

## **Supplementary information file**

### **Integrated analysis of microRNA and mRNA expression profiles in abdominal adipose tissues in chickens**

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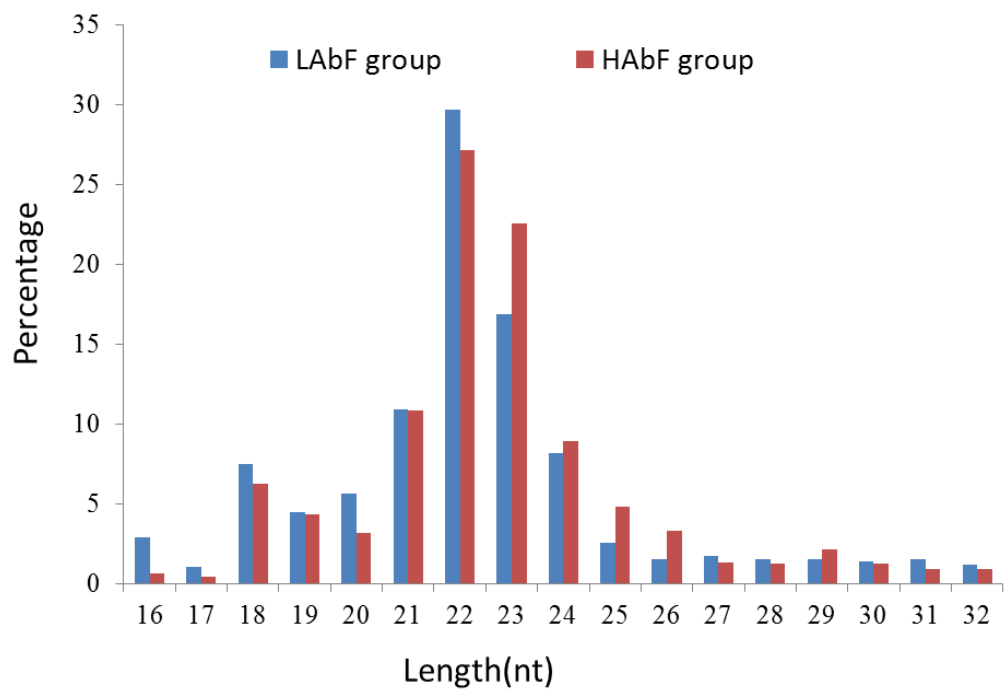
# These authors contributed equally to this work.

#### **Supplemental Figure Legends**

**Figure S1. Length distribution of small RNAs. LAbF: low-abdominal fat libraries; HAbF: high-abdominal fat libraries.**

**Figure S2. Exonic rates of HAbF and LAbF libraries regarding the mRNA-seq experiments. (A) Exonic rates of LAbF group (B) Exonic rates of LAbF group; LAbF: low-abdominal fat libraries; HAbF: high-abdominal fat libraries.**

Figure S1

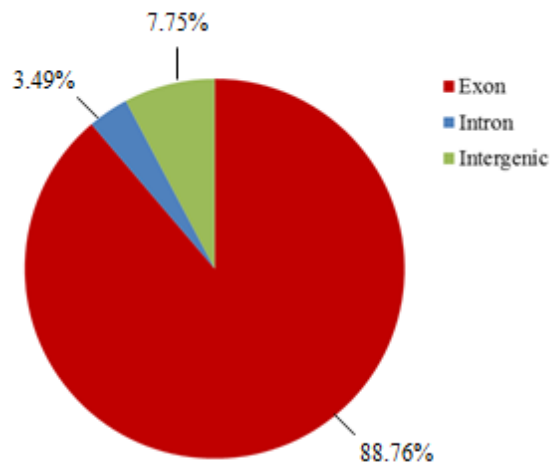


**Figure S2**

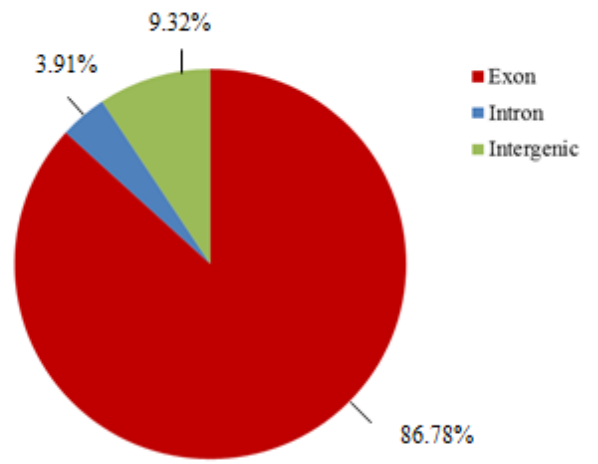
LABF: 66424

HAbF: 63618

**A**



**B**



**Table S3. Produced Reads and Aligned Reads of HAbF and LAbF libraries regarding the mRNA-seq experiments**

|                |                   | LABF     | Valid Ratio (reads)% | HAbF     | Valid Ratio(reads)% |
|----------------|-------------------|----------|----------------------|----------|---------------------|
| Produced Reads | Raw Reads         | 49242752 | 100%                 | 57429740 | 100%                |
|                | Valid Reads       | 49242752 |                      | 57429740 |                     |
| Aligned Reads  | Total Valid reads | 49226144 | 100.00%              | 57351996 | 100.00%             |
|                | Read-1            | 8552400  | 17.37%               | 11029633 | 19.23%              |
|                | Read-2            | 8340873  | 16.94%               | 10814590 | 18.86%              |
|                | Alignment         | 16893273 | 34.32%               | 21844223 | 38.09%              |
|                | Unmapped          | 32332871 | 65.68%               | 35507773 | 61.91%              |

LABF: low-abdominal fat libraries

HAbF: high-abdominal fat libraries

Alignment: The total number of reads mapped to the reference genome

Unmapped: The total number of reads that were not mapped to the reference genome

**Table S6. q-PCR primers for genes**

| Gene name      | Accession Number | Sequence (5' to 3')                                    |
|----------------|------------------|--|
| <i>AKR1D1</i>  | NM_001277393.1   | F: GGATGAAACGTGGGTAAATG<br>R: CTCTGATGCGTTGTGGATTG     |
| <i>APOA5</i>   | XM_417939.4      | F: AGCAGATCATGTTCGCTGAAG<br>R: TTCCTTCAGATTTGTGAACTC   |
| <i>CYP11A1</i> | NM_001001756.1   | F: TTCCTTCAGATTTGTGAACTC<br>R: CACAGAATGCTTCCTTGTGT    |
| <i>SOCS3</i>   | NM_204600.1      | F: CCTCTGCCGTAAGACTGTCA<br>R: TTTCCCTCTGCCAGCCTCTT     |
| <i>APOA1</i>   | NM_205525.4      | F: GGACCAGTTCTCCGCCAAGT<br>R: TGCACCAGAGGCGTCATC       |
| <i>SCP2</i>    | XM_004936799.1   | F: TAAGCGAAGGAATGAAAC<br>R: AGAAGATATGGGTAGCAC         |
| <i>CTBP1</i>   | NM_001012890.1   | F: CTTTGCTTTCAGCCGTCAC<br>R: ATGGTTCGCTTGGGTGGT        |
| <i>PRKAR2B</i> | XM_001232696.3   | F: ATGGACATTGCCGACACC<br>R: GGTCTTCATTCAGGTGG          |
| <i>PLTP</i>    | NM_001162406.1   | F: TTCTGCTGATGGTGTCCACATC<br>R: GGAACTCATAGACCTTCCTGAG |
| <i>FADS2</i>   | NM_001160428.2   | F: TCCTCACTTTTGTGAGTTTCT<br>R: CTGAGAGCTAAGCCAGTCTTTG  |
| <i>PECR</i>    | NM_001006522.1   | F: AACAGTGTTGCTCCTGGAATAG<br>R: ATCTCCTCAGGAACTGCTGATC |
| <i>PTGES</i>   | NM_001194983.1   | F: GCTCAGGAAGAAGGCATTTG<br>R: TACACAGCTCCAAGGAAGAG     |
| <i>SCD</i>     | NM_204890.1      | F: TGCTACAGGAGGAGGAGTTCT<br>R: CTTCTCACGGTAGGTTTCATC   |
| <i>ABCD3</i>   | NM_001012597.1   | F: CGTGTTCTTGGTGAGTTGTG<br>R: TTCCTTCAGCACCTGGTCAGG    |
| <i>ACSL1</i>   | NM_001012578.1   | F: CAAAGGAGAAGGTGAGGTGTG<br>R: CTTCAACGTACCGTTTGGTAG   |
| <i>LAMA2</i>   | XM_419746.4      | F: CCAGGAATGTGAGTGTGATCAATAT                           |

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|                              |                |  |
|------------------------------|----------------|--|
|                              |                | R: AGAAGTCTCTCTGGTGCTCGCT  |
| <i>CHAD</i>                  | XM_004946335.1 | F: TCCTGCTTCTTCTTCCCACCACA<br>R: GTTTGCTCAGGCACCTTGGGGAT               |
| <i>GART</i>                  | NM_001001469.1 | F: TTCTCAAGTTGGCGTCTCTGGTGAT<br>R: TGTGTGCATAAGCTTTCACGTGGC            |
| <i>AKT1</i>                  | NM_205055.1    | F: TGGCACATTCATTGGCTAC<br>R: CTCCAGCATCAAACCTAC                        |
| <i>RAP1B</i>                 | NM_001007852.1 | F: GGTTCTTGGTTCTGGAGGTGTT<br>R: ATCATCAGTGTCTTTGACTCGAAGA              |
| <i>ITGA11</i>                | XM_413930.4    | F: AAGGATGCCTATTTTGGCTACA<br>R: ACAGAGTGACTCTTCTAGGTTGAG               |
| <i>CAV2</i>                  | NM_001007086.1 | F: CGCATCTTCATGGACGACGACAAC<br>R: GCAGATCCACACCTTGTCGAAGGAG            |
| <i>ACSL1</i><br><i>3'UTR</i> | NM_001012578.1 | F:CAACTCGAGACAGTGGATTGAGTAAAGTGG<br>R:TAAGCGGCCCGCATGCAGAAATATTTATTTTG |

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**Table S7. miRNA-specific primers for q-PCR\***

| <b>miRNA</b>    | <b>Primers</b>            |
|-----------------|---------------------------|
| gga-miR-19a-3p  | TGTGCAAATCTATGCAAAACTGA   |
| gga-miR-19b-3p  | TGTGCAAATCCATGCAAAACTGA   |
| gga-miR-17-5p   | CAAAGTGCTTACAGTGCAGGTAGT  |
| gga-miR-30e-5p  | TTTCAGTCGGATGTTTACAGC     |
| gga-miR-103-3p  | AGCAGCATTGTACAGGGCTATGA   |
| gga-miR-27b-3p  | TTCACAGTGGCTAAGTTCTGC     |
| gga-miR-26a-5p  | TTCAAGTAATCCAGGATAGGC     |
| gga-miR-30d     | TGTA AACATCCCCGACTGGAAG   |
| gga-miR-142-3P  | TGTGCAAATCCATGCAAAACTGA   |
| gga-miR-122-5P  | TGGAGTGTGACAATGGUGTTTGT   |
| gga-miR-3535    | GGATATGATGACTGATTATCTGAAA |
| gga-miR-301b-3p | CAGTGCAATAGTATTGTCAAAGCAT |
| gga-miR-133c-3p | TTGGTCCCCTTCAACCAGCTGC    |
| gga-miR-146b-5p | TGAGAACTGAATTCCATAGGCG    |
| gga-miR-215-5p  | ATGACCTATGAATTGACAGAC     |
| gga-miR-200a-3p | TAACACTGTCTGGTAACGATGT    |
| gga-miR-92-3p   | TATTGCACTTGTCCCGGCCTG     |
| gga-miR-133a-3p | TTGGTCCCCTTCAACCAGCTGT    |
| gga-miR-204     | TTCCCTTTGTCATCCTATGCCT    |
| gga-miR-144-3p  | CTACAGTATAGATGATGTACTC    |
| U6              | GTGACCCACGATGTGTATTCGC    |