SUPPLEMENTARY TABLES

Supplementary Table 1. Paired treatment naïve LN and PB CLL samples: patient characteristics.

		Number	%
Median age (years)		56 (33-73)	
Gender			
	Male	10	59
	Female	7	41
Rai Stage			
	I	5	29.5
	II	4	23.5
	III	4	23.5
	IV	4	23.5
IGHV mutation			
	Un-mutated	10	59
	Mutated	4	23.5
ZAP70			
	+	9	53
	-	7	41
CD38			
	+	9	53
	-	8	47
17p deletion			
	Deleted	5	29.5
	Non deleted	12	70.5

Supplementary Table 2. Clinical and laboratory parameters of CLL patients treated with ibrutinib.

		Number	%
Median age (years)		66 (33 - 85)	
Gender			
	Male	22	55
	Female	18	45
Median absolute lymphocytic count ALC (x10^9/L)			
	ALC pre-treatment (min. - max.)	75.6 (0.5 - 402)	
	ALC 28 days post-treatment (min. - max.)	87 (2.6 - 475.3)	
Rai Stage			
	I	8	20
	II	3	7.5
	III	5	12.5
	IV	24	60
IGHV mutation			
	Unmutated	23	57.5
	Mutated	17	42.5
ZAP70			
	+	12	30
	-	15	37.5
CD38			
	+	15	37.5
	-	25	62.5
17p deletion			
	Deleted	23	57.5
	Non deleted	17	42.5
Nodal response to ibrutinib			
	Responders	25	62.5
	Non-responders	13	32.5

Supplementary Table 3. RT and PCR primers.

Primer	Sequence
let-7a_F	5'- GGG CCT GAG GTA GTA GGT TGT ATA GTT -3'
let-7a-3p_F	5'- GGG GCC CCT ATA CAA TCT ACT GTC TTT C -3'
let-7g_F	5'- GGC CGT GAG GTA GTA GTT TGT ACA GTT -3'
miR-9_F	5'- GGG CCT CTT TGG TTA TCT AGC TGT ATG A -3'
miR-15a_F	5'- GTG CCT AGC AGC ACA TAA TGG TTT GTG -3'
miR-16_F	5'- GTG CCT AGC AGC ACG TAA ATA TTG GCG -3'
miR-17_F	5'- GGC AAA GTG CTT ACA GTG CAG GTA G -3'
miR-20a_F	5'- GGG CCT AAA GTG CTT ATA GTG CAG GTA G -3'
miR-21_F	5'- GGG CCC TAG CTT ATC AGA CTG ATG TTG A -3'
miR-22_F	5'- GGC AGT TCT TCAGTGGCAAGC TTT A-3'
miR-29a_F	5'- CCC GGA CTG ATT TCT TTT GGT GTT CAG -3'
miR-29c-3p_F	5'- GGC CTA GCA CCA TTT GAA ATC GGT TA -3'
miR-29c_F	5'- GGT GAC CGA TTT CTC CTG GTG TTC -3'
miR-34a_F	5'- GGT GGC AGT GTC TTA GCT GGT TGT -3'
miR-106b_F	5'- GTG CCT AAA GTG CTG ACA GTG CAG AT -3'
miR-146b-F	5'- GGC CTGAGAACTGAATTCCATAGGCT-3'
miR-150_F	5'- GTC TCC CAA CCC TTG TAC CAG TG -3'
miR-155_F	5'- GGG CCT TAA TGC TAA TCG TGA TAG GGG T -3'
miR-181b_F	5'- TGA CGA ACA TTC ATT GCT GTC GG -3'
miR-185_F	5'- GCT GGA GAG AAA GGC AGT TCC TGA -3'
miR-223_F	5'- GTG CCC GTG TAT TTG ACA AGC TGA GTT -3'
miR-650_F	5'- AGG AGG CAG CGC TCT CAG GAC -3'
RNU44_F	5' - GGC AAA TGC TGA CTG AAC ATG AAG GTC - 3'
Reverse transcription anchor primer	5’- CGA CTC GAT CCA GTC TCA GGG TCC GAG GTA TTC GAT CCT AAC CCT CTC CTC GGT ATC GAG TCG CAC TTT TTT TTT TTT V - 3’
PCR reverse primer	5' - GTC CGA GGT ATT CGA TCC TAA C - 3'
TaqMan probe	5' - 6-FAM/ TCT CCT CGG /ZEN/ TAT CGA GTC GCA CT /IABKFQ/ - 3'

Supplementary Table 4: Gene list of the nanoString nCounter assay.

AKT1
ARID1A
ARID1B
ARID2
ASXL1
ATM
BAX
CDKN1A
CYLD
DAPK1
DNMT3A
E2F1
FBXW7
FOXP1
GPS2
HDAC1
IBTK
IDH1
IKBKB
KLF4
LDOC1
MAP2K1
MRE11A
NFKBIA
NOTCH1
PDCD1
PHLPP
PTEN
RARRES3
RB1
RUNX1
RUNX3
SAMHD1
SF3B1
SIRT1
SMAD4
SOCS1
TCF21
TET2
TNFAIP3
TP53
WT1
XPO1
GUSB
HPRT1
TBP

Supplementary Table 5. Differential miRNA expression in circulating CLL cells from 38 patients compared to circulating B cells from 33 healthy controls.

miRNA	Median (IQR) in CTRL	Median (IQR) in CLL	Fold	*P* value	Trend in CLL
Let-7a	129.6 (77.8-237)	767.6 (397-1080)	6	< 0.0001	Up
Let7a-3p	0.1 (0.04-0.2)	0.76 (0.3-2.4)	7	< 0.0001	Up
Let-7g	29.8 (18.8-50.7)	185.6 (60-342)	6	< 0.0001	Up
miR-9	0.02 (0.01-0.1)	0.13 (0.02-0.9)	6.5	0.002	Up
miR-15a	39.4 (13.7-196)	869.7 (146.6-8131)	22	< 0.0001	Up
miR-16	66 (33.6-195.7)	1303 (453.7-2239)	19	< 0.0001	Up
miR-17	0.6 (0.3-2)	6 (1.8-12.5)	10	< 0.0001	Up
miR-20a	2.2 (1.2-8)	15.5 (5.8-34.3)	8	< 0.0001	Up
miR-21	15.05 (6.8-30.2)	505.2 (202-655)	32	< 0.0001	Up
miR-22	0.02 (0.02-0.06)	0.2 (0.02-0.4)	15	0.0009	Up
miR-29a	0.1 (0.02-0.5)	1.6 (0.4-3.7)	16	< 0.0001	Up
miR-29c-3p	45.6 (26-83.5)	681 (313-1126)	15	< 0.0001	Up
miR-29c	0.1 (0.06-0.3)	0.8 (0.3-1.4)	8	< 0.0001	Up
miR-34a	0.5 (0.1-1.02)	43.7 (12.4-174)	87	< 0.0001	Up
miR-106b	1.3 (0.3-5.4)	9 (1.8-39)	7	0.0007	Up
miR-146b	14.4 (4.8-44.7)	127.4 (23-586.3)	9	< 0.0001	Up
miR-150	6.9 (3.9-21)	192 (30.6-336)	30	< 0.0001	Up
miR-155	10.6 (3.5-23.8)	307.4 (153.6-698)	29	< 0.0001	Up
miR-181b	0.66 (0.5-1.1)	0.24 (0.07-0.85)	-2.5	0.01	Down

miR-185	0.7 (0.2-1.5)	2.4 (1-3.7)	3	< 0.0001	Up
miR-223	0.03 (0.01-0.16)	0.17 (0.07-0.4)	5	0.0017	Up
miR-650	0.001 (0.0005-0.01)	0.085 (0.008-0.3)	85	< 0.0001	Up

Twenty-two miRNAs were assayed by TaqMan qPCR and with standard curves in PB CLL cells and circulating B-cells from healthy controls. The median and interquartile ranges of the miRNA quantity (fmoles/ng of total RNA) are shown. CTRL, healthy control; IQR, interquartile range. *P* values calculated by Student's T-test.

Supplementary Table 6. Differential miRNA expression in PB CLL cells from 38 patients pre- and post-treatment (day 28) with ibrutinib.

miRNA	Median in CLL patient samples pre-ibrutinib treatment (IQR) fmoles/ng total RNA	Median in CLL patient samples post-ibrutinib treatment (IQR) fmoles/ng total RNA	Fold change	*p*-value Wilcoxon	Trend
Let7a	805.2 (421-1079.7)	782 (446.5-1090)	1	0.9	-
Let7a-3p	0.78 (0.36-2.4)	0.6 (0.3-2.4)	-1.3	0.25	-
Let7g	204.7 (76-342)	156.3 (94-321.2)	-1.3	0.5	-
miR-9	0.15 (0.04-0.9)	0.06 (0.01-0.3)	-2.5	0.2	-
miR-15a	1079 (281-8131)	550.4 (152.5-3033)	-2	0.08	-
miR-16	1315 (501.3-2239)	1279.8 (594-2219.3)	1	0.8	-
miR-17	6.4 (2.4-12.5)	5.6 (2.3-12.8)	-1.1	0.9	-
miR-20a	17.2 (7.3-34.3)	19.5 (10-37)	1.1	0.5	-
miR-21	530.9 (240.9-655)	324 (131.7-576)	-1.6	0.3	-
miR-22	0.2 (0.04-0.4)	0.06 (0.02-0.15)	-3.33	0.0008	Down
miR-29a	1.7 (0.7-3.7)	2 (0.6-5.5)	1.17	0.3	-
miR-29c-3p	688.7 (351.5-1126)	817.2 (291.1-1586.5)	1.18	0.59	-
miR-29c	0.8 (0.4-1.4)	0.7 (0.3-1.2)	-1.1	0.78	-
miR-34a	49.3 (14.6-174)	8.9 (3.4-45.3)	-5.56	0.01	Down
miR-106b	13 (2.1-39)	9.2 (3.7-22.2)	-1.4	0.67	-
miR-146b	151.5 (68.3-687.8)	27.6 (7.8-81.2)	-5.56	< 0.0001	Down
miR-150	200.3 (68.3-336)	227.4 (99-495)	1.1	0.45	-
miR-155	343.9 (163.6-698)	239 (122.5-469)	-1.4	0.08	-

miR-181b	0.26 (0.078-0.85)	0.1 (0.02-0.24)	-2.6	0.019	Down
miR-185	2.6 (1.3-3.7)	1.8 (0.9-2.6)	-1.4	0.079	-
miR-223	0.19 (0.1-0.4)	0.15 (0.05-0.3)	-1.3	0.1	-
miR-650	0.1 (0.009-0.3)	0.06 (0.006-0.2)	-1.4	0.9	-

The miRNA level was quantified by TaqMan qPCR and with standard curves. The median and interquartile range of the miRNA quantity (fmoles/ng of total RNA) are shown. Pre-tx, pre-treatment; post-tx, post-treatment; IQR, interquartile range. *P* values calculated by Wilcoxon paired test.

Supplementary Table 7. Differential miRNA expression in PB CLL cells from 38 patients pre- and post-treatment (day 28) with ibrutinib: Responders and Non-Responders.

miRNA	Responders (N=24) Median change in CLL cells post-ibrutinib treatment compared to pre-treatment (IQR) Percent Change	Non-Responders (N=12) Median change in CLL cells post-ibrutinib treatment compared to pre-treatment (IQR) Percent Change	Responders Pre-treatment compared to post-ibrutinib p-value	Non-Responders Pre-treatment compared to post-ibrutinib p-value	Responder Pre-treatment compared to Non-Responder Pre-treatment p-value
Let7a	4.36% (-38.11%-136.23%)	-14.4% (-54.4%-44.43%)	0.65	0.53	0.73
Let7a-3p	-0.18% (-63.17%-67.95%)	-13.3% (-84.8%-71.4%)	0.58	0.27	0.63
Let7g	-34.62% (-60.35% - 149.8%)	0.63% (-43.42%-185.9%)	0.3	0.8	0.89
miR-9	-60.24% (-92.25% -160.5%)	-88.82% (-94.1% - 29.6%)	0.58	0.11	0.48
miR-15a	-57.41% (-92.34%-58.30%)	6.13% (-47.15%-777.0%)	0.08	0.94	0.39
miR-16	10.64% (-60.89%-588.72%)	-30.66% (-59.66%-33.57%)	0.84	0.2	0.65
miR-17	4.29% (-66.41%-209.4%)	-31.75% (-59.16 – 151.5%)	0.88	0.70	0.90
miR-20a	55.89% (-58.59% - 437.4%)	50.77% (-38.64% - 77.88%)	0.66	0.5	0.78
miR-21	-13.11% (-70.92% - 98.68%)	-66.26% (-76.46 – 9.94%)	0.90	0.16	0.54
miR-22	-59.44% (-92.1% - 25.3%)	-39.09% (-92.89% - -4.27%)	**0.02***	**0.015***	0.20
miR-29a	151.1% (-66.67% - 558.2%)	-4.29% (-65.52% - 123.7%)	0.4	0.3	0.95
miR-29c-3p	36.94% (-43.49% -113.29%)	-6.08% (-54.51%-149.11%)	0.22	0.8	0.90
miR-29c	23.30% (-57.91% - 98.1%)	17.5% (-46.23 – 77.1%)	0.95	0.70	0.76
miR-34a	-70.17% (-90.36% - 31.22%)	-71.82% (-93.71% - 11.23%)	**0.007****	0.13	0.88
miR-106b	76.46%	-24.47%	0.50	0.80	0.17

	(-85.90% - 1140.9%)	(-90.03 – 219.6%)			
miR-146b	-87.49% (-925-39 – -58.81%)	-87.8% (-93.65 - -75.1%)	**0.001*** **	**0.02***	0.41
miR-150	85.8% (-56.26% - 379.4%)	2.37% (-40.78% - 165.0%)	0.25	1	0.22
miR-155	-14.10% (-64.37% - 137.15%)	-53.79% (-74.38% - -36.9%)	0.60	**0.028***	0.70
miR-181b	-76.19% (-96.27% - 10.94%)	5.34% (-92.64% - 79.02%)	**0.024***	0.48	0.72
miR-185	-39.68% (-77.86% - 8.39%)	-47.13% (-60.1% - 106.6%)	**0.049***	0.81	0.87
miR-223	-51.1% (-88.00% - 191.4%)	-56.79% (-76-84% - -21.7%)	0.53	0.08	**0.007****
miR-650	-19.15% (-96-77% - 2647.51%)	-4.29% (-65.52% - 123.7%)	0.98	0.9	0.67

The miRNA level was quantified by TaqMan qPCR and with standard curves. The median and interquartile range of the miRNA percentage change from pre-treatment to post-treatment are shown. Pre-tx, pre-treatment; post-tx, post-treatment; IQR, interquartile range. *P* values calculated by Wilcoxon paired test. Significant p-values are bolded and marked with asterisks (* p-value < 0.05 ** p-value < 0.01 *** p-value < 0.001)

Supplementary Table 8. Differential miRNA expression in PB CLL cells from 38 patients pre- and post-treatment (day 28) with ibrutinib: Absolute values of miRNA in CLLs that were found to be significant for comparisons in responders and non-responders.

	Responders			Non-Responders		
miRNA	Median in CLL patient samples pre-ibrutinib treatment (IQR) fmoles/ng total RNA	Median in CLL patient samples post-ibrutinib treatment (IQR) fmoles/ng total RNA	P Value	Median in CLL patient samples pre-ibrutinib treatment (IQR) fmoles/ng total RNA	Median in CLL patient samples post-ibrutinib treatment (IQR) fmoles/ng total RNA	P Value
miR-22	0.119 (0.03 – 0.42)	0.045 (0.013 – 0.15)	0.02	0.282 (0.15 – 0.49)	0.115 (0.018 – 0.18)	0.015
miR-34a	48.64 (13.1 – 175.65)	9.00 (3.70 – 32.75)	0.007	52.17 (22.74 – 92.26)	7.54 (3.41 – 45.32)	0.13
miR-146b	202.65 (45.71 - 725.67)	41.32 (10.95 - 95.78)	0.001	127.41 (80.79 – 203.58)	12.53 (7.32 – 31.1)	0.02
miR-155	265.95 (163.6 – 846.9)	310.79 (152.3 – 496.5)	0.6	402.00 (204.4 – 652.9)	198.93 (97.53 – 445.25)	0.028
miR-181b	0.289 (0.09 – 1.49)	0.09 (0.02 – 0.26)	0.024	0.21 (0.09 – 0.75)	0.1 (0.03 – 0.18)	0.48
miR-185	3.28 (0.89 - 3.86)	1.88 (0.66 – 2.60)	0.049	2.45 (1.69 – 3.00)	1.65 (0.97 – 3.79)	0.81
miR-223	0.14 (0.07 – 0.28)	0.14 (0.034 – 0.29)	0.53	0.42 (0.31-1.74)	0.22 (0.91 – 0.56)	0.08

The miRNA level was quantified by TaqMan qPCR in duplicate and with standard curves. The median and interquartile range of the miRNA quantity (fmoles/ng of total RNA) are shown. Pre-tx, pre-treatment; post-tx, post-treatment; IQR, interquartile range.

Supplementary Table 9. mRNA counts of putative tumor suppressor targets of miR-22, miR-34a, miR-146b, and miR-181b in PB CLL cells from 38 patients pre- and post-treatment (day 28) with ibrutinib.

mRNA	Avg. (SD) pre-tx	Avg. (SD) post-tx	Fold change	*P* value	Trend in post-tx
ARID1B	578 (±325)	787 (±377)	1.4	0.011	Up
ARID2	490 (±260)	635 (±275)	1.3	0.027	Up
ATM	274 (±130)	332 (±209)	1.2	0.046	Up
CYLD	2132 (±1124)	3014 (±1298)	1.4	0.033	Up
FOXP1	1001 (±950)	1561 (±1304)	1.6	0.023	Up
HDAC1	740 (±303)	981 (±410)	1.3	0.012	Up
IBTK	141 (±159)	172 (±133)	1.2	0.04	Up
PTEN	1090 (±406)	1272 (±668)	1.2	0.05	Up
SMAD4	834 (±402)	1159 (±588)	1.4	0.003	Up

mRNA counts were obtained from nanoString nCounter assay. Avg., average; SD, standard deviation; pre-tx, pre-treatment; post-tx, post-treatment. *P* values calculated by Wilcoxon paired test.

Supplemental Table 10. Differential gene expression between CLL cells in PB and in LN.

mRNA	Median (IQR) in PB	Median (IQR) in LN	Fold change	*P* value	Trend
ARID1B	7 (4.6-8.3)	5 (3.3-6.2)	-1.4	0.01	Down
ARID2	20.9 (18.4-27.3)	22.8 (15.6-32.3)	1.1	0.36	-
ATM	31.1 (25.6-36.3)	45.2 (19.9-56.7)	1.3	0.11	-
CYLD	2.5 (1.7-3.5)	1.6 (1.3-2)	-1.6	0.04	Down
FOXP1	68.6 (52-72)	49.4 (35-74)	-1.4	0.006	Down
HDAC1	68.6 (52-72)	49.4 (35-74)	-1.4	0.4	-
IBTK	7 (4.6-8.3)	5 (3.3-6.2)	-1.4	0.06	-
PTEN	2.5 (1.7-3.5)	1.6 (1.3-2)	-1.5	0.22	-
SMAD4	68.6 (52-72)	49.4 (35-74)	-1.4	0.33	-

Gene expression was determined by TaqMan qPCR performed in triplicate. RNA from 17 paired and treatment naïve PB and LN CLL cells was used. The median and interquartile range of the relative mRNA expression are shown. *P* values calculated by Wilcoxon paired test.

Supplementary Table 11. Differential gene expression in cell lines treated with Ibrutinib

mRNA	Cell Line	Percent Change Untreated to Treated	*P* value
ARID1b	MEC1	56.69%	0.0005
ARID2	MEC1	35.21%	0.0028
ATM	MEC1	35.48%	0.039
CYLD	MEC1	19.49%	0.0014
FOXP1	MEC1	199.22%	0.0055
HDAC1	MEC1	65.82%	0.033
IBTK	MEC1	45.42%	0.0037
PTEN	MEC1	20.57%	0.066
SMAD4	MEC1	12.89%	0.0038
ARID1b	SP53	175.97%	0.001
ARID2	SP53	155.97%	0.0009
ATM	SP53	290.76%	0.0005
CYLD	SP53	65.35%	0.01
FOXP1	SP53	164.80%	0.0002
HDAC1	SP53	76.92%	0.002
IBTK	SP53	157.62%	0.006
PTEN	SP53	180.27%	0.0001
SMAD4	SP53	118.89%	0.002

Gene expression was determined by TaqMan qPCR performed in triplicate. RNA from MEC1 and SP53 cell lines treated with of Ibrutinib for 48 hours was compared to untreated cells. Percent change in expression levels is shown from untreated cells to treated cells with the associated p-value. *P* values calculated by Student’s t-test.

Supplementary Table 12. Differential gene expression in cell lines transfected with pre-miRNA and anti-miRNA constructs.

Pre-miR						**Anti-miR**				
		MEC-1		SP53			MEC-1		SP53	
mRNA	**Transfection**	***% Change***	**p-value**	***% Change***	**p-value**	**Transfection**	***% Change***	**p-value**	***% Change***	**p-value**
ARID1b	pre-miR 34a	-23.67%	0.007	-49.02%	0.014	anti-miR 34a	0.69%	0.91	-9.02%	0.86
ATM	pre-miR 34a	1.89%	0.75	-19.30%	0.067	anti-miR 34a	28.62%	0.28	178.04%	0.003
CYLD	pre-miR 34a	-52.39%	0.0004	-10.26%	0.31	anti-miR 34a	-34.15%	0.066	-3.92%	0.83
FOXP1	pre-miR 34a	-19.23%	0.10	-1.21%	0.75	anti-miR 34a	-14.99%	0.53	898.78%	0.011
HDAC1	pre-miR 34a	-20.06%	0.03	-27.21%	0.001	anti-miR 34a	39.56%	0.03	922.51%	0.001
IBKT	pre-miR 34a	-35.81%	0.02	-14.88%	0.087	anti-miR 34a	-3.66%	0.52	10.68%	0.59
PTEN	pre-miR 34a	-30.63%	0.065	-18.63%	0.25	anti-miR 34a	-8.25%	0.71	-4.54%	0.78
SMAD4	pre-miR 34a	-16.37%	0.029	-24.57%	0.06	anti-miR 34a	265.02%	0.002	354.67%	0.023
ARID1b	pre-miR 146b	-46.84%	0.0002	-34.79%	0.066	anti-miR 146b	16.21%	0.15	175.97%	0.001
ATM	pre-miR 146b	-36.18%	0.03	-24.32%	0.033	anti-miR 146b	21.67%	0.08	412.87%	0.003
CYLD	pre-miR 146b	-47.34%	0.01	-19.99%	0.12	anti-miR 146b	-38.44%	0.071	-8.15%	0.64
FOXP1	pre-miR 146b	-50.98%	0.0002	13.62%	0.06	anti-miR 146b	8.21%	0.33	8.63%	0.22
HDAC1	pre-miR 146b	-40.83%	0.004	-29.26%	0.02	anti-miR 146b	46.65%	0.009	880.40%	0.001
IBKT	pre-miR 146b	-12.83%	0.23	-25.19%	0.03	anti-miR 146b	-4.06%	0.41	-3.42%	0.81
PTEN	pre-miR 146b	-9.15%	0.48	-28.97%	0.13	anti-miR 146b	-6.68%	0.38	-33.34%	0.083
SMAD4	pre-miR 146b	-37.43%	0.0014	-28.88%	0.026	anti-miR 146b	847.99%	0.0005	369.78%	0.00001

Gene expression was determined by TaqMan qPCR performed in triplicate. RNA from MEC1 and SP53 cell lines transfected with pre-miRNA constructs or anti-miRNA constructs was compared to those treated with scramble control oligos. Percent change in expression levels is shown from untreated cells to treated cells with the associated p-value. *P* values calculated by Student's t-test

Supplementary Table 13. Differential gene expression of proliferation markers in cell lines transfected with anti-miRNA constructs.

Marker	Cell/Transfection	Percent Change	P-Value
KI67	MEC1 anti-miR 34a	-7.49%	0.231
TOP2a	MEC1 anti-miR 34a	-17.81%	0.152
TPX	MEC1 anti-miR 34a	-28.86%	0.02
KI67	MEC1 anti-miR 146b	-18.34%	0.38
TOP2a	MEC1 anti-miR 146b	-23.54%	0.31
TPX	MEC1 anti-miR 146b	-23.01%	0.049
KI67	SP53 anti-miR 34a	-15.63%	0.035
TOP2a	SP53 anti-miR 34a	-30.34%	0.0225
TPX	SP53 anti-miR 34a	-34.09%	0.0001
KI67	SP53 anti-miR 146b	-30.55%	0.003
TOP2a	SP53 anti-miR 146b	-27.13%	0.026
TPX	SP53 anti-miR 146b	-2.55%	0.69

Gene expression was determined by TaqMan qPCR performed in triplicate. RNA from MEC1 and SP53 cell lines transfected with anti-miRNA constructs was compared to those treated with scramble control oligos. Percent change in expression levels is shown from untreated cells to treated cells with the associated p-value. *P* values calculated by Student's t-test