## buffer and response factor

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#### **Supplementary Fig S1**

Supplementary Fig. S1. mRNA expressions of inflammatory factors in LPS- and LRM-induced Beta-TC-6 cells. LRM-treated Beta-TC-6 cells showing a significant increase in Il-1a, Il-6 and TNF-a mRNAs expression levels, while LPS does not have a significant effect. LPS+/–, incubation with or without 2 µg/ml LPS for 12 h; LRM+/–, incubation with or without LRM (2 µg/ml LPS induced RAW264.7 cell culturing medium mixed with common cell medium at a ratio of 1:3(v/v)) for 12 h. Data are expressed as Mean $\pm$ SD (n=3); \**P* <0.05 and \*\**P* < 0.01 vs LRM–.

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## **Supplementary Fig S2**



**Supplementary Fig. S2. Effects of miR-30a mimics on ROS in LPS-induced RAW 264.7 and Beta-TC-6 cells.** (a and b) Fluorescence microscopy showing that miR-30a significantly inhibited the production of ROS in both LPS-induced RAW264.7 cells and LRM-induced Beta-TC-6 cells. (c and d) Relative fluorescence intensity assay showing that miR-30a significantly inhibited the production of ROS in both LPS-induced Raw264.7

cells and LRM-induced Beta-TC-6 cells. LPS+/–, incubation with or without LPS; LRM+/–, incubation with or without LRM; NC, negative controls of miRNA mimics; NC-i, negative controls of miRNA inhibitors or siRNA; miR-30a-i, miRNA-30a inhibitor; and si-IL1a, silencing mRNA fragment of Il-1a. Data are expressed as the Mean $\pm$ SD (n=3); \*\**P* < 0.01 vs. NC or NC-i (LPS/LRM+), respectively.

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**Supplementary Fig S3** 



**Supplementary Fig S3 (a) The uncropped images of Western blotting in Raw24.7 cells.** Western blotting showing that miR-30a mimics significantly inhibit the increases of pp65, pIKBa and p62 in RAW264.7 and Beta-TC-6 cells after 24 h of LPS and LRM, respectively. 1 LPS-NC, 2 LPS+NC, 3 LPS+miR30a, 4 LPS+NCi, 5 LPS+miR30ai, 6 LPS+silL1a



**Supplementary Fig S3 (b) The uncropped images of Western blotting in Beta-TC-6 cells.** Western blotting showing that miR-30a mimics significantly inhibit the increases of pp65, pIKBa and p62 in Beta-TC-6 cells after 24 h of LRM. 1 LRM-NC, 2 LRM+NC, 3 LRM+miR30a, 4 LRM+NCi, 5 LRM+miR30ai, 6 LRM+silL1a

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## **Supplementary Fig S3**



Supplemental Fig S3. Summary of effects and potential mechanisms of miR-30a on inflammation regulation and islet protection.

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#### **Supplementary Method S1**

#### ROS assay

In brief, the 2,7-Dichlorodi-hydrofluorescein diacetate (DCFH-DA) fluorescence probe was transported into the cells and then hydrolyzed into 2,7-dichlorodi-hydrofluorescein (DCFH). Intracellular active oxygen binds to DCFH and causes DCFH to emit fluorescence, which can be detected through fluorescence microscopy (excitation wavelength: 485 nm; emission wavelength: 525 nm). In this study, RAW264.7 and Beta-TC-6 cells ( $5 \times 10^4$  per well) were seeded into 24-well plates for 12 h of attachment. After replacing the medium, the cells were transfected with miRNA or siRNA mimics for 12 h. Subsequently, LPS (2) mg/mL final concentration) and LRM (1:3, v/v) was added to the medium with RAW264.7 and Beta-TC-6 cells for 6–24 h after medium replacement, respectively. Subsequently, the medium from each plate was replaced with fresh medium (without FBS) containing DCFH-DA (10 mM final concentration), and the plates were incubated for 20 min. The cells were then washed three times with fresh medium (without FBS) and immediately observed under a fluorescence microscope magnified at 200× (LEICA DMI6000B, German). Six random areas with the same size from the captured image of each sample were selected. The gray density of the fluorescence intensity in each area was calculated using ImageJ software, and the average value of each sample was obtained with three biological

repetitions for further statistical analysis. We defined the average gray density values of fluorescence intensity from negative controls of miRNAs treated with LPS or LRM as 1, and all values were normalized to this value.

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#### **Supplementary Method S2**

#### miRNA and mRNA q-PCR

For the miRNA assay, miR-30a was analyzed using the miRNA assay kit (GenePharma, Shanghai, China) in accordance with the manufacturer's instructions. The U6 gene was used as an internal control for normalization. In brief, the reverse transcription (RT) reaction was performed using a PrimeScript<sup>TM</sup> First Strand cDNA Synthesis Kit (Takara, Dalian, China). PCR was confirmed by SYBR Green I dye (Takara, Dalian, China) with an ABI PRISM 7300 Real-time PCR System (Applied Biosystems, USA). The primers for the mRNA assay were synthesized from Invitrogen (supplemental Table S2). Actin was used as an internal control for normalization. RT was performed using a PrimeScriptTM 1st Strand cDNA Synthesis Kit (Takara, Dalian, China) in accordance with the manufacturer's instructions. Q-PCR analysis was conducted using SYBR® Green I dye according to the manufacturer's protocol (Takara, Dalian, China) in an ABI PRISM 7300 Real-time PCR System, USA). The fold change was calculated using the 2<sup>-ddCt</sup> method of relative quantification. All experiments were conducted in triplicate.

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#### **Supplementary Method S3**

#### Western blot analysis

Cell lysis extracts were separated by SDS-PAGE (12%) and transferred onto nitrocellulose transfer membranes (PALL 66485, BioTrace NT, USA). The membranes were blocked with 5% non-fat dry milk for 1 h and left to react overnight at 4 °C with rabbit polyclonal anti-I Kappa B alpha (IKBa, 1:2000, #44D4, Cell Signaling Technology, USA), anti-pIKBa (1:2000, #14D4, Cell Signaling Technology, USA), anti-p65 (1:2000, #3033, Cell Signaling Technology, USA), anti-phospho-p65 (1:2000, #3039, Cell Signaling Technology), p62 (1:2000, PM045, Medical & Biological Laboratories Co., Ltd., Japanese), LC3 (1:2000, L7543, Sigma–Aldrich Co.). After rinsing, the membranes were soaked in blocking buffer with secondary antibodies (purified polyclonal antibody to rabbit or to mouse, 1:200–5000, KPL, USA) for an hour. After rinsing again, the membranes were visualized with the chemiluminescence method (Cat 32106, Pierce<sup>TM</sup> ECL Western Blotting Substrate, ThermoFisher Scientific, USA).

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## Supplemental Table S1 Nucleic acid sequences for miRNAs and siRNA mimics.

Gene names	Sequences (5' to 3')
miR-30a mimics	UGUAAACAUCCUCGACUGGAAG
Negative controls	UUCUCCGAACGUGUCACGUTT
miR-30a inhibitors	CUUCCAGUCGAGGAUGUUUACA
miRNA inhibitor NC	CAGUACUUUUGUGUAGUACAA

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## Supplemental Table S2 Primers of mouse IL1a 3'-UTR and its mutated fragments

Gene	Primers (5' to 3')
names	
IL1a-3'UTR	Forward: GCCTCTAGATATTTCGGGAGTCTATTC
	Reverse: GCCCTCGAGTAGAGTCTTTTTGATCCTC
IL1a-3'UTR-	Forward: TGAAAGCTAAGCCTCTTTGTAAGAGAAGAG
mut	Reverse: TTTAGAATTACAGAGACTCAGCACA

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Gene	NCBI	Primers (5' to 3')	Sizes
names	Accession		( <b>bp</b> )
	No.		
Mouse	NM_01055	Forward: TCTGCCATTGACCATCTC	182
IL1a	4.4	Reverse: ATCTTCCCGTTGCTTGAC	
Mouse	NM_03116	Forward: CTGCAAGAGACTTCCATCCAG	131
IL6	8	Reverse: GTGGTATAGACAGGTCTGTTGG	
Mouse	NM_01369	Forward: GGGCTTCCAGAACTCCA	213
TNFa	3.2	Reverse: GCTACAGGCTTGTCACTCG	
Mouse	NM_00838	Forward: CACTTCCTACCCCTGCTGG	81
Ins1	6	Reverse: ACCACAAAGATGCTGTTTGACA	
Mouse	NP_00117	Forward: GCTTCTTCTACACACCCATGTC	147
Ins2	2013.1	Reverse: AGCACTGATCTACAATGCCAC	
Mouse		Forward: GCCGCCACCCAGTTTAC	190

## Supplemental Table S3 Primers for PCR.

PDX-1	NM_00881	Reverse: CCCAGGCTCGGTTCCATT	
	4.3		
Mouse	NM_01089	Forward: GACCCAGAAACTGTCTAAAATAGAGACA	105
NeouroD1	4	Reverse: AAGGAGACCAGATCAGGGCTTT	
Mouse	NM_00127	Forward: GCTGAGGCTGATGAAAAACA	87
CREM	1505.1	Reverse: GCCACACGATTTTCAAGACA	
Mouse	NM_02156	Forward: GGGGAGAGGGAGGTTTAGTG	213
BHLHE22	0.4	Reverse: CCCTTTCATCACTTGCCAAT	
Mouse	NM_00739	Forward: GTGACGTTGACATCCGTAAAGA	245
Actin	3	Reverse: GCCGGACTCATCGTACTCC	
Human	NM_00057	Forward: ATCATGTAAGCTATGGCCCACT	131
IL1a	5	Reverse: CTTCCCGTTGGTTGCTACTAC	
Human	NM_00110	Forward: CATGTACGTTGCTATCCAGGC	250
Actin	1.3	Reverse: CTCCTTAATGTCACGCACGAT	