Table S1 The specific primers for the RT-PCR

|  |  |  |
| --- | --- | --- |
| Gene | Primers | Sequences (5’- 3’) |
| *myh1* | RT-MYH1\_F | TCAAGCAGAAGCAGCGTGAGGAG |
| RT-MYH1\_R | CGGATAGCACAGAGCCTTCAGCAT |
| *myh4* | RT-MYH4\_F | TGATGCCAAGAGTGCCTGCTACG |
| RT-MYH4\_R | CTGTCCTCTCCTCCTGAGTGTCCA |
| *gtr12* | RT-GTR12\_F | ACCTGCTCATCTCCATGACCTTCC |
| RT-GTR12\_R | TATCTCCTCCAGCGTGCGACCT |
| *tri16* | RT-TRI16\_F | CGCACAAGCACACTCATCACAAGA |
| RT-TRI16\_R | TCATATGGTGGCGGCTTCACTTCT |
| *crem* | RT-CREM\_F | ATAACGCCAGCTCCAGCCTTCC |
| RT-CREM\_R | CGGGCAGCTTCCCTGTTCTTCA |
| *ttc9a* | RT-TTC9A\_F | TGGAGAATGCAGAGCTGGAGTGTT |
| RT-TTC9A\_R | CGGATCGGTACAGAGCCTTGAAGT |
| *jun* | RT-JUN\_F | CTCTCCTGATGTGGGCTTGCTGAA |
| RT-JUN\_R | CTCCTGCTCGTCGGTGACATTCTT |
| *tri65* | RT-TRI65\_F | CCAGCAGAGAATCCAGGACAGAGA |
| RT-TRI65\_R | TCCATCAGACGGATCAGGTCAGTG |
| *fmo5* | RT-FMO5\_F | CGGTGGTTGGAGGAGGAAGTTCAG |
| RT-FMO5\_R | AATGCTCGCTCTGTCTGGCTCTG |
| *b3gt2* | RT-B3GT2\_F | GGCGGGTGTCTTACTCCAGTTGT |
| RT-B3GT2\_R | AGGCGTTGTGCTTGTTGCTCTG |
| *tnni2* | RT-TNNI2\_F | CGACAAGGTGGACGAGGAGAGGTA |
| RT-TNNI2\_R | AGCATGGAGTCAGCGGACATACG |
| *pprc1* | RT-PPRC1\_F | ACCGCTGCTACTGTGTCTGCTC |
| RT-PPRC1\_R | GGTGAGGGTTTGGTGGACTTGCTA |
| *ghr* | RT-GLIS1\_F | GCAGCAAGGATGTCTGTACGGAGA |
| RT-GLIS1\_R | AGAGTGAGAGGCGGACGGAGTT |
| *ptgis* | RT-PTGIS\_F | TCTGGCAGCAGTGAAGAAGGAGTT |
| RT-PTGIS\_R | GCAGCGGTGAGTCTGAGTGTCT |
| *sdhb* | RT-SDHB\_F | GCTGTCCTGTCTGTTCTGTTGTGG |
| RT-SDHB\_R | CCGAACCATCACCATCATGCCAGA |
| *stc2* | RT-STC2\_F | GAAGTGTGGAGACGAGGTCAGGTT |
| RT-STC2\_R | GTGGCTGTGGATTGCTGTGGAAG |
| *nr4a1* | RT-NR4A1\_F1 | CCTTGGTGGGAAATGGCTATGTGG |
| RT-NR4A1\_R1 | GCTACTGCGTTGTGGCTGAATGAA |
| *nr4a1\_1* | RT-NR4A1\_1\_F2 | AACGCCTCCTGTCAGCACTACG |
| RT-NR4A1\_1\_R2 | CGATTCCGCCTCCTCTTGTCCA |
| *pde4d* | RT-PDE4D\_F | CTCCATCTCAGCCGACAAGTTCCA |
| RT-PDE4D\_R | TACTGCCACTGTAGCCCTCCTCTT |
| *s41a1* | RT-S41A1\_F | CGGAGATCGTGGTGGCATTGGA |
| RT-S41A1\_R | TCATCACTCTCGTTGCTCTGGCTT |
| *pdp1* | RT-PDP1\_F | CGAGCCAGAGATCACGTACCACAA |
| RT-PDP1\_R | CCACGATACGAACCACCTCCTGTC |
| *tutla* | RT-TUTLA\_F | TGGCTCATCCTCAGCAGCAACAT |
| RT-TUTLA\_R | ACATTGACAGACTCGCTCGGTTCA |
| *klf13* | RT-KLF13\_F | TGGCAAATCATCCCACCTCAAAGC |
| RT-KLF13\_R | CGGAGCGGGCGAACTTCTTACT |
| *htr1a* | RT-HTR1A\_F | CGGCTGGCATCTCCTTCGCTAT |
| RT-HTR1A\_R | CGCTGGAGTGAGAGTCATCATCCT |
| *mxra5* | RT-MXRA5\_F | GGCTCCAAGGTAGAGGCACCATAC |
| RT-MXRA5\_R | GCAGGACAGCAAGGTCTCCATCA |
| *actb* | RT-actb-F | GATCTGGCATCACACCTTCTAC |
| RT-actb-R | CACCGGAGTCCATGACAATAC |

Table S2 Summary of transcriptome data generated from the brown-marbled grouper samples.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Total reads | Unmapped reads | Unique mapped reads | Unique mapped rate | Multiple mapped reads | Multiple mapped ratio | Mapping ratio |
| H1 | 52,012,402 | 1,527,697 | 50,143,406 | 96.46% | 311,300 | 0.60% | 97.06% |
| H2 | 63,030,193 | 1,156,861 | 61,217,878 | 97.12% | 655,454 | 1.04% | 98.16% |
| H3 | 53,917,347 | 1,015,204 | 52,382,921 | 97.15% | 419,222 | 0.78% | 97.93% |
| L1 | 51,476,226 | 943,598 | 50,292,002 | 97.70% | 240,626 | 0.47% | 98.17% |
| L2 | 65,202,821 | 1,307,107 | 63,538,208 | 97.45% | 357,506 | 0.55% | 98.00% |
| L3 | 68,502,049 | 1,377,230 | 66,770,737 | 97.47% | 354,082 | 0.52% | 97.99% |

Chart

Description automatically generatedFig.S1 GO assignment of the differentially expressed genes; red bar indicates up-regulated genes, and green bar indicates down-regulated gene

Graphical user interface, application

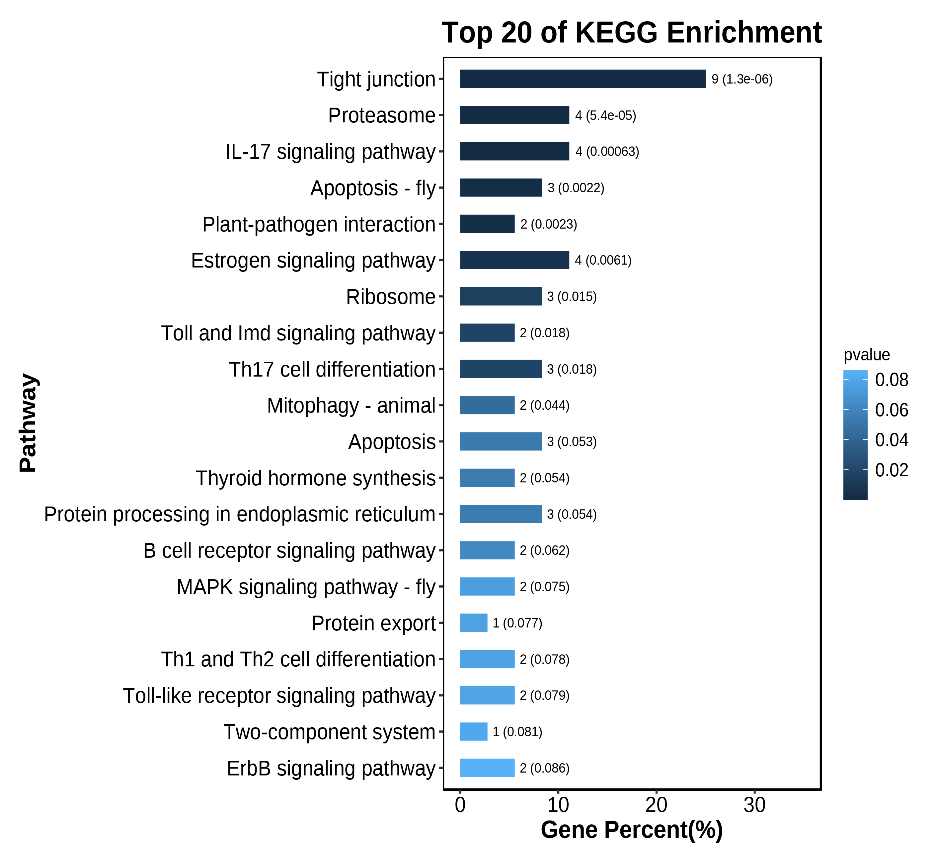
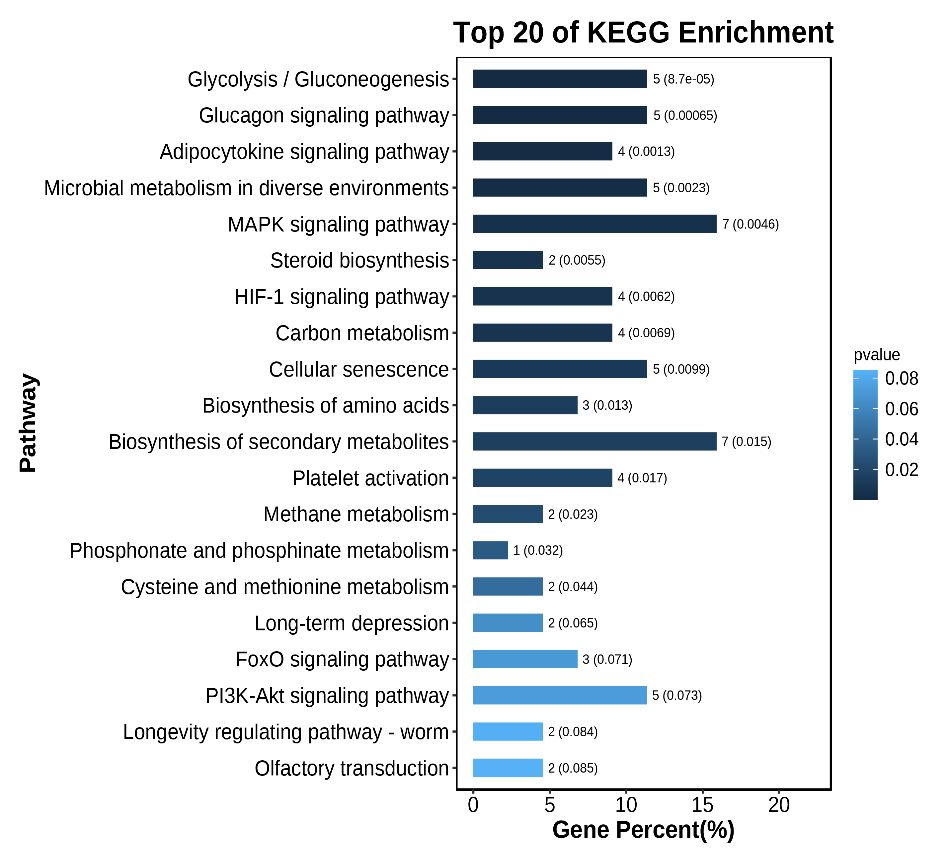
Description automatically generated

Fig.S2 Bar plots of down-regulated genes in fast-growing grouper of GO functional enrichment analyses. A: Top 20 of GO Enrichment (Biological Process); B: Top 20 of GO Enrichment (Cellular Component); C: Top 20 of GO Enrichment (Molecular Function).

Graphical user interface

Description automatically generated

Fig.S3 Bar plots of up-regulated genes in fast-growing grouper of GO functional enrichment analyses. A: Top 20 of GO Enrichment (Biological Process); B: Top 20 of GO Enrichment (Cellular Component); C: Top 20 of GO Enrichment (Molecular Function).



A

B

Fig.S4 A: The bar plot of up-regulated genes in fast-growing grouper of KEGG enrichment analyses. B: The bar plot of down-regulated genes in fast-growing grouper of KEGG enrichment analyses.

+Chart

Description automatically generated with medium confidence

Fig.S5 Heat Map of the top 50 features for each phenotype in GSEA\_data. H1, H2, H3: the fast-growing group. L1, L2, L3: the slow-growing group. red indicates upregulated gene, and bule indicates downregulated gene.

Diagram, engineering drawing

Description automatically generatedFig.S6 L represent the slow-growing group; H represent the fast-growing group. The qPCR analysis of gene expression in slow- and fast-growing group. The y-axis indicates relative expression level between the samples of slow- and fast-growing group using the Relative Quantitation. *b3gt2*, Hexosyltransferase; *crem*, cAMP-responsive element modulator; *ghr*, Growth hormone receptor; *fmo5*, Flavin-containing monooxygenase 5; *ttc9a*, Tetratricopeptide repeat protein 9A; *myh4*, Myosin-4; tri65, Tripartite motif-containing protein 65; *tnni2*, Troponin I, fast skeletal muscle; *myh1*, Myosin-1; *pprc1*, Peroxisome proliferator-activated receptor gamma coactivator-related protein 1; *jun*, Transcription factor Jun; *ptgis*, Prostacyclin synthase; *sdhb*, Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial; *tri16*, Trichothecene 8-O-acetyltransferase; *gtr12*, Solute carrier family 2, facilitated glucose transporter member 12; *tutla*, Protein turtle homolog A; *klf13*, Krueppel-like factor 13; *pde4d*, cAMP-specific 3',5'-cyclic phosphodiesterase 4D; *s41a1*, Solute carrier family 41 member 1; *stc2*, Stanniocalcin-2; *nr4a1*, Nuclear receptor subfamily 4 group A member 1; *htr1a*, 5-hydroxytryptamine receptor 1A; *pdp1*, PWWP domain-containing protein 1; *mxra5*, Matrix-remodeling-associated protein 5. Significant differences at the P < 0.05, P < 0.01, P < 0.001 level are indicated by \*, \*\*, \*\*\* above the columns.