

## **Supplementary Material**

# **Predictors and Management of Antiplatelet-Related Bleeding Complications for Acute Coronary Syndrome in Chinese Elderly Patients**

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## *Supplementary Material*

# **The landscape of non-coding RNA in an adult pig model of intrauterine growth restriction**

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**Supplementary Table S1. Formula milk**

| Ingredients                             | Percent(%) |
|-----------------------------------------|------------|
| Whole milk powder                       | 58.00      |
| Whey protein concentrate                | 25.00      |
| Casein                                  | 5.70       |
| Coconut oil                             | 10.00      |
| CaH <sub>2</sub> PO <sub>4</sub> (22%P) | 0.10       |
| Choline chloride                        | 0.10       |
| Vitamin mixture <sup>1</sup>            | 0.10       |
| Mineral mixture <sup>2</sup>            | 0.50       |
| L-Arg                                   | 0.06       |
| DL-Met                                  | 0.06       |
| L-Lys.HCl                               | 0.30       |
| L-Thr                                   | 0.03       |
| L-Trp                                   | 0.05       |
| Total                                   | 100.00     |
| Nutrient content <sup>3</sup>           | Content    |
| Crude protein, %                        | 25.30      |
| Digestible energy, MJ/kg                | 18.39      |
| Calcium, %                              | 1.02       |
| Total phosphorus, %                     | 0.81       |
| Available phosphorus, %                 | 0.67       |
| Digestive-Lysine, %                     | 1.93       |
| Digestive -Methionine, %                | 0.63       |
| Digestive -Arginine, %                  | 0.86       |

Note 1: Contents per kg of diet: vitamin A, 0.94 mg; vitamin E, 20 mg; vitamin D3, 10 µg; vitamin B1, 1.50 mg; vitamin B2, 5 mg; vitamin B6, 2 mg; vitamin B12, 40 µg; vitamin K3, 1 mg; folic acid, 1.50 mg; nicotinic acid, 20 mg; pantothenic acid, 15 mg; biotin, 0.1 mg. Note 2: contents per kg of diet: Zn, 90 mg; Mn, 4.0 mg; Fe, 90 mg; Cu, 6.0 mg; Se, 0.3 mg; I, 0.2 mg. Note 3: Nutrient levels were calculated values.

**Supplementary Table S2. Ingredient composition and nutrient levels of experimental diets**  
(as fed basis, %)

| <b>Ingredients</b>                 | <b>7-11kg</b> | <b>11-25kg</b> | <b>25-50kg</b> | <b>50-75kg</b> | <b>75-100kg</b> |
|------------------------------------|---------------|----------------|----------------|----------------|-----------------|
| Corn grain                         | 27.19         | 35.00          | 68.57          | 75.13          | 78.03           |
| Expand corn                        | 25.00         | 23.68          | 0.00           | 0.00           | 0.00            |
| Soybean oil                        | 2.50          | 1.80           | 3.00           | 3.00           | 3.00            |
| Sucrose                            | 2.00          | 2.00           | 2.00           | 0.00           | 0.00            |
| Wheat bran                         | 0.00          | 0.00           | 3.00           | 3.00           | 5.00            |
| Whey powder                        | 12.00         | 7.00           | 0.00           | 0.00           | 0.00            |
| Soybean meal                       | 8.00          | 12.00          | 18.20          | 15.50          | 10.90           |
| Full-fat soybean                   | 5.00          | 8.00           | 0.00           | 0.00           | 0.00            |
| Soy protein concentrate            | 5.00          | 3.00           | 0.00           | 0.00           | 0.00            |
| Whole milk powder                  | 3.00          | 0.00           | 0.00           | 0.00           | 0.00            |
| Fishmeal (CP 62.5 %)               | 4.00          | 3.00           | 2.00           | 0.00           | 0.00            |
| Plasma protein powder              | 3.00          | 1.00           | 0.00           | 0.00           | 0.00            |
| L-Lys·Hcl                          | 0.45          | 0.46           | 0.42           | 0.44           | 0.40            |
| DL-Met                             | 0.15          | 0.16           | 0.14           | 0.12           | 0.10            |
| L-Thr                              | 0.15          | 0.16           | 0.14           | 0.15           | 0.14            |
| L-Try                              | 0.01          | 0.02           | 0.03           | 0.03           | 0.03            |
| Choline chloride 50%               | 0.15          | 0.10           | 0.10           | 0.10           | 0.10            |
| CaCO <sub>3</sub>                  | 1.00          | 0.92           | 0.90           | 0.89           | 0.80            |
| CaHPO <sub>4</sub>                 | 0.10          | 0.40           | 0.70           | 0.84           | 0.70            |
| NaCl                               | 0.30          | 0.30           | 0.30           | 0.30           | 0.30            |
| Premix <sup>1</sup>                | 1.00          | 1.00           | 0.50           | 0.50           | 0.50            |
| Total                              | 100.00        | 100.00         | 100.00         | 100.00         | 100.00          |
| <b>Nutrient levels<sup>2</sup></b> |               |                |                |                |                 |
| DE (Kcal/kg)                       | 3.58          | 3.48           | 3.39           | 3.40           | 3.39            |
| CP (%)                             | 19.55         | 18.35          | 15.68          | 13.73          | 12.18           |
| Ca (%)                             | 0.79          | 0.71           | 0.66           | 0.59           | 0.52            |
| STTD P (%)                         | 0.39          | 0.34           | 0.31           | 0.27           | 0.25            |
| SID Lys (%)                        | 1.36          | 1.23           | 0.98           | 0.85           | 0.73            |
| SID Met+cys (%)                    | 0.74          | 0.69           | 0.55           | 0.55           | 0.42            |
| SID Thr (%)                        | 0.80          | 0.73           | 0.58           | 0.52           | 0.46            |
| SID Trp (%)                        | 0.22          | 0.20           | 0.17           | 0.15           | 0.13            |

Note 1: Contents per kg of diet for 7-25 kg BW Period: Fe, 150 mg; Cu, 195 mg; Zn, 150 mg; Mn, 30 mg; I, 0.3 mg; Se, 0.3 mg; vitamin A, 12000 IU; vitamin D, 3200 IU; vitamin E, 80 mg; vitamin K<sub>3</sub>, 32.50 mg; vitamin B<sub>1</sub>, 2.30 mg; vitamin B<sub>2</sub>, 6.50 mg; vitamin B<sub>6</sub>, 5 mg; vitamin B<sub>12</sub>, 50 µg; nicotinic acid, 45 mg; pantothenic acid, 20 mg, folic acid, 1.50 mg; biotin, 0.15 mg; enzyme preparation and preservatives. Contents per kg of diet for 7-25 kg BW Period: Fe, 120 mg; Cu, 17 mg; Zn, 100 mg; Mn, 25 mg; I, 0.3 mg; Se, 0.2 mg; vitamin A, 5512 IU; vitamin D, 2250 IU; vitamin E, 24 mg; vitamin K<sub>3</sub>, 3 mg; vitamin B<sub>2</sub>, 6 mg; vitamin B<sub>6</sub>, 3 mg; vitamin B<sub>12</sub>, 24 µg; pantothenic acid, 15 mg, folic acid, 1.20 mg; biotin, 0.15 mg; enzyme preparation and preservatives. Note 2: Nutrient levels were calculated values.

**Supplementary Table S3. Information of primers used to perform Q-PCR**

| Gene symbol                     | Forward primer (5'-3')  | Reverse primer (5'-3')         |
|---------------------------------|-------------------------|--------------------------------|
| <i>COX2</i>                     | GCACCCCGACATAGAGAGC     | CTGCGGAGTGCAGTGTTCT            |
| <i>GCG</i>                      | GAATCAACACCATCGGTCAAAT  | CTCCACCCATAGAATGCCCAGT         |
| <i>TCONS-00115337</i>           | CGTTTCCCTGGGTCATAA      | GGTTGCTCTGTGCTTTGC             |
| <i>TCONS-00052043</i>           | GCTAACTGTGGGCTAAGTG     | TAGGTCGCAACCGTGTAT             |
| <i>TCONS-00152611</i>           | GGCAGATGGCAAGTGATT      | AGGGGTTGAGACCAGAGT             |
| <i>ATF4</i>                     | CAGGGTGAAGTGGAATCT      | GGAGTCAGGGCTCATACA             |
| <i>TCF7</i>                     | GTCACCACGCTGCCATCC      | ACCGCTCTTCTTCTTGC              |
| <i>CPT1</i>                     | GTGGGCGACTAACTATGTG     | CCAGTTTACGGCGATACA             |
| <i>miR-214</i>                  | ACAGCAGGCACAGACAGGCAG   | R-primer (Uni-miR qPCR Primer) |
| <i>miR-22-3p</i>                | AAGCTGCCAGTTGAAGAACTGT  | R-primer (Uni-miR qPCR Primer) |
| <i>miR-122</i>                  | TGGAGTGTGACAATGGTGTTTGT | R-primer (Uni-miR qPCR Primer) |
| <i>circRNA16347</i>             | TGGAGACAGGTGGTAGTGG     | TACGAAAAGTGGAATCTATGTG         |
| <i>circRNA7964</i>              | GGGAACTTGGAACATACCT     | GAGACCTCTTGCTCTACTACAC         |
| <i>circRNA21610</i>             | ATTGCTTAGACTGATCCTTGG   | TGAGTACAGGCCACTATTAAA          |
| <i>circRNA3281</i>              | TTCCTATCTTCTAAACGATTCC  | TCCCTACATTTTCACAGCA            |
| <i>circRNA4816</i> (Divergent)  | GGAAAGATAATAATAAGCCACC  | CAGTCTGTAGAATGAGGGAGT          |
| <i>circRNA4816</i> (Convergent) | TTCCTTCTACTCAGATTTCTCTC | AAATTTCTCAAATTCAGGTTGGC        |
| <i>ACTB</i> (Divergent)         | AGAAGGTGTGGTGCCAGA      | GTGAGAAGATGACCCAGATCA          |
| <i>ACTB</i> (Convergent)        | TCTGGCACCACACCTTCT      | TGATCTGGGTCATCTTCTCAC          |
| <i>TBP</i>                      | GATGGACGTTTCGGTTTAGG    | AGCAGCACAGTACGAGCAA            |
| <i>TOP2B</i>                    | AACTGGATGATGCTAATGATGCT | TGGAAAACTCCGTATCTGTCTC         |

*COX2*: cytochrome c oxidase subunit I; *GCG*: glucagon; *ATF4*: activating transcription factor 4; *TCF7*: transcription factor 7; *CPT1*: carnitine palmitoyltransferase 1; *ACTB*: actin beta; *TBP*: TATA-box binding protein; *TOP2B*: DNA topoisomerase II beta. Uni-miR qPCR Primer included in commercial kits.

**Supplementary Table S4. Summary of transcriptome alignment**

| Group                          | Normal-1              | Normal-2              | Normal-3              | IUGR-1                | IUGR-2                | IUGR-3                |
|--------------------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|-----------------------|
| Total Raw Reads                | 182462984<br>(16.42G) | 188671562<br>(16.98G) | 188490354<br>(16.96G) | 212157764<br>(19.09G) | 191055696<br>(17.20G) | 198755512<br>(17.89G) |
| Valid Data                     | 181246976<br>16.31G   | 186904702<br>16.82G   | 186844562<br>16.82G   | 210590742<br>18.95G   | 189842370<br>17.09G   | 197354938<br>17.76G   |
| Valid Ratio (reads)            | 0.99                  | 0.99                  | 0.99                  | 0.99                  | 0.99                  | 0.99                  |
| Q20%                           | 99.50                 | 99.55                 | 99.63                 | 99.53                 | 99.53                 | 99.54                 |
| Q30%                           | 93.83                 | 94.22                 | 95.24                 | 94.11                 | 94.06                 | 94.20                 |
| Total mapped ratio %           | 72.49                 | 70.11                 | 69.57                 | 70.68                 | 73.79                 | 73.96                 |
| Unique Mapped ratio %          | 66.90                 | 64.32                 | 64.30                 | 65.61                 | 68.56                 | 68.68                 |
| Multi Mapped reads %           | 5.59%                 | 5.78%                 | 5.27%                 | 5.07%                 | 5.23%                 | 5.28%                 |
| PE Mapped reads %              | 32.81%                | 31.51%                | 31.14%                | 30.96%                | 33.47%                | 33.45%                |
| Map to sense strand %          | 33.75%                | 32.40%                | 32.43%                | 33.34%                | 34.62%                | 34.67%                |
| Map to antisense strand %      | 33.16%                | 31.92%                | 31.87%                | 32.26%                | 33.94%                | 34.01%                |
| Splice reads %                 | 20.67%                | 18.20%                | 17.21%                | 18.07%                | 21.61%                | 21.66%                |
| Back-spliced junctions reads % | 2.30%                 | 2.21%                 | 2.44%                 | 3.21%                 | 2.54%                 | 1.85%                 |
| GC content %                   | 46                    | 45                    | 45                    | 45                    | 46                    | 45                    |

**Supplementary Table S5. List of identified lincRNAs (part)**

| class_code | CPC_Score | CNCI_Score | gene_id     | Normal1/FPKM | Normal2/FPKM | Normal3/FPKM | UIUC1/FPKM | UIUC2/FPKM | UIUC3/FPKM |
|------------|-----------|------------|-------------|--------------|--------------|--------------|------------|------------|------------|
| "u"        | -1.36E+00 | -2.87E-01  | XLOC_011392 | 4.35E+00     | 2.24E+00     | 1.98E+00     | 1.32E+00   | 2.81E+00   | 3.28E+00   |
| "u"        | -1.16E+00 | -1.39E-01  | XLOC_011432 | 7.14E-01     | 6.95E-01     | 8.39E-01     | 1.14E+00   | 4.93E-01   | 6.14E-01   |
| "u"        | -1.20E+00 | -2.17E-01  | XLOC_011439 | 9.50E+00     | 1.29E+01     | 9.79E+00     | 8.46E+00   | 9.42E+00   | 8.70E+00   |
| "u"        | -1.35E+00 | -1.88E-01  | XLOC_011487 | 1.13E+00     | 6.55E-01     | 1.47E+00     | 4.01E-01   | 7.34E-01   | 1.21E+00   |
| "u"        | -1.09E+00 | -1.02E-01  | XLOC_011496 | 7.91E-01     | 2.39E-01     | 6.04E-01     | 1.67E-01   | 3.75E-01   | 1.27E-01   |
| "u"        | -1.08E+00 | -1.72E-01  | XLOC_011505 | 1.40E-01     | 2.96E-01     | 7.12E-01     | 5.33E-01   | 1.97E-01   | 2.26E-01   |
| "u"        | -1.16E+00 | -1.15E-01  | XLOC_011517 | 5.55E-01     | 6.45E-01     | 6.59E-01     | 4.59E-01   | 1.27E-01   | 5.34E-02   |
| "u"        | -1.18E+00 | -2.05E-01  | XLOC_011543 | 2.31E-01     | 5.40E-01     | 2.41E-01     | 8.77E-01   | 3.56E-01   | 3.15E-01   |
| "u"        | -1.47E+00 | -1.05E-01  | XLOC_011575 | 3.31E-01     | 1.01E+00     | 5.50E-01     | 6.75E-01   | 4.65E-01   | 4.11E-01   |
| "u"        | -1.19E+00 | -3.19E-01  | XLOC_011691 | 7.84E-01     | 6.25E-01     | 9.06E-01     | 6.58E-01   | 7.94E-01   | 1.42E+00   |
| "u"        | -1.15E+00 | -1.64E-01  | XLOC_011697 | 2.23E-01     | 3.21E-01     | 2.30E-01     | 7.21E-02   | 8.15E-01   | 8.46E-01   |
| "u"        | -1.07E+00 | -1.23E-01  | XLOC_011771 | 1.70E+00     | 8.77E-01     | 1.46E+00     | 1.40E+00   | 1.29E+00   | 1.28E+00   |
| "u"        | -1.30E+00 | -1.05E-01  | XLOC_011776 | 9.13E-01     | 7.36E-01     | 1.06E+00     | 1.05E+00   | 1.25E+00   | 9.50E-01   |
| "u"        | -1.22E+00 | -1.97E-01  | XLOC_011795 | 1.51E+00     | 9.47E-01     | 7.69E-01     | 1.34E+00   | 7.19E-01   | 5.32E-01   |
| "u"        | -1.05E+00 | -1.43E-01  | XLOC_011858 | 9.07E-01     | 4.45E-01     | 6.27E-01     | 7.13E-01   | 2.92E-01   | 6.70E-01   |
| "u"        | -1.31E+00 | -1.06E-01  | XLOC_011863 | 6.40E-01     | 6.63E-01     | 7.51E-01     | 6.76E-01   | 3.35E-01   | 6.98E-01   |
| "u"        | -1.16E+00 | -1.06E-01  | XLOC_011899 | 5.42E+00     | 4.00E+00     | 2.63E+00     | 2.46E+00   | 4.05E+00   | 5.11E+00   |
| "u"        | -1.10E+00 | -1.15E-01  | XLOC_011916 | 4.50E-01     | 4.19E-01     | 9.81E-01     | 6.02E-01   | 4.23E-01   | 2.59E-01   |
| "u"        | -1.09E+00 | -1.58E-01  | XLOC_011924 | 5.34E-01     | 1.26E+00     | 1.91E+00     | 8.30E-01   | 8.27E-01   | 1.11E+00   |
| "u"        | -1.13E+00 | -1.02E-01  | XLOC_011950 | 7.11E-01     | 1.02E+00     | 1.37E+00     | 9.93E-01   | 4.95E-01   | 6.59E-01   |
| "u"        | -1.35E+00 | -2.50E-01  | XLOC_012103 | 6.37E-01     | 7.09E-01     | 3.76E-01     | 1.05E+00   | 1.05E+00   | 3.33E-01   |
| "u"        | -1.03E+00 | -1.70E-01  | XLOC_012103 | 8.94E-01     | 9.68E-01     | 4.22E-01     | 6.79E-01   | 2.38E-01   | 5.49E-01   |

**Supplementary Table S6. List of differentially expressed lincRNAs (part)**

| class_code | gene_id     | sample_1 | sample_2 | UIUC_fpkms | Normal_fpkms | log2(fold_change) | p_value | q_value  | significant |
|------------|-------------|----------|----------|------------|--------------|-------------------|---------|----------|-------------|
| "u"        | XLOC_016397 | UIUC     | Normal   | 0.362753   | 0            | inf               | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_018428 | UIUC     | Normal   | 2.5077     | 1.04343      | 1.26504           | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_018432 | UIUC     | Normal   | 3.13715    | 1.26621      | 1.30894           | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_019712 | UIUC     | Normal   | 0.531614   | 0            | inf               | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_021629 | UIUC     | Normal   | 0          | 0.421627     | -inf              | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_024126 | UIUC     | Normal   | 0          | 0.525645     | -inf              | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_028606 | UIUC     | Normal   | 0          | 0.422127     | -inf              | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_028940 | UIUC     | Normal   | 1.65104    | 0.574544     | 1.52288           | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_029652 | UIUC     | Normal   | 0.342792   | 0.97758      | -1.51188          | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_029653 | UIUC     | Normal   | 1.62964    | 3.58267      | -1.13648          | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_031202 | UIUC     | Normal   | 8.09281    | 19.0529      | -1.2353           | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_035280 | UIUC     | Normal   | 1.19789    | 3.28567      | -1.45569          | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_035369 | UIUC     | Normal   | 2.64       | 0.497152     | 2.40878           | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_035378 | UIUC     | Normal   | 6.6998     | 1.42643      | 2.23171           | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_035978 | UIUC     | Normal   | 0          | 0.433994     | -inf              | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_036495 | UIUC     | Normal   | 0          | 1.4728       | -inf              | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_037380 | UIUC     | Normal   | 0.461934   | 0            | inf               | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_037599 | UIUC     | Normal   | 1.93664    | 0.42518      | 2.18741           | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_042062 | UIUC     | Normal   | 20.2625    | 5.18928      | 1.9652            | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_042063 | UIUC     | Normal   | 46.2025    | 14.5196      | 1.66997           | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_045828 | UIUC     | Normal   | 4.28761    | 1.21709      | 1.81673           | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_046179 | UIUC     | Normal   | 0          | 0.556549     | -inf              | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_046227 | UIUC     | Normal   | 3.30401    | 17.1048      | -2.37212          | 0.00005 | 9.53E-03 | yes         |
| "u"        | XLOC_046234 | UIUC     | Normal   | 0          | 1.49895      | -inf              | 0.00005 | 9.53E-03 | yes         |

**Supplementary Table S7. GO terms annotation for neighbor gene functions of predicated lncRNAs (cis-regulation)**

| GO_ID      | GO_Term                                                                                | GO_function        | GO_class | S gene<br>number | TS gene<br>number | B gene<br>number | TB gene<br>number | pvalue   |
|------------|----------------------------------------------------------------------------------------|--------------------|----------|------------------|-------------------|------------------|-------------------|----------|
| GO:0004869 | cysteine-type endopeptidase inhibitor activity                                         | molecular_function | 7        | 4                | 118               | 7                | 6643              | 3.18E-06 |
| GO:0010951 | negative regulation of endopeptidase activity                                          | biological_process | 11       | 5                | 118               | 21               | 6643              | 2.63E-05 |
| GO:0005576 | extracellular region                                                                   | cellular_component | 3        | 15               | 118               | 284              | 6643              | 1.36E-04 |
| GO:0003884 | D-amino-acid oxidase activity                                                          | molecular_function | 7        | 2                | 118               | 2                | 6643              | 3.13E-04 |
| GO:0016641 | "oxidoreductase activity, acting on the CH-NH2<br>group of donors, oxygen as acceptor" | molecular_function | 6        | 2                | 118               | 2                | 6643              | 3.13E-04 |
| GO:0007026 | negative regulation of microtubule<br>depolymerization                                 | biological_process | 9        | 3                | 118               | 9                | 6643              | 4.25E-04 |
| GO:0050786 | RAGE receptor binding                                                                  | molecular_function | 6        | 2                | 118               | 3                | 6643              | 9.28E-04 |
| GO:0048037 | cofactor binding                                                                       | molecular_function | 4        | 2                | 118               | 3                | 6643              | 9.28E-04 |
| GO:0051301 | cell division                                                                          | biological_process | 5        | 5                | 118               | 45               | 6643              | 1.13E-03 |
| GO:0004064 | arylesterase activity                                                                  | molecular_function | 7        | 2                | 118               | 4                | 6643              | 1.83E-03 |
| GO:0050832 | defense response to fungus                                                             | biological_process | 7        | 2                | 118               | 5                | 6643              | 3.02E-03 |
| GO:0045669 | positive regulation of osteoblast differentiation                                      | biological_process | 9        | 3                | 118               | 17               | 6643              | 3.10E-03 |
| GO:0005815 | microtubule organizing center                                                          | cellular_component | 11       | 4                | 118               | 37               | 6643              | 3.97E-03 |
| GO:0045071 | negative regulation of viral genome replication                                        | biological_process | 9        | 3                | 118               | 19               | 6643              | 4.30E-03 |
| GO:0050727 | regulation of inflammatory response                                                    | biological_process | 7        | 3                | 118               | 19               | 6643              | 4.30E-03 |
| GO:0008150 | biological_process                                                                     | biological_process | 2        | 82               | 118               | 3817             | 6643              | 4.52E-03 |
| GO:0031012 | extracellular matrix                                                                   | cellular_component | 3        | 5                | 118               | 64               | 6643              | 5.38E-03 |
| GO:0005102 | receptor binding                                                                       | molecular_function | 5        | 6                | 118               | 93               | 6643              | 6.00E-03 |



|            |                                                                                                         |                    |    |    |     |      |      |          |
|------------|---------------------------------------------------------------------------------------------------------|--------------------|----|----|-----|------|------|----------|
| GO:0020037 | heme binding                                                                                            | molecular_function | 6  | 4  | 118 | 42   | 6643 | 6.29E-03 |
| GO:0005856 | cytoskeleton                                                                                            | cellular_component | 9  | 8  | 118 | 159  | 6643 | 7.13E-03 |
| GO:0005874 | microtubule                                                                                             | cellular_component | 11 | 4  | 118 | 44   | 6643 | 7.43E-03 |
| GO:0016705 | "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen" | molecular_function | 5  | 3  | 118 | 23   | 6643 | 7.47E-03 |
| GO:0000281 | mitotic cytokinesis                                                                                     | biological_process | 7  | 2  | 118 | 8    | 6643 | 8.17E-03 |
| GO:0005814 | centriole                                                                                               | cellular_component | 10 | 3  | 118 | 24   | 6643 | 8.42E-03 |
| GO:0005575 | cellular_component                                                                                      | cellular_component | 2  | 63 | 118 | 2805 | 6643 | 8.91E-03 |
| GO:0005506 | iron ion binding                                                                                        | molecular_function | 8  | 4  | 118 | 48   | 6643 | 1.01E-02 |
| GO:0021983 | pituitary gland development                                                                             | biological_process | 12 | 2  | 118 | 9    | 6643 | 1.04E-02 |
| GO:0030855 | epithelial cell differentiation                                                                         | biological_process | 7  | 3  | 118 | 26   | 6643 | 1.05E-02 |
| GO:0001824 | blastocyst development                                                                                  | biological_process | 10 | 2  | 118 | 10   | 6643 | 1.28E-02 |

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**Supplementary Table S8. KEGG pathways annotation for neighbor gene functions of predicated lncRNAs (cis-regulation)**

| pathway_name                            | gene_list                                                               | S gene number | TS gene number | B gene number | TB gene number | pvalue   |
|-----------------------------------------|-------------------------------------------------------------------------|---------------|----------------|---------------|----------------|----------|
| Steroid hormone biosynthesis            | HSD17B2;CYP1A1;CYP7A1                                                   | 3             | 30             | 11            | 1407           | 1.29E-03 |
| PPAR signaling pathway                  | PCK1;CYP7A1;AQP7                                                        | 3             | 30             | 15            | 1407           | 3.35E-03 |
| Mismatch repair                         | RFC4;EXO1                                                               | 2             | 30             | 5             | 1407           | 4.23E-03 |
| Progesterone-mediated oocyte maturation | RINGO;CCNB3;CDC2                                                        | 3             | 30             | 20            | 1407           | 7.81E-03 |
| D-Arginine and D-ornithine metabolism   | DAO                                                                     | 1             | 30             | 1             | 1407           | 2.13E-02 |
| Starch and sucrose metabolism           | GYS2;GCK                                                                | 2             | 30             | 12            | 1407           | 2.54E-02 |
| Pyruvate metabolism                     | PCK1;ME3                                                                | 2             | 30             | 16            | 1407           | 4.38E-02 |
| Metabolic pathways                      | ATP6V1G1;INPP1;PCK1;<br>RPIA;HSD17B2;GCK;CYP1A1;<br>NNMT;ME3;DAO;CYP7A1 | 11            | 30             | 309           | 1407           | 4.61E-02 |
| Insulin signaling pathway               | PCK1;GYS2;GCK                                                           | 3             | 30             | 39            | 1407           | 4.77E-02 |
| Primary bile acid biosynthesis          | CYP7A1                                                                  | 1             | 30             | 3             | 1407           | 6.27E-02 |

|                                              |            |   |    |    |      |          |
|----------------------------------------------|------------|---|----|----|------|----------|
| Butirosin and neomycin biosynthesis          | GCK        | 1 | 30 | 3  | 1407 | 6.27E-02 |
| Glycolysis / Gluconeogenesis                 | PCK1;GCK   | 2 | 30 | 24 | 1407 | 9.08E-02 |
| p53 signaling pathway                        | CCNB3;CDC2 | 2 | 30 | 25 | 1407 | 9.74E-02 |
| DNA replication                              | RFC4       | 1 | 30 | 6  | 1407 | 1.22E-01 |
| Oocyte meiosis                               | RINGO;CDC2 | 2 | 30 | 30 | 1407 | 1.32E-01 |
| Citrate cycle (TCA cycle)                    | PCK1       | 1 | 30 | 7  | 1407 | 1.40E-01 |
| Cell adhesion molecules (CAMs)               | CD4;PVRL1  | 2 | 30 | 33 | 1407 | 1.55E-01 |
| Retinol metabolism                           | CYP1A1     | 1 | 30 | 8  | 1407 | 1.59E-01 |
| Nicotinate and nicotinamide metabolism       | NNMT       | 1 | 30 | 8  | 1407 | 1.59E-01 |
| Maturity onset diabetes of the young         | GCK        | 1 | 30 | 8  | 1407 | 1.59E-01 |
| Proximal tubule bicarbonate reclamation      | PCK1       | 1 | 30 | 8  | 1407 | 1.59E-01 |
| Metabolism of xenobiotics by cytochrome P450 | CYP1A1     | 1 | 30 | 9  | 1407 | 1.77E-01 |
| Collecting duct acid secretion               | ATP6V1G1   | 1 | 30 | 10 | 1407 | 1.94E-01 |

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**Supplementary Table S9. List of identified circRNAs (part)**

| Accession | Normal-<br>1_count | Normal-<br>2_count | Normal-<br>3_count | UIUC-<br>1_count | UIUC-<br>2_count | UIUC-<br>3_count | mean_fpkms_U | mean_fpkms_C | geneName           |
|-----------|--------------------|--------------------|--------------------|------------------|------------------|------------------|--------------|--------------|--------------------|
| ciRNA103  | 3.00               | 3.00               | 4.00               | 3.00             | 2.00             | 0.00             | 0.47         | 1.08         | E2F5               |
| ciRNA105  | 12.00              | 20.33              | 12.50              | 10.50            | 6.83             | 8.50             | 0.09         | 0.18         | ARMC1              |
| ciRNA111  | 10.00              | 18.00              | 5.00               | 5.00             | 6.00             | 7.00             | 1.49         | 3.20         | CERS2              |
| ciRNA113  | 3.00               | 4.00               | 1.00               | 0.00             | 0.00             | 1.00             | 0.12         | 1.19         | PPM1J              |
| ciRNA130  | 60.30              | 28.10              | 56.48              | 55.83            | 169.28           | 139.91           | 20.50        | 9.74         | FADS1              |
| ciRNA131  | 59.30              | 28.10              | 56.48              | 53.83            | 168.28           | 139.91           | 20.52        | 9.77         | FADS1              |
| ciRNA132  | 59.30              | 28.10              | 56.48              | 53.83            | 168.28           | 139.91           | 20.62        | 9.82         | FADS1              |
| ciRNA133  | 59.30              | 28.10              | 56.48              | 53.83            | 168.28           | 139.91           | 20.82        | 9.91         | FADS1              |
| ciRNA138  | 3.00               | 7.00               | 11.00              | 4.00             | 1.00             | 0.00             | 0.61         | 2.89         | ENSSSCG00000026230 |
| ciRNA141  | 3.00               | 6.00               | 3.00               | 0.00             | 0.00             | 2.00             | 0.05         | 0.36         | DIAPH1             |
| ciRNA15   | 5.00               | 9.00               | 8.00               | 2.00             | 5.00             | 2.00             | 0.98         | 2.82         | EIF4G1             |
| ciRNA155  | 2.00               | 1.00               | 1.00               | 1.00             | 0.00             | 0.00             | 0.06         | 0.25         | GRAMD1B            |
| ciRNA156  | 37.00              | 53.00              | 33.00              | 24.00            | 24.00            | 24.00            | 1.14         | 2.29         | STT3A              |
| ciRNA162  | 742.41             | 435.34             | 358.02             | 363.82           | 390.09           | 501.29           | 12.38        | 26.12        | TDO2               |
| ciRNA164  | 676.50             | 523.54             | 193.50             | 217.00           | 243.00           | 272.54           | 5.81         | 23.31        | ENSSSCG00000008951 |
| ciRNA187  | 1.00               | 12.00              | 12.00              | 6.00             | 6.00             | 0.00             | 1.00         | 2.41         | ENSSSCG00000017868 |
| ciRNA19   | 6.00               | 7.00               | 3.00               | 0.00             | 5.00             | 4.00             | 0.24         | 0.51         | SUPT4H1            |
| ciRNA199  | 28.80              | 74.60              | 35.40              | 18.51            | 25.80            | 34.88            | 0.42         | 0.87         | GHR                |
| ciRNA205  | 0.00               | 2.00               | 2.50               | 0.00             | 1.00             | 1.00             | 0.21         | 0.58         | ENSSSCG00000023854 |
| ciRNA206  | 32.00              | 96.00              | 58.00              | 35.00            | 14.00            | 16.00            | 0.96         | 3.18         | CUX2               |
| ciRNA210  | 643.43             | 123.54             | 453.54             | 132.43           | 303.67           | 372.56           | 7.70         | 33.36        | ENSSSCG00000010488 |
| ciRNA217  | 8.00               | 3.00               | 0.00               | 1.00             | 0.00             | 4.00             | 0.60         | 1.55         | RNH1               |

**Supplementary Table S10. List of identified differentially expressed circRNAs (part)**

| Accession    | mean_fpk_m_U | mean_fpk_m_C | regulation | log2<br>fold_change | pvalue | FDR  | significant | chr   | exon<br>Count | geneName           |
|--------------|--------------|--------------|------------|---------------------|--------|------|-------------|-------|---------------|--------------------|
| circRNA4816  | 222.65       | 17.15        | up         | 3.70                | 0.00   | 0.00 | yes         | chr5  | 7             | PPFIBP1            |
| circRNA8864  | 724.43       | 89.15        | up         | 3.02                | 0.00   | 0.00 | yes         | chr17 | 4             | TMX4               |
| circRNA11290 | 125.19       | 455.54       | down       | -1.87               | 0.01   | 0.00 | yes         | chr11 | 4             | TNFRSF19           |
| circRNA13759 | 73.01        | 18.36        | up         | 1.99                | 0.00   | 0.00 | yes         | chr8  | 1             | KLB                |
| circRNA21610 | 59.68        | 15.80        | up         | 1.92                | 0.00   | 0.00 | yes         | chr8  | 2             | KLB                |
| circRNA7964  | 63.31        | 19.09        | up         | 1.73                | 0.00   | 0.00 | yes         | chr8  | 3             | KLB                |
| circRNA16347 | 133.26       | 53.09        | up         | 1.33                | 0.02   | 0.01 | yes         | chr2  | 5             | HMGCR              |
| circRNA20143 | 8.47         | 3.38         | up         | 1.33                | 0.04   | 0.00 | yes         | chr17 | 3             | ENSSSCG00000007235 |
| circRNA8699  | 2.68         | 1.12         | up         | 1.26                | 0.01   | 0.01 | yes         | chr12 | 3             | GLP2R              |
| circRNA13147 | 1.32         | 0.58         | up         | 1.19                | 0.02   | 0.00 | yes         | chr2  | 2             | ANKRD31            |
| circRNA21524 | 20.57        | 9.85         | up         | 1.06                | 0.01   | 0.01 | yes         | chr9  | 1             | ME3                |
| ciRNA514     | 1.14         | 0.55         | up         | 1.04                | 0.02   | 0.00 | yes         | chr1  | 1             | ATP5A1             |
| circRNA21209 | 1.09         | 0.54         | up         | 1.01                | 0.01   | 0.00 | yes         | chr2  | 4             | ANKRD31            |
| circRNA3512  | 3.53         | 7.08         | down       | -1.00               | 0.03   | 0.01 | yes         | chrX  | 5             | GK                 |
| circRNA10766 | 3.03         | 6.10         | down       | -1.01               | 0.02   | 0.00 | yes         | chr9  | 3             | SOAT1              |
| circRNA15307 | 4.49         | 9.09         | down       | -1.02               | 0.03   | 0.01 | yes         | chrX  | 4             | GK                 |
| circRNA3281  | 7.48         | 15.19        | down       | -1.02               | 0.03   | 0.01 | yes         | chr18 | 7             | DPY19L1            |
| circRNA15182 | 1.31         | 2.66         | down       | -1.03               | 0.02   | 0.01 | yes         | chr18 | 4             | CFTR               |
| circRNA6021  | 7.13         | 14.54        | down       | -1.03               | 0.01   | 0.00 | yes         | chr3  | 7             | ENSSSCG00000008621 |
| ciRNA372     | 1.35         | 2.76         | down       | -1.03               | 0.04   | 0.01 | yes         | chr3  | 1             | ABCG8              |
| circRNA7648  | 24.07        | 49.39        | down       | -1.04               | 0.01   | 0.00 | yes         | chr9  | 4             | TBCEL              |
| circRNA14852 | 143.15       | 294.01       | down       | -1.04               | 0.02   | 0.01 | yes         | chr15 | 11            | ENSSSCG00000016159 |
| ciRNA556     | 0.42         | 0.86         | down       | -1.04               | 0.02   | 0.01 | yes         | chr13 | 1             | ATP5O              |

|              |        |        |      |       |      |      |     |            |    |                    |
|--------------|--------|--------|------|-------|------|------|-----|------------|----|--------------------|
| circRNA8200  | 31.79  | 65.60  | down | -1.05 | 0.04 | 0.01 | yes | chr8       | 2  | ADAD1              |
| circRNA15306 | 3.92   | 8.11   | down | -1.05 | 0.01 | 0.00 | yes | chrX       | 7  | GK                 |
| circRNA2417  | 238.06 | 493.89 | down | -1.05 | 0.02 | 0.01 | yes | chr15      | 5  | ENSSSCG00000016159 |
| circRNA13636 | 25.52  | 53.16  | down | -1.06 | 0.01 | 0.00 | yes | chr9       | 3  | TBCEL              |
| circRNA18201 | 12.42  | 26.35  | down | -1.09 | 0.00 | 0.00 | yes | chrX       | 8  | GK                 |
| circRNA3511  | 2.80   | 5.95   | down | -1.09 | 0.01 | 0.00 | yes | chrX       | 2  | GK                 |
| circRNA4538  | 79.74  | 175.99 | down | -1.14 | 0.03 | 0.00 | yes | chr6       | 3  | CTH                |
| circRNA3510  | 33.19  | 73.75  | down | -1.15 | 0.01 | 0.01 | yes | chrX       | 3  | GK                 |
| circRNA20810 | 86.52  | 193.58 | down | -1.16 | 0.03 | 0.00 | yes | chr6       | 6  | CTH                |
| circRNA12528 | 86.87  | 195.94 | down | -1.17 | 0.04 | 0.00 | yes | chr6       | 6  | CTH                |
| circRNA4537  | 101.98 | 234.41 | down | -1.20 | 0.03 | 0.00 | yes | chr6       | 2  | CTH                |
| circRNA12776 | 1.48   | 3.44   | down | -1.22 | 0.01 | 0.00 | yes | chr4       | 3  | GRHL2              |
| ciRNA690     | 0.09   | 0.23   | down | -1.26 | 0.03 | 0.00 | yes | chr13      | 1  | MASP1              |
| circRNA7561  | 0.89   | 2.13   | down | -1.26 | 0.00 | 0.00 | yes | chr9       | 10 | ENSSSCG00000014943 |
| ciRNA544     | 0.41   | 1.01   | down | -1.30 | 0.02 | 0.01 | yes | JH118445.1 | 1  | ENSSSCG00000001071 |
| circRNA5643  | 2.26   | 5.59   | down | -1.30 | 0.00 | 0.00 | yes | chr3       | 1  | ENSSSCG00000023626 |

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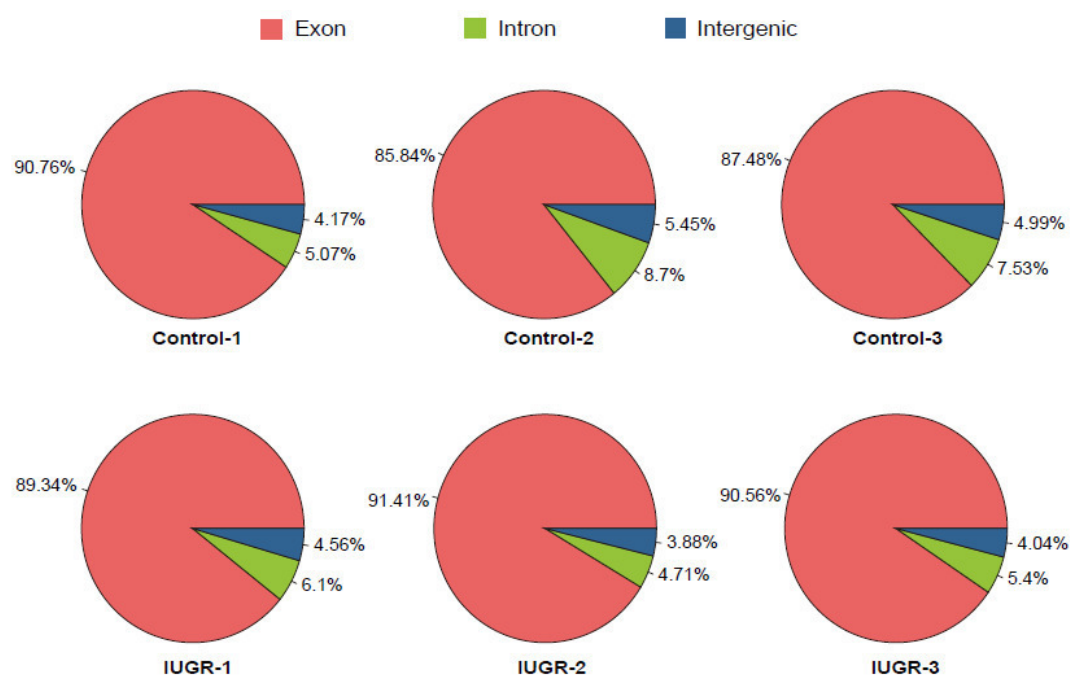
**Supplementary Table S11. List of miRNAs target of top 10 differentially expressed lincRNAs (part)**

| circRNA     | chr   | exon Count | geneName | miRNA           | Site Type | TargetScan score | TargetScan score_percentile | Miranda score | Miranda _Energy |
|-------------|-------|------------|----------|-----------------|-----------|------------------|-----------------------------|---------------|-----------------|
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-1277    | m8        | (0.21)           | 70.00                       | 155.00        | (14.83)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-196a    | m8        | (0.31)           | 88.00                       | 141.00        | (11.53)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-196b-5p | m8        | (0.31)           | 88.00                       | 140.00        | (12.03)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-199a-3p | 8mer      | (0.34)           | 89.00                       | 140.00        | (13.41)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-4339    | 8mer      | (0.31)           | 88.00                       | 157.00        | (19.02)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-542-3p  | m8        | (0.17)           | 59.00                       | 147.00        | (14.07)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-664-5p  | m8        | (0.30)           | 87.00                       | 168.00        | (26.14)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-676-5p  | m8        | (0.24)           | 77.00                       | 146.00        | (11.80)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-7135-5p | 8mer      | (0.30)           | 87.00                       | 142.00        | (16.18)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-7140-5p | m8        | (0.17)           | 58.00                       | 150.00        | (18.10)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-9787-3p | m8        | (0.19)           | 61.00                       | 153.00        | (15.04)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-9805-3p | 8mer      | (0.36)           | 95.00                       | 147.00        | (18.36)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-9828-3p | m8        | (0.21)           | 72.00                       | 140.00        | (16.51)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-9842-5p | m8        | (0.22)           | 78.00                       | 154.00        | (25.37)         |
| circRNA4816 | chr5  | 7.00       | PPFIBP1  | ssc-miR-9850-5p | m8        | (0.22)           | 78.00                       | 162.00        | (23.19)         |
| circRNA8864 | chr17 | 4.00       | TMX4     | ssc-miR-142-5p  | m8        | (0.18)           | 57.00                       | 156.00        | (11.58)         |
| circRNA8864 | chr17 | 4.00       | TMX4     | ssc-miR-499-5p  | m8        | (0.19)           | 64.00                       | 156.00        | (16.78)         |
| circRNA8864 | chr17 | 4.00       | TMX4     | ssc-miR-532-3p  | m8        | (0.14)           | 53.00                       | 140.00        | (21.18)         |

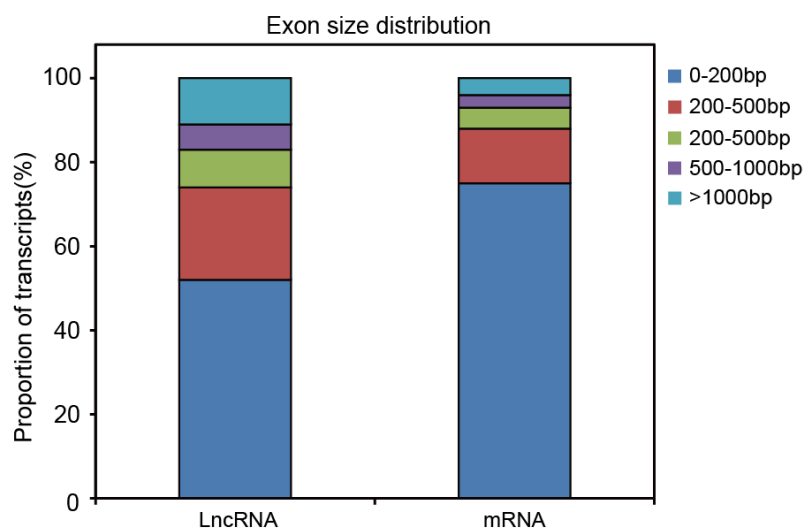
|              |       |      |          |                 |      |        |       |        |         |
|--------------|-------|------|----------|-----------------|------|--------|-------|--------|---------|
| circRNA11290 | chr11 | 4.00 | TNFRSF19 | ssc-miR-122     | 8mer | (0.18) | 66.00 | 150.00 | (19.24) |
| circRNA11290 | chr11 | 4.00 | TNFRSF19 | ssc-miR-127     | 8mer | (0.34) | 92.00 | 156.00 | (26.56) |
| circRNA13759 | chr8  | 1.00 | KLB      | ssc-miR-30a-5p  | 8mer | (0.31) | 88.00 | 163.00 | (20.25) |
| circRNA13759 | chr8  | 1.00 | KLB      | ssc-miR-30b-5p  | 8mer | (0.31) | 88.00 | 171.00 | (22.54) |
| circRNA13759 | chr8  | 1.00 | KLB      | ssc-miR-30c-5p  | 8mer | (0.31) | 88.00 | 167.00 | (22.14) |
| circRNA13759 | chr8  | 1.00 | KLB      | ssc-miR-30d     | 8mer | (0.31) | 88.00 | 165.00 | (24.12) |
| circRNA13759 | chr8  | 1.00 | KLB      | ssc-miR-30e-5p  | 8mer | (0.31) | 88.00 | 169.00 | (22.96) |
| circRNA13759 | chr8  | 1.00 | KLB      | ssc-miR-361-3p  | m8   | (0.23) | 78.00 | 151.00 | (16.13) |
| circRNA13759 | chr8  | 1.00 | KLB      | ssc-miR-504     | 8mer | (0.33) | 92.00 | 144.00 | (18.59) |
| circRNA13759 | chr8  | 1.00 | KLB      | ssc-miR-9791-3p | 8mer | (0.46) | 98.00 | 142.00 | (10.46) |
| circRNA21610 | chr8  | 2.00 | KLB      | ssc-miR-30a-5p  | 8mer | (0.29) | 86.00 | 163.00 | (20.25) |
| circRNA21610 | chr8  | 2.00 | KLB      | ssc-miR-30b-5p  | 8mer | (0.29) | 87.00 | 171.00 | (22.54) |
| circRNA21610 | chr8  | 2.00 | KLB      | ssc-miR-30c-5p  | 8mer | (0.29) | 87.00 | 167.00 | (22.14) |
| circRNA21610 | chr8  | 2.00 | KLB      | ssc-miR-30d     | 8mer | (0.29) | 86.00 | 165.00 | (24.12) |
| circRNA21610 | chr8  | 2.00 | KLB      | ssc-miR-30e-5p  | 8mer | (0.29) | 86.00 | 169.00 | (22.96) |
| circRNA21610 | chr8  | 2.00 | KLB      | ssc-miR-361-3p  | m8   | (0.23) | 78.00 | 151.00 | (16.13) |
| circRNA21610 | chr8  | 2.00 | KLB      | ssc-miR-490     | m8   | (0.22) | 75.00 | 144.00 | (14.04) |
| circRNA21610 | chr8  | 2.00 | KLB      | ssc-miR-490-3p  | m8   | (0.22) | 75.00 | 144.00 | (14.04) |
| circRNA21610 | chr8  | 2.00 | KLB      | ssc-miR-504     | 8mer | (0.33) | 92.00 | 144.00 | (18.59) |

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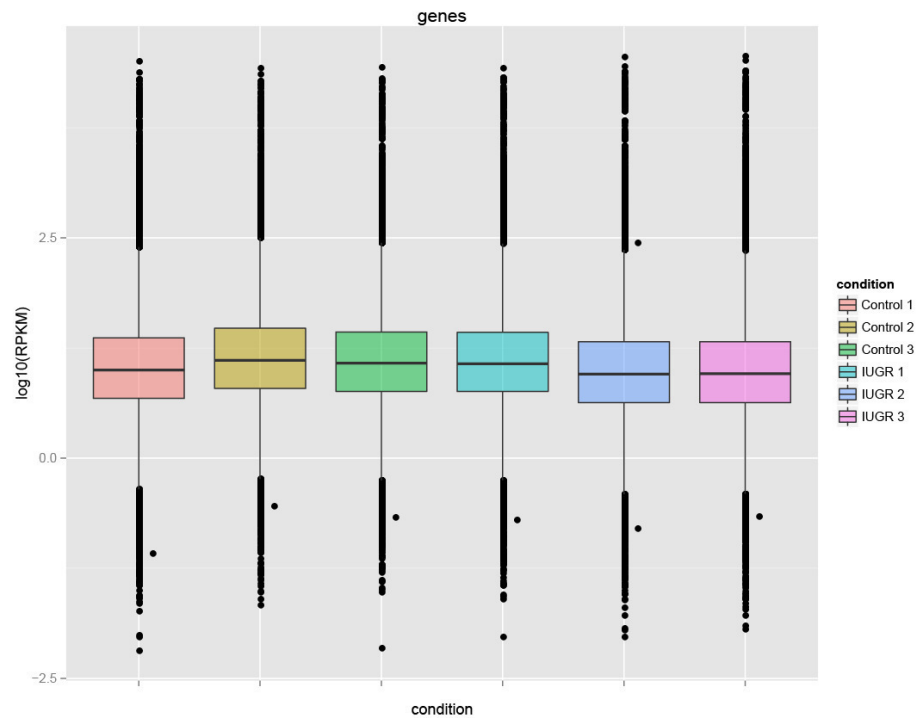




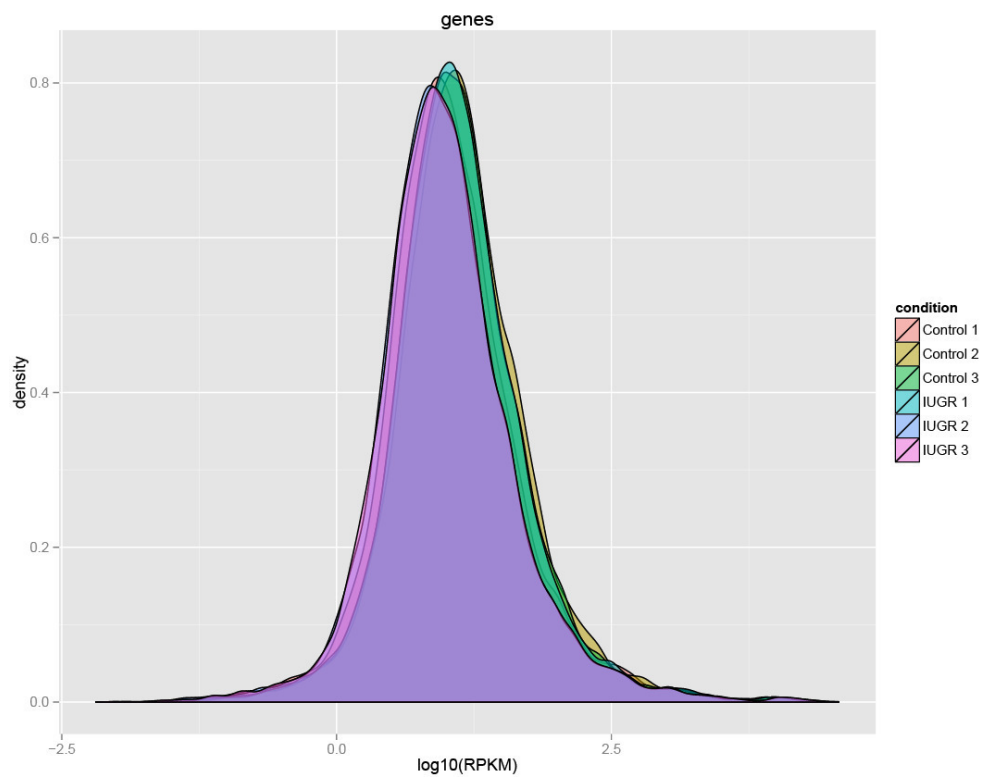
**Supplementary Figure S1. The distribution of reads in genome sites.**



**Supplementary Figure S2. The distribution of exon size in porcine lncRNA and mRNA transcripts.**



**Supplementary Figure S3. Boxplot of average circRNA expression levels**



**Supplementary Figure S4. Expression density of circRNA\_.**