

Effects of Starvation on the Physiology and Liver Transcriptome of Yellowcheek (*Elopichthys bambusa*)

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Table S1. Basic information of sequencing data. F8C, un-starved yellowcheek samples collected on the eighth day after starvation experiment; F28C, un-starved yellowcheek samples collected on the 28th day after starvation experiment; F8, starved yellowcheek samples collected on the eighth day after starvation experiment; F28, starved yellowcheek samples collected on the 28th day after starvation experiment.

Sample	RawReads	RawBases	CleanReads	CleanBases	ValidBases	Q30	GC
F28_1	47.74M	7.16G	47.22M	6.79G	94.80%	94.83%	46.88%
F28_2	50.10M	7.52G	49.57M	7.15G	95.08%	94.86%	47.45%
F28_3	47.03M	7.05G	46.54M	6.70G	95.00%	94.86%	47.01%
F28C_1	49.52M	7.43G	48.99M	7.05G	94.93%	94.86%	47.50%
F28C_2	47.81M	7.17G	47.31M	6.75G	94.14%	95.11%	48.48%
F28C_3	46.92M	7.04G	46.28M	6.60G	93.75%	94.17%	47.08%
F8_1	49.59M	7.44G	49.00M	7.05G	94.79%	94.30%	46.95%
F8_2	49.42M	7.41G	48.77M	7.04G	94.95%	94.15%	47.04%
F8_3	48.91M	7.34G	48.29M	6.91G	94.26%	94.37%	46.61%
F8C_1	46.71M	7.01G	46.19M	6.65G	94.86%	94.77%	46.97%
F8C_2	47.15M	7.07G	46.61M	6.71G	94.80%	94.76%	46.95%
F8C_3	44.02M	6.60G	43.54M	6.28G	95.06%	94.80%	46.77%

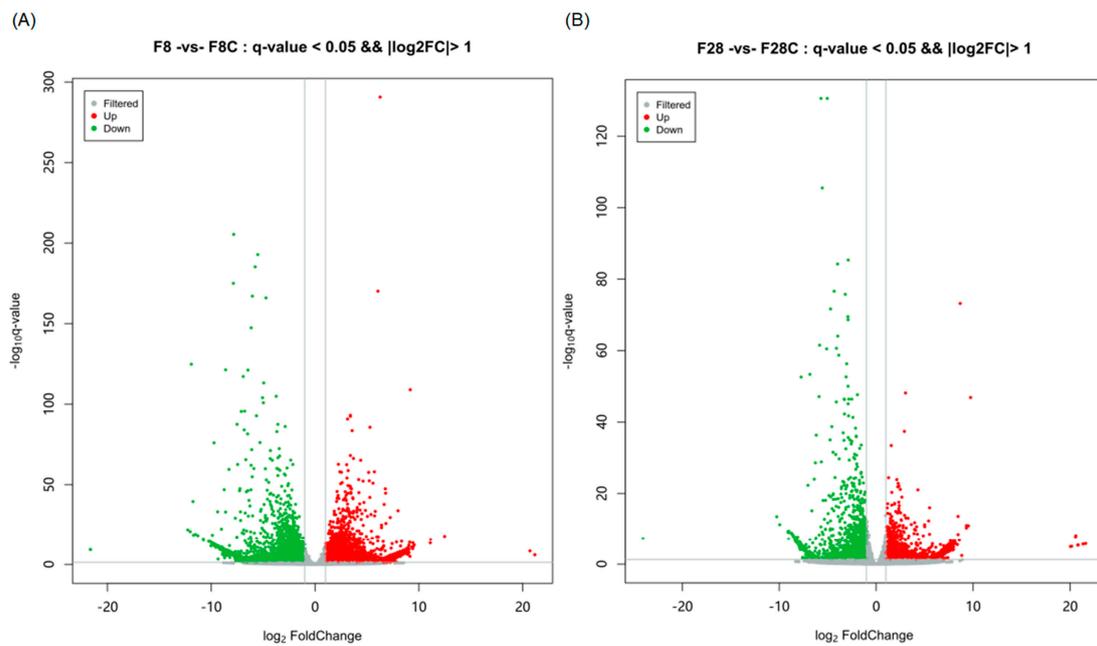


Figure S1. Volcano plots shows differentially expressed genes caused by starvation for eight (A) and 28 (B) days. F8C, un-starved yellowcheek samples collected on the eighth day after starvation experiment; F28C, un-starved yellowcheek samples collected on the 28th day after starvation experiment; F8, starved yellowcheek samples collected on the eighth day after starvation experiment; F28, starved yellowcheek samples collected on the 28th day after starvation experiment.

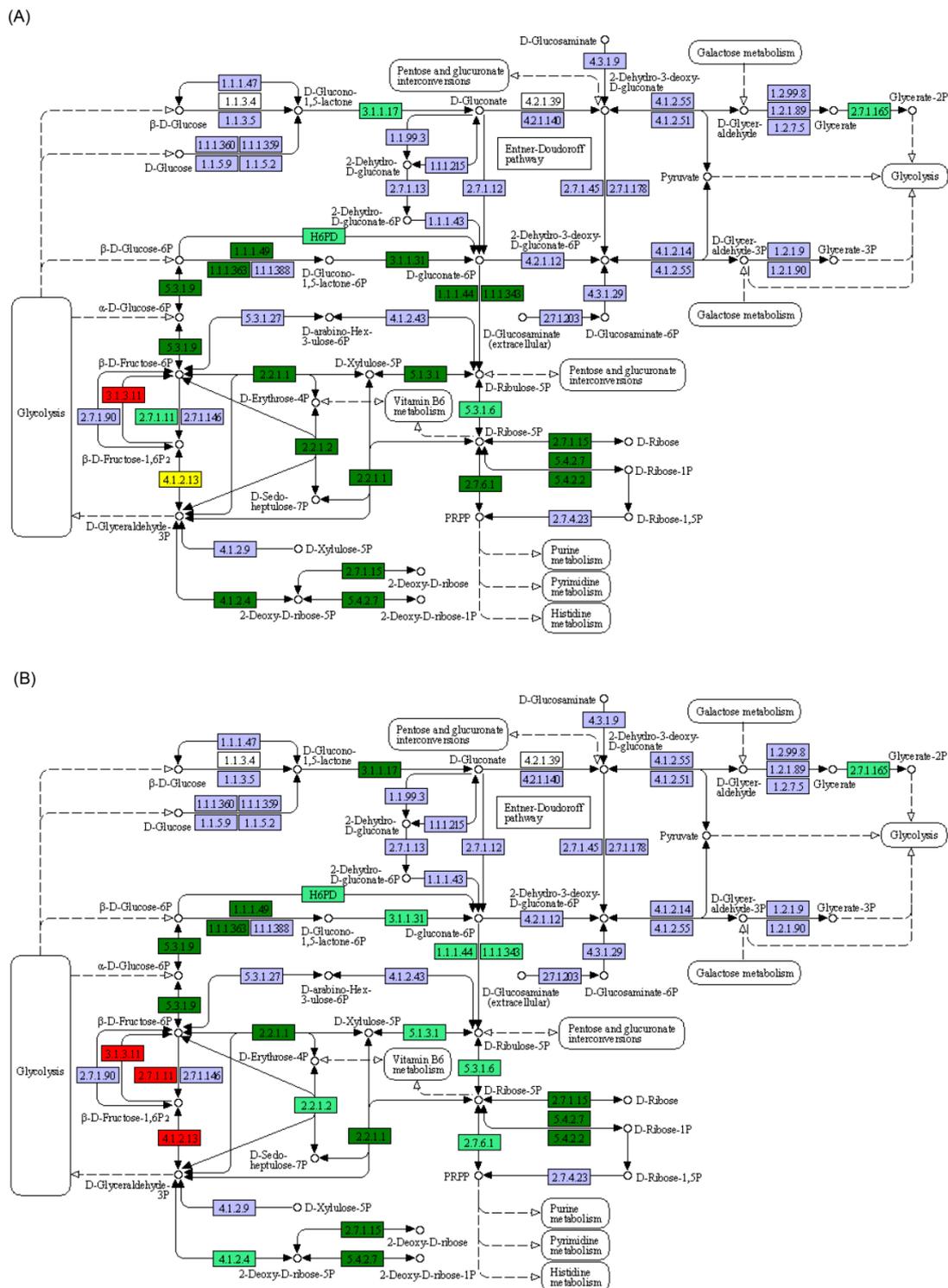


Figure S2. KEGG pathway showed significantly up- and down-regulated genes participate in pentose phosphate in the liver transcriptome of yellowcheek starved for eight (A) and 28 (B) days compared with the control. Red indicates significantly up-regulated genes, dark green indicates significantly down-regulated genes, yellow indicates both up- and down-regulated genes in the corresponding genes, light green indicates that the genes of the species annotated on the map, light purple indicates that the genes were not annotated on the map, and white indicates unknown genes.

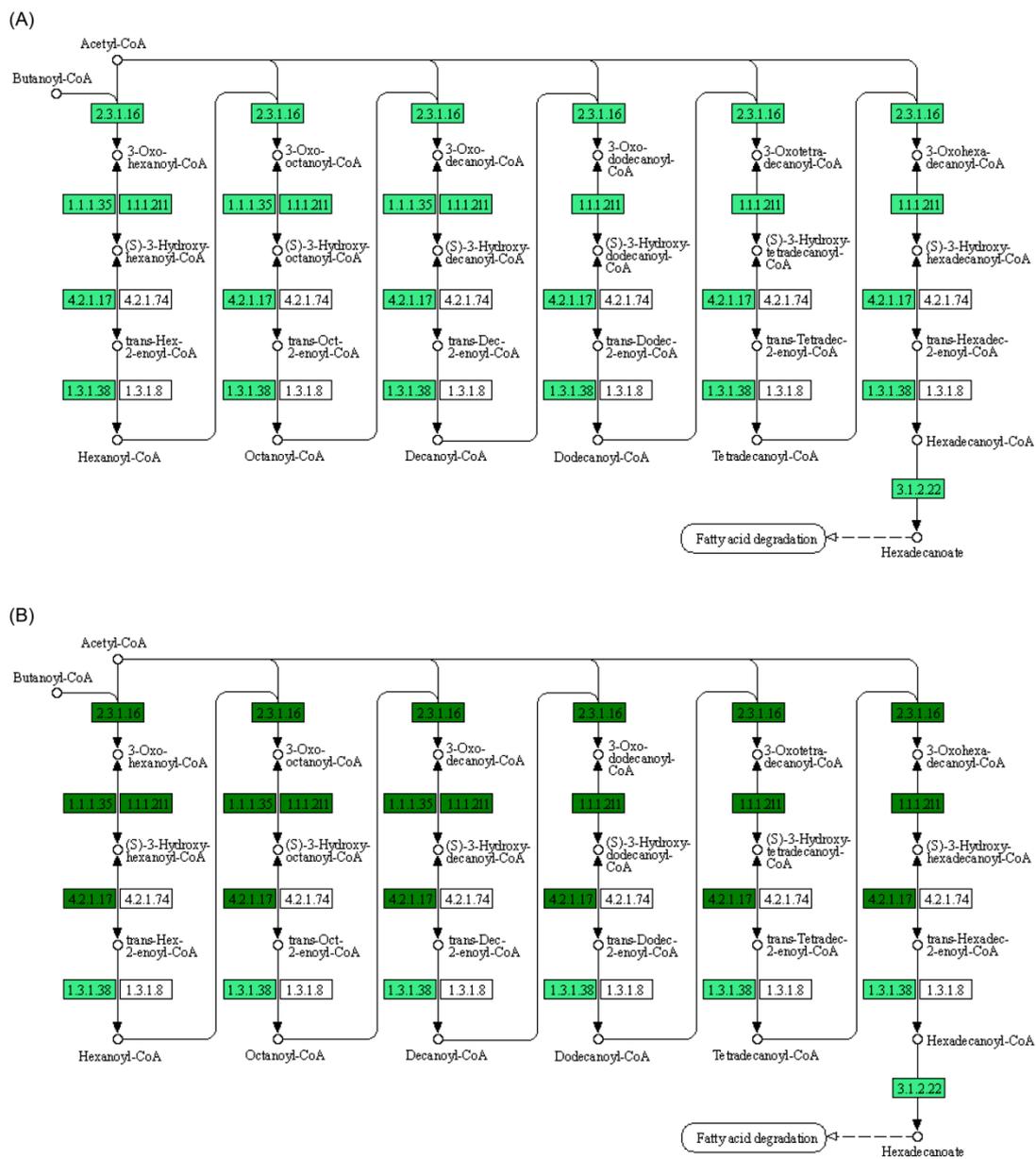


Figure S4. KEGG pathway showed significantly up- and down-regulated genes participate in fatty acid elongation in mitochondria ($4 < n < 16$) in the liver transcriptome of yellowcheek starved for eight (A) and 28 (B) days compared with the control. Red indicates significantly up-regulated genes, dark green indicates significantly down-regulated genes, yellow indicates both up- and down-regulated genes in the corresponding genes, light green indicates that the genes of the species annotated on the map, light purple indicates that the genes were not annotated on the map, and white indicates unknown genes.

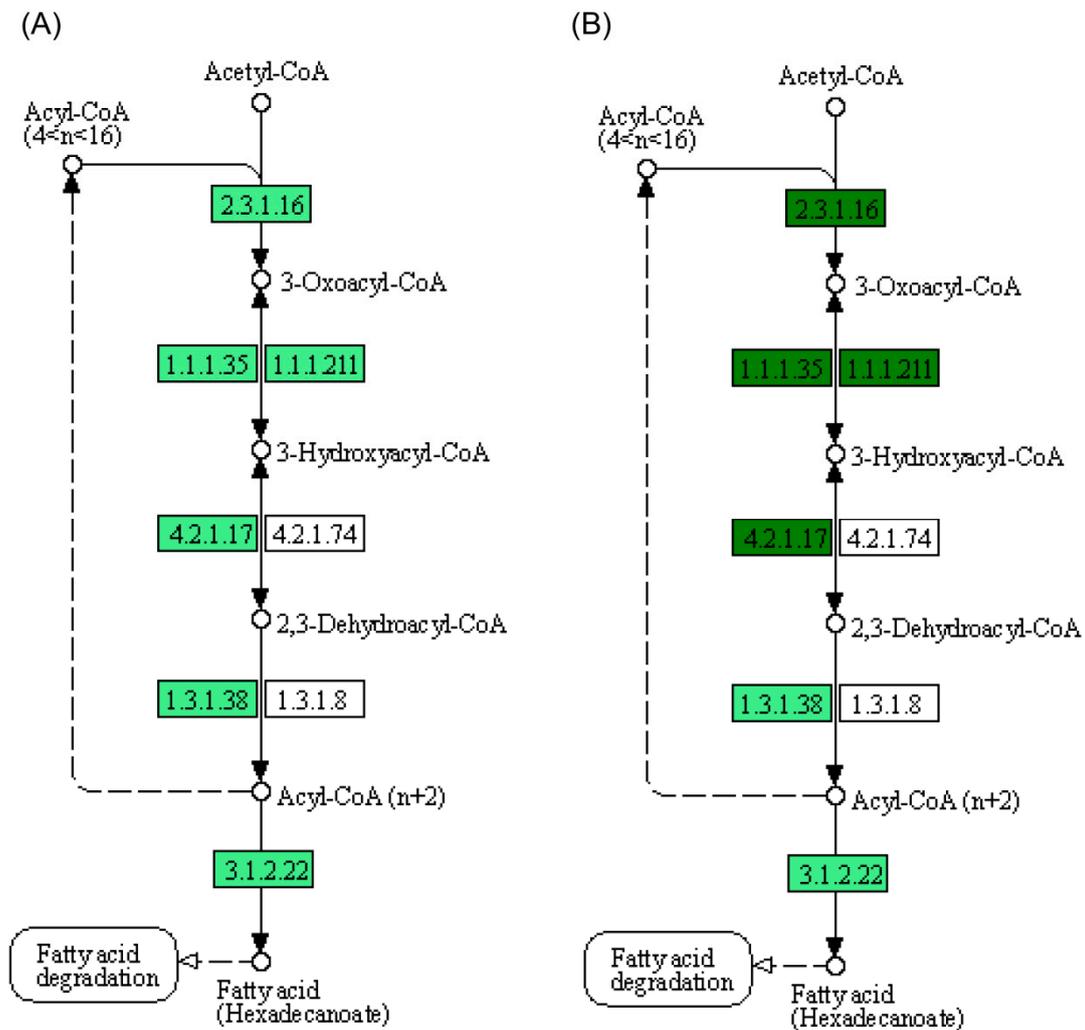


Figure S5. KEGG pathway showed significantly up- and down-regulated genes participate in general forms of fatty acid elongation in mitochondria ($4 < n < 16$) in the liver transcriptome of yellowcheek starved for eight (A) and 28 (B) days compared with the control. Dark green indicates significantly down-regulated genes, light green indicates that the genes of the species annotated on the map, and white indicates unknown genes.

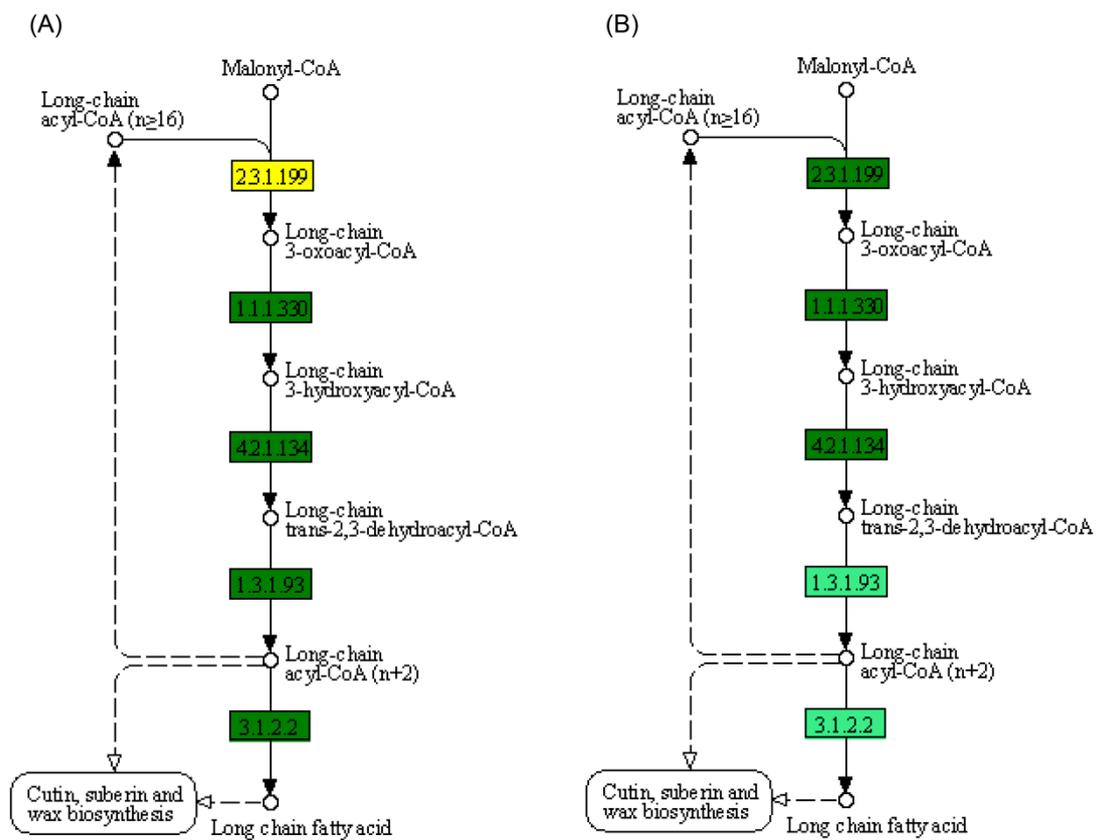


Figure S6. KEGG pathway showed significantly up- and down-regulated genes participate in fatty acid elongation in endoplasmic reticulum ($n \geq 16$) in the liver transcriptome of yellowcheek starved for eight (A) and 28 (B) days compared with the control. Dark green indicates significantly down-regulated genes, yellow indicates both up- and down-regulated genes in the corresponding genes, and light green indicates that the genes of the species annotated on the map.

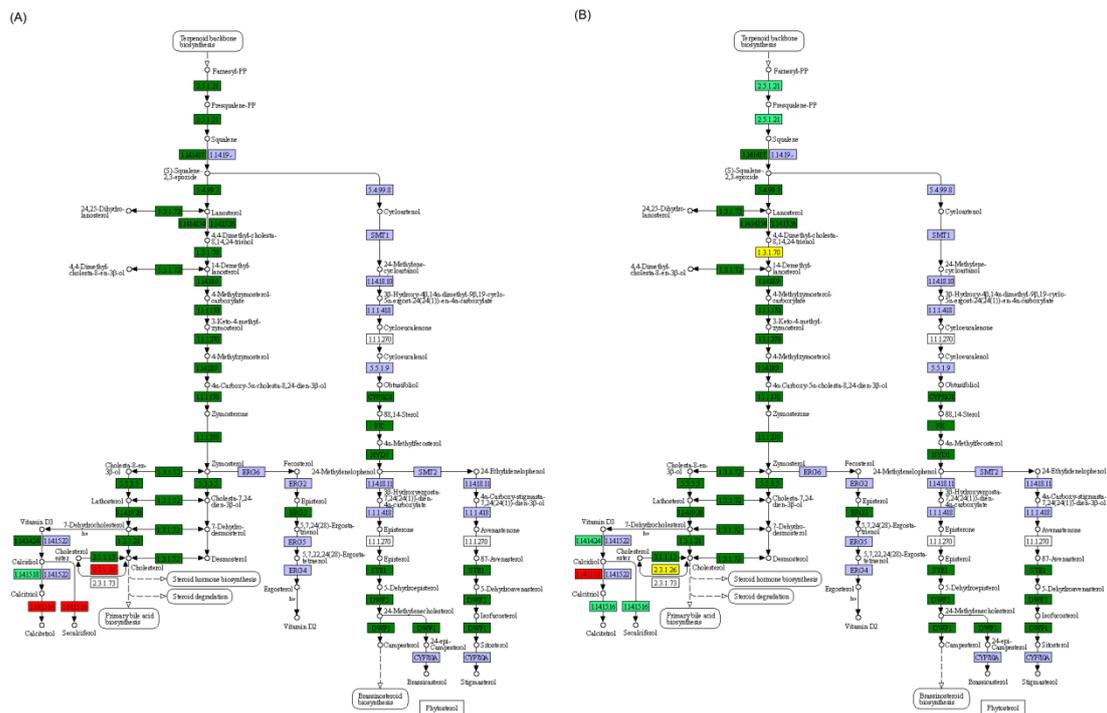


Figure S7. KEGG pathway showed significantly up- and down-regulated genes participate in steroid biosynthesis in the liver transcriptome of yellowcheek starved for eight (A) and 28 (B) days compared with the control. Red indicates significantly up-regulated genes, dark green indicates significantly down-regulated genes, yellow indicates both up- and down-regulated genes in the corresponding genes, light green indicates that the genes of the species annotated on the map, light purple indicates that the genes were not annotated on the map, and white indicates unknown genes.