Supplementary material

Primer sequences for qRT-PCR

Gene	sequence
ICAM3 forward	5′-GGAGTTCCTTTTGCGGGTG-3′
ICAM3 reverse	5′-TCAGAGCTGGGACAATCAGTA-3′
IRF5 forward	5′-GGGCTTCAATGGGTCAACG-3′
IRF5 reverse	5′-GCCTTCGGTGTATTTCCCTG-3′
IKZF1 forward	5′-TTCCGTGATCCTTTTGAGTGC-3′
IKZF1 reverse	5′-CTCGCGTTATGTGCGACGA-3′
CD206 forward	5′-CTACAAGGGATCGGGTTTATGGA-3′
CD206 reverse	5′-TTGGCATTGCCTAGTAGCGTA-3′
IRF4 forward	5′- GCTGATCGACCAGATCGACAG-3′
IRF4 reverse	5′-CGGTTGTAGTCCTGCTTGC-3′
ICAM1 forward	5′-ATGCCCAGACATCTGTGTCC-3′
ICAM1 reverse	5′-GGGGTCTCTATGCCCAACAA-3′
CCL17 forward	5′-AGGGAGCCATTCCCCTTAGA-3′
CCL17 reverse	5′-CTCTTGTTGTTGGGGTCCGA-3′
CCL24 forward	5′-TCTGCAAGGACCCGAGCTATT-3′
CCL24 reverse	5′-TGACCACTCGGTTCTCAGGA-3′
CD163 forward	5′-GACGCATTTGGATGGATCATGT-3′
CD163 reverse	5′-CCCACCGTCCTTGGAATTTGA
GAPDH forward	5′-ACGGATTTGGTCGTATTGGGC-3′
GAPDH reverse	5′-TTGACGGTGCCATGGAATTG-3′

Analysis pipeline for RNAseq procedure

Data preprocessing:

Sample ID	Raw reads	depth	Raw bases(G)
Con-1	40,579,030	40M	6.09
Con-2	43,012,668	43M	6.49

IL-32(10ng/ml)-1	47,062,514	47M	7.11
IL-32(10ng/ml)-2	49,708,672	49M	7.47
IL-32(40ng/ml)-1	53,093,038	53M	7.96
IL-32(40ng/ml)-2	44,297,068	44M	6.69

1) Raw reads were filtered to get the clean Reads by Seqtk software;

2) Hisat2 (version: 2.0.4) software was adopted for clean Reads mapping genome. The genome file is ftp://ftp.ensembl.org/pub/release-83/fasta/homo_sapiens/dna/Homo_sapiens.GRCh38.dna.primary_assembly.fa.gz;

3) Convert the aligned sam files to Bam files with samtools;

4) Bam files were assembled and quantified by Stringtie (version: 1.3.0);

5) The edgeR package in R software was used to perform differential gene analysis to calculate Fold-change, p-value and q-value.