

Table S1. Sequence of the primers used for qPCR.

Gene Symbol	Primer name	5'→3' primer sequence
Ccl2	mCcl2_F	catccacgtgttggtca
	mCcl2_R	gatcatcttgctggtgaatga
Ccl5	mCcl5_F	tgcagaggactctgagacagc
	mCcl5_R	gagtgggtgccgagccata
Ccl11	mCcl11_F	agagctccacagcgcttct
	mCcl11_R	gcaggaagtgggatgga
Ccl19	mCcl19	Taqman Mm00839967_g1
Cxcl1	mCxcl1_F	Taqman Mm04207460_m1
Cx3cl1	mCx3cl1_F	catccgctatcagctaaacca
	mCx3cl1_R	cagaagcgtctgtgctgtgt
Cxcl10	mCxcl10_F	gctgccgtcattttctgc
	mCxcl10_R	tctcactggccccgcatc
Il6	mIl6_F	acaagtcggaggcttaattacacat
	mIl6_R	ttgccattgcacaactcttttc
Il1 β	mIl1 β _F	tcgctcagggtcacaagaaa
	mIl1 β _R	catcagaggcaaggaggaaaac
Tnfa	mTnfa_F	catcttctcaaaattcgagtgacaa
	mTnfa_R	tgggagtagacaaggtacaaccc
PGC1 α	mPGC1 α _F	ttccaaaaagaagtccatacaca
	mPGC1 α _R	gataaagttgtggtttggcttga
PGC1 β	mPGC1 β _F	gacgtggacgagctttcact
	mPGC1 β _R	gagcgtcagagcttctgtgt
CCL5	hCCL5_F	cctcattgctactgcctct
	hCCL5_R	ggtgtgggtgccgaggaata

CCL19	hCCL19_F	tcagcctgctggttctctg
	hCCL19_R	gcagtcttcagcatcattgg
CXCL1	hCXCL1_F	catcgaaaagatgctgaacagt
	hCXCL1_R	ataagggcagggcctcct
CX3CL1	hCX3CL1_F	ccacettctgccatctgac
	hCX3CL1_R	atgttgcatctcgtcacacc
CXCL5	hCXCL5_F	ccttttctaaagaaagtcatccaga
	hCXCL5_R	tgggttcagagacctccaga
CXCL10	hCXCL10_F	gaaagcagttagcaaggaaaggt
	hCXCL10_R	gacatatactccatgtagggaagtga

Table S2. DAVID (Database for Annotation, Visualization, and Integrated Discovery) analysis of human adipocyte microarray data.

Term	Count	%	P-value	Benjamini
109. Chemokines families	10	0.3	1.80E-02	7.70E-01
18. Cytokines astrocytes	7	0.2	4.40E-02	8.30E-01

Table S3. Gene set enrichment analysis of human adipocyte microarray data according to gene ontology.

Name	NES	NOM p-value	FDR q-value
RECEPTOR_BINDING	-1.9952039	0	0.39522976
PROTEIN_KINASE_CASCADE	-1.9937165	0.006198347	0.20004994
G_PROTEIN_COUPLED_RECPTOR_BINDING	-1.9729283	0.006741573	0.15669367
DEFENSE_RESPONSE	-1.9172692	0.007317073	0.16777436
LOCOMOTORY_BEHAVIOR	-1.8803759	0.002197802	0.16598015
CYTOKINE_ACTIVITY	-1.8572822	0.10752688	0.15733895
CHEMOKINE_ACTIVITY	-1.7575725	0.018390805	0.24868898
SIGNAL_TRANSDUCTION	-1.7564824	0.003267974	0.21920505
CHEMOKINE_RECEPTOR_BINDING	-1.7551912	0.020618556	0.19606276
BEHAVIOR	-1.7498477	0.01754386	0.18191557

NES : normalized enrichment score

NOM p-value : The nominal p value

FDR : False Discovery Rate

Table S4. List of chemokines regulated by ATRA.

Chemokines	Down regulation fold change in ATRA+TNFα/TNFα condition
CCL5	-2.2509918
CCL13	-3.1270533
CCL3L3	-1.7154679
CCL18	-1.5367765
CCL19	-5.6640778
CCL22	-1.5474644
CCL23	-1.6318715
CCL25	-1.5530369
CXCL11	-3.9912832
CXCL10	-2.8700345
CXCL13	-1.4731226
CXCL1	-1.698609
CX3CL1	-3.1594527
CXCL5	-1.8439337
CXCL6	-1.571521
CXCL17	-1.5607669
CXCL3	-1.327791

Table S5. List of chemokine receptors regulated by ATRA.

Chemokine receptors	Down regulation fold change in ATRA+TNFα/TNFα condition
CCR2	-1.6563766
CCR1	-1.6749991
CCRL2	-1.6172404
CCR9	-1.6099906
CXCR3	-1.6277624