<Supplementary data>

Method for identification of plant origin

Genomic DNA extraction

Approximately 0.1 g of the sample was used for DNA sequencing analysis and genomic DNA extraction was extracted using CTAB buffer. The sample was mixed with 500 μl of CTAB buffer and 5 μl of β-mercaptoethanol and reacted at 65℃ for 30 minutes. It was treated twice with CIA (chloroform:isoamyl alcohol, 24:1) and centrifuged to take the supernatant containing nucleic acid. The nucleic acid was separated using silica magnetic beads. The sample was washed twice with 500 μl of 70% ethanol and dried, and then eluted with 50 μl of TE buffer.

PCR amplification

To prepare the composition of PCR reactant, the sample was mixed with approximately 20 ng of template DNA, 1 unit of hot-start Taq polymerase, 2 μl of 10X PCR buffer, 2 mM $MgCl_2$, 0.2 mM dNTP and each 5 pM primer pair, and added distilled water to fill to a total volume of 20 μl. DNA amplification was performed as a denaturation phase at 94℃ for 5 minutes, followed by 94℃ for 30 seconds, 55℃ for 30 seconds and 72℃ for 1 minute under the setting at 35 cycles, followed by the final extension step at 72℃ for 5 minutes in *AllInOneCycler*™ 96 well PCR system (Bioneer, Daejeon, Korea). The PCR amplicon was electrophoresed on a 1% agarose gel. The amplification of ITS 1, and ITS 2 was achieved using the ITS 1 (5' TCCGTAGGTGAACCTGCGG) and ITS 2 (5' TCCTCCGCTTATTGATATGC) primers.

DNA sequencing

The amplicon was mixed with 10 ng of DNA, 2 µl of 5X sequencing buffer, 3.75 pM one-direction primer and BigDye Terminator V3.1 kit (Applied Biosystems, ThermoFisher scientific, USA) the mixture was performed as 98℃ for 5 seconds, 50℃ for 5 seconds and 60℃ for 4 minutes under the setting at 25 cycles. After BigDye cycling PCR reaction, it was added to 100 µl of Magnesil Green (Promega, USA) for purification. The dye-terminated nucleic acid fragments were eluted with 20 µl of distilled water. The sequencing analysis was performed on an ABI3130XL automatic sequencer (Applied Biosystems, ThermoFisher scientific, USA) and the products were separated in 36 cm capillary filled with POP-7TM polymer.

Phylogenetic analysis

The complete contig sequence, which was aligned based on the forward and reverse direction of the decoded nucleotide sequence data, was used to identify plant origin from the GeneBank (NCBI, http://www.ncbi.nlm.nih.gov/BLAST/).

Result

The result of DNA sequencing was verified using the BLAST tool.

It was identified that the DNA sequence of the sample (200708_CA) was identical to the DNA sequence of *Cuscuta australis* R. Br. and that the DNA sequence of the sample (200708_CJ) was the same as that of *Cuscuta Japonica* Choisy. The contig sequences used for plant origin verification is summarized in Table S1.

Table S1. Contig sequences of Cuscutae Semen samples

Sample name	Contig sequence
200708_CA	AAGGATCATTGTCGAACCCTCGCGGTAGAATGACTTGCTA ACCTGTACCAATTATTGATTCGAATGTCGGGGTGCCGTCT TTCTGATTTGCCCACGACGAACAAAAACACCGGCGCAGC AGCGCCAAGGAATATAATAATGAGTGTGCAACCTCGCAG AGCTTAGTTATGCTGCCTGTGAGCTTTGCATCCTTTTAATA AAAATGACTCTCGGCAATGGATATCTCGGCTCTTGCATCG ATGAAGAACGTAGCGAAATGCGATACGTGGTGTGAATTG CAGAATCCCGCGAACCATCGAAACTTTGAACGCAAGTTG CGCCTCAAGCCATTCGGTTGAGGGCACGTATGCTTGGGTG TCATGCATTATGTCTCCCCTCTCGTGTGTGGAGTGGGAAT AGATCCTGGCCTCCTGGGCCCTTCCTTGGGCGTGGTTGGC CGAAAATGTTGTCCTTGATTTTGTTGATGTCTTGGTGTGCG GTGGATGTGCCAGGTGTGCATAGTTGCCAGCCTTGCTCGG CTTCATTGTGGCGTCGGGATCCTATGAAGCTGCCGGTTTT

	GGCTCTTTGATTGCGACCCCAAGTCAGGCGAGACT ACCCGCTGAGTTTAAACAA
200708_CJ	TTAAACTCAGCGGGTAGTCCCGCCTGACCTGGGGTCGCGG TCAGAGAGCCAGCTCACACCAGCTCAAAAGGGTCAAAAT CCCAAGATGACTGGGCACGACGCGACGATAAGCACACTA GGTACGACCACCACTCGCCGTGACGTCAGTCGTCAAGGA CCAACATTTCAGCCAGCCGCATCCAAGGTCGGGCACGGG AGGCCATCATCCGCTCCCCGCTCCGCAACGGGAGGGGAG CGACGCGATGCGTGACGCCCAGGCAGACGTGCCCTCGGC CTGACGGCTTTGGGCGCAACTTGCGTTCAAAGACTCGATG GTTCACGGGATTCTGCAATTCACACCAAGTATCGCATTTC GCTACGTTCTTCATCGATGCGAGAGCCGAGATATCCGTTG CCGAGAGTCGTTTATGTTATTAAAGACGCCAACGCCACCC ATGCACCCGCGGACGGGGCACGATGGCCCGACGATCTCG TTTGAGTAGTCCTTGGCGCGTTCCGCGCCGGGGGTTCGTT GATCATTGGAGGCGCGTGCCCGAGAGAACAGCCCCCAAT GAATGTGTTGTATGTGAAACAGGTTCTCGAGTCGTTCTG CTGGGCAGGTTTCGACAATGATCCTT

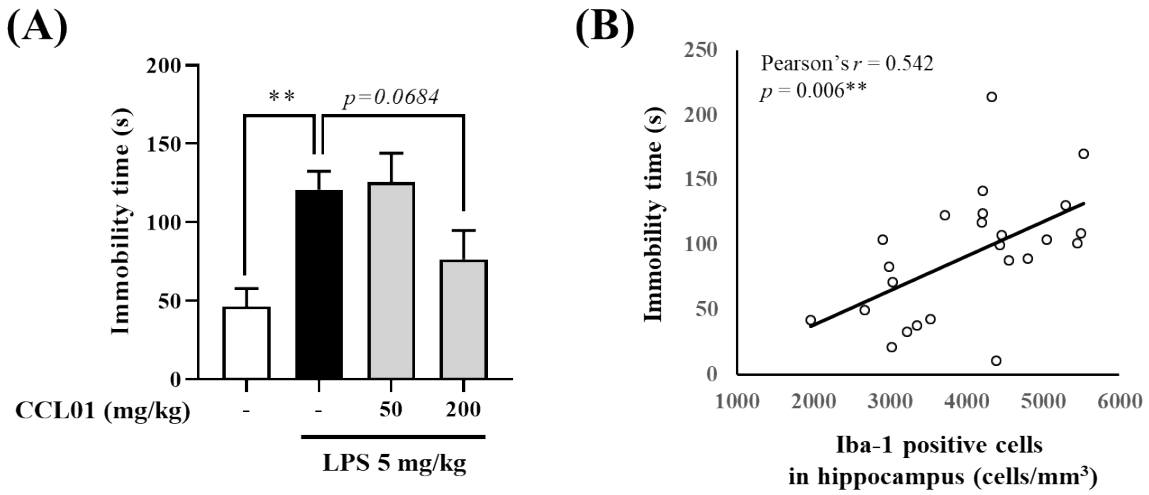
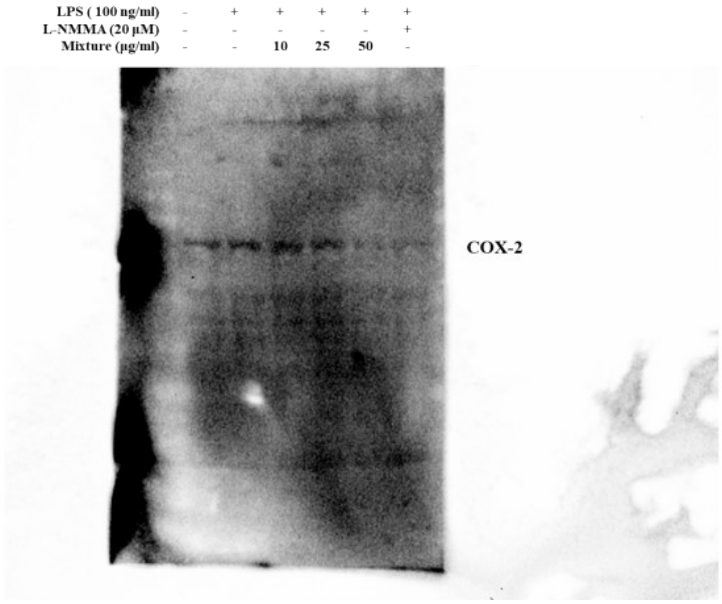


Fig. S1. The effects of CCL01 on depressive behavior in LPS-injected mice and the correlation between anti-neuroinflammatory and anti-depressive effects of CCL01. Mice were administered with MT104 (50 or 200 mg/kg, *p.o.*) for consecutive 5 days and injected with LPS (5 mg/kg, *i.p.*) on the fifth day. (A) Three hours after LPS injection, tail suspension test (TST) was performed, and the immobility time was analyzed. All data are presented as the mean ± SEM (n = 6 – 7). $^{**}p < 0.01$ vs. normal group. (B) Correlation scatter plots analyzed between Iba-1-positive cell counts and immobility time. Pearson's r value with significance ($^{**}p < 0.01$) was obtained from correlation analysis.

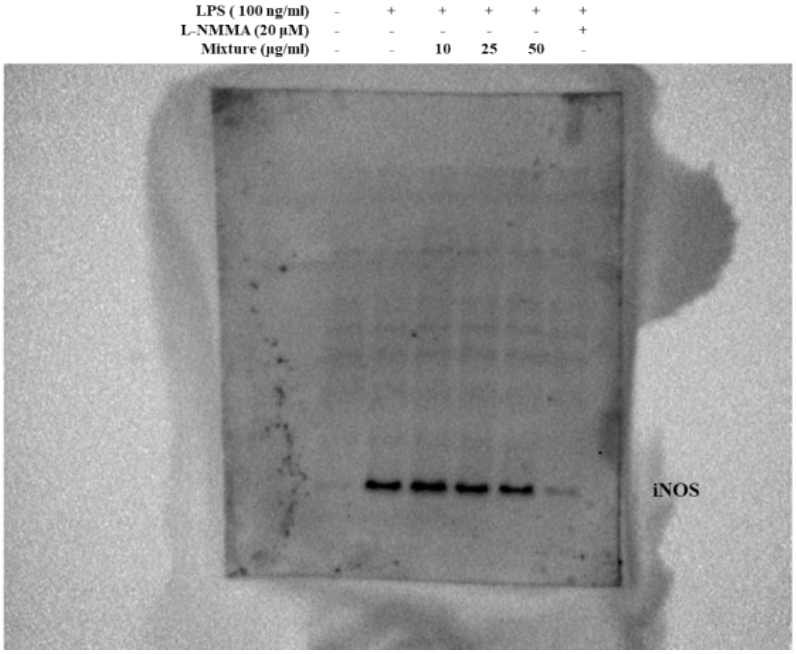
<Western images>

Fig.3_Data

1) COX-2



2) iNOS



3) α-Tubulin

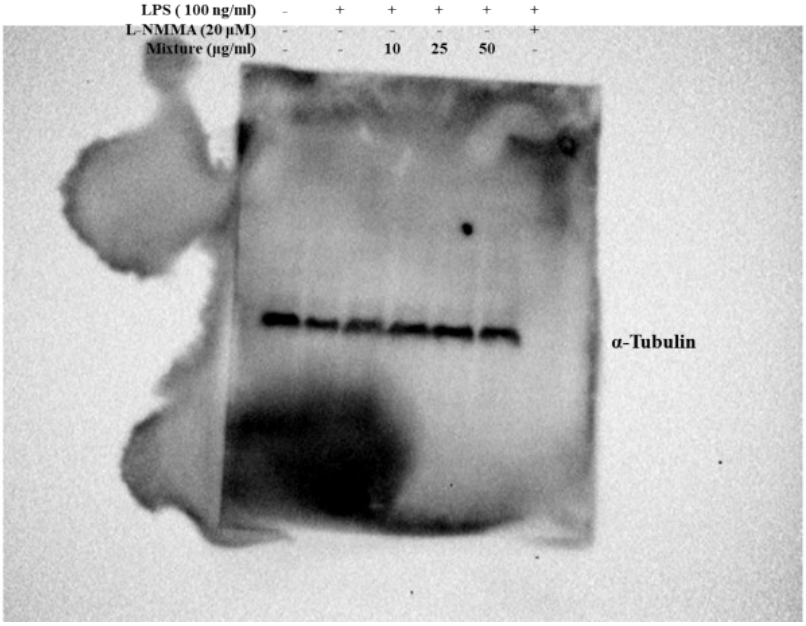
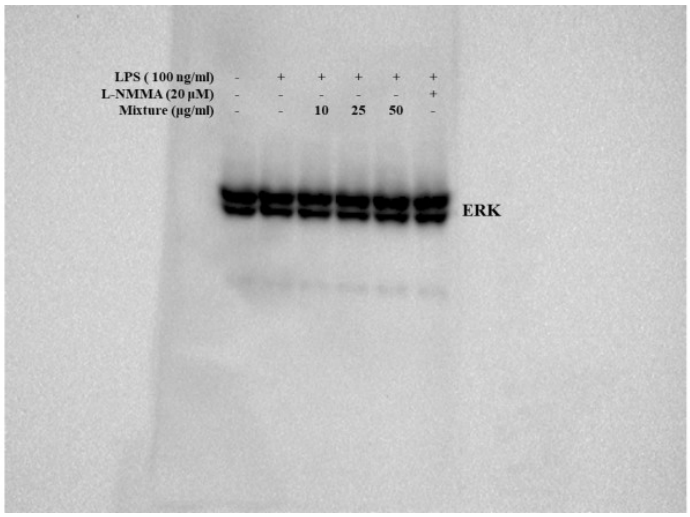
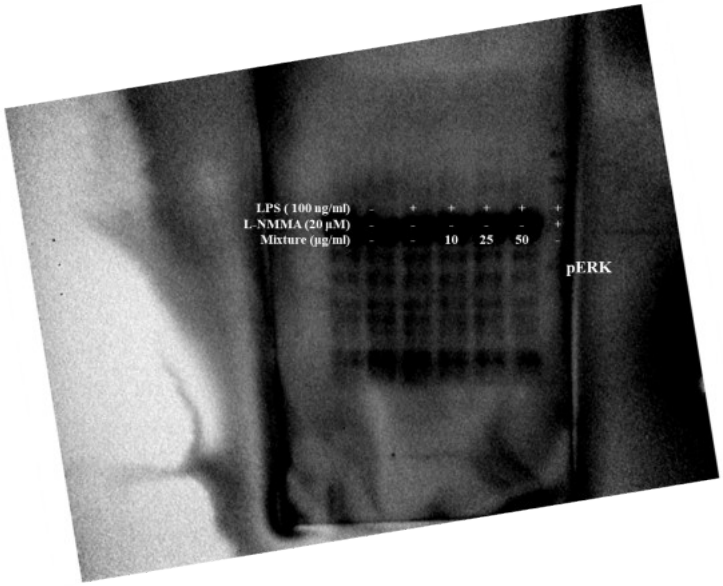


Fig.4_Data

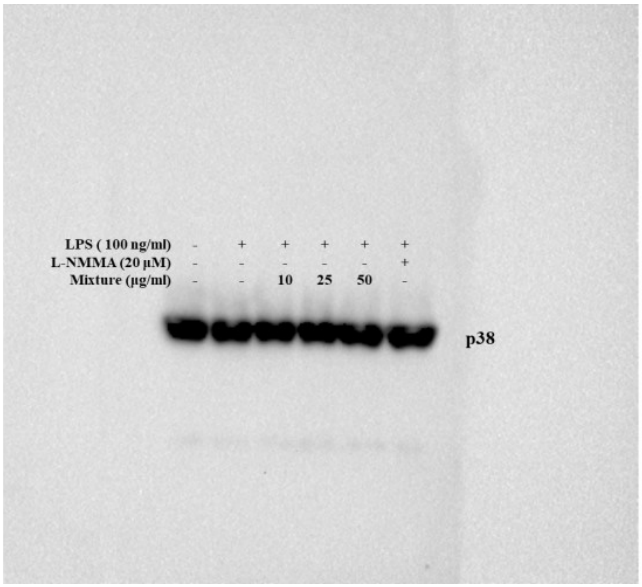
1) ERK



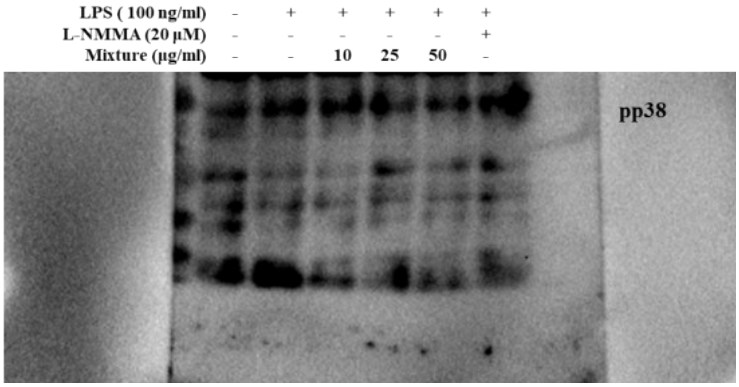
2) p-ERK



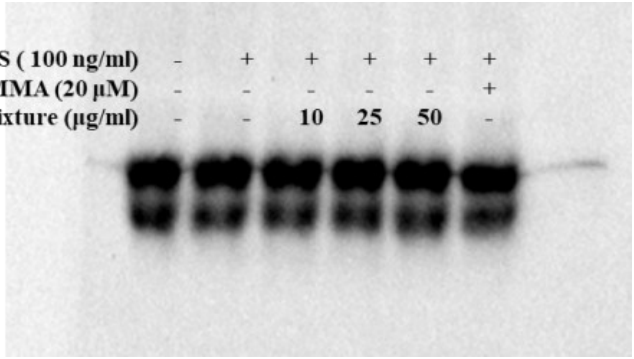
3) p38


LPS (100 ng/ml) - + + + + +
L-NMMA (20 μM) - - - - - +
Mixture (μg/ml) - - 10 25 50 -
p38

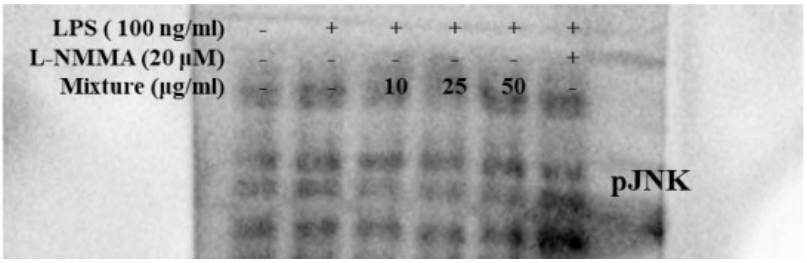
4) p-p38


LPS (100 ng/ml) - + + + + +
L-NMMA (20 μM) - - - - - +
Mixture (μg/ml) - - 10 25 50 -
pp38

5) JNK



6) p-JNK



7) α-Tubulin

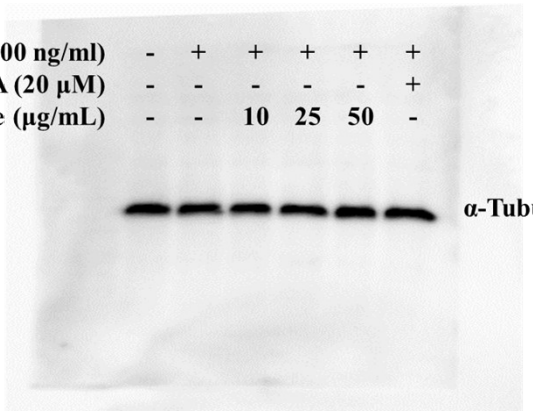
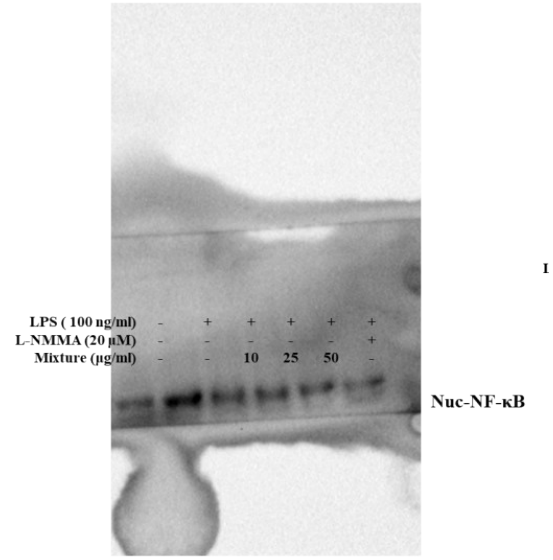
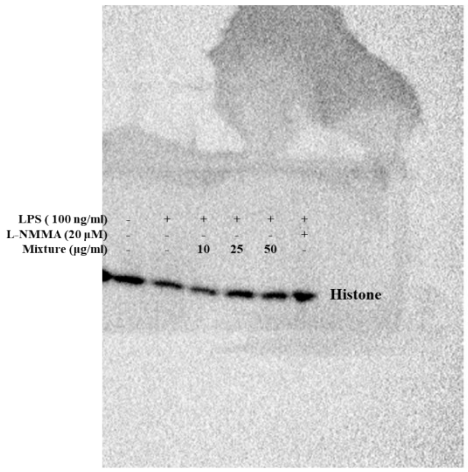


Fig.5_Data

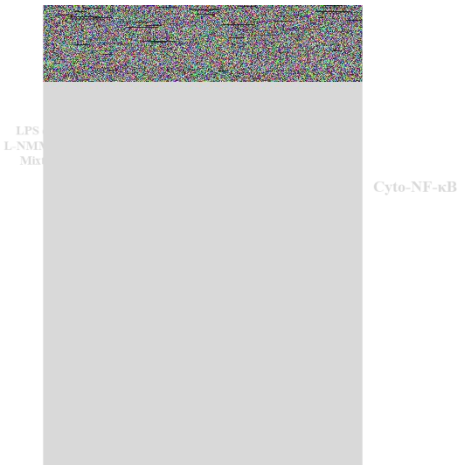
1) Nuc-NF-κB



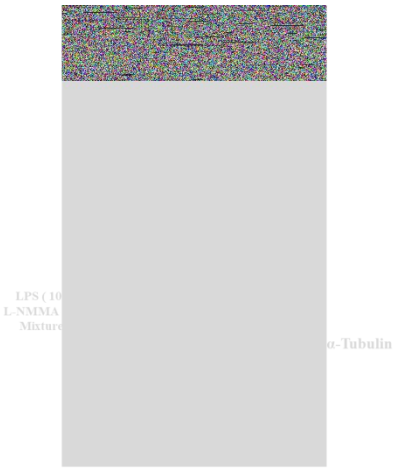
2) Histone



3) Cyt-NF-κB



4) α-Tubulin



5) Cyt-IκB

6) Cyt-p-IκB

7) α-Tubulin

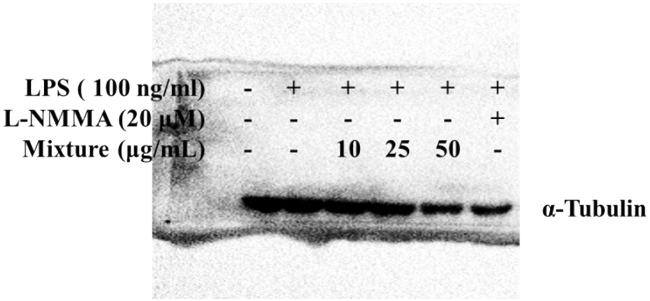
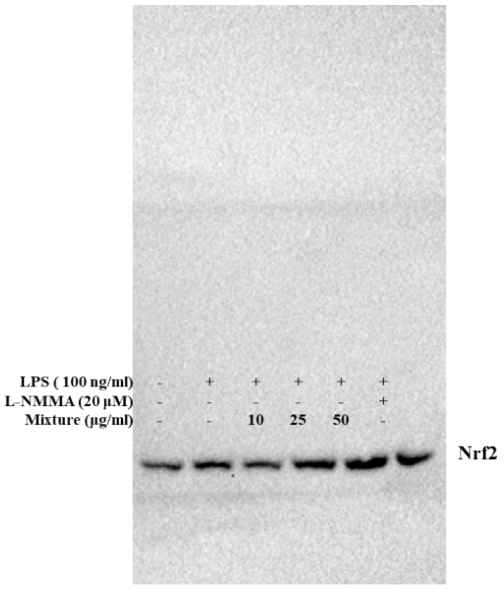
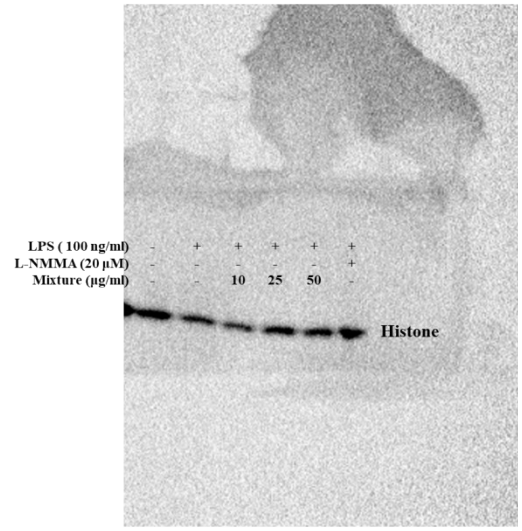


Fig.6_Data

1) Nrf2



2) Histone



3) HO-1

4) α-Tubulin