**Supplemental Table 1** Primers used for quantitative real-time PCR analysis.

|  |  |  |  |
| --- | --- | --- | --- |
| Genes | Forward primer (5’-3’) | Reverse primer (5’-3’) | Accession no. |
| ***chrebp*** | ACCATCACTCTCCAGCAAGC | ATGACGGTGGGTGTGGTTAC | MK002238 |
| ***srebp1*** | CTGGGTCATCGCTTCTTTGTG | TCCTTCGTTGGAGCTTTTGTCT | JX992742 |
| ***pparγ*** | ACGCCCCGTTCGTTATCC | TGAGCAGAGTCACCTGGTCATTG | JX992741 |
| ***lxrα*** | ACATGCGTCGAAAGTGTCAG | CTGTTTCTGCATGGCGACTA | KJ814240.1 |
| ***fas*** | AACTAAAGGCTGCTGGTTGCTA | CACCTTCCCGTCACAAACCTC | JN579124 |
| ***accα*** | GGGGTTTTCACGCTGCTTC | GGTTCTGATTGGGTCGTCCTG | JX992746 |
| ***scd1*** | AGACCATCGTGTCCATCACA | TGGCATTTAGAACAAGTGCG | KJ818303.1 |
| ***lpl*** | AGCGATTGGTGGGAGGATTAT | TGAGCACGGTCCAGTTTCCT | JX992743.1 |
| ***sumo1*** | TGGCCAGGACAACAGTGAAA | CTAGTCGTTCCAGTAGCCGC | MH192975 |
| ***sumo2*** | CGAGAAGCCCAAGGAAGGAG | TGTCCGTCTCGTTAATGGGC | MH192976 |
| ***sumo3*** | CGCCGCTCAGCAAGTTAATG | CCGCCCGTTTGTTGTTGAAA | MH192977 |
| ***sae1*** | TCTGACCTGGGCTTGGAGTA | TAATCTGGTGTCGTGCGCTT | MH192978 |
| ***uba2*** | CTGGTCAACGTTGTGCACTG | CATGGTGCTGGAGGAAGGTT | MH192979 |
| ***ubc9*** | TGATGAACTGGGAGTGTGCC | GCCTCCAGTCTTTGTCCTCC | MH192980 |
| ***pias1*** | CTCCTGCTGAACCGTTTCCT | GAGCTGTAGATGTCCGAGCC | MH192981 |
| ***senp1*** | CGCCTCATCATCACCAGGAA | TTCTTAGTCCAGCGCCGTAC | MH192982 |
| ***senp2*** | TCCTCATCCCTTTGCACCTG | GCTGGTCACCGTCCACTTTA | MH192983 |
| ***senp3*** | AGAGCTGGAAAACATGGCGA | TGCCGTGATACCCGTTCAAA | MH192984 |
| ***18s rRNA*** | AGCTCGTAGTTGGATCTCGG | CGGGTATTCAGGCGAGTTTG | KP938527 |
| ***β-actin*** | GGACTCTGGTGATGGTGTGA | CTGTAGCCTCTCTCGGTCAG | EU161066 |
| ***rpl7*** | GGCAAATGTACAGGAGCGAG | GCCTTGTTGAGCTTGACGAA | KP938522 |
| ***tuba*** | TCAAAGCTGGAGTTCTCGGT | AATGGCCTCGTTATCCACCA | KP938526 |
| ***b2m*** | GCTGATCTGCCATGTGAGTG | TGTCTGACACTGCAGCTGTA | KP938520 |
| ***elfa*** | GTCTGGAGATGCTGCCATTG | AGCCTTCTTCTCAACGCTCT | KU886307 |
| ***gapdh*** | TTTCAGCGAGAGAGACCCAG | ATGACTCTCTTGGCACCTCC | KP938521 |
| ***tbp*** | AGCAAAGAGTGAGGAGCAGT | ACTGCTGATGGGTGAGAACA | KP938525 |
| **SUMO1-6×His** | GTGGAATATCATGTCAGACACG | CTAATGGTGATGGTGATGATGGTCGTTCCAGTAGCCGCCGGTCT |  |
|  | ctagcgtttaaacttaagcttATGTCAGACACGGAGACAAAACC | aacgggccctctagactcgagCTAATGGTGATGGTGATGATGGTC |  |
| **UBC9-6×His** | ATGTCTGGTATAGCGCTGAG | TTAATGGTGATGGTGATGATGGGGAGAAAACTTTTTGGCTTGTGCT |  |
|  | ctagcgtttaaacttaagcttATGTCTGGTATAGCGCTGAGTCG | aacgggccctctagactcgagTTACTTATCGTCGTCATCCTTGTAATC |  |
| **SREBP1-Flag** | ATGAATAATAATATGTCTTTT | CTACTTATCGTCGTCATCCTTGTAATCCAGAGCCATCCGTGA |  |
|  | ctagcgtttaaacttaagcttATGAATAATAATATGTCTTTTGACGATCC | aacgggccctctagactcgagCTACTTATCGTCGTCATCCTTGTAATC |  |
| **K145R** | AGGTGagaCAGCCCAAAGCTCAAACCGCTCAA | TTTGGGCTGtctCACCTGACTTGGGGCCACAG |  |
| **K254R** | GTTCATCaggGCAGAATCTCTCCTCCTCACCA | ATTCTGCcctGATGAACTGAGGCTGCAACAAG |  |
| **K264R** | CCTGagaCCAGACGTATCTATGATAACTACAGTCACG | ATACGTCTGGtctCAGGGTGGTGAGGAGGAGAGA |  |
| **K392R** | CCAGAAACTAagaCAGGAGAACATGGCTCTCAAAAT | CCTGtctTAGTTTCTGGTTGGACTGCTGAAGG |  |
| **K419R** | GGATGTAagaGCTGAACTTCCCACTCCTCCAG | GTTCAGCtctTACATCCACCTCCATGGCCACC |  |

Abbreviations: *18s rRNA*, Ribosomal RNA; *acc*, acetyl-CoA carboxylase ; *b2m*, beta-2-microglobulin; *chrebp*, carbohydrate response element binding protein; *elfa*, translation elongation factor; *fas*, fatty acid synthase; *gapdh*, glyceraldehyde-3-phosphate dehydrogenase; *hprt*, hypoxanthine-guanine phosphoribosyltransferase; *lpl*, lipoprotein lipase; *lxr*, liver X receptors; *ppar*, peroxisome proliferator-activated receptor; *pias1*, protein inhibitor of activated STAT1; *rpl7*, ribosomal protein L7; *sae1*, SUMO-activating enzyme subunit 1; *scd1*, stearoyl-CoA desaturase 1; *senp*, sentrin-specific protease; *srebp1*, sterol-regulator element-binding protein-1; *sumo*, small ubiquitin-related modifier; *tbp*, TATA-box-binding protein; *tuba*, tubulin alpha chain; *uba2*, SUMO-activating enzyme subunit 2; *ubc9*, ubiquitin-conjugating enzyme 9. Mutants with the K145R, K254R, K264R, K392R and K419R mutations were generated from wild-type (WT) SREBP1 by site-directed mutagenesis.

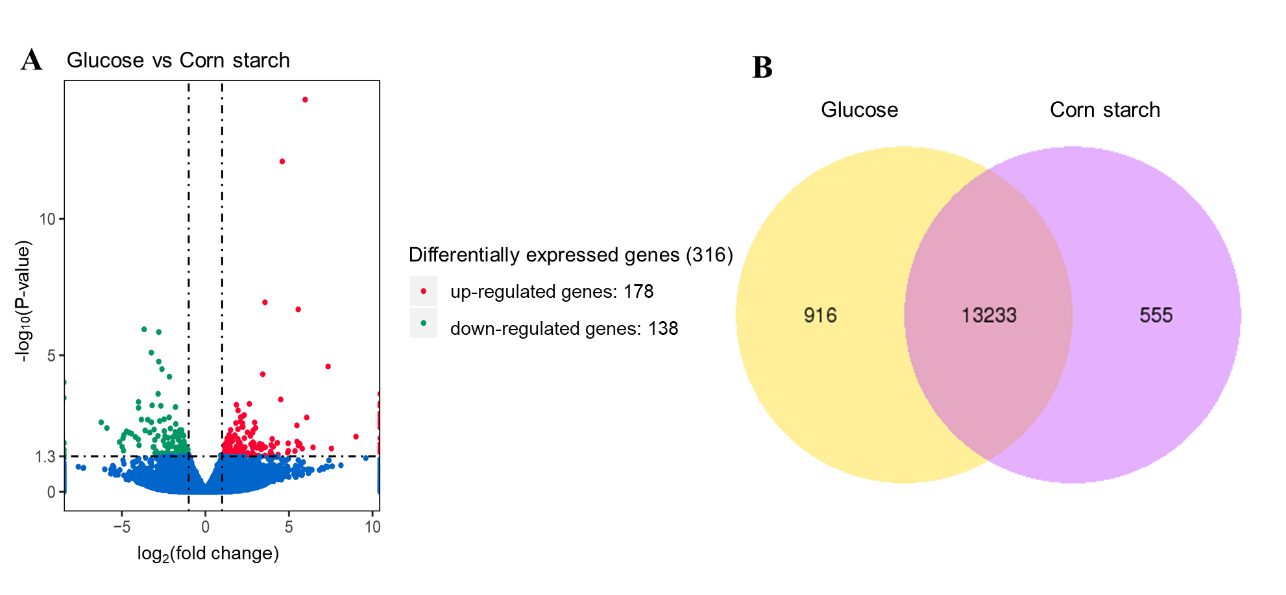
**Supplemental Table 2** Summary of output statistics by Illumina sequencing

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Sample | Raw reads | Clean reads | clean bases | Clean data ratio (%) | Q20(%) | GC content(%) |
| G1 | 59548100 | 57778704 | 8.67G | 97.03% | 97.10 | 44.46 |
| G2 | 65504136 | 64091922 | 9.61G | 97.84% | 97.57 | 46.13 |
| G3 | 56059086 | 54537518 | 8.18G | 97.29% | 97.62 | 46.25 |
| C1 | 60168574 | 58669406 | 8.80G | 97.51% | 97.16 | 46.02 |
| C2 | 52970302 | 51157316 | 7.67G | 96.58% | 97.40 | 46.27 |
| C3 | 57799794 | 56538698 | 8.48G | 97.82% | 97.26 | 46.12 |

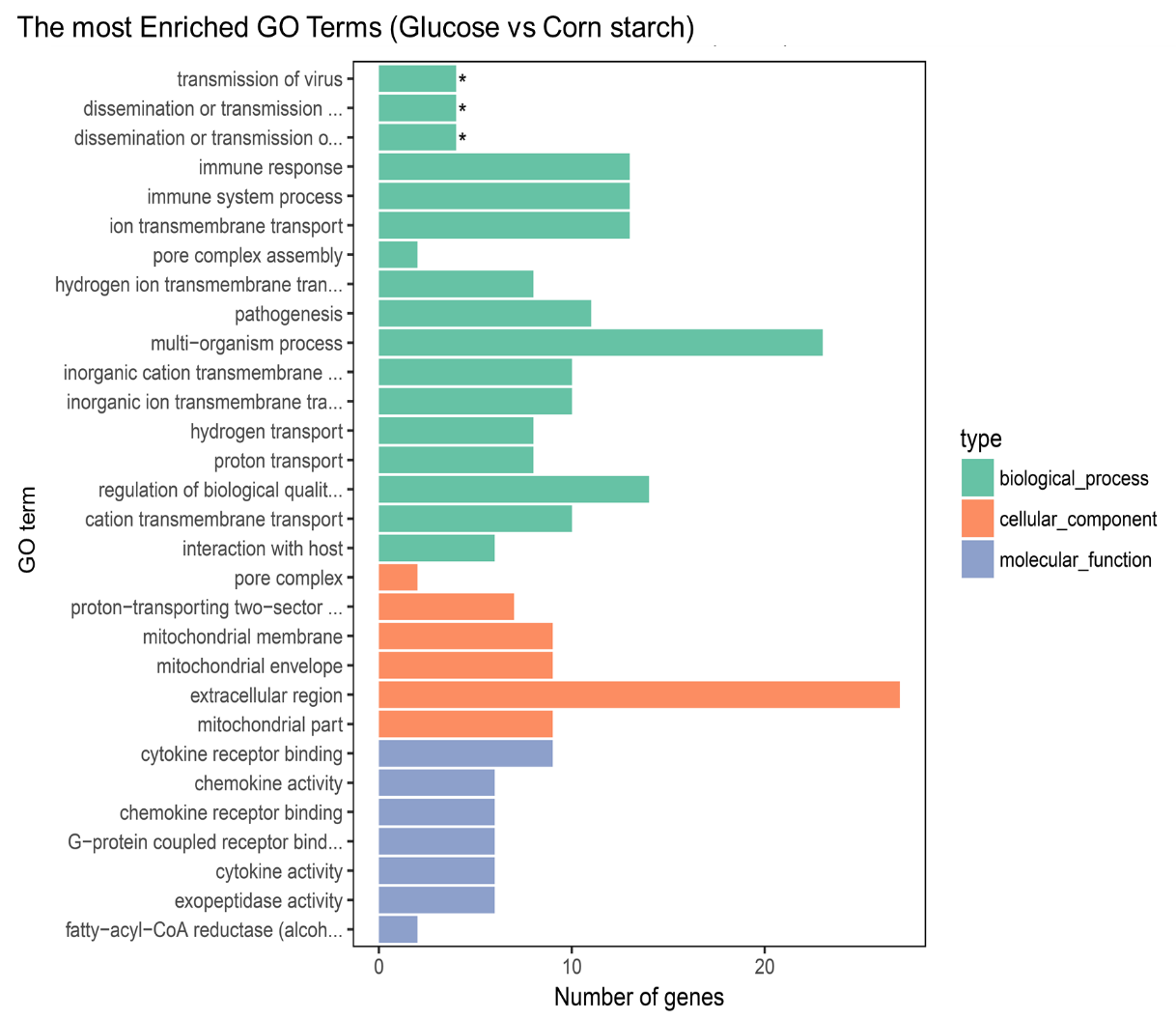
Q20 indicates a base call accuracy of 99% (1:100 probability of incorrect base call); GC percentage is proportion of guanidine and cytosine nucleotides among total nucleotides.

**Supplemental Table 3** Alignment statistics of reads align to reference gene

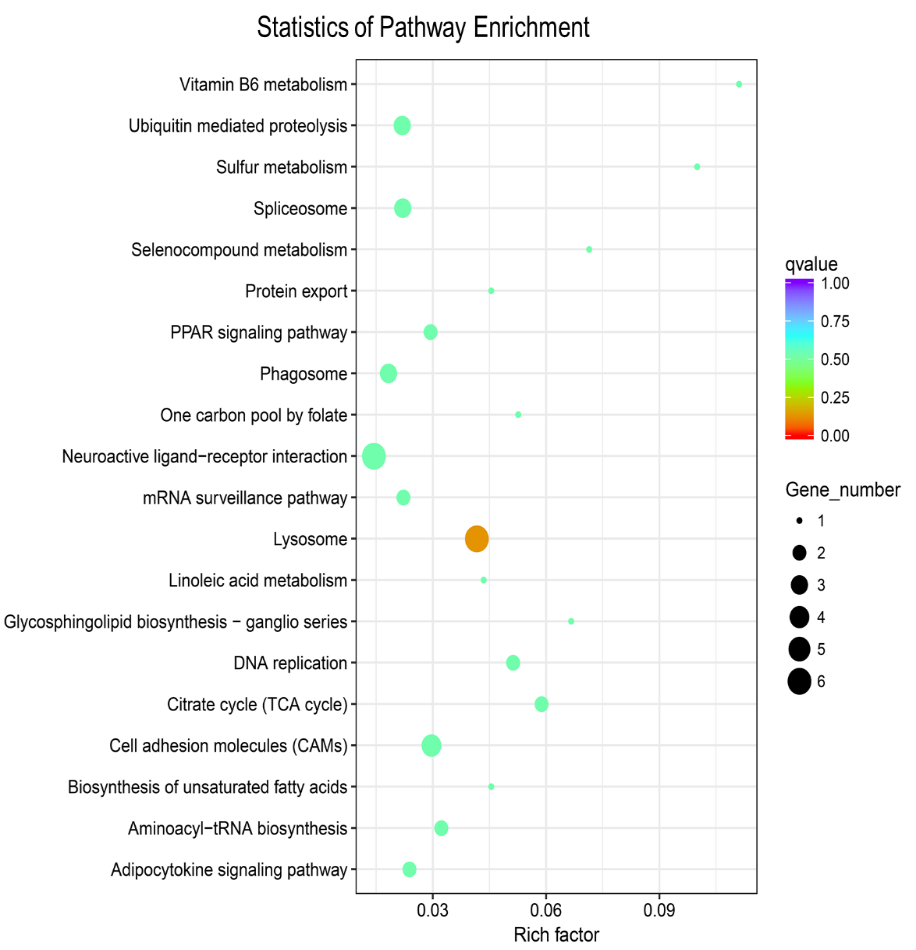
|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | Total reads | Total mapped reads (%) | Unique match (%) | Multiple mapped (%) |
| G1 | 57778704 | 81.21 | 66.84 | 14.37 |
| G2 | 64091922 | 82.19 | 68.27 | 13.93 |
| G3 | 54537518 | 80.69 | 66.82 | 13.86 |
| C1 | 58669406 | 81.37 | 67.53 | 13.84 |
| C2 | 51157316 | 81.29 | 67.78 | 13.5 |
| C3 | 56538698 | 81.54 | 68.11 | 13.43 |



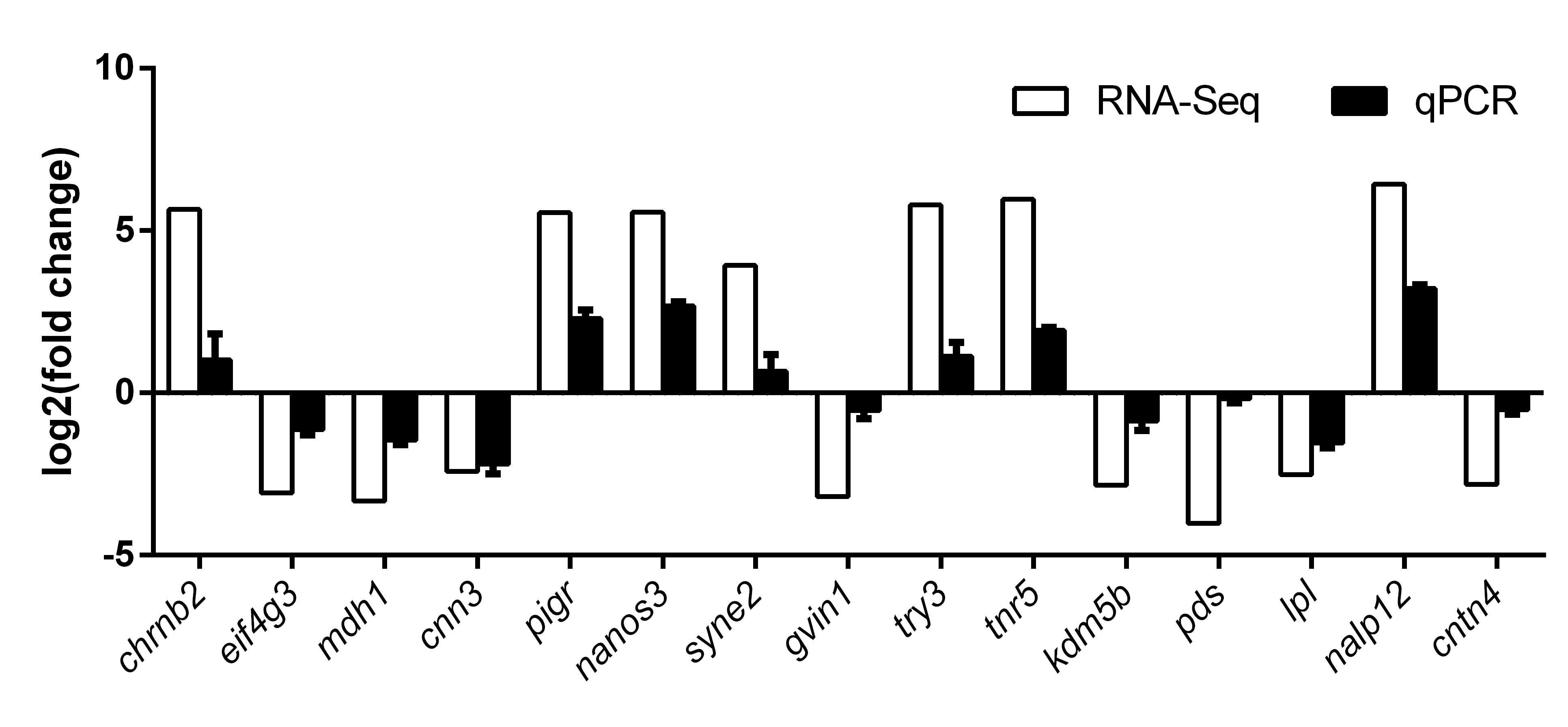
**Supplemental Figure 1** (A)Scatter plots showing the correlation between the gene expression profiles of Glucose and Corn starch groups. X-axis and Y-axis mean log2 value of gene expression. (B) Venn diagram analysis of the differentially expressed genes following glucose and corn starch groups. Differentially expressed genes are shown in red (up-regulated expression) and green (down-regulated expression). Blue means genes that were not differentially expressed.



**Supplemental Figure 2** GO functional classification of DEGs. X axis means number of DEGs (the number is presented by its square root value). Y axis represents GO terms. All GO terms are grouped into three ontologies: green for biological process, orange for cellular component and blue for molecular function.

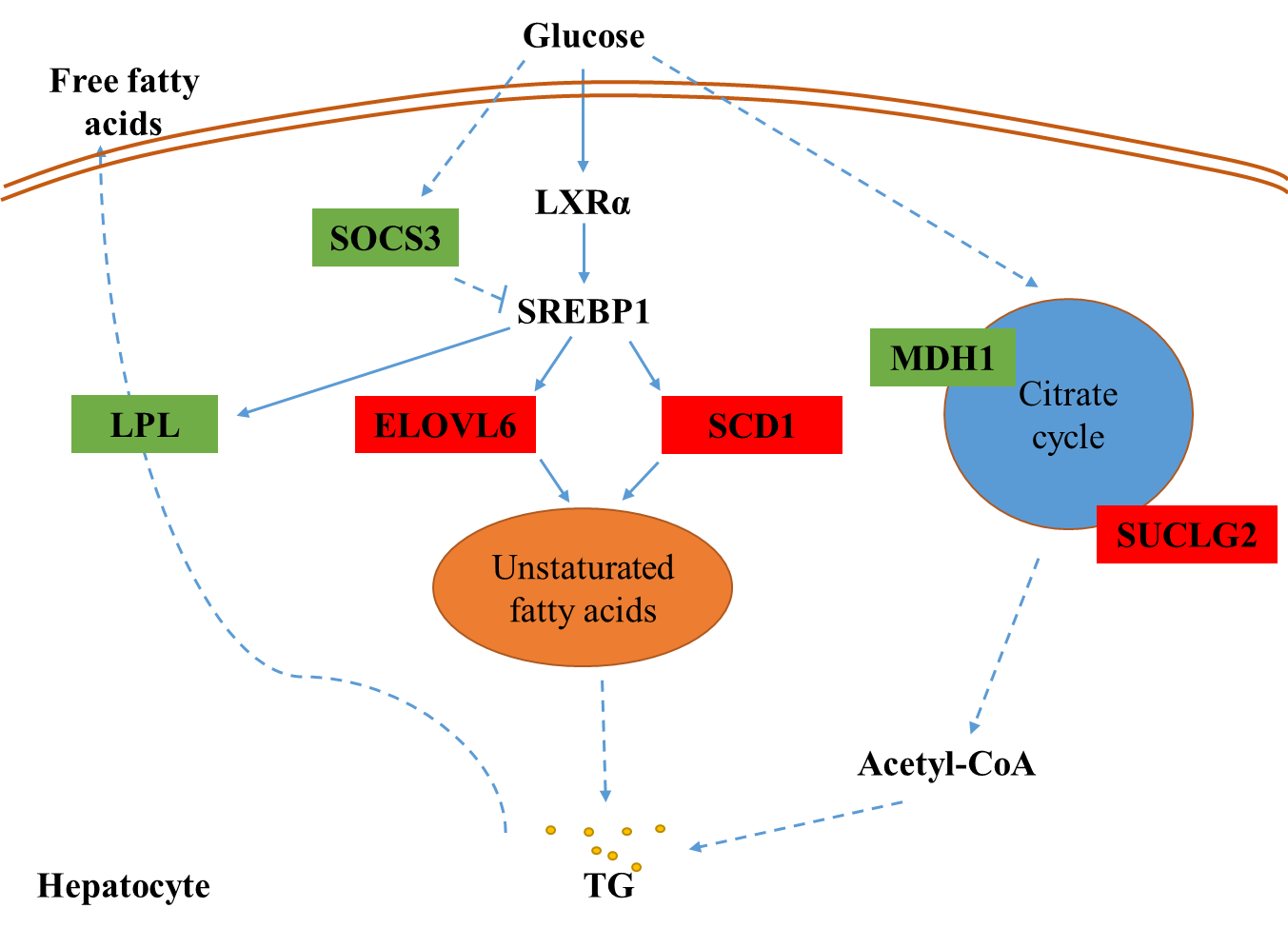


**Supplemental Figure 3** KEGG functional classification of DEGs. X-axis means rich factor (the ratio of the number of differentially expressed genes enriched in the pathway to the number of the annotation genes). Y-axis means KEGG pathway terms, and different color represents different qvalue (Qvalue refers to the Pvalue after multiple hypothesis test corrections, and the closer to 0, the more significant enriched).



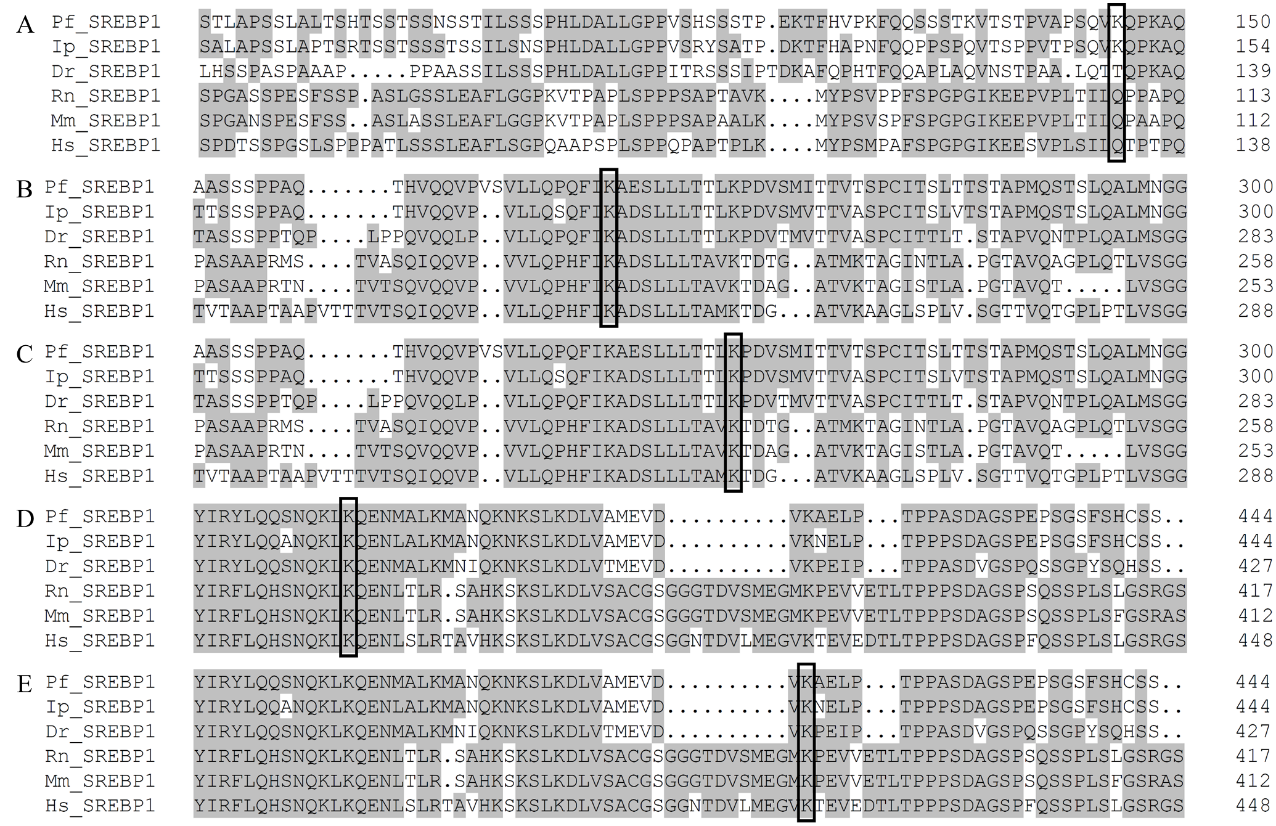
**Supplemental Figure 4** Comparison of mRNA levels between RNA-Seq and qPCR results. The y-axis is the gene expressed log2(fold change) and the x-axis is the gene name. mRNA levels were normalized to housekeeping genes (*rpl7* and *b2m*) expressed as a ratio of the glucose group. Values are mean ± SEM. qPCR, quantitative PCR; SEM, standard errors of the mean.

Abbreviations: *chrnb2*, neuronal acetylcholine receptor subunit beta 2; *cnn3*, calponin 3; *cntn4*, contactin 4; *eif4g3*, eukaryotic translation initiation factor 4 gamma 3; *gvin1*, interferon induced very large GTPase 1; *kdm5b*, lysine specific demethylase 5b; *lpl*, lipoprotein lipase; *mah1*, malate dehydrogenase 1; *nanos3*, nanos C2HC type zinc finger 3; *nalp12*, NACHT, LRR and PYD domains-containing protein 12; *pds*, pendred syndrome; *pigr*, polymeric immunoglobulin receptor; *syne2*, nesprin 2; *tnr5*, tumor necrosis factor receptor superfamily member 5; *try3*, trypsin 3.



**Supplemental Figure 5** Differentially expressed genes involved in lipogenesis. The up-regulated genes (P < 0.05, and the absolute value of log2(ratio)≥1) are highlighted in red, and the down-regulated genes are highlighted in green. The non-DEGs are highlighted in black.

Abbreviations: ELOVL6, elongation of very long chain fatty acids protein 6; LPL, lipoprotein lipase; LXRα, liver X receptor α; MDH1, malate dehydrogenase 1; SCD1, stearoyl-CoA desaturase 1; SOCS3, suppressor of cytokine signaling 3; SREBP1, sterol regulatory element binding protein 1; SUCLG2: succinyl-CoA synthetase beta subunit; TG, Triglyceride.



**Supplemental Figure 6** Multiple amino acid sequences alignment of SREBP1 from *P. fulvidraco* and other species. Accession numbers as follows (*Pelteobagrus fulvidraco* (Pf), *Ictalurus punctatus* (Ip), *Danio rerio* (Dr), *Rattus norvegicus* (Rn), *Mus musculus* (Mm) and *Homo sapiens* (Hs)): XM\_027139065.1, XM\_017452596.1, DQ836065.1, NM\_001276708.1, XM\_006532716.3, BC057388.1). The SUMOylation sites of SREBP1 K145 (A), K254 (B), K264 (C), K392 (D) and K419 (E) are boxed. And K254, K264, K392 and K419 in SREBP1 are conserved among the six species.

C:\Users\acer\Desktop\0429\SUMO0507\位图0507\Fig.S7.tif

**Supplemental Figure 7** The domain structure of SREBP1 from *Pelteobagrus fulvidraco*. The mSin3A-associated proteins 130 C- terminus (SAP130-C, yellow), polyunsaturated fatty acid synthase PfaA (Omega-3 PfaA, green) and basic Helix-Loop-Helix-zipper domain (bHLH-zip, red) are indicated. Positions of lysines (K) of SUMOylation sites of SREBP1 K145, K254, K264, K392 and K419 are boxed.