Supplemental Materials and Methods

Cell Lines and Treatments

The P493-6 cell line was maintained in RPMI supplemented with 10% fetal bovine serum and antibiotics at 37C and 5% CO_2. HBL-1, TMD8, U2932, SUDHL4, Pfeiffer, and Karpas 422 cell lines were maintained in RPMI supplemented with 10% fetal bovine serum, 2mM L-glutamine, and antibiotics at 37C and 5% CO_2. OCI-LY10 and OCI-LY1 cell lines were maintained in IMDM supplemented with 20% fetal bovine serum, 2mM L-glutamine, 50μM β-ME and antibiotics at 37C and 5% CO_2. P493-6 cells were treated with 1μM doxycycline for 48 hours to repress transgenic Myc. SMARTpool siRNAs, miRNA mimics, and miRNA hairpin inhibitors (Dharmacon) were transfected by electroporation using the AMAXA system and Reagent V (Lonza). Cells were harvested for western blotting and RNA isolation or treated with α-IgM 48 hours after electroporation as described in the text. All siRNA, miRNA mimic, and miRNA hairpin inhibitor treatments (alone or in combination with BCR ligation) were performed at least three times. DLD1 Dicer hypomorph cells were maintained in McCoy's supplemented with 10% fetal bovine serum and antibiotics at 37C and 5% CO_2. miRNAs (20 nM) and psi-CHECK2 plasmid constructs were transfected using Lipofectamine 2000 (Invitrogen).

Cytosolic Calcium Measurements

P439-6 cells were loaded with the calcium indicator fura-2 AM (3 μM; Invitrogen) for 20 min at room temperature and then were allowed to adhere to Poly-L-lysine coated coverglass (#1.5, Fisher Scientific) for 5 min. Residual dye and non-adherant cells were removed by perfusing the imaging chamber with extracellular bath solution (155 mM NaCl, 4.5 mM KCl, 2 mM CaCl2, 1 mM MgCl2, 5 mM glucose, 10 mM HEPES, pH 7.4). Ca^{2+} measurements were performed using a Leica DMI 6000 fluorescence microscope equipped with a Hamamatsu Orca ER camera and controlled with Leica Application Suite software. The fluorescence emission ratio at 510 nm was recorded following excitation at 340 and 380 nm with a monochromator (TILL photonics). Intracellular Ca2+ images were captured every 2 seconds and are represented as the Fura-2 fluorescence emission ratio. After 100 s of baseline recording (40-60 individual cells per experiment) were stimulated by addition of anti-IgM antibody (final concentration = 5 μg/ml) to imaging chamber. Mean Fura-2 ratio values were plotted (Origin Lab, Microcal). Pseudocolor

ratio images at resting and peak cytosolic Ca^{2+} concentrations shown are representative of three individual experiments. Statistical analysis (**p < 0.01, *p < 0.05, n.s.= not significant) of the mean ratio (± S.E.M. n=3) was calculated at each time point with student t-test.

Western blotting and Antibodies

Western blotting was performed as previously described [31]. Signals were detected by either ECL (Pierce) or Odyssey Infrared Imager (LI-COR Biosciences). Representative blots are shown. Antibody information is described in the table.

Antibody	Dilution	System	Company	Catalog #
c-Myc	1:500	ECL	Calbiochem	OP10
actin	1:50,000	ECL/Odyssey	Sigma	A3854
phosho-BLNK	1:1000	Odyssey	Santa Cruz	sc-28517
total-BLNK	1:1000	Odyssey	Santa Cruz	sc-8003
GAPDH	1:20,000	ECL/Odyssey	Abcam	ab9484
FCRL4	1:1000	Odyssey	R&D Systems	AF2426
FCGR2B	1:1000	Odyssey	Santa Cruz	sc-12815
CD22	1:1000	Odyssey	Santa Cruz	sc-7932
CD72	1:1000	Odyssey	Santa Cruz	sc-1707
Pten	1:1000	Odyssey	Santa Cruz	sc-7974
phospho-SYK	1:1000	ECL	Cell Signaling	#2710
total-SYK	1:1000	Odyssey	Cell Signaling	#2712
phospho-ERK	1:1000	Odyssey	Cell Signaling	#9101
total-ERK	1:1000	Odyssey	Cell Signaling	#9102
phospho-Akt	1:1000	Odyssey	Cell Signaling	#4060
total-Akt	1:1000	Odyssey	Cell Signaling	#2920
phospho-GSK3-beta	1:1000	Odyssey	Cell Signaling	#9323
total-GSK3-beta	1:1000	Odyssey	Cell Signaling	#9315
phospho-PLCgamma2	1:1000	Odyssey	Cell Signaling	#3871
total-PLCgamma2	1:1000	Odyssey	Cell Signaling	#3872
phospho-c-Myc	1:1000	ECL	Abcam	ab79318
goat anti-mouse-HRP	1:5000	ECL	GE Healthcare	NA931V
goat anti-rabbit-HRP	1:5000	ECL	GE Healthcare	NA934V
goat anti-mouse-680	1:10,000	Odyssey	Licor	926-32220
goat anti-mouse-800	1:10,000	Odyssey	Licor	926-32210
goat anti-rabbit-680	1:10,000	Odyssey	Licor	827-11081
goat anti-rabbit-800	1:10,000	Odyssey	Licor	926-32211
donkey anti-goat-680	1:10,000	Odyssey	Licor	926-32224
donkey anti-goat-800	1:10,000	Odyssey	Licor	926-32214

Antibody Table: Table listing the antibodies used in this study. Antibody dilution, detection method, source, and catalog number are shown.

qPCR

Total RNA was isolated using TRIzol reagent (Invitrogen). For miRNAs, RT and qPCR was performed using Taqman miRNA assays and Taqman Gene Expression Master Mix (Invitrogen and Life Technologies). miRNA expression was analyzed normalized to that of RNU6B. For mRNAs, cDNAs were prepared with random hexamers using High Capacity cDNA RT kit (Life Technologies). qPCR was performed using PowerSYBR Green PCR Master Mix (Life Technologies). mRNA qPCR oligo sequences are listed in the table below. qPCR reactions were performed on an Applied Biosystems Viia7 machine and analyzed with Viia7 RUO software (Life Technologies).

Gene	Strand	Sequence (5`-3`)
FCRL4	FWD	CAGAGATGGCGAGGTCATCC
	REV	ACCCCTCACTGTTTCAGCAC
FCRGR2B	FWD	ATTCCCACCCACACGCAGCC
	REV	TGGCACGTGTACTCCCCGCT
CD22	FWD	CATCTCCTCGGCCCCTGGCT
	REV	ATCCAGACGCAGGCCCCCTC
CD72	FWD	CGGTCAAGTCGGAGCAGCCA
	REV	GGCCGAGCAGGAGGTATCGC

qPCR Primers: Sequences of oligos used for qPCR in this study.

Luciferase Assay Constructs

Construct	Strand	Sequence (5`-3`)
FCRL4 WT	top	TCGAGCTGTGTCTTTGAGTTACTAATTAGTTTATATGAGAATAATTCTTGCAATAA ATGAAGAAGGAATAAAAGAAATAGGAAGCCACAAATTTGTATGC
	bottom	GGCCGCATACAAATTTGTGGCTTCCTATTTCTTTTATTCCTTCTTCATTTATTGCAA GAATTATTCTCATATAAACTAATTAGTAACTCAAAGACACAGC
FCRL4 mut	top	TCGAGCTGTGTCTTTGAGTTACTAATTAGTTTATATGAGAATAATTCTTATGGCA AATGAAGAAGGAATAAAAGAAATAGGAAGCCACAAATTTGTATGC
	bottom	GGCCGCATACAAATTTGTGGCTTCCTATTTCTTTTATTCCTTCTTCATTTGCCATAA GAATTATTCTCATATAAACTAATTAGTAACTCAAAGACACAGC
FCRGR2B WT	top	TCGAGCCTGAAAGCCACAGACAATATGGTCCCAAATAACCGACTGCACCTTCTGT GCTTCAGCTCTTCTTGACATCAAGGCTCTTCCGTTCCACATCCGC
	bottom	GGCCGCGGATGTGGAACGGAAGAGCCTTGATGTCAAGAAGAGCTGAAGCACA GAAGGTGCAGTCGGTTATTTGGGACCATATTGTCTGTGGCTTTCAGGC
FCRGR2B mut	top	TCGAGCCTGAAAGCCACAGACAATATGGTCCCAAATAACCGACTGCGATCTCTG TGCTTCAGCTCTTCTTGACATCAAGGCTCTTCCGTTCCACATCCGC
	bottom	GGCCGCGGATGTGGAACGGAAGAGCCTTGATGTCAAGAAGAGCTGAAGCACA GAGATCGCAGTCGGTTATTTGGGACCATATTGTCTGTGGCTTTCAGGC
CD22 WT	top	TCGAGGAGACCTCCCCCGGACTGCGATGACACGGTCACTTATTCAGCATTGCAC AAGCGCCAAGTGGGCGACTATGAGAACGTCATTCCAGATTTTCCGC
	bottom	GGCCGCGGAAAATCTGGAATGACGTTCTCATAGTCGCCCACTTGGCGCTTGTGC AATGCTGAATAAGTGACCGTGTCATCGCAGTCCGGGGGAGGTCTCC
CD22 mut	top	TCGAGGAGACCTCCCCCGGACTGCGATGACACGGTCACTTATTCAGCATCATGT AAGCGCCAAGTGGGCGACTATGAGAACGTCATTCCAGATTTTCCGC
	bottom	GGCCGCGGAAAATCTGGAATGACGTTCTCATAGTCGCCCACTTGGCGCTTACAT GATGCTGAATAAGTGACCGTGTCATCGCAGTCCGGGGGAGGTCTCC

3`UTR Sequences used in Luciferase Sensor Assays: 100bp oligos (top/bottom) were annealed and ligated into the psi-CHECK2 vector prior to luciferase sensor assays.

Supplemental Table Legends

Table S1: List of miRNAs whose seed sequences are significantly enriched for in Myc repressed genes. SigTerms analysis for Myc repressed genes performed as described in Figure 1B. miRNA family, Count in Selected Genes (Myc repressed), Count in Total Population (all genes), and p-value (for significance of enrichment) are shown. A p-value <0.05 was considered significant. Highlighted in gray are miR-17~92 cluster family members.

Table S2: List of BCR signaling pathway genes in the GSEA Core Enrichment from the analysis described in Figure 1E. The rank in gene list, rank metric score, running enrichment score, and whether the gene was part of the core enrichment are listed for each gene.

Table S1

miRNA	Count in Selected Genes	Count in Total Population	P-value
miR-17-5p/20/93.mr/106/519.d	257	861	4.57757E-13
miR-19	233	803	1.22339E-10
miR-130/301	181	635	6.09481E-08
miR-101	152	527	3.19812E-07
miR-106/302	152	530	4.64903E-07
miR-29abc	201	739	5.00558E-07
miR-144	158	570	2.57328E-06
miR-30a/30a-5p/30b/30b-5p/30cde/384-5p	240	934	4.64204E-06
miR-24	113	392	1.0339E-05
miR-124/506	290	1172	1.27895E-05
miR-25/32/92/92ab/363/367	161	607	2.98719E-05
miR-200bc/420	182	702	3.83135E-05
miR-129/129-5p	89	304	4.63514E-05
miR-125/351	144	538	4.81392E-05
miR-181	198	779	6.23717E-05
miR-199/199-5p	96	336	6.69199E-05
miR-448	118	431	8.1477E-05
miR-145	125	466	0.000133324
miR-27ab	199	796	0.000161799
let-7/98	183	726	0.000186473
miR-1/206	136	521	0.000255384
miR-142-3p	68	233	0.000377847
miR-205	73	254	0.000388636
miR-128	169	673	0.000391783
miR-204/211	107	399	0.000394271
miR-153	120	462	0.000698202
miR-410	98	370	0.001049154
miR-377	82	310	0.002656373
miR-26ab/1297	138	561	0.002920415
miR-543	107	422	0.003043551
miR-202/202-3p	129	522	0.003304671
miR-335/335-5p	41	138	0.00352046
miR-326/330/330-5p	66	244	0.003736146
miR-134	28	88	0.005191281
miR-23ab	170	721	0.00656575
miR-299/299-3p	17	47	0.006694901
miR-137	171	726	0.00669797
miR-495/1192	121	501	0.009297715
miR-103/107	102	415	0.009677737
miR-10	45	163	0.010078127
miR-139-5p	58	220	0.010927588
miR-221/222	67	260	0.011328075
miR-18ab	46	169	0.012195112
miR-122	33	114	0.012367098
miR-22	73	288	0.012668242
miR-21/590-5p	49	183	0.0136047
miR-186	106	441	0.016173455
miR-182	170	740	0.017466684
miR-149	60	235	0.019089883
miR-214/761	89	367	0.020722141
miR-431	23	77	0.023007859
miR-148/152	112	475	0.023620136
miR-329/362-3p	47	180	0.023915642
miR-140/140-5p/876-3p	55	216	0.025176433
miR-340/340-5p	185	819	0.025324998
miR-133	105	444	0.025624931
miR-219/219-5p	58	230	0.026461986
miR-143	58	230	0.026461986
miR-411	18	58	0.028515933
miR-491/491-5p	24	83	0.030049037
miR-146	29	105	0.033471896
miR-135	105	453	0.042140828
miR-324-5p	21	73	0.042682824
miR-138	81	342	0.043642956
miR-96/1271	155	690	0.044547608
miR-320/320abcd	106	460	0.04749761
miR-132/212	60	247	0.048198374
miR-496	21	74	0.048826871
miR-374/374ab	90	386	0.049565791
miR-758	33	126	0.049587005

Table S2

GENE SYMBOL	GENE_TITLE	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	82	1.497612	0.0358117	Yes
CD72	CD72 molecule	316	1.217139	0.0517105	Yes
CD79B	CD79b molecule, immunoglobulin-associated beta	365	1.181588	0.0812907	Yes
CD22	CD22 molecule	458	1.130725	0.1059406	Yes
RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	469	1.123899	0.1369072	Yes
INPP5D	inositol polyphosphate-5-phosphatase, 145kDa	478	1.116441	0.1678217	Yes
PTPN6	protein tyrosine phosphatase, non-receptor type 6	483	1.110545	0.1988872	Yes
LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	504	1.102927	0.2284672	Yes
NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	583	1.064506	0.2523573	Yes
SYK	spleen tyrosine kinase	606	1.0516	0.2803281	Yes
PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	675	1.021646	0.3038008	Yes
MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	682	1.019721	0.3321409	Yes
IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	684	1.019494	0.3608715	Yes
CD19	CD19 molecule	980	0.907527	0.3630991	Yes
VAV2	vav 2 oncogene	1030	0.889369	0.3843421	Yes
CD79A	CD79a molecule, immunoglobulin-associated alpha	1079	0.874241	0.4052369	Yes
CD81	CD81 molecule	1119	0.860496	0.4264578	Yes
PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	1183	0.842902	0.4452763	Yes
PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5, p101	1239	0.825645	0.4642422	Yes
NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	1355	0.789222	0.4774157	Yes
NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	1453	0.763531	0.4912922	Yes
AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	1463	0.761216	0.512089	Yes
NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	1547	0.740658	0.5264305	Yes
VAV1	vav 1 oncogene	1657	0.712369	0.5379085	Yes
PRKCB1	protein kinase C, beta 1	1682	0.70515	0.5559302	Yes
GSK3B	glycogen synthase kinase 3 beta	1785	0.679978	0.5670486	Yes
NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	1995	0.630941	0.5682872	Yes
PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)	2221	0.577061	0.566733	Yes
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	2291	0.559542	0.5770677	Yes
IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	2333	0.551841	0.5894075	Yes
NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	2345	0.548847	0.6040442	Yes
PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	2725	0.480303	0.5875306	No
IFITM1	interferon induced transmembrane protein 1 (9-27)	2782	0.470827	0.5963903	No
NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	2965	0.438817	0.594343	No
BLNK	B-cell linker	3119	0.41018	0.5937885	No
NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	3509	0.341426	0.5725566	No
VAV3	vav 3 oncogene	4166	0.247813	0.5274836	No
FCGR2B	Fc fragment of IgG, low affinity IIb, receptor (CD32)	4320	0.223402	0.521651	No
FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	4422	0.210078	0.5195699	No
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	4512	0.196047	0.5180448	No
BTK	Bruton agammaglobulinemia tyrosine kinase	5425	0.070241	0.4476316	No
NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	5545	0.054297	0.4397193	No
CARD11	caspase recruitment domain family, member 11	6312	-0.04503	0.3801836	No
AKT2	v-akt murine thymoma viral oncogene homolog 2	6651	-0.08759	0.355827	No
NFKBIB	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	8316	-0.30724	0.2324145	No
PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide	9113	-0.41921	0.1810712	No
PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)	9495	-0.47929	0.1643702	No
RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	10371	-0.66127	0.1135961	No
PPP3R1	protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, alpha isoform	10737	-0.75501	0.1059569	No
KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	10753	-0.76036	0.1262532	No
HRAS	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	11079	-0.85002	0.1244743	No

Supplemental Figure Legends

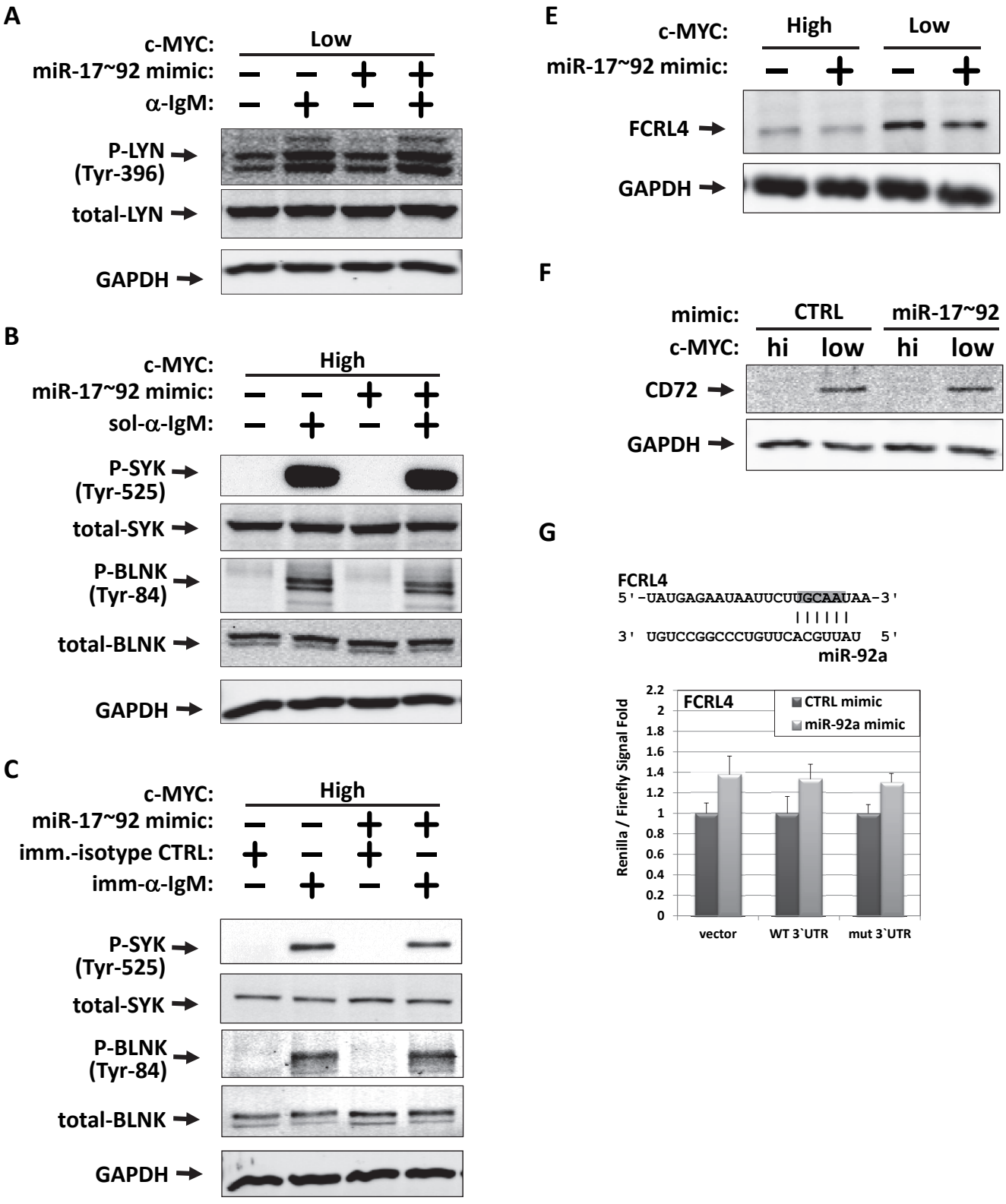
Figure S1. A. P493-6 cells were grown and treated with control mimic or miR-17~92 mimic mix for 48 hours prior to treatment with immobilized anti-IgM for 6 hours. Western blotting was performed for P-LYN, total-LYN, and GAPDH. **B-C**, Western blotting was performed for P-SYK, total-SYK, P-BLNK, total-BLNK, and GAPDH. **B.** P493-6 cells were grown and treated with control mimic or miR-17~92 mimic mix for 48 hours prior to addition of 10 μg/mL soluble anti-IgM for 15 minutes. **C.** P493-6 cells were grown and treated with control mimic or miR-17~92 mimic mix for 48 hours prior to treatment with immobilized anti-IgM (imm-α-IgM) or immobilized isotype control (imm-isotype-CTRL) for 6 hours. **D-E.** P493-6 cells grown in the absence (Myc^{HIGH}) or presence (Myc^{LOW}) of 1 μM doxycycline were treated with control mimic or miR-17~92 mimic mix for 48 hours. Changes in CD72 **(D)** and FCRL4 **(E)** protein levels were examined by Western blotting. GAPDH was utilized as a loading control. **F.** Dual luciferase assays performed in HCT-116 Dicer hypomorph cells cotransfected with FCRL4 3`UTR luciferase sensors and either control or miRNA mimics. Schematic of predicted 3`UTR-miRNA interactions are depicted (top panel). Shaded nucleotides indicate regions mutated to disrupt the mRNA-miRNA interaction in the mut 3`UTR constructs. Changes in luciferase activity upon treatment with miRNA mimics are plotted (bottom panel). Values were normalized to luciferase activity from control mimic transfected cells. Error bars represent standard deviation of 3 independent experiments.

Figure S2. A. P493-6 cells were treated, or not, with 1 μM doxycycline for 48 hours prior to addition of 10 μg/mL soluble anti-IgM for 2 minutes. Western blotting was performed for P-PLCγ2 , total-PLCγ2 , and actin. Bands were quantified and the ratio of P-PLCγ2/total-PLCγ2 is shown. **B.** P493-6 cells were left untreated, or treated with 1 μM doxycycline for 24 hours or 48 hours prior to addition of anti-IgM. Cytosolic Ca2+ levels in P493-6 cells were monitored by fluorescence microscopy using the ratiometric Ca2+ indicator dye Fura-2. Mean trace of three independent experiments are plotted (top); n.s.= not significant. **C-D**. Independent triplicate cytosolic Ca^{2+} measurements following BCR crosslinking by anti-IgM. Cytosolic Ca^{2+} levels in P493-6 cells were monitored by fluorescence microscopy using the ratiometric Ca^{2+} indicator dye Fura-2. **C.** P493-6 cells were grown in the presence (MYC^{LOW}) of 1 μM doxycycline and treated with control mimic or miR-17~92 mimic mix for 48 hours prior to addition of anti-IgM.

D. P493-6 cells (MYC^{HIGH}) were treated with control short hairpin inhibitor or miR-17~92 short hairpin inhibitor mix for 48 hours prior to addition of anti-IgM. **E.** P493-6 cells were grown in the absence (Myc^{HIGH}) or presence (Myc^{LOW}) of 1 μM doxycycline and treated with control mimic or miR-17~92 mimic mix for 48 hours prior to treatment with immobilized anti-IgM (imm-α-IgM) or immobilized isotype control (imm-isotype-CTRL) for 6 hours. Western blotting was performed for P-ERK, total-ERK, Myc, and GAPDH.

Figure S3. A. DLBCL cell line subtype by COO and CCC classifications. For **B-D.** The HBL-1, TMD8, U2932, OCI-LY10, OCI-LY1, SUDHL4, Pfeiffer, Karpas 422, and P493-6 cell lines were grown and harvested for protein extract and RNA isolation. **B**. Western blotting was performed for Myc, P-Myc Ser62, and actin. **C**. qPCR was performed for the *mir17hg* primary transcript and miR-17~92 mature microRNAs. U1 and RNU6B RNAs (respectively) were used as loading controls. Levels are relative to the P493-6 cell line. **D.** Western blotting was performed for SYK, BLNK, and actin. **E.** Normalized levels of mir17hg were plotted versus the average mature miR-17~92 abundance for DLBCL tumors. Linear regression was performed and the R value and Pearson correlation p-value are shown.

Figure S1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α-IgM:
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GAPDH
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miR-17~92 mimic:
sol-α-IgM:
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total-SYK
P-BLNK (Tyr-84)
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GAPDH
C
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miR-17~92 mimic:
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E
c-MYC:
High
Low
miR-17~92 mimic:
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miR-17~92
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hi
low
hi
low
CD72
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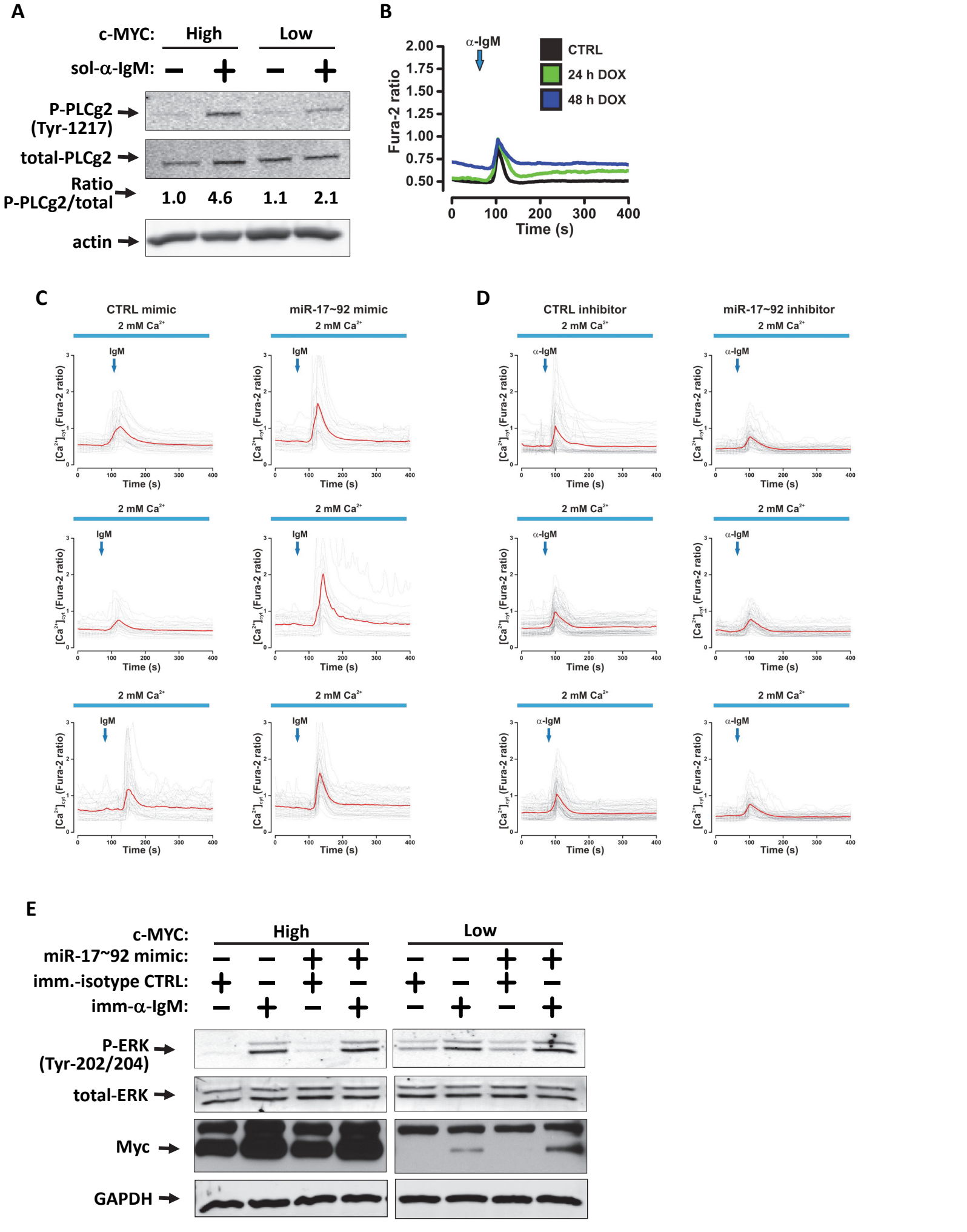
vector
WT 3`UTR
mut 3`UTR

Figure S2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High
Low
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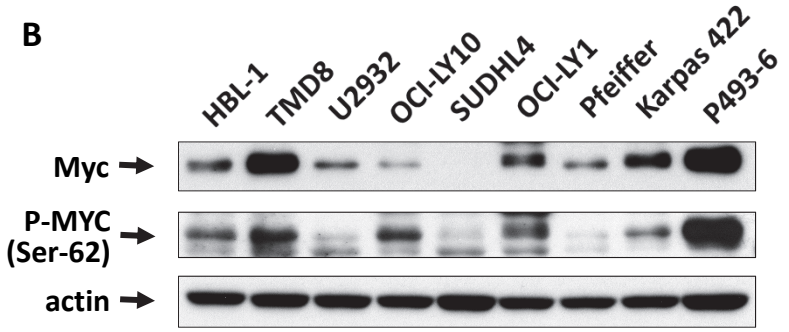
4.6
1.1
2.1
actin
B
α-IgM
CTRL
24 h DOX
48 h DOX
Fura-2 ratio
Time (s)
C
CTRL mimic
miR-17~92 mimic
D
CTRL inhibitor
miR-17~92 inhibitor
2 mM Ca2+
IgM
α-IgM
[Ca2+]cyt (Fura-2 ratio)
Time (s)
E
c-MYC:
High
Low
miR-17~92 mimic:
imm.-isotype CTRL:
imm-α-IgM:
P-ERK (Tyr-202/204)
total-ERK
Myc
GAPDH

Figure S3

A

	COO	CCC
HBL-1	ABC-DLBCL	BCR
TMD8	ABC-DLBCL	BCR
U2932	ABC-DLBCL	BCR
OCI-LY10	ABC-DLBCL	BCR
SUDHL4	GCB-DLBCL	BCR
OCI-LY1	GCB-DLBCL	BCR
Pfeiffer	GCB-DLBCL	OxPhos
Karpas 422	GCB-DLBCL	OxPhos

B



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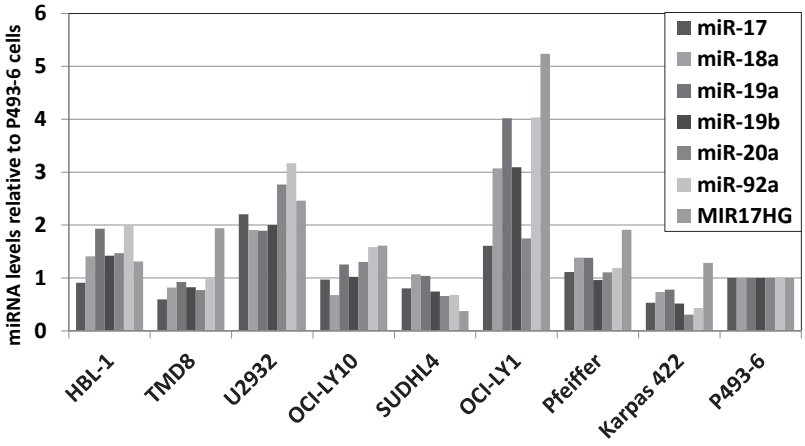
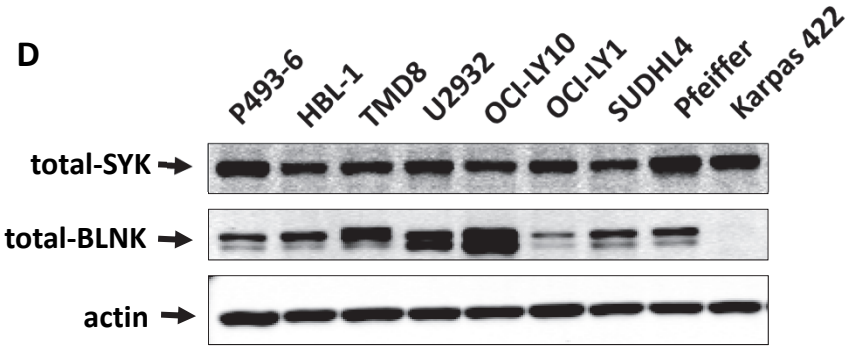


D



E