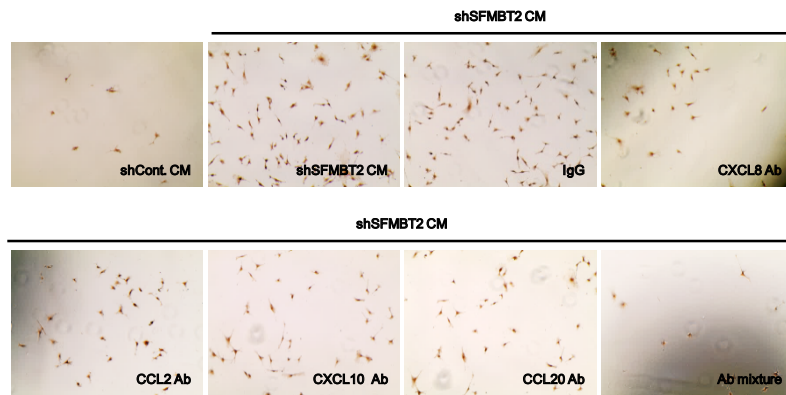
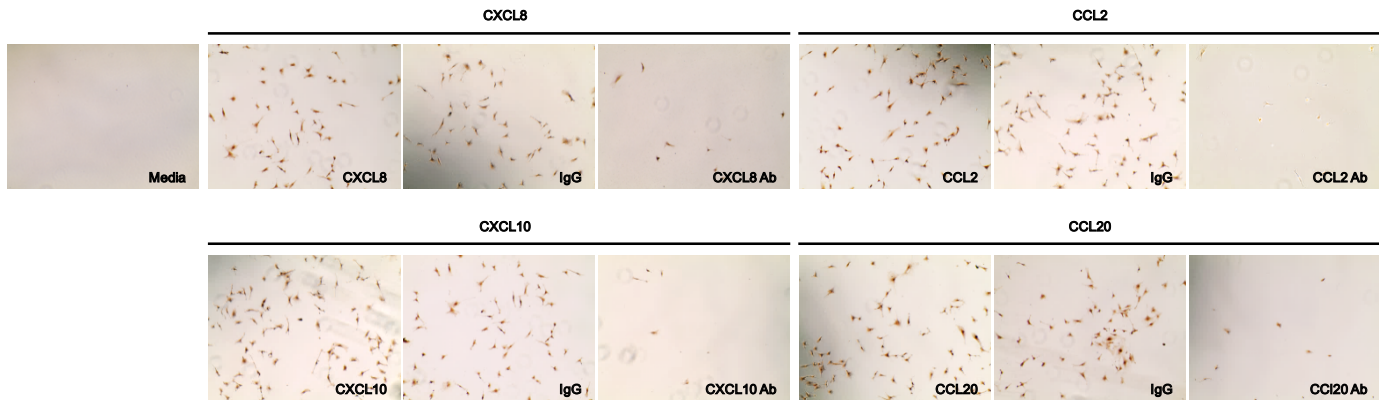
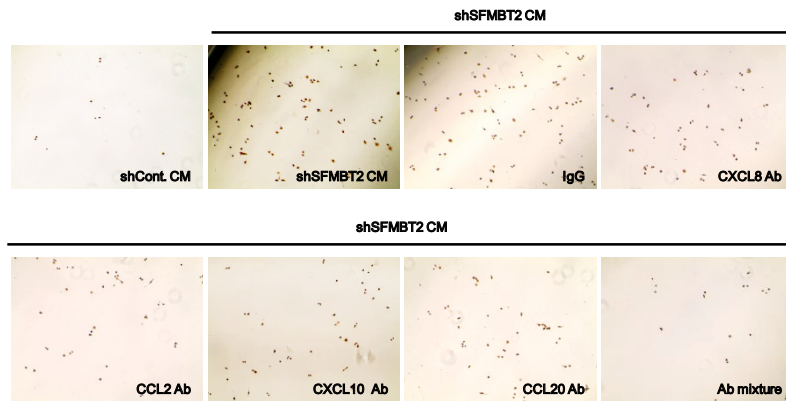
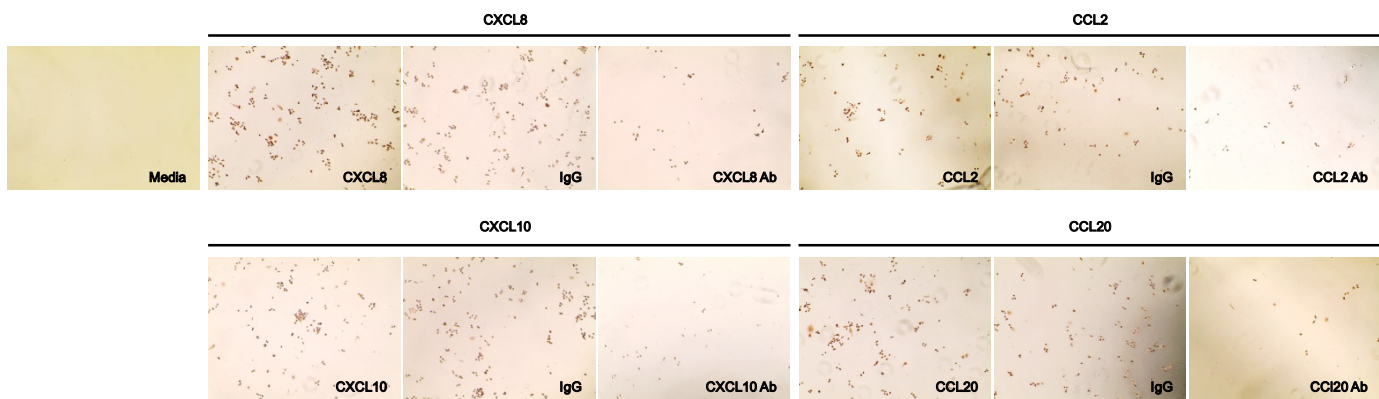
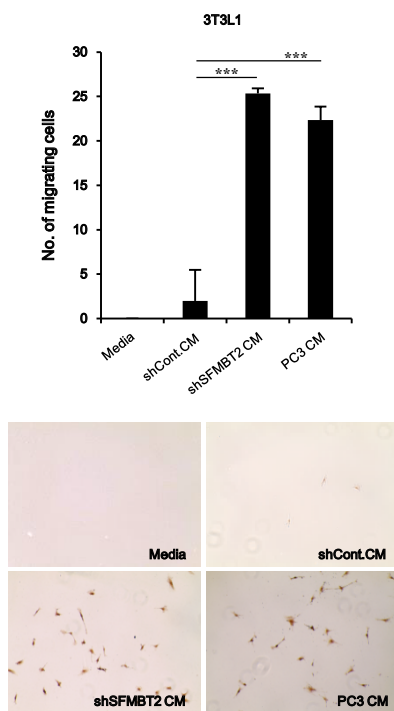
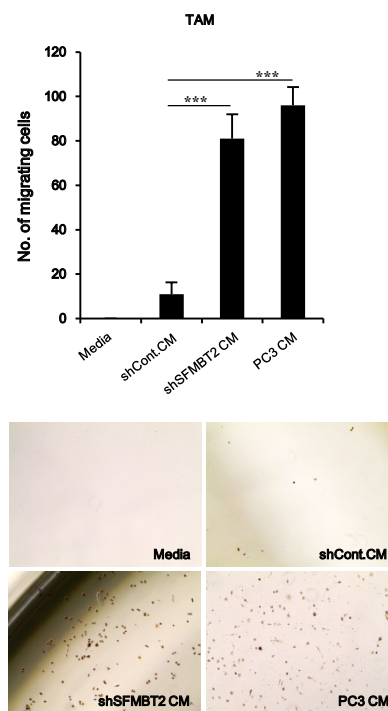
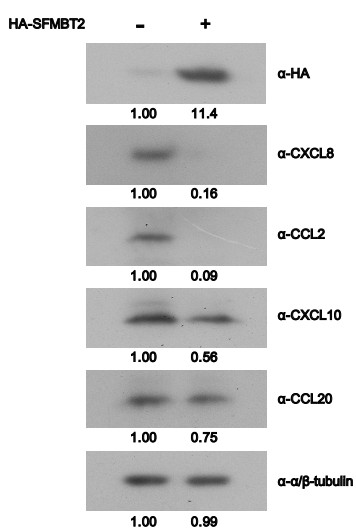
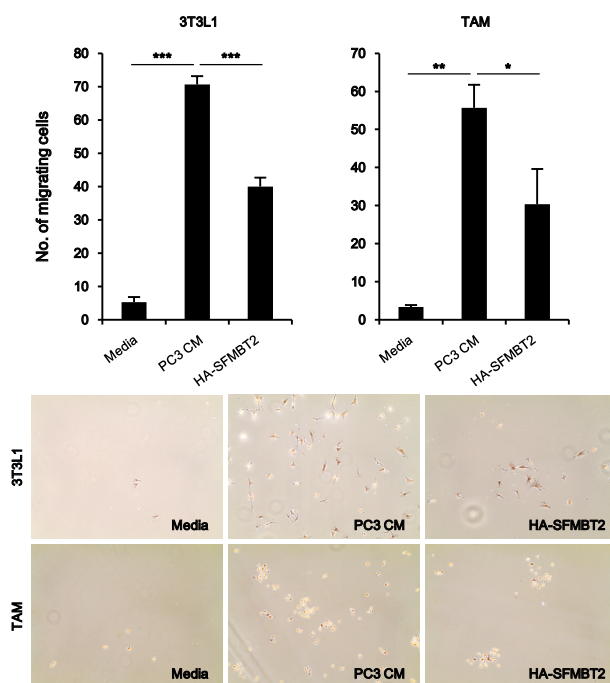
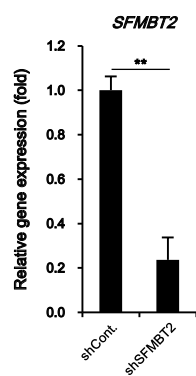
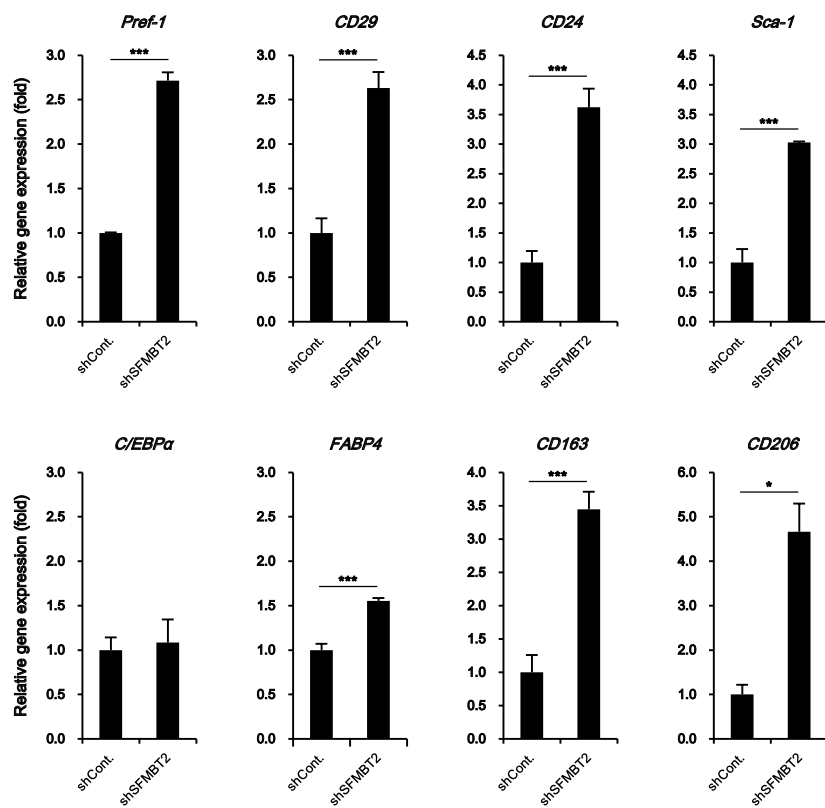


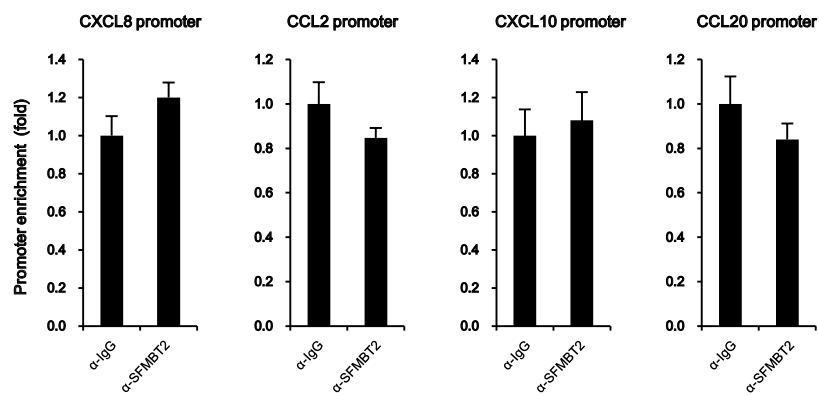
A**B****C****D**

A**B****C****D**

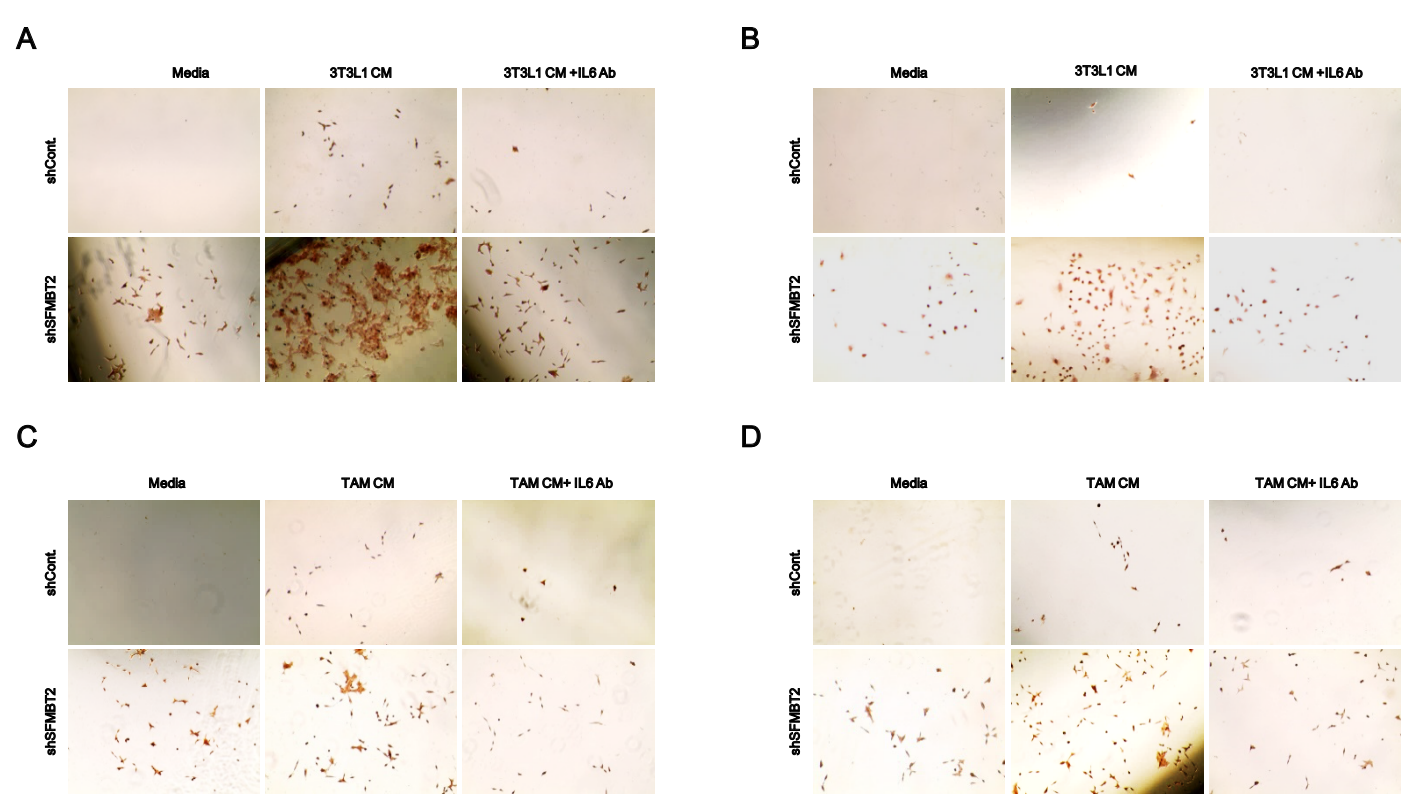
Supplementary Figure S2.

A**B**

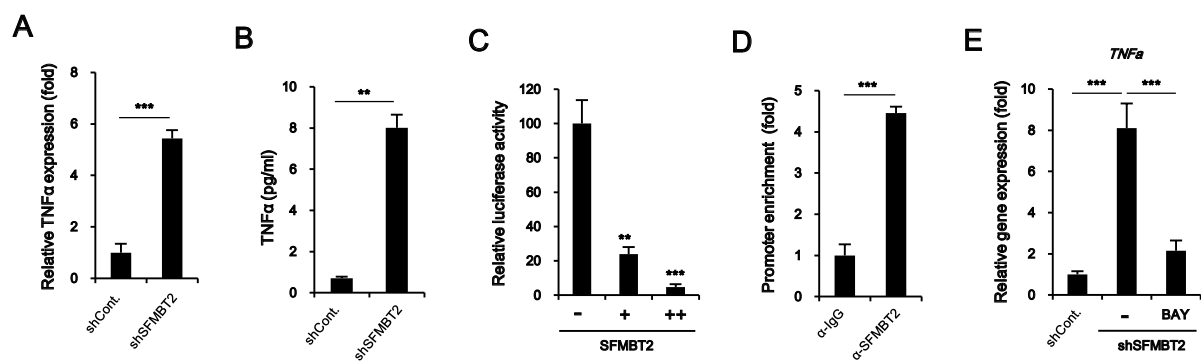
Supplementary Figure S3.



Supplementary Figure S4.



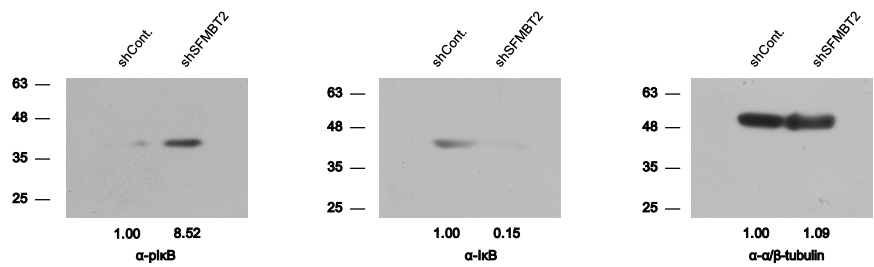
Supplementary Figure S5.



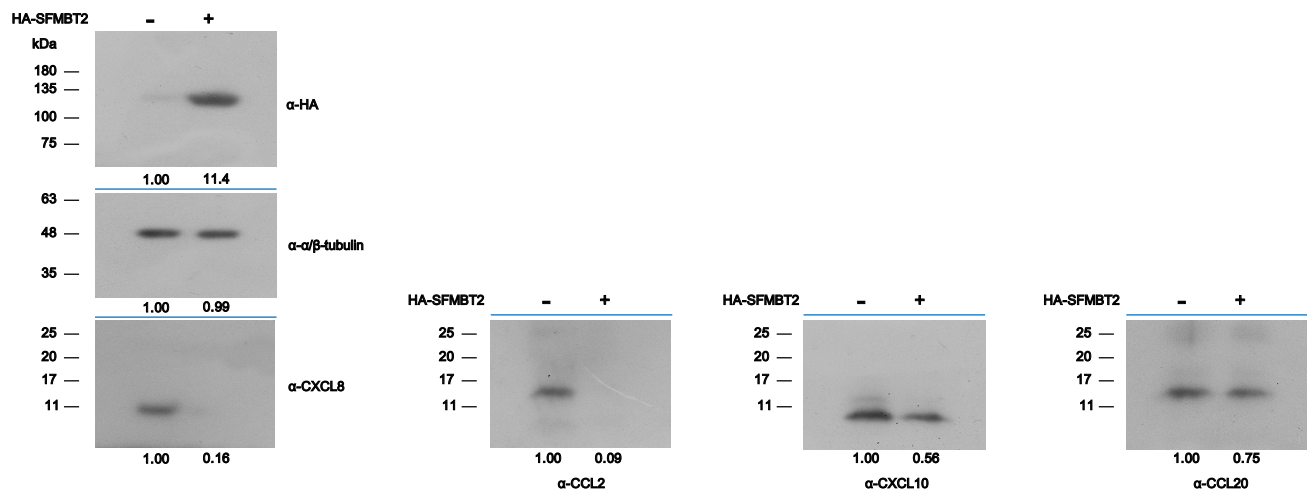
Supplementary Figure S6.

Full blots from Figure 5D (A) and Figure S2C (B)

A



B



Supplementary Figure S7.

Table S1. Oligonucleotides used in this study.

Gene	Forward Primer	Reverse Primer
qRT-PCR Primers		
hSFMBT2	5'- TGACGTAGTCATCGCGATT -3'	5'- ACCAGTCAAGTCACGTATGAGAA -3'
hCXCL8	5'- ACTGAGAGTGATTGAGAGTGGAC -3'	5'- AACCCCTCTGCACCCAGTTTTTC -3'
hCCL2	5'- ATCACCAGCAGCAAGTGTC -3'	5'- AGGTGGTCCATGGAATCCTG -3'
hCXCL10	5'- CAGCAGAGGAACCTCCAGTC -3'	5'- GCAGGTACAGCGTACAGTTC -3'
hCCL20	5'- TGCTGTACCAAGAGTTTGCTC -3'	5'- CGCACACAGACAACTTTTTCTTT -3'
hTNF α	5'- GAGGCCAAGCCCTGGTATG -3'	5'- CGGGCCGATTGATCTCAGC -3'
h18s rRNA	5'- GTAACCCGTTGAACCCATT -3'	5'- CCATCCAATCGGTAGTAGCG -3'
mIL6	5'- TAGTCCTTCTACCCCAATTTCC -3'	5'- TTGGTCCTTAGCCACTCCTTC -3'
mCCR2	5'- ACACCCTGTTTCGCTGTAGG -3'	5'- GATTCCTGGAAGGTGGTCAA -3'
mCCR4	5'- GGAAGGTATCAAGGCATTTGGG -3'	5'- GTACACGTCGTCATGGACTT -3'
mCCR6	5'- CTGCACTAGTGAGCGTGTGG -3'	5'- ACCTCTTCTAGGGAGCATGG -3'
mCXCR1	5'- ATTCGTGTGCGTGGGCATCT -3'	5'- CCCGCAAGGTCATCCGAAAA -3'
mCXCR2	5'- GACACAGCTCCAGTTAGGGATG -3'	5'- CGAGGTGCTAGGATTTGAGC -3'
mCXCR3	5'- GCTGTAGCCGATGTTCTGCTGGTG -3'	5'- TGCACTATGCTCAGATATCTGTC -3'
mPref-1	5'- AGTGCGAAACCTGGGTGTC -3'	5'- GCCTCCTGTTGAAAGTGGTCA -3'
mCD24	5'- TTCTGGCACTGCTCCTACC -3'	5'- GCGTTACTTGATTGTTGGGGAA -3'
mCD29	5'- ACTGTGATGCCGTATATTAGCAC -3'	5'- GATATGCGTTGCTGACCAACA -3'
mCD163	5'- AAGCATTACTGTCATCATAG -3'	5'- CTCCACCTACAAGTCTAA -3'
mCD206	5'- CAGGTGTGGGCTCAGGTAGT -3'	5'- TGTGGTGAGCTGAAAGGTGA -3'
mSca-1	5'- ACAGCACAGGCAGGAAGACT -3'	5'- TCGGTATTATCTTCGGGGC -3'
mC/EBP α	5'- TGGACAAGAACAGCAACGAG -3'	5'- TCACTGGTCAACTCCAGCA -3'
mFABP4	5'- AAGGTGAAGAGCATCATAACCCT -3'	5'- TCACGCCTTTCATAACACATTCC -3'
m18s rRNA	5'- AGTCCCTGCCCTTTGTACACA -3'	5'- CGATCCGAGGGCCTCACTA -3'
ChIP Primers		
CXCL8 (p65)	5'- GGGCCATCAGTTGCAAATC -3'	5'- TTCCTTCCGGTGGTTTCTTC -3'
CCL2 (p65)	5'- TGGAAAAAGTGTCTCGTCCTGAC -3'	5'- GCTGCTGTCTCTGCCTCTTATTGA -3'
CXCL10 (p65)	5'- AGGAGCAGAGGGAAATTCGTAAC -3'	5'- AACGTGGGGCTAGTGTGCCA -3'
CCL20 (p65)	5'- TGAGGAAAAAGCAGGAAGTTT -3'	5'- GTACACAGAAGGCGTGTTGC -3'
CXCL8 (YY1)	5'- CCCCCACATTACTCAGAAAGTTACTC -3'	5'- GGTGTTAGAAACAAGATCATGGAT GATTTTCTTTA -3'
CCL2 (YY1)	5'- CCCCATTTGCTCATTTGGTCTCAG -3'	5'- TGCTGGAGGCGAGAGTGCGA -3'
CXCL10 (YY1)	5'- CCTTTTCTCACACATTCTAGATACCATC -3'	5'- CCTGCTTTGACAGGGTCAAAGATC -3'
CCL20 (YY1)	5'- CAGGGTCTTCTTCATGACAGCAC -3'	5'- ACAGCGATACAAAGGTCAGCCC -3'
TNF α (YY1)	5'- AACTTTCCAAATCCCCGCCCCC -3'	5'- CCAGCGGAAACTTCCTTGGTG -3'
Promoter cloning Primer		
TNF α promoter	5'- ATGCGGTACCGAGCTCCTGGGAGATATGGC CACA -3'	5'- ATGCGATATCTCAGTGCTCATGGTGTC CTT TCCAG -3'

Table S2. Antibodies used in this study.

Antibody	Cat #	Company	Application
CXCL8	ab89336	Abcam	IHC, WB
CCL2	MABN712	Millipore	IHC, WB
CXCL10	ab8098	Abcam	IHC, WB
CCL20	ab9829	Abcam	IHC, WB
Pref-1	33697	Novus Biologicals	IHC
CD29	ab183666	Abcam	IHC
CD163	A8383	ABclonal	IHC
CD206	A8301	ABclonal	IHC
RFP	AE020	ABclonal	IHC
pI κ B	2859S	Cell signaling	WB
I κ B	ab7217	Abcam	WB
HA	AE008	ABclonal	WB
α/β -tubulin	2148	Cell signaling	WB
p65	ab7970	Abcam	ICC, ChIP
p50	ab7971	Abcam	ICC, ChIP
AcH3	06-599	Millipore	ChIP
p300	sc-585	Santa Cruz Biotechnology	ChIP
IL6	A11114	ABclonal	IHC
Anti-Rabbit IgG–TRITC	T6778	Sigma	IHC, ICC
Anti-Mouse IgG–FITC	F0257	Sigma	IHC
Anti-Mouse IgG–HRP	sc-2005	Santa Cruz Biotechnology	WB
Anti-Rabbit IgG–HRP	sc-2357	Santa Cruz Biotechnology	WB

IHC: Immunohistochemistry, **WB:** Western blot, **ICC:** Immunocytochemistry, **ChIP:** Chromatin Immunoprecipitation

Table S3. Chemokines and Cytokines used in this study.

Chemokine/Cytokine	Cat #	Company
CXCL8	200-08M	Pepro Tech
CCL2	300-04	Pepro Tech
CXCL10	300-12	Pepro Tech
CCL20	300-29A	Pepro Tech
IL4	200-04	Pepro Tech
IL13	200 13	Pepro Tech

Table S4. Characteristics of prostate cancer patients in tissue array used in this study.

Characteristics	N (%)
Gender	Male
Mean age in year (range)	64.98 (44-72)
Mean preoperative PSA ng/ml (range)	26.64 (0.5-161)
pTNM pathologic classification	
pT2a	1 (2.5%)
pT2b	7 (17.5%)
pT3	32 (80.0%)
Gleason score	
4-7	17 (42.5%)
8-10	23 (57.5%)

N: Patient number, **PSA:** Prostate-specific antigen, **pTNM:** Pathological tumor-node-metastasis

pT2a: Tumor affects one-half of one lobe or less

pT2b: Tumor affects more than one-half of one lobe but not both lobes

pT3: Tumor extends beyond the prostate

Table S5. Relationship between expression level of SFMBT2 and Gleason Score.

Gleason Score	SFMBT2 expression			Total cases (%)
	High (%)	Moderate (%)	Low (%)	
= 2	8 (88.88%)	1 (11.11%)	0 (0%)	9 (100%)
≤ 7	1 (5.90%)	8 (47.06%)	8 (47.06%)	17 (100%)
≥ 8	1 (4.34%)	2 (8.70%)	20 (86.96%)	23 (100%)

There is significant difference $P<0.001$.