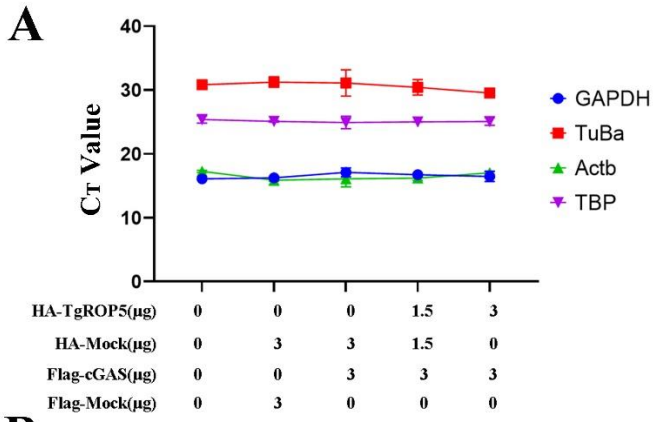


B

Target markers	GAPDH	TuBa	Actb	TBP
Minimum	16.10	29.53	15.87	24.91
Maximum	17.10	31.24	17.27	25.37
Range	1.002	1.713	1.394	0.4604
Mean	16.52	30.62	16.49	25.08
Std. Deviation	0.4001	0.6884	0.6139	0.1720
Std. Error of Mean	0.1789	0.3079	0.2745	0.07694

Figure S1 | Different housekeeping genes expressed in different cells 1 μg of total RNA, isolated from different cells with TRIzol regents, was reverse transcribed into cDNA with HiScript® III RT SuperMix for qPCR Kits. The cDNA was quantified using AceQ Universal SYBR qPCR Master Mix Kits. The CT values of different housekeeping genes including GAPDH, TuBa, Actb and TBP were measured and analyzed. (A) The CT value in different cells. (B) Descriptive statistics of different genes expressing.

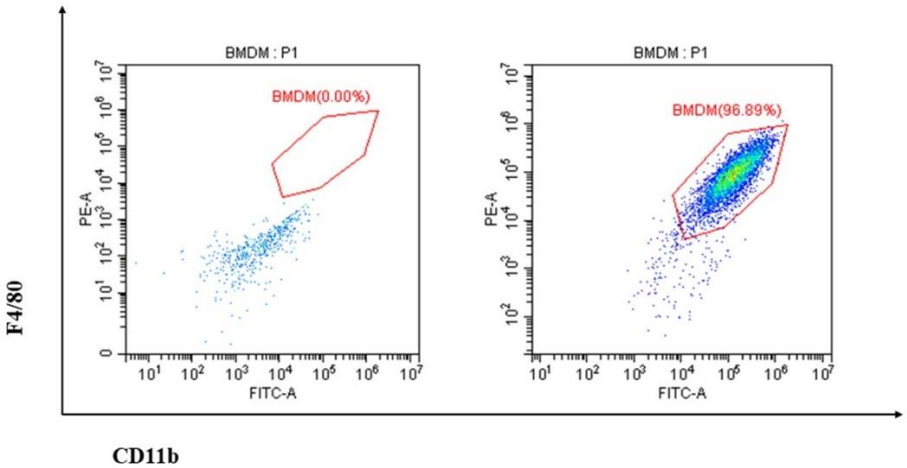


Figure S2 | Flow CytoMetry analysis of BMDM BMDM were generated from C57BL/6J mice and resuspended in macrophage differentiation media for 7 days in a 5% CO 2 humidified tissue culture incubator. The BMDM were harvested for FCA. The Flow CytoMetry analysis was performed using a BD AccuriTM C6 Plus flow cytometer (BD Biosciences). All data sets were analyzed with Flowjo software (TreeStar, Ashland, OR, United States).



Figure S3 | The sequences and information for the deletion mutants of ROP5 (A) The amino acid sequences of full-length and deletion mutants of ROP5(The putative domains were highlighted). (B) The information of the putative domains identified in ROP5. This information were analyzed with online tools (http://smart.embl-heidelberg.de/(accessed on 3 August 2021)).

Table S1 | primers used in this study

Primers	Sequences from 5′ to 3′	Used to
ROP5-F ROP5-R	ATAGGATCCATGGCGACGAAGCTCGCTAGACTAG ATACTCGAGTCAAGCGACTGAGGGCGCAGCAGT	Amplify sequence of ROP5
mcGAS-F mcGAS-R	AATGGTACCATGGAAGATCCGCGTAGAAGGACG CCACTCGAGTCAAAGCTTGTCAAAAATTGGAAAC	Amplify sequence of cGAS
mSTING-F mSTING-R	CCAGAATTCTATGCCATACTCCAACCTGCATCCAG TTACTCGAGTCAGATGAGGTCAGTGCGGAGTG	Amplify sequence of STING
mTBK1-F mTBK1-R	ATCGGATCCATGCAGAGCACCTCCAACCAT AATGGGCCCCTAAAGACAGTCCACATTGCG	Amplify sequence of TBK1
mIRF3-F mIRF3-R	CCAGAATTCTATGGAAACCCCGAAACCGCG CCACTCGAGTCAGATATTTCCAGTGGCCTG	Amplify sequence of IRF3
R5ΔPD1-F R5ΔPD1-R	ATAGGATCCATGCGGAAGAGACTTGCTCAGCACTTC ATACTCGAGTCAAGCGACTGAGGGCGCAGCAGT	Amplify truncated ROP5
R5ΔPD2-F R5ΔPD2-R	GAAGAGACTTGCTCAGCACACGCCGAGGTGGCTCTCCGGT ACCGGAGAGCCACCTCGGCGTGTGCTGAGCAAGTCTCTTC	Amplify truncated ROP5
R5ΔPD3-F R5ΔPD3-R	AGGTGGCTCTCCGGTCTCCCGCTGCTGGACCCTTCGTTTCAT TGAAACGAAGGGTCCAGCAGCGGGAGACCGGAGAGCCACCT	Amplify truncated ROP5
R5ΔPD4-F R5ΔPD4-R	ATAGGATCCATGGCGACGAAGCTCGCTAGACTAG ATACTCGAGCTGCACGAAGTCAGGCACAGGTAT	Amplify truncated ROP5
qIFN-β-F qIFN-β-R	CAGCTCCAAGAAAGGACGAAC GGCAGTGTAACTCTTCTGCAT	qPCR analyses
qISG56-F qISG56-R	CTGAGATGTCACTTCACATGGAA GTGCATCCCCAATGGGTTCT	qPCR analyses
qIL-6-F qIL-6-R	TAGTCCTTCCTACCCCAATTTCC TTGGTCCTTAGCCACTCCTTC	qPCR analyses
qCXCL-10-F qCXCL-10-R	CCAAGTGCTGCCGTCATTTTC GGCTCGCAGGGATGATTTCAA	qPCR analyses
qISG15-F qISG15-R	GGTGTCCGTGACTAACTCCAT TGGAAAGGGTAAGACCGTCCT	qPCR analyses
qActb-F qActb-R	GGCTGTATTCCCCTCCATCG CCAGTTGGTAACAATGCCATGT	qPCR analyses
qTuBa-F qTuBa-R	AGCTCTTCTGCTTGGAGCAC GTTAGCTGCATCCTCCTTGC	qPCR analyses
qTBP-F qTBP-R	GCCTTCCACCTTATGCTCA TGTGTGGGTTGCTGAGATGT	qPCR analyses
qGAPDH-F qGAPDH-R	AGGTCGGTGTGAACGGATTTG TGTAGACCATGTAGTTGAGGTCA	qPCR analyses
qTgB1-F qTgB1-R	AACGGGCGAGTAGCACCTGAG TGGGTCTACGTCGATGGCATGACAAC	qPCR analyses
gRNA-F gRNA-R	GATCGGTCACCGACTCGAAGGTTTTAGAGCTAGAAATA AACTTGACATCCCCATTTAC	Construct gRNA plasmid

pUC19-F pUC19-R	GGCGTAATCATGGTCATAGC ACTGGCCGTCGTTTTACAAC	Amplify linerized vector
DHFR-F DHFR-R	CAACCCGCGCAGAAGACATC GGACACGCTGAACTTGTGGC	Amplify UTR sequence
5′UTR-F 5′UTR-R	GTTGTAAAACGACGGCCAGTAATACACA TCCTGCATGCCG GATGTCTTCTGCGCGGGTTGCTGGCAGAT GTTGTGAGGTC	Amplify homologous
3′UTR-F 3′UTR-R	GCCACAAGTTCAGCGTGTCCGAAAACGG CTCTGCCAACGG GCTATGACCATGATTACGCCACTGTACAC ACGACTACCAG	Amplify homologous
PCR1-F PCR1-R	GGTTTCTGAGTGGTGACAGA ATTTGTGAGGACGACTCACG	Identify ROP5 knockout strain
PCR2-F PCR2-R	AGGATGAATTCCTACCCAGC TCTCTAAACGGTATGGTGCC	Identify ROP5 knockout strain
PCR3-F PCR3-R	AGTTGCTGACGAAACCCATC TTTTCAGGTGTGAAGCGTCC	Identify ROP5 knockout strain