

Figure S1. Allele discrimination plot (single-nucleotide polymorphism assay, rs3746444). Alleles as wild-type homozygous A/A (lower right red cluster), heterozygous A/G (middle green cluster) and mutant homozygous G/G (upper left blue cluster) were retrieved using allele-calling software.

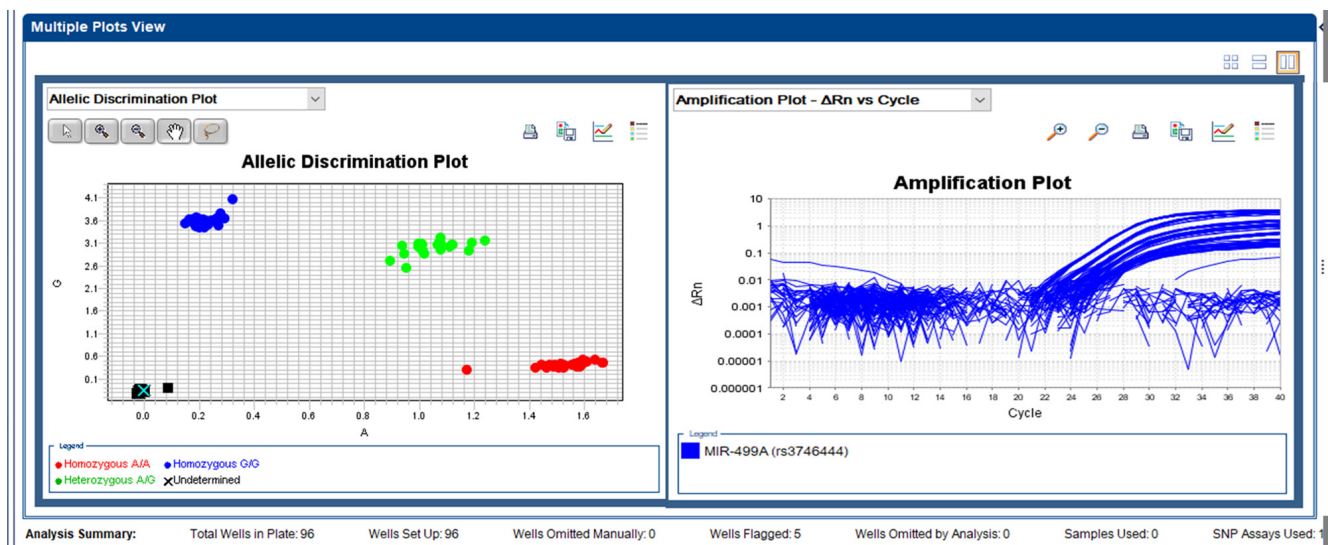


Figure S2. Secondary stem-loop structure of the miR-499a precursor, found in *Homo sapiens* (length, 90 nucleotides). This structure is annotated by seven databases, including European Nucleotide Archive, miRBase, Ensembl, NCBI Reference Sequence, Rfam, GENCODE and HUGO Gene Nomenclature Committee. Human miRNA *hsa-mir-449a* precursor sequence is a product of the miR-449a gene (MIR449A). The black nucleic acid bases are the same type as those present in the template, green bases indicate that these bases are not the same as the template, while red base indicates inserted new nucleotide. Data source, <https://rnacentral.org/rna/URS00006A0D74/9606.miR/miRNA,microRNA>.

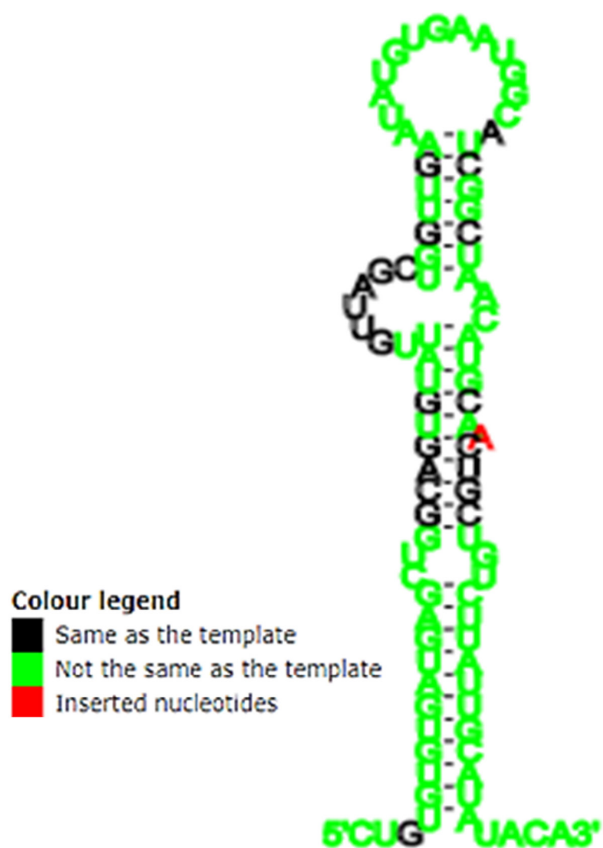


Table SI. Summary of the molecular and biological functions of miR-499a.

Molecular function/biological process (GO)	Evidence code	(Refs.)
mRNA binding involved in post-transcriptional gene silencing (1903231)	IDA	(11-14)
Gene silencing by miRNA (0035195)	IDA	(11-14)
miRNA-mediated inhibition of translation (0035278)	IDA	(13)
Negative regulation of myoblast proliferation (2000818)	IDA	(11)
Positive regulation of blood vessel endothelial cell migration (0043536)	IDA	(13)
Positive regulation of cardiac muscle cell differentiation (2000727)	IDA	(11)
Positive regulation of vascular-associated smooth muscle cell migration (1904754)	IDA	(13)
Positive regulation of vascular endothelial cell proliferation (1905564)	IDA	(13)
Positive regulation of vascular smooth muscle cell proliferation (1904707)	IDA	(13)
Transition between fast and slow fiber (0014883)	ISS	(14)

Data source (14). miR/miRNA, microRNA; GO, Gene Ontology; IDA, inferred from direct assay; ISS, inferred from sequence or structural similarity.