**Materials and Methods**

*Reagents*

Lipopolysaccharide (LPS) was purchased from Sigma (L3024, St. Louis, MO). MiR-155 mimics and control, miR-155 inhibitors and inhibitor control were from GenePharma (Shanghai, China). Anti-SOCS1 antibody were purchased from Abcam (ab62584, Cambridge, MA). Anti-TAB2 (A9867) and Anti-β-actin (AC026) antibodies were purchased from Abclonal (Wuhan, China).

*Cell culture and transfection*

The Raw264.7 cells were obtained from American Type Culture Collection (ATCC) and maintained in Dulbecco’s modified Eagle medium (DMEM) with 10% fetal bovine serum (FBS; Gibco). The thioglycolate-elicited mouse peritoneal macrophages were cultured in RPMI-1640 medium with 10% FBS. A total of 1×104 cells was seeded into 96-well plates and incubated overnight. JetSI-ENDO transfection reagents (114-15, Poly-plus-transfection, Strasbourg, France) were used for the co-transfection of plasmids and RNAs as previously described (Liu, et al., 2011; Liu, et al., 2019).

*Detection of cytokine production*

IL-6 and TNF-α in the supernatants were measured with ELISA kits (88-7064-22, 88-7346-22, eBioscience, USA) ，according to the manufacturer’s protocols as previously described (Liu, et al., 2012).

*RNA Sequencing and Data Analysis*

Total RNA was extracted using an RNeasy Micro Plus kit (74136, QIAGEN, Dusseldorf, Germany) according to the manufacturer’s instructions and sent to BGI Genomics for library construction. The library products were sequenced via MGIseq-2000 by BGI Genomics. The sequencing reads were filtered by SOAP nuke without quality problems. Genome mapping was done by HISAT. Clean reads were mapped to the mm10 reference genome using Bowtie2, and gene expression indicated by RPKM (Reads Per Kilobases per Million reads) was calculated by RSEM. Differentially expressed genes (DEG) were detected with Deseq2 using generalised linear model assuming negative binomial distributions by at least 2-fold change and FDR lower than 0.05.

*Biotin-based Pulldown Assay*

The capture of miR-155–bound ceRNAs in a pull-down assay with biotinylated miR-155 was performed as described previously (Dash, et al., 2018; Wang, et al., 2018). Briefly, RAW264.7 cells were transfected with biotinylated miR-155 mimics or controls (50 nmol/L) and stimulated with or without LPS at 6 hours after transfection. The biotin-coupled RNA complex was pulled down by incubating the cell lysates with streptavidin-coated magnetic beads (No. 88817, Pierce Biotechnology). The abundance of TAB2 and SOCS1 in the bound fractions was measured by Real-time PCR.

*RNA isolation and real-time PCR (qPCR)*

Total RNA was extracted with TRIzol (Invitrogen). Real-time quantitative PCR, using SYBR Green detection chemistry, was performed on a CFX-TOUCH PCR System (BioRAD, USA). For miRNA analysis, the reverse-transcriptase primer for miR-155 was 5’-GTC GTATCC AGT GCA GGG TCC GAG GTA TTC GCA CTG GAT ACG ACCCCC TA-3’. Quantitative PCR primers were 5’-CTC GTG GTTAAT GCTAAT TGT GA-3’ (forward) and 5 -GTG CAG GGT CCG AGG T-3’ (reverse). U6 small nuclear RNA was quantified using its reverse primers for reverse-transcriptase reaction and its forward and reverse primers for qPCR, which were 5’-CTC GCT TCG GCA GCA CA-3’ (forward) and 5’-AAC GCT TCA CGA ATT TGCGT-3’ (reverse).The relative expression level of miRNA was normalized by U6 expression. For murine TAB2, the primers were 5’-GGG GGT GGT CTC CCC AA CCT-3’ (forward) and 5’-ACT CAG TTT CCG GGC TTC GCT-3’ (reverse); For murine SOCS1, the primer was 5’-CCA CTC CGA TTA CCG GCG CATC-3’ (forward) and 5’-GAG CGC GAA GAA GCA GTT CCGT-3’ (reverse). For murine IL-6，the primer was 5’- CC CCA ATT TCC AAT GCT CTC C -3’(forward) and 5’- CGC ACT AGG TTT GCC GAG TA -3’ (reverse). For murine MyD88, 5’-GAA ACT CCA CAG GCG AGC GT -3’ (forward) and 5’-ACT CCC ACG TTA AGC GCG AC-3’ (reverse). For murine TNFa, the primer was 5’- TAG CCC ACG TCG TAG CAA AC -3’ (forward) and 5’- GCA GCC TTG TCC CTT GAA GA -3’ (reverse). For murine SHIP1, 5’- GTA CAA CTT GCC GTC CTG GT -3’ (forward) and 5’- TCT ACA GTG CCA GGA CCA TTC-3’ (reverse). The relative expression of mRNA was normalized by the β-actin.

*Western blot analysis*

The cells were washed twice with cold PBS and lysed with cell lysis buffer (Cell Signaling Technology) added PMSF. Protein concentrations of the cell lysis extracts were measured with BCA assay (Pierce, Rockford, IL). Equal amount of cell lysates were prepared and loaded to SDS/PAGE gel, transferred into PVDF membrane, and blotted as we did previously(Liu, et al., 2012; Song, et al., 2017) .

*Statistical analysis*

Statistical significance was finished by Student’s *t* test, analysis of variance (ANOVA) using GraphPad Prism 7.0, with a p value less than 0.05 considered as statistically significant. Correlation was assessed by means of Spearman’s rho test.All the experiments were repeated at least three times.

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