

## Supplemental data

**Fig. S1 Principal component analysis (PCA) plots for lncRNA expression cluster of HC FLS and RA FLS.**

**Fig. S2 Localization of LINK-A by nuclear/cytoplasm fractionation.** RT-qPCR analysis of cytoplasmic and nuclear fraction of HC FLSs revealed that LINK-A expression was enriched in cytoplasm. Values are expressed relative to expression level of nucleus. GAPDH served as a cytoplasmic marker; U6 served as a nuclear marker.

**Fig. S3** Correlation of synovial LINK-A expression with the synovitis score (A) and DAS28-ESR (B) in RA patients. LINK-A expression and synovitis score of RA patients were evaluated by ISH and H&E staining, respectively. Correlation analysis was performed by Spearman's rank order correlation test.

**Fig. S4** The quantification of the percentage of LINK-A-positive cells in synovial tissues from RA patients treated with prednisone or MTX (GC+MTX) and those with no therapy (naive). Data are shown as the mean  $\pm$  SD.

**Fig. S5 Efficiency of LINK-A knockdown.** RA FLS were transfected with specific LINK-A siRNA1-3 for 48 h, and silencing efficiency was evaluated by RT-qPCR. Data show the silencing efficiency of LINK-A siRNA from 3 independent experiments. Ct values are normalized to  $\beta$ -actin. \*\*\*\* $P < 0.001$  vs. control siRNA (siC), by 1-way ANOVA

**Fig. S6 Effect of LINK-A knockdown on the expression and activity of RhoA, Rac1 and CDC42.** RA FLS were transfected with LINK-A siRNA 2 or LINK-A siRNA 3 for 48 h. (A) Effect of LINK-A knockdown on the expression of RhoA, Rac1 and CDC42. The protein expression was measured by Western blot. Data (lower panel) are expressed as the mean  $\pm$  SD of densitometry quantification of Western blot from at least 6 independent experiments (B) Effect of LINK-A knockdown on the activity of CDC42, Rac1 and RhoA. The activity of RhoA, Rac1 and CDC42 was detected using G-LISA. Data are expressed as the mean  $\pm$  SD from at least 6 independent experiments. \* $P < 0.05$  vs. control siRNA (siC), by 1-way ANOVA

**Fig. S7 Expression of HIF-1 $\alpha$  in FLS from RA patients and healthy control (HC) subjects.** HIF-1 $\alpha$  expression was determined by RT-qPCR. Data are presented as the mean  $\pm$  SD

from at least 3 independent experiments.  $**P < 0.01$  vs. HC FLS, by Student's *t* test

**Fig. S8 Efficiency of HIF-1 $\alpha$  knockdown.** RA FLS were transfected with HIF-1 $\alpha$  siRNA 1-3 for 48 h and subjected to RT-qPCR analysis (**A**) and Western blot (**B**). A representative blot of at least 3 independent experiments is shown. The data shown are the mean  $\pm$  SD from at least 3 independent experiments.  $****P < 0.001$  vs. siC, by 1-way ANOVA

**Fig. S9 Effect of HIF-1 $\alpha$  knockdown on migration, invasion in RA FLSs.** RA FLS were transfected with siRNA-2 and siRNA-3 for HIF-1 $\alpha$  (si HIF-1 $\alpha$ -2, si HIF-1 $\alpha$ -3) or siC. Migration (**A**) and invasion (**B**) were evaluated using a Boyden chamber. An invasion assay was performed using inserts coated with a Matrigel basement membrane matrix. The migrated or invaded FLSs were stained violet using a Diff-Quick kit (left panel, original magnification, 100  $\times$ ). The migration or invasion index represents the number of migrated or invaded cells normalized to siC-treated cells. Data show the mean  $\pm$  SD for samples from 4 different RA patients.  $****P < 0.001$  vs. siC, by 1-way ANOVA

**Fig. S10 Effect of HIF-1 $\alpha$  knockdown on expression and secretion of MMPs and pro-inflammatory cytokines.** RA FLS were transfected with siRNA-2 and siRNA-3 for HIF-1 $\alpha$  (si HIF-1 $\alpha$ -2, si HIF-1 $\alpha$ -3) or siC with or without TNF- $\alpha$  stimulation for 24 hours. The mRNA expression of MMP and cytokine was detected using RT-qPCR assay. Ct values were normalized to  $\beta$ -actin values. MMP and cytokine secretion was measured using ELISA. (**A** and **B**) Effect of HIF-1 $\alpha$  knockdown on expression and secretion of MMPs. (**C** and **D**) Effect of HIF-1 $\alpha$  knockdown on expression and secretion of proinflammatory cytokines. Data are presented as the mean  $\pm$  SD.  $*P < 0.05$ ,  $**P < 0.01$  vs. siC,  $^{\#}P < 0.05$ ,  $^{\#\#}P < 0.01$  vs. siC + TNF- $\alpha$ , by 1-way ANOVA

**Fig. S11 Effect of miRNAs inhibition or mimics on the expression of MMPs (A and C) and pro-inflammatory cytokines (B and D) in RA FLSs.** RA FLS were treated with miRNAs inhibitors or mimics with or without TNF- $\alpha$  stimulation for 24 hours. MMP and pro-inflammatory cytokine expression was measured by RT-qPCR. Ct values were normalized to  $\beta$ -actin values. Data are presented as the mean  $\pm$  SD.  $*P < 0.05$ ,  $**P < 0.01$  vs. siC, by 1-way ANOVA

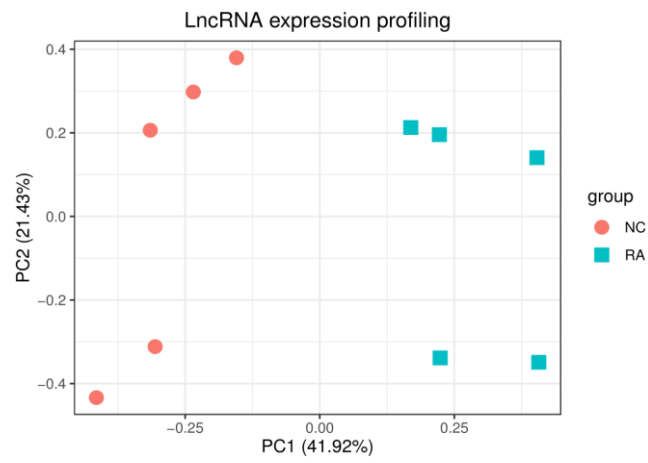
**Fig. S12 Effect of miRNA1262 inhibition or mimics on secretion of MMPs (A and B) and pro-inflammatory cytokines (C and D) in RA FLSs.** RA FLSs were treated with

miRNA 1262 (miR-1262) mimics or inhibitors for 24 hours. MMPs and cytokines secretion was measured using ELISA. Data are presented as the mean  $\pm$  SD. \* $P$  < 0.05, \*\* $P$  < 0.01 vs. siC, by 1-way ANOVA

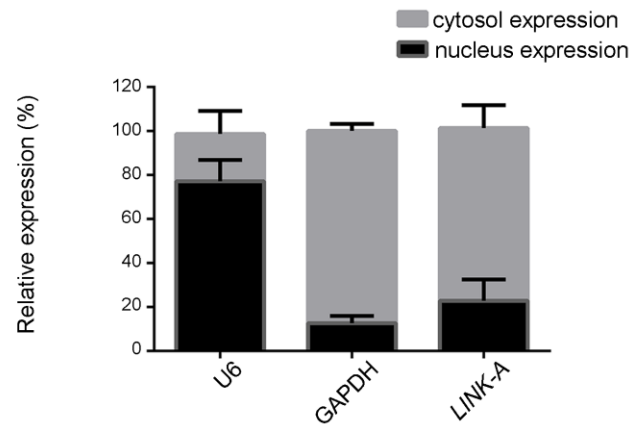
**Fig. S13 Effect of miRNA1262 inhibition or mimics on the proliferation of RA FLSs.** RA FLSs were treated with miRNA 1262 (miR-1262) inhibitors (A) or mimics (B) for 24 hours. EdU incorporation assay (D) was used to evaluate the proliferation. Representative images show proliferation of RA FLSs labeled with EdU (red) and nuclei stained with Hoechst 33342 (blue) (original magnification, 100  $\times$ ). Graphs (lower panels) indicate the mean  $\pm$  SD of 8 independent experiments involving 8 different RA patients.

**Fig. S14 Decreased levels of miRNA 1262 (miR-1262) in FLS from patients with RA.** Expression of miR-1262 was measured using RT-qPCR assay. Ct values were normalized to  $\beta$ -actin values. Data are presented as the mean  $\pm$  SD. \* $P$  < 0.05 vs. HC FLS, by Student's  $t$  test

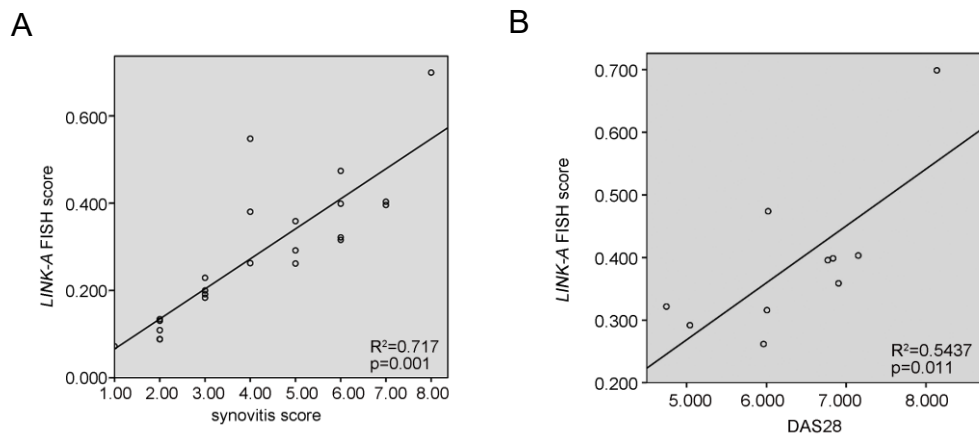
**Fig.S1**



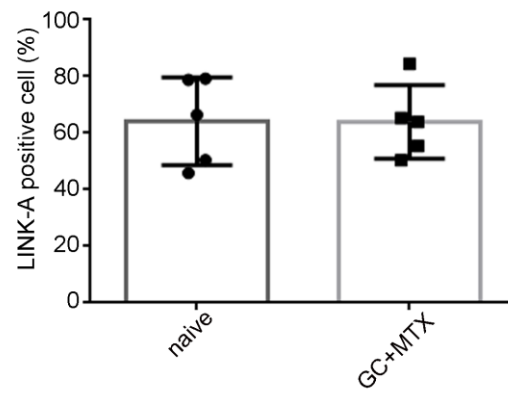
**Fig.S2**



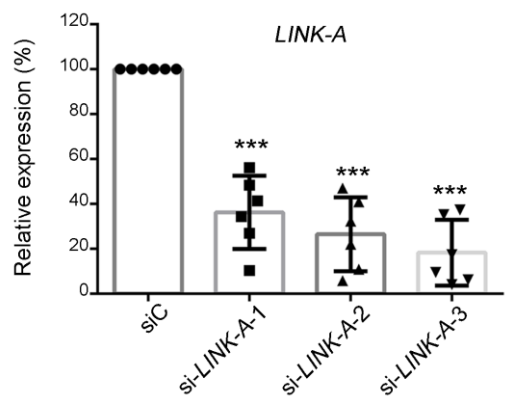
**Fig.S3**



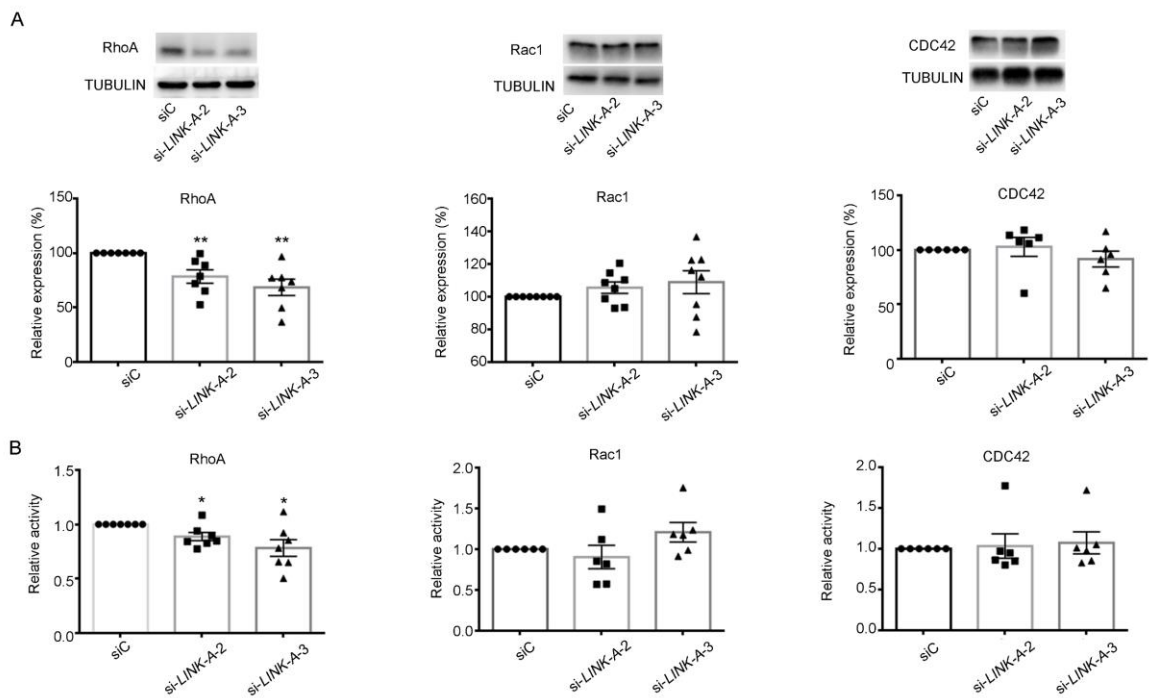
**Fig.S4**



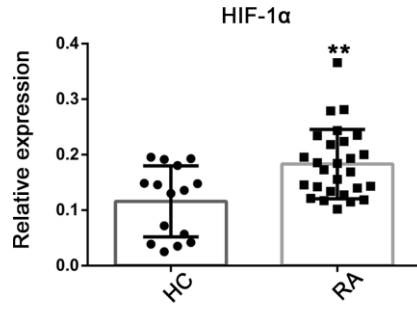
**Fig.S5**



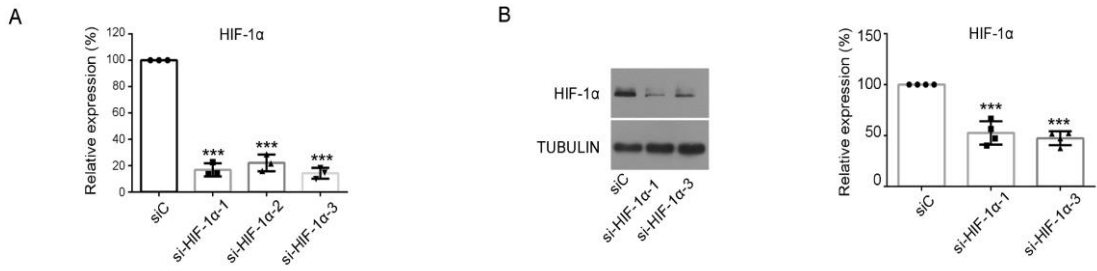
**Fig.S6**



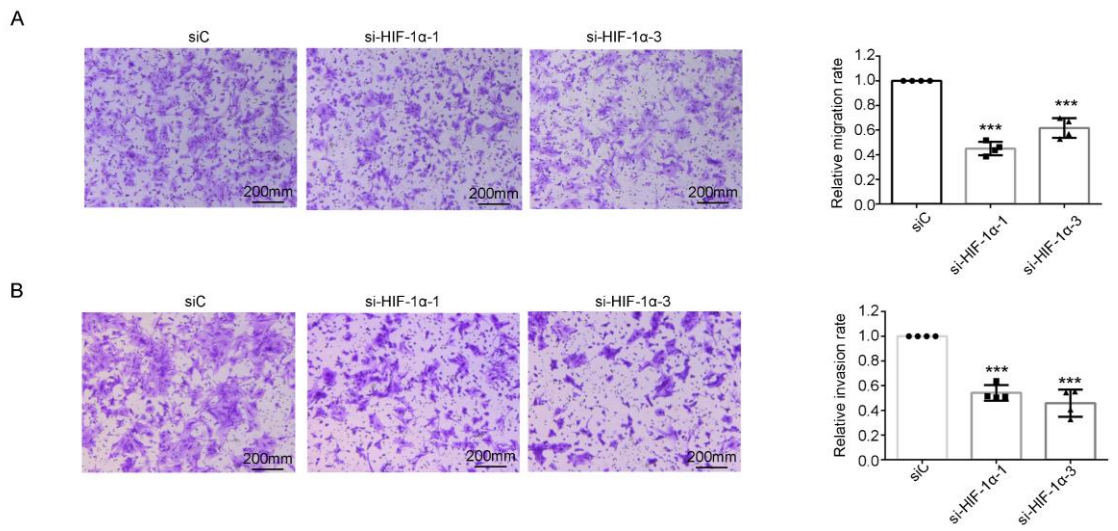
**Fig.S7**



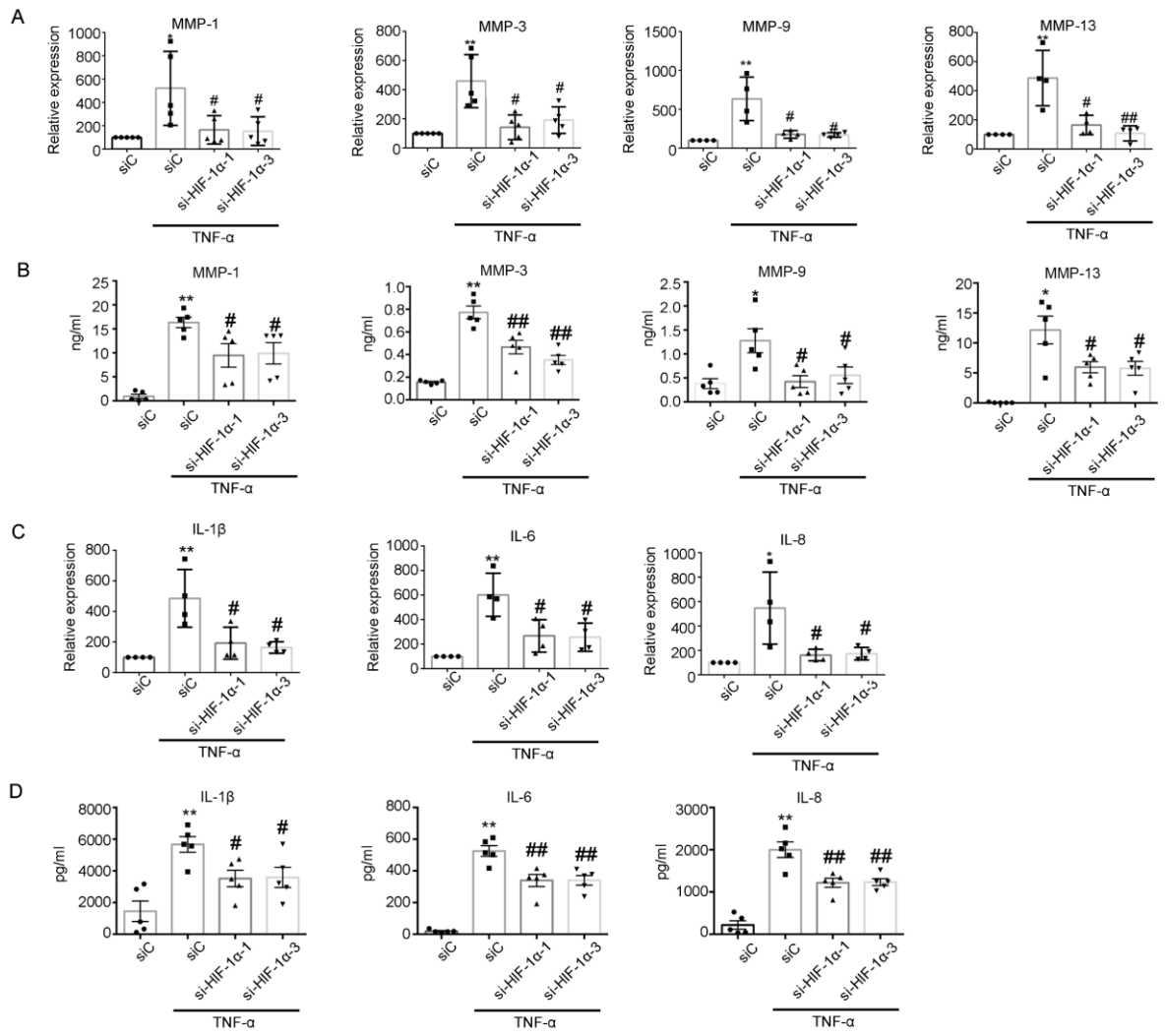
**Fig.S8**



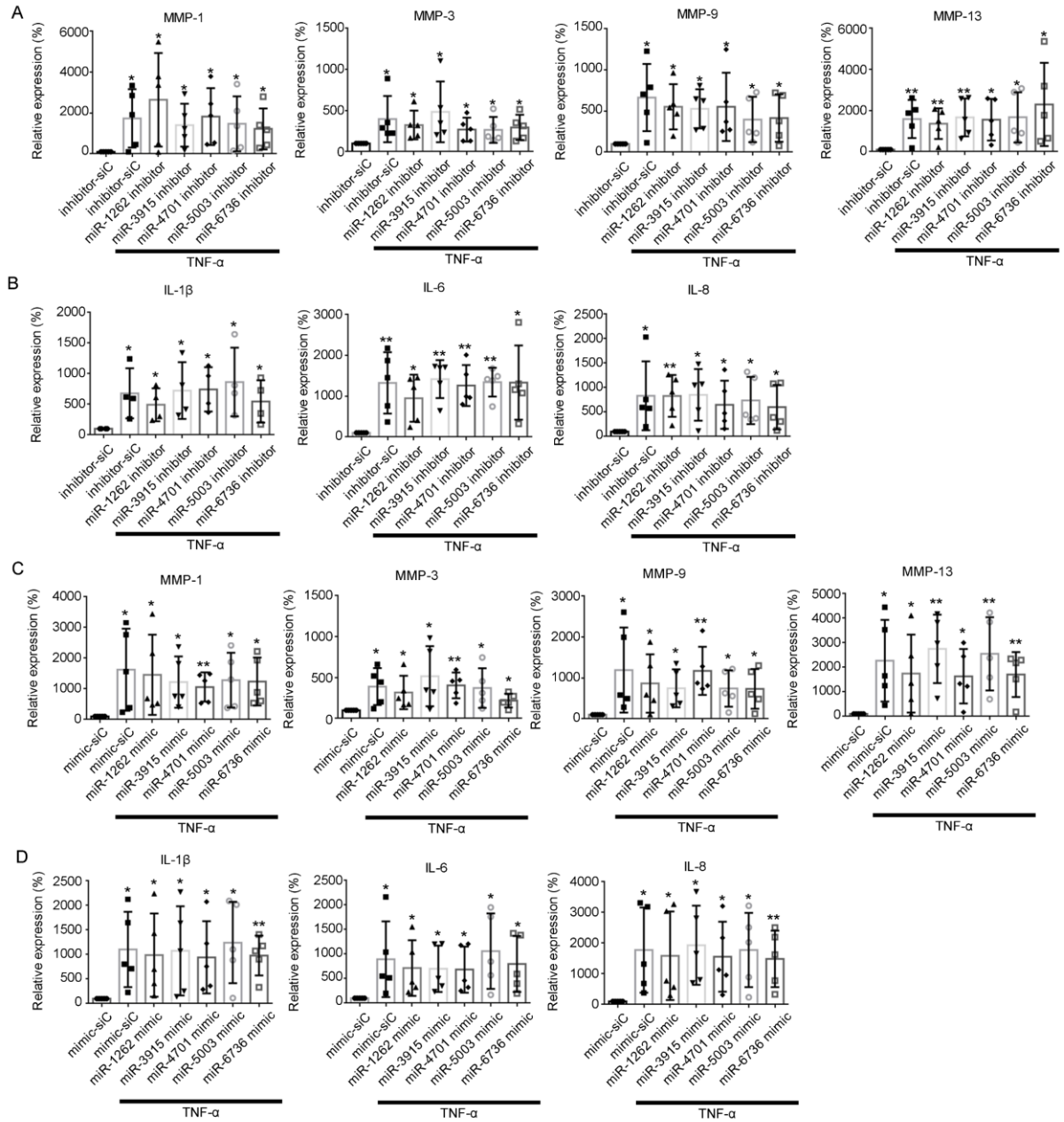
**Fig.S9**



**Fig.S10**

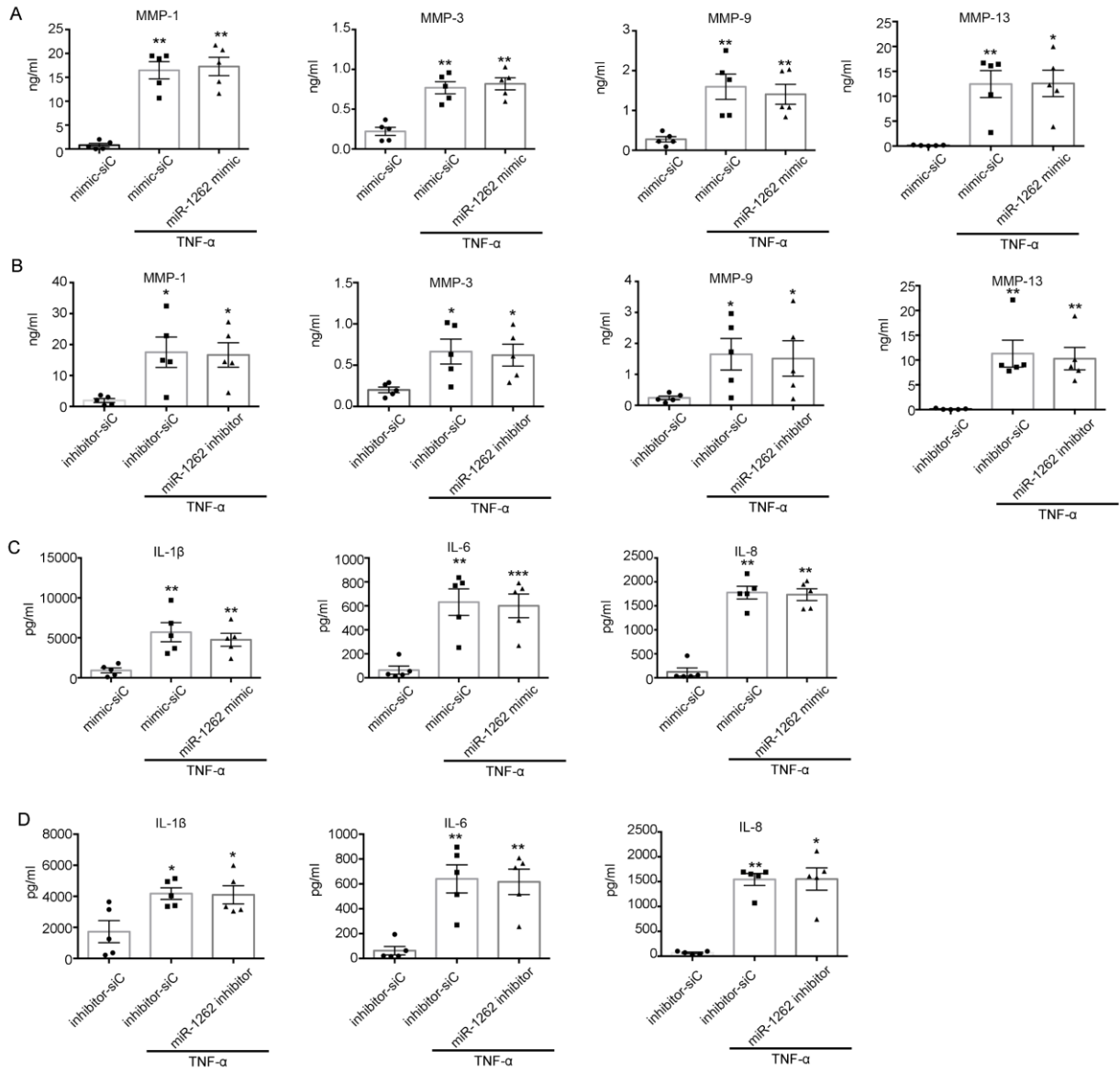


**Fig.S11**

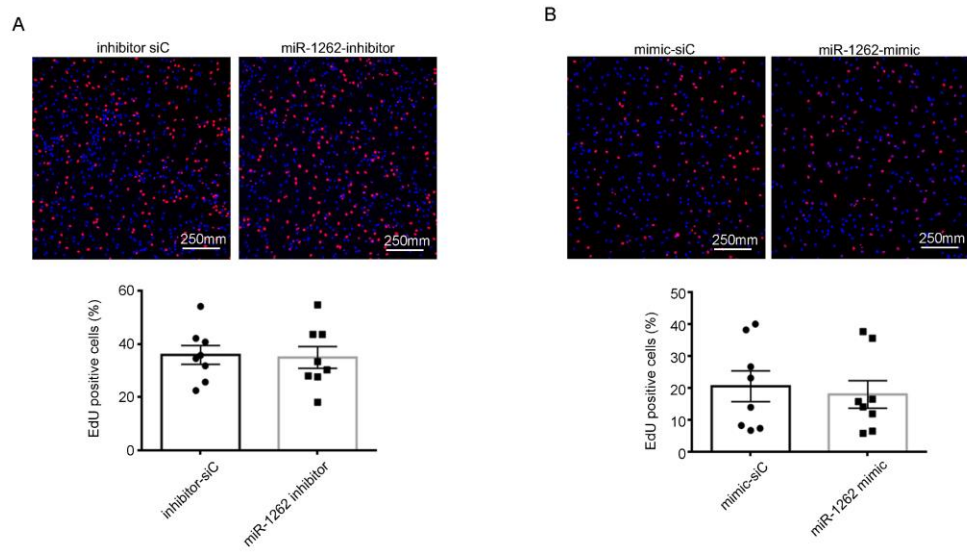




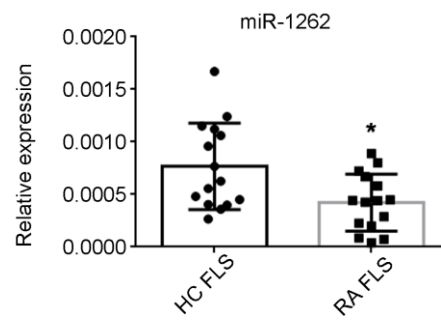
**Fig.S12**



**Fig.S13**



**Fig.S14**



## Tables

**Table S1. Demographic and clinical features of patients with active RA.**

Age, yrs (mean ± SD)	57.6±9.6
Female, <i>n</i> (%)	25 (83.3)
Male, <i>n</i> (%)	5 (16.7)
Disease duration, yrs (mean±SD)	5.7±6.8
Rheumatoid factor-positive, <i>n</i> (%)	25 (83.3)
Anti-CCP-positive, <i>n</i> (%)	16 (53.3)
DAS28 (CRP) (mean±SD)	5.2 ± 1.4
Previous medications, <i>n</i> (%)	
Prednisone (<10mg/d)	13 (43.3)
Methotrexate	7 (23.3)
Leflunomide	3(10.0)
Sulfasalazine	1 (3.3)
Hydroxychloroquine	3 (10.0)

**Table S2 Sequences of RACE primers**

LINK-A 5' RACE	GCAGAGCATCCCTGTTTCCC
LINK-A 3' RACE	GCTAAAGGCATCTTTGTCCG
UPM	CTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGT

**Table S3 Sequences of RT-PCR primers**

Name	Forward	Reverse
β-actin	TCAAGATCATTGCTCCTCCTGAG	ACATCTGCTGGAAGGTGGACA
GAPDH	GCACCGTCAAGGCTGAGAAC	TGGTGAAGACGCCAGTGGGA
LINK-A	TTCCCCATTTTTCTTTTTT	CTCTGGTTGGGTGACTGGTT
HIF-1α	ATCCATGTGACCATGAGGAAAATG	TCGGCTAGTTAGGGTACACTTC
PTK6	ACCTGGAGTCGCAGAATTACA	GCCTGGCTAACCCGAAGTC
LRRK2	CCTGTTGTGGAAGTGTGGGA	TCTCTTTCTGCTTTTGTGTACCT
MMP-1	CTCTGGAGTAATGTCACACCTCT	TGTTGGTCCACCTTTCATCTTC
MMP-3	TGTAAAGAAACCTTCTGCAA	TTTAAAACACAGTATGCCCAA
MMP-9	TGTACCGCTATGGTTACTCTCG	GGCAGGGACAGTTGCTTCT
MMP-13	TCCTGATGTGGGTGAATACAATG	GCCATCGTGAAGTCTGGTAAAAT
MMP-14	CATCTGTGACGGGAACTTTGA	GGCAGTGTGATGGACGCA
IL-1β	ATGATGGCTTATTACAGTGCCAA	GTCGGAGATTCGTAGCTGGA
IL-6	ACTCACCTCTTCAGAACGAATTG	CCATCTTTGGAAGGTTTCAGGTTG
IL-8	ACTGAGAGTGATTGAGAGTGGAC	AACCCTCTGCACCCAGTTTTTC
hsa-miR-1262	ATGGGTGAATTTGTAGAAGGAT	
hsa-miR-3915	TTGAGGAAAAGATGGTCTTATT	
hsa-miR-4701-3p	TGGGTGATGGGTGTGGTGT	
hsa-miR-5003-3p	TACTTTTCTAGTTGTTGGGG	
hsa-miR-6736-5p	GGGTGAGGGCATCTGTGGT	

**Table S4 Sequences of siRNA**

---

siRNA: <i>LINK-A</i>	1	TGTCTAAGGTGGAGATTAC
	2	AGATGTAGTTCTAGTTCAT
	3	GGTCTTCATTCTTACGCTT
siRNA : HIF-1 $\alpha$	1	GGAACATGATGGTTCACCT
	2	CTACCCACATACATAAAGA
	3	CCAGCAACTTGAGGAAGTA
siRNA : PTK6	1	CCGAGCTTGTGAACTACCA
	2	GTGCGGCACTACAAGATCT
	3	ACGAGGCGGTGTCCTTCCT
siRNA : LRRK2	1	GCATCATGGTTGAATGCTT
	2	GTACTCTCCTGGTCATCAA
	3	GCAACTGACTGAATTTGTT

---