Figure S1

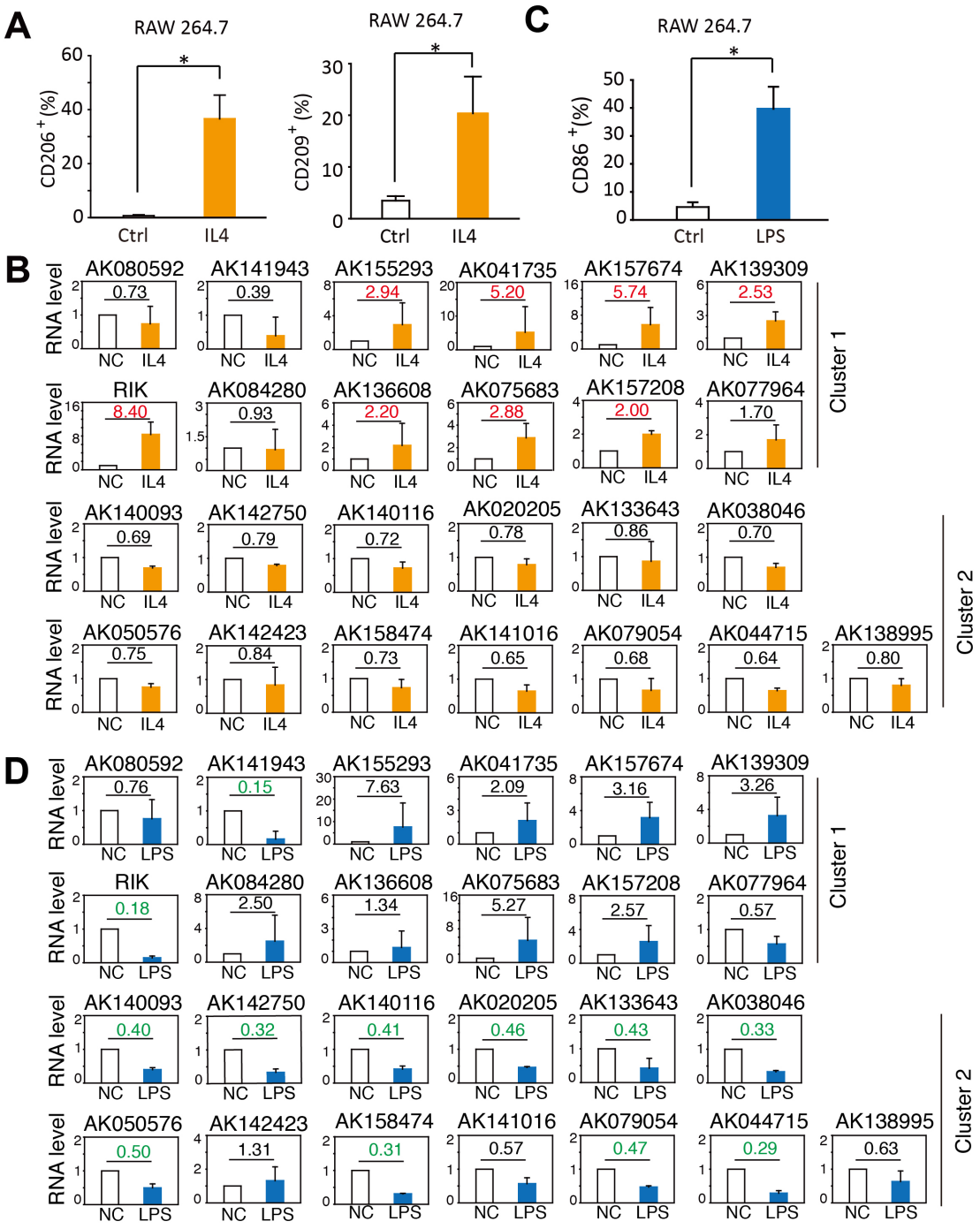


Figure S1: (**A**) Flow cytometric analysis was performed to analyze the percentage of $CD206^+$ cells or $CD209^+$ cells in IL4-triggered M2 polarization model. RAW264.7 cells were treated with IL4 (10 ng/mL) for 72 hours and the expression of CD206 or CD209 was analyzed. The statistical data is from three independent experiments and the bar indicates the SD values (*:

p<0.05). (**B**) Validation of 25 lncRNAs in IL4-triggered M2 polarization model by qRT-PCR. RAW264.7 cells were treated with IL4 (10 ng/mL) for 24 hours and qRT-PCR was used to verify the changes of lncRNAs. (**C**) Flow cytometric analysis was performed to analyze the percentage of $CD86^+$ cells in LPS-triggered M1 polarization model. RAW264.7 cells were treated with LPS (10 ng/mL) for 72 hours and the expression of CD86 was analyzed. The statistical data is from three independent experiments and the bar indicates the SD values (*: p<0.05). (**D**) Validation of 25 lncRNAs changed in LPS-triggered M1 polarization model by qRT-PCR. RAW264.7 cells were treated with LPS (10 ng/mL) for 24 hours and qRT-PCR was used to verify the changes of lncRNAs. The relative gene expression is normalized to control group (without treatment) and the number indicates the mean value from triplicates.

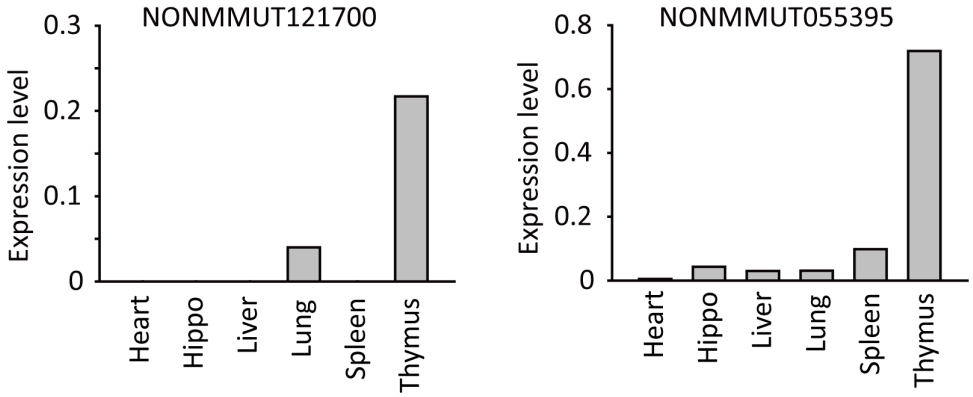
Figure S2

A

The conservation analysis of lncRNA-MM2P

Sequences producing significant alignments	Scores (bits)	Value
NONMMUT121700	3400	0.0
NONMMUT055395	3400	0.0

B



C

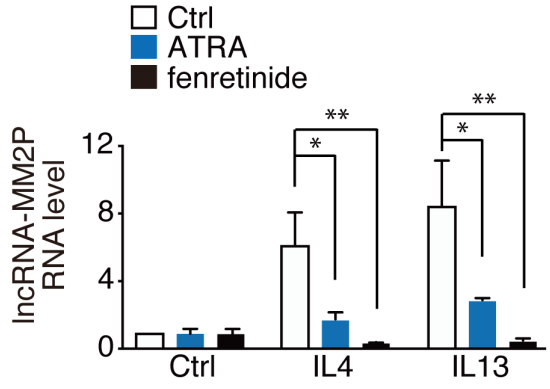


Figure S2: (**A**) The conservation annotation of the lncRNA-MM2P presented by the NONCODE database. Scores and value represented the conservation of the lncRNA-MM2P. Value = 0.0 suggested that the lncRNA-MM2P is highly similar to the transcripts. (**B**) The expression profile of the referred transcripts in different organs. (**C**) The expression level of lncRNA-MM2P in IL4- and IL13- treated RAW264.7 cells after ATRA or fenretinide cotreatment. The data

is show as fold change comparing to control group. The statistical data is from three independent experiments and the bar indicates the SD values (*: $p<0.05$; **: $p<0.01$).

Figure S3

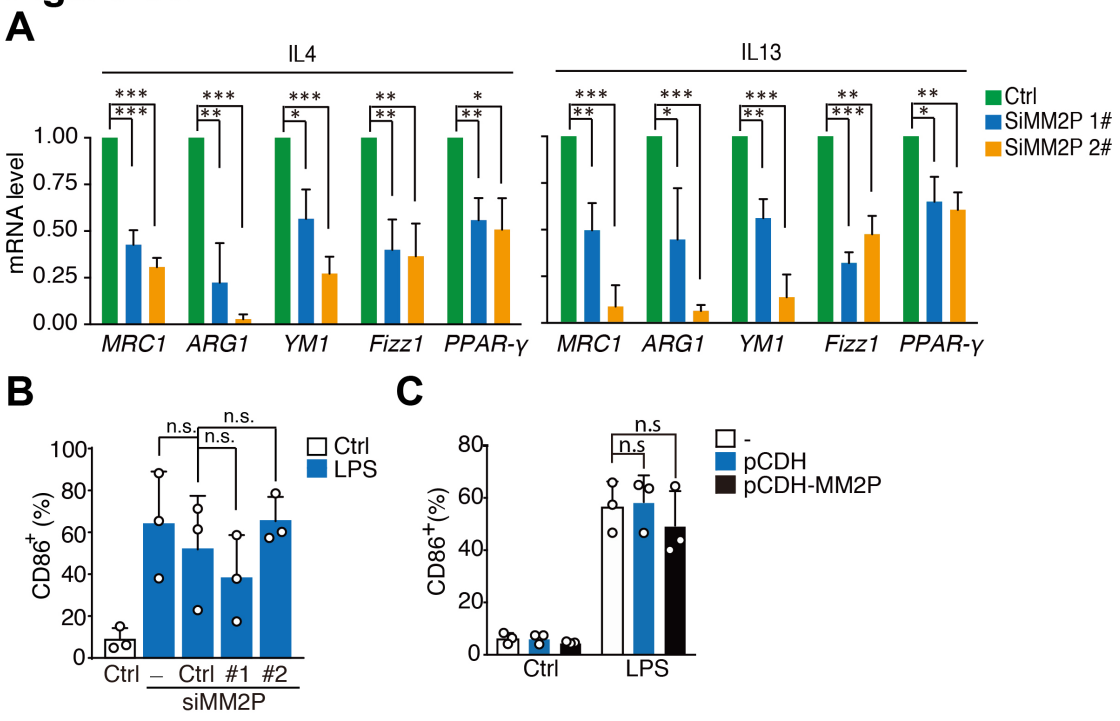


Figure S3: (**A**) The mRNA level of M2 polarization marker genes in BMDMs cells were quantified by qRT-PCR and normalized to 18s rRNA expression. The data is show as fold change comparing to control group. The statistical data is from three independent experiments and the bar indicates the SD values (*: $p<0.05$, **: $p<0.01$, ***: $p<0.001$). (**B**) RAW264.7 cells were transfected with siRNAs specifically targeting lncRNA-MM2P or control siRNAs for 12 hours and then stimulated with LPS (10 ng/mL) for 72 hours. Flow cytometric analysis was performed to analyze the percentage of $CD86^+$ cells. The statistical data is from three independent experiments and the bar indicates the SD values (n.s.: no statistic difference). (**C**) Flow cytometric analysis was performed to analyze the percentage of $CD86^+$ cells after overexpression of lncRNA-MM2P in RAW264.7 cells treated with LPS. The statistical data is from three independent experiments and the bar indicates

the SD values (n.s.: no statistic difference).

Figure S4

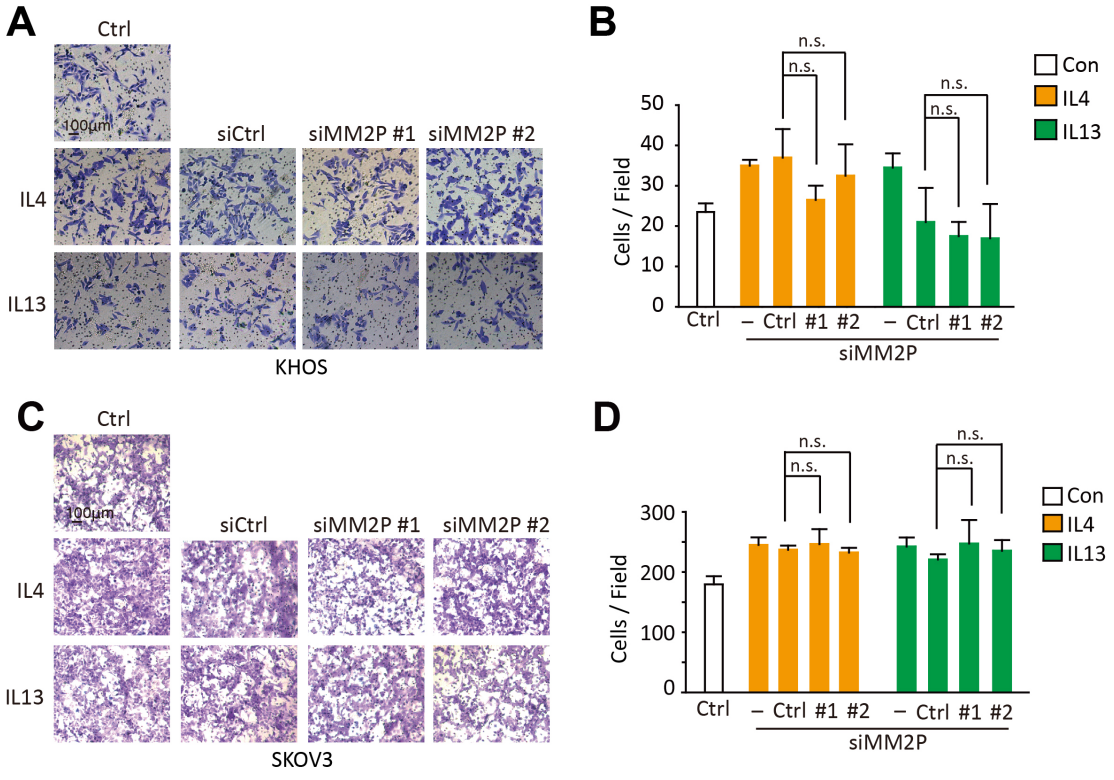
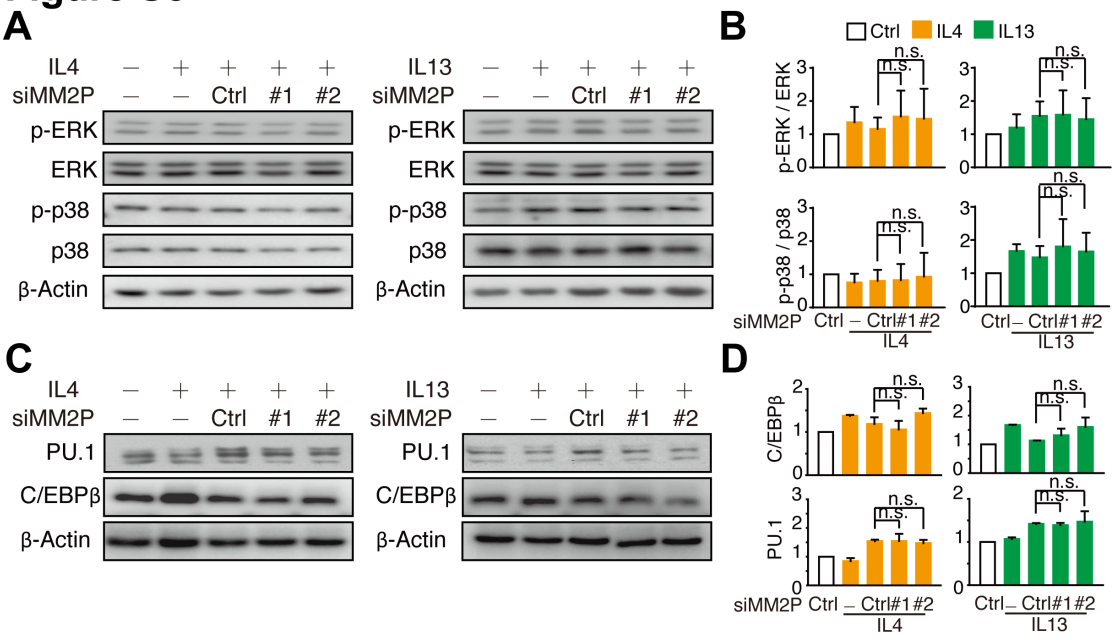


Figure S4: (**A**) Transwell assay was performed to determine the migration of KHOS cells. KHOS cells were treated with different conditioned medium of RAW264.7 cells for 12 hours using a 24-well Transwell chamber, and the migrated cells were stained with crystal violet. Scale bar = 100 μm. (**B**) Statistical analysis of (**A**). The statistical data is from three independent experiments and the bar indicates the SD values (n.s.: no significant difference). (**C**) Transwell assay was performed to determine the migration of SKOV3 cells. SKOV3 cells were treated with different conditioned medium of RAW264.7 cells for 12 hours using a 24-well Transwell chamber, and the migrated cells were stained with crystal violet. Scale bar = 100 μm. (**D**) Statistical analysis of (**C**). The statistical data is from three independent experiments and the bar indicates the SD values (n.s.: no significant

difference).

Figure S5



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99 **Figure S5:** (**A**) RAW264.7 cells were transfected with siRNAs specifically
100 targeting lncRNA-MM2P or control siRNAs for 12 hours and then 12 hours
101 later stimulated with IL13 or IL4 for 30min. Western blot detected the
102 expression of p-ERK1/2, ERK1/2, p-p38 and p38 in RAW264.7 cells. (**B**)
103 Quantitative analysis of (**A**). The statistical data is from six independent
104 experiments and the bar indicates the SD values (n.s., no significant
105 difference). (**C**) RAW264.7 cells were transfected with siRNAs specifically
106 targeting lncRNA-MM2P or control siRNAs for 12 hours and then 12 hours
107 later stimulated with IL13 or IL4 for 30min. Western blot detected the
108 expression of PU.1 and C/EBPβ in RAW264.7 cells. (**D**) Quantitative analysis
109 of (**C**), the expression is normalized to β-Actin. The statistical data is from
110 three independent experiments and the bar indicates the SD values (n.s., no
111 significant difference).

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