

S2 Table. Primers used for miRNA cloning and qPCR expression analysis.

miRNA	Primer sequence	Amplified fragment size	Use
mir-299	Fw: ACACACACCTCGAGAGTTCTGCCTTGGGAAATCG	489 bp ^a	miRNA cloning
	Rv: ACACACACGGATCCTGTTTGGCACTGAGGAGAAG		
mir-541	Fw: ACACACACCTCGAGGTTCCACTCCTGCTGACTCC	554 bp ^a	miRNA cloning
	Rv: ACACACACGGATCCTATCAACAGCTGGCTGACCA		
mir-508	Fw: ACACACACGGATCCGCATGCCTCCTTTGGACAAG	511 bp ^a	miRNA cloning
	Rv: ACACACACCTCGAGATTTGTTGCCACTGAAGAGA		
mir-503	Fw: ACACACACGGATCCGGGGTGCCAAATGAAGCAT	395 bp ^a	miRNA cloning
	Rv: ACACACACCTCGAGGCTCGCGTCTCTGTTTCC		
mir-938	Fw: CACACACAAGATCTCCAATCATTCTGGCAGTGA	549 bp ^a	miRNA cloning
	Rv: CACACACACTGCAGTTCATTGCTTGTGGGATCA		
hsa-miR-299-3p	Fw: AGTATGTGGGA T GGTAAACC	46 bp	qPCR analyses
	Rv: GGTCCAGTTTTTTTTTTTTTTTAAGC		
ptr-miR-299-3p	Fw: GTATGTGGGA C GGTAAACC	45 bp	qPCR analyses
	Rv: GGTCCAGTTTTTTTTTTTTTTTAAGC		
hsa-miR-503-3p	Fw: CGCAGGG G GTATTGTTTC	44 bp	qPCR analyses
	Rv: GTTTTTTTTTTTTTTTCTGGCA		
ptr miR-503-3p	Fw: CGCAGGG A GTATTGTTTC	44 bp	qPCR analyses
	Rv: GTTTTTTTTTTTTTTTCTGGCA		
hsa-miR-508-3p	Fw: CAGTGATTGTAGCCTTTT G GA	48 bp	qPCR analyses
	Rv: AGGTCCAGTTTTTTTTTTTTTTCTAC		
ptr-miR-508-3p	Fw: GCAGTGATTGTAGCCTTTT T GA	49 bp	qPCR analyses
	Rv: AGGTCCAGTTTTTTTTTTTTTTCTAC		
hsa-miR-541-3p mml-miR-541-3p ^b	Fw: CAGTGGTGGGCACAGA	46 bp	qPCR analyses
	Rv: GTCCAGTTTTTTTTTTTTTTTAGTCC		
hsa-miR-938-5p	Fw: CAGTGCCCTTAAAGGTGA	43 bp	qPCR analyses
	Rv: CAGTTTTTTTTTTTTTTACTGGGT		

Nucleotides shown in bold letters indicate the difference between the human and non-human miRNA variants. ^aThe cloning fragment size includes the precursor miRNA sequence plus 120-300 bp at both extremes and primers tail recognized by the restriction enzyme. ^bNon-human variants were chimpanzee miRNA sequences, except miR-541-3p, for which we used the macaque sequence due to the pre-miRNA has not been described in chimpanzee. Same primers were used for human and macaque miR-541-3p qPCR amplification since they did not match the nucleotide substitution between both variants.