

Supplementary information

Comparative transcriptome analysis to investigate the potential role of miRNAs in milk protein/fat quality

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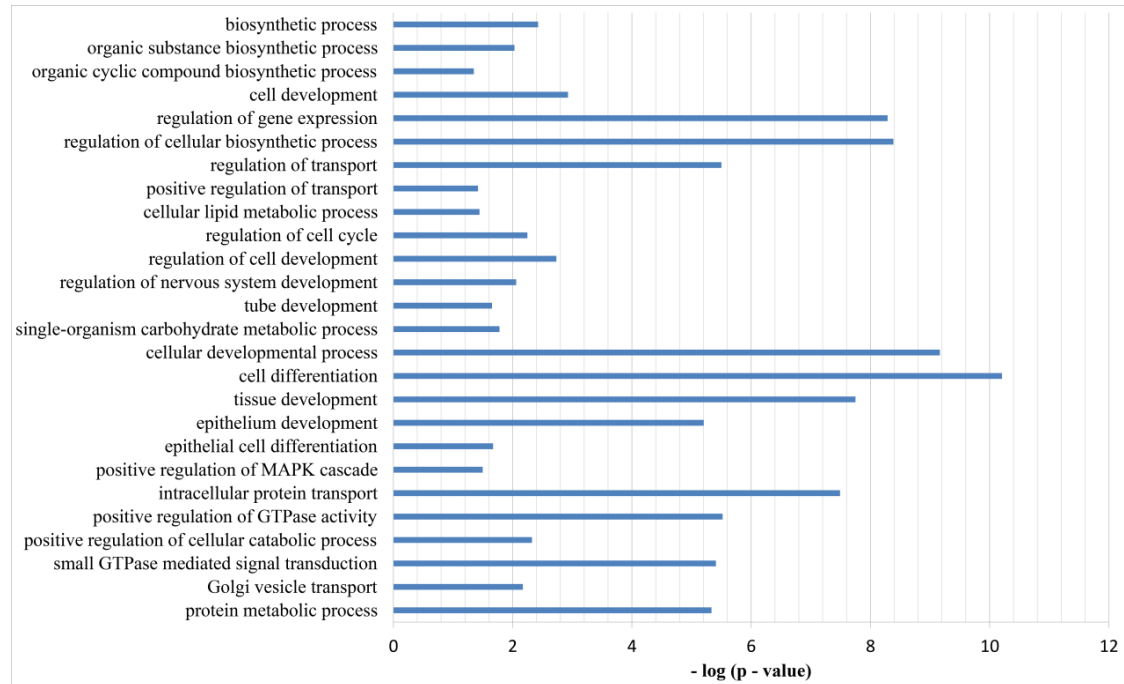
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Table S1. Concentrate composition of lactating and dry cow rations

Concentrate composition (%)	Lactating	Dry
Corn	/	67.5
Cottonseed	15	8
Rapeseed	8	6
Soybean meal	12	/
Extruded soybean	30	4
Wheat bran	/	10
Limestone	2	1.5
Sodium bicarbonate	2	1
Calcium bicarbonate	2.7	1
Sodium chloride	1.5	/
DDGS	24	/
Methionine	0.8	/
Mineral and vitamin premix	2	1

Figure S1. Functional enrichment analysis and pathways classification targets of differentially expressed miRNAs. **(A)** Functional enrichment analysis of targets by 38 differentially expressed miRNAs in H and L group. **(B)** Pathway classification of targets by 38 differentially expressed miRNAs in H and L group.

A



B

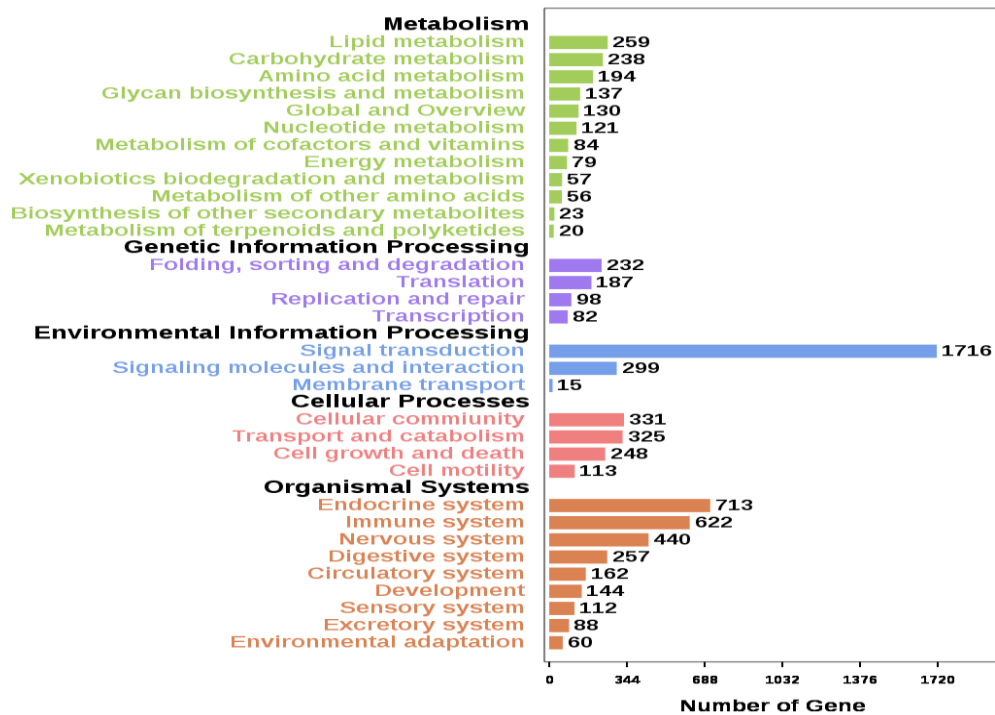
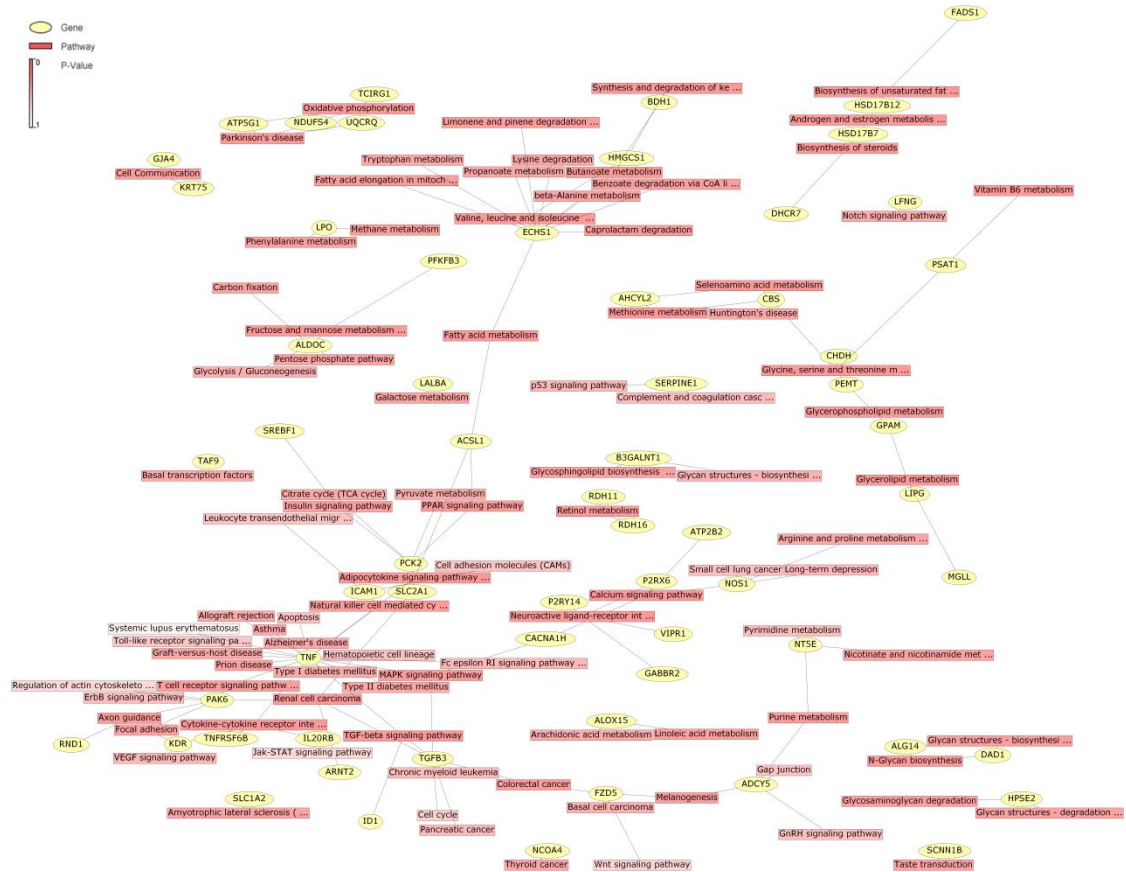


Figure S2. (A) Gene pathway network analysis results indicated that signal transduction, cell cycle and metabolism were the most important pathway in H vs. L of putative gene. (B) Gene correlation was analysis based on pathway from KEGG database, showing that most genes have one association on the same pathway of the same database.

A



B

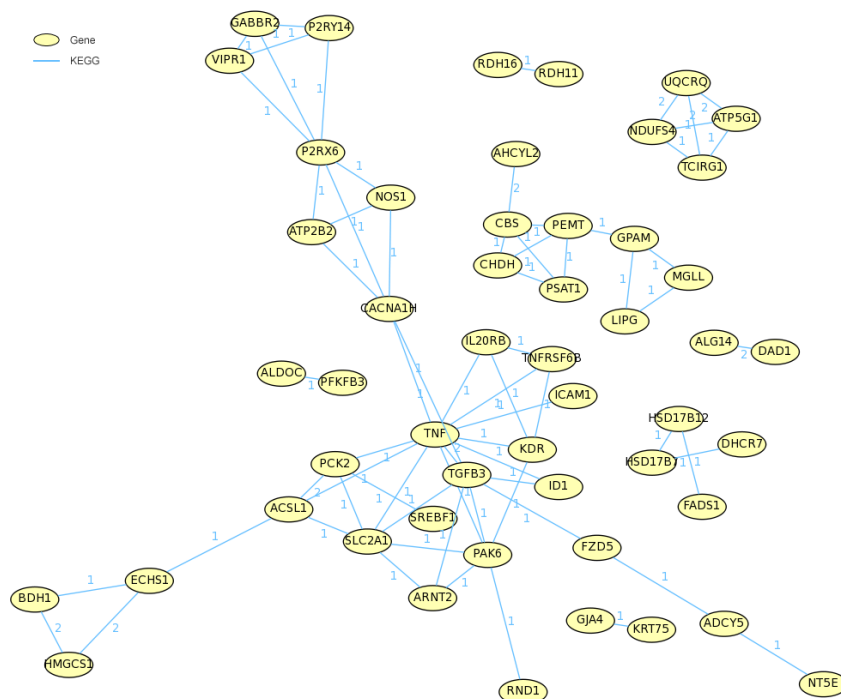


Table S2. RIP gene differentially expressed in L compared to H sample.

Gene symbol	Difference in log₂ FC (L / H)	P value
<i>LALBA</i>	2.82	4.99E-07
<i>ABCG2</i>	2.51	7.52E-06
<i>HSTN</i>	2.47	7.78E-05
<i>CSN1S1</i>	1.98	2.77E-04
<i>TMEM120B</i>	1.69	1.83E-03
<i>WNT5A</i>	-2.24	2.22E-03
<i>FASN</i>	1.56	3.70E-03
<i>PAEP</i>	1.48	5.69E-03
<i>CSN1S2</i>	1.45	6.93E-03
<i>SLC34A2</i>	1.44	7.31E-03
<i>RHOF</i>	1.45	7.66E-03
<i>SLC39A8</i>	1.37	1.15E-02
<i>CSTB</i>	1.53	1.50E-02
<i>MFGE8</i>	1.26	1.82E-02
<i>GPAM</i>	1.19	2.59E-02

Figure S3. qPCR validation of the miRNAs and mRNAs expression. (a) L compared to D, (b) H compared to D, (c) H compared to L, (d) L compared to H of RIP – seq and mRNA – seq, L compared to H of qPCR.

