,CXCL2,CXCL8,HIF1A,ICAM1,IL1B,IL6,NOS2	cell movement of leukocytes	100% (1/1)
MIF	2.828	10	8	ACTA2,CD44,CXCL8,HIF1A,IL1B,IL6,MMP1,NOS2	invasion of cells	100% (1/1)
PRKCD	2.828	10	8	CCL20,CXCL8,IL1B,IL6,LIF,SERPINE1,SOCS1,VEGFA	chemotaxis	100% (1/1)
PTGS2	2.828	10	8	CCL2,CXCL5,CXCL8,IL1B,IL6,NOS2,TGM2,VEGFA	cell movement of breast cancer cell lines	0% (0/1)
PTGS2	2.828	10	8	CCL2,CXCL5,CXCL8,IL1B,IL6,NOS2,TGM2,VEGFA	migration of breast cancer cell lines	0% (0/1)
TLR4	2.828	10	8	CCL2,CD44,CXCL2,CXCL8,ICAM1,IL1B,NFKBIA,NOD2	recruitment of phagocytes	100% (1/1)
TNFRSF1A	2.828	10	8	CCL2,CD44,CXCL1,CXCL2,CXCL8,ICAM1,IL1B,SERPINE1	recruitment of phagocytes	100% (1/1)
TNFSF12	2.828	10	8	CCL2,CXCL2,CXCL6,CXCL8,ICAM1,IL1B,IL6,S100A9	migration of granulocytes	0% (0/1)

Regulators	Consistency Score	Node Total	Target Total	Target Molecules	Diseases & Functions	Known Regulator-Disease/Function Relationship
miR-155-5p (miRNAs w/seed UAAUGCU)	2.828	10	8	CCL20,CXCL1,CXCL2,CXCL8,IL1B,IL6,SERPINE1,SOCS1	chemotaxis	0% (0/1)
JUN	2.75	18	16	CCL2,CCL8,CD44,CXCL5,CXCL8,IL1B,IL6,LIF,MMP1,NFKBIA,NGF,NOS2,PLAUR,PTGS2,SERPINE1,VEGFA	cell movement of tumor cell lines	100% (1/1)
COL18A1	2.714	13	11	CCL2,F3,FGF2,HIF1A,IL6,MMP1,NOS2,PTGS2,SERPINE1,THBS1,VEGFA	neoplasia of cells	100% (1/1)
EGFR	2.714	13	11	CXCL8,F3,ICAM1,IL1B,IL6,NOS2,PLAUR,PTGS2,SERPINE1,TGM2,VEGFA	leukocyte migration	100% (1/1)
PTGS2	2.683	7	5	CCL2,CXCL8,IL1B,IL6,NOS2	activation of myeloid cells	100% (1/1)
ZC3H12A	2.683	7	5	CCL2,IL1B,IL6,NOS2,TNFRSF1B	leukocyte migration	100% (1/1)
RELA	2.673	16	14	CCL2,CCL20,CD44,CXCL1,CXCL2,CXCL8,HIF1A,ICAM1,IL1B,IL6, NOS2,PTGS2,TGM2,VEGFA	adhesion of immune cells	100% (1/1)
CD40LG	2.667	11	9	CCL2,CXCL8,IL1B,IL6,NAMPT,NFKBIA,NOS2,PTGS2,VEGFA	invasion of cells	100% (1/1)
CSF2	2.667	11	9	CCL2,CD38,CXCL8,ICAM1,IL1B,IL6,NOS2,TGM2,TNFRSF1B	cell movement of leukocytes	100% (1/1)
IL6	2.667	11	9	CCL2,CCL20,CXCL2,CXCL6,ICAM1,NOS2,PTGS2,SAA1,VEGFA	migration of phagocytes	100% (1/1)
CAMP	2.646	9	7	CCL2,CCL20,CCL7,CXCL1,CXCL8,IL1B,IL6	chemotaxis	100% (1/1)
CCL5	2.646	9	7	CCL2,CD44,CXCL2,CXCL8,IL1B,IL6,PLAUR	adhesion of blood cells	100% (1/1)
EGR1	2.646	9	7	CCL2,CD44,CXCL2,CXCL8,ICAM1,IL1B,VEGFA	accumulation of blood cells	100% (1/1)
EGR1	2.646	9	7	CCL2,CD44,CXCL2,CXCL8,ICAM1,IL1B,VEGFA	accumulation of leukocytes	100% (1/1)
EGR1	2.646	9	7	CCL2,CD44,CXCL2,CXCL6,CXCL8,ICAM1,IL1B	cell movement of neutrophils	0% (0/1)
EGR1	2.646	9	7	CCL2,CD44,CXCL2,CXCL6,CXCL8,ICAM1,IL1B	migration of granulocytes	0% (0/1)
ERK	2.646	9	7	CCL2,FGF2,ICAM1,IL1B,IL6,LIF,PTGS2	formation of osteoclasts	0% (0/1)
IL1B	2.646	9	7	CCL2,FGF2,ICAM1,IL11,IL6,LIF,PTGS2	formation of osteoclasts	100% (1/1)

Regulators	Consistency Score	Node Total	Target Total	Target Molecules	Diseases & Functions	Known Regulator-Disease/Function Relationship
Immunoglobulin	2.646	9	7	CCL2,CCL7,CCL8,CXCL2,IL1B,NFKBIA,NOS2	cell movement of myeloid cells	100% (1/1)
Immunoglobulin	2.646	9	7	CCL2,CCL7,CCL8,CXCL2,IL1B,NFKBIA,NOS2	cell movement of phagocytes	100% (1/1)
LCN2	2.646	9	7	CCL20,CXCL2,CXCL6,IL1B,IL1RN,IL6,NOS2	inflammatory response	100% (1/1)
MAP2K3	2.646	9	7	CCL8,ICAM1,IL1B,IL6,NOS2,SERPINE1,VEGFA	leukocyte migration	100% (1/1)
NLRP12	2.646	9	7	CXCL2,CXCL6,CXCL8,ICAM1,IL1B,IL6,NOS2	migration of neutrophils	100% (1/1)
NOD2	2.646	9	7	CCL2,CXCL8,ICAM1,IL1B,IL6,NFKBIA,NOS2	activation of leukocytes	100% (1/1)
NOD2	2.646	9	7	CCL2,CXCL2,CXCL8,ICAM1,IL1B,IL6,NOS2	migration of granulocytes	0% (0/1)
PI3K (complex)	2.646	9	7	CEBPB,CXCL8,HIF1A,IL6,NOS2,PTGS2,VEGFA	invasion of tumor cell lines	100% (1/1)
STAT1	2.646	9	7	CCL2,CCL20,CXCL2,HIF1A,ICAM1,IL6,NOS2	migration of phagocytes	0% (0/1)
STK11	2.646	9	7	CCL2,HIF1A,IL6,NOS2,PTGS2,SERPINE1,VEGFA	leukocyte migration	0% (0/1)
TAB1	2.646	9	7	CCL20,CFB,CXCL8,IL1B,IL6,PTGS2,SAA1	cell movement of leukocytes	0% (0/1)
TLR2	2.646	9	7	CCL2,CXCL2,CXCL8,IL1B,IL6,PTGS2,SOCS1	chemotaxis	100% (1/1)
TLR2	2.646	9	7	CCL2,CXCL2,CXCL8,ICAM1,IL1B,IL6,NOS2	migration of granulocytes	0% (0/1)
TLR9	2.646	9	7	CD38,CXCL8,IL1B,IL6,PTGS2,SERPINE1,SOCS1	chemotaxis	100% (1/1)
miR-155-5p (miRNAs w/seed UAAUGCU)	2.646	9	7	CCL20,CXCL1,CXCL2,CXCL8,IL1B,IL6,SERPINE1	inflammatory response	0% (0/1)
HIF1A	2.598	14	12	CXCL2,CXCL8,FYN,GPER1,HSPB1,IL1B,IL6,NOS2,PIM2,PTGS2,SLC40A1,VEGFA	cellular homeostasis	100% (1/1)
IL1A	2.53	12	10	CCL2,CD44,CXCL5,CXCL8,FGF2,IL1B,IL32,IL6,NOS2,SERPINE1	migration of breast cancer cell lines	0% (0/1)

Regulators	Consistency Score	Node Total	Target Total	Target Molecules	Diseases & Functions	Known Regulator-Disease/Function Relationship
BCL3	2.5	6	4	CXCL8,ICAM1,IL1B,IRF1	activation of leukocytes	100% (1/1)
C5AR1	2.5	6	4	CXCL2,FCER1G,IL1B,IL6	inflammatory response	100% (1/1)
PRDM1	2.5	6	4	CXCL2,CXCL6,IL1B,IL6	cell movement of leukocytes	100% (1/1)
PRDM1	2.5	6	4	CXCL2,CXCL6,IL1B,IL6	inflammatory response	100% (1/1)
PTGS2	2.5	6	4	ICAM1,IL1B,NOS2,VEGFA	vascularization	100% (1/1)
PTGS2	2.5	6	4	ICAM1,IL1B,NOS2,VEGFA	vascularization of absolute anatomical region	100% (1/1)
ERK1/2	2.475	10	8	CD44,F3,FGF2,ICAM1,IL1B,IL6,SERPINE1,VEGFA	binding of tumor cell lines	100% (1/1)
JUN	2.475	10	8	IL1B,IL24,IL6,LIF,NFKBIA,NGF,PLAUR,PTGS2	differentiation of tumor cell lines	100% (1/1)
Mek	2.475	10	8	CXCL8,HIF1A,IL1B,IL6,NGF,PTGS2,SERPINE1,TNFAIP3	leukocyte migration	100% (1/1)
PDGF BB	2.475	10	8	CCL2,CCL8,CD44,CXCL8,IL1B,IL6,PTGS2,VEGFA	migration of phagocytes	0% (0/1)
RET	2.475	10	8	CCL2,CCL20,CXCL8,IL1B,IL6,MMP1,PLAUR,S100A9	migration of tumor cell lines	0% (0/1)
TLR3	2.475	10	8	CCL20,CD38,CXCL2,CXCL8,IL1B,IL6,PTGS2,SERPINE1	chemotaxis	0% (0/1)
Alpha catenin	2.449	8	6	CXCL2,IL1B,IL6,PTGS2,S100A9,TGM2	adhesion of immune cells	0% (0/1)
Alpha catenin	2.449	8	6	CXCL2,CXCL6,IL1B,IL6,S100A9,SAA1	migration of neutrophils	0% (0/1)
CCL5	2.449	8	6	C5AR1,CCL2,CD44,CXCL2,CXCL8,IL1B	accumulation of myeloid cells	100% (1/1)
CCL5	2.449	8	6	C5AR1,CCL2,CD44,CXCL2,CXCL8,IL1B	accumulation of phagocytes	100% (1/1)
CCL5	2.449	8	6	CCL2,CD44,CXCL2,CXCL8,IL1B,PLAUR	adhesion of endothelial cells	0% (0/1)
CD14	2.449	8	6	CCL2,CXCL2,ICAM1,IL1B,IL6,PTGS2	adhesion of immune cells	100% (1/1)

Regulators	Consistency Score	Node Total	Target Total	Target Molecules	Diseases & Functions	Known Regulator-Disease/Function Relationship
CD14	2.449	8	6	CCL2,CXCL2,IL1B,IL6,PTGS2,SOCS1	chemotaxis	0% (0/1)
CITED2	2.449	8	6	CXCL1,CXCL8,HIF1A,IL6,MMP1,VEGFA	cell movement	100% (1/1)
DUSP1	2.449	8	6	CXCL2,CXCL8,IL1B,IL6,NOS2,S100A9	migration of neutrophils	0% (0/1)
EGF	2.449	8	6	CD44,CEBPB,CXCL8,NGF,PTGS2,VEGFA	activation of phagocytes	0% (0/1)
EGR1	2.449	8	6	CCL2,CD44,CXCL2,CXCL8,IL1B,VEGFA	accumulation of myeloid cells	100% (1/1)
EGR1	2.449	8	6	CCL2,CD44,CXCL2,CXCL8,IL1B,VEGFA	accumulation of phagocytes	100% (1/1)
ERK1/2	2.449	8	6	CCL2,CD44,CXCL8,FGF2,IL1B,VEGFA	accumulation of phagocytes	0% (0/1)
ERK1/2	2.449	8	6	CCL2,CD44,CXCL8,ICAM1,IL1B,VEGFA	adhesion of endothelial cells	0% (0/1)
F7	2.449	8	6	CXCL2,CXCL8,IL1B,LIF,PLAUR,VEGFA	adhesion of immune cells	0% (0/1)
F7	2.449	8	6	CXCL2,CXCL8,IL1B,LIF,PLAUR,VEGFA	chemotaxis	100% (1/1)
F7	2.449	8	6	CXCL2,CXCL8,F3,IL1B,PLAUR,VEGFA	leukocyte migration	100% (1/1)
FBXO32	2.449	8	6	CCL20,CXCL2,CXCL6,IL1B,IL6,PTGS2	cell movement of leukocytes	0% (0/1)
FBXO32	2.449	8	6	CCL20,CXCL2,CXCL6,IL1B,IL6,PTGS2	chemotaxis	0% (0/1)
FBXO32	2.449	8	6	CCL20,CXCL2,CXCL6,IL1B,IL6,PTGS2	inflammatory response	0% (0/1)
IL15	2.449	8	6	CCL2,CD44,CXCL2,IL6,NOS2,TGFBR2	cell movement of leukocytes	100% (1/1)
IL1B	2.449	8	6	CCL2,FGF2,HIF1A,NGF,PTGS2,VEGFA	flow of blood	100% (1/1)
IL1B	2.449	8	6	FGF2,ICAM1,NGF,PTGS2,PTX3,VEGFA	permeability of vasculature	0% (0/1)
IL1	2.449	8	6	CCL2,CXCL8,IL6,MMP1,MMP13,PTGS2	activation of cells	100% (1/1)
KLK5	2.449	8	6	CCL20,CXCL2,ICAM1,IL1B,IL6,S100A9	adhesion of immune cells	0% (0/1)
KLK5	2.449	8	6	CCL20,CXCL2,ICAM1,IL1B,IL6,S100A9	cell movement of leukocytes	100% (1/1)

Regulators	Consistency Score	Node Total	Target Total	Target Molecules	Diseases & Functions	Known Regulator-Disease/Function Relationship
P38 MAPK	2.449	8	6	CEBPB,CXCL8,IL1B,NGF,NOS2,PTGS2	concentration of fatty acid	100% (1/1)
PTGS2	2.449	8	6	CCL2,CXCL8,ICAM1,IL1B,NOS2,VEGFA	cell movement of antigen presenting cells	100% (1/1)
TBK1	2.449	8	6	CXCL8,ICAM1,IL6,NFKBIZ,PTGS2,VEGFA	activation of leukocytes	0% (0/1)
TBK1	2.449	8	6	CXCL2,CXCL8,ICAM1,IL6,PTGS2,VEGFA	adhesion of immune cells	0% (0/1)
TBK1	2.449	8	6	CXCL2,CXCL8,ICAM1,IL6,PTGS2,VEGFA	migration of phagocytes	0% (0/1)
TRAF6	2.449	8	6	CCL2,CXCL2,CXCL8,ICAM1,IL1B,IL6	adhesion of immune cells	0% (0/1)
TRAF6	2.449	8	6	CCL2,CXCL2,CXCL8,ICAM1,IL1B,IL6	migration of granulocytes	0% (0/1)
mir-146	2.449	8	6	CCL2,CCL7,CXCL8,IL1B,IL6,SOCS1	chemotaxis	0% (0/1)
IL17A	2.333	11	9	CEBPB,CXCL1,CXCL5,ICAM1,IL1B,IL1RN,IL6,NOS2,PTGS2	development of lymphatic system	100% (1/1)
APP	2.309	14	12	CCL20,CTGF,CXCL2,FGF2,IL1B,IL6,MME,NOS2,NRP1,PLAT,PTGS2, SERPINE1	migration of tumor cell lines	100% (1/1)
BCL3	2.309	5	3	ICAM1,IL1B,IRF1	proliferation of lymphocytes	100% (1/1)
BCL3	2.309	5	3	ICAM1,IL1B,IRF1	proliferation of mononuclear leukocytes	100% (1/1)
C5AR1	2.309	5	3	FCER1G,IL1B,IL6	differentiation of lymphatic system cells	100% (1/1)
C5AR1	2.309	5	3	FCER1G,IL1B,IL6	fatty acid metabolism	100% (1/1)
C5AR1	2.309	5	3	FCER1G,IL1B,IL6	metabolism of eicosanoid	100% (1/1)
C5AR1	2.309	5	3	FCER1G,IL1B,IL6	synthesis of eicosanoid	100% (1/1)

Regulators	Consistency Score	Node Total	Target Total	Target Molecules	Diseases & Functions	Known Regulator-Disease/Function Relationship
C5AR1	2.309	5	3	FCER1G,IL1B,IL6	synthesis of fatty acid	100% (1/1)
IL1RN	2.309	5	3	CD44,IL1B,IRF1	accumulation of myeloid cells	100% (1/1)
IL1RN	2.309	5	3	CD44,IL1B,IRF1	accumulation of phagocytes	100% (1/1)
NAMPT	2.309	5	3	CXCL8,IL6,MMP1	invasion of tumor cell lines	100% (1/1)
NOD2	2.309	5	3	ICAM1,IL1B,IL6	cell-mediated response	100% (1/1)
PGF	2.309	5	3	CCL2,CCL20,CXCL8	chemotaxis of tumor cell lines	100% (1/1)
PGF	2.309	5	3	CCL2,CCL20,CXCL8	homing of tumor cell lines	100% (1/1)
C5	2.268	9	7	CXCL2,CXCL8,F3,IL1B,IL6,MMP1,SERPINE1	cell movement	100% (1/1)
CHUK	2.268	9	7	CXCL2,CXCL6,CXCL8,IL6,NGF,PTGS2,VEGFA	chemotaxis	100% (1/1)
EGFR	2.268	9	7	CEBPB,CXCL8,ICAM1,IL1B,IL6,TGM2,VEGFA	cell viability of blood cells	0% (0/1)
EZH2	2.268	9	7	CXCL1,CXCL2,CXCL8,IL6,PTGS2,SAA1,VEGFA	migration of phagocytes	0% (0/1)
FOS	2.268	9	7	CCL2,CD44,CXCL8,F3,ICAM1,SERPINE1,VEGFA	recruitment of blood cells	100% (1/1)
IL17A	2.268	9	7	CXCL1,CXCL5,ICAM1,IL1B,IL6,NOS2,PTGS2	Lymphocyte homeostasis	100% (1/1)
IL17A	2.268	9	7	CXCL1,CXCL5,ICAM1,IL1B,IL6,NOS2,PTGS2	T cell homeostasis	100% (1/1)
INSIG1	2.268	9	7	ACSL4,CXCL2,CXCL6,IL6,NFKBIZ,PLD1,S100A9	cell movement	0% (0/1)
PLG	2.268	9	7	CCL2,F3,FYN,IL1B,IL6,PTGS2,SERPINE1	migration of tumor cell lines	100% (1/1)
PRKCA	2.268	9	7	CCL2,CXCL2,NOS2,PTGS2,S100A9,SERPINE1,VEGFA	migration of phagocytes	0% (0/1)
TGFA	2.268	9	7	CCL20,CXCL2,CXCL8,IL6,PTGS2,SERPINE1,VEGFA	migration of phagocytes	0% (0/1)
TNF	2.268	9	7	CCL2,IL1B,LIF,NGF,SOCS1,TYMP,VEGFA	activation of protein	0% (0/1)

Regulators	Consistency Score	Node Total	Target Total	Target Molecules	Diseases & Functions	Known Regulator-Disease/Function Relationship
BIRC3	2.236	7	5	CCL2,CXCL1,CXCL8,IL1B,IL6	adhesion of immune cells	0% (0/1)
BIRC3	2.236	7	5	CCL2,CXCL1,CXCL8,IL1B,IL6	cellular homeostasis	0% (0/1)
BIRC3	2.236	7	5	CCL2,CXCL1,CXCL8,IL1B,IL6	chemotaxis	0% (0/1)
BIRC3	2.236	7	5	CCL2,CXCL1,CXCL8,IL1B,IL6	inflammatory response	100% (1/1)
BIRC3	2.236	7	5	CCL2,CXCL1,CXCL8,IL1B,IL6	migration of granulocytes	0% (0/1)
C3	2.236	7	5	CXCL2,IL1B,IL6,NOS2,VEGFA	leukocyte migration	100% (1/1)
CHUK	2.236	7	5	CXCL2,CXCL6,CXCL8,IL6,NGF	chemotaxis of leukocytes	100% (1/1)
Cg	2.236	7	5	ICAM1,PLAT,PTGS2,PTX3,VEGFA	permeability of vasculature	100% (1/1)
FCGR2A	2.236	7	5	CCL2,CXCL2,IL1B,IL6,VEGFA	adhesion of immune cells	100% (1/1)
FCGR2A	2.236	7	5	CCL2,CXCL2,IL1B,IL6,VEGFA	chemotaxis	100% (1/1)
FCGR2A	2.236	7	5	CCL2,CXCL2,IL1B,IL6,VEGFA	leukocyte migration	100% (1/1)
Fcer1	2.236	7	5	CCL2,CXCL8,FYN,IL1B,IL6	adhesion of immune cells	100% (1/1)
Fcer1	2.236	7	5	CCL2,CXCL8,FYN,IL1B,IL6	cellular homeostasis	100% (1/1)
Fcer1	2.236	7	5	CCL2,CXCL8,FYN,IL1B,IL6	invasion of cells	0% (0/1)
Fcer1	2.236	7	5	CCL2,CXCL8,FYN,IL1B,IL6	migration of tumor cell lines	0% (0/1)
IKBKB	2.236	7	5	CCL2,CXCL2,CXCL6,CXCL8,IL1B	chemotaxis of neutrophils	100% (1/1)
IKBKB	2.236	7	5	CCL2,IL1B,NGF,PTGS2,VEGFA	flow of blood	0% (0/1)
IKBKB	2.236	7	5	ICAM1,NGF,PTGS2,PTX3,VEGFA	permeability of vasculature	0% (0/1)
IL22	2.236	7	5	CXCL2,IL1B,LBP,NOS2,SAA1	cell movement of myeloid cells	100% (1/1)

Regulators	Consistency Score	Node Total	Target Total	Target Molecules	Diseases & Functions	Known Regulator-Disease/Function Relationship
IL22	2.236	7	5	CXCL2,IL1B,LBP,NOS2,SAA1	cell movement of phagocytes	0% (0/1)
IRAK2	2.236	7	5	CXCL2,CXCL8,IL1B,IL6,NOS2	inflammatory response	0% (0/1)
IRAK2	2.236	7	5	CXCL2,CXCL8,IL1B,IL6,NOS2	migration of neutrophils	0% (0/1)
Jnk	2.236	7	5	CXCL8,ICAM1,IL1B,IL6,TGM2	cell viability of leukocytes	100% (1/1)
KLF2	2.236	7	5	CXCL2,F3,HIF1A,IL6,PTGS2	leukocyte migration	100% (1/1)
KLF2	2.236	7	5	CXCL2,F3,HIF1A,IL6,PTGS2	neoplasia of cells	0% (0/1)
KRT17	2.236	7	5	CXCL2,CXCL6,IL1B,IL6,MMP13	cell movement	0% (0/1)
Lymphotoxin	2.236	7	5	CCL2,ICAM1,IL1B,IL6,MMP1	activation of cells	100% (1/1)
Lymphotoxin	2.236	7	5	CCL2,ICAM1,IL1B,IL6,MMP1	cell movement	100% (1/1)
NR1H3	2.236	7	5	IL1B,IL6,NFKBIA,NOS2,PTGS2	invasion of cells	0% (0/1)
PARP1	2.236	7	5	IL1B,IL6,NOS2,PTGS2,SOCS1	metabolism of eicosanoid	0% (0/1)
PARP1	2.236	7	5	IL1B,IL6,NOS2,PTGS2,SOCS1	synthesis of eicosanoid	0% (0/1)
PF4	2.236	7	5	ACTA2,CCL2,CXCL8,IL1B,IL6	invasion of cells	0% (0/1)
PLA2G4A	2.236	7	5	CXCL8,IL1B,IL6,NOS2,PTGS2	activation of myeloid cells	0% (0/1)
PLA2G4A	2.236	7	5	CXCL8,IL1B,IL6,NOS2,PTGS2	activation of phagocytes	0% (0/1)
PLA2G4A	2.236	7	5	CXCL8,IL1B,IL6,NOS2,PTGS2	cell movement of leukocytes	100% (1/1)
PLA2G4A	2.236	7	5	CXCL8,IL1B,IL6,NOS2,PTGS2	inflammatory response	0% (0/1)
PLA2G4A	2.236	7	5	CXCL8,IL1B,IL6,NOS2,PTGS2	invasion of cells	0% (0/1)
PPRC1	2.236	7	5	CXCL8,ESM1,LAMB3,NAMPT,PTGS2	invasion of tumor cell lines	0% (0/1)
PRKCE	2.236	7	5	CEBPB,IL6,NOS2,PTGS2,VEGFA	activation of phagocytes	100% (1/1)
PRKCE	2.236	7	5	CEBPB,IL6,NOS2,PTGS2,VEGFA	invasion of tumor cell lines	100% (1/1)

Regulators	Consistency Score	Node Total	Target Total	Target Molecules	Diseases & Functions	Known Regulator-Disease/Function Relationship
PRKCE	2.236	7	5	CEBPB,IL6,NOS2,PTGS2,VEGFA	metabolism of eicosanoid	0% (0/1)