

Table S1. Information of different species miR-31 in phylogenetic tree

| Gene | Species | Number |
|------------|--------------------|-------------|
| gga-miR-31 | Chicken | NR_031499.1 |
| hsa-miR-31 | Human | NR_029505.1 |
| mmu-miR-31 | House Mouse | NR_029747.1 |
| bmo-miR-31 | Domenstic Silkworm | NR_107250.1 |
| cfa-miR-31 | Dog | NR_049225.1 |
| eca-miR-31 | Horse | NR_032994.1 |
| tgu-miR-31 | Zebra finch | NR_049153.1 |
| bta-miR-31 | Cattle | NR_049716.1 |
| dre-miR-31 | Zebra fish | NR_034276.1 |
| ola-miR-31 | Japanese Medaka | NR_107194.1 |
| ptr-miR-31 | Chimpanzee | NR_032004.1 |
| ssc-miR-31 | Pig | NR_128414.1 |
| ocu-miR-31 | Rabbit | NR_162489.1 |
| cgr-miR-31 | Chinese hamster | NR_105204.1 |
| mml-miR-31 | Rhesus Monkey | NR_032003.1 |
| rno-miR-31 | Norway Rat | NR_031845.1 |

Table S2. Primers sequences of gga-miR-31-5p promoter different recombinant vectors

| Name of fragment | Length of product | Primer sequence (5'-3') |
|------------------|-------------------|------------------------------------------------------------------------------------------------|
| pGL3-miR-31-2180 | 2226bp | F2:attctctatcgataggtaccCCTGCAAGGTCACAGTGAAAC R2:gcttacttagatcgagatctcgagCTTGTTAGAAAGCCATCTG |
| pGL3-miR-31-1344 | 1390bp | F3:attctctatcgataggtaccAAGCTGAACTTCATACAC R2:gcttacttagatcgagatctcgagCTTGTTAGAAAGCCATCTG |
| pGL3-miR-31-584 | 630bp | F4:attctctatcgataggtaccGATCACTTACAGCATGCTG R2:gcttacttagatcgagatctcgagCTTGTTAGAAAGCCATCTG |
| Fragment 1 | 213bp | dF1:attctctatcgataggtaccCCTGCAAGGTCACAGTGAAAC dR1:caagtctacaATTAACACATTAAAGCCTTTCCCTC |
| Fragment 2 | 2023bp | dF2:atgtgttaatTGTAGACTTGTTTGTTGTC dR2: gcttacttagatcgagatctcgagCTTGTTAGAAAGCCATCTG |
| Fragment 3 | 405bp | dF1: attctctatcgataggtaccCCTGCAAGGTCACAGTGAAAC dR3: catctgttgaTTCTGATTAAGTAGAAAAATTAATTGTAG |
| Fragment 4 | 1831bp | dF3: ttaatcagaaTCAACAGATGGTTTGCTTTG dR2: gcttacttagatcgagatctcgagCTTGTTAGAAAGCCATCTG |
| Fragment 5 | 202bp | dF2: atgtgttaatTGTAGACTTGTTTGTTGTC dR3: catctgttgaTTCTGATTAAGTAGAAAAATTAATTGTAG |

Note: The lowercase letters are homologous arms.

Table S3. Prediction of transcription factors in the gga-miR-31-5p promoter region

| Promoter region | Transcription factor |
|-----------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| -584bp~+1bp | Ap-1, Atf, C/Ebpalpha, C/Ebpbeta, Cp1, CREB, CRE-BP1, D1, Ftz, GATA-1, GR, Hb, HNF-3, HSF1_(Long), ICSBP, MEB-1, NF-1, Oct-1, Oct-2.1, P40x, RAP1, Sp1, SRF, TBP, Zen-1 |
| -1344bp~-584bp | C/EBPalpha, Antp, AP-1, GCN4, C/EBPgamma, Sp1, GR, PR, NF-1, C/EBP, SRF, TBP, IRF-1, ADR1, CRE-BP1, GATA-1, ATF-a, Oct-1, Odd, C/EBPbeta, CPE_binding_pro, CREB, MEB-1, GCR1, C/EBPdelta, GLO, Hb, Ftz, Pit-1, HOXA4 |
| -2180bp~-1344bp | HNF-4alpha1, GR, c-Jun, CFF, HSTF, NF-E2, ER, Oct-1, NF-1, RAR-alpha1, C/EBPepsilon, MEB-1, ICSBP, Antp, C/EBPalpha, PR, TBP, Oct-11, Pit-1a, RAP1, HNF-3, Sp1, C/EBPbeta, SRF, HNF-1C, GCN4, GATA-1, HNF-1, REB1, REV-ErbAalpha, Odd, T3R-alpha, CPE_binding_pro, C/EBPgamma, LyF-1, Oct-2.1, ETF, PU.1 |