

Table S1. Primers used for *ACCα*, *CPT1α1b*, *FAS* and *PPARγ* promoter cloning

Gene	Forward primer (5'-3')	Reverse primer (5'-3')	Step
<i>ACCα</i>	CCATCCGAGTGAGGTTGT GG	AAGTGCTGTCCGAGTTGA GA	PCR
	ACGATGGACTCCAGAGC GGCCGCVVNVNNNCCAA	CGAGACGACTTGATGCA AGCTAATA	hiTAIL- PCR1
	ACGATGGACTCCAGAG	GAAATGAGTCGGCAAGC TATTCTGATGTGG	hiTAIL- PCR2
	ACGATGGACTCCAGAG	CACAACCTCACTCGGATG GATGTTCGTT	hiTAIL- PCR3
<i>CPT1α1b</i>	TGAACGCCAAATCGACAT CCT	GTGGAGGCCTGACAGATA AAC	PCR
	ACGATGGACTCCAGAGC GGCCGCVVNVNNNCCAA	TTCGGTACTGATGCAGAT TTAGGAT	hiTAIL- PCR1
	ACGATGGACTCCAGAG	CTAGGACGAAGAACGGT TCAGTTTAAGACAC	hiTAIL- PCR2
	ACGATGGACTCCAGAG	AAGTAATGGCTTCTCCGC CCTATGTAGTG	hiTAIL- PCR3
<i>FAS</i>	AAAGCAGTAAGAAGACC AAC	GCTATGACGATTTCTCTCC ATG	PCR
	ACGATGGACTCCAGAGC GGCCGCVVNVNNNCCAA	CTTAGGGTGTGAACTACT GACG	hiTAIL- PCR1
	ACGATGGACTCCAGAG	TTCTGCGTAGTCTAGACA AGC	hiTAIL- PCR2
	ACGATGGACTCCAGAG	CTGAGCTGCCTTGTAAGT CCT	hiTAIL- PCR3
<i>PPARγ</i>	TGGGATTTGGTCTAAGCA CTC	TGTAGTTGTTCTCATGGG CTCT	PCR
	ACGATGGACTCCAGAGC GGCCGCVVNVNNNCCAA	CACGAAGCTGACGTAAC AAGATGCTTTC	hiTAIL- PCR1
	ACGATGGACTCCAGAG	GACTTCCTGTTGCTTCAC CCGCTGCTT	hiTAIL- PCR2
	ACGATGGACTCCAGAG	CATGTGGTTGTGCTGTGA GGTG	hiTAIL- PCR3

Table S2. Primers used for 5'-deletion plasmids construction

Gene	Primers	Forward primer (5'-3')	Reverse primer (5'-3')
<i>ACCα</i>	pG13-402/ +51	ctatcgataggtaccgagctcTCCATC CTCGTGTACCGTCA	cagtaccggaatgccaagcttCTCACT CGGATGGATGTTTCG
	pG13-793/ +51	ctatcgataggtaccgagctcCTGTTC TTCCCAGATCTCACA	cagtaccggaatgccaagcttCTCACT CGGATGGATGTTTCG
	pG13-1154 /+51	ctatcgataggtaccgagctcTCGGTA TCTGAAGACTTGACTC	cagtaccggaatgccaagcttCTCACT CGGATGGATGTTTCG
	pG13-1518 /+51	ctatcgataggtaccgagctcTTGCTC CGTTCTGCTAAATG	cagtaccggaatgccaagcttCTCACT CGGATGGATGTTTCG
	pG13-1914 /+51	ctatcgataggtaccgagctcTGGATG GATGGATAAATGGAAGT	cagtaccggaatgccaagcttCTCACT CGGATGGATGTTTCG
	pG13-2234 /+51	ctatcgataggtaccgagctcGTGTAT ACAGTAGATGTTGGCTT	cagtaccggaatgccaagcttCTCACT CGGATGGATGTTTCG
<i>CPT1α1b</i>	pG13-387/ +24	ctatcgataggtaccgagctcTTAAAT GGTTAGGTGTTAGGTGG	cagtaccggaatgccaagcttGCTTCT CCGCCCTATGTAGT
	pG13-726/ +24	ctatcgataggtaccgagctcCTGAAG AATCAAAGGAAAGGTG	cagtaccggaatgccaagcttGCTTCT CCGCCCTATGTAGT
	pG13-1120 /+24	ctatcgataggtaccgagctcGTTTCGT GGGCATATTTGTTG	cagtaccggaatgccaagcttGCTTCT CCGCCCTATGTAGT
	pG13-1480 /+24	ctatcgataggtaccgagctcGCACAG ACCTGATTGCTGA	cagtaccggaatgccaagcttGCTTCT CCGCCCTATGTAGT
	pG13-1709 /+24	ctatcgataggtaccgagctcCCCTAA TTCTAACGAGCAAGCC	cagtaccggaatgccaagcttGCTTCT CCGCCCTATGTAGT
	pG13-2155 /+24	ctatcgataggtaccgagctcGGGATT AACTCTGTGGACTGG	cagtaccggaatgccaagcttGCTTCT CCGCCCTATGTAGT
<i>FAS</i>	pG13-326/ +39	ctatcgataggtaccgagctcCCTACA AGATGCAACACCTC	cagtaccggaatgccaagcttGGTCTT CTTACTGCTTTGGTT
	pG13-746/ +39	ctatcgataggtaccgagctcTCTGAT TCGTTTACGGTCCTC	cagtaccggaatgccaagcttGGTCTT CTTACTGCTTTGGTT
	pG13-1152 /+39	ctatcgataggtaccgagctcATATAG CCGTTGCACTACACAG	cagtaccggaatgccaagcttGGTCTT CTTACTGCTTTGGTT
	pG13-1380 /+39	ctatcgataggtaccgagctcTGTA TGACTTGTCAGCTCT	cagtaccggaatgccaagcttGGTCTT CTTACTGCTTTGGTT
	pG13-1525 /+39	ctatcgataggtaccgagctcGTACAA AATGTGCCATCCGAG	cagtaccggaatgccaagcttGGTCTT CTTACTGCTTTGGTT
	pG13-1960 /+39	ctatcgataggtaccgagctcTGTGCC AACATTTACCCCTG	cagtaccggaatgccaagcttGGTCTT CTTACTGCTTTGGTT
<i>PPARγ</i>	pG13-439/ +63	ctatcgataggtaccgagctcTGGTTA TGGCACAAATGCAAC	cagtaccggaatgccaagcttTTGGTG ATACTGAGCTTCGTAAT
	pG13-671/ +63	ctatcgataggtaccgagctcTTGGCT ATAAATGCATCCTG	cagtaccggaatgccaagcttTTGGTG ATACTGAGCTTCGTAAT
	pG13-784/ +63	ctatcgataggtaccgagctcCATGCC ATGTTCCCTGGAC	cagtaccggaatgccaagcttTTGGTG ATACTGAGCTTCGTAAT

pGl3-1241 /+63	ctatcgataggtaccgagctcTTGACT GGAAATCGGTTTATACT	cagtaccggaatgccaagcttTTGGTG ATACTGAGCTTCGTAAT
pGl3-1575 /+63	ctatcgataggtaccgagctcTGGTAG GGAAGAGTACCTGA	cagtaccggaatgccaagcttTTGGTG ATACTGAGCTTCGTAAT
pGl3-2033 /+63	ctatcgataggtaccgagctcTGCGGT GTCCAACATACTCA	cagtaccggaatgccaagcttTTGGTG ATACTGAGCTTCGTAAT

Table S3. The reference binding site sequences

Name	Binding site sequences
CREB	TGAGCT
HNF4 α	CAAAGT
MTF-1	TNTGCACACG
NF- κ B	GGGANTTCC
NF-Y	CCAAT
PPAR α	GGNAAAGGT
PPAR γ	GGNAAAGG
SP1	CCCCNCCCC
SREBP1	TCACCCA
STAT3	TTCTNGGAA
STAT5	TTCCNNGAA
TATA-box	TATAAA

Table S4. Primers used for site-mutation analysis

Gene	Primers	Forward primer (5'-3')	Reverse primer (5'-3')
<i>CPT1a1b</i>	CMut-STA T3-1	CTAtcgaggtgtctTGTTTTTAAT GTTTGCTGATTTTTTTA	ACAagacacctgaTAGCTGTT AAATAGCTAAATGGTGC A
	CMut-STA T3-2	AAAcaggatctgctAAGAAATA AAATAAATACACTGGCAA CTAT	CTTagcagatcctgTTTAAATA ATTATGTATGTA ACTATT TACACCACT
<i>FAS</i>	FMut-STA T3-1	GAAAcacattagagAGATTCCAG TACGATAACTTTACATGC	TCTctctaatgtgTTCATATTT TTTAAATATGATGTTGAT TAAAG
	FMut-STA T3-2	AGCcaccatacgaGCAGTCAA GATTCGAAATTACAACA	TGCttcgtatggtgGCTTTGCCT TTTTACCAGGTTT
	FMut-STA T3-3	ACAAtgcagctagctCCAAATTCC TTTTATGTGTCGACA	TGGagctagctgcaTGTGACCC TTAAAAGTACAGACATG G

Table S5. Primers used for electrophoretic mobility-shift assay

Primers		Forward primer (5'-3')	Reverse primer (5'-3')
CPT1 α 1b -STAT3-1	Biotin-probe	Biotin-CTAATTCACGTAAATG TTT	Biotin-AAACATTTACGTGAA TTAG
	Mutative-competitor	CTATCGAGGTGTCTTGTTT	AAACAAGACACCTCGATAG
FAS -STAT3-3	Biotin-probe	Biotin-CACAAACACCTGGAA CCAA	Biotin-TTGGTTCCAGGTGTTT GTG
	Mutative-competitor	CACAAGCAAGTCTATCGTA	TACGATAGACTTGCTTGTG

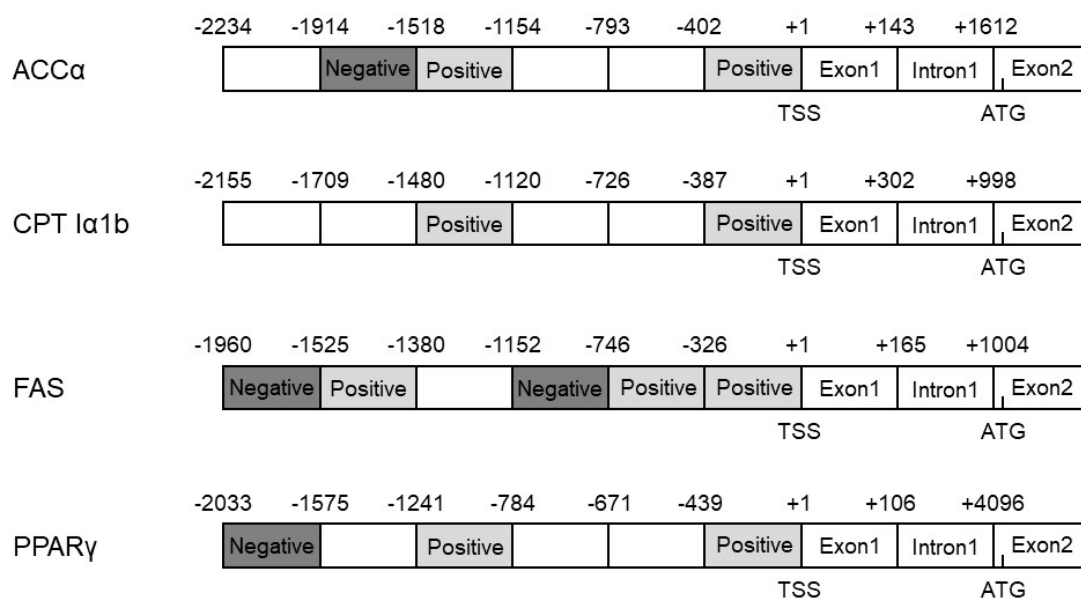


Figure S1 The schematic diagram of *ACC α* , *CPT1 α 1b*, *FAS* and *PPAR γ* gene structure. Positive: the region that positively regulated the promoter activity. Negative: the region that negatively regulated the promoter activity. TSS: transcription start site. ATG: translation initiation site.

CACAGCTCCA GCTCTGTGTA TACAGTAGAT GTTGGCTTTA AGCCCAACAC TTTTTCCTCC CTTTACTTAT CAGACAGTTT TCTGATAAAA AAAAAAATAA -2150
 AGAAATTGGA GAGCACAGTT ATCACAAAGAA ACTATTACTA AACTGTGTGC TCTGAAATG TACAACAAA CATTCTGAAA TTCAGAGGAC ATTTAGTTTG -2050
 TTGGACTTTC AGATTTCAGA AGTCAAATG AGAAGTAGCT CTTTATTCTT TTTTTCCTCC TTTTTCCTCC GATTCCATAA CTTCTTATAT TCAGTAACTG -1950

HNf4a
 TAAACAATT GCTGCACAAA AAATGGATGG ATGGATGGAT GGATGGATAA ATGGAAGTAA TAAGAAACAT GGTGAAATAA TTACAGATTT TTCCCATTTA -1850
 TTGTATGGT ATTTTATATAT GACACAAAAA CATATATGAA TCATTTACAT TACAGCTGAT ATAAACACTC GTTATAGCAA ACACCTGTGT ACTTCGTTTA -1750

STAT3
 TCAATTTTAC ATGAAAAGCA CTGACACTGT AGACTTCTTC CATAAATGTA AGACATTAGT CTTAGATTGC ATTTGGTCTT CAGTATACAT GTCCTTGTTA -1650
 ACATCATACA CATCTTTAGT TGGTACTTAA CAATAACGTA TTAAGAGCAA ATCTGATCAA TCTGATAAGT GCTGCAATCA TTTTTCCTCC ACCCAGAATT -1550
 GGTCATAGCA TAGTATTTAA CTGACTTAT TTGCTCCGT TCTGCTAAAT GTTCACATAT AAATGATTTA TGATGAATGT TTTTATGATG ATGTGTGACTG -1450
 TTTTAAAGTC AGATTTCTTT TTGCTGCTG AGAACATTTG AGGTGAATCA AGCTTTTGT TATTTTCTCC TTCCATGAAT CCCTTCTAAG GTCTCATGTT -1350

CCACTGCCTG TTTTATCTGG CAGTAGGACA GGTGATGTCT GCATGATCAT TAAACTTTGA GCTGAACCTG AACCTAAAAA TCACGCTTGC ACAAGACTGA -1250

PPAR/RXR
 TATTTTATCG TTCTGAATCA ACCCGTTTAC ACAATAGTTA GATTGGATGC CAATGCCTCT GTGCTACGTC TGAGTGAATC CGGGTCGAAG GTGCTTCGGT -1150
 ATCTGAAGAC TTGACTCTAT CTACAGTTAG CTGAAGTATT GAACATTAT TTAAGAGACA TTTCATCCAA AGTGCCTTCC GGTGAGCCT TCAGATGAC -1050
 GGTTAAAATC TACTGGGATT CGACCTCACA ACCTTCTGCT CGGTATTTCA TATTCAGTAT GATACTGACA CCGAAATGTT CCTTGATACC TAAGTAGATC -950
 TTCTAGGTTG ATGGGATGTG ACTGTATCGG TGCAATCAGTA CAACAGCACA CACATTAGCA TCATTATAAT GACTGCTGTG GAATGAAATA AAAATGTTCA -850
 GTAAATAGAT TAGTATTTAA GGCAATTTAC GTCAATCTCT TAAGAAATGAT AAATATCTGT TCTTCCAGTA TCTACAGAG ATTTCCATAC ATGTGTGACTG -750
 TTTTGGAAAG GACAACCTTG GACATGTTTA ATACTTGGAG ACTGTTTGT TTTTGGACA ACTGAACCAC ATTATTTATCC CAAATCGCTC GTCTTGTAT -650

HNf4a
 TGCAATGATA AGACATGCAA ACTTTTGA CTTATGTTAT TTGCATTACA TGTGATAATG TTATTTATTT TAGATCCCTA AAGCTATCTG AACCTTGTGA -550
 CTCAATTATA TCTATAAAAA AAATAAGAAAT AAATCATTAA ATCATTTATG CGAGTCTTTT TCCCTTCTGC TTATTTATTC TTTTCTGTTT TATTGCATTT -450
 CTTATTGCAA ATTTTATTTT TTGTATATATA AATAAAATGG AAAAAATCCC ATCTCTCTGT ACCGTACCTT TTAATTCATA AACGATTTT AGTCGGATCA -350

PPARy
 GCGGATACCG CGCACAAAAA CGCGGACCAC CAGACCTCT CTCTCATGG TTACACCTCT CTTTATTTGC ATATCAAAAC CGGCCCTAA CTGAACACAG -250

SREBP1
 AAATTCCTATT CGCTCATTCG TTCGGCGTGA GACTCTTAAA GTTCATAGTT CGACAATCTG CAGTAACTTC ACTCGACTCC CCGTTTTTAC ATCCCACCTG -150
 CATTCCGACA TAACGCTTCC TTGTTTTGTG ATTGACTCAT ACAGCTGTCC AATCAGAGAC CAGAACTCGG GTGTACAATT TACATATGAC CAATCAGAGC -50

NF-Y **NF-Y**
 AAAACAGACC GGCAAATTCC AATACGGGTA GGATAAAAAA ACGCTTCCGG TGAGTAGCTA AGCTTATTTA CTCGAAAGCT AACGCTAGCT GAATATTAGC +51

TATA-box **TSS**

Figure S2 Nucleotide sequence of yellow catfish *ACCα* promoter. Numbers are relative to the transcription start site (+1). The putative transcription factor binding sites are underlined. The highlighted sequences show putative transcription factor binding sites of STAT3.

CCTAACACTT TCTTTCCACT GACGCTCTTC CGGGGTTTAT TTTTGGCGAG AGGACTGCAA CAAATCTATG GACTGGAGTA GGGATTAAC CTGTGGACTG -2132
 GAGTTGGGAT TAAATATGTG GACTGGAGAA ATTACTAAAT CTCTGGACTG GAGTACTGAC TAAATGTGTG GACTGGAGTA AAAAACTAAT TCATTCATTC -2032
 ATTCGTTTAT TCATTCATTC ATTTTCTACC GCTTTTTCAA TTCAATTTCA TTTATTTGTA TATTTACTTT TAAAAATTC CATTGTCTCA AAGCAGCTAT -1932
 ACAGAAGTAT GGAACAGAA GAGAGAGATA TAAATAAATC AAACAATAAA ACAACAAAC AAACAACAA ATAAAGAAAG AAAGAAAGAA AGAAAGAAAG -1832
 AAGAAGAAGA AGAAGAAGA GAAGAAGAAG AAGAACGGAT AAAAAATAAT AAATGAATAT ATACAATTTA AGTTTAAAAA AAGATTTAACT -1732
 TAAAATTTAA AATACTATAT ATCTATCCCT AATCTAACC AGCAAGCCGA AGGTGACTGC GGCAAGGAAA AACTCCCTGA GAAGATATGA GGAATAAAC -1632
 TTGAGAGGAA CCAGACTCAG AAGGGAACCC ATCCCTCATTT GGGTGACACT GAACAGGACA TAAATGTAAT GTAAAAAAA AAGTCCCTTT CTACACAGT -1532
 TGATGCAACT GAGAGCTTCT GAAAAACTAA TGGGTCATCG TAAACTCTGA GTTCAGCACA GACCTGATTG CTGATCAAGA CCAGACCATA CAGTTGACTG -1432
 ACACAACATT GATTCAAAAG AAGGCATGAT AATCTCTGGG CGGCTCCATC CACAACAATC CCATGAGACA CTTGCTGAAA ACAAGATTGT AGTAAAAAAC -1332
 AAATTACTGC TGAAGTATTA AATACACCTA TGGATCAAG TATTACTAAA TAAGTATATA TCTACACTCA CTGTCCACTT TATTAGAAAC ATTCATGCTT -1232
 TTATTGAATC AGAGAATAA CAGCAGCTCG ATTACTATGC ACCATAGTGA ACATTAATTT TAAATTTAA AATTGAATAT TAGGAATAGT GGACAGCAAT -1132
 GGATTCCTTA CTATGGTTCC TGGGCATATT TGTGCTTCA GCTCATTAAT CTGTCTTTTA TCGCAGTCGT TTTGTTTTGT TTTGTTTTGT TTAGTCCACA -1032

MTF-1 **STAT3**
 GGTTAAATCC TTGCACCAAT TAGCTATTTA ACAGCTAATT CACGTAATA TTTTAAATGT TTGCTGATTT TTTTAAACGT TAGAATAGTT CTGCACTAAA -932
 TGTTTGTAT TTTAAGACAA AATATAATTT TGTACCCAT ACAAAATTT TTAATTTTAA GTCTTTAGTA TTAATAAAT GAATAGTGGT GTAATAGTT -832

STAT3
 ACATACATAA TTATTTAAAC ATGTTGGAAAT AAGAAATAAA ATAAATACAC TGCCAACACT GTAAGCGTTA TTTTAAATGTT TTTATTACAT ACTTACTTTT -732
 CTTTCTATTC TGAAGATCA AAGGAAGGT GTATGAGACA GTAGTGAGAC CAGCTCTGCT GTATGGGTTA GAGACTGTAG CTGTGAGGAT CAGACATGAG -632
 GCAGAGATGG CCGTAGCAGA TATGAGGATG TTGAGGTTCT CTTTAGGAGT GACAAGGATG GACAGGATTA GGAACGAGTG CATCAGAGGG ACGGCTCAGG -532

MTF-1
 TTGGCTGTTT TGTGGACAAG GTCAAGAGG ATAGATTTAG ATGGTTTGGG CATGTACAAA TGAGGGAGAT TGTATATTTG GTAGAAATGAT GTTGGAAATG -432
 GAGGTGAGGT CAAGAGGAAG GACAAAGAGA AGATATATGG GCATGAAGTT AAATGGTTAG GTGTTAGGTG GAAACAGATT ATTTGCTGTG GCATTTTGGC -332

HNf4a **PPARα/RXR**
 TTTCTTTTAA TTCTCTTAT ACAAACTTGT CCTCTCTTTC ATCTGAGGGA TTCGATATTA TAAAAATAGC CACATGATTT ACATTGACAG GATTTTTTGT -232

SP1
 GTGAAACTTT GTGTGCTGCC ATTTTGGCCA GGACTCCCTG GTAGAAGAGA TTTTTTTTAA TCTCAATGGG ATTATTCTCG GTAAAAATAA AGATAAATAA -132

SP1
 ATAAAAATAA ATAAATTTAT GCCTAAATTA ACAGCAGAAAT AAATAAATAA ATCTCTCCG CACCCTAGG GGGCGGTGTG CACATTAAGT AAGTCTGAGG -32

SP1
 TTGAATCCCA AAAATCTGTA ATGTAAACAA AGTGCACTAC ATAGGGCGGA GAAGCCATTA CTTTCTTTTA CTTATAGTGT GCCTATGTGC GGCCTGTGTA +69

TSS

Figure S3 Nucleotide sequence of yellow catfish *CPT 1a1b* promoter. Numbers are relative to the transcription start site (+1). The putative transcription factor binding sites are underlined. The highlighted sequences show putative transcription factor binding sites of STAT3.

CAGTCCCTGC AATAAGCCAG GAGCTCAGTC AAATCTGCAT CTAGGCAGCT GTGTACACAA AATGTGCCAA CATTTCACCC TGTTACTTT TAGGTTTCAT -1913

AGATCTAAGT GGTTCAAATC AAGCACAGTT CTCAGTACCC TTCTGAACTT TTAATCAACA TCATATTTAA AAAATATGAA AATCCTAAAA GAGATTCCAG -1813

TACGATAACT TTACATGCAG GGTACACAG CACACCATT TGTGACCTTA TGTGTTGATG CCCCCTGCATG GGCTTCCCTCT GAATAATTTA CAGATACTGT -1713

TCCTGTGTCA GCCAGAGCAG AGGAAAATAG AAATACACCA CATCCCGGAT TACCAGTTCA AGTTCCAGGGC TTGAAAGCAG TGATCCAGGA GAGAAACAAA -1613

AAAGCCAGAA CTACATCTGA ACCTGGTAAA AAGGCAAAGC CAGCTGGAAA GGCAGTCAAG ATTCGAAATT ACAACATTAA AGACTGAAAC TATGCAGGTA -1513

CAAAAATGTGC CATCCGAGCA AGATTTTGAA ACTATTTAAC AAACCCGGAT GTTGTGTTTT ATGAATCGTG AGTTCAAATA TGTGAAATAT TTGTTACCTT -1413

TACTGAACTC TAAACTCTGT GGGTTCCTTG TAAAATGTAC CTTGTAAATG ACTTGTCAAG TCTGTCAATG AAAATAAAAA ATGTTTTTGT AATAATAAAA -1313

PPAR α /RXR

TATTTTTATA CTCAATAACT CAATACTGTG GTTGTATTTT ACCTGCAAG TATACACCTA CTTATGCCTA TAGTTTCTTA CACTTAGCAG TAAGGAAGTA -1213

TGTCGTGTGT CATCACCTGT CTAACCTGTC TCAAGTCAAG TCAAGGAGCT TTTATTGTCA TTCAACCAT ATATAGCCGT TGCACTACAC AGTGAAATGA -1113

GACGTTTCTC CAGGACCATG GTGCTACACA AAACAAGATG GCAATGGAGT GTTTTGAACA TAGTCGTGTA TGTAGCACAC TTTGGTTTCT CACTAGCTGC -1013

TTTATTATAC ACTCTATTTT AATCTACAAT CTGTGTTGCT TTCTGACCAC AGCAGGATG TTGGTTGCAT ATTTTGTGTT CAAAATGATC ACGAGATGTT -913

CAACCGCTTC TCAGACGAGC TGTGGGCTT GATACAGATG TTCCAGCACC ACACATACAC ACAAACTCAA AGATGCCATG AGGTGGTCC ATGTCTGTAC -813

TTTTAAGGGT CACAAAACCC TGGAACAAA TTCCTTTTAT GTGTCGACAA ACTTGGCCAA TCAACCTGAT TCTGATTCTG ATTCGTTTAC GGTCTCCAT -713

CCATGGACGC TGTGTGGTTA AACCGAGCAC TGAACTGTAA AGACTCTTGC GCTTTAACTA TAAACAGTAT AAAACATCTA TAGAGTGAAC CGAAATAACC -613

CCGTTAAACG ACACGCCCTC TTGATGACCT CACAGGCTAC GCTTGTCTTT AGCAGGACGC CTTAATCGGT TCCTCATCAC CTCACCCCTAT ATCAGAAACA -513

CGCCCTTTCT TCGTCTGAT TGGCCAAAAG TCAACGTCAA TCACGAAACT GTGTGATCTG CAAGCTGTG CACGTGAAAC ATCCCAAAAT CACTGAAATA -413

PPAR γ

AATGGCTTC ACAGCAGTAT TGTAAACTCA GTTTAACATT AATATATTTG TCCCTAGCTG ATTTAAAGCT TTTTGAAAT AGCACTCGTA CATTTTCTTA -313

CAAGATGCAA CACCTCATTT TAAGACACAC ACACACACAA TGACGCTAT ATCTAATCTT GACCCAGATT CATTAGGCAA TAAGGCAATG TACTTGTCTA -213

GGTTACTGTG ATAGCATGCA TCTGTGCATG ATGTTGCACA TAAACCTTCC ATTTATGATC TGAACCTGAA TAACCTGTGT TTTTAGCGGG AATTAACGTT -113

AGGACATCAG CTCAGTGGTT GGAATGTTGA TCCCTGCCCTC CTTCTCATT GACTAGAAA CCCAAGGCAA CTGTCAGCCC ATGTGGCGTG GCTATACAC -13

NF-Y **NF-Y**

ATGGCACACA TTTAAATGAA ACAGACATCA GTGCAAAAGC AACCARAAGCA GTAAGAAGAC CAACACTCAG AAAAAAGGGG TTATTAATCC ACATTCACAG +78

TATA-box **TSS**

Figure S4 Nucleotide sequence of yellow catfish *FAS* promoter. Numbers are relative to the transcription start site (+1). The putative transcription factor binding sites are underlined. The highlighted sequences show putative transcription factor binding sites of STAT3.

GAGGAAGCTG AGGAAGCGCG GGAACCTCA GGAGAGACAT CAACTGTTAA CTCATGCCTA TTAAGGCAA TTGGAGGAAA GTTCATGTCC TCCGATATTG -2072

TGCAAGAGCA AATTTCCAG GGGCTACACA ATAAAGATTG CGGTGTCCAA CATACTCATC AGAAAGGGTG TTTGCAGCAA ATCTGATTTG TCATCAAGGG -1972

CTGGAGAGA ATGTTACAGT AACCGATTGC TTAACATCCG TCCTCATGTA CTTGTGCATG TTTTAAATGTT TTCTCCAGGG ATTTGGATTG AAAAGCATGA -1872

CREB

GATCATAATT AGTCATGTGC TAGAACGTTA GAGGAGTTGC AATGTGCTTG CATAAATGTG TGTGTGTGCG TGTGTGTGTG TGCATGCGTG TGTGTGTGTG -1772

TGTGCATGCG TGTGTGTGTG TGTGAGACGT TGCTTTGTGG TCTACAGCAG CAGTAAACT AGCTCAGGAT CATTGCTTG AATTGCAT TGTAAATGTC -1672

GAGTCAGCTG TTGPGAAAG TTTGTACTTT TGTGGAAAGT TTGTACTTTT CTGTTTTTTC TTTCCACTTT TCTAATGTTA ATGACAGCTT TTCTATTGGT -1572

AGGGAAGAGT ACCTGAATTT TATTAACTTA ATTTACACTA AAAACACAAA CTGAAAAAAA AAAATTACTT CACAAAAAAG GATTAATAAT ATTTGGCAATA -1472

GGTGCATCCC AAAATTCAGT TTGCAATATT CTCTGCCATT TTGTAGTAAA AATGTAGACA AGTTAACAGT GGAAATTTCTA ACAAGTGGAA GTGCACTCGA -1372

NF-kB

AGCACGCCGA TGACGCCTT ATTCAACCTA ATAAACAGCG AGTGGAAATG CACTTCAACC GTTGTAGCTT TCTTACACAA AAGGAAAGGG GCATTGAAAA -1272

AGTATAATTT TTTATGATGG CCACCGAACA TTGACTGGAA ATCGGTTTAT ACTTCCAGTG TAGTTTCACA TTTGAGACGA TACTCCCTTA AAATTCGTAC -1172

ACTAAACAGT AAAGTGCTTA GTGCAAGTGC TTAGTCATTT GGGACACAGC TGACGAGACT GGATTTTACC AAATTTTACC ACATATATAT TCGTGTAAACA -1072

AGCCCTCTTA TTTTGGCAA CACCCACTGG ACAAAATTATG CTAAGTTACC CAACATGGTG GAATGATCTA GAACAGGATA ACAGCAGATT TAGTGTTCCT -972

GGAAATTGAG CTTGTACCTA TTTAATTAAT TTAGATAAGT GGTTTACATG ACATATTATC CATATTCTCT AAAAGTCATG CAATCTTTTG TTTTFTTTT -872

TGTTTCTCAG TCTGGGTGAA GTTGGGTGCA CCAGACTGCA GACTACTGCA GGCTGTTAT TACAARAATG TGTCTGTGTG AAAGACACAT GCCATGTTC -772

CTGGACAAA CCTAGTTTTA GCACAAAACC GTTTAGCAGA AAATGGTTCA TTTTAAATGG AGAAGGCTTT GTTATCTATT ATTATCTAGA AGCAGTGTATG -672

TTGGCTATAA ATGCATCTTG CTTGAATAGA TTCTTTTTTT TTTAATCAGC GTATTTGTGG TATTTTGGTG TGTAACCTAA TATAATACTG TGTGTGTCCA -572

ATAACATGAT CTTTATTGCC AGTATTTGCA AATGCTTAGT GTGGCACGTG TGAATATAT GGAATCATT TTCCAGTAGG AATGAAATGT GTCGTGTTAC -472

HNFI4a

TTGGTAAAAG TGCTTTTCGA ATCGTTTAAA CATGTTTATG GCACAAATGC AACATATTTCT ACTATAAGAT TTTTGAATA ACAACACAGC AACCATAACA -372

AACACACACA CACACAAA CAACACACACA CACATACTGT ACACAAAAA TCTGATAGTA AAGCTACTAT CGGTCAACAT GACTGTCTATG ATCATAGGAT -272

CTGAGGTCAG GGCCTCTCAG TAGTGACACT GAAAATGTCA CGGTGTAGAG AAAGCATCTT GTTACGTCAG CTTCGTGTTA TAAATTTATC CAGGGGAAGA -172

AGTGATCCAT CCACCTTTCT GTAAGAGAAA GTGGAAGACA GAAAAGCAGC GGGTGAAGCA ACAGGAAGTC ATCTGGCTAG CCGATCACCT CACAGACAAA -72

NF-Y

CCACATGATG GTTAGCTGTC TGCACCTTTG CTGAGGCCAT GCAGTGTA AAATCAAGTTC CTGTTCAATT TGTGTAGAAC ACTTGACCAG TTACCAAAGT +29

TATA-box **TSS**

Figure S5 Nucleotide sequence of yellow catfish *PPAR γ* promoter. Numbers are relative to the transcription start site (+1). The putative transcription factor binding sites are underlined. The highlighted sequences show putative transcription factor binding sites of STAT3.