Table S1. References used for selection of the investigated genes and polymorphisms

GENE	Variant ID	References
AGO1	rs636832	[38-40]
DROSHA	rs10035440	[20, 41]
	rs3805500	[19-21]
MIR219-1	rs107822	[42, 43]
	rs213210	[31, 43]
MIR146a	rs2910164	[12, 44]
MIR300	rs12894467	[45, 46]
MIR499a	rs3746444	[12, 26]
MIR608	rs4919510	[47, 48]
MIR938	rs2505901	[31, 34]

Table S2. Characterization of the polymorphisms analyzed in the present study and their quality control parameters

GENE	rs	ALLELE	FUNCTION	QUALITY CONTROL			
				MAF	Genotyping rate	HWE*	Status
AGO1	rs636832	A>G	Intron variant	36%	80%	0.33887	Included
DROSHA	rs10035440	T>C	Intron variant	15%	81%	1.0000	Included
DROSHA	rs3805500	G>A	Intron variant	49%	83%	0.20689	Included
MIR146a	rs2910164	G>C	Mature miRNA variant	29%	86%	0.12694	Included
MIR219-1	rs213210	A>G	Regulatory region variant	17%	89%	0.02196	Included
MIR219-1	rs107822	C>T	TF binding site	37%	80%	0.07143	Included
MIR300	rs12894467	T>C	Non-coding transcript exon variant	39%	90%	0.00204	Included
MIR499a	rs3746444	A>G	Mature miRNA variant	18%	86%	0.11173	Included
MIR608	rs4919510	G>C	Mature miRNA variant	36%	86%	1.0000	Included
PRE-MIR-938	rs2505901	C>T	Intron variant	40%	81%	0.00859	Included

*Significance adjusted for multiple comparisons by the Bonferroni correction ($P \leq 0.001$).