Supplementary information

Supplementary Table 1: The primer sequences used for qPCR		
Genes	Forwards (5'to3')	Reverse (5'to3')
Mouse- Tnfα	CCCTCACACTCAGATCATCTTCT	GCTACGACGTGGGGCTACAG
Mouse- iNOS	GTTCTCAGCCCAACAATACAAGA	GTGGACGGGTCGATGTCAC
Mouse- IL-6	TAGTCCTTCCTACCCCAATTTCC	TAGTCCTTCCTACCCCAATTTCC
Mouse-IL1β	TGGAAAAGCGGTTTGTCTTC	TACCAGTTGGGGGAACTCTGC
Mouse- Arg1	GTGAAGAACCCACGGTCTGT	GCCAGAGATGCTTCCAACTG
Mouse-CD163	GCCATAACTGCAGGCACAAA	GTTGGTCAGCCTCAGAGACA
Mouse-GAPDH	AGGTCGGTGTGAACGGATTTG	GGGGTCGTTGATGGCAACA

TABLE S1 List of primers used for RT-qPCR.



Figure S1. (A-B) Cell viability analysis using the CCK-8 assay in BV2 cells and HT22 cells (The values are presented as mean \pm SD; ***p<0.001, one-way ANOVA; n = 5 per group).



Figure S2. (A) The morphology of BV2 cells after different treatment. **(B-C)** Representative flow cytometric analysis of LPS-induced BV2 cells in each group (The values are presented as mean \pm SD; **p<0.01, ***p<0.001, one-way ANOVA). **(D)** Representative immunofluorescent staining of iNOS (green) and IBA-1 (red) in BV2 cells in each group. Nuclei were counterstained with DAPI (blue). Scale bar, 20 µm.



Figure S3. (A) Western blot analysis and quantification in BV2 cells (The values are presented as mean \pm SD; **p*<0.05, ***p*<0.01, ****p*<0.001, one-way ANOVA). (**B**) RT-qPCR analysis of pro-inflammatory and anti-inflammatory related genes expression in BV2 cells. All data were normalized to GAPDH expression (The values are presented as mean \pm SD; **p*<0.05, ***p*<0.01, ****p*<0.001, one-way ANOVA).



Figure S4. (A) The morphology of HT22 cells after co-culture with BV2 cells. (B-C) Flow cytometry analysis of HT22 cell apoptosis in each group (The values are presented as mean \pm SD; ***p<0.001, one-way ANOVA). (D) Western blot analysis and quantification of caspase-3, Bcl-2 and Bax expression in HT22 cells (The values are presented as mean \pm SD; *p<0.05, **p<0.01, ***p<0.001, one-way ANOVA).