**Supplementary Tables:**

**Table S1.** The specific primer information of DEmRNAs were verified by qPCR.

| Gene | GenBank ID | Primer sequence (5′→3′) | Product size (bp) | Annealing temperature/℃ | Application |
|---|---|---|---|---|---|
| *PP1A* | NM_001308578.1 | F: TGGCAAGTCCATCTATGGCG<br>R: ATGCTTGCCATCCAACCACT | 157 | 60 | qPCR |
| *KIAA2013* | XM_042257240.1 | F: CTCTTCAGTCCAGGTGTGGAA<br>R: ATCTGGTCCCGCTCCCTATG | 149 | 60 | |
| *PDPR* | XM_027977618.2 | F: GTAAAGGGAGGCTCTGTGTGAA<br>R: GCATCGCGTCTGTCAGCAAC | 84 | 60 | |
| *HSP90AA1* | XM_027957416.2 | F: TTCAAACTCGTCAGACGCCC<br>R: TGGTGAGGGTTCGATCTTGC | 125 | 60 | |
| *ATP5PB* | XM_004002318.4 | F: TACCTGACAATGCTGTCCCG<br>R: TTGCCTGCAATACCCCTGG | 100 | 60 | |
| *JUP* | XM_027974516.2 | F: CTCCAAACGCAGCCACCAT<br>R: CGAGTGGATGCCAGAGTCAT | 101 | 60 | |
| *CD52* | NM_001368857.1 | F: ATCTCCAAAAGTGCTGCCCA<br>R: CCAGGACTCCAGTTTGTATCTGA | 117 | 60 | |
| *PABPC4* | XM_042246030.1 | F: AGCTGCTCAGAAGGATTCAAA<br>R: TGGTTCTTGGTGTTGAGGTCC | 102 | 60 | |
| *EEF1AKMT2* | XM_015103491.3 | F: ACAGGAGAAATCTGGTTTGGAG<br>R: CCAAATTTTGCAAGTTCAACCAGC | 140 | 60 | |
| *SAMD9* | XM_042248377.1 | F: AGGAGACAAGTAAACATCACAAC<br>R: GGGCATGAAGGAAATAACACAGG | 180 | 60 | |
| *HINT1* | XM_012178158.3 | F: TGAGGATGACCAGTGTCTTGC<br>R: TTCTTCAGGCCCAGATCAGC | 177 | 60 | |
| *CLN5* | NM_001082595.1 | F: AGTAGCAACCATATCAGGAGGC<br>R: CTTTTTCGGGCTGGCTTGGA | 112 | 60 | |
| *EIF4A2* | XM_027957453.2 | F: GCTGTCTTTTCAGTCCGGCA<br>R: GGCCGCCATGTTCTCTGTTA | 82 | 60 | |
| *AGGF1* | XM_012180676.4 | F: CCTCGAATTCACAGGAGCCA<br>R: TCTGCTGCAGCTCTCAAACT | 94 | 60 | |
| *BTBD1* | XM_042242645.1 | F: TGACCGGATCAGGTTCACAG<br>R: CCGTGGGGCCATGAATAGAG | 80 | 60 | |
| *PSMD4* | NM_001104928.1 | F: TGGTCTAGGAGAACCGGTCG<br>R: CACTGTTGTCCACGCAAACC | 81 | 60 | |
| *EPHX2* | XM_042243107.1 | F: GCCGTGGACATGAAAGGCTA<br>R: CCTGAGCGATGCCCAACTTA | 118 | 60 | |
| *RPS3* | XM_004016328.5 | F: CCCTAAGAAGCCTCTGCCTG<br>R: GCGGCCAAGGAGACCTATTA | 153 | 60 | |
| *CREB3L2* | XM_027968851.2 | F: GACTTGTCCCCTCTGTCACG<br>R: GGCATGAGGAATCAACCCCA | 102 | 60 | |
| *THEM4* | XM_027975113.2 | F: GACGGCCTGGGCTTTGAATA<br>R: CACCTCCATGAAGGAATCCAGG | 115 | 60 | |
| *RPL19* | XM_012186026.3 | F: AATGCCAATGCCAACTC<br>R: CCCTTTCGCTACCTATACC | 151 | 60 | Reference gene |
| *β-actin* | NM_001009784.3 | F: GCTGTATTCCCCTCCATCGT<br>R: GGATACCTCTCTTGCTCTGG | 97 | 60 | |

**Table S2.** The specific primer information of DEmRNAs were verified by qPCR.

| miRNA | Forward primer sequence (5′→3′) | Reverse primer sequence (5′→3′) | Application |
|---|---|---|---|
| miR-1388-y | TAATCTCAGGTTCGTCAGCCCG | mRQ 3′ primer (the same below) | qPCR |
| miR-508-x | CGCTACTCCAGAGGGTGTCATTC | | |
| miR-146-y | TGCCCTAGGGACTCAGTTCTG | | |
| novel-m0114-5p | TCATGGACAAGCTGTGTGGCA | | |
| miR-432-x | CGTCTTGGAGTAGGTCATTGGGAA | | |
| oar-miR-493-5p | CGCGTTGTACATGGTAGGCTTTCATT | | |
| oar-miR-432 | CTCTTGGAGTAGGTCATTGGGTGG | | |
| novel-m0011-3p | CGCAAAGCCCAAACGAACTTTTTGT | | |
| miR-21-y | CAACAGCAGTCGATGGGCTG | | |
| miR-2312-z | CGCGAAAACCTGAATGAACTTATCGG | | |
| *U6* | ACGGACAGGATTGACAGATT | TCGCTCCACCAACTAAGAA | Reference gene |
| *18S* | GTGGTGTTGAGGAAAGCAGACA | TGATCACACGTTCCACCTCATC | |

Table S3. Overview of the reads and quality control of the 12 libraries of the mRNA sequencing from heart tissue of Tibetan sheep.

| Samples | Raw dates | Clean date (bp) | Clean reads | Q20 (%) | Q30 (%) | GC (%) | Total mapped (%) | Unique mapped (%) |
|---|---|---|---|---|---|---|---|---|
| TS25-1 | 52,438,044 | 7,722,757,719 | 51,832,014 | 7,569,587,009 (98.02%) | 7,278,354,660 (94.25%) | 3,778,936,844 (48.93%) | 50,022,319 (96.79%) | 45,569,911 (88.17%) |
| TS25-2 | 40,532,686 | 5,961,146,045 | 39,913,902 | 5,843,395,824 (98.02%) | 5,605,990,742 (94.04%) | 2,914,627,392 (48.89%) | 38,839,248 (97.54%) | 35,698,373 (89.65%) |
| TS25-3 | 37,641,638 | 5,518,848,781 | 36,951,444 | 5,408,095,609 (97.99%) | 5,184,161,006 (93.94%) | 2,679,017,708 (48.54%) | 35,896,587 (97.41%) | 32,883,365 (89.23%) |
| TS25-4 | 36,673,766 | 5,409,888,006 | 36,211,232 | 5,308,023,556 (98.12%) | 5,098,460,498 (94.24%) | 2,626,025,203 (48.54%) | 35,239,534 (97.55%) | 32,291,835 (89.39%) |
| TS35-1 | 51,230,844 | 7,559,983,984 | 50,702,270 | 7,409,134,814 (98.00%) | 7,122,152,279 (94.21%) | 3,681,900,499 (48.70%) | 48,857,374 (96.60%) | 44,624,922 (88.24%) |
| TS35-2 | 36,486,182 | 5,350,596,612 | 35,848,724 | 5,245,158,103 (98.03%) | 5,031,535,650 (94.04%) | 2,556,687,013 (47.78%) | 34,752,193 (97.22%) | 31,706,201 (88.70%) |
| TS35-3 | 38,087,166 | 5,601,473,419 | 37,487,256 | 5,488,801,101 (97.99%) | 5,259,521,340 (93.90%) | 2,682,399,494 (47.89%) | 36,355,096 (97.25%) | 33,167,695 (88.72%) |
| TS35-4 | 41,890,282 | 6,161,110,959 | 41,253,662 | 6,037,817,325 (98.00%) | 5,787,657,704 (93.94%) | 2,957,693,620 (48.01%) | 40,037,341 (97.34%) | 36,566,526 (88.90%) |
| TS45-1 | 57,047,798 | 8,410,349,118 | 56,406,366 | 8,249,638,545 (98.09%) | 7,940,258,407 (94.41%) | 4,151,544,963 (49.36%) | 54,398,619 (96.92%) | 50,010,008 (89.10%) |
| TS45-2 | 38,744,938 | 5,703,075,667 | 38,171,996 | 5,582,064,063 (97.88%) | 5,343,544,765 (93.70%) | 2,737,300,929 (48.00%) | 36,981,929 (97.32%) | 33,971,358 (89.40%) |
| TS45-3 | 39,797,284 | 5,859,859,462 | 39,235,458 | 5,741,010,565 (97.97%) | 5,502,908,424 (93.91%) | 2,848,130,715 (48.60%) | 38,026,361 (97.44%) | 34,999,744 (89.68%) |
| TS45-4 | 39,436,788 | 5,789,924,579 | 38,772,316 | 5,664,699,657 (97.84%) | 5,420,688,641 (93.62%) | 2,828,894,666 (48.86%) | 37,608,406 (97.35%) | 34,538,207 (89.40%) |

**Table S4.** Overview of the reads and quality control of the 12 libraries of the miRNA sequencing from heart tissue of Tibetan sheep.

| Samples | Raw reads | High quality reads | Clean tags | Match genome (%) | Not match exon (%) |
|---|---|---|---|---|---|
| TS25-1 | 8,998,259 (100%) | 8,918,227 (99.1106%) | 8,894,072 (99.7292%) | 6,775,008 (76.17%) | 8,863,799 (99.66%) |
| TS25-2 | 15,836,840 (100%) | 15,714,524 (99.2276%) | 15,650,919 (99.5952%) | 11,951,266 (76.36%) | 15,557,978 (99.41%) |
| TS25-3 | 12,863,043 (100%) | 12,772,606 (99.2969%) | 12,720,617 (99.5930%) | 9,561,405 (75.16%) | 12,619,315 (99.20%) |
| TS25-4 | 12,645,103 (100%) | 12,556,923 (99.3027%) | 12,503,917 (99.5779%) | 9,410,228 (75.26%) | 12,450,586 (99.57%) |
| TS35-1 | 11,580,446 (100%) | 11,468,520 (99.0335%) | 11,433,349 (99.6933%) | 8,834,054 (77.27%) | 11,412,562 (99.82%) |
| TS35-2 | 15,128,103 (100%) | 15,021,639 (99.2963%) | 14,954,031 (99.5499%) | 11,281,087 (75.44%) | 14,844,695 (99.27%) |
| TS35-3 | 12,708,893 (100%) | 12,621,979 (99.3161%) | 12,570,388 (99.5913%) | 9,501,310 (75.58%) | 12,492,083 (99.38%) |
| TS35-4 | 12,785,289 (100%) | 12,646,746 (98.9164%) | 12,577,249 (99.4505%) | 9,462,170 (75.23%) | 12,495,343 (99.35%) |
| TS45-1 | 9,308,060 (100%) | 9,243,247 (99.3037%) | 9,223,364 (99.7849%) | 7,314,664 (79.31%) | 9,199,355 (99.74%) |
| TS45-2 | 13,555,629 (100%) | 13,443,656 (99.1740%) | 13,369,350 (99.4473%) | 10,078,220 (75.38%) | 13,233,318 (98.98%) |
| TS45-3 | 10,447,470 (100%) | 10,370,054 (99.2590%) | 10,334,989 (99.6619%) | 7,988,228 (77.29%) | 10,275,477 (99.42%) |
| TS45-4 | 14,437,359 (100%) | 14,312,563 (99.1356%) | 14,257,869 (99.6179%) | 10,872,250 (76.25%) | 14,141,986 (99.19%) |