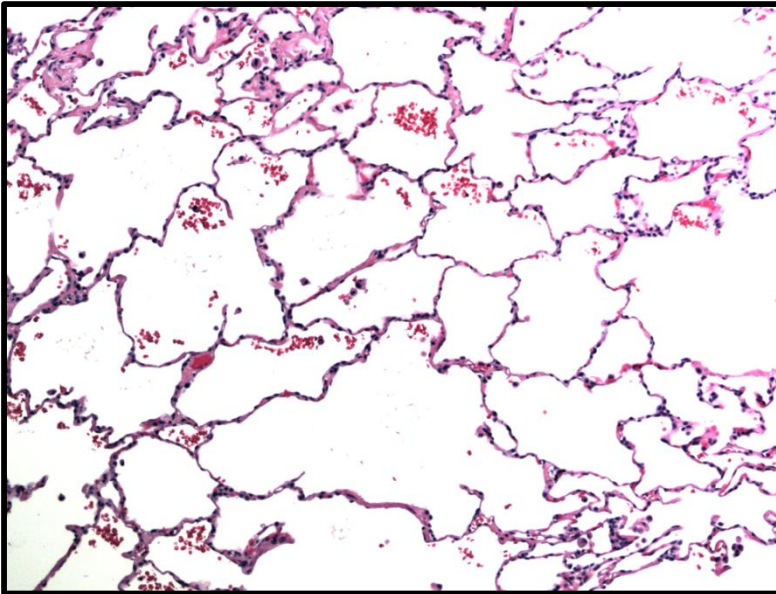
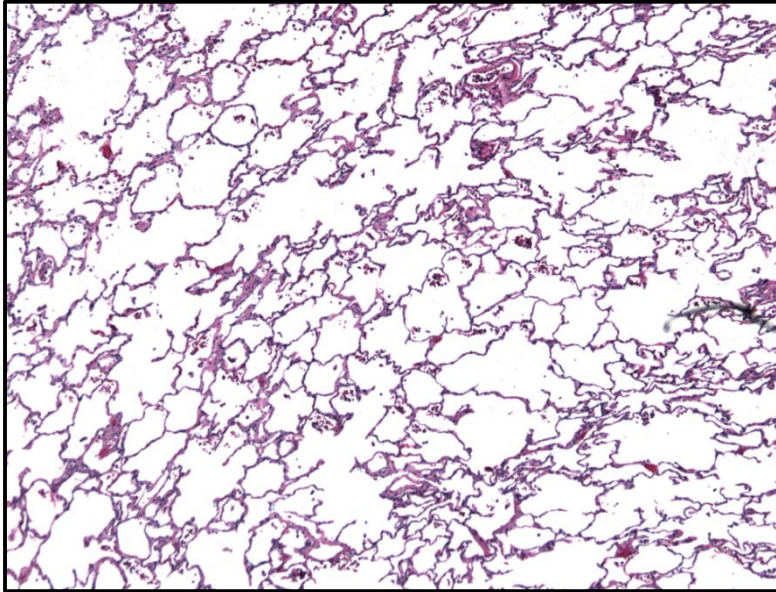
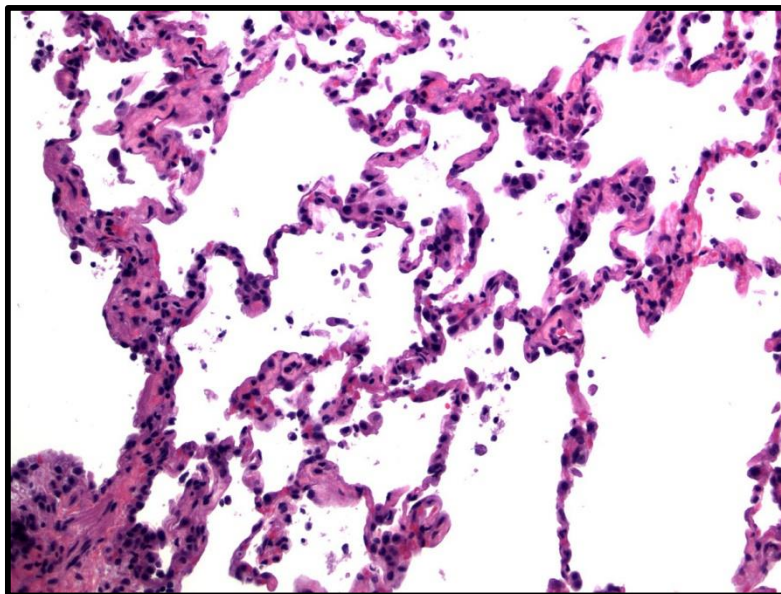
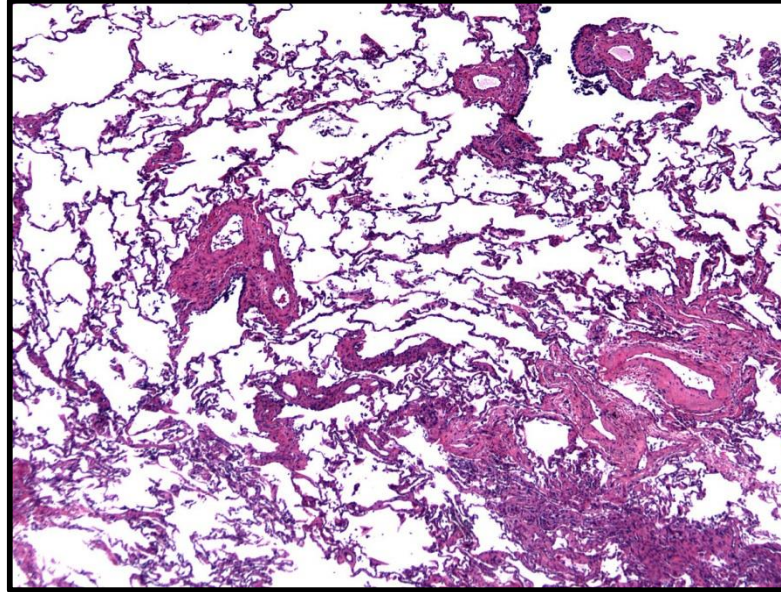


A

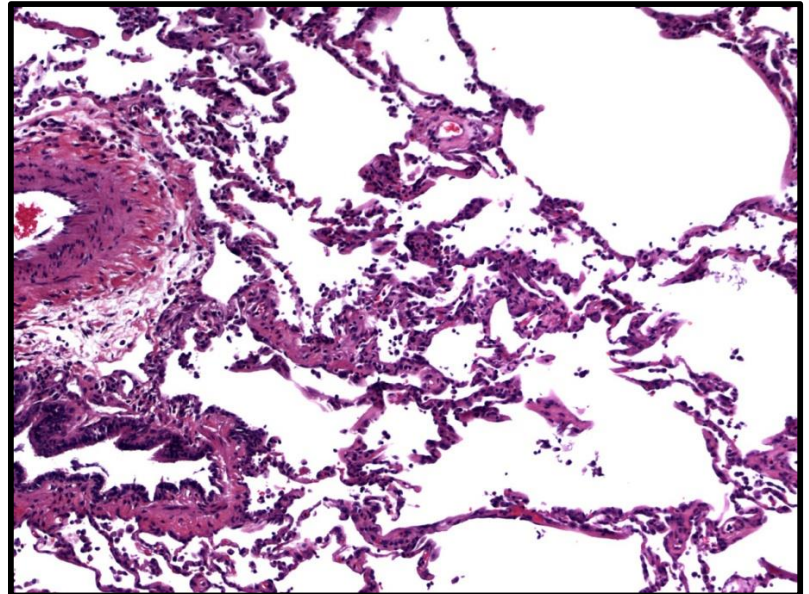
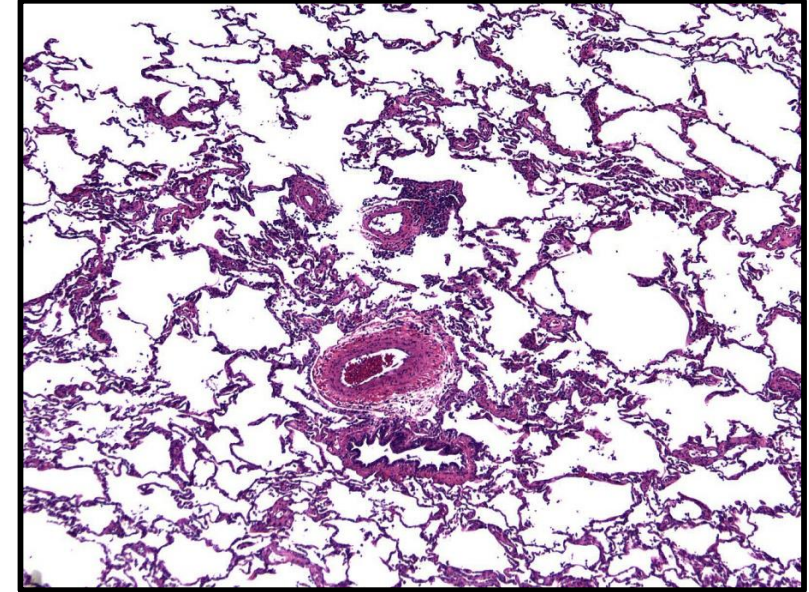
Control group



Ischemia group



Reperfusion group



B

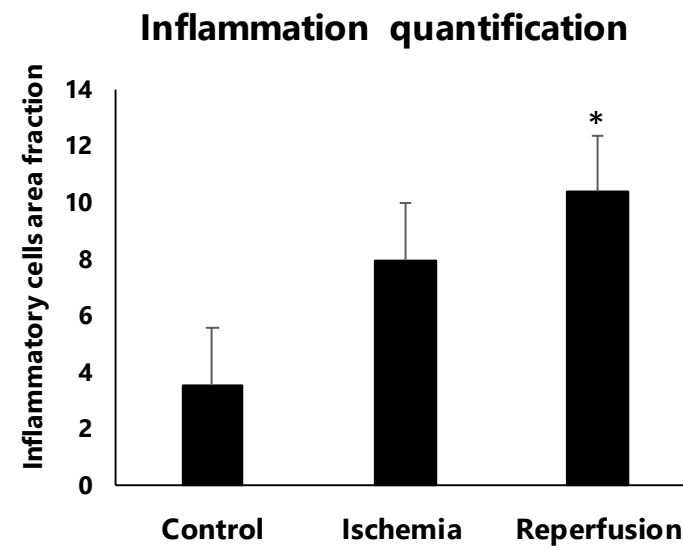
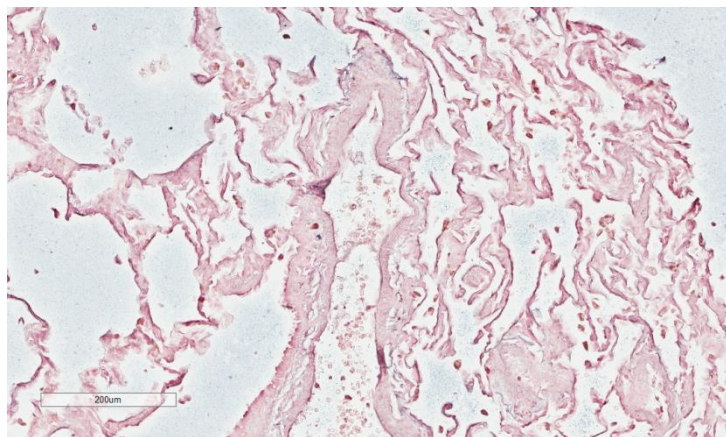
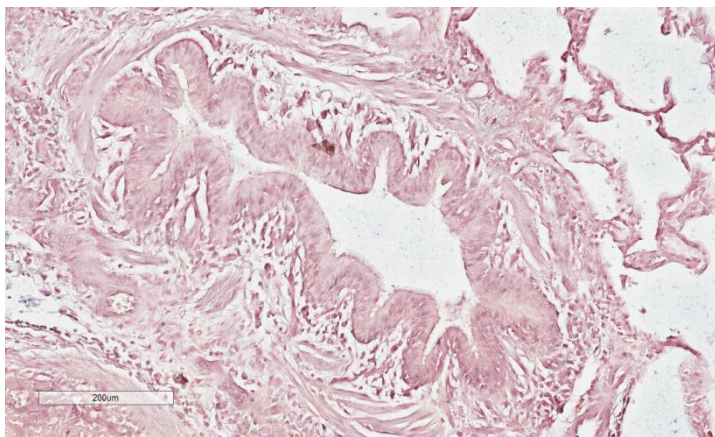


Figure S1

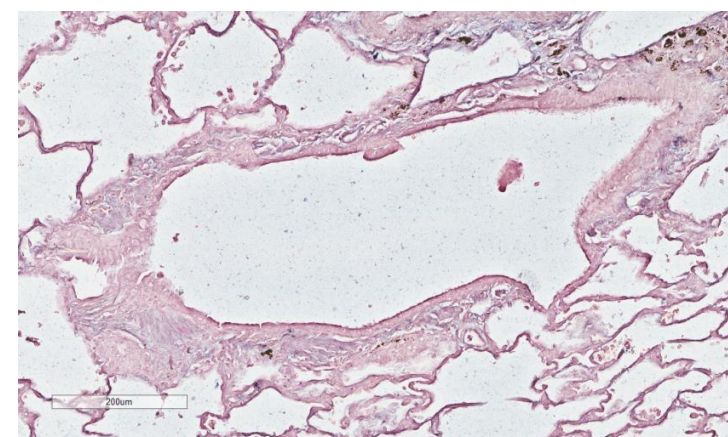
A No Probe



Control group



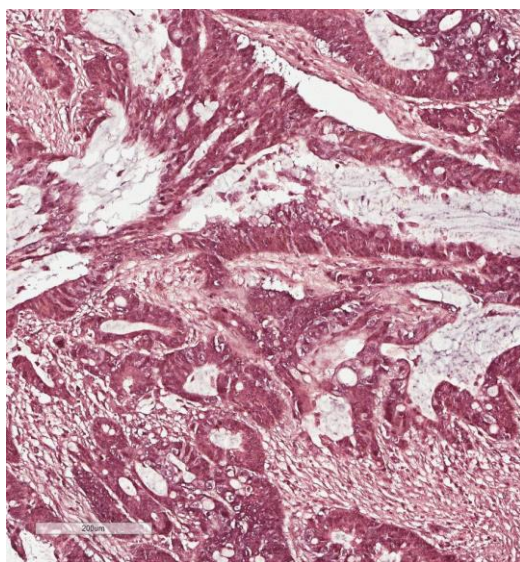
Ischemia group



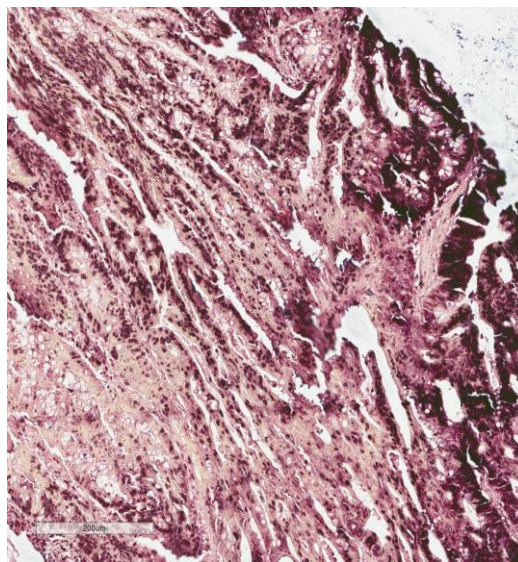
Reperfusion group

Figure S2

B Positive Control

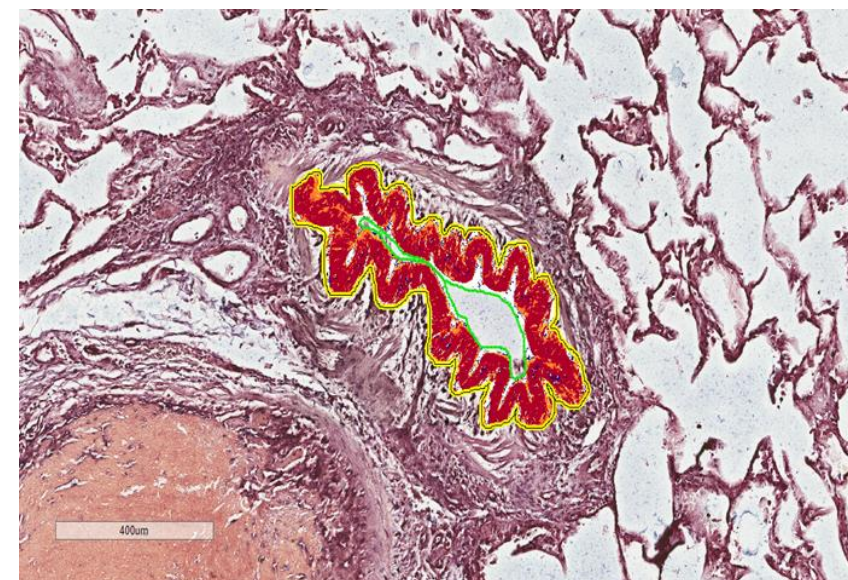


miR-17



miR-548

C Positivity quantification



Figures

Figure S1. A. Hematoxylin and eosin staining of normal lung tissue, after ischemia, and after reperfusion (IRI) showing minimal architecture changes (upper panels, 40x) with increased patchy infiltration of inflammatory cells after ischemia and reperfusion (lower panels, 100x). **B.** Inflammation quantification showing increased infiltration of inflammatory cells in the Ischemia and Reperfusion groups compared to the Control group ($p=0.08$ and 0.01 , respectively).

Figure S2. (A) In-situ hybridization assay of miR-17 & miR-548 in human lung tissues with no miR probe (B) Positive control: In-situ hybridization assay of miR-17 & miR-548 in colorectal adenocarcinoma cells (10 x). (C) Quantification of miR expression positivity in the lung tissue

Tables

Table S1. Donor characteristics of Ex Vivo Lung Perfusion (EVLP)

EVLP #	Age	Sex	Smoking history (>20 p/y)	BD or DCD	Cause of death	P/F ratio
#1	18	Male	None	BD	Head trauma	263
#2	66	Female	None	BD	Anoxia	316
#3	58	Female	None	BD	Anoxia	272
#4	35	Male	None	BD	Anoxia	87
#5	67	Female	None	BD	Drug abuse overdose	198
#6	39	Female	None	DCD	Anoxia	97
#7	54	Female	None	BD	Cerebrovascular accident	250
#8	47	Female	None	BD	Head trauma	228
#9	73	Male	None	BD	Cerebrovascular accident	267
#10	75	Male	None	BD	Cerebrovascular accident	298
#11	48	Male	None	BD	Cerebrovascular accident	128
#12	28	Female	None	BD	Anoxia	260
#13	44	Male	None	DCD	Anoxia	347
#14	33	Male	None	BD	Anoxia	150
#15	57	Male	None	BD	Anoxia	168
#16	40	Female	None	BD	Anoxia	122
#17	58	Male	None	BD	Head trauma	296
#18	34	Female	None	BD	Head trauma	248
#19	51	Male	None	DCD	Head trauma	132
#20	53	Male	None	BD	Head trauma	162
#21	34	Male	None	DCD	Anoxia	301
#22	43	Female	None	DCD	Drug abuse overdose	281
#23	59	Male	None	BD	Anoxia	248
#24	66	Male	None	BD	Cerebrovascular accident	325

20 p/y: 20 pack years, BD: brain dead, DCD: donation after circulatory death, P/F: PaO₂/FiO₂ ventilator settings

Table S2. Control donor characteristics

Donor #	Age	Sex	Smoking history (< 50 p/y)	BD or DCD	Cause of death	P/F ratio
#1	18	M	Yes	DCD	Head trauma (gunshot)	217
#2	64	F	Yes	DCD	Head trauma	293
#3	28	F	Yes	DCD	Cerebrovascular accident	316
#4	55	M	Yes	DCD	Anoxia	303
#5	30	M	Yes	BD	Head trauma (gunshot)	359
#6	54	F	Yes	BD	Cerebrovascular accident	406

50 p/y: 50 pack years, BD: brain dead, DCD: donation after cardiac death, P/F: PaO₂/FiO₂ ventilator settings

Table S3. Downstream analysis for miR-17 and miR-548b showing expected target genes related to lung injury

Downstream Targets	miR-17-3p		miR-548b-3p	
	Target gene	Gene name	Target gene	Gene name
Interleukin	IL1R1 IL16 IL17RA IL17RD IL17REL IL18BP IL20 IL20RB IL21R IL22RA1 IL36RN IL4R IL5 IL5RA IL6R IL7R ILF3	interleukin 1 receptor, type I interleukin 16 interleukin 17 receptor A interleukin 17 receptor D interleukin 17 receptor E-like interleukin 18 binding protein interleukin 20 interleukin 20 receptor beta interleukin 21 receptor interleukin 22 receptor, alpha 1 interleukin 36 receptor antagonist interleukin 4 receptor interleukin 5 (colony-stimulating factor, eosinophil) interleukin 5 receptor, alpha interleukin 6 receptor interleukin 7 receptor interleukin enhancer binding factor 3, 90kDa	IL17A IL18R1	interleukin 17A interleukin 18 receptor 1
Mutual targets	IRAK4 IL6ST IL1RAPL1 IL1RN IRAK1BP1	interleukin-1 receptor-associated kinase 4 interleukin 6 signal transducer interleukin 1 receptor accessory protein-like 1 interleukin 1 receptor antagonist interleukin-1 receptor-associated kinase 1 binding protein 1	IRAK4 IL6ST IL1RAPL1 IL1RN IRAK1BP1	interleukin-1 receptor-associated kinase 4 interleukin 6 signal transducer interleukin 1 receptor accessory protein-like 1 interleukin 1 receptor antagonist interleukin-1 receptor-associated kinase 1 binding protein 1
Cytokine	CRLF3 CIAPIN1 CLNK DOCK5 SOCS3	cytokine receptor-like factor 3 cytokine induced apoptosis inhibitor 1 cytokine-dependent hematopoietic cell linker dedicator of cytokinesis 5 suppressor of cytokine signaling 3	DOCK7 SOCS6	dedicator of cytokinesis 7 suppressor of cytokine signaling 6
Mutual targets	CISH SOCS2 SOCS7	cytokine inducible SH2-containing protein suppressor of cytokine signaling 2 suppressor of cytokine signaling 7	CISH SOCS2 SOCS7	cytokine inducible SH2-containing protein suppressor of cytokine signaling 2 suppressor of cytokine signaling 7

TNF	C1QTNF1 C1QTNF6 LITAF RIPK1 TNFAIP2 TNFAIP8L3 TNFRSF12A TNFRSF13C TNFRSF19 TNFRSF1B TNFSF15 TNFSF8 TRADD TRAF1 TRAF6	C1q and tumor necrosis factor related protein 1 C1q and tumor necrosis factor related protein 6 lipopolysaccharide-induced TNF factor receptor (TNFRSF)-interacting serine-threonine kinase 1 tumor necrosis factor, alpha-induced protein 2 tumor necrosis factor, alpha-induced protein 8-like 3 tumor necrosis factor receptor superfamily, member 12A tumor necrosis factor receptor superfamily, member 13C tumor necrosis factor receptor superfamily, member 19 tumor necrosis factor receptor superfamily, member 1B tumor necrosis factor (ligand) superfamily, member 15 tumor necrosis factor (ligand) superfamily, member 8 TNFRSF1A-associated via death domain TNF receptor-associated factor 1 TNF receptor-associated factor 6, E3 ubiquitin protein ligase	FBF1 NGFRAP1 TNFSF4 TNFRSF10 A	Fas (TNFRSF6) binding factor 1 nerve growth factor receptor (TNFRSF16) associated protein 1 tumor necrosis factor (ligand) superfamily, member 4 tumor necrosis factor receptor superfamily, member 10a
Mutual targets	C1QTNF8 TRAF3 TNFSF14 TNFSF18 TNFRSF11A TNFRSF9 TNFAIP8	C1q and tumor necrosis factor related protein 8 TNF receptor-associated factor 3 tumor necrosis factor (ligand) superfamily, member 14 tumor necrosis factor (ligand) superfamily, member 18 tumor necrosis factor receptor superfamily, member 11a, NFKB activator tumor necrosis factor, alpha-induced protein 1 (endothelial) tumor necrosis factor, alpha-induced protein 8	C1QTNF8 TRAF3 TNFSF14 TNFSF18 TNFRSF11A TNFRSF9 TNFAIP8	C1q and tumor necrosis factor related protein 8 TNF receptor-associated factor 3 tumor necrosis factor (ligand) superfamily, member 14 tumor necrosis factor (ligand) superfamily, member 18 tumor necrosis factor receptor superfamily, member 11a, NFKB activator tumor necrosis factor, alpha-induced protein 1 (endothelial) tumor necrosis factor, alpha-induced protein 8
Immune	AIRE IRGQ IGBP1 IGLL1 IGDCC3 IGSF10 ILDR2 KIR3DL1 KIR3DL2 KIR2DL4 LRIT2 LRIG2 LILRA1 OSCAR RBPJL SEMA3E SEMA4B SEMA4F TIGIT VSIG10L	autoimmune regulator immunity-related GTPase family, Q immunoglobulin (CD79A) binding protein 1 immunoglobulin lambda-like polypeptide 1 immunoglobulin superfamily, DCC subclass, member 3 immunoglobulin superfamily, member 10 immunoglobulin-like domain containing receptor 2 killer cell immunoglobulin-like receptor, 3 domains, long cytoplasmic tail, 1 killer cell immunoglobulin-like receptor, 3 domains, long cytoplasmic tail, 2 killer cell immunoglobulin-like receptor, 2 domains, long cytoplasmic tail, 4 leucine-rich repeat, immunoglobulin-like and transmembrane domains 2 leucine-rich repeats and immunoglobulin-like domains 2 leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 osteoclast associated, immunoglobulin-like receptor recombination signal binding protein for immunoglobulin kappa J region-like sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F T cell immunoreceptor with Ig and ITIM domains V-set and immunoglobulin domain containing 10 like	BIVM HIVEP2 HIVEP3 ISLR2 IGSF11 LRIT3 SEMA3A SEMA3D SEMA3G WFIKKN2	basic, immunoglobulin-like variable motif containing human immunodeficiency virus type I enhancer binding protein 2 human immunodeficiency virus type I enhancer binding protein 3 immunoglobulin superfamily containing leucine-rich repeat 2 immunoglobulin superfamily, member 11 leucine-rich repeat, immunoglobulin-like and transmembrane domains 3 sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2
Mutual targets	IGSF3 TIMD4	immunoglobulin superfamily, member 3 T-cell immunoglobulin and mucin domain containing 4	IGSF3 TIMD4	immunoglobulin superfamily, member 3 T-cell immunoglobulin and mucin domain containing 4

Apoptosis	AREL1 AIFM1 AIFM2 BCL2L11 BCL2L13 CASP3 CASP5 CASP6 CASP8 CIAPIN1 NAIF1 PERP SYVN1	apoptosis resistant E3 ubiquitin protein ligase 1 apoptosis-inducing factor, mitochondrion-associated, 1 apoptosis-inducing factor, mitochondrion-associated, 2 BCL2-like 11 (apoptosis facilitator) BCL2-like 13 (apoptosis facilitator) caspase 3, apoptosis-related cysteine peptidase caspase 5, apoptosis-related cysteine peptidase caspase 6, apoptosis-related cysteine peptidase caspase 8, apoptosis-related cysteine peptidase cytokine induced apoptosis inhibitor 1 nuclear apoptosis inducing factor 1 PERP, TP53 apoptosis effector synovial apoptosis inhibitor 1, synoviolin	XIAP	X-linked inhibitor of apoptosis
Mutual targets	AEN CASP10 CASP2 CASP9 PAWR	apoptosis enhancing nuclease caspase 10, apoptosis-related cysteine peptidase caspase 2, apoptosis-related cysteine peptidase caspase 9, apoptosis-related cysteine peptidase PRKC, apoptosis, WT1, regulator	AEN CASP10 CASP2 CASP9 PAWR	apoptosis enhancing nuclease caspase 10, apoptosis-related cysteine peptidase caspase 2, apoptosis-related cysteine peptidase caspase 9, apoptosis-related cysteine peptidase PRKC, apoptosis, WT1, regulator
Chemokines	ACKR2 CCL14 CCR6 CCR7 CMKLR1 CXCL1 CXCL17 CXCL2 CXCL9 FAM19A1 XCR1	atypical chemokine receptor 2 chemokine (C-C motif) ligand 14 chemokine (C-C motif) receptor 6 chemokine (C-C motif) receptor 7 chemokine-like receptor 1 chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) chemokine (C-X-C motif) ligand 17 chemokine (C-X-C motif) ligand 2 chemokine (C-X-C motif) ligand 9 family with sequence similarity 19 (chemokine (C-C motif)-like), member A1 chemokine (C motif) receptor 1	CCR2 CCR8 CCR9 CX3CR1 CXCL10 CXCL11 CXCR4 PPBP XCL1	chemokine (C-C motif) receptor 2 chemokine (C-C motif) receptor 8 chemokine (C-C motif) receptor 9 chemokine (C-X3-C motif) receptor 1 chemokine (C-X-C motif) ligand 10 chemokine (C-X-C motif) ligand 11 chemokine (C-X-C motif) receptor 4 pro-platelet basic protein (chemokine (C-X-C motif) ligand 7) chemokine (C motif) ligand 1
Mutual Targets	CXCR2	chemokine (C-X-C motif) receptor 2	CXCR2	chemokine (C-X-C motif) receptor 2
TOLL	TOLLIP TIRAP	toll interacting protein toll-interleukin 1 receptor (TIR) domain containing adaptor protein		
Mutual Targets	TLR4 TLR5 TLL2	toll-like receptor 4 toll-like receptor 5 tolloid-like 2	TLR4 TLR5 TLL2	toll-like receptor 4 toll-like receptor 5 tolloid-like 2
HIF	EGLN1 HIGD1A HIGD2B HIF1A HIF3A HYOU1	egl-9 family hypoxia-inducible factor 1 HIG1 hypoxia inducible domain family, member 1A HIG1 hypoxia inducible domain family, member 2B hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) hypoxia inducible factor 3, alpha subunit hypoxia upregulated 1		
Mutual Targets	EGLN3	egl-9 family hypoxia-inducible factor 3	EGLN3	egl-9 family hypoxia-inducible factor 3

Table S4. Predicted miR-17-3p interaction with target genes related to lung injury

Mediators	mRNA / miRNA	Predicted consequential pairing of target region (top) and miRNA (bottom)
<i>CXCL2</i>	Position 86-92 of <u>CXCL2</u> 3' UTR hsa-miR-17-3p	5' ...GAAAGAGAGACACAG CUGCAGAG ... 3' GAUGUUCACGGAAGU GACGUCA
<i>L-1β</i>	Position 1486-1493 of <u>IL1R1</u> 3' UTR hsa-miR-17-3p	5' ...UCUCUGGUCAGGCC ACUGCAGA ... 3' GAUGUUCACGGAAG UGACGUCA
	Position 2679-2685 of <u>IRAK4</u> 3' UTR hsa-miR-17-3p	5' ...CCGUGCUAGUAUGGCC CUGCAGAA ... 3' GAUGUUCACGGAAGU - - - - GACGUCA
	Position 1641-1647 of <u>IL1RAPL1</u> 3' UTR hsa-miR-17-3p	5' ... CAAUCACAAAGGAAU CUGCAGAG ... 3' GAUGUUCACGGAAGU GACGUCA
	Position 42-48 of <u>IL1RN</u> 3' UTR hsa-miR-17-3p	5' ...UCUUGCAUGGCAAG ACUGCAGG ... 3' GAUGUUCACGGAAG UGACGUCA 3
	Position 976-982 of <u>IL1RN</u> 3' UTR hsa-miR-17-3p	5' ...ACCGGGCUGGGAGCU CUGCAGAG ... 3' GAUGUUCACGGAAGU GACGUCA
	Position 3882-3888 of <u>IRAK1BP1</u> 3' UTR hsa-miR-17-3p	5' ...GCUCAAUCAUAGCUU ACUGCAGC ... 3' GAUGUUCACGGAAG UGACGUCA
<i>IL-6</i>	Position 1143-1149 of <u>IL6R</u> 3' UTR hsa-miR-17-3p	5' ...GAUCAAACGGUUUU ACUGCAGC ... 3' GAUGUUCACGGAAG UGACGUCA
	Position 1380-1386 of <u>IL6ST</u> 3' UTR hsa-miR-17-3p	5' ...AGUACUCAAACAGA ACUGCAGU ... 3' GAUGUUCACGGAAG UGACGUCA
<i>IL-17</i>	Position 643-649 of <u>IL17RA</u> 3' UTR hsa-miR-17-3p	5' ...AGAUUGUGCCAUUGC ACUGCAGC ... 3' GAUGUUCACGGAAG - - UGACGUCA
	Position 3448-3454 of <u>IL17RA</u> 3' UTR hsa-miR-17-3p	5' ...GUGCAAUCAUGGCUC ACUGCAGC ... 3' GAUGUUCACGGAAG UGACGUCA
	Position 2217-2223 of <u>IL17RD</u> 3' UTR hsa-miR-17-3p	5' ...AUGGGAAUCGUUGCC CUGCAGAU ... 3' GAUGUUCACGGAAGU GACGUCA
	Position 1147-1153 of <u>IL17REL</u> 3' UTR	5' ...GUCUGCUGAGCCUCC- CUGCAGAU ...

	hsa-miR-17-3p Position 2207-2213 of <u>IL17REL</u> 3' UTR hsa-miR-17-3p Position 2330-2336 of <u>IL17REL</u> 3' UTR hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA 5' ...GUGGUCGCACCCCAUCUGCAGAU... 3' GAUGUUCACGGAAGUGACGUCA 5' ...AGACUGGAGAGGGGGCUGCAGAG... 3' GAUGUUCACGGAAGUGACGUCA
<i>TNF-α</i>	Position 135-141 of <u>C1QTNF8</u> 3' UTR hsa-miR-17-3p	5' ...AGGCCCGGCCAGAGUCUGCAGAA... 3' GAUGUUCACGGAAGUGACGUCA
	Position 2136-2142 of <u>TRAF3</u> 3' UTR hsa-miR-17-3p	5' ...UAAAGGAAGGACUUCUGCAGAA... 3' GAUGUUCACGGAAGUGACGUCA
	Position 3201-3207 of <u>TRAF3</u> 3' UTR hsa-miR-17-3p	5' ...CUUGUCCCGCGGAGCCUGCAGAG... 3' GAUGUUCACGGAAGUGACGUCA
	Position 4506-4513 of <u>TRAF3</u> 3' UTR hsa-miR-17-3p	5' ...AUCUUUACUUAUUAGACUGCAGA... 3' GAUGUUCACGGAAGUGACGUCA
	Position 5225-5231 of <u>TRAF3</u> 3' UTR hsa-miR-17-3p	5' ...GACGCUGCACAGCAUCUGCAGAU... 3' GAUGUUCACGGAAGUGACGUCA
	Position 517-524 of <u>TNFSF14</u> 3' UTR hsa-miR-17-3p	5' ...AGAAGACCCACGUAGACUGCAGA... 3' GAUGUUCACGGAAGUGACGUCA
	Position 200-206 of <u>TNFSF18</u> 3' UTR hsa-miR-17-3p	5' ...GACUUUUGGUUGGAUCUGCAGAG... 3' GAUGUUCACGGAAGUGACGUCA
	Position 1785-1791 of <u>TNFRSF11A</u> 3' UTR hsa-miR-17-3p	5' ...UAGCCAACAUAAAGAACUGCAGG... 3' GAUGUUCACGGAAGUGACGUCA
	Position 3512-3518 of <u>TNFRSF11A</u> 3' UTR hsa-miR-17-3p	5' ...GCGUGGAGUAAAAUGCUGCAGAG... 3' GAUGUUCACGGAAGUGACGUCA
	Position 1879-1885 of <u>TNFRSF9</u> 3' UTR hsa-miR-17-3p	5' ...UCUGAACAAUAGUCUACUGCAGU... 3' GAUGUUCACGGAAGUGACGUCA
	Position 3578-3584 of <u>TNFAIP8</u> 3' UTR	5' ...AGAUUGUACCACUGCACUGCAGC...

	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 776-782 of <u>C1QTNF1</u> 3' UTR	5' ...CUGGGUCCCCAGGCC UGCAGAU ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 978-984 of <u>C1QTNF1</u> 3' UTR	5' ...AACACCUCAAGCAGC ACUGCAGU ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 878-884 of <u>C1QTNF6</u> 3' UTR	5' ...GCUCAGGCCUGCACC- ACUGCAGC ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 88-95 of <u>LITAF</u> 3' UTR	5' ...ACCAUUACUGUCCCA ACUGCAGA ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 655-662 of <u>LITAF</u> 3' UTR	5' ...CUUUGAGAUUCUGUA ACUGCAGA ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 113-119 of <u>RIPK1</u> 3' UTR	5' ...AUAGGGGUUCUGUGU UGCAGAA ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 1343-1349 of <u>RIPK1</u> 3' UTR	5' ...ACCCUGAAAUGGGG UGCAGAG ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 1243-1249 of <u>TNFAIP2</u> 3' UTR	5' ...AUGGCAUCAAGGCUC ACUGCAGC ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 1030-1036 of <u>TNFAIP8L3</u> 3' UTR	5' ...UUCAGGUUGAUGAUCC UGCAGAG ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 3273-3279 of <u>TNFAIP8L3</u> 3' UTR	5' ...UCAUAUAUCUGAGCC UGCAGAA ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 258-264 of <u>TNFRSF12A</u> 3' UTR	5' ...GACACUGACUAAGGA ACUGCAGC ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 121-127 of <u>TNFRSF13C</u> 3' UTR	5' ...GGGACCAGGCUAACU UGCAGAA ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 7481-7487 of <u>TNFRSF13C</u> 3' UTR	5' ...GCCCCGCGGGGCUUG UGCAGAU ...

	hsa-miR-17-3p	3' GAUGUUCACGGAAGUG ACGUCA
	Position 2379-2385 of <u>TNFRSF19</u> 3' UTR	5' ...CUGUGGCUUCUUGUGCUGCAGAA...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUG ACGUCA
	Position 425-431 of <u>TNFRSF1B</u> 3' UTR	5' ...CCCCAGCAUCCUUUU UCUGCAGAG ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUG ACGUCA
	Position 1530-1536 of <u>TNFRSF1B</u> 3' UTR	5' ...CCCAGGGCCAGGGCC UCUGCAGAG ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUG ACGUCA
	Position 3060-3066 of <u>TNFSF15</u> 3' UTR	5' ...CAGCACCUCUACUGU UCUGCAGAU ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUG ACGUCA
	Position 443-449 of <u>TNFSF8</u> 3' UTR	5' ...GGAUACUUCUUUU AUUCUGCAGAU ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUG ACGUCA
	Position 3006-3012 of <u>TNFSF8</u> 3' UTR	5' ...GUGCUAUCUUGGCUC ACUGCAGC ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGU ACGUCA
	Position 342-348 of <u>TRADD</u> 3' UTR	5' ...ACUUCAUCCUGGGUG UCUGCAGAU ...
TOLL-like receptor	hsa-miR-17-3p	3' GAUGUUCACGGAAGUG ACGUCA
	Position 350-356 of <u>TRADD</u> 3' UTR	5' ...CUGGGUGCUGCAGAU ACUGCAGU ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAG --- UGACGUCA
	Position 6158-6164 of <u>TRAF1</u> 3' UTR	5' ...AGUGCCAGACACGGC ACUGCAGG ...
Apoptosis	hsa-miR-17-3p	3' GAUGUUCACGGAAG --- - UGACGUCA
	Position 1140-1146 of <u>TRAF6</u> 3' UTR	5' ...UGCUGUAGCCUAACA ACUGCAGG ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAG -- UGACGUCA
	Position 446-452 of <u>TLR4</u> 3' UTR	5' ...AAAUUCUACUUGAUG ACUGCAGU ...
TOLL-like receptor	hsa-miR-17-3p	3' GAUGUUCACGGAAGU ACGUCA
	Position 2471-2477 of <u>TOLLIP</u> 3' UTR	5' ...CCUCUCCUCUCCCC UCUGCAGAU ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUG ACGUCA
Apoptosis	Position 263-269 of <u>CASP3</u> 3' UTR	5' ...UGACCUACUCUCAUG UCUGCAGAG ...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUG ACGUCA
	Position 471-477 of <u>CASP8</u> 3' UTR	5' ...UUUCCUACCGAAAC CCUCUGCAGAG ...

	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 1905-1911 of <u>CASP9</u> 3' UTR	5' ...CUGAAGCACCCCGGACUGCAGU...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 2382-2388 of <u>BCL2L11</u> 3' UTR	5' ...CCUUUUUGGAAACUUACUGCAGG...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 4154-4161 of <u>BCL2L11</u> 3' UTR	5' ...AUACUGCUGUAAAUACUGCAGA...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 218-225 of <u>BCL2L13</u> 3' UTR	5' ...GAAUACCCUGGAAUCACUGCAGA...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 2241-2247 of <u>BCL2L13</u> 3' UTR	5' ...AAGACUGAGGCUGCUCUGCAGAU...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 3416-3422 of <u>BCL2L13</u> 3' UTR	5' ...UGAGGACUGCUUCCUACUGCAGC...
	hsa-miR-17-3p	3' GAUGUUCACGGAAG--UGACGUCA
	Position 2669-2676 of <u>PERP</u> 3' UTR	5' ...GCUUCAAAACCAUAGACUGCAGA...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA
	Position 3212-3218 of <u>PERP</u> 3' UTR	5' ...CAGAUUUAAAAUUCUGCAGAC...
	hsa-miR-17-3p	3' GAUGUUCACGGAAGUGACGUCA

Table S5. Predicted miR-548b-3p interaction with target genes related to lung injury

Mediators	mRNA / miRNA	Predicted consequential pairing of target region (top) and miRNA (bottom)
<i>CXCL10</i>	Position 104-110 of <u>CXCL10</u> 3' UTR hsa-miR-548b-3p	5' ...UGUCAAGCCAUAUUGUUCUUAG... 3' UGUUUUCGUUGACUCCAAGAAC
	Position 256-262 of <u>CXCL10</u> 3' UTR hsa-miR-548b-3p	5' ...CUACUGAGGUGCUAUGUUCUUAG... 3' UGUUUUCGUUGACUCCAAGAAC
<i>L-1β</i>	Position 209-215 of <u>IRAK4</u> 3' UTR hsa-miR-548b-3p	5' ...UUAGUAUCACCCCCAGUUCUUAC... 3' UGUUUUCGUUGACUCCAAGAAC
	Position 3008-3014 of <u>IL1RAPL1</u> 3' UTR hsa-miR-548b-3p	5' ...UCAAAGAUAUCAUCCGGUUCUUU... 3' UGUUUUCGUUGACUCCAAGAAC
	Position 854-860 of <u>IL1RN</u> 3' UTR hsa-miR-548b-3p	5' ...AAUGUGGCUCUGGGGUUCUUU... 3' UGUUUUCGUUGACUCCAAGAAC
	Position 3622-3628 of <u>IRAK1BP1</u> 3' UTR hsa-miR-548b-3p	5' ...AUUUAAUAGUAAGGAGUUCUUAU... 3' UGUUUUCGUUGACUCCAAGAAC
	<i>IL-6</i>	Position 2858-2864 of <u>IL6ST</u> 3' UTR hsa-miR-548b-3p
<i>IL-17</i>		Position 114-120 of <u>IL17A</u> 3' UTR hsa-miR-548b-3p
	<i>TNF-α</i>	Position 1342-1348 of <u>C1QTNF8</u> 3' UTR hsa-miR-548b-3p
Position 2022-2028 of <u>TRAF3</u> 3' UTR hsa-miR-548b-3p		5' ...UCGAAGCGUCCGUUGUUCUUAU... 3' UGUUUUCGUUGACUC-CAAGAAC
Position 1798-1804 of <u>TNFSF14</u> 3' UTR hsa-miR-548b-3p		5' ...ACCUGGAUCUGUCUAGUUCUUAG... 3' UGUUUUCGUUGACUCCAAGAAC
Position 1303-1309 of <u>TNFSF18</u> 3' UTR hsa-miR-548b-3p		5' ...AAUUAGCUACUUGCAGGUUCUUG... 3' UGUUUUCGUUGACUCCAAGAAC
Position 3122-3128 of <u>TNFRSF11A</u> 3' UTR hsa-miR-548b-3p		5' ...UGGAUCAGCUUGGUGGUUCUUC... 3' UGUUUUCGUUGACUCCAAGAAC

	Position 5758-5764 of <u>TNFRSF11A</u> 3' UTR	5' ...AAAUGAAUGUUUAAAGUUCUAG...
	hsa-miR-548b-3p	3' UGUUUUCGUUGACUCCAAGAAC
	Position 6209-6215 of <u>TNFRSF11A</u> 3' UTR	5' ...AUUCACCAACAUAUGGGUUCUUU...
	hsa-miR-548b-3p	3' UGUUUUCGUUGACU--CCAAGAAC
	Position 3924-3930 of <u>TNFRSF9</u> 3' UTR	5' ...GUCUUGGUUAUUCUUGGUUCUUU...
	hsa-miR-548b-3p	3' UGUUUUCGUUGACUCCAAGAAC
	Position 4884-4890 of <u>TNFAIP8</u> 3' UTR	5' ...AGGCACUUGCGUUUGUUCUUA...
	hsa-miR-548b-3p	3' UGUUUUCGUUGACUCCAAGAAC
	Position 954-960 of <u>FBF1</u> 3' UTR	5' ...AAAGAACAGGCAGAUUGUUCUUAU...
	hsa-miR-548b-3p	3' UGUUUUCGUUGACUCCAAGAAC
	Position 1288-1294 of <u>NGFRAP1</u> 3' UTR	5' ...GAGUACAACUCUUGUGGUUCUUG...
	hsa-miR-548b-3p	3' UGUUUUCGUUGACU----CCAAGAAC
	Position 1306-1313 of <u>NGFRAP1</u> 3' UTR	5' ...UCUUGGGAUUACAUAUGGUUCUUA...
	hsa-miR-548b-3p	3' UGUUUUCGUUGACUCCAAGAAC
	Position 1641-1647 of <u>NGFRAP1</u> 3' UTR	5' ...GAAACUACUCUGUAAGUUCUUA...
	hsa-miR-548b-3p	3' UGUUUUCGUUGACUCCAAGAAC
	Position 2628-2634 of <u>TNFSF4</u> 3' UTR	5' ...UCCAAAUCAUAUUUGUUCUUA...
	hsa-miR-548b-3p	3' UGUUUUCGUUGACUCCAAGAAC
TOLL-like receptor	Position 2464-2470 of <u>TNFRSF10A</u> 3' UTR	5' ...AAAUUUAUGUAUUUGGUUCUUG...
	hsa-miR-548b-3p	3' UGUUUUCGUUGACUCCAAGAAC
	Position 1250-1257 of <u>TLR4</u> 3' UTR	5' ...GUCUGGAUUAAUGGGGUUCUUA...
	hsa-miR-548b-3p	3' UGUUUUCGUUGACUCCAAGAAC
	Position 2075-2081 of <u>TLR4</u> 3' UTR	5' ...CCUCUCAUGUUAAGUGUUCUUA...
	hsa-miR-548b-3p	3' UGUUUUCGUUGACUCCAAGAAC
	Position 2626-2632 of <u>TLR4</u> 3' UTR	5' ...AUGCUUGGUGGAUACGUUCUUA...
	hsa-miR-548b-3p	3' UGUUUUCGUUGACUCCAAGAAC

<i>Apoptosis</i>	Position 2316-2323 of <u>CASP9</u> 3' UTR	5' ...GCCUGACCUAUUUCU GGUUCUUA ...
	hsa-miR-548b-3p	 3' UGUUUUCGUUGACU CCAAGAAC