

Supplementary Table SI. Primer sequences for real-time qPCR

Name	Primer	Sequence
Mus Gapdh	Forward	5'AACTTTGGCATTGTGGAAGG3'
	Reverse	5'GTCTTCTGGGTGGCAGTGAT3'
Mus Cxcl10	Forward	5'CCAAGTGTGCGTCATTTTC3'
	Reverse	5'GGCTCGCAGGGATGATTTCAA3'
Mus Mmp9	Forward	5'GCGTCGTGATCCCACTTAC3'
	Reverse	5'CAGGCCGAATAGGAGCGTC3'
Mus Cxcr2	Forward	5'GCCCTGCCCATCTTAATTCTAC3'
	Reverse	5'ACCCTCAAACGGGATGTATTGT3'
Mus IL-1 α	Forward	5'CGAAGACTACAGTTCTGCCATT3'
	Reverse	5'GACGTTTCAGAGTTCTCAGAG3'
Mus Ccr1	Forward	5'AGTGAGAAGAAGGTCAAAGCCG3'
	Reverse	5'GTTGGTCCACAGAGAGGAAGGG3'

Supplementary Table SII. Differentially expressed genes (DEGs) in two comparisons.

	Total DEGs	Up-regulated genes	Down-regulated genes
CS vs. SA	621	350	271
CS + MCC950 (10) vs. CS	765	599	166

Supplementary Table SIII. Identification of the hub genes by PPI analysis

Genes	CS vs. SA		CS + MCC950(10) vs. CS	
	Log ₂ FC	P-adjusted	Log ₂ FC	P-adjusted
Mmp9	1.21	5.28E-03	-1.93	7.14E-11
IL-1 α	1.90	1.69E-07	-1.04	4.72E-03
Cxcr2	2.17	1.36E-02	-1.85	1.33E-02
Cxcl10	1.72	4.86E-02	-2.39	4.10E-11
Ccr1	1.66	7.30E-05	-1.56	4.75E-06

Supplementary Table SIV. MCODE scores of genes in the top 1 cluster module

Genes	MCODE Cluster	MCODE scores
Mmp9	Cluster 1	8.672727
Cxcl10	Cluster 1	8.672727
Il1rn	Cluster 1	8.672727
Ccl22	Cluster 1	8.672727
Ccl2	Cluster 1	8.672727
Tnf	Cluster 1	8.672727
Ccl12	Cluster 1	8.672727
Cxcr2	Cluster 1	7.822222
IL-1 α	Cluster 1	7.822222
Ccr1	Cluster 1	7.822222
Ccl9	Cluster 1	7.822222

Supplementary Table SV. Hub gene related GO enrichment terms

Biological process	Enrichment score	P-value
Immune response (GO:0006955)	69.13	1.41E-18
Inflammatory response (GO:0006954)	44.98	1.05-E14
Chemokine-mediated signaling pathway (GO:0070098)	244.06	3.97E-14
Chemotaxis (GO:0006935)	94.18	1.76E-13
Positive regulation of leukocyte migration (GO:0002687)	228.14	2.45E-07

Molecule function	Enrichment score	P-value
Cytokine activity (GO:0005125)	62.75	4.60E-14
Chemokine activity (GO:0008009)	213.30	1.56E-11
Chemokine receptor activity (GO:0004950)	166.58	6.20E-05
C-X-C chemokine receptor activity (GO:0016494)	249.87	4.00E-03
Fibronectin binding (GO:0001968)	54.66	1.81E-02

Cell component	Enrichment score	P-value
Extracellular space (GO:0005615)	9.99	7.64E-09
Extracellular region (GO:0005576)	9.27	1.49E-08
External side of plasma membrane (GO:0009897)	16.38	6.98E-05
Mast cell granule (GO:0042629)	291.52	3.43E-03
Neuronal cell body (GO:0043025)	8.48	4.51E-03

Supplementary Table SVI. Hub gene related KEGG enrichment pathways

KEGG	Enrichment score	P-value
MAPK signaling pathway (mmu04010)	5.34	5.18E-02
Cytokine-cytokine receptor interaction (mmu04060)	26.98	1.73E-14
Chemokine signaling pathway (mmu04062)	28.77	7.11E-10
Necroptosis (mmu04217)	9.02	1.97E-02
Toll-like receptor signaling pathway (mmu04620)	15.86	6.69E-03
RIG-I-like receptor signaling pathway (mmu04622)	22.43	3.40E-03
C-type lectin receptor signaling pathway (mmu04625)	14.02	8.49E-03
IL-17 signaling pathway (mmu04657)	43.13	5.11E-08