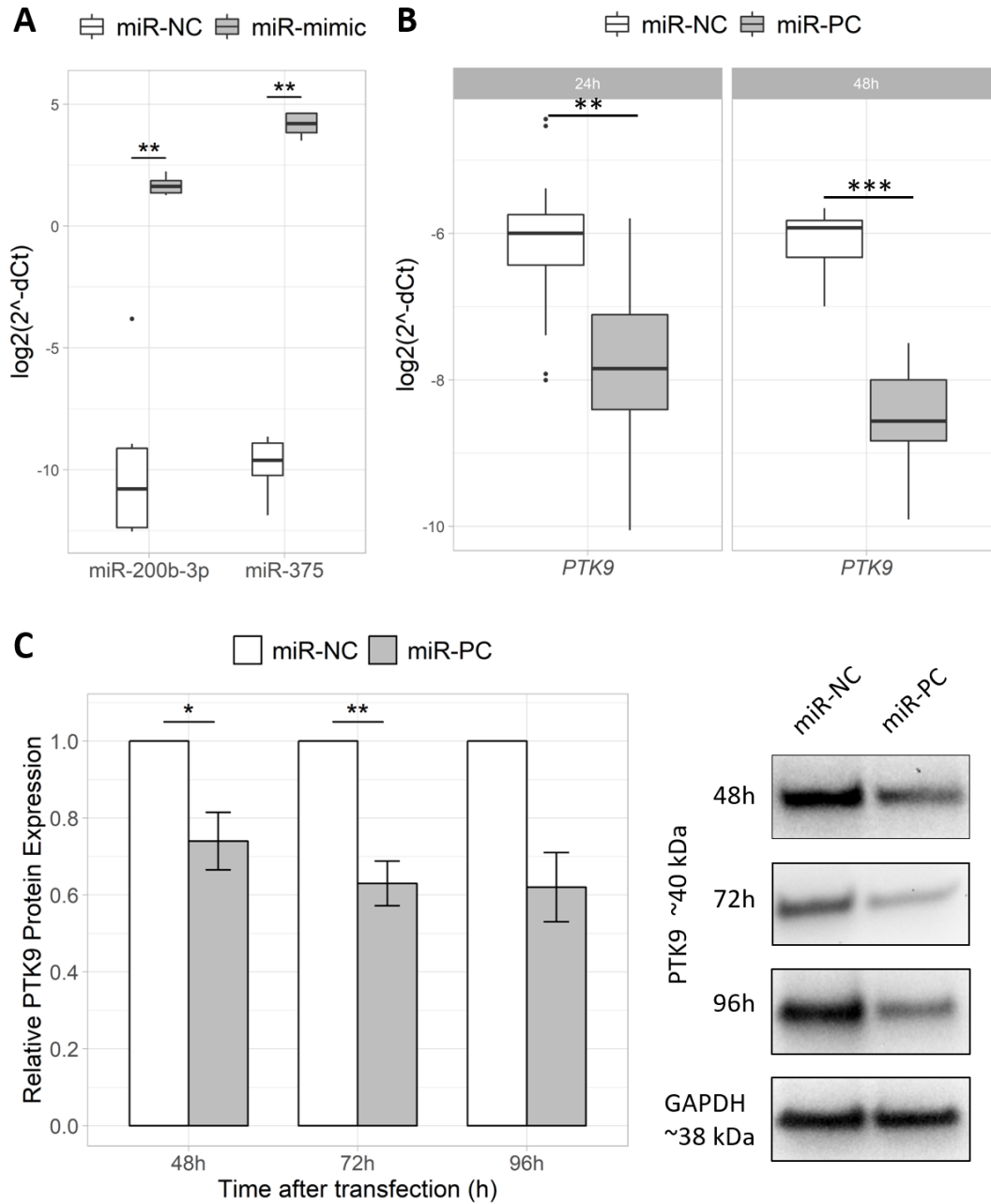


Supplementary data



**Figure S1:** Evaluation of miRNA transfection and silencing efficiency. (A) Upregulation of miRNAs miR-375-3p and miR-200b-3p was observed after transfection with corresponding miRNA mimics; (B) PTK9 gene was downregulated after transfection with miRvana miRNA Mimic miR-1 positive control and (C) PTK9 protein was downregulated after transfection with miRvana miRNA Mimic miR-1 positive control. miR-NC—miRNA mimic negative control, miR-PC—miRNA mimic positive control. \*  $p < 0.05$ , \*\*  $p < 0.005$ , \*\*\*  $p < 0.0005$ .

**Table S1:** Binding positions and insert sequences for the construction of pMIR-REPORT-Luciferase vectors, used for the investigation of direct miRNA-target binding. The sequences coding the predicted microRNA binding sites in the 3'UTR of the target genes are highlighted in grey. Changed nucleotides in the mutant insert sequences are colored in red.

Mature miRNA ID	Mature miRNA Accession Number	Target Symbol	Target Ensembl Number	miRNA Binding Position	Insert type	Insert sequences (5' to 3')		
						Forward	Reverse	
miR-375-3p	MIMAT0000728	KIT	ENSG00000157404	453-459	Wt	Forward	CTGCGCACTAGTTGGAAAACAGAACATCATTAGAACAAAGGACAGAGTATGAACACCTGAAGCTTAATAAA	
						Reverse	TTTATTAAGCTTCAGGTGTTCACTCTGTCCTTTGTTCTAATGATGTTCTGTTTTCCAAGTGTGCGCAG	
					Mut	Forward	CTGCGCACTAGTTGGAAAACAGAACATCATTAGATGAAAGGACAGAGTATGAACACCTGAAGCTTAATAAA	
						Reverse	TTTATTAAGCTTCAGGTGTTCACTCTGTCCTTTATCATTAATGATGTTCTGTTTTCCAAGTGTGCGCAG	
					549-555	Wt	Forward	CTGCGCACTAGTAAAAAATGATCCCAAGTGTGAACAAAAGATGCTCTTCTGTGGACCAAAGCTTAATAAA
							Reverse	TTTATTAAGCTTTGGTCCACAGAAGAGCATCTTTGTTACACTTGGGGATCATTTTTACTAGTGTGCGCAG
				Mut		Forward	CTGCGCACTAGTAAAAAATGATCCCAAGTGTGAAAGGAAAGATGCTCTTCTGTGGACCAAAGCTTAATAAA	
						Reverse	TTTATTAAGCTTTGGTCCACAGAAGAGCATCTTTCTTACACTTGGGGATCATTTTTACTAGTGTGCGCAG	
				855-861	Wt	Forward	CTGCGCACTAGTATAACCACAAAGCACAGTTTGAACAAAATCTCCTCTTTAGCTGATGAAGCTTAATAAA	
						Reverse	TTTATTAAGCTTCATCAGCTAAAAGAGGAGATTTGTTCAAAGTGTGCTTTGTGGTTATACTAGTGTGCGCAG	
					Mut	Forward	CTGCGCACTAGTATAACCACAAAGCACAGTTTGAAGGAAATCTCCTCTTTAGCTGATGAAGCTTAATAAA	
						Reverse	TTTATTAAGCTTCATCAGCTAAAAGAGGAGATTTCTTCAAAGTGTGCTTTGTGGTTATACTAGTGTGCGCAG	
miR-200b-3p	MIMAT0000318	EGFR	ENSG00000146648	5849-5855	Wt	Forward	TGCGCACTAGTAAAGTTTTGCAATGATGAAAGCAGTATTTGTACAAATGAAAAGCAGAAAAGCTTAATAAA	
						Reverse	TTATTAAGCTTTTCTGCTTTTCATTTGTACAAACTGCTTTCATCATTGCAAAACTTACTAGTGTGCGCA	
					Mut	Forward	CTGCGCACTAGTAAAGTTTTGCAATGATGAAAGCAGCCTTTGTACAAATGAAAAGCAGAAAAGCTTAATAAA	
						Reverse	TTTATTAAGCTTTTCTGCTTTTCATTTGTACAAAGGCTGCTTTCATCATTGCAAAACTTACTAGTGTGCGCA	
				5927-5933	Wt	Forward	TGCGCACTAGTAAATGTTGATTGTGCATTGAGTATTAATAAATTAGATGTATATTATAAGCTTAATAAA	
						Reverse	TTATTAAGCTTATAATATACATCTAATTTTTAATACTCAATGCACAATCAACATTTCACTAGTGTGCGCA	
					Mut	Forward	CTGCGCACTAGTAAATGTTGATTGTGCATTGAGTCTTAAATAAATTAGATGTATATTATAAGCTTAATAAA	
						Reverse	TTTATTAAGCTTATAATATACATCTAATTTTTAGGACTCAATGCACAATCAACATTTCACTAGTGTGCGCA	
		ETV1		Wt	Forward	CTGCGCACTAGTCTTTTTGCATATAGACTCCAGTATTAGTTACTTTCATTCTAAAATTAAGCTTAATAAA		
					Reverse	TTTATTAAGCTTAATTTTGAATGAAAGTAACTAATACTGGAGTCTATATGCAAAAAAGACTAGTGTGCGCAG		
				Mut	Forward	CTGCGCACTAGTCTTTTTGCATATAGACTCCAGGCTTAGTTACTTTCATTCTAAAATTAAGCTTAATAAA		
					Reverse	TTTATTAAGCTTAATTTTGAATGAAAGTAACTAAGCCTGGAGTCTATATGCAAAAAAGACTAGTGTGCGCAG		

**Table S2.** Predicted pairing of target region and miRNA (data obtained from the TargetScanHuman database). The microRNA-target binding sites are highlighted in grey. Changed nucleotides in the mutant insert sequences are colored in red.

	Predicted pairing of target region (top) and miRNA (bottom)	
	Wild type target sequence	Mutant target sequence
Position 453-459 of KIT 3' UTR	5' ...AACAGAAUCAUUAAGAACAAG...	5' ...AACAGAAUCAUUAAGATGAAAG...
hsa-miR-375	3' AGUGCGCUCGGCUUGCUUGUUU	3' AGUGCGCUCGGCUUGCUUGUUU

Position 549-555 of KIT 3' UTR	5' ...AUGAUCCCCAAGUGUGAACAAAA... 	5' ...AUGAUCCCCAAGUGUGAA <b>GG</b> AAA... 
hsa-miR-375	3' AGUGCGCUCGGCUUGCUUGUUU	3' AGUGCGCUCGGCUUGCUUGUUU
Position 855-861 of KIT 3' UTR	5' ...CACAAAGCACAGUUUGAACAAAA... 	5' ...CACAAAGCACAGUUUGAA <b>GG</b> AAA... 
hsa-miR-375	3' AGUGCGCUCGGCUUG-- CUUGUUU	3' AGUGCGCUCGGCUUG-- CUUGUUU
Position 5849-5855 of EGFR 3' UTR	5' ...UUGCAAUGAUGAAAGCAGAUUUU... 	5' ...UUGCAAUGAUGAAAGCAG <b>CC</b> UUU... 
hsa-miR-200b-3p	3' AGUAGUAAUGGUCCGUCAUAAU	3' AGUAGUAAUGGUCCGUCAUAAU
Position 5927-5933 of EGFR 3' UTR	5' ...GUUGAUUGUGCAUUGAGAUUUA... 	5' ...GUUGAUUGUGCAUUGAG <b>CC</b> UUA... 
hsa-miR-200b-3p	3' AGUAGUAAUGGUCCGUCAUAAU	3' AGUAGUAAUGGUCCGUCAUAAU
Position 4455-4462 of ETV1 3' UTR	5' ...UUUGCAUUAUAGACUCCAGAUUA... 	5' ...UUUGCAUUAUAGACUCCAG <b>GC</b> UUA... 
hsa-miR-200b-3p	3' AGUAGUAAUGGUCCGUCAUAAU	3' AGUAGUAAUGGUCCGUCAUAAU