**Table S1** Primer sequences used in this study

|  |  |  |
| --- | --- | --- |
| Subject | Forward primer (5’-3’) | Reverse primer (5’-3’) |
| qRT-PCR (β-actin)1 | GAGCACGGTATTGTGACCAACT | CTCTGTGAGCAGGACAGGGT |
| qRT-PCR (fabp4)2 | CTTCCAGCGAGAACTTTGATGA | TCACCAGGTTGGGCTTTGC |
| qRT-PCR (PPARγ)3 | CACCGCAGAGCGAAGAACACC | GACGCCATAGTGAAACCCCG |
| fabp4 overexpression4 | CCCAAGCTTATGGTTGAGCAGTTTGTAGGAACC | CCGCTCGAGTTAAACCCTCTCGTAGGTCCTCAGT |
| cloning of fabp4 promoter5 | ACTAATACACGAGCATCGCCGT | AAGTCAAAGTCCAGGTTCCTACAA |
| cloning of fabp4 promoter5 | GGACTAGGGCTGCAACTAACC | CGGCGATGCTCGTGTATT |
| cloning of fabp4 promoter5 | AAAACCTCAAACGGCACA | AATGGTTAGTTGCAGCCCTA |
| D16 | CGGGGTACCCAAATACAACTTTAACTCACCTGCC | CCCAAGCTTTGGTGAAGATGACGCTCAGATGT |
| D26 | CGGGGTACCAGCAGGAGTGATTGGTTGGGA | CCCAAGCTTTGGTGAAGATGACGCTCAGATGT |
| D36 | CGGGGTACCAATCGACAAGTTCTGCAGCTCTAG | CCCAAGCTTTGGTGAAGATGACGCTCAGATGT |
| D46 | CGGGGTACCCATCAAACTATTCAGGGACCCAT | CCCAAGCTTTGGTGAAGATGACGCTCAGATGT |
| D56 | CGGGGTACCTTCCCTTCAATCAAACACACC | CCCAAGCTTTGGTGAAGATGACGCTCAGATGT |
| D66 | CGGGGTACCAATACAACTTTAACTCACCTGCCTT | CCCAAGCTTAGTACTGGTTTTAACCAGCAGATGG |
| construction of deletion mutant (F1, R1)6 | CGGGGTACCAATACAACTTTAACTCACCTGCCTT | CCCAAGCTTAGTACTGGTTTTAACCAGCAGATGG |
| construction of deletion mutant (F2, R2)7 | AGTTTTTGTTT**TTCCGCAAT**GCAACA | TGTTGC**ATTGCGGAA**AAACAAAAACT |

1The gene sequence of β-actin (KX987228.1) was obtained from NCBI, and the primers were designed in regions conserved with *Epinephelus coioides* β-actin (AY510710.2)

2The gene sequence of fabp4 (MN562216) was obtained from NCBI, and the primers were designed in regions conserved with *Epinephelus coioides* fabp4 gene (*Epinephelus coioides* fabp4 sequence was obtained from our non-public whole-genome sequencing data)

3The sequence of *T.ovatus* PPARγ was obtained from our non-published sequence provided by Dr. Li M M, and the primers were designed in heterogeneous regions with *Epinephelus coioides* PPARγ (Epinephelus coioides PPARγ sequence was obtained from our non-public whole-genome sequencing data)

4The bases underlined are the sites and protective bases for Hind Ш (5′-CCCAAGCTT-3′) and Xho I (5′-CCGCTCGAG-3′)

5The complete promoter sequence of fabp4 was obtained by three separate PCR amplification. Finally, the obtained sequences were spliced together

6The bases underlined are the sites and protective bases for Kpn I (5′-CGGGGTACC-3′) and Hind Ш (5′-CCCAAGCTT-3′)

7The bases bolded are the predicted binding site of PPARγ, and the bases underlined “CCG” are mutated from the original “AAG”.

**Figure S1** Effect of dietary n-3 LC-PUFA on *fabp4* gene expression in *T. ovatus* liver. Values are means ± SD. Means at a time without a common symbol are significantly different (*P*≤0.05).



**Figure S2** Effect of PPARγ overexpression, fabp4 overexpression, BMS309403, and GW9662 on the contents of fatty acids. Values are means ± SD.



**Figure S3** The distribution of possible PPARγ binding sites in *T. ovatus fabp4* core promoter region. The bold sections represent the predicted binding sites that located at -1882bp to -1864bp and -1774bp and -1766bp, respectively.

