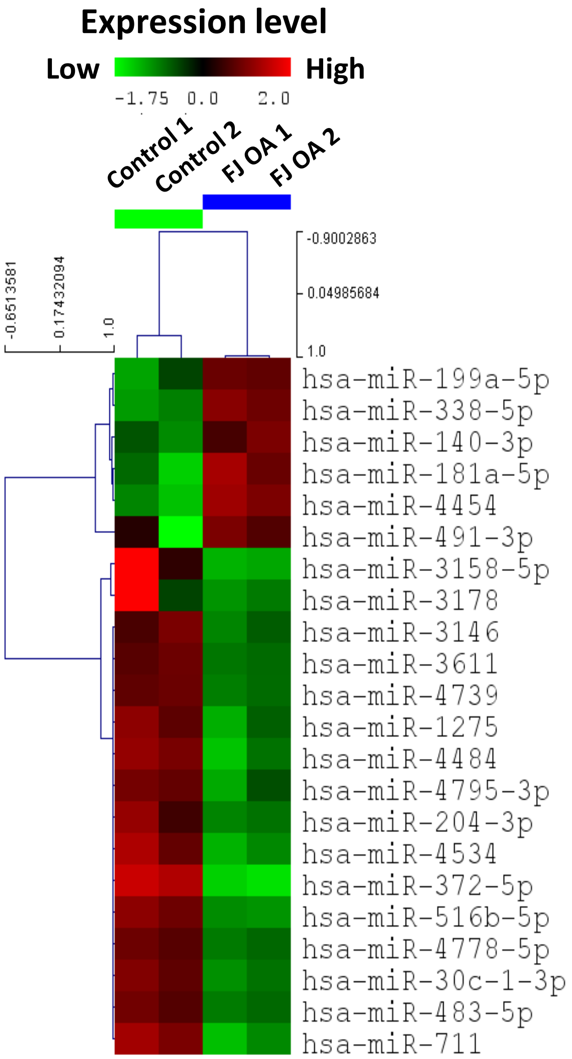
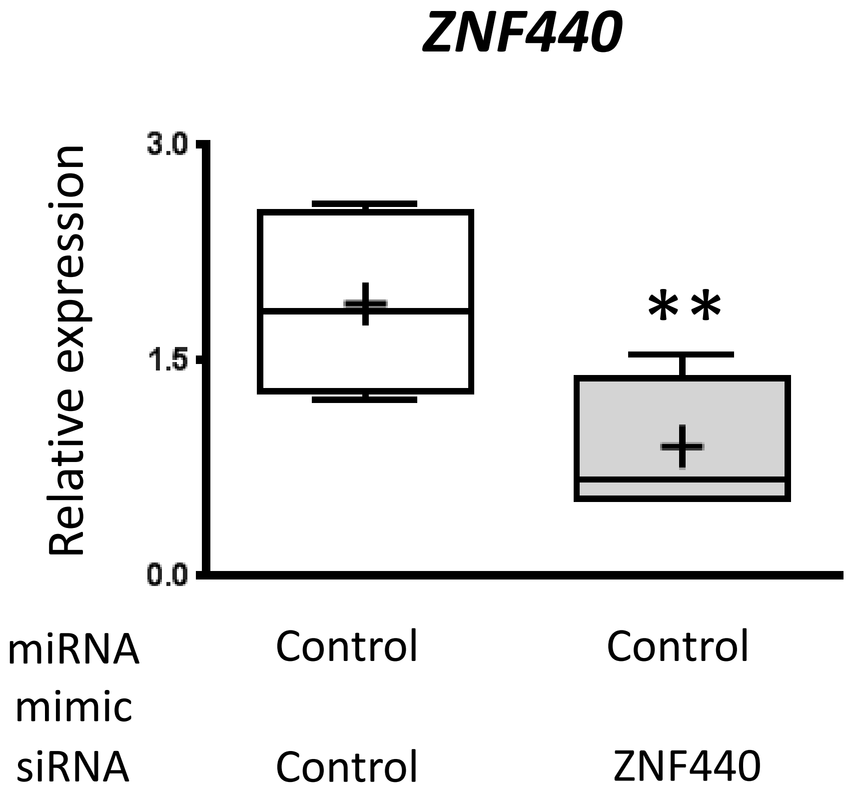
Supplemetal Figure 1.



Supplemental Figure 1: Heatmap showing 22 microRNAs (miRNAs) exhibiting ≥ 1.5-fold change (out of 2,100 miRNAs screened) in their expression between control (n=2) and facet joint osteoarthritis (FJ OA) cartilage (n=2; each FJ OA sample is pooled from 3 separate cartilage specimens). Entire microarray data is accessible at http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE79258.

Supplemental Figure 2.



Supplemental Figure 2: Expression of zinc finger protein 440 (*ZNF440*) in facet joint osteoarthritis (FJ OA) chondrocytes co-transfected with control microRNA (miRNA) mimic and control siRNA or control miRNA mimic and ZNF440 siRNA (n=5/each group). The result showed a significant decrease in the expression of *ZNF440* in FJ OA chondrocytes transfected with ZNF440 siRNA compared to control siRNA. Data presented as box / whisker plots. Horizontal lines and cross marks indicate the medians and the means, boxes indicate 25th to 75th percentiles, and whiskers indicate minimum and maximum values of the dataset. **, $p<0.01$ as determined by two-tailed Student's T-test.

Supplemental Table 1. Seven microRNAs (miRNAs) identified during screening phase (exhibiting ≥ 2.0-fold change in the expression) were further validated by real-time PCR (RT-PCR) in n=21 control and n=34 FJ OA cartilage. Out of 7 microRNAs tested, expression of two miRNAs (miR-181a-5p and miR-4454) was significantly elevated in FJ OA cartilage compared to control cartilage.

Screening phase (microRNA array)				**Validation phase (RT-PCR)**
MicroRNAs (≥ 2.0-fold)	Mean fold change		Up or Down regulation	
	Control	FJ OA		***P* value**
miR-372-5p	1	-2.99495	↓	0.154
miR-3158-5p	1	-2.38262	↓	0.647
miR-711	1	-2.26024	↓	0.256
miR-4454	1	2.249572	↑	**<0.01****
miR-4534	1	-2.16688	↓	0.167
miR-181a-5p	1	2.150419	↑	**<0.01****
miR-4484	1	-2.13305	↓	0.353

**, *p*<0.01, as determined using two-tailed Student's T test.

Supplemental Table 2. Results of Ordinal logistic regression models of FJ OA grade assessed by MRI grading scale (0, 1, 2, or 3) and Spearman's rank correlations between miRNA expression and FJ OA grade in 55 subjects

	miR-181a-5p	**miR-4454**
Odds ratio for increased grade	3.237073	2.0454479
p value*	0.008188489	0.006106278
AIC	139.2706	139.3924
Spearman's rank correlation	0.424 (p = 0.0012†)	0.460 (p = 0.0004†)

Correlations between miRNA expression and FJ OA grade were assessed with Spearman's rank-order correlation coefficient. The correlation coefficients were 0.42 for miR-181a-5p expression and 0.46 for miR-4454 expression; both were statistically significant. AIC; Akaike information criterion.

*null hypothesis: OR = 1
† null hypothesis: correlation coefficient = 0

Supplemental Table 3. Table showing a summary of up-regulation or down-regulation in the expression of inflammatory, catabolic, anabolic and cell death mediators in facet joint osteoarthritis (FJ OA) chondrocytes treated with microRNA (miR) 181a-5p or miR-4454 mimic/inhibitor.

		Inflammatory mediators			Catabolic mediator	Cartilage Matrix Molecule	Cell death Mediator
miRNAs treatment		***TNFA***	***IL6***	***MCP1***	***MMP13***	***COL2A1***	***PARP p85***
mimics	**miR-181a-5p**	↑	↑	↑	↑	↓	↑
	miR-4454	↑	↑	↑	**NS**	↓	↑
Inhibitors	**miR-181a-5p**	**NS**	↓	**NS**	↓	↑	↓
	miR-4454	↓	↓	↓	↓	↑	↓

TNFA; tumor necrosis factor-alpha*, IL6*; interleukin-6, *MCP1*; monocyte chemoattractant protein-1, *MMP13*; metalloproteinase-13, *COL2A1*; type II collagen, PARP p85; poly (ADP-ribose) polymerase, NS; not significant.

Supplemental Table 4. Significantly enriched pathways (total 247 pathways) associated with miR-181a-5p and miR-4454 using pathDIP (1)

Pathway Source	Pathway Name	p-value	Pathway Source	Pathway Name	p-value
reactome	Influenza Virus Induced Apoptosis	1.00E-04	reactome	mTORC1 mediated signalling	0.003084
biocarta	nf kb signaling pathway	6.43E-04	biocarta	akt signaling pathway	0.003157
pid	Canonical NF kappaB pathway	9.07E-04	pid	HIV 1 Nef Negative effector of Fas and TNF alpha	0.003228
pharmgkb	Tacrolimus Cyclosporine Pathway Pharmacodynamics	0.001187	reactome	RIP mediated NFkB activation via ZBP1	0.003283
wikipathways	NOD pathway	0.001413	ontocanro	Nemo	0.003393
pharmgkb	Glucocorticoid Pathway Peripheral Tissue Pharmacodynamics	0.001497	reactome	NF kB activation through FADD RIP 1 pathway mediated by caspase 8 and 10	0.003395
reactome	Regulation of mRNA stability by proteins that bind AU rich elements	0.001573	biocarta	hiv 1 nef negative effector of fas and tnf	0.003592
ipavs	FAS_signaling_in_cardiac_hypertrophy	0.001804	biocarta	erythropoietin mediated neuroprotection through nf kb	0.003663
reactome	FCERI mediated NF kB activation	0.002049	ipavs	beta3_integrin_mediated_Ub_for_NFkB_activation_Proteins	0.003989
ipavs	Wnt_signaling_in_cardiomyocyte_hypertrophy	0.002154	biocarta	cd40l signaling pathway	0.004267
biocarta	internal ribosome entry pathway	0.002219	wikipathways	Structural Pathway of Interleukin 1 IL 1	0.004404
kegg	RIG I like receptor signaling pathway Homo sapiens human	0.002234	reactome	Signaling by Wnt	0.004448
wikipathways	EBV LMP1 signaling	0.002293	biocarta	acetylation and deacetylation of rela in nucleus	0.004472
kegg	Influenza A Homo sapiens human	0.002637	reactome	TCF dependent signaling in response to WNT	0.004710
reactome	Activation of NF kappaB in B cells	0.003035	reactome	AUF1 hnRNP D0 destabilizes mRNA	0.004914

Supplemental Table 4 continued (2)

Pathway Source	Pathway Name	p-value	Pathway Source	Pathway Name	p-value
pid	Role of Calcineurin dependent NFAT signaling in lymphocytes	0.005403	wikipathways	Osteopontin Signaling	0.007227
pid	IL1 mediated signaling events	0.005431	reactome	S6K1 signalling	0.008032
biocarta	double stranded rna induced gene expression	0.005543	wikipathways	NLR Proteins	0.008341
reactome	TAK1 activates NFkB by phosphorylation and activation of IKKs complex	0.005727	reactome	RIG I MDA5 mediated induction of IFN alpha beta pathways	0.008416
reactome	Metabolism of mRNA	0.005835	pid	TNF receptor signaling pathway	0.008770
biocarta	toll like receptor pathway	0.006177	pharmgkb	Carbamazepine Pathway Pharmacokinetics	0.008869
reactome	mTOR signalling	0.006316	pid	FOXA1 transcription factor network	0.008920
kegg	Pathways in cancer Homo sapiens human	0.006421	kegg	Herpes simplex infection Homo sapiens human	0.009206
reactome	Interleukin 1 signaling	0.006452	wikipathways	IL 1 signaling pathway	0.009598
kegg	Osteoclast differentiation Homo sapiens human	0.006486	reactome	TCR signaling	0.009768
reactome	NOTCH1 Intracellular Domain Regulates Transcription	0.006532	pid	Class I PI3K signaling events mediated by Akt	0.009875
wikipathways	TNF alpha Signaling Pathway	0.006816	kegg	Measles Homo sapiens human	0.009981
wikipathways	TNF alpha Signaling Pathway 1	0.006816	kegg	Prostate cancer Homo sapiens human	0.010014
reactome	TRAF6 mediated NF kB activation	0.006929	reactome	HIV Life Cycle	0.010022
pid	BCR signaling pathway	0.00701	reactome	Fc epsilon receptor FCERI signaling	0.010456

Supplemental Table 4 continued (3)

Pathway Source	Pathway Name	p-value	Pathway Source	Pathway Name	p-value
reactome	ZBP1 DAI mediated induction of type I IFNs	0.010712	reactome	Signaling by NOTCH1	0.013609
ehmn	Lysine metabolism	0.010908	reactome	Signaling by NOTCH1 HD Domain Mutants in Cancer	0.013609
humancyc	methylglyoxal degradation III	0.011062	reactome	Signaling by NOTCH1 HD PEST Domain Mutants in Cancer	0.013609
reactome	Cytosolic sensors of pathogen associated DNA	0.011312	reactome	Signaling by NOTCH1 PEST Domain Mutants in Cancer	0.013609
reactome	Signaling by NOTCH	0.011818	reactome	Signaling by NOTCH1 in Cancer	0.013609
biocarta	tnfr2 signaling pathway	0.011973	reactome	Signaling by NOTCH1 t 7 9 NOTCH1 M1580_K2555 Translocation Mutant	0.013609
reactome	Innate Immune System	0.012395	biocarta	inactivation of gsk3 by akt causes accumulation of b catenin in alveolar macrophages	0.013700
wikipathways	RANKL RANK Signaling Pathway	0.012475	biocarta	signal transduction through il1r	0.013700
biocarta	cadmium induces dna synthesis and proliferation in macrophages	0.012894	pid	Calcium signaling in the CD4 TCR pathway	0.014418
reactome	Release of eIF4E	0.012924	ontocanro	TGF	0.014599
reactome	Serotonin receptors	0.013245	biocarta	nfkb activation by nontypeable hemophilus influenzae	0.014789
reactome	Regulated proteolysis of p75NTR	0.013245	netpath	TCR	0.014871
ipavs	Cardiac_Hypertrophy	0.013263	reactome	Translocation of GLUT4 to the plasma membrane	0.015344
kegg	Epstein Barr virus infection Homo sapiens human	0.013453	reactome	Transport of the SLBP independent Mature mRNA	0.015395
reactome	FBXW7 Mutants and NOTCH1 in Cancer	0.01361	wikipathways	B Cell Receptor Signaling Pathway	0.015720

Supplemental Table 4 continued (4)

Pathway Source	Pathway Name	p-value	Pathway Source	Pathway Name	p-value
reactome	Downstream TCR signaling	0.015726	humancyc	acetone degradation I to methylglyoxal	0.017582
pid	Regulation of cytoplasmic and nuclear SMAD2 3 signaling	0.015825	biocarta	yaci and bcma stimulation of b cell immune responses	0.017910
reactome	Deadenylation of mRNA	0.01604	reactome	Energy dependent regulation of mTOR by LKB1 AMPK	0.018021
reactome	Regulation of AMPK activity via LKB1	0.016276	pid	Notch mediated HES HEY network	0.018491
biocarta	fas signaling pathway cd95	0.016303	pid	Signaling events mediated by HDAC Class I	0.018888
reactome	Transport of the SLBP Dependant Mature mRNA	0.016366	reactome	LRR FLII interacting protein 1 LRRFIP1 activates type I IFN production	0.018997
reactome	Transport of Mature mRNAs Derived from Intronless Transcripts	0.016694	reactome	NOD1 2 Signaling Pathway	0.018997
biocarta	mapkinase signaling pathway	0.016759	spike	Apoptosis	0.018997
netpath	IL1	0.016873	wikipathways	Nanomaterial induced apoptosis	0.019101
kegg	Hepatitis B Homo sapiens human	0.016973	reactome	G2 M Transition	0.019134
ipavs	RANK_Singnaling_Pathway_in_Osteoclast_resorption	0.016988	wikipathways	Androgen receptor signaling pathway	0.019439
reactome	Transport of Mature mRNA Derived from an Intronless Transcript	0.017025	wikipathways	Toll like receptor signaling pathway	0.019508
biocarta	chaperones modulate interferon signaling pathway	0.017108	kegg	B cell receptor signaling pathway Homo sapiens human	0.019571
reactome	IRAK1 recruits IKK complex	0.017575	kegg	NF kappa B signaling pathway Homo sapiens human	0.019950
reactome	IRAK1 recruits IKK complex upon TLR7 8 or 9 stimulation	0.017575	spike	Caspases Cascade	0.019979

Supplemental Table 4 continued (5)

Pathway Source	Pathway Name	p-value	Pathway Source	Pathway Name	p-value
reactome	Mitotic G2 G2 M phases	0.020205	reactome	MyD88 cascade initiated on plasma membrane	0.022385
netpath	AndrogenReceptor	0.020399	reactome	TRAF6 mediated induction of NFkB and MAP kinases upon TLR7 8 or 9 activation	0.022385
reactome	TRAF3 dependent IRF activation pathway	0.020824	reactome	Toll Like Receptor 10 TLR10 Cascade	0.022385
reactome	HSF1 dependent transactivation	0.020898	reactome	Toll Like Receptor 5 TLR5 Cascade	0.022385
kegg	Viral carcinogenesis Homo sapiens human	0.02096	kegg	Thyroid hormone signaling pathway Homo sapiens human	0.022434
biocarta	carm1 and regulation of the estrogen receptor	0.021366	systems.biology.org	Toll Like_receptor_signaling_network	0.022464
reactome	Nucleotide binding domain leucine rich repeat containing receptor NLR signaling pathways	0.021366	reactome	MyD88 dependent cascade initiated on endosome	0.022796
reactome	Toll Like Receptor 9 TLR9 Cascade	0.021378	reactome	Toll Like Receptor 7 8 TLR7 8 Cascade	0.022796
reactome	Downstream signaling events of B Cell Receptor BCR	0.021778	pid	Osteopontin mediated events	0.022865
reactome	MyD88 Mal cascade initiated on plasma membrane	0.021845	biocarta	ceramide signaling pathway	0.023041
reactome	Toll Like Receptor 2 TLR2 Cascade	0.021845	kegg	Circadian rhythm Homo sapiens human	0.023072
reactome	Toll Like Receptor TLR1 TLR2 Cascade	0.021845	spike	Apoptosis Anti Apoptosis Network	0.023847
reactome	Toll Like Receptor TLR6 TLR2 Cascade	0.021845	reactome	TRAF6 Mediated Induction of proinflammatory cytokines	0.023986
wikipathways	Corticotropin releasing hormone	0.021845	reactome	Smooth Muscle Contraction	0.024049
pharmgkb	Phenytoin Pathway Pharmacokinetics	0.021882	pid	Glucocorticoid receptor regulatory network	0.024225

Supplemental Table 4 continued (6)

Pathway Source	Pathway Name	p-value	Pathway Source	Pathway Name	p-value
reactome	Late Phase of HIV Life Cycle	0.024507	wikipathways	TCR Signaling Pathway	0.027373
biocarta	bone remodeling	0.024706	systems.biology.org	hepatocyte_v2 9	0.027441
smpdb	Intracellular Signalling Through Adenosine Receptor A2b and Adenosine	0.024774	signalink	TGF Ncore	0.027442
biocarta	eukaryotic protein translation	0.024907	kegg	Wnt signaling pathway Homo sapiens human	0.027732
biocarta	overview of telomerase rna component gene hterc transcriptional regulation	0.025026	reactome	HIV Infection	0.027768
systems.biology.org	beta_cell_v2 3	0.025379	wikipathways	Energy Metabolism	0.027986
reactome	PKB mediated events	0.025443	spike	NFkB Signaling Network	0.028001
spike	Hearing and Vision Proteins	0.025444	pid	Ceramide signaling pathway	0.028547
biocarta	tnf stress related signaling	0.025531	biocarta	trefoil factors initiate mucosal healing	0.028548
smpdb	Intracellular Signalling Through Adenosine Receptor A2a and Adenosine	0.025625	kegg	HTLV I infection Homo sapiens human	0.028751
wikipathways	FAS pathway and Stress induction of HSP regulation	0.026055	kegg	Epithelial cell signaling in Helicobacter pylori infection Homo sapiens human	0.029005
reactome	mRNA Editing	0.026144	wikipathways	Histone Modifications	0.029236
reactome	S6K1 mediated signalling	0.026453	biocarta	multi step regulation of transcription by pitx2	0.029540
reactome	p75NTR signals via NF kB	0.02685	biocarta	mets affect on macrophage differentiation	0.030098
wikipathways	Apoptosis	0.027078	reactome	Xenobiotics	0.030368
kegg	Oxytocin signaling pathway Homo sapiens human	0.027226	ipavs	TWEAK_signaling_pathway	0.030562

Supplemental Table 4 continued (7)

Pathway Source	Pathway Name	p-value	Pathway Source	Pathway Name	p-value
wikipathways	TOR Signaling	0.03069	ontocanro	Apoptosis_Human	0.033904
netpath	Leptin	0.031112	wikipathways	TWEAK Signaling Pathway	0.033908
pid	FOXM1 transcription factor network	0.031165	reactome	AMPK inhibits chREBP transcriptional activation activity	0.034365
reactome	Vpr mediated induction of apoptosis by mitochondrial outer membrane permeabilization	0.031281	pid	TRAIL signaling pathway	0.034952
wikipathways	ErbB Signaling Pathway	0.031289	wikipathways	SIDS Susceptibility Pathways	0.035319
reactome	Signaling by the B Cell Receptor BCR	0.031538	reactome	JNK c Jun kinases phosphorylation and activation mediated by activated human TAK1	0.035776
wikipathways	Estrogen signaling pathway	0.031741	pid	Atypical NF kappaB pathway	0.035832
kegg	Legionellosis Homo sapiens human	0.031836	reactome	Import of palmitoyl CoA into the mitochondrial matrix	0.035932
kegg	NOD like receptor signaling pathway Homo sapiens human	0.031838	kegg	AMPK signaling pathway Homo sapiens human	0.036064
netpath	RAGE	0.032038	pid	Fc epsilon receptor I signaling in mast cells	0.036370
wikipathways	Cardiac Hypertrophic Response	0.032324	pid	Regulation of nuclear SMAD2 3 signaling	0.036460
reactome	Eukaryotic Translation Elongation	0.033264	reactome	Constitutive Signaling by NOTCH1 t 7 9 NOTCH1 M1580_K2555 Translocation Mutant	0.036636
wikipathways	Aryl Hydrocarbon Receptor	0.033307	kegg	Adipocytokine signaling pathway Homo sapiens human	0.036660
kegg	Small cell lung cancer Homo sapiens human	0.033393	kegg	mTOR signaling pathway Homo sapiens human	0.036941
biocarta	mechanism of gene regulation by peroxisome proliferators via ppara	0.033406	kegg	Cytosolic DNA sensing pathway Homo sapiens human	0.037226
spike	MYO3A Interacting Proteins in the Auditory System	0.033605	pid	Signaling mediated by p38 alpha and p38 beta	0.038868

Supplemental Table 4 continued (8)

Pathway Source	Pathway Name	p-value	Pathway Source	Pathway Name	p-value
pid	Validated targets of C MYC transcriptional activation	0.038878	reactome	Organelle biogenesis and maintenance	0.046194
reactome	formation of the beta catenin TCF transactivating complex	0.039201	netpath	TNFalpha	0.046725
wikipathways	Nanoparticle triggered regulated necrosis	0.040472	pid	p38 MAPK signaling pathway	0.046816
wikipathways	miRNA Biogenesis	0.04077	pid	CD40 CD40L signaling	0.046834
biocarta	pelp1 modulation of estrogen receptor activity	0.040813	biocarta	keratinocyte differentiation	0.046876
wikipathways	Integrated Lung Cancer Pathway	0.041742	reactome	cGMP effects	0.046900
reactome	Translation	0.043285	wikipathways	Integrated Breast Cancer Pathway	0.047652
pid	FoxO family signaling	0.043886	kegg	Shigellosis Homo sapiens human	0.047654
reactome	Hormone sensitive lipase HSL mediated triacylglycerol hydrolysis	0.043953	reactome	TRAF6 mediated IRF7 activation	0.047717
ontocanro	SASP_Senescene Associated Secretory Phenotype_	0.043984	biocarta	hypoxia and p53 in the cardiovascular system	0.048361
wikipathways	Notch Signaling Pathway 1	0.04441	pid	Regulation of Androgen receptor activity	0.048837
kegg	T cell receptor signaling pathway Homo sapiens human	0.044477	kegg	Regulation of autophagy Homo sapiens human	0.049355
kegg	MAPK signaling pathway Homo sapiens human	0.044773	wikipathways	Neural Crest Differentiation	0.049355
biocarta	human cytomegalovirus and map kinase pathways	0.044999	netpath	Oncostatin_M	0.050474
pid	Validated transcriptional targets of AP1 family members Fra1 and Fra2	0.045179	reactome	Formation of the Editosome	0.050943
kegg	Toll like receptor signaling pathway Homo sapiens human	0.045327	reactome	mRNA Editing C to U Conversion	0.050943
reactome	Mitochondrial biogenesis	0.046195			

Supplemental Table 5. Relative expression of predicted target gene candidates associated with both microRNA (miR)-181a-5p and miR-4454 assessed by real-time PCR (RT-PCR) analysis

Gene	Control mimic	miR-181a-5p mimic (*P* value compared to control)	miR-4454 mimic (P value compared to control)
ZNF454	0.50±0.03	0.51±0.04 (0.90)	0.60±0.12 (0.45)
ZNF440	0.39±0.06	0.69±0.07 (***0.01****)	0.91±0.20 (***0.04****)
MLL1	0.44±0.04	0.46±0.04 (0.76)	0.42±0.02 (0.68)
KDM5A	0.49±0.12	0.51±0.11 (0.92)	0.76±0.18 (0.25)
EIF4A2	1.00±0.12	1.27±0.10 (0.12)	0.85±0.10 (0.36)
MBOAT2	0.46±0.03	0.57±0.03 (***0.04****)	0.49±0.06 (0.62)
ATM	0.40±0.05	0.39±0.03 (0.93)	0.35±0.02 (0.38)
LRRC32	0.70±0.17	0.62±0.10 (0.69)	0.81±0.14 (0.63)
LARP4	0.35±0.06	0.37±0.05 (0.81)	0.48±0.07 (0.17)
CARD8	0.87±0.22	0.98±0.20 (0.72)	1.14±0.23 (0.41)

Supplemental Table 5. The expression of zinc finger protein 440 (*ZNF440*) (n=6/each group) is significantly upregulated in facet joint osteoarthritis (FJ OA) chondrocytes treated with miR-181a-5p or miR-4454 mimic compared to control mimic. The expression of *MBOAT2* is upregulated only when FJ OA chondrocytes are treated with miR-181a-5p, not miR-4454. Other genes did not show any significant differences between miR-181a-5p or miR-4454 and control mimic treatments. Each relative expression in RT-PCR products was calculated by the $2^{-\Delta Ct}$ method. Data were normalized to glyceraldehyde 3-phosphate dehydrogenase (GAPDH). The data are expressed as mean ± SEM. *, $p<0.05$. The significance between control mimic and miR-181a-5p or miR-4454 mimic treatments was determined using a two-tailed Student's T test. *ZNF454;* zinc finger protein 454, *ZNF440*; zinc finger protein 440, *MLL1*; mixed-lineage leukemia 1, *KDM5A*; lysine demethylase 5A, *EIF4A2*; eukaryotic translation initiation factor 4A2, *MBOAT2*; membrane bound O-acyltransferase domain containing 2, *ATM*; ATM serine/threonine kinase, *LRRC32;* leucine rich repeat containing 32, *LARP4;* la ribonucleoprotein domain famiy member 4, *CARD8*; caspase recruitment domain family member 8.

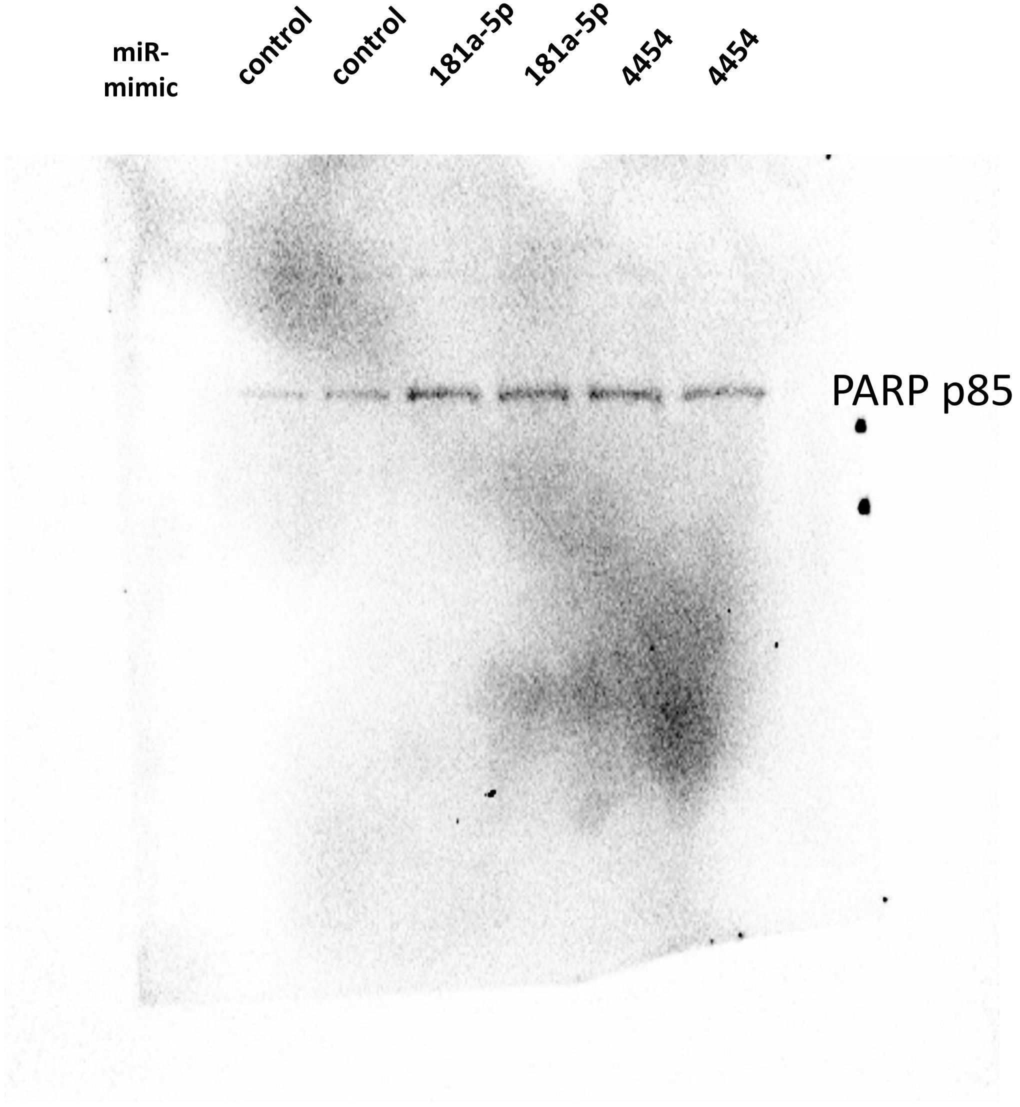
Supplemental Table 6. Gene sequences of primers, mimics, and inhibitors for quantitative real-time PCR

Genes	Forward primer (5'-3')	Reverse primer (5'-3')
GAPDH	CAGAACATCATCCCTGCCTCT	GCTTGACAAAGTGGTCGTTGAG
MMP13	TCCCAGGAATTGGTGATAAGTAGA	CTGGCATGACGCGAACAAA
COL2A1	TGGACGATCACGAAACC	GCTGCGGATGCTCTCAATCT
TNFA	GTCTCCTACCAGACCAAG	CAAAGTAGACCTGCCCAGACTC
IL6	TGACAAACAAATTCGGTACATCCT	TCTGCCAGTGCCTCTTTGCT
MCP1	CTCTGCCGCCCTTCTGTG	TGCATCTGGCTGAGCGAG
ZNF440	CATCATGCCCAGCTGCAACC	ATGGCACTGCTGGTTTTGGG
ZNF454	TGCCTCCATAGCACTTTGCC	GCCACATCCTTGAAGGTCACC
MLL1	ACTGTGGCGCCAAGAAATGC	TCAGCGTTGCTTTGGATGGC
KDM5A	TGTGCAAAAGGGGGAGAAGG	AACACTTGACGGCACACCTG
EIF4A2	GAGCCACTTGTCATGCCTGC	ACACGACTTGACCCTGACCG
MBOAT2	TGAAACAAGCCCTCCCATGC	ACGGACAAGTGCTGAGGTTG
ATM	CCAGCAAATTCTAGTGCCAGTCAG	TGAGGTGGATTAGGAGCAGGATC
LRRC32	TCAAGCGGCTCAATCTTGCC	TTGTTTCGCAGGTCCAGCAC
LARP4	AGACCCGGAAGCAGTTGTTG	AAGGACACACACTCGCCTTG
CARD8	GATGGAGTCGTAGGGGCCTGAG	CTCCCTCATCAGGGGCTTCACG
miRCURY LNA PCR primers (5'-3')		
hsa-miR-372-5p	CCUCAAAUGUGGAGCACUAUUCU	
hsa-miR-3158-5p	CCUGCAGAGAGGAAGCCCUUC	
hsa-miR-711	GGGACCCAGGGAGAGACGUAAG	
hsa-miR-4454	GGAUCCGAGUCACGGCACCA	
hsa-miR-4534	GGAUGGAGGAGGGGUCU	
hsa-miR-181a-5p	AACAUUCAACGCUGUCGGUGAGU	
hsa-miR-4484	AAAAGGCGGGAGAAGCCCCA	
miRCURY LNA microRNA Mimic (5'-3')		
hsa--miR-181a-5p	AACAUUCAACGCUGUCGGUGAGU	
hsa-miR-4454	GGAUCCGAGUCACGGCACCA	
cel-miR-39-3p (control)	TCACCGGGTGTAAATCAGCTTG	
miRCURY LNA Power Inhibitor (5'-3')		
hsa-miR-181a-5p	ACTCACCGACAGCGTTGAATG	
hsa-miR-4454	TGGTGCCGTGACTCGGATC	
Negative control A	TAACACGTCTATACGCCCA	

Supplemental Table 6. Sequences of primers, microRNA mimics and inhibitors used in this study. *GAPDH*; glyceraldehyde 3-phosphate dehydrogenase, *MMP13;* metalloproteinase-13, *COL2A1*; type II collagen, *TNFA*; tumor necrosis factor-alpha*, IL6*; interleukin-6, *MCP1*; monocyte chemoattractant protein-1, *ZNF440*; zinc finger protein 440, *ZNF454;* zinc finger protein 454 , *MLL1*; mixed-lineage leukemia 1, *KDM5A*; lysine demethylase 5A, *EIF4A2*; eukaryotic translation initiation factor 4A2, *MBOAT2*; membrane bound O-acyltransferase domain containing 2, *ATM*; ATM serine/threonine kinase, *LRRC32;* leucine rich repeat containing 32, *LARP4;* la ribonucleoprotein domain famiy member 4, *CARD8*; caspase recruitment domain family member 8.

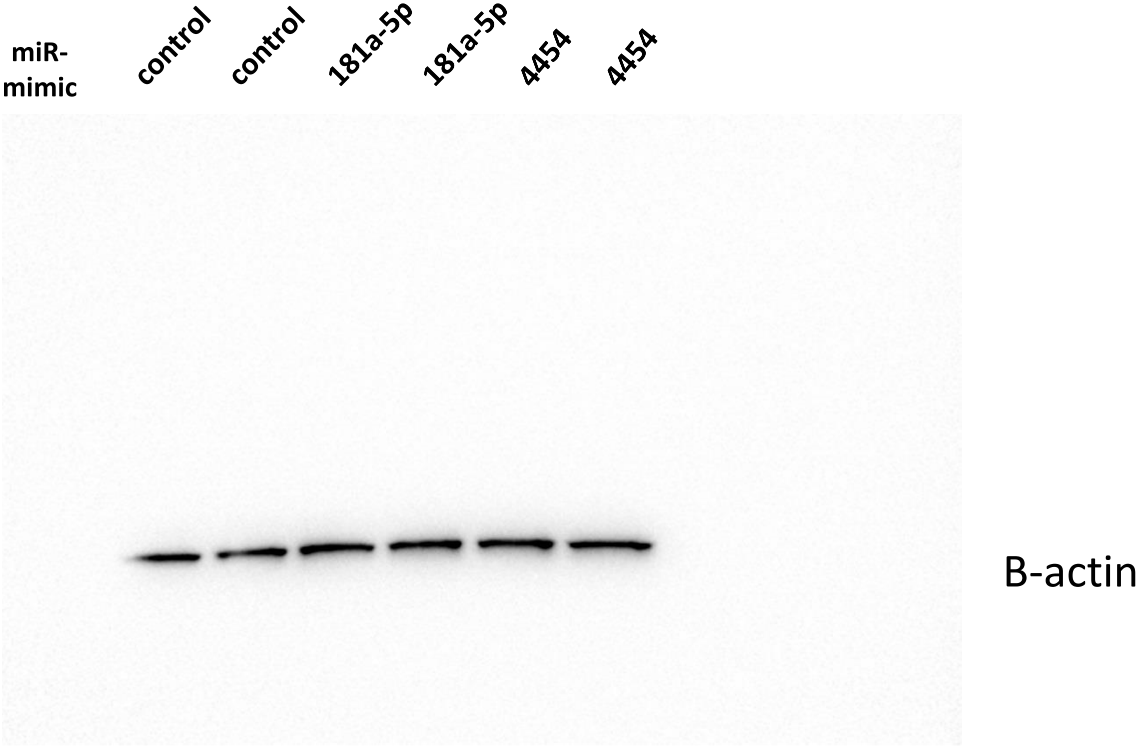
Full unedited gel for Figure 3B

PARP p85 Blot



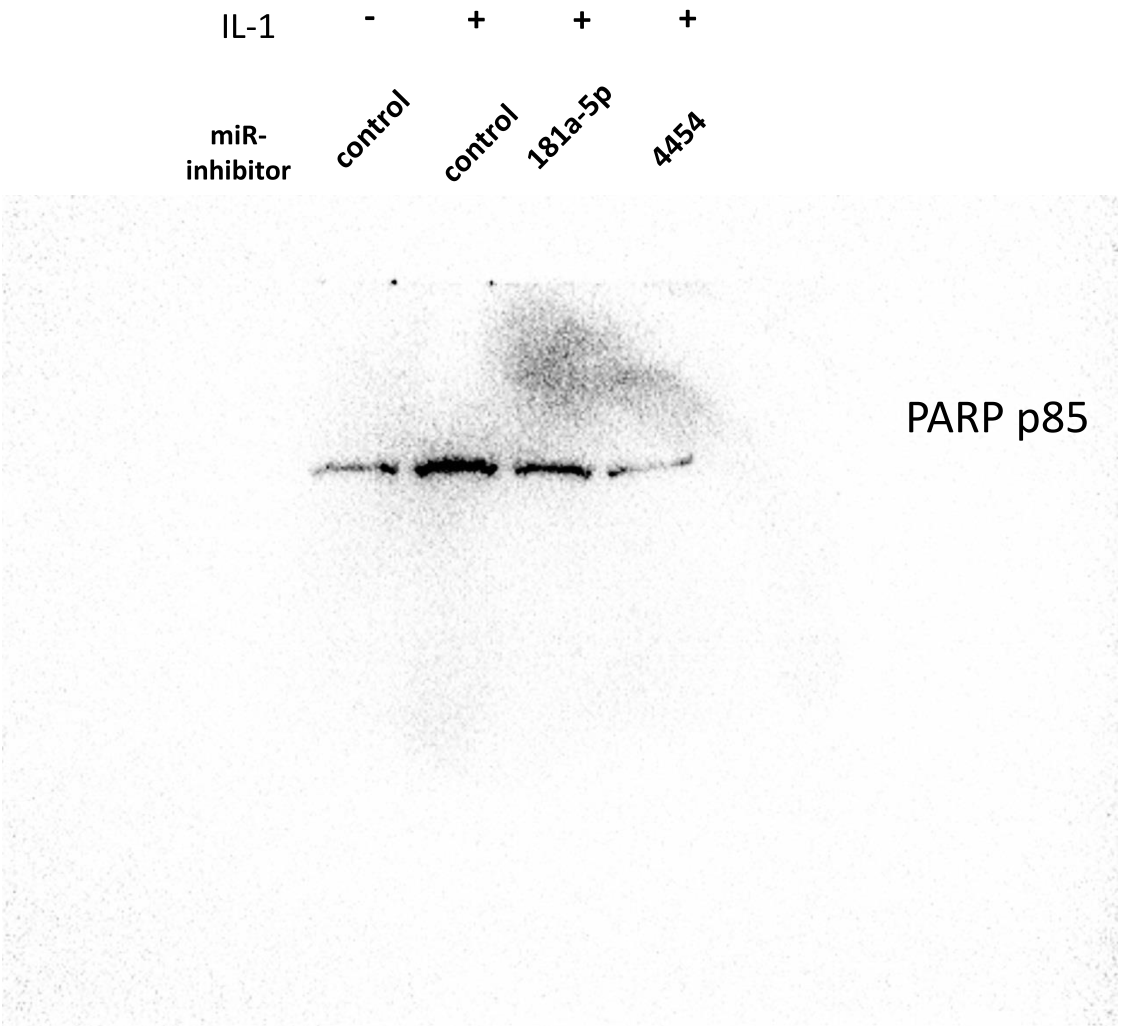
Full unedited gel for Figure 3B

B-actin blot



Full unedited gel for Figure 3E

PARP p85 Blot



Full unedited gel for Figure 3E

B-actin blot

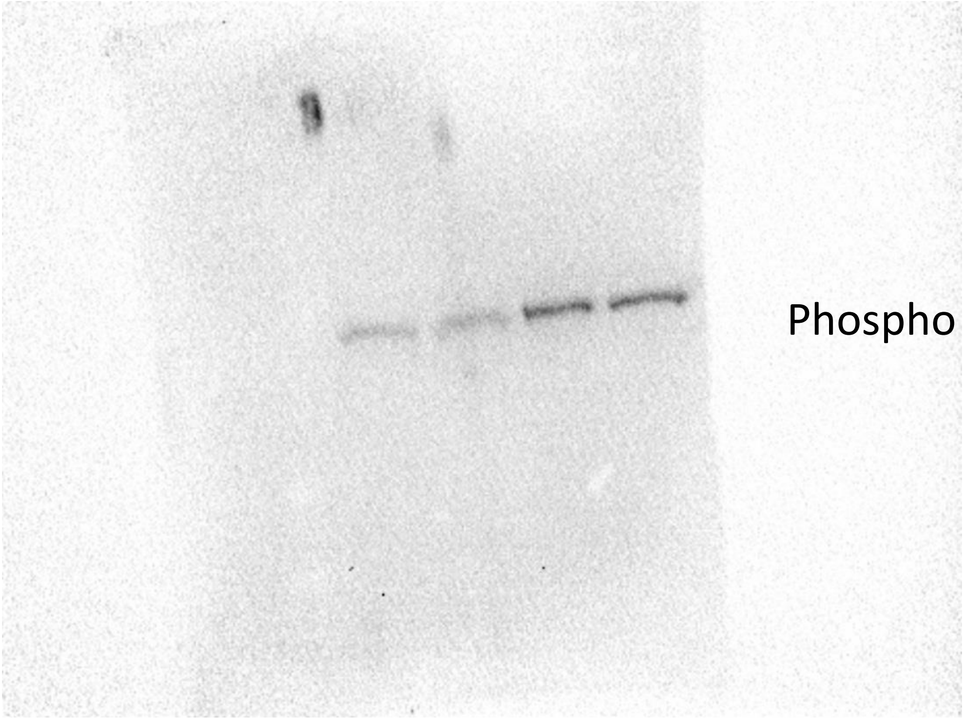
IL-1	-	+	+	+
miR-inhibitor	**control**	**control**	**181a-5p**	**4454**

B-actin

Full unedited gel for Figure 4E

Phospho-p65 Blot

IL1b - IL1b - IL1b + IL1b +

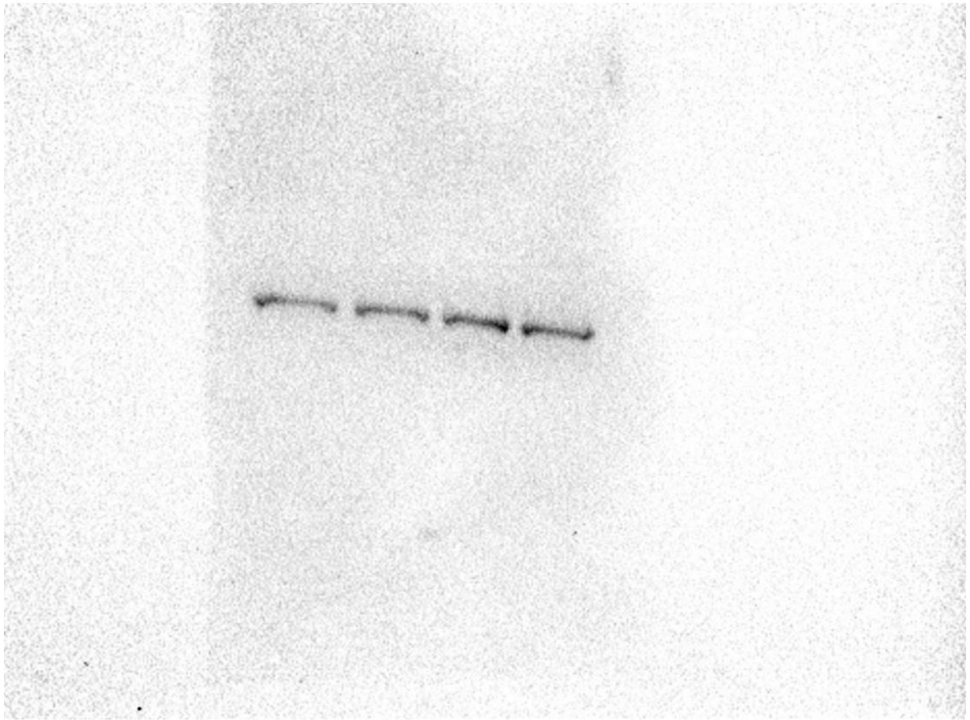


Phospho p65

Full unedited gel for Figure 4E

p65 Blot

IL1b - IL1b - IL1b + IL1b +



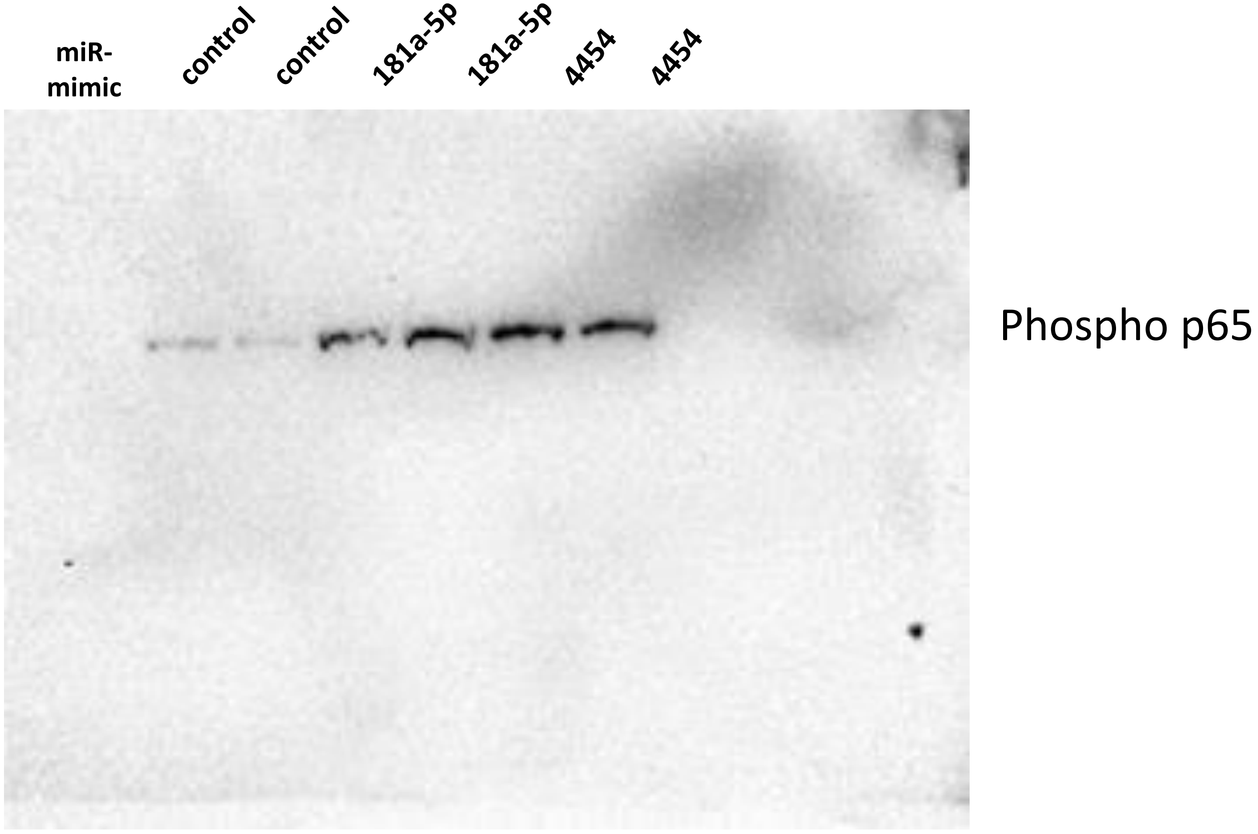
p65

Full unedited gel for Figure 4E

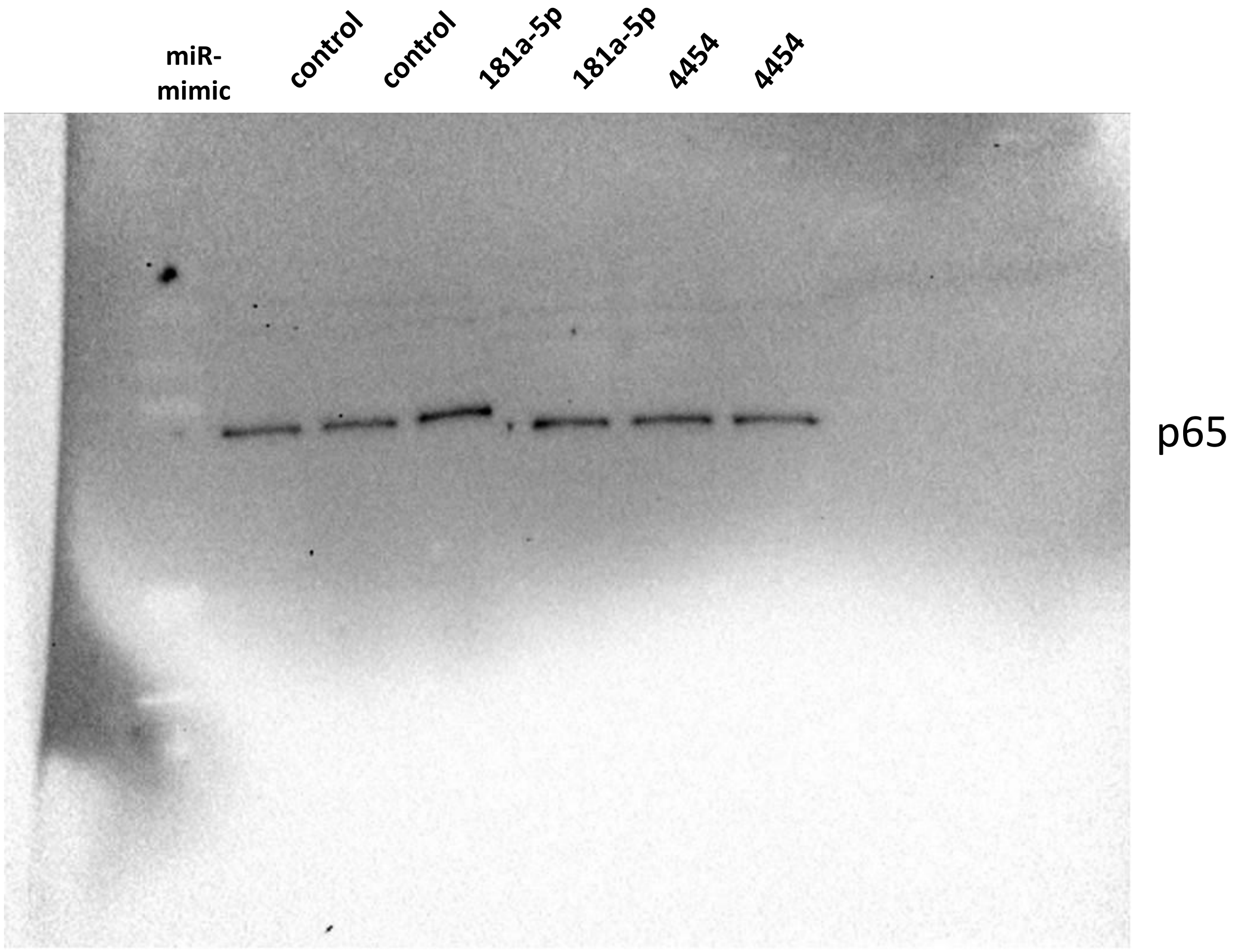
B-actin Blot

Full unedited gel for Figure 4F

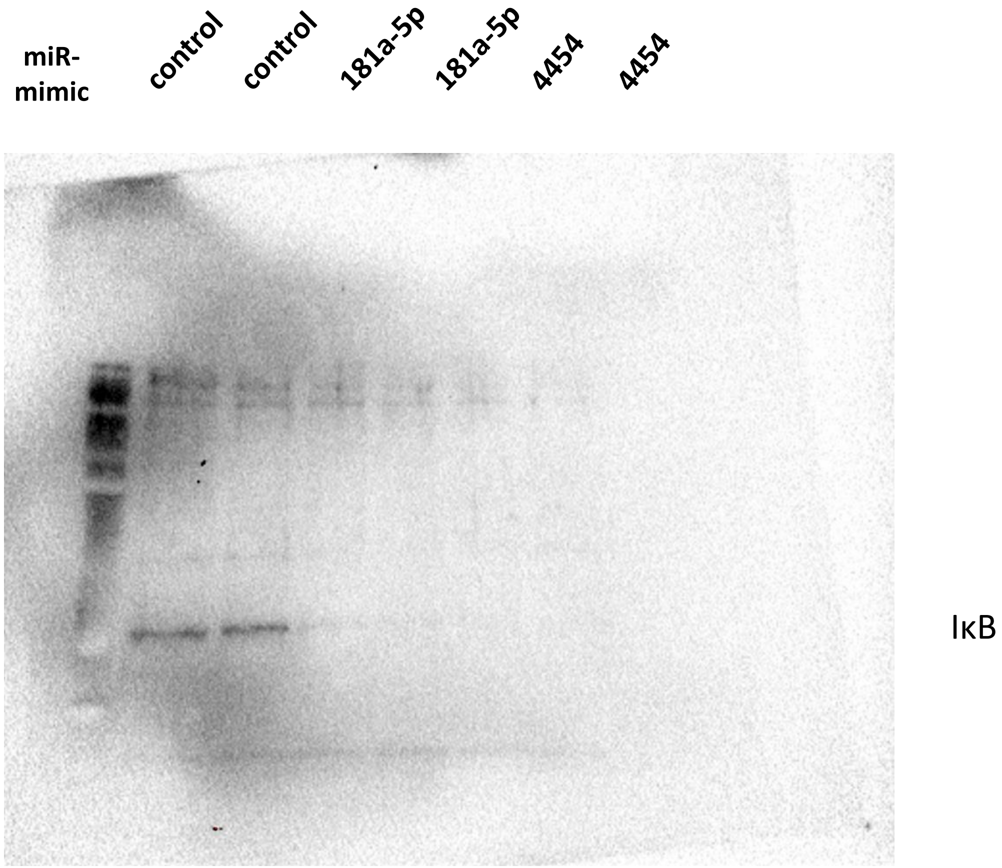
Phospho-p65 Blot



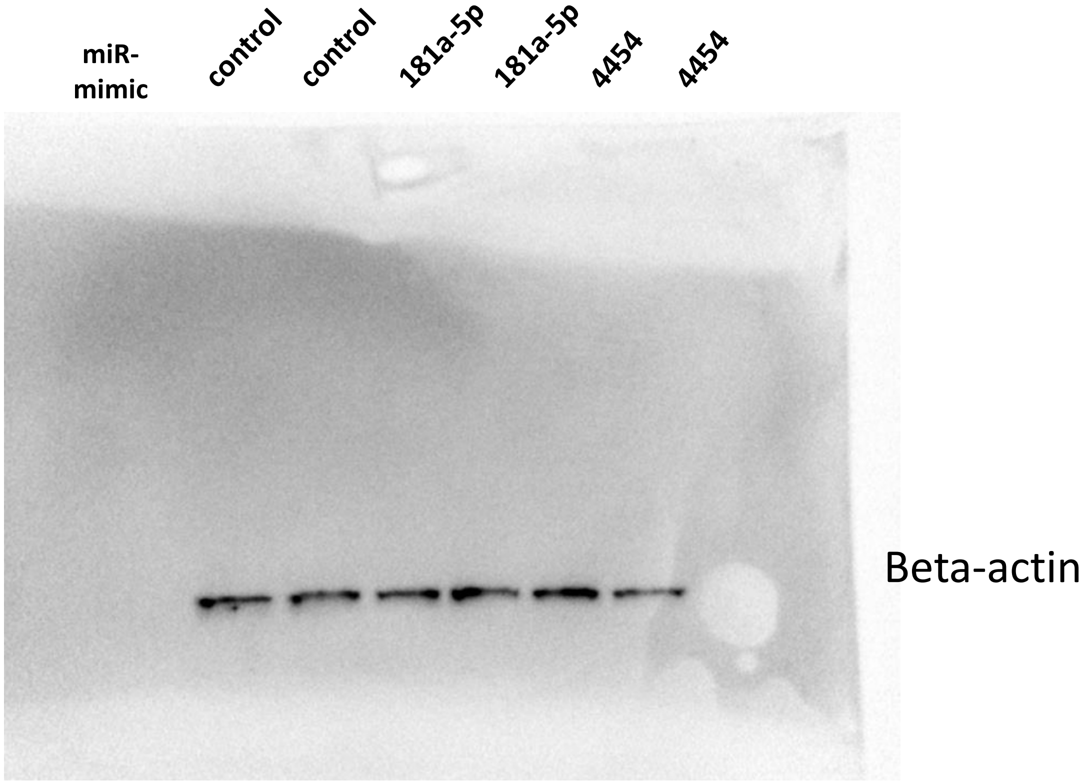
Full unedited gel for Figure 4F P65 Blot



Full unedited gel for Figure 4F IκB Blot

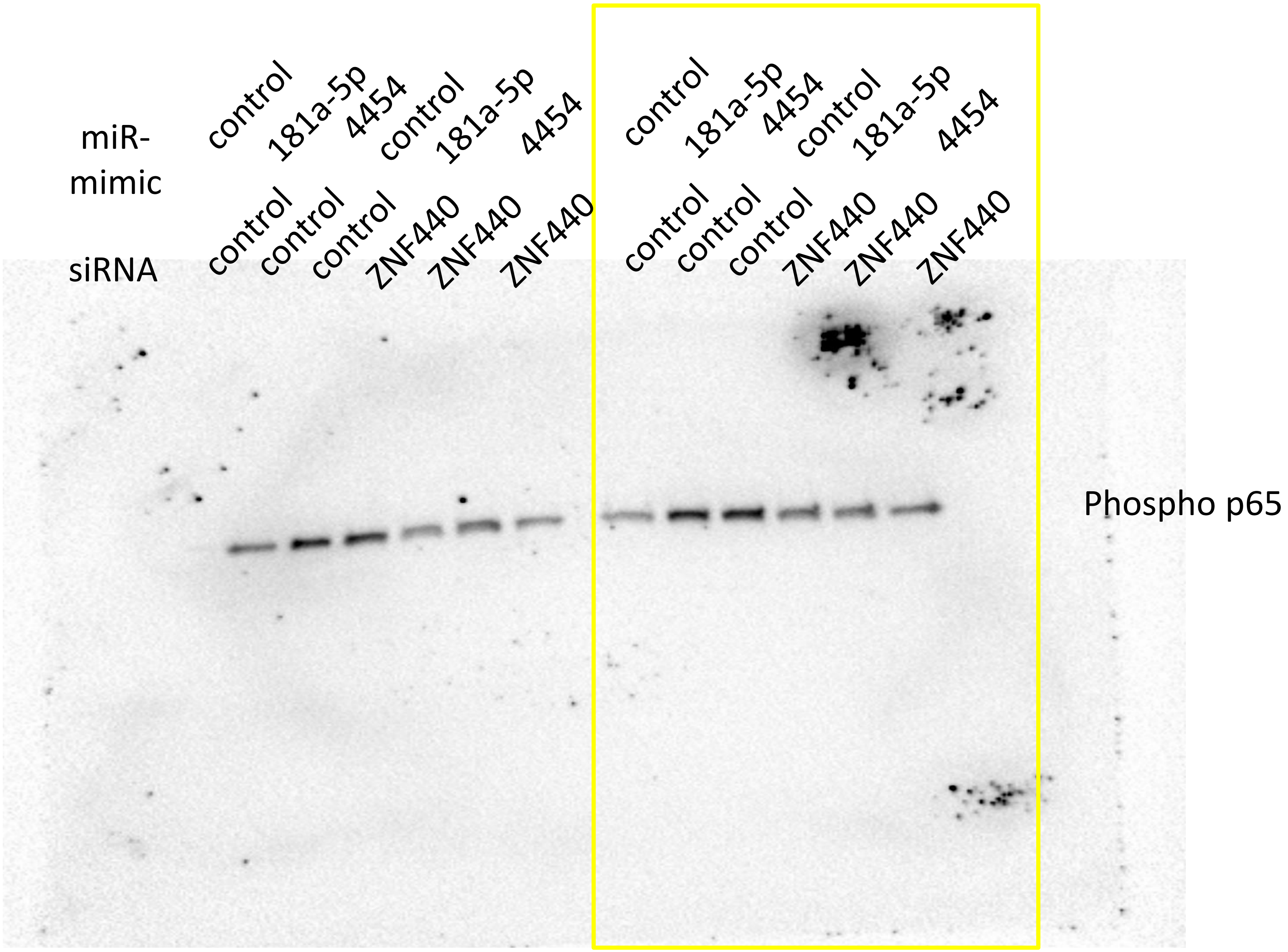


Full unedited gel for Figure 4F Beta-actin Blot



Full unedited gel for Figure 4G

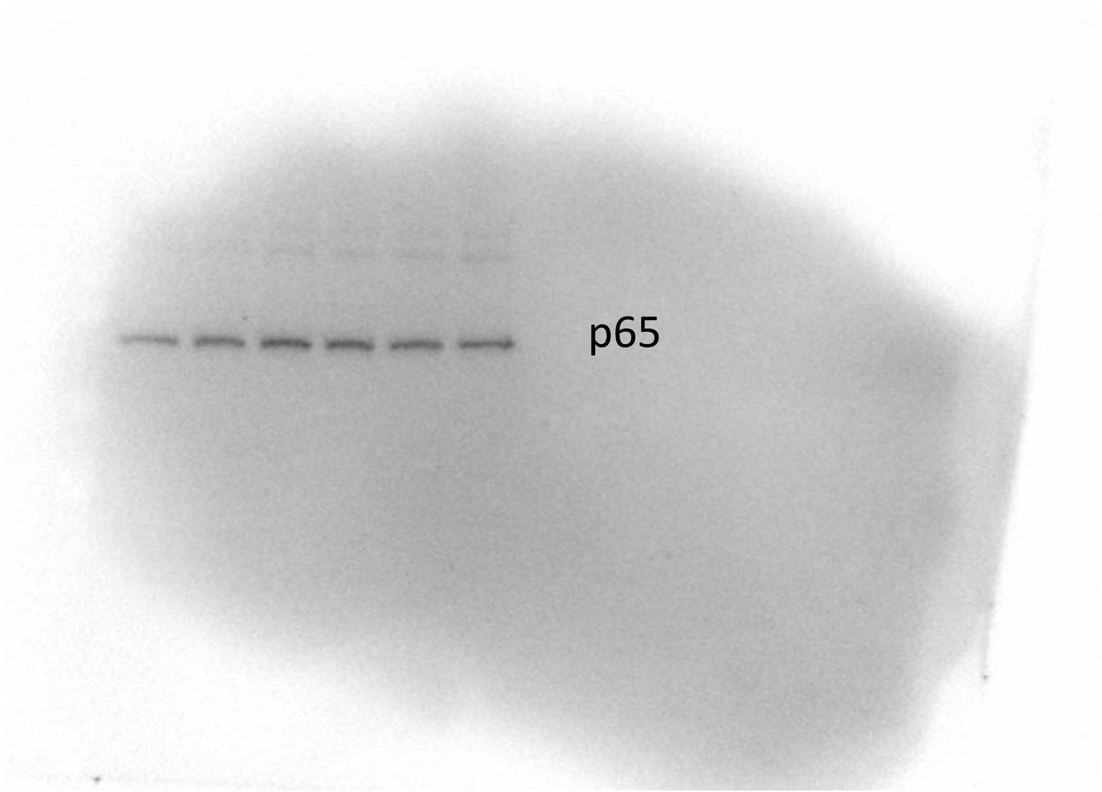
Phospho-p65 Blot



Full unedited gel for Figure 4G

p65 Blot

miR-mimic	control	181a-5p	4454	control	181a-5p	4454
siRNA	control	control	control	ZNF440	ZNF440	ZNF440



Full unedited gel for Figure 4G

b-actin Blot

miR-mimic	control	181a-5p	4454	control	181a-5p	4454
siRNA	control	control	control	ZNF440	ZNF440	ZNF440