Supplementary materials

Supplementary materials include patient and primer information, cytokine arrangement of cytokine antibody array, Tarbase and Targetscan database verification information, and gene literature summary.

Supplementary table 1:Schematic diagram of miR-15/107 gene family sequence

name	Accession number	sequence
hsa-miR-15a-5p	MIMAT0000068	U**AGCAGC**ACAUAAUGGUUUGUG
hsa-miR-16-5p	MIMAT0000069	U**AGCAGC**ACGUAAAUAUUGGCG
hsa-miR-103a-3p	MIMAT0000101	**AGCAGC**AUUGUACAGGGCUAUGA
hsa-miR-195-5p	MIMAT0000461	U**AGCAGC**ACAGAAAUAUUGGC
hsa-miR-107	MIMAT0000104	**AGCAGC**AUUGUACAGGGCUAUCA
hsa-miR-424-5p	MIMAT0001341	C**AGCAGC**AAUUCAUGUUUUGAA
hsa-miR-497-5p	MIMAT0002820	C**AGCAGC**ACACUGUGGUUUGU
hsa-miR-503-5p	MIMAT0002874	U**AGCAGC**GGGAACAGUUCUGCAG
hsa-miR-646	MIMAT0003316	A**AGCAGC**UGCCUCUGAGGC
hsa-miR-6838-5p	MIMAT0027578	A**AGCAGC**AGUGGCAAGACUCCU

Supplementary table 2: Patient characteristics

Patient	Gender	Age (years)	Disease duration (years)	RF (IU/ml)	ESR (mm/h)	CRP (mg/l)
OA1	Female	68	16	9	8	3
OA2	Female	71	18	4	9	9
OA3	Male	76	23	3	16	4
OA4	Female	72	12	7	17	8
OA5	Female	58	13	6	7	2
OA6	Male	71	13	5	12	9
OA7	Female	63	12	6	21	6
OA8	Male	72	18	7	7	10
RA1	Male	64	12	254	53	13
RA2	Female	48	10	131	51	62
RA3	Female	53	7	378	31	15
RA4	Female	51	9	63	45	45
RA5	Female	55	6	157	57	27
RA6	Male	69	11	59	53	22
RA7	Female	74	12	257	59	17
RA8	Female	62	10	212	43	18

RF, rheumatoid factor; ESR, erythrocyte sedimentation rate; CRP, C-reactive protein; CCP, cyclic citrullinated peptide

Anti-CCP antibody are all positive for RA patitents.

Supplementary table 3: MiRNA mimic and inhibitor sequence information

name	product	Sequence (from 5′ to 3′)
miRNA NC	Mimic	Sense UUCUCCGAACGUGUCACGUTT Antisense ACGUGACACGUUCGGAGAATT
miR-424-5p	Mimic	Sense CAGCAGCAAUUCAUGUUUUGAA Antisense CAAAACAUGAAUUGCUGCUGUU
miR-497-5p	Mimic	Sense CAGCAGCACACUGUGGUUUGU Antisense AAACCACAGUGUGCUGCUGUU
miRNA NC	Inhibitor	CAGUACUUUUGUGUAGUACAA
miR-424-5p	Inhibitor	UUCAAAACAUGAAUUGCUGCUG
miR-497-5p	Inhibitor	ACAAACCACAGUGUGCUGCUG

NC: negative control

Supplementary table 4: siRNA sequence information

name	product	Sequence (from 5′ to 3′)
NC siRNA	siRNA	Sense UUCUCCGAACGUGUCACGUTT Antisense ACGUGACACGUUCGGAGAATT
***DICER1* siRNA 1**	siRNA	Sense GGACCAUUUACUGACAGAATT Antisense UUCUGUCAGUAAAUGGUCCTT
***DICER1* siRNA 2**	siRNA	Sense GGCCAUUGGACACAUCAAUTT Antisense AUUGAUGUGUCCAAUGGCCTT
***DICER1* siRNA 3**	siRNA	Sense CCUCCUGGUUAUGUAGUAATT Antisense UUACUACAUAACCAGGAGGTT

Supplementary table 5: Primer information

Gene symbol	Ta *(℃)		Sequences (from 5′ to 3′)
hsa-miR-15a-5p	60	Forward	UAGCAGCACAUAAUGGUUUGUG
hsa-miR-16-5p	60	Forward	UAGCAGCACGUAAAUAUUGGCG
hsa-miR-103a-3p	60	Forward	AGCAGCAUUGUACAGGGCUAUGA
hsa-miR-195-5p	60	Forward	UAGCAGCACAGAAAUAUUGGC
hsa-miR-107	60	Forward	AGCAGCAUUGUACAGGGCUAUCA
hsa-miR-424-5p	60	Forward	CAGCAGCAAUUCAUGUUUUGAA
hsa-miR-497-5p	60	Forward	CAGCAGCACACUGUGGUUUGU
hsa-miR-503-5p	60	Forward	UAGCAGCGGGAACAGUUCUGCAG
hsa-miR-646	60	Forward	AAGCAGCUGCCUCUGAGGC
hsa-miR-6838-5p	60	Forward	AAGCAGCAGUGGCAAGACUCCU
RNU6 (U6 small nuclear RNA)	60	Forward	CTCGCTTCGGCAGCACA
		Reverse	AACGCTTCACGAATTTGCGT
IL1B	59	Forward	AGAAGTACCTGAGCTCGCCA
		Reverse	CTGGAAGGAGCACTTCATCTGT
IL6	61	Forward	CAATCTGGATTCAATGAGGAGAC
		Reverse	CTCTGGCTTGTTCCTCACTACTC
IL8	61	Forward	TGGAGAAGTTTTTGAAGAGGGCT
		Reverse	ACAGACCCACACAATACATGAAG
MMP3	59	Forward	AGTCTTCCAATCCTACTGTTGCT
		Reverse	TCCCCGTCACCTCCAATCC
MMP13	59	Forward	AATATCTGAACTGGGTCTTCCAAAA
		Reverse	CAGACCTGGTTTCCTGAGAACAG
TGFB	59	Forward	CTAATGGTGGAAACCCACAACG
		Reverse	TATCGCCAGGAATTGTTGCTG
TLR3	54	Forward	GCTAGCAGTCATCCAACAGAATC
		Reverse	AGTCAACTTCAGGTGGCTGC
TLR4	54	Forward	AATCTAGAGCACTTGGACCTTTCC
		Reverse	GGGTTCAGGGACAGGTCTAAAGA
BCL2	60	Forward	AGGCTGGGATGCCTTTGTGG
		Reverse	TTTGTTTGGGGCAGGCATGT
TRIM23	60	Forward	AACAAACAGGATGTTGCTGGAG
		Reverse	GAGCCAGTCCAACCCTTCAT
SUMO3	60	Forward	GAGAGGCAGGGCTTGTCAAT
		Reverse	CGGGCCCTCTAGAAACTGTG

CEP55	60	Forward	ACTTTTGGAGAAAATTCGAGTCCT
		Reverse	GTTGGTCTCTCAGTCGCTGT
E2F1	60	Forward	GCCATCCAGGAAAAGGTGTGA
		Reverse	GTGATGTCATAGATGCGCCG
CCNA2	60	Forward	CCAGGAGAATATCAACCCGGA
		Reverse	GGTGCAACCCGTCTCGT
KCNN4	60	Forward	CCGAGAGGCAGGCTGTTAAT
		Reverse	CAGACGATCTTGCCCCACAT
GAPDH	60	Forward	CACCCACTCCTCCACCTTTG
		Reverse	CCACCACCCTGTTGCTGTAG

*：Annealing Temperature

Supplementary table 6:
Cytokine arrangement of RayBio® C-Series human cytokine antibody array C5.

	A	B	C	D	E	F	G	H	I	J	K
1	POS	POS	POS	POS	NEG	NEG	ENA-78	G-CSF	GM-CSF	GRO	GRO-α
2	I-309	IL-1α	IL-1β	IL-2	IL-3	IL-4	IL-5	IL-6	IL-7	IL-8	IL-10
3	IL12-p40	IL-13	IL-15	IFN-γ	MCP-1	MCP-2	MCP-3	M-CSF	MDC	MIG	MIP-1β
4	MIP-1-	RANTES	SCF	SDF-1	TARC	TGF-β1	TNF-α	TNF-β	EGF	IGF-1	Angiogenin
5	OSM	TPO	VEGF	PDGF-BB	Leptin	BDNF	BLC	CK β8-1	Eotaxin	Eotaxin-2	Eotaxin-3
6	FGF-4	FGF-6	FGF-7	FGF-9	FLT-3 Ligand	Fractalkine	GCP-2	GDNF	HGF	IGFBP-1	IGFBP-2
7	IGFBP-3	IGFBP-4	IL-16	IP-10	LIF	LIGHT	MCP-4	MIF	MIP-3α	NAP-2	NT-3
8	NT-4	OPN	OPG	PARC	PIGF	TGF- b 2	TGF- b 3	TIMP-1	TIMP-2	POS	POS

Supplementary table 7:
Dysregulated genes in RASF after gain of miR-424 function detected by using mRNA deep sequencing

Gene Symbol	Regulation after transfected with mimic	padj	Function in literature	Outcome after transfected with mimic
ZNF367	Down	6.56E-08	ZNF367 knockdown increased proliferation in vitro and vivo, also increased cellular invasion and migration. [1]	Promote the proliferation
BTRC	Down	3.80E-08	BTRC is negative factors controlling IκB degradation in the type 1 TNF receptor (TNF-RI) and IL-1R pathways uponTNF-α and IL-1β stimulation. [2]	inhibit the degradation of IkB
CCNA2	Down	0.00832	CCNE2 or CCNA2 silencing markedly decreased abl cell and CWR22Rv1 cell growth. [3]	inhibit proliferation
CD83	Down	0.00162	In mixed leukocyte reaction (MLR), sCD83 inhibits DC-mediated T cell activation and proliferation.[4]	Promote the proliferation
CDC6	Down	0.01602	Down-regulation of CDC6 in HO8910 cells decreased cell proliferation and colony formation.[5]	inhibit proliferation
CEP55	Down	0.00328	knockdown of CEP55 markedly inhibited cell viability and proliferation and CEP55-silenced cells were obviously arrested in the G0/G1 phase and presented significant cell apoptosis .[6]	inhibit proliferation and promote apoptosis
			CEP55 knockdown significantly induced cell cycle arrest at G1 phase and suppressed OS cell proliferation, migration and invasion. [7]	inhibit proliferation
E2F1	Down	0.01955	E2F1 silencing effectively downregulated expression of canonical E2F target genes and suppressed RANKL-induced osteoclast genesis. [8]	Suppress osteoclast genesis
E2F2	Down	3.65E-05	In embryonic fibroblasts (MEF) of E2F2 knockout mice, the expression of IL-1α, IL-1β and TNF-α was suppressed. [9]	Upregulate the expression of IL-1α, IL-1β, and TNF-α
			Silencing E2F2 suppresses the proliferation, migration, and invasion of RASFs in vitro.[10]	inhibit proliferation
KCNN4 (KCa3.1)	Down	0.00240	Different concentrations of the KCa3.1 inhibitor significantly reduced the proliferation of RASFs. [11]	inhibit proliferation
STMN1	Down	0.00111	Inhibition of STMN1 showed a decrease in cell proliferation.[9]	inhibit proliferation

Supplementary table 8:
Dysregulated genes in RASF after gain of miR-497 function detected by using mRNA deep sequencing

Gene Symbol	Regulation after transfected with mimic	padj*	Function in literature	Outcome after transfected with mimic
BCL2	Down	1.10E-06	SF Treg cells transcribing high levels of Bcl-2 and microRNA-21 demonstrate limited apoptosis in RA[12].	Promote apoptosis
TRIM23	Down	8.16E-11	Overexpression of TRIM23 can activate the NF-κB pathway[13]	Inhibit NF-κB pathway
SUMO3	Down	1.28E-07	The knockdown of SUMO-2/3 significantly increased the TNF-α and IL-1β, induced expression of MMP-3 and MMP-13, accompanied by increased NF-κB activity[14].	Promote NF-kB pathway

* : p-value adjusted

Supplementary table 9: Validated miR-424 target genes from Tarbase.

Gene name	miRNA name	Experiments throughput	Cell lines	Tissues
PDCD4	hsa-miR-424-5p	low: 0 high: 6	BETA Cells, 293S, HEK293, HELA	Pancreas, Cervix, Kidney
BCL2	hsa-miR-424-5p	low: 0 high: 3	EF3DAGO2, HEK293, HELA	Cervix, Kidney
CCNE1	hsa-miR-424-5p	low: 3 high: 5	THP1, HEPG2, HELA, 293S, HEK293	Peripheral Blood, Liver, Cervix, Kidney
CCNE2	hsa-miR-424-5p	low: 1 high: 0	THP1	Peripheral Blood
CCND1	hsa-miR-424-5p	low: 2 high: 11	THP1, HEPG2, MDAMB231, HEK293,293S, HS5, HS27A	Mammary Gland, Peripheral Blood, Liver, Kidney, Bone Marrow
CCND3	hsa-miR-424-5p	low: 1 high: 0	HEPG2	Liver

Supplementary table 10: Validated miR-497 target genes from Tarbase.

Gene name	miRNA name	Experiments throughput	Cell lines	Tissues
PDCD4	hsa-miR-497-5p	low: 0 high: 8	BETA Cells, 293S, HELA	Pancreas, Cervix, Kidney, Brain
BCL2	hsa-miR-497-5p	low: 0 high: 2	EF3DAGO2, HELA	Cervix
CCNE1	hsa-miR-497-5p	low: 5 high: 3	HELA, 293S, MDAMB231, SKHEP1, HEPG2, HEK293T	Mammary Gland, Liver, Cervix, Kidney
CCND1	hsa-miR-497-5p	low: 5 high: 7	HEK293A, SGC7901, SKHEP1, HEPG2,293S, HS5, HS27A, HMSC	Gastric, Liver, Kidney, Bone Marrow
CCND3	hsa-miR-497-5p	low: 3 high: 0	SKHEP1, HEPG2	Liver

Supplementary table 11: Validated DICER1 and miRNA target relationship from Tarbase

Gene name	miRNA name	Experiments throughput	Cell lines	Tissues
DICER1	hsa-miR-424-5p	low: 1 high: 2	THP1, MDAMB231,293S	Peripheral Blood, Mammary Gland, Kidney
DICER1	hsa-miR-497-5p	low: 0 high: 3	293S	Kidney

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