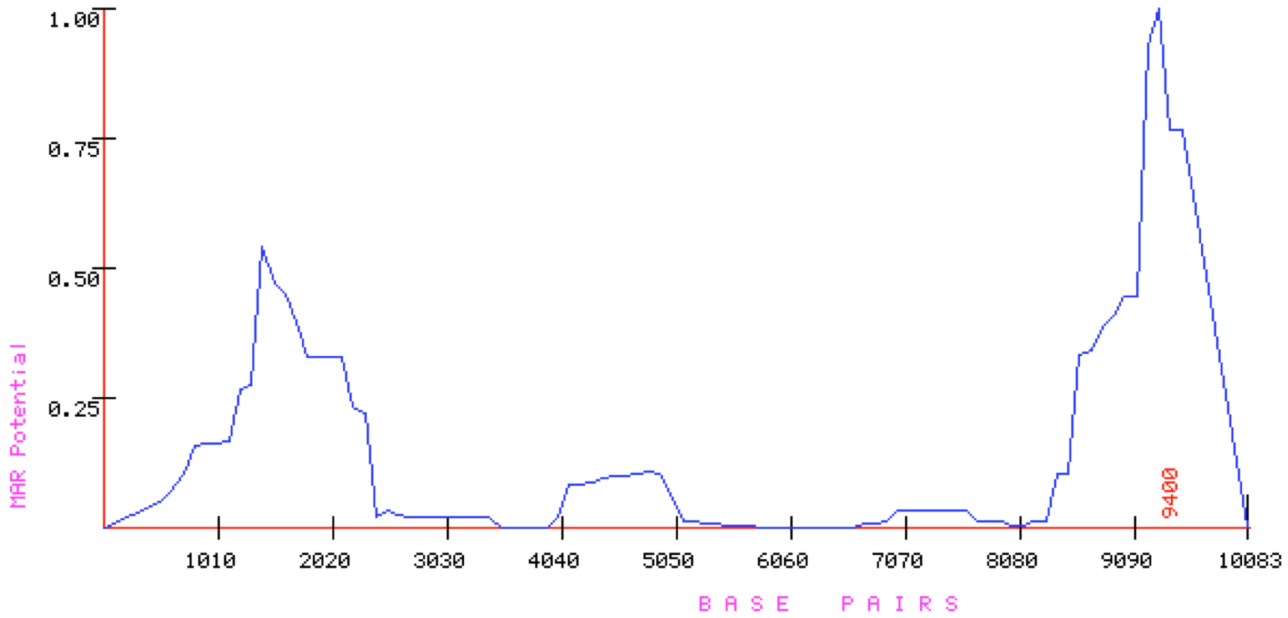
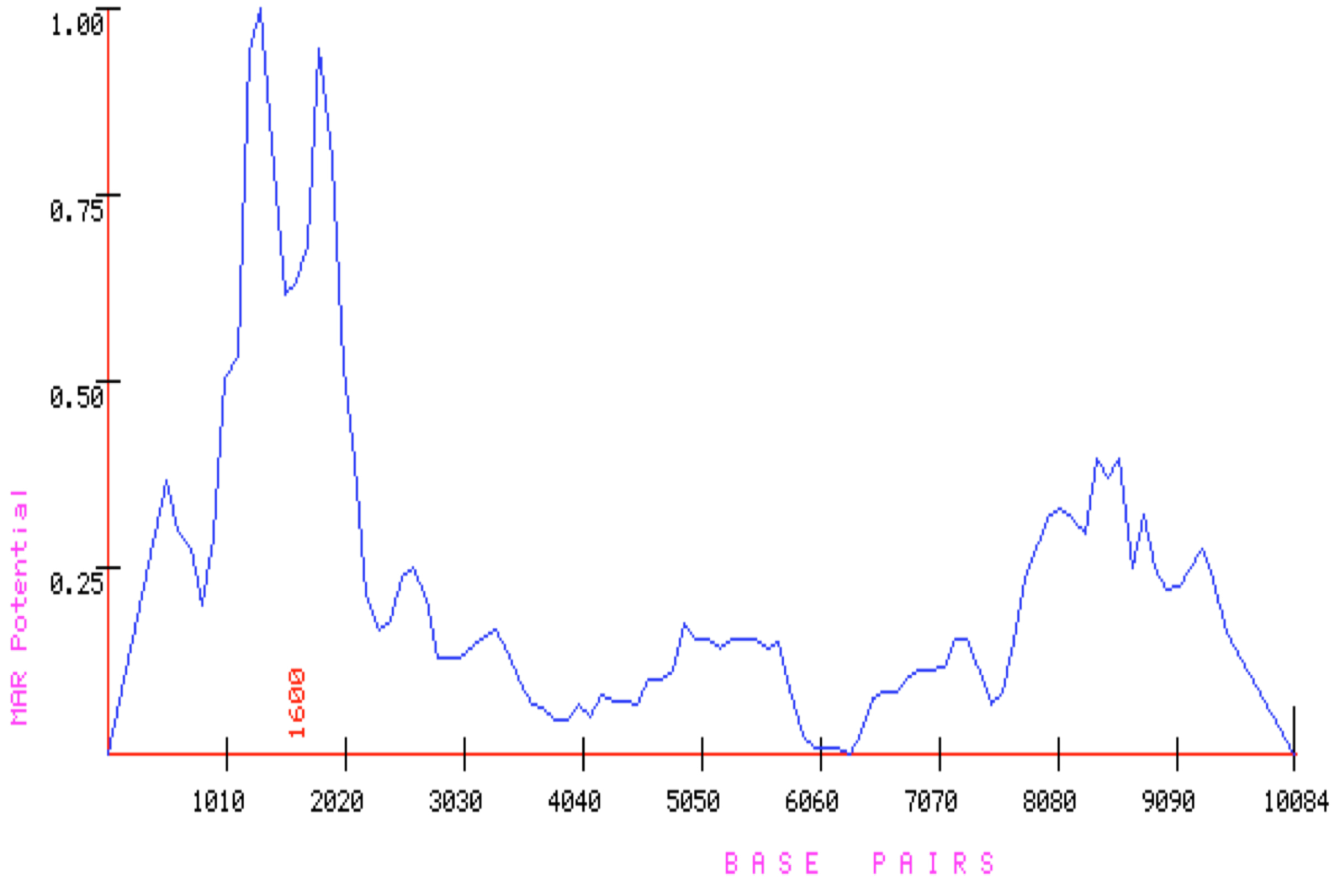
Supplementary Figure 1

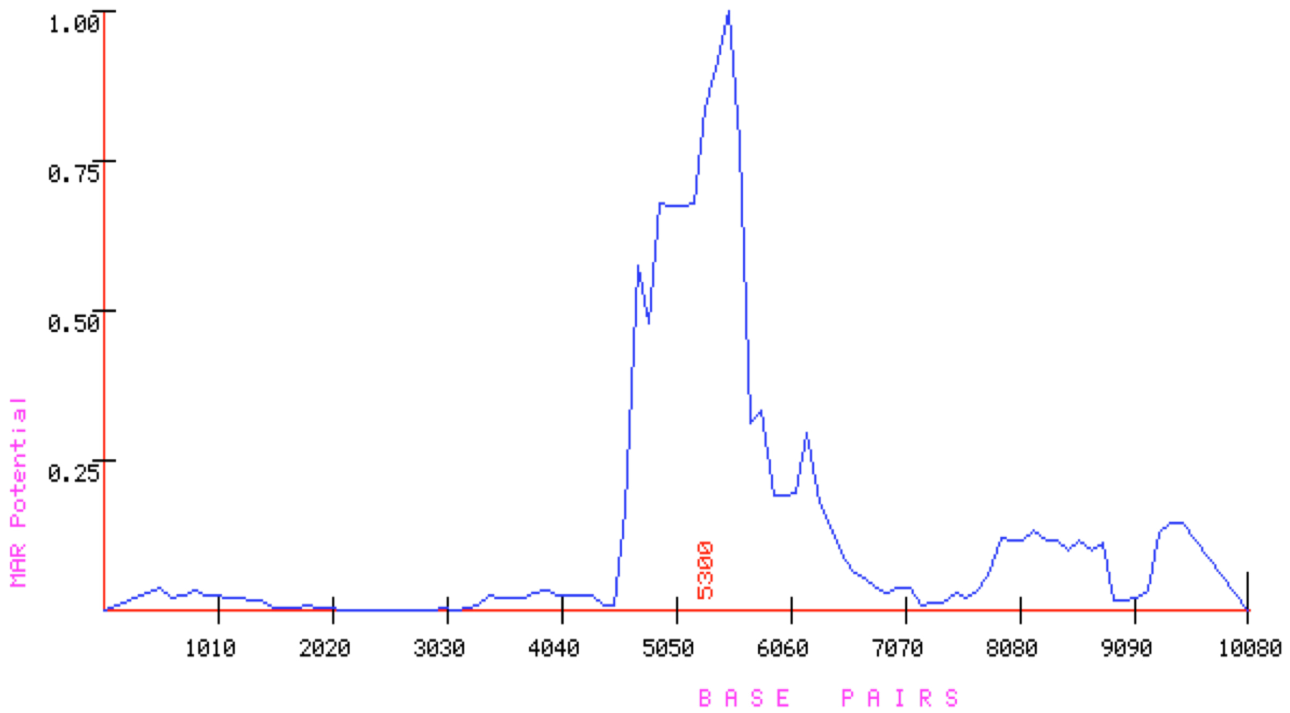
a) hsa-let-7b



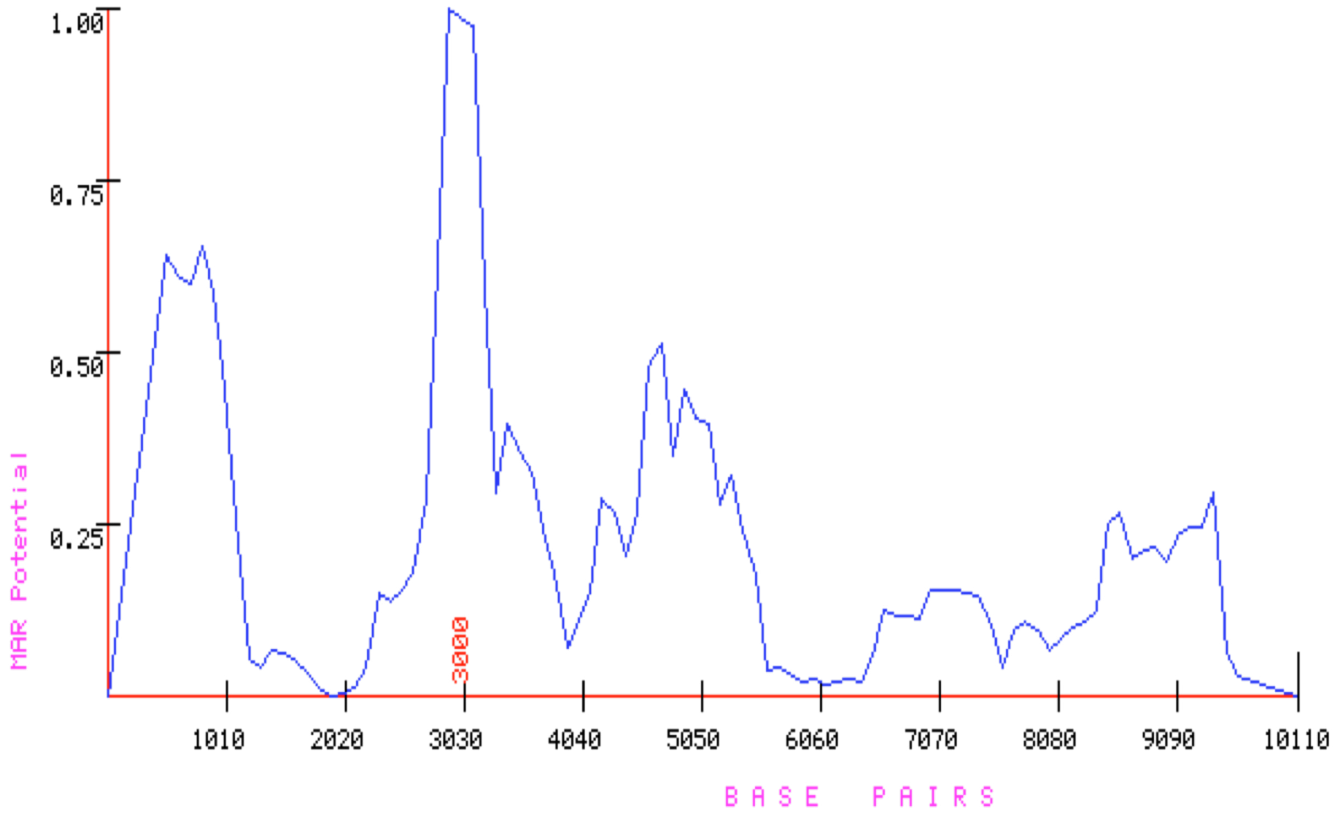
b) hsa-miR-17


1.00
0.75
0.50
0.25
MAR Potential
1600
1010
2020
3030
4040
5050
6060
7070
8080
9090
10084
BASE PAIRS

c) hsa-miR-93

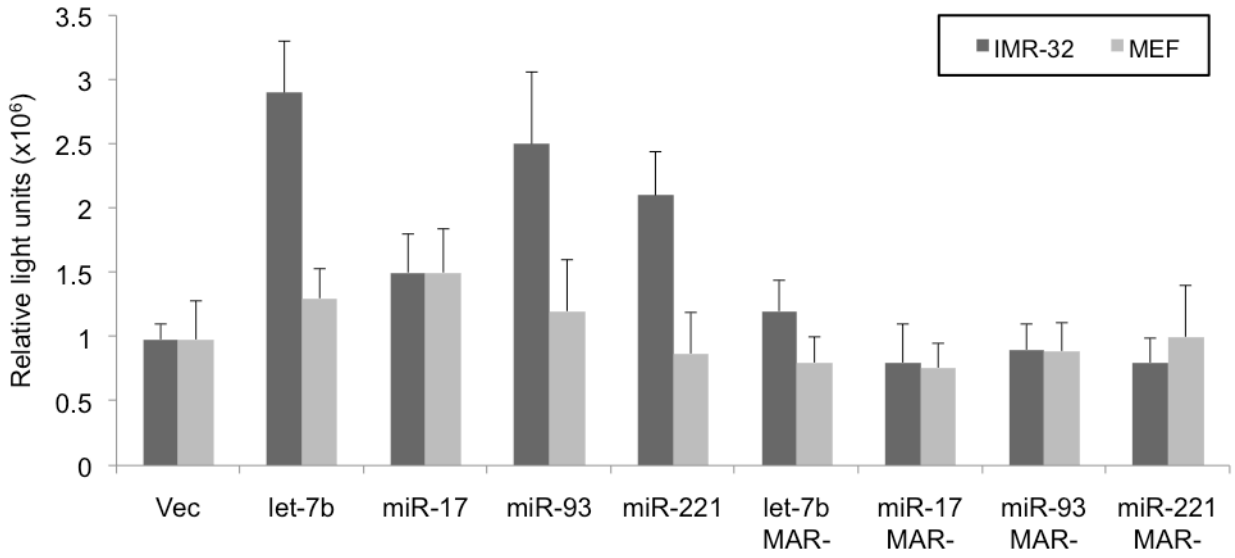

1.00
0.75
0.50
0.25
MAR Potential
5300
1010
2020
3030
4040
5050
6060
7070
8080
9090
10080
BASE PAIRS

d) hsa-miR-221



Prediction of putative MARs (peak position indicated in red) upstream of each of the miRNAs aberrantly expressed in neuroblastoma.

Supplementary Figure 2



Luciferase reporter assays were performed in IMR-32 or MEF cells employing 1 μg PGL2 constructs, where MAR elements from each of the indicated miRNAs were cloned upstream of luciferase gene. In a control experiment, the encompassing regions excluding the core MAR element (MAR-) were cloned upstream of luciferase gene to check for reporter activity. We seeded $1x10^5$ cells in 24 well plates, co-transfected them with GFP and 1μg of luciferase plasmids. We performed luciferase assays 48h post-transfection. Briefly, cells were washed once in 1X PBS and collected by centrifugation at 2500 rpm. The pellet was lysed in 1X passive lysis buffer on ice and after centrifugation at 13000 rpm for 10 min, protein was estimated. Equal amount of protein (100 μg) was used to perform the reporter assay using Dual reporter luciferase assay kit (Promega). Samples were loaded in duplicates and repeated as three individual experiments, to evaluate the fold increase in the reporter activity.