Table S1 Primers used for quantitative real-time PCR verification

| Gene | Primer sequence | Accession number |
|---|---|---|
| *rpl-17* | F-AGAAATGCCCCATCTCCA<br>R-CCCTGTCTCCGTCTTGTTG | XM_020587712.1 |
| *col1a1* | F:CTTTAAGTGTACCATGCGCTGT<br>R:ATTTGCCGGTTTTCACGGGT | XM_020625331.1 |
| *s6k1* | F:TCAGGATACCACTATGGAGTTCAC<br>R:TACAGCGGCGTTCACACTTG | XM_020612395.1 |
| *fabp2* | F:GGCATTGACCGCCATCTCTT<br>R:TGTCTCGCCAGGTCAAACAG | XM_020602138.1 |
| *acsl4* | F:ATTGTGGTGGACTGGTTG<br>R:CTACATGAGCACCAAGACTG | XM_020591041.1 |
| *ube3a* | F:ACGCACACAAACAATCTCAAGT<br>R:GCATGGGGCAAGACAGTCA | XM_020588829.1 |
| *ube2b* | F:GTTATCAGGTGGCGATGGAG<br>R:GTAGACTCGTATGGGTTGTAAGG | XM_020611979.1 |

*rpl-17*, ribosomal protein L17; *col1a1*, collagen alpha-1(I); *fabp2*, fatty acid binding protein 2; *s6k1*, ribosomal protein S6 kinase beta-1; *acsl4*, acyl-CoA synthetase long-chain family member 4; *ube3a,* ubiquitin-protein ligase E3A; *ube2b*, ubiquitin conjugating enzyme E2 B.

Table S2 The differentially expressed genes involved in Ribosome

| Gene name | Gene description | Regulate | FC | P-value |
|---|---|---|---|---|
| rpl10a | ribosomal protein L10a | up | 2.52 | 1.40E-02 |
| rps27a | ribosomal protein S27a | up | 2.04 | 4.10E-02 |
| LOC109956091 | 60S ribosomal protein L36a | up | 2.07 | 2.53E-02 |
| rpl6 | ribosomal protein L6 | up | 2.21 | 2.90E-02 |
| rps13 | ribosomal protein S13 | up | 2.42 | 1.89E-02 |
| mrpl33 | mitochondrial ribosomal protein L33 | up | 2.03 | 4.46E-02 |
| rplp2 | ribosomal protein lateral stalk subunit P2 | up | 3.06 | 1.86E-03 |
| rps2 | ribosomal protein S2, transcript variant X2 | up | 2.39 | 1.05E-02 |
| rpl38 | ribosomal protein L38 | up | 2.48 | 1.94E-02 |
| LOC109963109 | 60S ribosomal protein L19-like | up | 2.52 | 6.89E-03 |
| rpl31 | ribosomal protein L31, transcript variant X2 | up | 2.22 | 1.81E-02 |

| | | | | |
|---|---|---|---|---|
| rpl17 | ribosomal protein L17 | up | 2.06 | 4.55E-02 |
| rps6 | ribosomal protein S6 | up | 2.16 | 3.71E-02 |
| rpl14 | ribosomal protein L14 | up | 2.23 | 9.86E-03 |
| LOC109967421 | 40S ribosomal protein S27-like | up | 13.73 | 1.13E-02 |
| rpl29 | ribosomal protein L29 | up | 2.34 | 1.28E-02 |
| rps25 | ribosomal protein S25 | up | 2.11 | 3.84E-02 |
| rps7 | ribosomal protein S7, transcript variant X1 | up | 2.64 | 8.80E-03 |
| rps3a | ribosomal protein S3A | up | 2.48 | 1.21E-02 |
| rpl23 | ribosomal protein L23 | up | 2.09 | 2.69E-02 |
| rpl27 | ribosomal protein L27 | up | 2.40 | 1.32E-02 |
| rpl13a | ribosomal protein L13a | up | 3.09 | 8.11E-04 |
| rps8 | ribosomal protein S8 | up | 2.57 | 1.01E-02 |
| mrpl21 | mitochondrial ribosomal protein L21 | down | 0.41 | 3.40E-03 |
| rpl24 | ribosomal protein L24 | up | 2.21 | 1.93E-02 |
| rps19 | ribosomal protein S19 | up | 2.61 | 7.94E-03 |
| uba52 | ubiquitin A-52 residue ribosomal protein fusion product 1 | up | 2.15 | 1.42E-02 |
| rps11 | ribosomal protein S11, transcript variant X1 | up | 2.46 | 6.43E-03 |
| rpl12 | ribosomal protein L12 | up | 2.66 | 1.13E-03 |
| rps12 | ribosomal protein S12 | up | 2.64 | 1.31E-03 |
| fau | FAU, ubiquitin like and ribosomal protein S30 fusion | up | 2.14 | 1.88E-02 |
| rpl37 | ribosomal protein L37 | up | 2.27 | 1.07E-02 |
| rpl18 | ribosomal protein L18 | up | 2.09 | 4.99E-02 |
| rps20 | ribosomal protein S20 | up | 2.78 | 2.20E-04 |
| rps26 | ribosomal protein S26 | up | 2.11 | 3.09E-02 |
| rpl23a | ribosomal protein L23a | up | 2.14 | 1.44E-02 |
| rps23 | ribosomal protein S23 | up | 2.91 | 4.78E-04 |
| LOC109969138 | 40S ribosomal protein S17, transcript variant X1 | up | 2.05 | 3.61E-02 |
| rps24 | ribosomal protein S24, transcript variant X1 | up | 2.16 | 3.83E-02 |
| rpl27a | ribosomal protein L27a | up | 2.12 | 2.70E-02 |
| mrpl16 | mitochondrial ribosomal protein L16, transcript variant X1 | down | 0.46 | 1.05E-02 |
| rpsa | ribosomal protein SA | up | 2.17 | 3.78E-02 |

Table S3 The differentially expressed genes involved in Ubiquitin mediated proteolysis

| Gene name | Gene description | Regulate | FC | P-value |
|---|---|---|---|---|
| trim37 | tripartite motif containing 37, transcript variant X1 | up | 2.67 | 3.52E-02 |
| rps27a | ribosomal protein S27a | up | 2.04 | 4.10E-02 |
| ube2i | ubiquitin conjugating enzyme E2 I, transcript variant X1 | down | 0.22 | 4.19E-02 |
| LOC109953363 | ubiquitin-protein ligase E3A | down | 0.49 | 8.51E-03 |
| anapc11 | anaphase promoting complex subunit 11 | down | 0.27 | 2.58E-04 |

| | | | | |
|---|---|---|---|---|
| LOC109958966 | ubiquitin-like modifier-activating enzyme 1 | down | 0.24 | 1.19E-02 |
| syvn1 | synoviolin 1, transcript variant X1 | down | 0.30 | 8.46E-03 |
| fbxw11 | F-box and WD repeat domain containing 11, transcript variant X1 | down | 0.36 | 4.87E-03 |
| cul1 | cullin 1, transcript variant X4 | down | 0.31 | 5.29E-04 |
| ddb1 | damage specific DNA binding protein 1 | up | 2.21 | 4.90E-02 |
| herc2 | HECT and RLD domain containing E3 ubiquitin protein ligase 2 | down | 0.40 | 4.45E-02 |
| uba1 | ubiquitin like modifier activating enzyme 1, transcript variant X1 | down | 0.47 | 2.11E-02 |
| ube2b | ubiquitin conjugating enzyme E2 B, transcript variant X1 | down | 0.45 | 5.13E-03 |
| LOC109973961 | ubiquitin-conjugating enzyme E2 Q2-like, transcript variant X1 | down | 0.35 | 2.13E-03 |
| LOC109962584 | probable E3 ubiquitin-protein ligase HERC4, transcript variant X2 | down | 0.20 | 3.07E-03 |
| trip12 | thyroid hormone receptor interactor 12, transcript variant X5 | down | 0.34 | 3.31E-03 |
| LOC109963682 | ubiquitin-conjugating enzyme E2 E2-like, transcript variant X1 | down | 0.27 | 3.14E-02 |
| LOC109963674 | ubiquitin-conjugating enzyme E2 E1, transcript variant X1 | down | 0.41 | 2.76E-04 |
| uba52 | ubiquitin A-52 residue ribosomal protein fusion product 1 | up | 2.15 | 1.42E-02 |
| huwe1 | HECT, UBA and WWE domain containing 1, E3 ubiquitin protein ligase | down | 0.46 | 7.69E-03 |
| LOC109957680 | cullin-3-like | down | 0.34 | 7.15E-04 |
| LOC109962585 | probable E3 ubiquitin-protein ligase HERC3 | down | 0.06 | 1.65E-02 |
| LOC109970578 | cullin-3-like | down | 0.43 | 2.13E-03 |
| cul4b | cullin 4B | down | 0.26 | 3.13E-04 |
| LOC109956179 | F-box only protein 2-like | up | 2.99 | 9.80E-03 |
| cdc27 | cell division cycle 27 | down | 0.31 | 3.80E-05 |
| LOC109969285 | ubiquitin-conjugating enzyme E2 R1-like | down | 0.40 | 1.25E-02 |

Table S4 The differentially expressed genes involved in mTOR signaling pathway

| Gene name | Gene description | Regulate | FC | P-value |
|---|---|---|---|---|
| LOC109954584 | phosphatidate phosphatase LPIN1-like, transcript variant X1 | down | 0.04 | 7.99E-14 |
| LOC109959759 | ras-related GTP-binding protein D-like, transcript variant X1 | down | 0.37 | 7.91E-03 |
| tsc2 | tuberous sclerosis 2, transcript variant X2 | up | 2.49 | 1.30E-02 |
| LOC109955468 | GTP-binding protein Rheb | down | 0.37 | 1.02E-02 |
| rps6ka3 | ribosomal protein S6 kinase A3, transcript variant X3 | up | 2.20 | 3.56E-03 |

| | | | | |
|---|---|---|---|---|
| LOC109966856 | phosphatidylinositol 3-kinase regulatory subunit gamma-like, transcript variant X4 | up | 4.34 | 2.63E-02 |
| LOC109959592 | ras-related GTP-binding protein A, transcript variant X1 | up | 2.03 | 3.81E-02 |
| fnip1 | folliculin interacting protein 1, transcript variant X1 | up | 4.28 | 7.75E-04 |
| lpin2 | lipin 2, transcript variant X1 | up | 3.35 | 2.44E-03 |
| lamtor5 | late endosomal/lysosomal adaptor, MAPK and MTOR activator 5 | up | 7.06 | 3.70E-03 |
| rps6ka6 | ribosomal protein S6 kinase A6 | up | 2.50 | 2.58E-02 |
| dvl2 | dishevelled segment polarity protein 2 | up | 2.37 | 1.88E-02 |
| clip1 | CAP-Gly domain containing linker protein 1, transcript variant X1 | down | 0.38 | 1.32E-02 |
| rps6 | ribosomal protein S6 | up | 2.16 | 3.71E-02 |
| wdr59 | WD repeat domain 59 | down | 0.30 | 2.56E-04 |
| ddit4 | DNA damage inducible transcript 4 | down | 0.26 | 1.62E-02 |
| LOC109957432 | hamartin-like | down | 0.41 | 2.43E-03 |
| LOC109972722 | segment polarity protein dishevelled homolog DVL-3-like, transcript variant X1 | up | 2.25 | 1.25E-03 |
| gsk3b | glycogen synthase kinase 3 beta, transcript variant X1 | down | 0.17 | 2.78E-04 |
| LOC109956162 | phosphatidate phosphatase LPIN2-like, transcript variant X1 | down | 0.38 | 1.61E-02 |
| raf1 | Raf-1 proto-oncogene, serine/threonine kinase, transcript variant X2 | down | 0.24 | 1.39E-03 |
| LOC109959930 | V-type proton ATPase subunit E 1-like, transcript variant X1 | up | 2.39 | 3.18E-02 |
| LOC109963978 | sestrin-2-like, transcript variant X1 | up | 2.43 | 4.27E-02 |
| LOC109955981 | keratin, type I cytoskeletal 18-like, transcript variant X1 | up | 2.09 | 4.90E-02 |
| akt1s1 | AKT1 substrate 1 | up | 2.35 | 7.02E-04 |
| atp6v1d | ATPase H+ transporting V1 subunit D | down | 0.33 | 3.21E-04 |
| LOC109966482 | insulin receptor substrate 1-B-like | down | 0.20 | 1.50E-05 |
| pten | phosphatase and tensin homolog, transcript variant X1 | down | 0.47 | 1.52E-02 |
| LOC109959155 | GATS-like protein 3 | up | 2.78 | 1.77E-02 |
| LOC109960282 | ribosomal protein S6 kinase beta-1-like | up | 2.34 | 3.33E-03 |
| lamtor4 | late endosomal/lysosomal adaptor, MAPK and MTOR activator 4 | up | 2.28 | 9.56E-03 |

Table S5 The differentially expressed genes involved in ECM-receptor interaction

| Gene name | Gene description | Regulate | FC | p-value |
|---|---|---|---|---|
| col6a2 | collagen type VI alpha 2 chain | up | 2.66 | 1.25E-02 |
| col4a6 | collagen type IV alpha 6 chain, transcript variant X1 | up | 2.34 | 2.39E-02 |
| LOC109971201 | collagen alpha-1(II) chain-like | up | 2.44 | 3.97E-02 |
| LOC109971731 | collagen alpha-3(VI) chain-like | up | 2.11 | 2.85E-02 |

| | | | | |
|---|---|---|---|---|
| LOC109966919 | syndecan-4-like | down | 0.29 | 6.31E-03 |
| LOC109969770 | tenascin-like | up | 13.08 | 3.82E-02 |
| LOC109969127 | integrin alpha-11-like | down | 0.43 | 3.12E-02 |
| col6a1 | collagen type VI alpha 1 chain | up | 2.91 | 5.90E-03 |
| LOC109964120 | fibronectin-like, transcript variant X1 | down | 0.43 | 4.12E-02 |
| itga7 | integrin subunit alpha 7, transcript variant X1 | down | 0.30 | 2.39E-05 |
| LOC109969769 | tenascin-like, transcript variant X4 | down | 0.18 | 6.96E-04 |
| col4a5 | collagen type IV alpha 5 chain, transcript variant X1 | up | 2.85 | 2.37E-02 |
| LOC109970053 | kunitz-type serine protease inhibitor BmKTT-2-like | up | 3.28 | 3.08E-03 |
| LOC109972354 | thrombospondin-4-B-like | down | 0.40 | 2.87E-02 |
| LOC109957036 | thrombospondin-4-B-like | up | 2.35 | 3.77E-02 |
| thbs3 | thrombospondin 3 | down | 0.34 | 2.69E-02 |
| LOC109974984 | laminin subunit alpha-1-like | down | 0.13 | 5.94E-05 |
| LOC109966907 | dystroglycan-like | up | 2.60 | 4.89E-04 |
| col1a2 | collagen type I alpha 2 chain | up | 2.50 | 2.42E-02 |
| LOC109970071 | collagen alpha-6(VI) chain-like | up | 2.91 | 6.31E-03 |
| itga6 | integrin subunit alpha 6, transcript variant X1 | up | 3.09 | 3.11E-02 |
| LOC109974887 | collagen alpha-1(I) chain-like, transcript variant X1 | up | 2.84 | 1.57E-02 |

Table S6 The differentially expressed genes involved in PPAR signaling pathway

| Gene name | Gene description | Regulate | FC | P-value |
|---|---|---|---|---|
| LOC109963008 | acyl-CoA desaturase-like | up | 5.35 | 1.36E-03 |
| LOC109963312 | very long-chain acyl-CoA synthetase-like | up | 6.64 | 1.16E-05 |
| LOC109955654 | cytochrome P450 27C1-like, transcript variant X2 | down | 0.30 | 2.58E-03 |
| acadm | acyl-CoA dehydrogenase, C-4 to C-12 straight chain | down | 0.47 | 2.38E-03 |
| LOC109956993 | long-chain-fatty-acid--CoA ligase 1-like | up | 2.65 | 3.68E-02 |
| LOC109963311 | very long-chain acyl-CoA synthetase-like | up | 15.35 | 8.41E-11 |
| acsl4 | acyl-CoA synthetase long-chain family member 4, transcript variant X3 | up | 3.30 | 1.28E-02 |
| LOC109968035 | fatty acid-binding protein, brain-like | up | 39.23 | 3.88E-06 |
| LOC109967077 | carnitine O-palmitoyltransferase 1, liver isoform-like | up | 2.46 | 1.82E-02 |
| LOC109963313 | very long-chain acyl-CoA synthetase-like | up | 30.29 | 4.15E-09 |
| LOC109974250 | perilipin-2-like, transcript variant X1 | down | 0.45 | 3.47E-02 |
| angptl4 | angiopoietin like 4 | down | 0.22 | 1.50E-04 |
| LOC109966867 | angiopoietin-related protein 4-like | down | 0.17 | 1.22E-02 |
| LOC109959447 | sorbin and SH3 domain-containing protein 1-like, transcript variant X1 | up | 2.29 | 5.49E-03 |
| LOC109971684 | retinoic acid receptor RXR-beta-A-like | up | 2.28 | 3.45E-04 |
| LOC109960743 | hydroxymethylglutaryl-CoA synthase, cytoplasmic-like, transcript variant X1 | down | 0.27 | 4.78E-03 |
| acaa1 | acetyl-CoA acyltransferase 1 | up | 2.25 | 4.75E-05 |
| fabp2 | fatty acid binding protein 2 | up | 2.87 | 4.68E-04 |