

```

From offset 559 to 580 | Folding energy = -37.900002 Kcal/mol
5'<-- target -->3'      -linker-      5'<-- microRNA -->3'
ACCTGGCTGAGGAGCTGGGCCA GCGGGACGC UGGCUCAGUUCAGCAGGAACAG
.((((.((((...(((((((( ----- )))))))))))...
A----CCTGGCTGAGGAGCTGGGCCA
      |||  |||  |||||
GACAAGGAC-GACU---UGACUCGGU

From offset 1074 to 1095 | Folding energy = -26.799999 Kcal/mol
5'<-- target -->3'      -linker-      5'<-- microRNA -->3'
GTTACTGGCTTCTCTTGAGTCA GCGGGACGC UGGCUCAGUUCAGCAGGAACAG
(((.(.((((...(((((((( ----- ))))))))...)))..
--GTTACTGGCTTCTCTTGAGTCA
   |||  ||  |||  |||||
GACAA-GGACGACUU-GACUCGGU

```

**Supplemental Figure S1. RNA22 analysis** (<http://cbcsrv.watson.ibm.com/rna22.html>). RNA22 analysis of the p16INK4A and miR-24 sequences yielded the predicted sites of miR-24 association with the p16 mRNA [CR (559-580) and 3'UTR (1074-1095)]. The default stringency settings were used:

- maximum number of allowed UN-base paired bases = 0 in seed/nucleus of 7 nucleotides
- minimum number of paired-up bases in heteroduplex = 14
- maximum folding energy for heteroduplex (Kcal/mol = -25)