

## Supporting Information

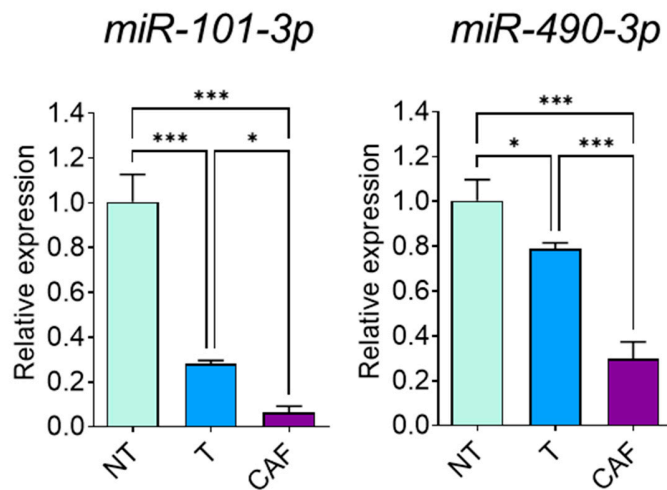
**Table S1.** The binding probability of miRs to *TGFBRI* mRNA were predicted by TargetScan 8.0

miRNAs	Position in the 3'-UTR	Seed match	Context++ score	Predicted relative KD
<i>hsa-miR-101-3p</i>	460-466	7mer-m8	-0.29	-3.849
	3993-4000	8mer	-0.24	-3.714
<i>hsa-miR-490-3p</i>	3933-3939	7mer-m8	-0.17	-3.435

**Table S2.** Primer sequences.

Gene		Sequence
<i>hsa-miR-101-3p</i>		5'-TACAGTACTGTGATAACTGAA-3'
<i>hsa-miR-490-3p</i>		5'-CAACCTGGAGGACTCCATGCTG -3'
<i>TGFBR1</i>	Forward	5'-GGGGATGGGGGAAATACGAC-3'
	Reverse	5'-CCAGAGCAGCCTTCAGTCAA-3'
<i>HMBS</i>	Forward	5'- GGAGGGCAGAAGGAAGAAAACAG -3'
	Reverse	5'-CACTGTCCGTCTGTATGCGAG-3'
<i>GAPDH</i>	Forward	5'-AGTATGACAACAGCCTCAAG-3'
	Reverse	5'-TCATGAGTCCTTCCACGATA-3'

**Figure S1. The qRT-PCR results of two miRs**



**Figure S2. Confirmation of mycoplasma-free cultures in this study**

