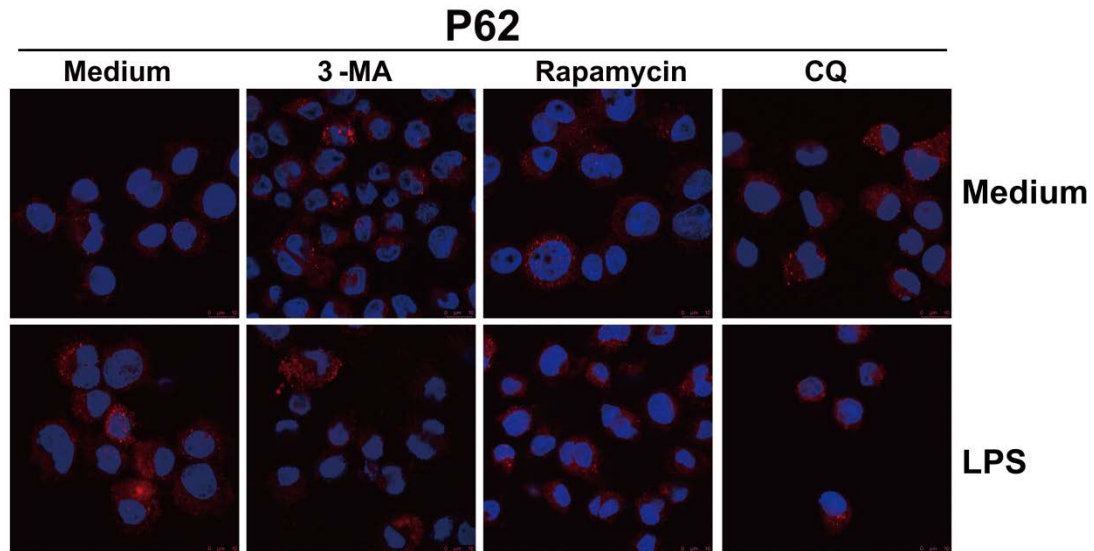


## Supplementary Files

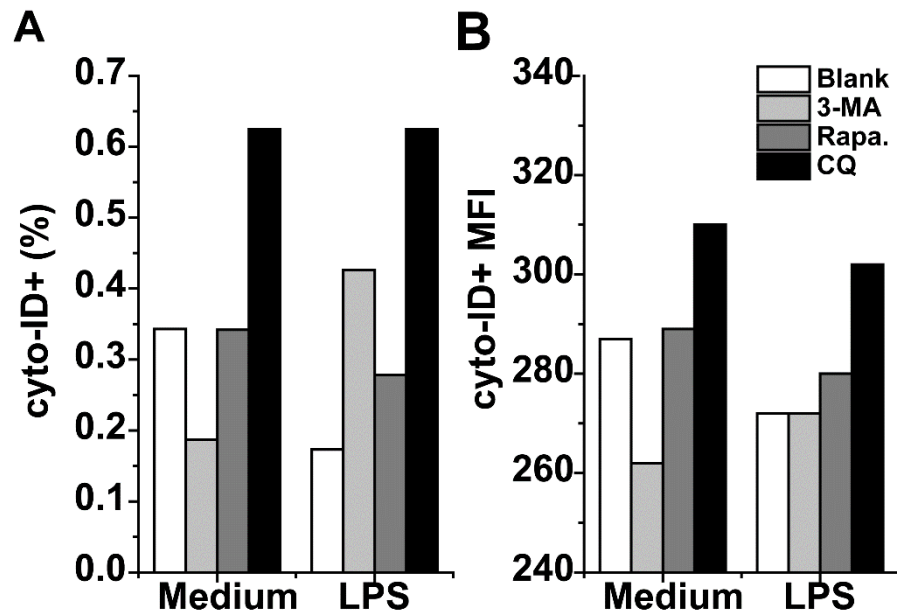
### Supplementary Figure 1.



#### Supplementary Figure 1. Immunofluorescence staining of P62/SQSTM1.

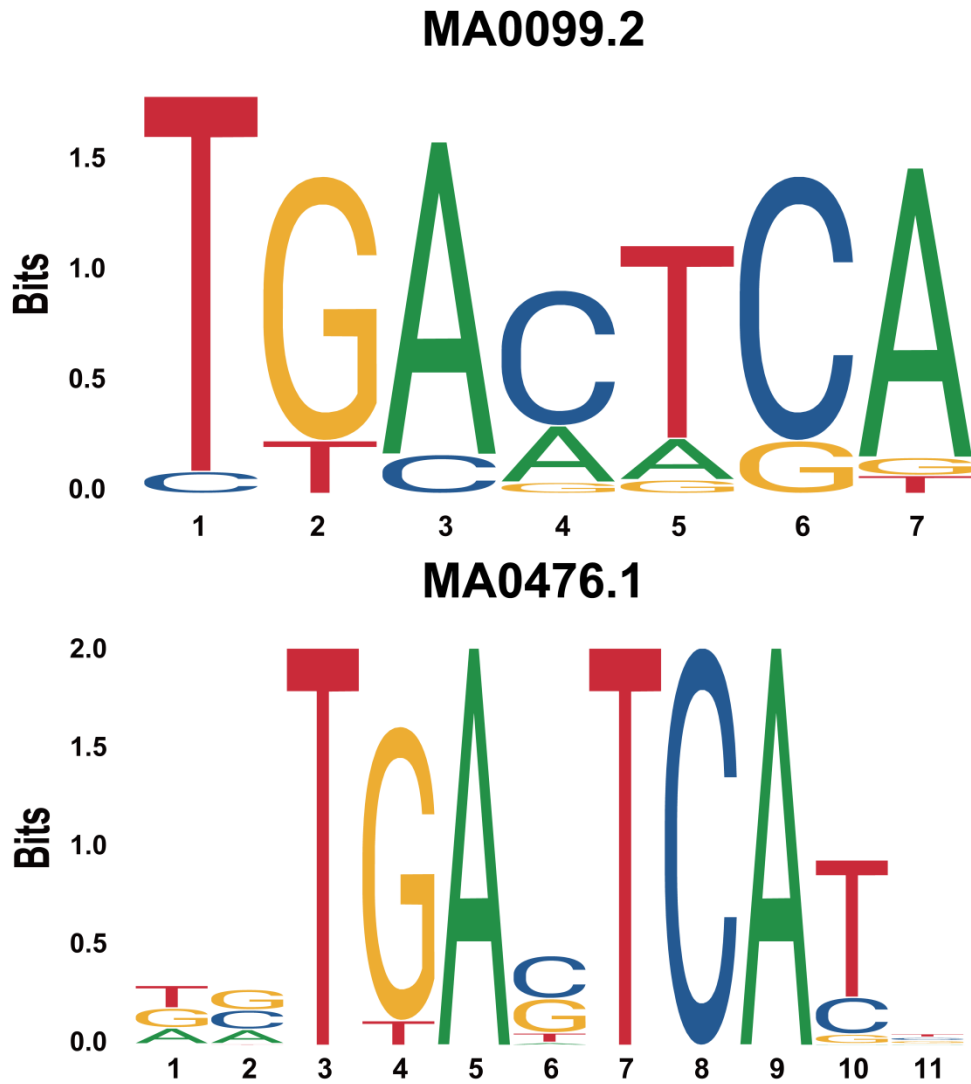
U937 cells were treated with 400 nM rapamycin, 20  $\mu$ M chloroquine (CQ), or 1 mM 3-methyladenine (3-MA) respectively with or without lipopolysaccharides (LPS,200ng/ml) stimulation for 2 hours. Thereafter, cells were stained with Alexa Fluor 647 conjugated anti- P62/SQSTM1 and observed with a confocal microscope. Neither CQ nor 3-MA treatment induced a significant upregulation of P62/SQSTM1.

Supplementary Figure 2.



Supplementary Figure 2. Flow cytometry analysis of autophagic U937 cells labeled with Cyto-ID kit.

U937 cells were treated with rapamycin, chloroquine, or 3-methyladenine respectively with or without lipopolysaccharides stimulation for 2 hours. With flow cytometry analysis, proportion (A) and mean fluorescence density (MFI) (B) of Cyto-ID labeled autophagic U937 cells were showed in columns.



**Supplementary Figure 3. Sequence logo of matrix profiles with putative binding sites of AP-1.**

With JASPAR database (<http://jaspar.cgb.ki.se>), matrix profiles MA0099.2 and MA0476.1 with putative binding sites of AP-1 transcription factors were identified in the IL-37 promoter region.

**Supplementary Table 1. Primer sequences used in this study.**

<b>Primer</b>	<b>Sequence (5'–3')</b>
Human	
IL-37	F: TTAGAAGACCCGGCTGGAAGCC R: AGATCTCTGGGCGTATGTAGT
IL-18	F: ATGGCTGCTGAACCAGTAGAAG R: CAGCCATACCTCTAGGCTGGC
IL-6	F: ACTCACCTCTTCAGAACGAATTG R: CCATCTTTGGAAGGTTTCAGGTTG
TNF- $\alpha$	F: GGCTCCAGGCGGTGCTTGTTTC R: AGACGGCGATGCGGCTGATG
IL-1R8	F: TCAGTGGCTCTGAACTGCAC R: GTACCAGAGCAGCACGTTGA
IL-18 $\alpha$	F: CACAGACACCAAAAGCTTCATC R: CAC AGT CAC TAG GCA CAC TAC
IL-1 $\beta$	F: ACAGATGAAGTGCTCCTTCCA R: GTCGGAGATTCGTAGCTGGAT
GAPDH	F: ACAGTCCATGCCATCACTG R: AGTAGAGGCAGGGATGATG
Rhesus macaque	
IL-37	F:TTAGAAGACCCGGCTGGAAGCC R:AGATCTCTGGGCGTATGTAGT
GAPDH	F: GTCTGGAAAAACCTGCCAAG R: ACCTGGTGCTCAGTGTAGCC

**Supplementary Table 2. Sequences and locations of AP1 putative binding sites within the promotor region of IL-37 analyzed with the JASPAR database.**

Matrix ID	Name	Score	Relative score	Start	End	Strand	Predicted sequence
MA0099.2	FOS::JUN	10.664	1	221	227	+	TGACTCA
MA0476.1	FOS	10.2377	0.92548	219	229	+	TTTGACTCACC
MA0099.2	FOS::JUN	8.18522	0.909521	257	263	+	TGCCTCA