

## Supplementary materials

**Table S1.** Primers used for qPCR.

Gene ID	Forward primer(5'→3')	Reverse primer(5'→3')
AKTIP	GGCAAAGGAGCGGATGTTC	CGGCTTCACCCAAGACAGA
AKT1S1	TGTTGCCAAGTTGCTGGTGAT	GTGGGAGAATGTAGAATACGTCTGA
CASP3	CTGGGCTTCAAGGTGGACAT	CCCGTGAGACGACAAGACAG
HYP	GGGAGGAAGATGACAGGATGG	CCCGAAGTTTACGACCGATT
CATB	ACGTCCGACTTCATGCACTACAC	ACGTCCGACTTCATGCACTACAC
CATL	GCCATCTTATCTGTCTGCTCAA	ACAGTTGCTTTGTAACGGATTCTC
TUA8	CGATCACAAGTTCGACCTCATG	ACCCAAATCCTCGTAATCCCT
CLAU-10	TCATCACCACAGCGACCTT	CCAGCATCGAGGGAAAGTC
MYO11	TATTCGCCAGGCCAACACT	GCCATCAGGAAACGATAGGAG
MYO10	TGTTCAAGGTGGGTCAGAGTAA	GGAAGCGTATAATGGTGTCACTG
ADGPL3	ACTTCATTTGGAGTTTCATAGGACC	ACCCACGATTTGATGTTGTCC
GJ32P	TCTTTATGTTGGCAATGTCCG	CTCTGAACTGCTGTTCTTCCTTTT
GJD3P	GGTTACCGCCCAGGACTACA	GAAAGCCAATCTCCGCCAC
GJ32PL	CCTCTTTGGCACATACATAACC	GGCACAGGGTGGAGACATT
rGAP	GGTGTTCGACATCGTTCCTGC	CTTCTTCGTACCTGGTATTTGAGG
18 S	CGGTGGTACTTTCTGTGC	TGTGGTAGCCGTTTCTCA

**Table S2.** Effects of PC diet on growth performance of tiger grouper after 8-week feeding trial.

Item	C	PC
SSI, %	0.13±0.05 <sup>a</sup>	0.12±0.04 <sup>a</sup>
HSI, %	0.188±0.41 <sup>a</sup>	1.62±0.5 <sup>a</sup>
SGR, %*day <sup>-1</sup>	3.67±0.75 <sup>a</sup>	3.45±0.17 <sup>a</sup>
WGR, %	35.12±1.92 <sup>a</sup>	33.08±2.12 <sup>a</sup>

SSI: Spleen somatic indices; HSI: hepatopancreas somatic indices; SGR: Specific growth rate; WGR: Weight gain rate; Data was presented as mean ± SE. Values with different superscripts in the same row were significantly different ( $P < 0.05$ ). The lack of superscript letter indicated no significant differences among groups ( $P > 0.05$ ).

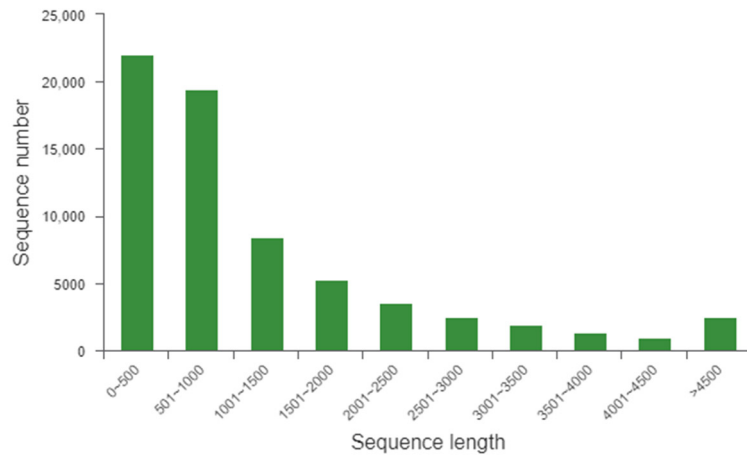
**Table S3.** Statistics of unigenes assembled.

Type	Resource
Total unigenes number	67825
Largest unigene length(bp)	22824
Smallest unigene length(bp)	201
Average unigene length(bp)	1369.6
<sup>a</sup> N50	2173
<sup>b</sup> E90N50	2750
GC percent	45.17
Mean mapped reads	1883.606843

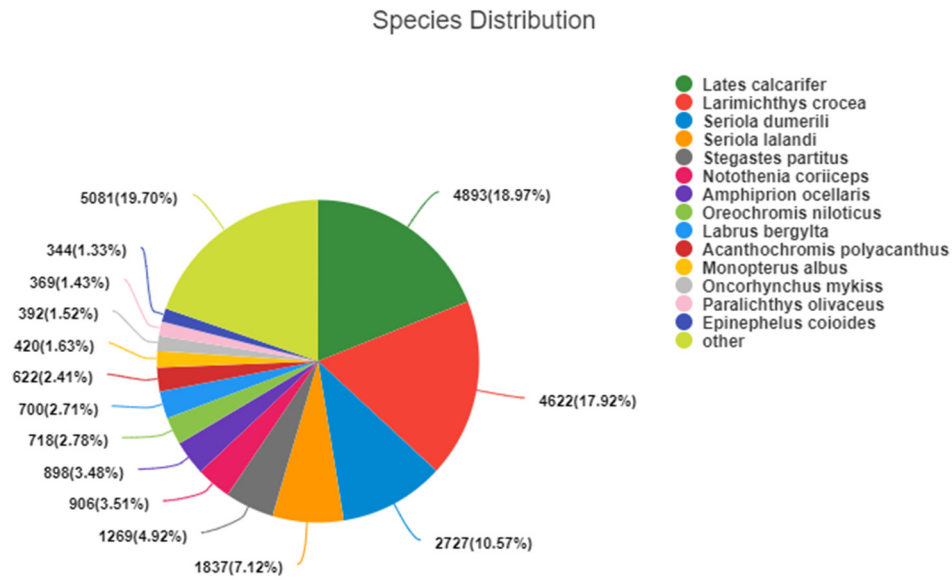
<sup>a</sup> : The assembled unigenes were sorted according to the length, N50 represents the length of the corresponding transcript when the length of unigenes is accumulated to half of the total length; <sup>b</sup> : The unigenes with the top 90% expression were sorted according to the length. E90N50 represents the length of the corresponding transcript when the length of the transcript is accumulated to half of the total length.

**Table S4.** Statistics of annotation results for intestine transcriptome unigenes.

Sample	Clean reads	Clean bases	Error rate (%)	Q20(%)	Q30(%)	GC content (%)
C_1	42868780	6402362666	0.0243	98.33	94.82	48.2
C_2	50759038	7554392639	0.0241	98.4	95	47.46
C_3	45485416	6789238074	0.0246	98.21	94.48	47.98
C_4	49994434	7458281090	0.0242	98.37	94.9	48.71
C_5	46643140	6953372256	0.0241	98.4	95	48.27
PC_1	56396278	8419828751	0.0241	98.41	95.02	48.69
PC_2	49936814	7450822733	0.0241	98.4	95.01	49.36
PC_3	48444140	7220277276	0.0239	98.48	95.2	48.56
PC_4	55973024	8354387035	0.0242	98.36	94.87	48.11
PC_5	49105230	7326443055	0.0244	98.29	94.71	48.53



**Figure S1.** The length distribution of the unigenes.



**Figure S2.** The species distribution based on Nr annotation.

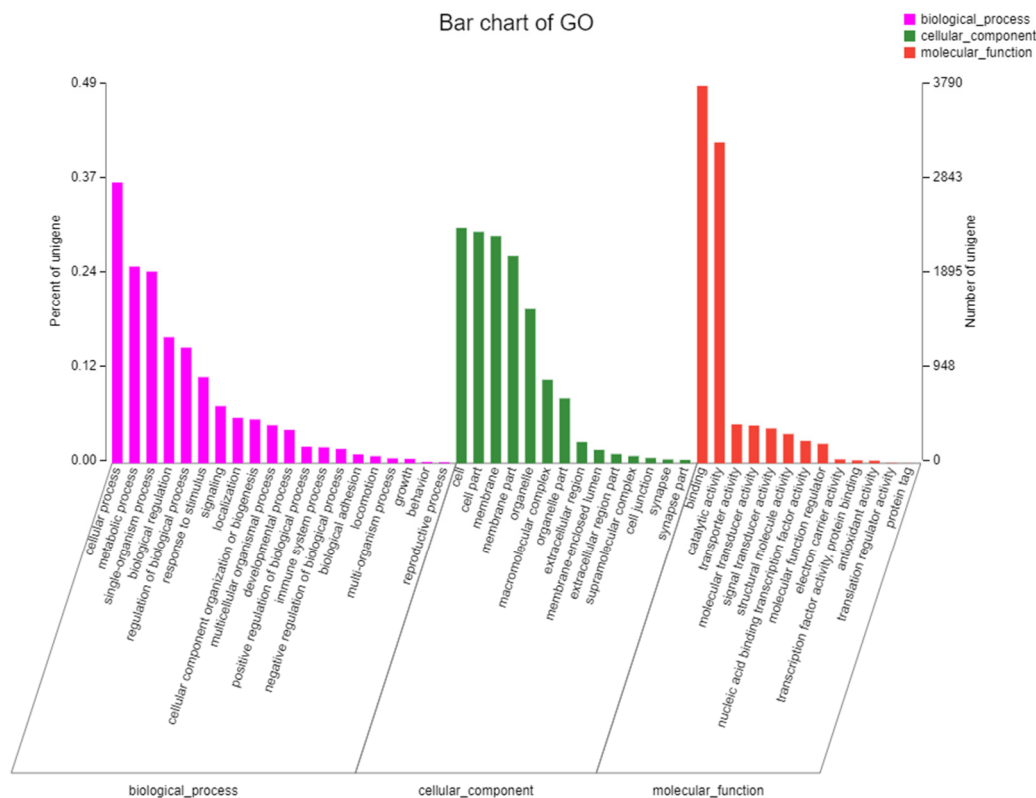


Figure S3. Top 47 annotated GO terms in the intestine transcriptome of *E. fuscoguttatus*.

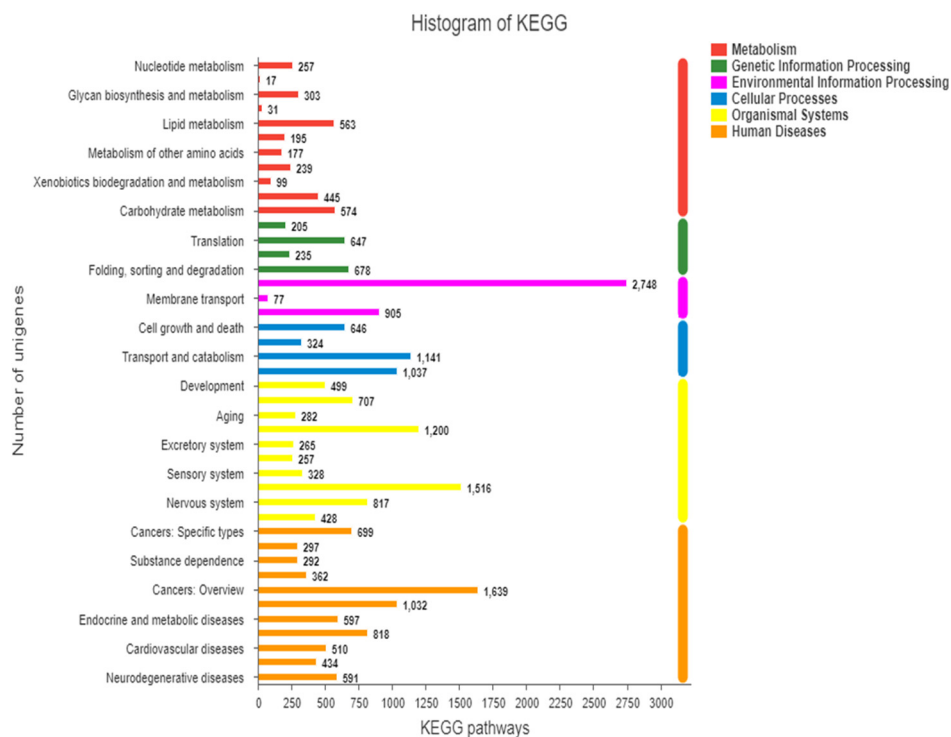


Figure S4. Annotated KEGG pathways in the intestine transcriptome of *E. fuscoguttatus*.