

Supplementary tables

Table S1. The specific primers for RT-PCR.

Gene	Primers	Sequences (5'- 3')
<i>myh1</i>	RT-MYH1_F	TCAAGCAGAAGCAGCGTGAGGAG
	RT-MYH1_R	CGGATAGCACAGAGCCTTCAGCAT
<i>myh4</i>	RT-MYH4_F	TGATGCCAAGAGTGCCTGCTACG
	RT-MYH4_R	CTGTCCTCTCCTCCTGAGTGTCCA
<i>gtr12</i>	RT-GTR12_F	ACCTGCTCATCTCCATGACCTTCC
	RT-GTR12_R	TATCTCCTCCAGCGTGCGACCT
<i>tri16</i>	RT-TRI16_F	CGCACAAGCACACTCATCACAAGA
	RT-TRI16_R	TCATATGGTGGCGGCTTCACTTCT
<i>crem</i>	RT-CREM_F	ATAACGCCAGCTCCAGCCTTCC
	RT-CREM_R	CGGGCAGCTTCCCTGTTCTTCA
<i>ttc9a</i>	RT-TTC9A_F	TGGAGAATGCAGAGCTGGAGTGTT
	RT-TTC9A_R	CGGATCGGTACAGAGCCTTGAAGT
<i>jun</i>	RT-JUN_F	CTCTCCTGATGTGGGCTTGCTGAA
	RT-JUN_R	CTCCTGCTCGTCGGTGACATTCTT
<i>tri65</i>	RT-TRI65_F	CCAGCAGAGAATCCAGGACAGAGA
	RT-TRI65_R	TCCATCAGACGGATCAGGTCAGTG
<i>fmo5</i>	RT-FMO5_F	CGGTGGTTGGAGGAGGAAGTTCAG
	RT-FMO5_R	AATGCTCGCTCTGTCTGGCTCTG
<i>b3gt2</i>	RT-B3GT2_F	GGCGGGTGTCTTACTCCAGTTGT
	RT-B3GT2_R	AGGCGTTGTGCTTGTGCTCTG
<i>tnni2</i>	RT-TNNI2_F	CGACAAGGTGGACGAGGAGAGGTA
	RT-TNNI2_R	AGCATGGAGTCAGCGGACATACG
<i>pprc1</i>	RT-PPRC1_F	ACCGCTGCTACTGTGTCTGCTC
	RT-PPRC1_R	GGTGAGGGTTTGGTGGACTTGCTA
<i>ghr</i>	RT-GLIS1_F	GCAGCAAGGATGTCTGTACGGAGA
	RT-GLIS1_R	AGAGTGAGAGGCGGACGGAGTT
<i>ptgis</i>	RT-PTGIS_F	TCTGGCAGCAGTGAAGAAGGAGTT
	RT-PTGIS_R	GCAGCGGTGAGTCTGAGTGTCT
<i>sdhb</i>	RT-SDHB_F	GCTGTCCTGTCTGTTCTGTTGTGG
	RT-SDHB_R	CCGAACCATCACCATCATGCCAGA
<i>stc2</i>	RT-STC2_F	GAAGTGTGGAGACGAGGTCAGGTT
	RT-STC2_R	GTGGCTGTGGATTGCTGTGGAAG
<i>nr4a1</i>	RT-NR4A1_F1	CCTTGGTGGGAAATGGCTATGTGG
	RT-NR4A1_R1	GCTACTGCGTTGTGGCTGAATGAA
<i>nr4a1_1</i>	RT-NR4A1_1_F2	AACGCCTCCTGTCAGCACTACG
	RT-NR4A1_1_R2	CGATTCCGCCTCCTCTTGTCCA
<i>pde4d</i>	RT-PDE4D_F	CTCCATCTCAGCCGACAAGTTCCA
	RT-PDE4D_R	TACTGCCACTGTAGCCCTCCTCTT
<i>s41a1</i>	RT-S41A1_F	CGGAGATCGTGGTGGCATTGGA

<i>pdp1</i>	RT-S41A1_R	TCATCACTCTCGTTGCTCTGGCTT
	RT-PDP1_F	CGAGCCAGAGATCACGTACCACAA
	RT-PDP1_R	CCACGATACGAACCACCTCCTGTC
<i>tutla</i>	RT-TUTLA_F	TGGCTCATCCTCAGCAGCAACAT
	RT-TUTLA_R	ACATTGACAGACTCGCTCGGTTCA
<i>klf13</i>	RT-KLF13_F	TGGCAAATCATCCACCTCAAAGC
	RT-KLF13_R	CGGAGCGGGCGAACTTCTTACT
<i>htr1a</i>	RT-HTR1A_F	CGGCTGGCATCTCCTTCGCTAT
	RT-HTR1A_R	CGCTGGAGTGAGAGTCATCATCCT
<i>mxra5</i>	RT-MXRA5_F	GGCTCCAAGGTAGAGGCACCATAC
	RT-MXRA5_R	GCAGGACAGCAAGGTCTCCATCA
<i>actb</i>	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 ratios	Mapping ratios
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%

Supplementary figures

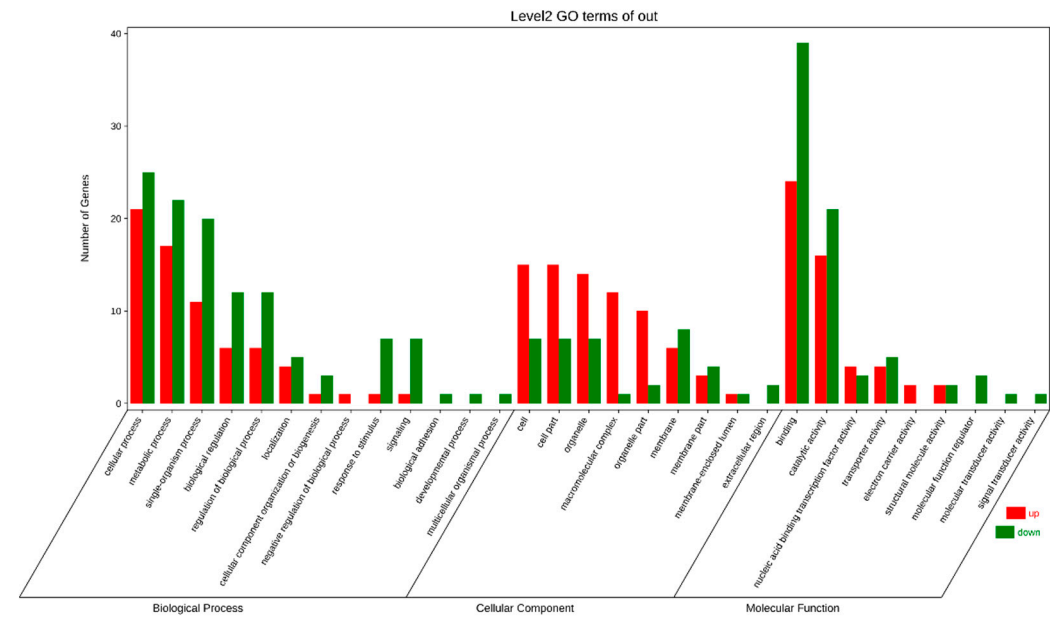
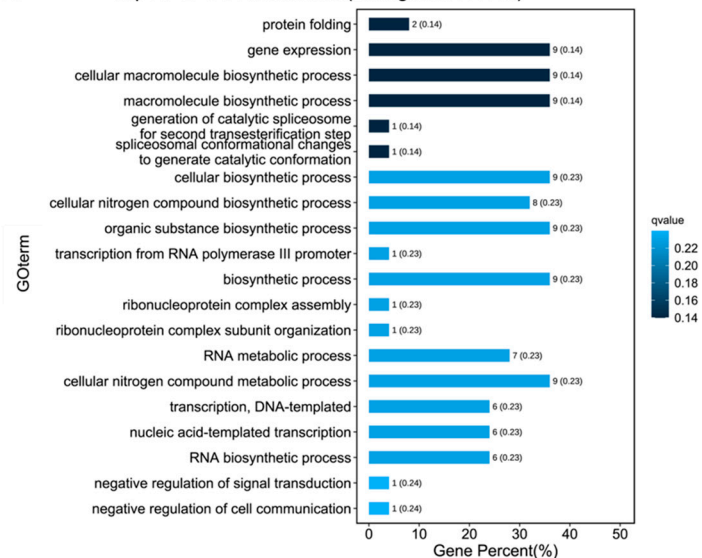
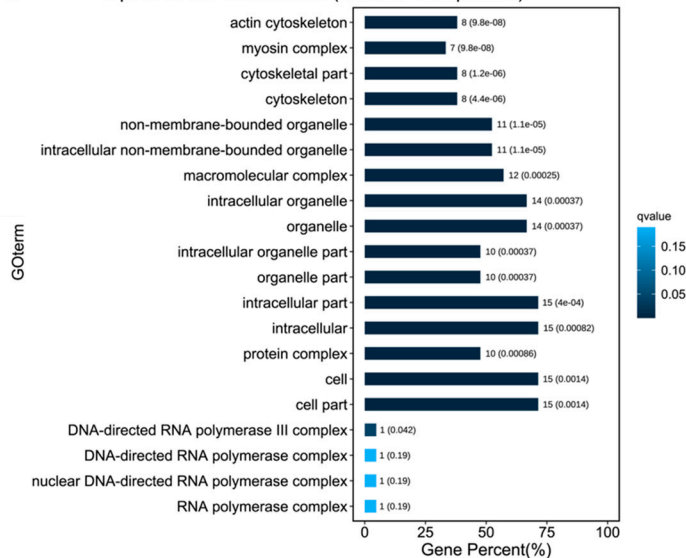


Fig. S1. GO assignment of the differentially expressed genes. Red bar indicates up-regulated genes, and green bar indicates down-regulated genes.

A Top 20 of GO Enrichment (Biological Process)



B Top 20 of GO Enrichment (Cellular Component)



C Top 20 of GO Enrichment (Molecular Function)

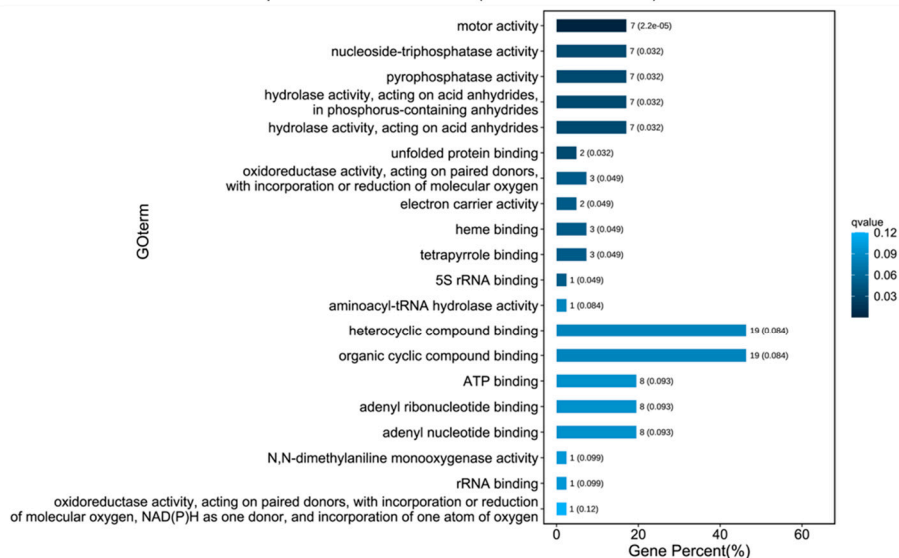


Fig.S2 Bar plots of down-regulated genes in fast-growing grouper of GO functional enrichment analyses. A: Top 20 of GO Enrichment (Biological Process); B: Top 20 of GO Enrichment (Cellular Component); C: Top 20 of GO Enrichment (Molecular Function).

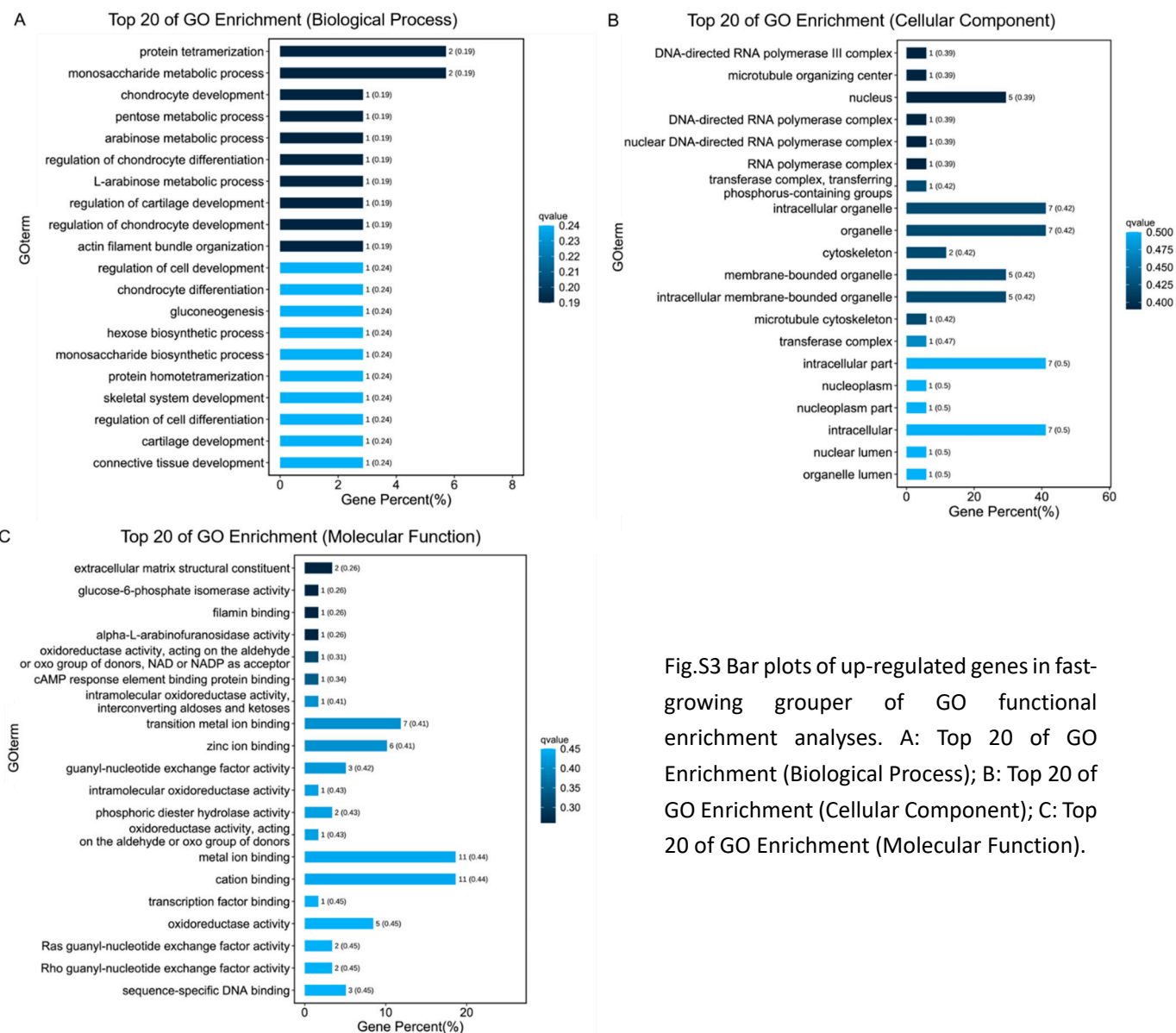


Fig.S3 Bar plots of up-regulated genes in fast-growing grouper of GO functional enrichment analyses. A: Top 20 of GO Enrichment (Biological Process); B: Top 20 of GO Enrichment (Cellular Component); C: Top 20 of GO Enrichment (Molecular Function).

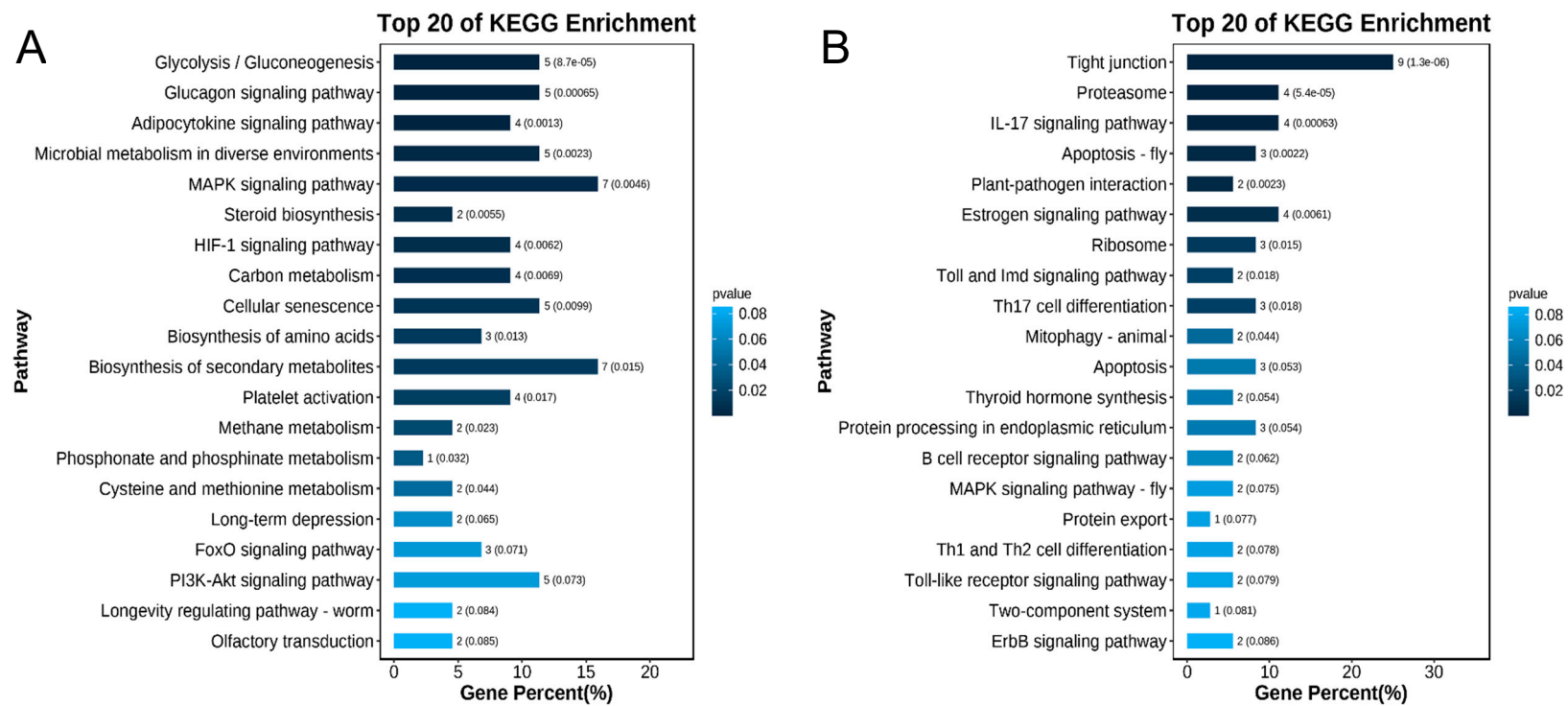


Fig.S4 A: Bar plot of up-regulated genes in the fast-growing group based on KEGG enrichment analyses. B: Bar plot of down-regulated genes in the fast-growing group based on KEGG enrichment analyses.

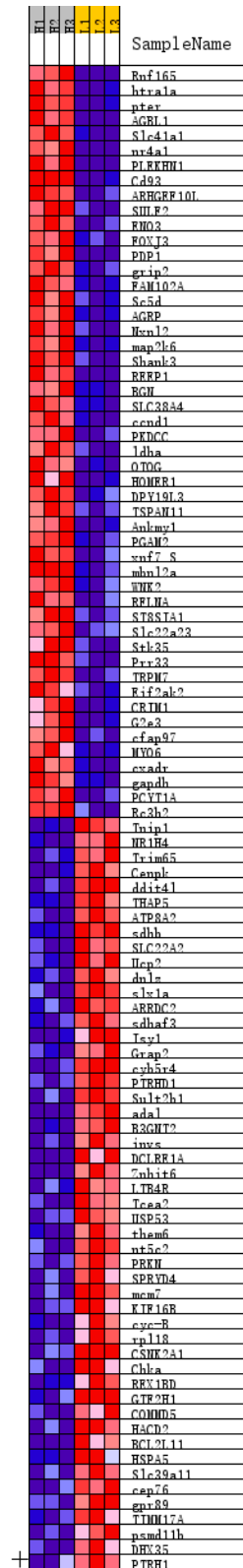


Fig. S5. Heat map of the top 50 features for each phenotype in the GSEA data. H1, H2, H3: the fast-growing group. L1, L2, L3: the slow-growing group. Red indicates up-regulated genes, and blue indicates down-regulated genes.

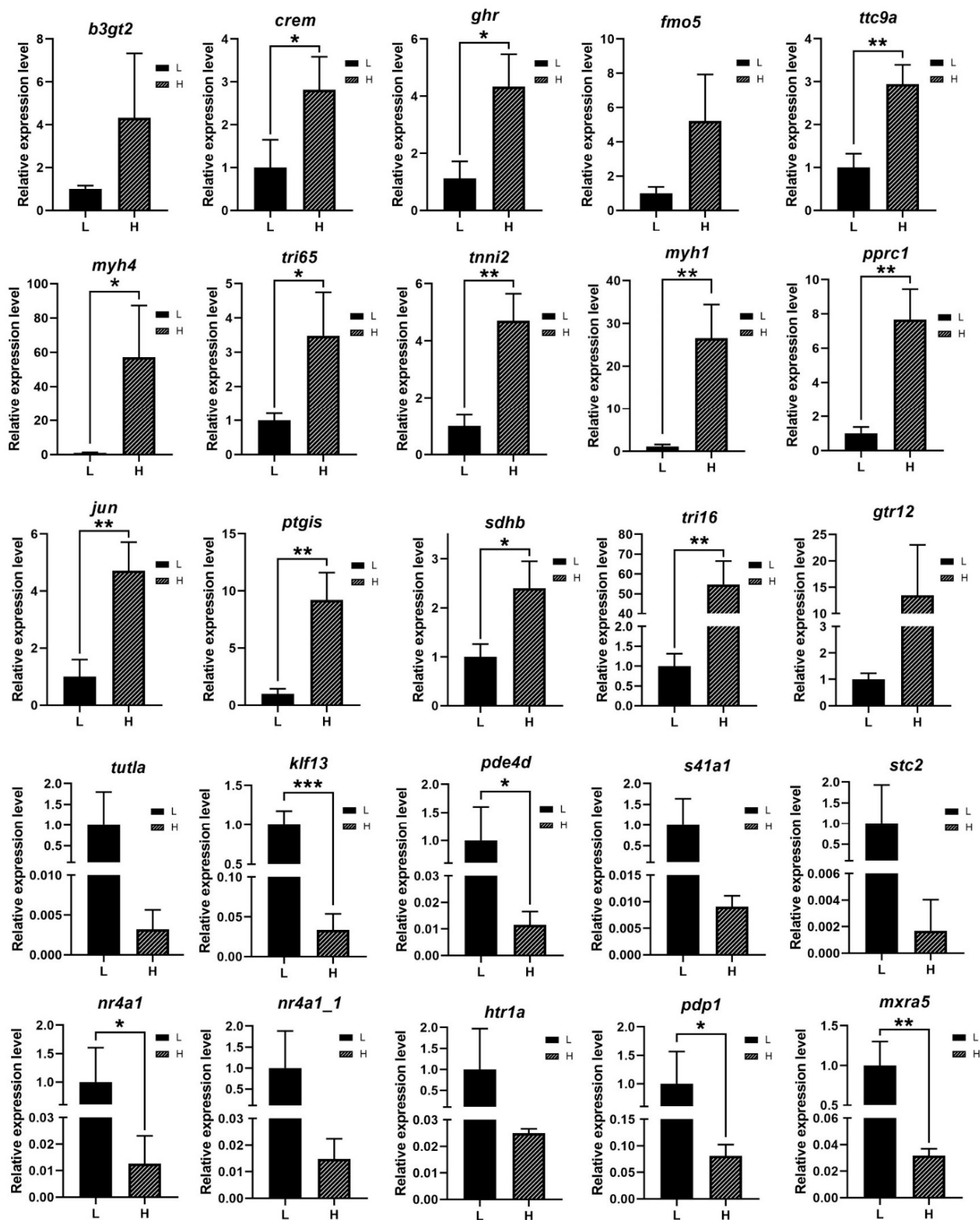


Fig. S6. L represent the slow-growing group; H represent the fast-growing group. The qPCR analysis of gene expression in the slow- and fast-growing groups. The y-axis indicates the relative expression level between the samples of the slow- and fast-

growing groups using the relative quantitation. *b3gt2*, hexosyltransferase; *crem*, cAMP-responsive element modulator; *ghr*, growth hormone receptor; *fmo5*, flavin-containing mono-oxygenase 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*, Kruppel-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 $P < 0.05$, $P < 0.01$, $P < 0.001$ levels are indicated by *, **, *** above the columns.