

Table SI. Reads of miR-1246 (31).

A, Pre-surgery		
Sequences	Reads	Base substitution
---TGGATTTTTGGAGCAGG--	128	
--ATGGATTTTTGGAGCAGG--	71	
---TGGATTTTTGGAGCA----	55	
---TGGATTTTTGGAGCAG---	43	
--ATGGATTTTTGGAGCA----	37	
----GGATTTTTGGAGCAGG--	23	
-AATGGATTTTTGGAGCAGG--	20	
--ATGGATTTTTGGAGCAGGA-	17	
--ATGGATTTTTGGAGCAG---	16	
--ATGGATTTTTGGAGC-----	11	
---TGGATTTTTGGAGCAGGA-	11	
AAATGGATTTTTGGAGCAGGA-	9	1:G>A
----GGATTTTTGGAGCAG---	8	
-----GATTTTTGGAGCAGG--	8	
-AATGGATTTTTGGAG-----	7	
-AATGGATTTTTGGAGCAG---	7	
-AATGGATTTTTGGAGCAGGA-	5	
-AATGGATTTTTGGAGC-----	3	
.-AATGGATTTTTGGAGCAGGGG	3	20:A>G
.---TGGATTTTTGGAGCAGGGG	3	18:A>G
.-ATGGATTTTTGGAGCAGGGG	2	19:A>G
GAATGGATTTTTGGAGC-----	2	
---TGGATTTTTGGAGCGGGA-	1	15:A>G
-----GATTTTTGGAGCAGGA-	1	
GAATGGATTTTTGGAGCAGGGG	1	21:A>G
GAATGGATTGTTGGAGCAGG--	1	10:T>G
Total:	493	
B, 7w post-surgery		
Sequences	Reads	Base substitution
---TGGATTTTTGGAGCAGG--	184	

---TGGATTTTTGGAGCA----	88	
---TGGATTTTTGGAGCAG---	80	
--ATGGATTTTTGGAGCAGG--	51	
-AATGGATTTTTGGAGCAGG--	30	
--ATGGATTTTTGGAGCA----	30	
--ATGGATTTTTGGAGCAG---	26	
----GGATTTTTGGAGCAGG--	21	
---TGGATTTTTGGAGCAGGA-	19	
--ATGGATTTTTGGAGCAGGA-	18	
--ATGGATTTTTGGAGC-----	16	
AAATGGATTTTTGGAGCAGGA-	14	1:G>A
----GGATTTTTGGAGCAG---	12	
-----GATTTTTGGAGCAGG--	10	
-AATGGATTTTTGGAGCAG---	9	
-AATGGATTTTTGGAGCAGGA-	6	
-AATGGATTTTTGGAGCA----	4	
-AATGGATTTTTGGAGC-----	4	
.-ATGGATTTTTGGAGCAGGGG	4	19:A>G
.-AATGGATTTTTGGAGCAGGGG	3	20:A>G
.----TGGATTTTTGGAGCAGGGG	3	18:A>G
GAATGGATTTTTGGAGCAGG--	3	
-AATGGATTTTTGGAGCAGGT-	1	20:A>T
.----TGGATTTTTGGAGCAGGAG	1	
---TGGATTTTTGGAGCAGT--	1	17:G>T
----GGATTTTTGGAGCAGGA-	1	
GAATGGATTTTTGGAGCAGGGG	1	21:A>G
GAATGGATTTTTGGAGCAGGA-	1	
-----ATTTTTGGAGCAGGA-	1	
Total:	642	
C, 12mo post-surgery		
Sequences	Reads	Base substitution
---TGGATTTTTGGAGCAGG--	1231	
---TGGATTTTTGGAGCA----	615	
---TGGATTTTTGGAGCAG---	392	

--ATGGATTTTTGGAGCAGG--	386	
--ATGGATTTTTGGAGCA----	204	
--ATGGATTTTTGGAGCAG---	140	
----GGATTTTTGGAGCAGG--	109	
-AATGGATTTTTGGAGCAGG--	88	
--ATGGATTTTTGGAGC-----	80	
---TGGATTTTTGGAGCAGGA-	80	
--ATGGATTTTTGGAGCAGGA-	66	
----GATTTTTGGAGCAGG--	65	
----GGATTTTTGGAGCAG---	64	
-AATGGATTTTTGGAGCAGGA-	38	
-AATGGATTTTTGGAGCA----	28	
AAATGGATTTTTGGAGCAGGA-	24	1:G>A
-AATGGATTTTTGGAGCAG---	22	
.---TGGATTTTTGGAGCAGGGG	18	18:A>G
..-ATGGATTTTTGGAGCAGGGG	8	19:A>G
.-AATGGATTTTTGGAGCAGGGG	5	20:A>G
-AATGGATTTTTGGAGC-----	4	
----GGATTTTTGGAGCAGGA-	4	
-----ATTTTTGGAGCAGGA-	4	
--ATGGATTTTTGGAGCAGGT-	2	19:A>T
----GATTTTTGGAGCAGGA-	2	
GAATGGATTTTTGGAGCAGG--	2	
-AATGGATTTTTGGAG-----	1	
-AATGGATTTTTGGAGAAGGA-	1	16:C>A
--ATGGATTTTTGGAGCAGGC-	1	19:A>C
--ATGGATTTTTGGAGCGGGA-	1	16:A>G
--ATGGATTTTTGAAGCAGGA-	1	12:G>A
--ATGGATTTATGGAGCAGG--	1	9:T>A
--ATGGAATTTTGGAGCAGG--	1	6:T>A
---TGGATTTTTGGAGCAGGC-	1	18:A>C
---TGGATTTTTGGAGCAGGT-	1	18:A>T
---TGGGTTTTTGGAGCAGGA-	1	4:A>G
---TGGATTTATGGAGCAGGA-	1	8:T>A

---TGGATTTTTGGAGCAAG--	1	16:G>A
GAATGGATTTTTGGAGCAGGA-	1	
GAATGGATTTTTGGAGCAGGG-	1	21:A>G
Total:	3695	
Green: miR-1246 5'(-2)		
Orange: miR-1246 5'(0)		
Red letter: canonical (miR-1246 0 0)		

Table SII. Target prediction of miR-1246 5'-isomiRs.

miR-1246 0 0		miR-1246 -1 0		miR-1246 -2 0	
Target Score	Gene Symbol	Target Score	Gene Symbol	Target Score	Gene Symbol
99	FAM53C	99	CBFA2T3	100	SGO1
96	C12orf71	99	COL22A1	99	RTKN2
94	LENEP	98	EHHADH	99	OSBPL6
94	GLRB	98	ONECUT2	99	PALM2-AKAP2
93	FPGT	97	SYT4	99	AKAP2
93	CREBL2	97	OSBPL6	99	HTRA3
92	SLC12A2	97	CADM2	99	ACER3
92	PLEKHB2	97	RGS5	99	EHHADH
92	QTRT2	96	EPC2	98	ITGA4
91	SCN3A	96	PRKACB	98	CBLL1
91	ANTXR2	96	XDH	98	EMP2
91	MRPS14	96	LRRTM2	98	EFNA5
91	ZNF425	95	BBOF1	98	ANKRD13C
91	RTKN2	95	CRTC1	98	KCNAB1
90	HECTD2	95	TREM2	98	OGN
90	ANKDD1B	95	KDM5A	98	WDR77
		95	RIMBP2	98	CFTR
				98	AKAP7
				98	ADARB2
				97	TNFRSF8
				97	FAM19A5
				97	ATF7IP
				97	KLHL6
				97	ONECUT2
				97	CBFA2T3
				97	KDM5A
				97	GTF2I
				97	NRXN1
				97	LRRTM2

					96	MSR1
					96	CPEB2
					96	CREB5
					96	RGS5
					96	GOLGA1
					96	ARL4C
					96	PRRG1
					96	ITPR2
					96	RPL34
					96	GYS2
					95	ORC5
					95	POU2F2
					95	ZNF569
					95	KLC1
					95	KIAA0355
					95	BPTF
					95	FNDC3A
					95	TMEM248
					95	UBA5
					95	PSMC2
					95	TUBGCP3
					95	COL8A1
					95	SLC4A7
					95	SYNPO2
					95	CAMK4

miRDB - Custom Prediction (<https://mirdb.org/custom.html>) was used. Genes predicted with target score of > 90 in miR-1246|0|0| and > 95 in miR-1246|-1|0| and miR-1246|-2|0|, respectively were shown.