SUPPLEMENT

Sixty Yanbian yellow steers raised in the Jilin Province Hunchun Animal Husbandry to the age of approximately 30 months were used in the study. All test cattle were fattened under the same feeding conditions until slaughter. Immediately after slaughter, samples of the longissimus dorsi muscle tissue were obtained. Based on the marbling pattern, three individuals each with a relatively high or low marbling grade were selected and assigned to the high- and low-fat groups, respectively. miRNA-Seq and RNA-Seq were conducted, and genes with differential expression were identified. The experimental procedures were approved by the Yanbian University Animal Care and Use Committee.

| hts miP 1271 mimiss (double strand) | 5'-CUUGGCACCUAGUAAGUACUCA-3' | | |
|-------------------------------------|------------------------------|--|--|
| bta-mix-12/1 minics (double-strand) | 5'-AGUACUUACUAGGUGCCAAGUU-3' | | |
| Mimios NC (double strend) | 5'-UUCUCCGAACGUGUCACGUTT-3' | | |
| Minnes NC (double-strand) | 5'-ACGUGACACGUUCGGAGAATT-3' | | |
| bta-miR-1271 inhibitor | 5'-UGAGUACUUACUAGGUGCCAAG-3' | | |
| Inhibitor NC | 5'-CAGUACUUUUGUGUAGUACAA-3' | | |

Table S1. miRNA sequence

| Table S2. | Primers | targeting | the seed | region | of the | candidate | target | gene A | TF3 |
|-----------|---------|-----------|----------|--------|--------|-----------|--------|--------|-----|
| | | | | - 0 - | | | | 0 | |

| Primer name | Primer sequence (5'-3') |
|-------------|---------------------------------------|
| ATF3-WT-F | CAT <u>GAGCTC</u> CGACACTGCTGTGACTTTT |
| ATF3-WT-R | CAG <u>TCTAGA</u> GCTTTCTTCCTGTGACCTT |
| ATF3-MUT-F | TTTGGATCAACAGAAAAGATGTCTTCCGC |
| ATF3-MUT-R | TTTCTGTTGATCCAAAACTGCACTCAGCGCTG |

Note. The underlined nucleotides represent enzyme cutting sites.

| Primer name | GenBank accession No. | Primer sequence (5'-3') |
|--------------|-----------------------|----------------------------|
| ATF3-F | NIM 001046102 2 | AAAGCAGAAAACACGAGTCCA |
| ATF3-R | NM_001040195.2 | AATGTGGTTTTCAATCGCAAG |
| PPARγ-F | NIN 191024 2 | CGAGAAGGAGAAGCTGTTGG |
| PPARγ-R | NM_181024.2 | TCAGCGGGAAGGACTTTATG |
| C/EBPa-F | NIM 176794 2 | TGGACAAGAACAGCAACGAG |
| C/EBPa-R | INM_1/0/84.2 | TCACTGGTCAACTCCAGCAC |
| β-Actin-F | NM 172070 2 | AGGCATCCTGACCCTCAAGTA |
| β-Actin-R | INM_173979.3 | GCTCGTTGTAGAAGGTGTGGT |
| bta-miR-1271 | MIMAT0009975 | CTTGGCACCTAGTAAGTACTCA |
| bta-let-7a | MIMAT0003844 | CGGTGAGGTAGTAGGGTTGTATAGTT |

 Table S3. Primers used for qRT-PCR analysis



Fig. S1. ATF3 is a candidate target gene of bta-miR-1271. a and b) miRNA-seq and RNA-seq analyze in longissimus dorsi muscle of Yanbian yellow cattle with high-fat groups (H1, H2, H3) and low-fat groups (L1, L2, L3). Data here is not fully shown. c) TargetScan prediction result. d) ATF3 coexists in both results.