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)