FIGURES

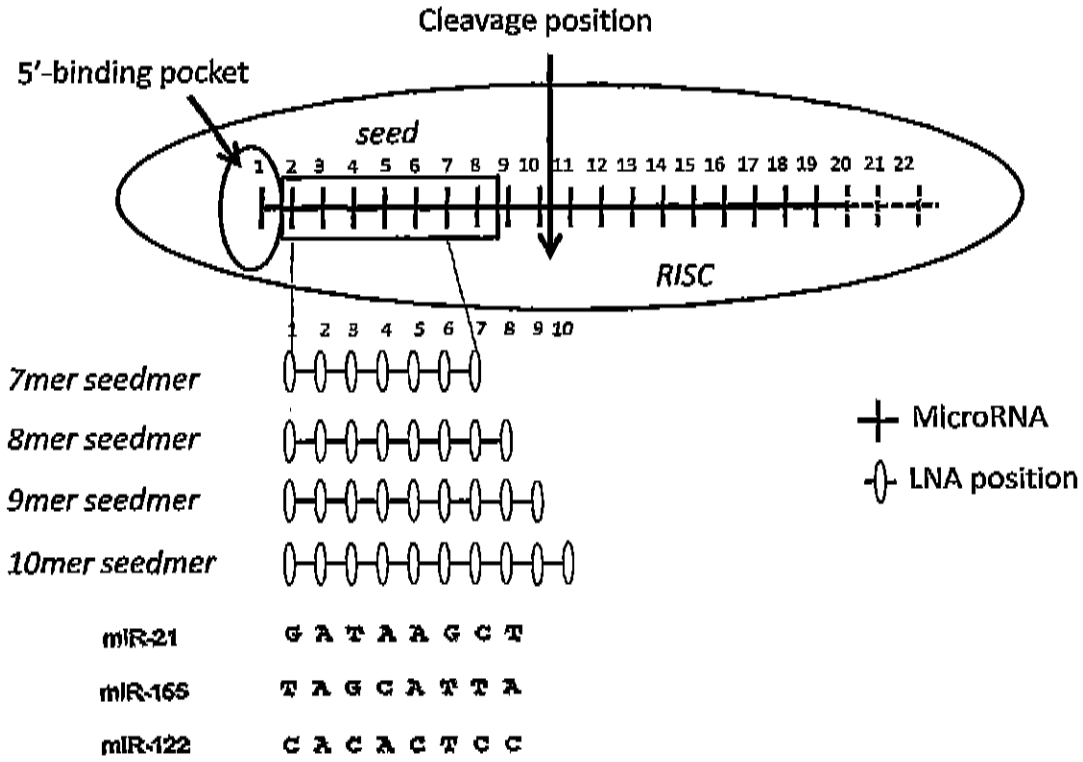


Figure 1

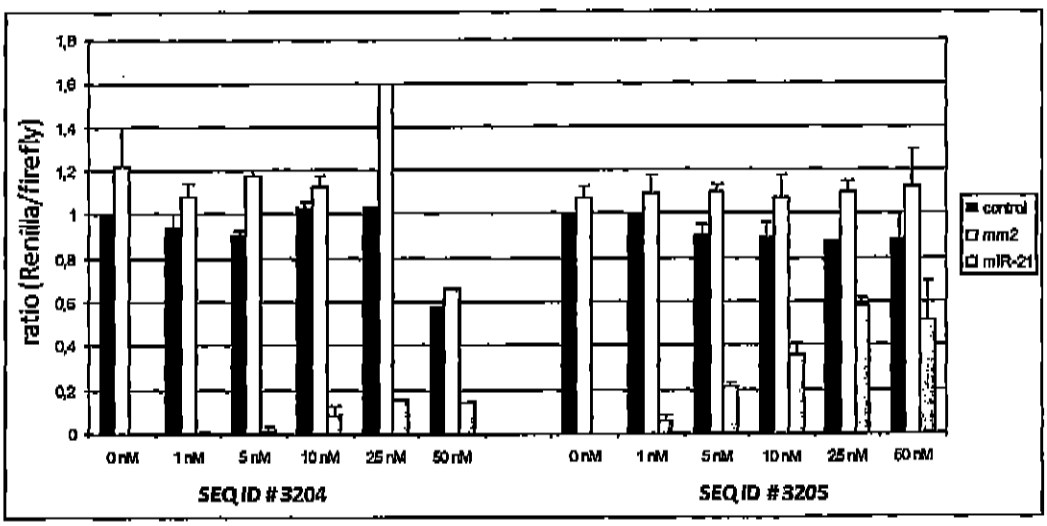


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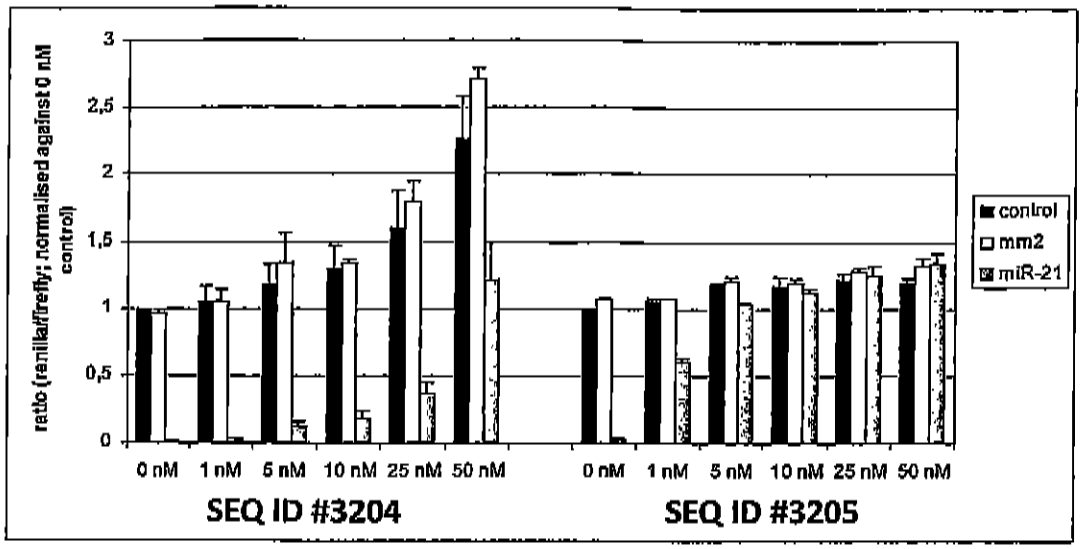


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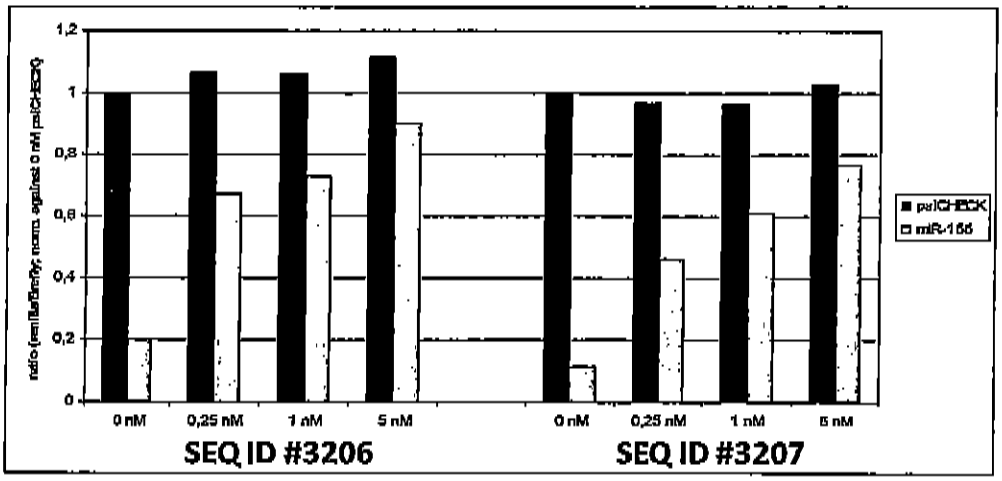


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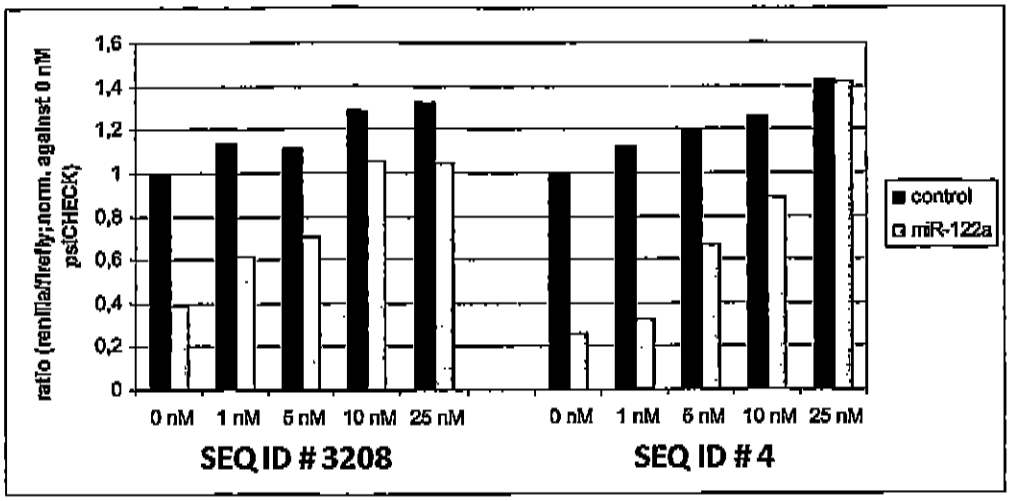


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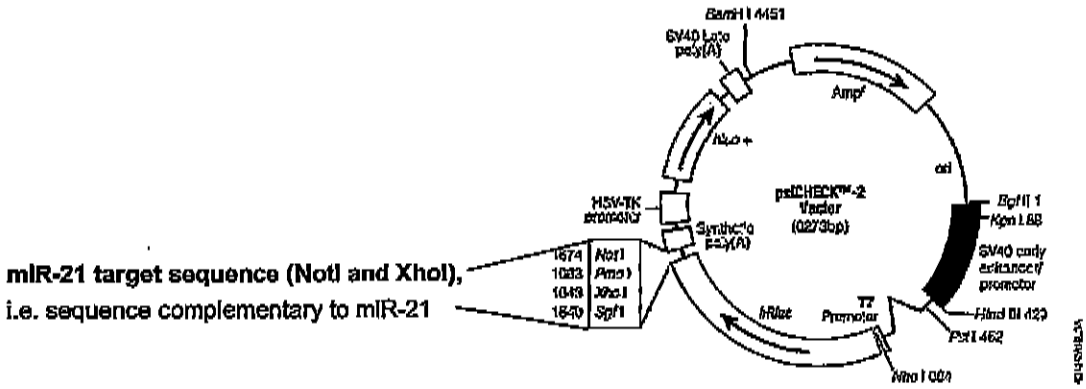


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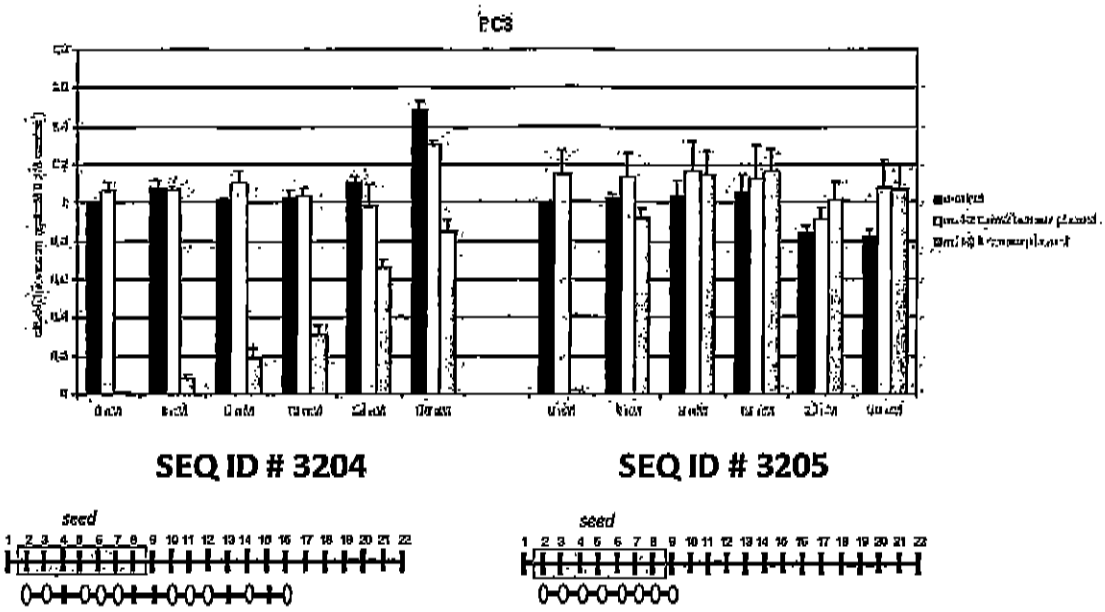


Figure 7

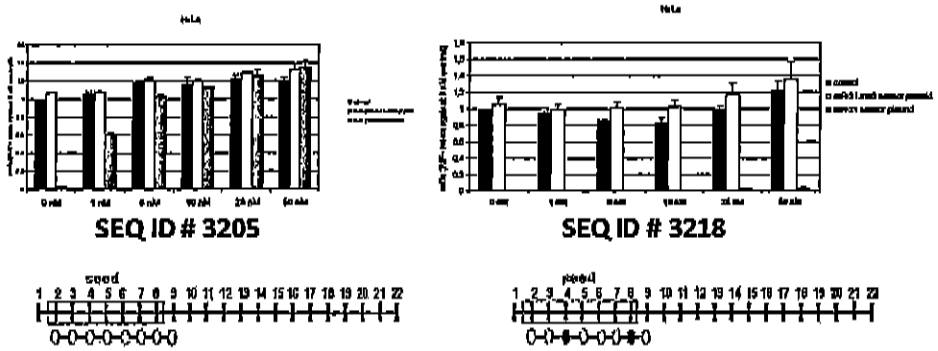


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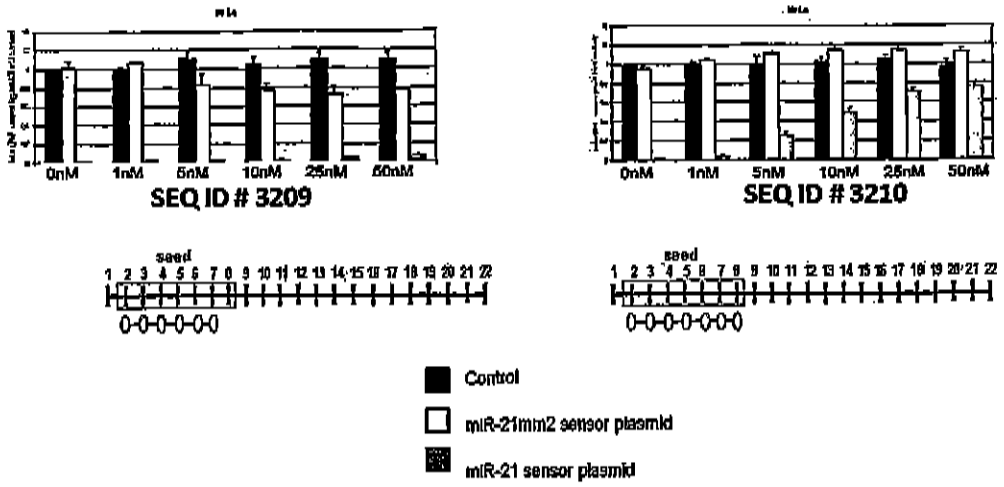


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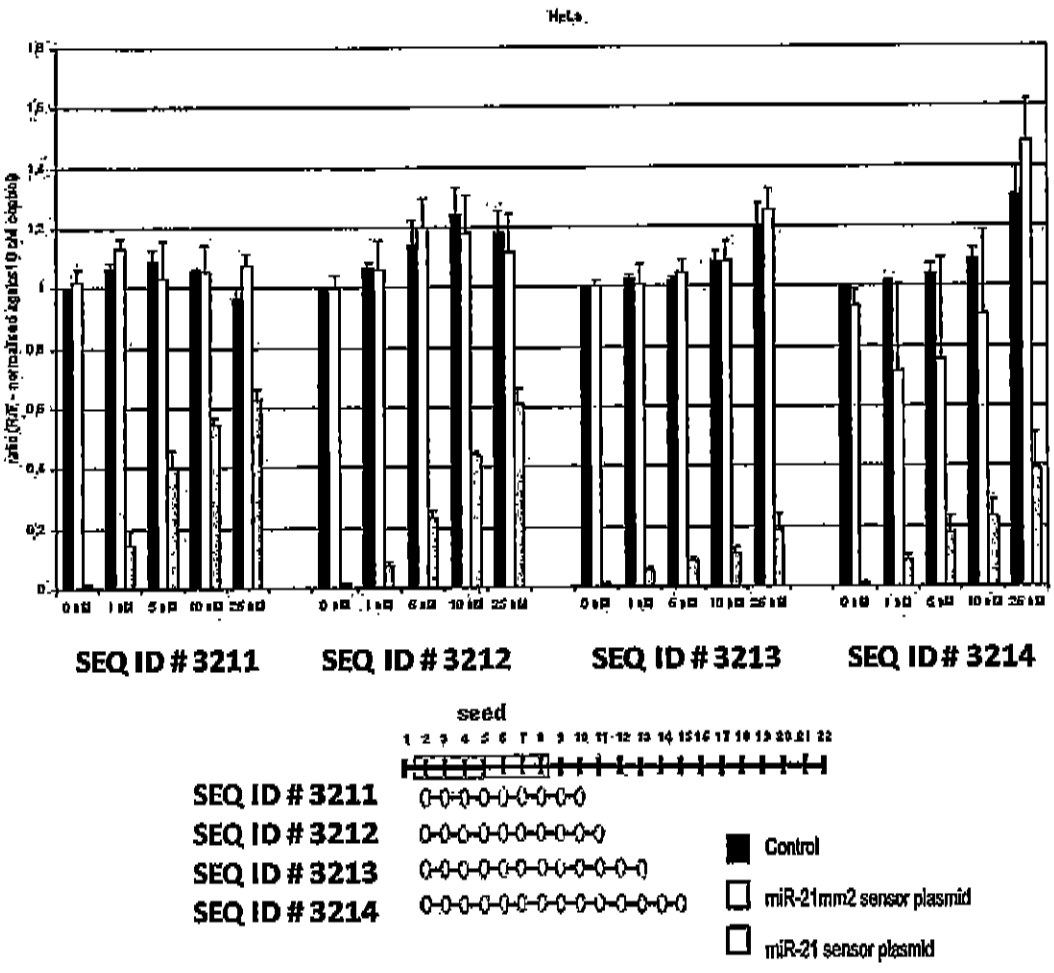


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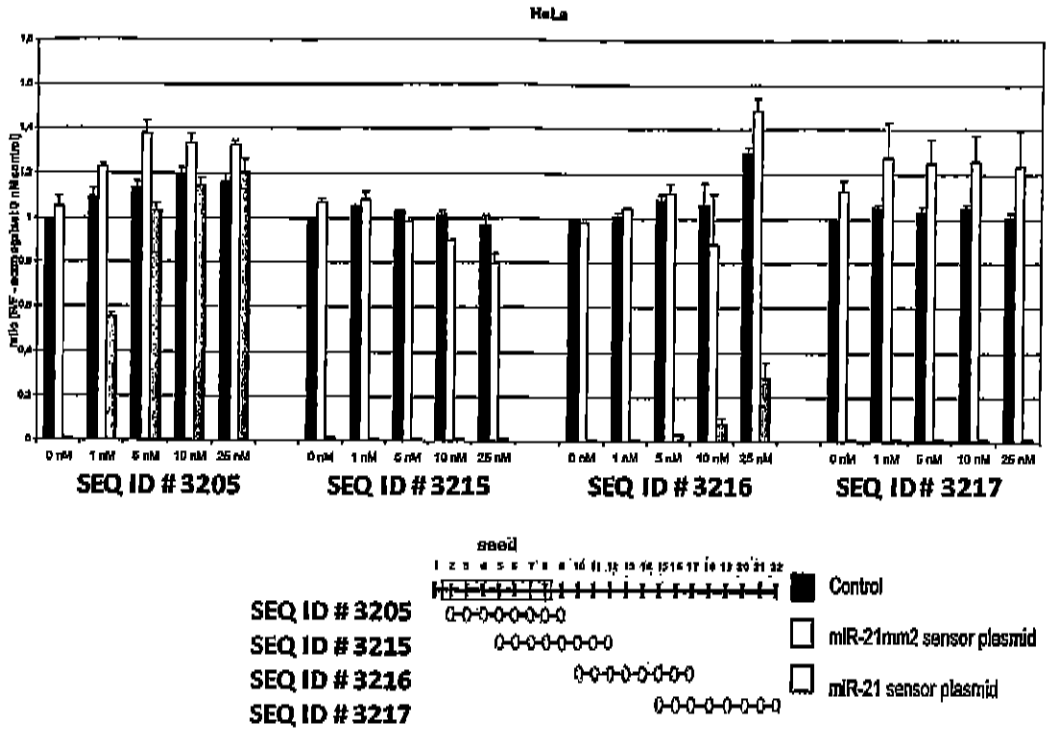


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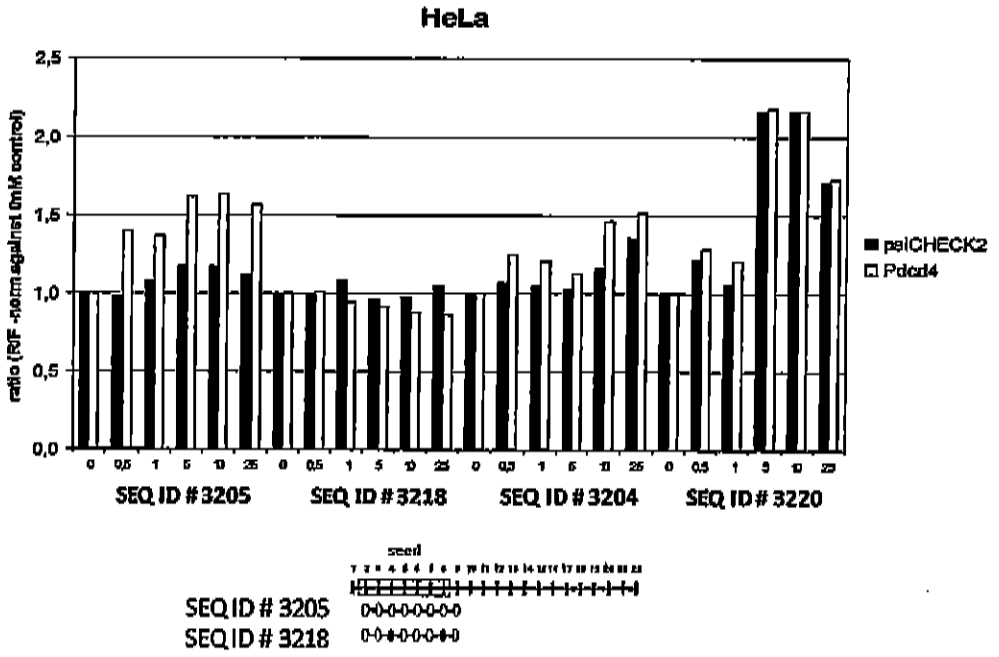


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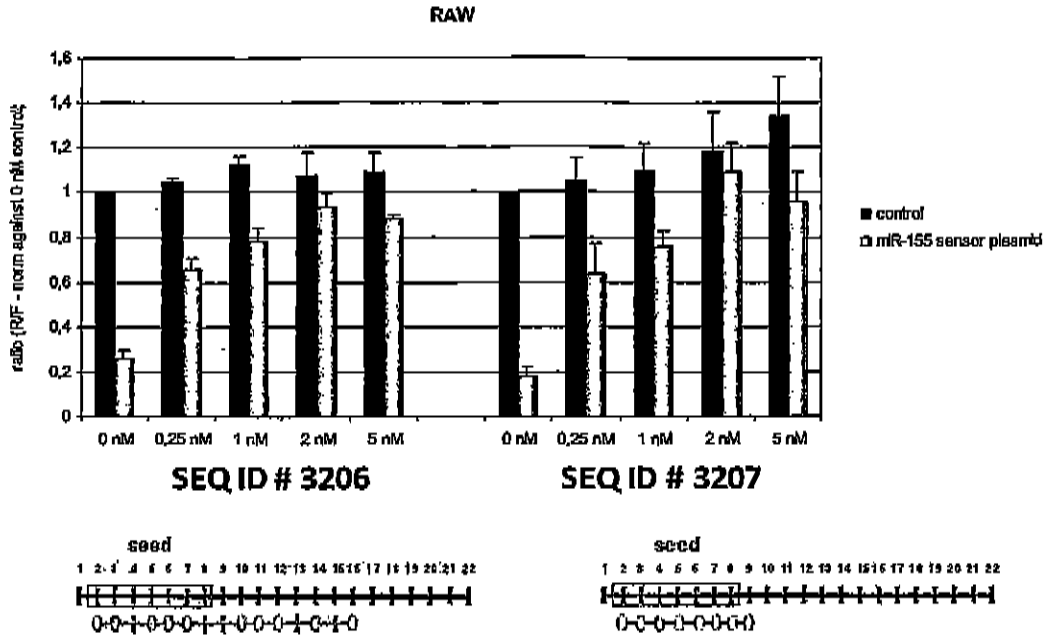


Figure 13



Figure 14

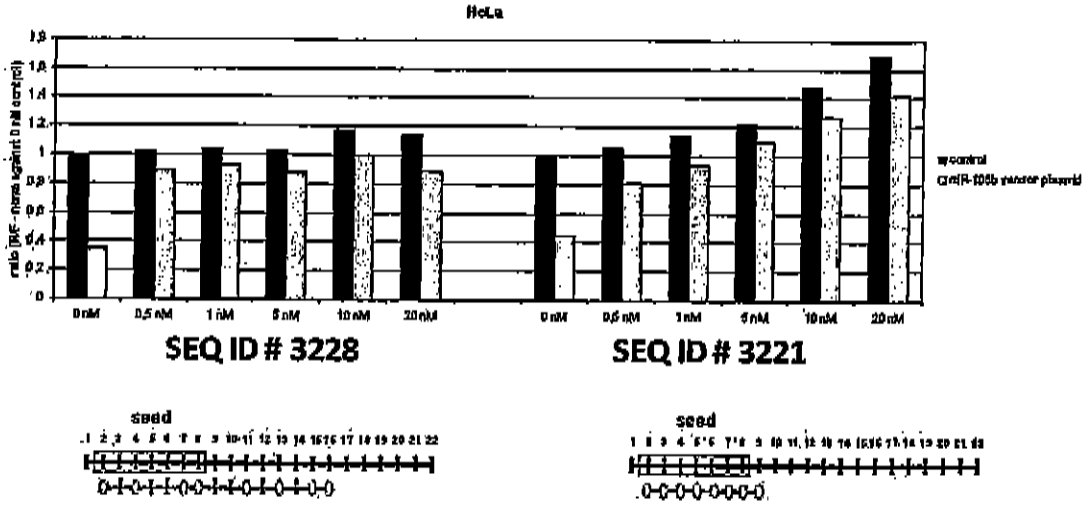


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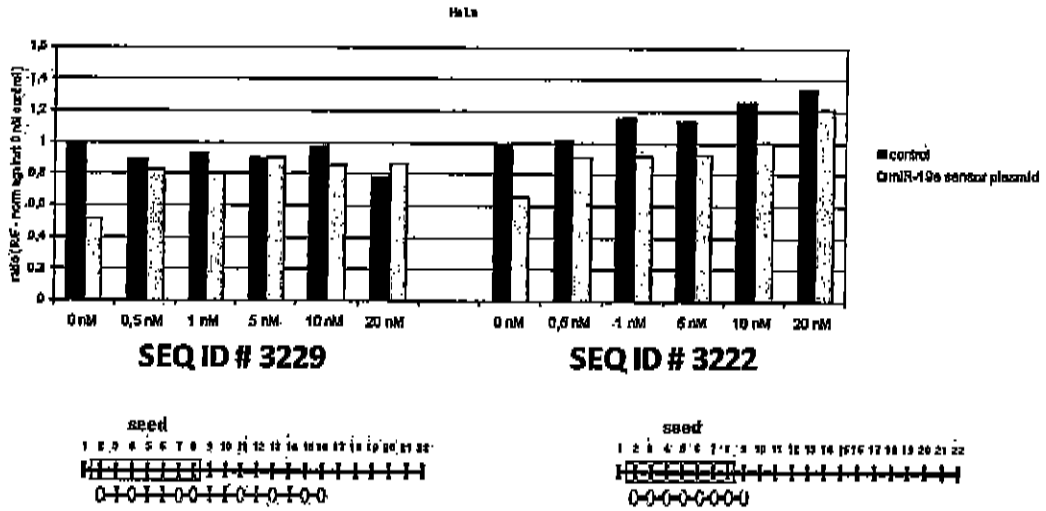


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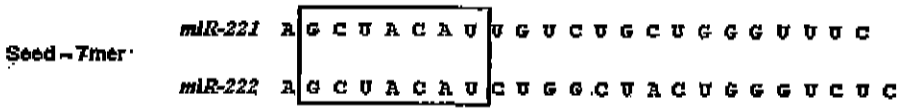


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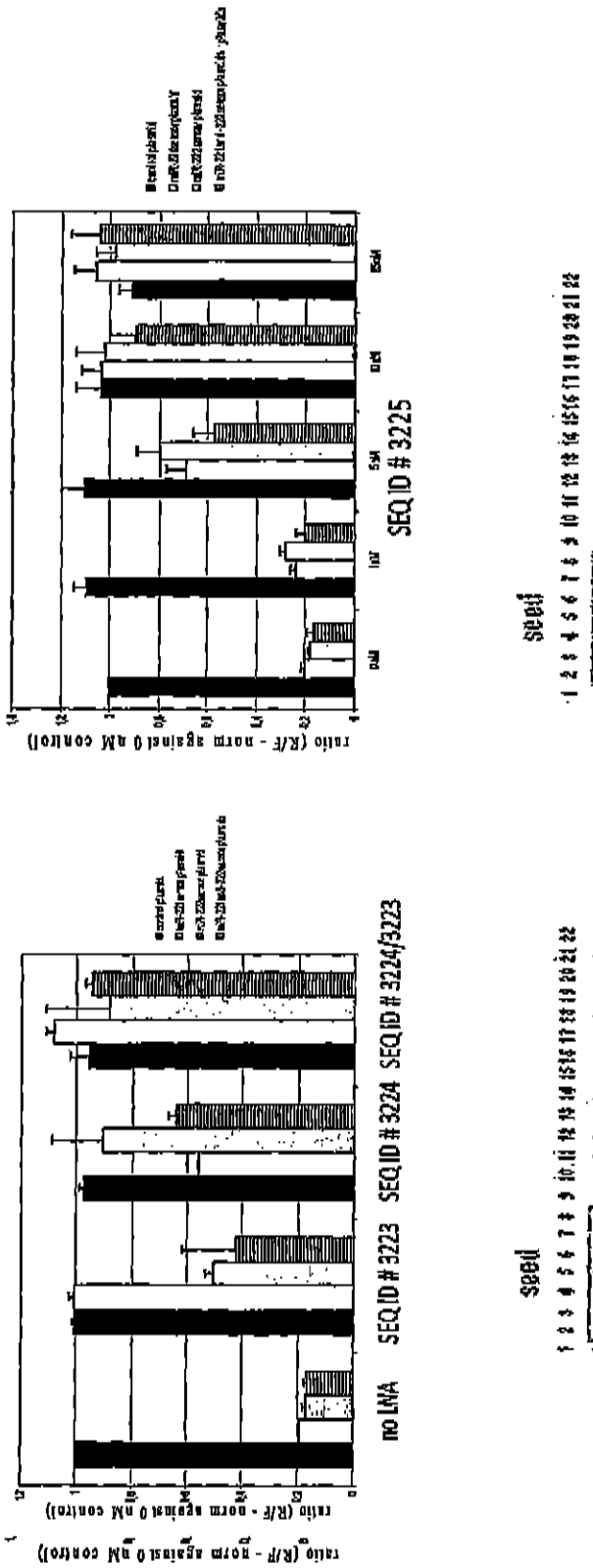

ratio (R/F - norm against 0 nM control)
no LNA
SEQ ID # 3223
SEQ ID # 3224
SEQ ID # 3224/3223
seed
SEQ ID # 3223
SEQ ID # 3224
ratio (R/F - norm against 0 nM control)
SEQ ID # 3225
seed
SEQ ID # 3225

Figure 18

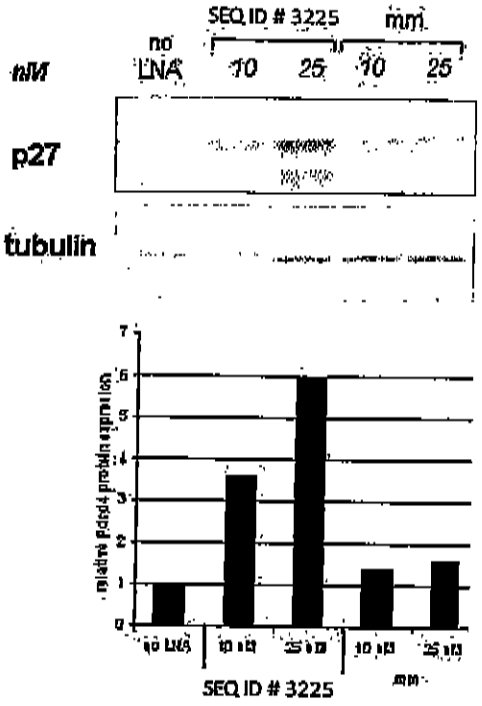


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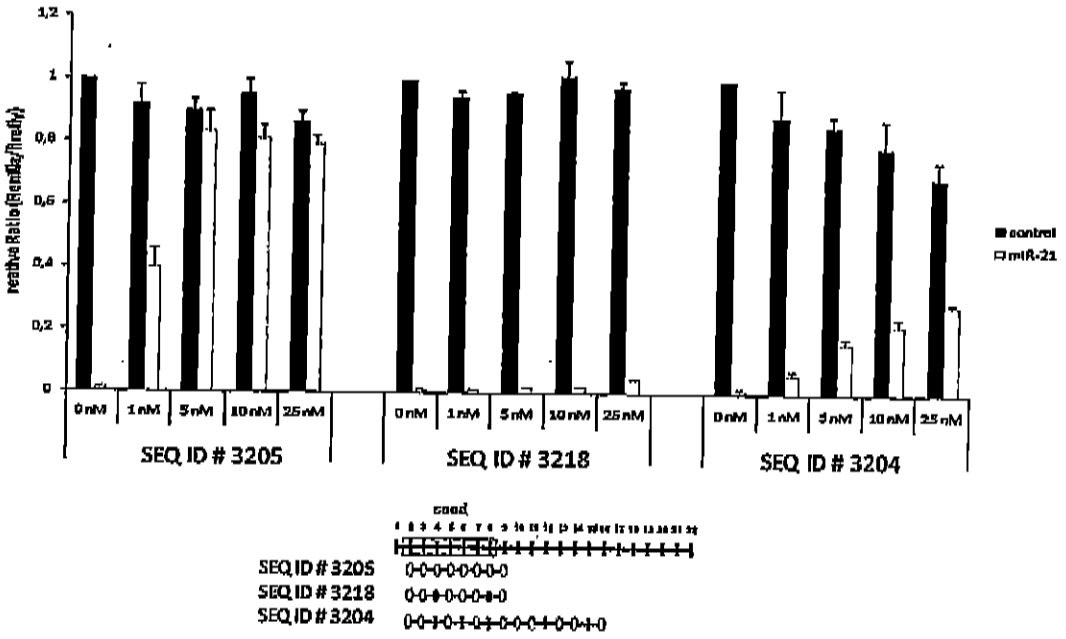


Figure 20

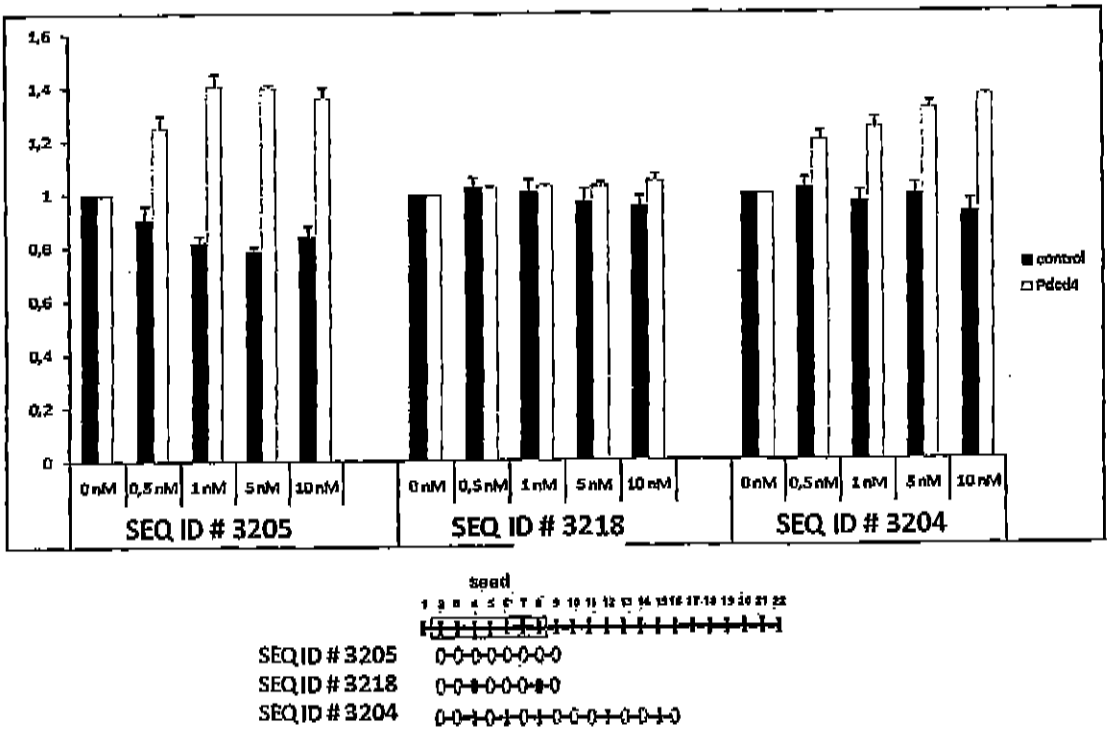
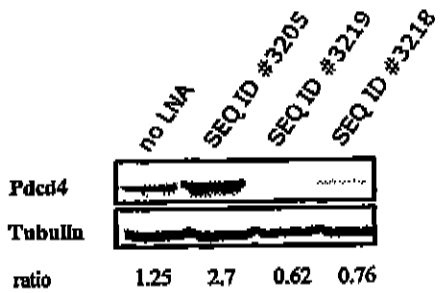


Figure 21



SEQ ID #3205	5´- GATAAGCT – 3´
SEQ ID #3219	5´- CGTAATGA– 3´
SEQ ID #3218	5´- GGTAAACT– 3´

Figure 22

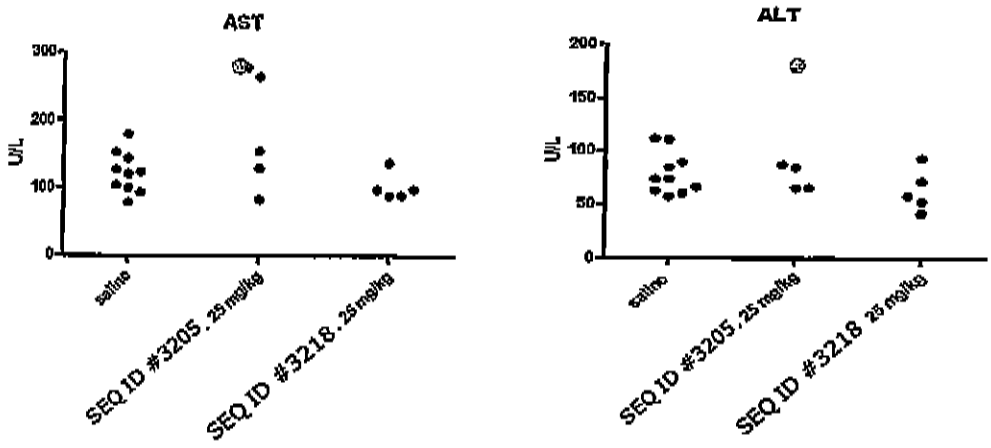


Figure 23

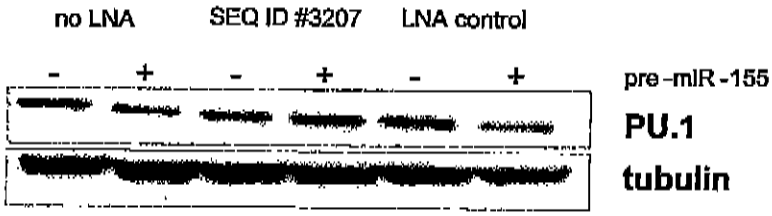
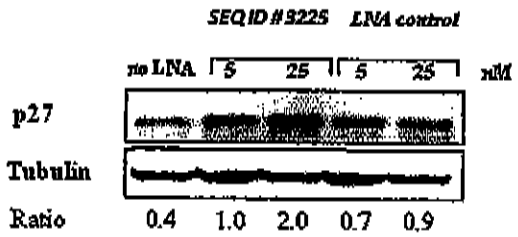


Figure 24



SEQ ID # 3225 5´- ATGTAGC -3´

LNA control 5´- GTAGACT -3´

Figure 25

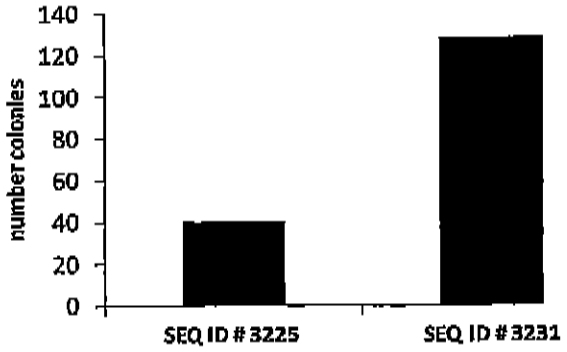

140
120
100
80
60
40
20
0
number colonies
SEQ ID # 3225
SEQ ID # 3231

Figure 26

Name	*Mature miRNA sequence*	*S (2-8)*	*ES (2-9)*	*NE (9-16)*	*Total (2-16)*
let-7a	UGAGGUAGUAGGUUGUAUAGUU	N/A	N/A	N/A	N/A
let-7b	UGAGGUAGUAGGUUGUGUGGUU	0	0	0	0
let-7c	UGAGGUAGUAGGUUGUAUGGUU	0	0	0	0
let-7d	AGAGGUAGUAGGUUGCAUAGUU	0	0	1	1
let-7e	UGAGGUAGGAGGUUGUAUAGUU	0	1	0	1
let-7f	UGAGGUAGUAGAUUGUAUAGUU	0	0	1	1
let-7g	UGAGGUAGUAGUUUGUACAGUU	0	0	1	1
let-7i	UGAGGUAGUAGUUUGUGCUGUU	0	0	1	1
miR-98	UGAGGUAGUAAGUUGUAUUGUU	0	0	1	1

Number	Compound	Sequence (5' to 3')[a]	Length (nt)	Complementary target(s)
1.	SEQ ID #3226	A-C-a-A-c-C-T-a-c-T-a-C-c-T-C	15	let-7a/b/c
2.	SEQ ID #3236	G-C-a-A-c-C-T-a-c-T-a-C-c-T-C	15	let-7d
3.	SEQ ID #3237	A-C-a-A-c-C-T-c-c-T-a-C-c-T-C	15	let-7e
4.	SEQ ID #3238	A-C-a-A-a-C-T-a-c-T-a-C-c-T-C	15	let-7g/i
5.	SEQ ID #3239	C-T-A-C-C-T-C	7	all members
6.	SEQ ID #3240	C-T-A-A-C-T-C	7	none
7.	SEQ ID #3227	A-C-T-A-C-C-T-C	8	all except let-7e
8.	SEQ ID #3232	T-A-C-C-T-C	6	all members
9.	SEQ ID #3234	T-N_1-C-T-A-C-C-T-C	9	all members[b]
10.	SEQ ID #3235	T-N_2-C-T-A-C-C-T-C	9	all members[b]

[a]Capital and lower case letters denote LNA and DNA, respectively.

[a]Both 9-mers theoretically target all members since they contain 2 different universally hybridizing chemistries at their 2nd position.

Figure 27

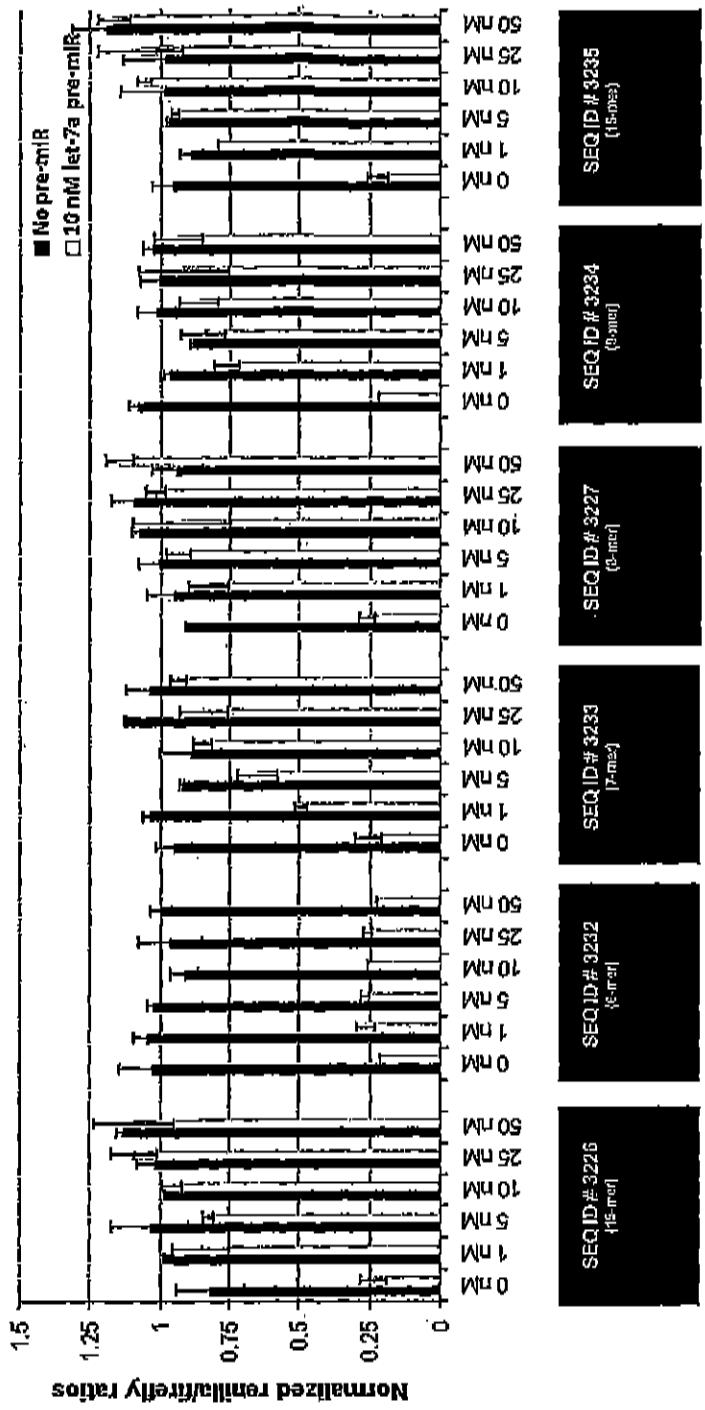

No pre-miR
10 nM let-7a pre-miR
Normalized renilla/firefly ratios
1.5
1.25
1
0.75
0.5
0.25
0
0 nM
1 nM
5 nM
10 nM
25 nM
50 nM
SEQ ID # 3226
(16-mer)
SEQ ID # 3232
(16-mer)
SEQ ID # 3233
(17-mer)
SEQ ID # 3227
(18-mer)
SEQ ID # 3234
(19-mer)
SEQ ID # 3235
(15-mer)

Figure 28

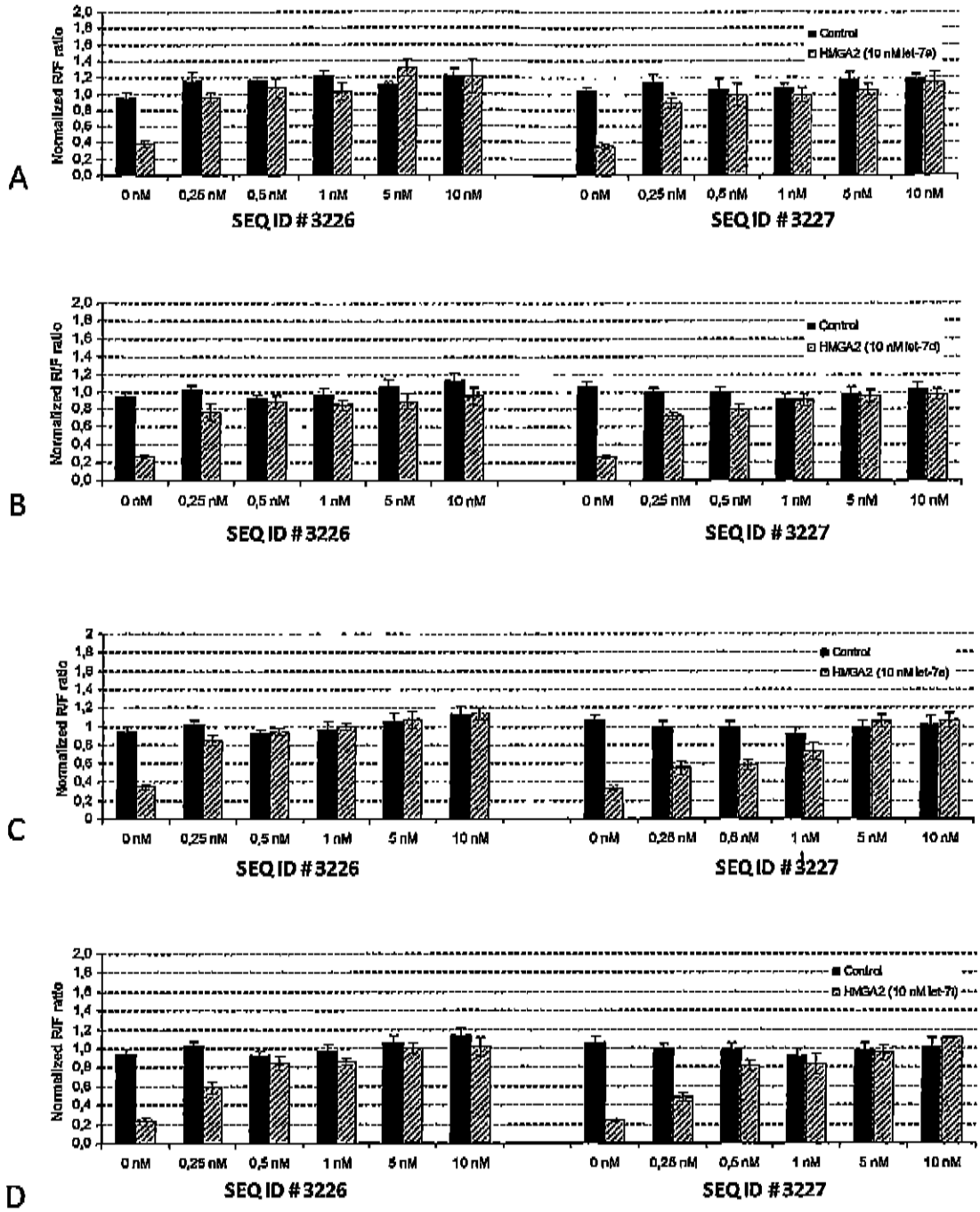

A
B
C
D
Normalized R/F ratio
Control
HMGA2 (10 nM let-7a)
HMGA2 (10 nM let-7d)
HMGA2 (10 nM let-7i)
0 nM
0,25 nM
0,5 nM
1 nM
5 nM
10 nM
SEQ ID # 3226
SEQ ID # 3227

Figure 29

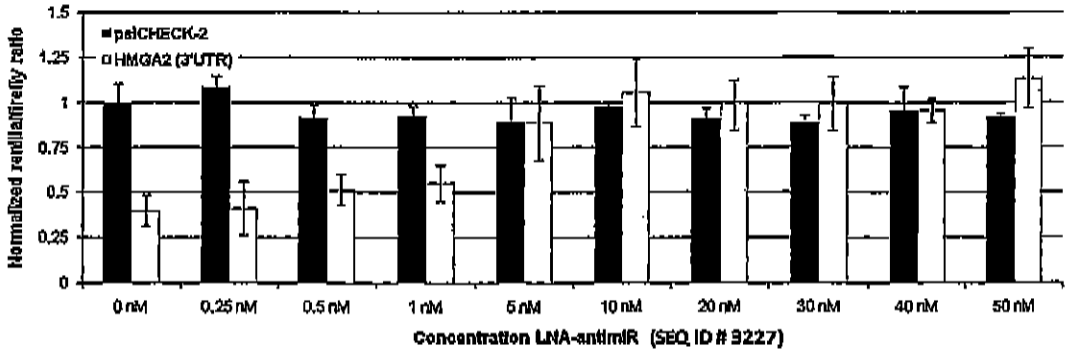


Figure 30

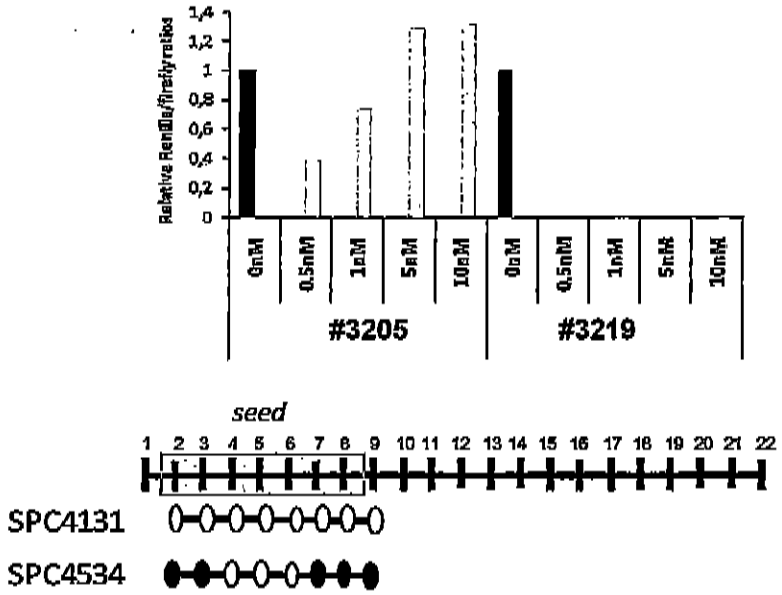


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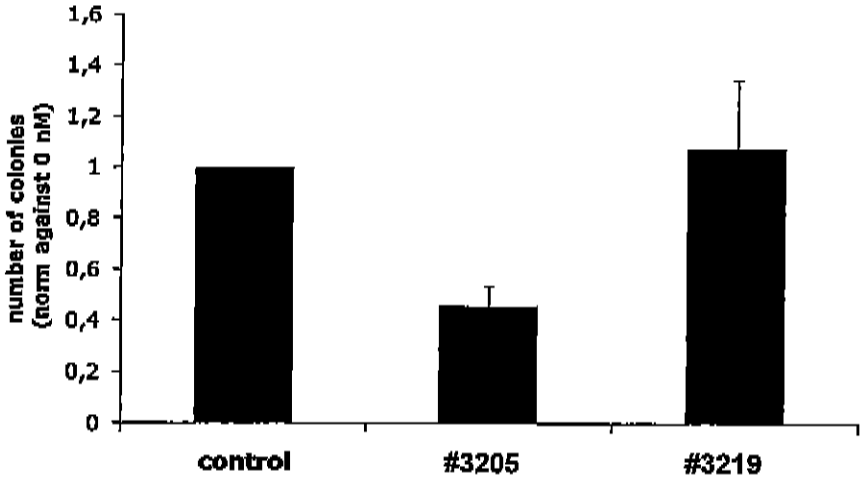


Figure 32.

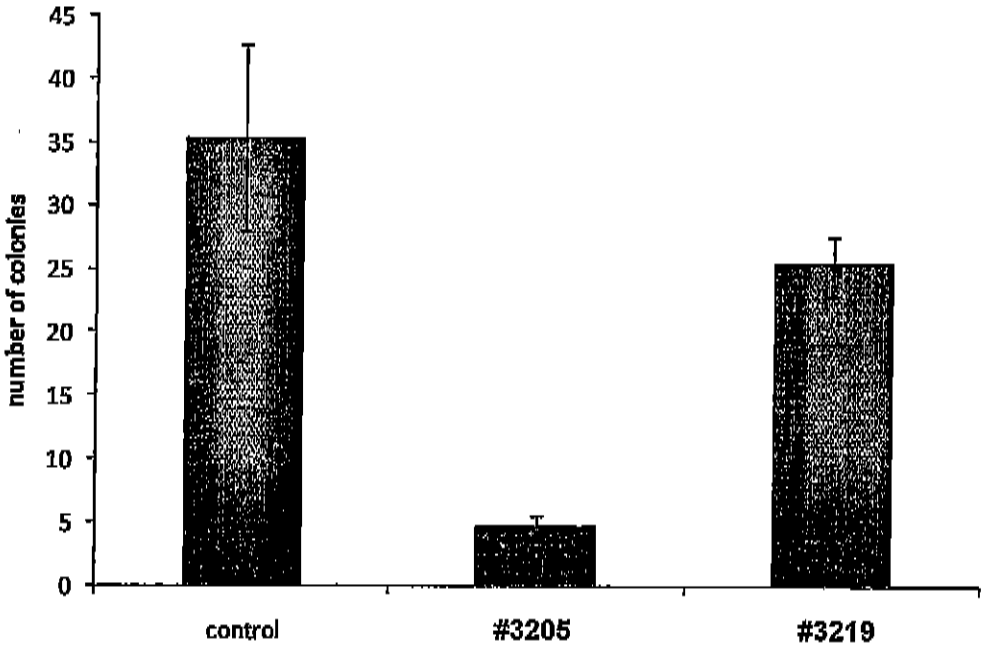
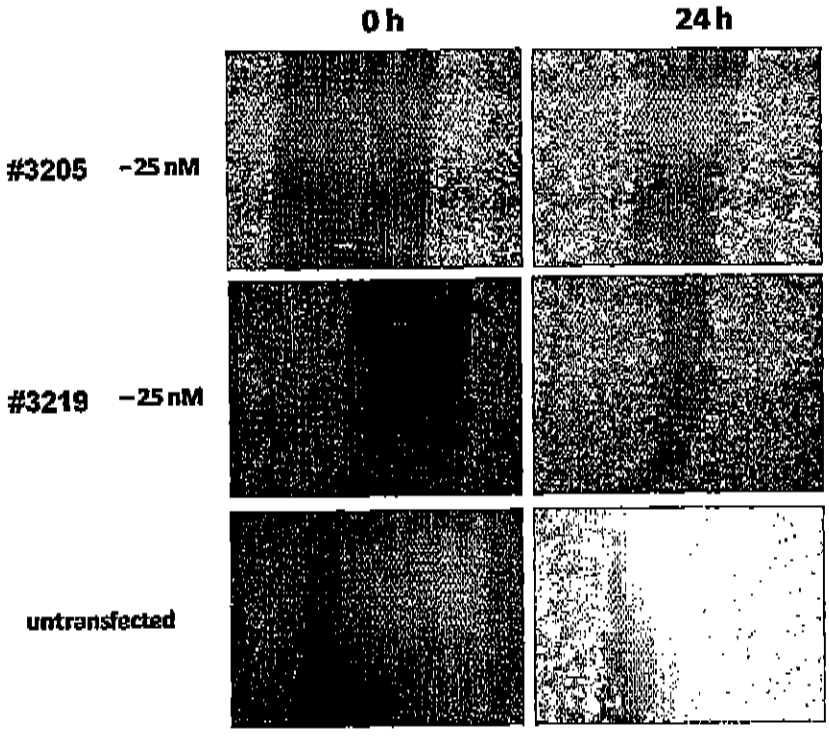
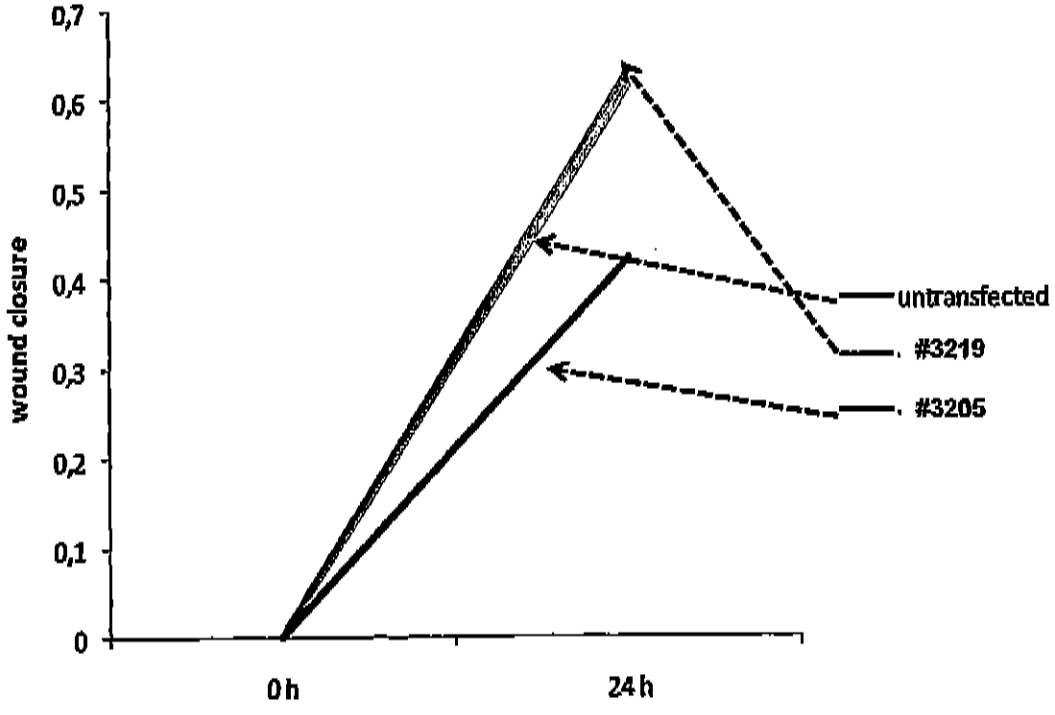


Figure 33.



(A)



(B)

Figure 34 A and B

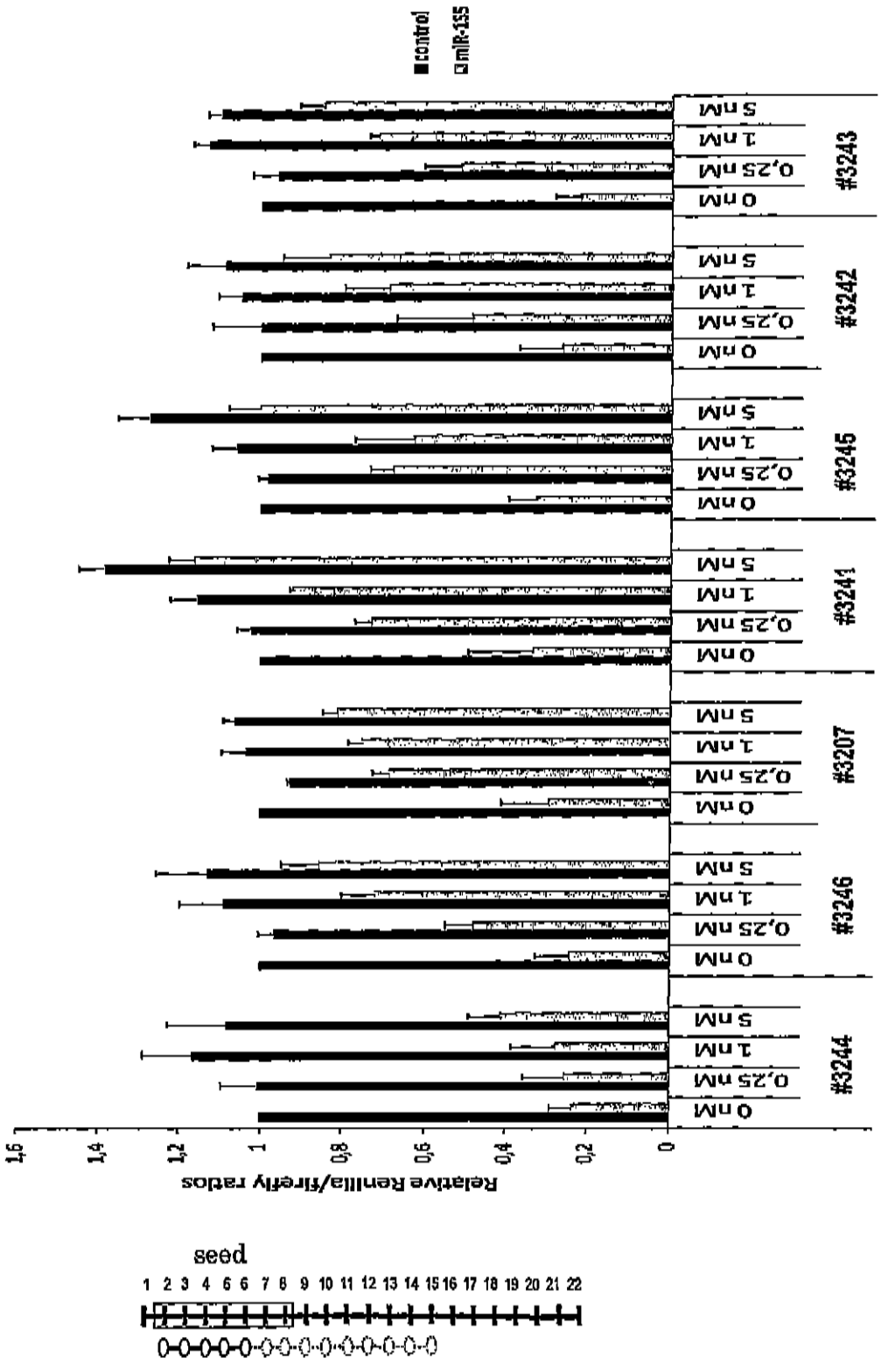
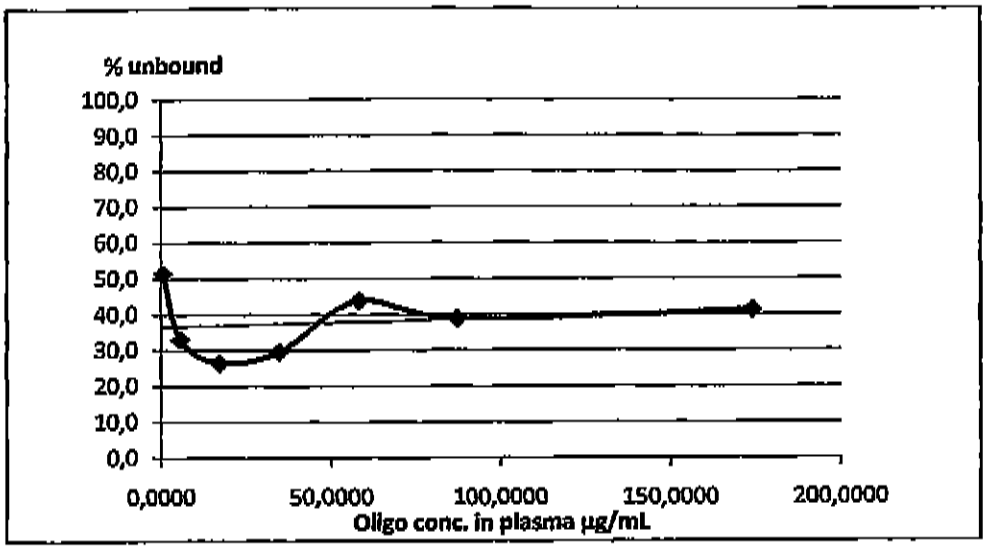
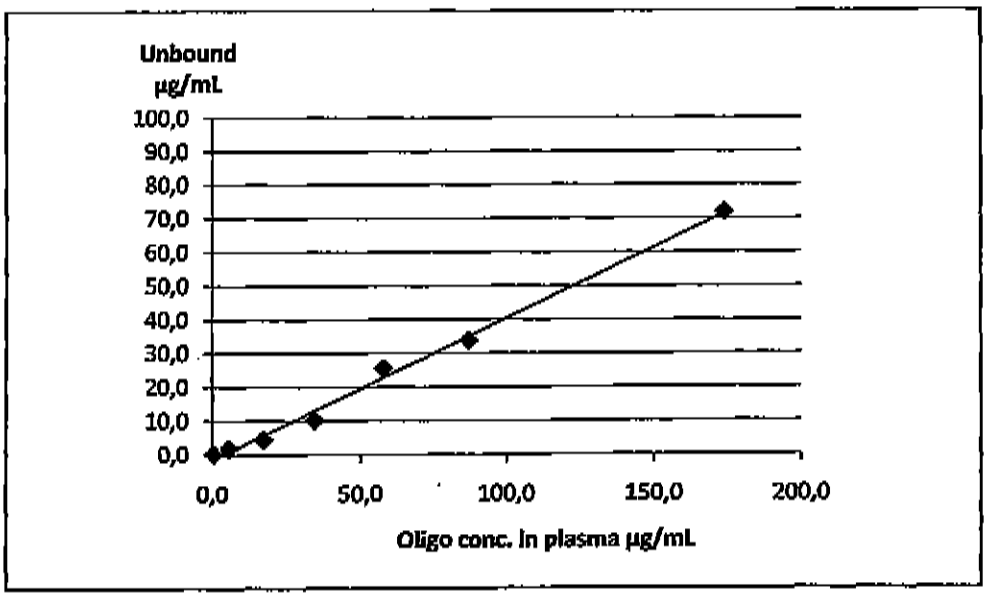

control
miR-155
#3243
#3242
#3245
#3241
#3207
#3246
#3244
0 nM
0,25 nM
1 nM
5 nM
Relative Renilla/firefly ratios
0
0,2
0,4
0,6
0,8
1
1,2
1,4
1,6
seed
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22

Figure 35.


% unbound
100,0
90,0
80,0
70,0
60,0
50,0
40,0
30,0
20,0
10,0
0,0
0,0000
50,0000
100,0000
150,0000
200,0000
Oligo conc. in plasma µg/mL

A)


Unbound
µg/mL
100,0
90,0
80,0
70,0
60,0
50,0
40,0
30,0
20,0
10,0
0,0
0,0
50,0
100,0
150,0
200,0
Oligo conc. in plasma µg/mL

B)

Figure 36.

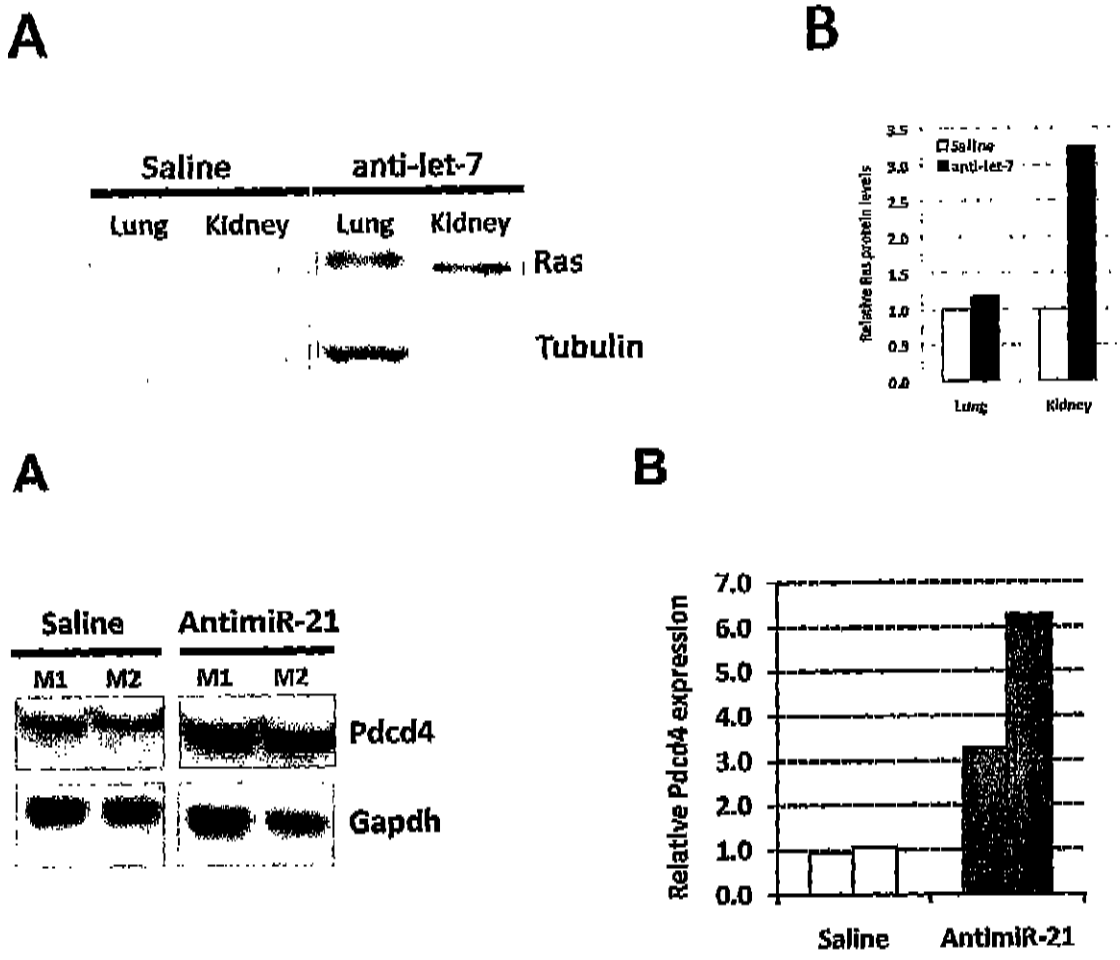

A
B
Saline
anti-let-7
Lung
Kidney
Lung
Kidney
Ras
Tubulin
Saline
anti-let-7
Relative Ras protein levels
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Lung
Kidney
A
B
Saline
AntimiR-21
M1
M2
M1
M2
Pdcd4
Gapdh
Relative Pdcd4 expression
7.0
6.0
5.0
4.0
3.0
2.0
1.0
0.0
Saline
AntimiR-21

Figure 37.

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<151> 2007-10-04

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<151> 2008-07-17

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gataagct 8

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tgataagct 9

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