

Table S1. Primers used for the cloning of *ctr1*, *ctr2* and *atox1* promoters in yellow catfish.

Genes	Forward primer (5'-3')	Reverse primer (5'-3')
<i>ctr1</i>	TGTGGAGCGACTTGTGTGTGGG	GACGAGGTCCTGACGGCTACCGGC
<i>ctr2</i>	CCCAAACGCAATTAAAAATGTTGA	TTATTATATAATCCAGCTACAGCTT
<i>atox1</i>	TACAAATATTAACCAGTATTTA	AAGAAGAAGAAAAAAGACACT

Table S2. Primers used for 5'-deletion plasmids construction of *ctr1*, *ctr2* and *atox1* promoters in yellow catfish

Genes	Primers	Forward primer (5'-3')	Reverse primer (5'-3')
<i>ctr1</i>	pGl3-470/+57	ctatcgataggtaccgagctcGACTACTTA CTATGTCCTTAGCCCTGTC	cagtaccggaatgccaagcttGACGAGG TCCTGACGGCTACC
	pGl3-796/+57	ctatcgataggtaccgagctcTCCACAGA AGCAGTTTTCAGTCATT	cagtaccggaatgccaagcttGACGAGG TCCTGACGGCTACC
	pGl3-1039/+57	ctatcgataggtaccgagctcAGTGCTGT GGTGCTGGTGAAG	cagtaccggaatgccaagcttGACGAGG TCCTGACGGCTACC
	pGl3-1359/+57	ctatcgataggtaccgagctcTGTGGAGC GACTTGTGTGTGG	cagtaccggaatgccaagcttGACGAGG TCCTGACGGCTACC
<i>ctr2</i>	pGl3-522/+43	ctatcgataggtaccgagctcGTCAAATT GCCGAAATACTCCAT	cagtaccggaatgccaagcttTTATTATAT AATCCAGCTACAGCTTTGTCC
	pGl3-1019/+43	ctatcgataggtaccgagctcCAACAGGC AGCAGCACCATA	cagtaccggaatgccaagcttTTATTATAT AATCCAGCTACAGCTTTGTCC
	pGl3-1557/+43	ctatcgataggtaccgagctcCGTCACTC TGTACTCAGGGAAGG	cagtaccggaatgccaagcttTTATTATAT AATCCAGCTACAGCTTTGTCC
	pGl3-1842/+43	ctatcgataggtaccgagctcCCCAAACG CAATTAAAAATGTTG	cagtaccggaatgccaagcttTTATTATAT AATCCAGCTACAGCTTTGTCC
<i>atox1</i>	pGl3-649/+43	ctatcgataggtaccgagctcTCAGCTAG TTCAGCGTGCAGAT	cagtaccggaatgccaagcttAAGAAGA AGAAAAAAGACACTCGG
	pGl3-1088/+43	ctatcgataggtaccgagctcCATTGACCT GCATATGGTTCATG	cagtaccggaatgccaagcttAAGAAGA AGAAAAAAGACACTCGG
	pGl3-1592/+43	ctatcgataggtaccgagctcGAAAGTTG GATCAAAATATATCACAAATC	cagtaccggaatgccaagcttAAGAAGA AGAAAAAAGACACTCGG
	pGl3-1825/+43	ctatcgataggtaccgagctcTACAAATAT TAACCAGTATTTATATGACAGT GG	cagtaccggaatgccaagcttAAGAAGA AGAAAAAAGACACTCGG

Table S3. Primers used for site-mutation analysis

Genes	Primers	Forward primer (5'-3')	Reverse primer (5'-3')
<i>ctr1</i>	Mut-ctr1-N RF2(1)	gttgacagtcagtagcagcATAACAGGGC CGTGTTATTAAAACA	ctgctactgactgtcaacattACACACCTG CTAACCTGGAGTGT
	Mut-ctr1-N RF2(2)	aaatcagaagcctggtgtgagGAACAGTG CTGTGGTGCTGGT	caccaggettctgatttgcaaGTTACAGGT AATATGACATCTATACAATATTA AAC
	Mut-ctr1-S REBP1(1)	atcccagtggtcacagtttagTCACGAGGG ATCGTTTTTTTTT	aactgtgaccactgggatgtggaGCGACTT GTGTGTGGGTGACC
	Mut-ctr1-S REBP1(2)	ccctccttgataagtaataagCCAGACGA TGTAACCTCTATTCTTATTTCC	tgacttatcaaggagggAGAAAGATCAC ATGACCAGTTTAGTCA
	Mut-ctr1-S REBP1(3)	accgacatagcgattgtcTGAACCTACAG TATTTACACACGGTATTG	gacaatcgctatgtcggttaataCTCGAATG AACAGTTTCTTAGCAGC
	Mut-ctr2-S REBP1(1)	agcatcacatcgactaggtTGCTAAACC GGTAGCCGGC	tagtgcatgtgatgctcgaAGCTAAACT TGACTAAACTAACTAGCTTTCT
<i>ctr2</i>	Mut-ctr2-S REBP1(2)	atgccagatatggcttgatcAGCAACTCCA CACAAAATGCC	caagccatatctggcatgtcTGCTGAGGA AAAGTCCAAAATCA
<i>atox1</i>	Mut-atox1- NRF2(1)	tcagtcagagtcggtacggctACAGTCAGT TCAAAGTGACAGAGTTTG	gtaccgactctgactgactTAGGGATGAT CGTTAAATTCCCA
	Mut-atox1- NRF2(2)	tcatgacaggctaggtgtccACAGGCAAC GGAGCTTCAAC	cacctagcctgtcatgattcGGTTCACAG AAGCACAACTATAGCG
	Mut-atox1- NRF2(3)	gcttgtcagagtcatgtataaaCAGTTTCTT CCATGACTGACGTTT	acatgactctgacaagccACAGTGATCA GCAGTTTCTTGTAGTG
	Mut-atox1- SREBP1(1)	gaaccgcgtgtcgtttcttCACACAGTATA AATGATAACATATAATGTGTCA	aaaacgacacgcgggtcgtAACACTGCCT AGGCGCTTGATT
	Mut-atox1- SREBP1(2)	agccgtcagaggtcgctactcgGTCAGCTG GTACAACTACCAGGG	tagcgacctctgacggctacAAGAAGACT AACAGGGAAAAGCATAA

Table S4. Primers used for electrophoretic mobility-shift assay

Primers		Forward primer (5'-3')	Reverse primer (5'-3')
<i>ctrl</i> -NRF2(1)	Biotin-probe	Biotin-GTAATGTGTGACAC AGACAGCAGCA	Biotin-TGCTGCTGTCTGTGTC ACACATTAC
	Mutative-co mpetitor	ACGGCTCTGACAGTCAG TGATCATG	CATGATCACTGACTGTCAGA GCCGT
<i>ctrl</i> -NRF2(2)	Biotin-probe	Biotin-TTGCAAAGTGACC AATCAGTGTGAG	Biotin-CTCACACTGATTGGT CACTTTGCAA
	Mutative-co mpetitor	CGATGGCTCAGAAGCCT GACTGACT	AGTCAGTCAGGCTTCTGAG CCATCG
<i>ctrl</i> -SREBP1 (1)	Biotin-Probe	Biotin-GAGAAAGATCACA TGACCAGTTTAG	Biotin-CTAAACTGGTCATGT GATCTTTCTC
	Mutative-co mpetitor	ACTCGCACCAGTGGTCAT GACCGGT	ACCGGTCATGACCACTGGT GCGAGT
<i>atox1</i> -NRF2(2)	Biotin-probe	Biotin-CGAATCAGTCACA AAGCAGTGTCCA	Biotin-TGGACACTGCTTTGT GACTGATTCG
	Mutative-co mpetitor	ATGCGACTGACAGGCTA GTCACTAG	CTAGTGACTAGCCTGTCAGT CGCAT
<i>atox1</i> -NRF2(3)	Biotin-probe	Biotin-TGGCTTGCTGAGA CAGCATATAAAC	Biotin-GTTTATATGCTGTCTC AGCAAGCCA
	Mutative-co mpetitor	CATAGGATCAGAGTCATG CGGCCGA	TCGGCCGCATGACTCTGATC CTATG
<i>atox1</i> -SREBP 1(1)	Biotin-probe	Biotin-TTACGAAATTAAGT GATTTTTCTTC	Biotin-GAAGAAAAATCACTT AATTTTCGTAA
	Mutative-co mpetitor	CGCATCGCCGCGTGTCGG CCGAGCT	AGCTCGGCCGACACGCGGC GATGCG
<i>atox1</i> -SREBP 1(2)	Biotin-probe	Biotin-GTAGCCGGTCACAT GATCTACTCGG	Biotin-CCGAGTAGATCATGT GACCGGCTAC
	Mutative-co mpetitor	ACGTATATCAGAGGTCGT GGACATA	TATGTCCACGACCTCTGATA TACGT

Table S5. Primers used for RT-qPCR analysis

Genes	Forward primer (5'-3')	Reverse primer (5'-3')	Accession No.
<i>ctr1</i>	TCAACACACCTGGAGAGA TG	CACCTGGATGACGTGAA GTA	KY646156
<i>ctr2</i>	CAAGGTGTGGAAGAACG TTC	GAACAATGTGCAGTCCT GTC	KY646157
<i>atox1</i>	TGACATGTGAAGGATGCT CT	AGGACCAATATACGTGA CAGT	KY660270
<i>β-actin</i>	GCACAGTAAAGGCGTTGT GA	ACATCTGCTGGAAGGTG GAC	EU161066
<i>elfa</i>	GTCTGGAGATGCTGCCAT TG	AGCCTTCTTCTCAACGC TCT	KU886307
<i>b2m</i>	GCTGATCTGCCATGTGAG TG	TGTCTGACACTGCAGCT GTA	KP938520
<i>hpri</i>	ATGCTTCTGACCTGGAAC GT	TTGCGGTTTCAGTGCTTT GAT	KP938523
<i>rpl7</i>	GGCAAATGTACAGGAGC GAG	GCCTTGTTGAGCTTGAC GAA	KP938522
<i>ubce</i>	TCAAGAAGAGCCAGTGG AGG	TAGGGGTAGTCGATGGG GAA	KP938524
<i>18s rRNA</i>	AGCTCGTAGTTGGATCTC GG	CGGGTATTCAGGCGAGT TTG	KP938527
<i>tbp</i>	AGCAAAGAGTGAGGAGC AGT	ACTGCTGATGGGTGAGA ACA	KP938525
<i>gapdh</i>	TTTCAGCGAGAGAGACCC AG	ATGACTCTCTTGGCACC TCC	KP938521
<i>tuba</i>	TCAAAGCTGGAGTTCTCG GT	AATGGCCTCGTTATCCA CCA	KP938526

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TGTGGAGCGA CTTGTGTGTG GGTGAGAGAG TGCTTGTGAG AGTGTTTGTG TGTAAAGAGT TATGTGGAAA AGAGTGTGTG GAAGAGAGTA TTTGTGTGTG -1259
                                         KLF4
TGATAGAGAG AGTGCACACG TAAGTGTGTG CTTGAACAAA AGACTACACG ATTTATAGTT ATAGAGTTAT AGTTCATGTC GGCCATGTTT GTAGGCCGTG -1159
                                         MRE          MAC1
ATGTTCTCTG TGAAATTGAG TCAAACTGAT ATTTTAAAGT TAATCATTTT TTAGTTCTGT TTAATATTGT ATAGATGTCA TATTACCTGT AACTTGCAAA -1059
GTGACCAATC AGTGTGAGGA ACAGTGTGTG GGTGTGGTG AAGTAAATCC AGTTATGAAG CTGTTTGGAG TTGTTGAGAA GAAAACGGTG TTGTAGCAGA -959
NRF2          CREB1
GCAGGTATAA TTTATTCTCC CTGGTTACCA TACTGTAGTA AACCAGAACAT CGTGTTTATC ATCATATATT AAATAACTCA GATCCAGTCC CACACTCCAG -859
GTTAGCAGGT GTGTAATGTG TGACACAGAC AGCAGCATAA CAGGGCCGTG TTATTAAAC ATTTCCACA GAAGCAGTTT CAGTCATTCT GCTCATACTG -759
                                         NRF2          MAC1
TACATTTAAG TTGTGTGTGT TTTTTGACAC ATTTTATACA CTATCTCAGG GACCTGTGCG TAAGAACTG TTCATTCGAG TATTAC TTCA CGCAAT ATTG -659
                                         MAC1          STAT3          SREBP1
TCTGAACCTA CAGTATTAC ACACGGTATT GACGCCGCTC GGTCCGCGCT GTTTTTTGTG TACTGTCTTT TTTGTATTTT GTGTGTGTC TTGTAACCTT -559
                                         MRE
TTGTCTGAAC TGTCTTGTCT GTCTTGTCTT GCACGTCTCT GTCTTGCCCT GTTGCACCA GGTACACAG TTGCACCTTA TGTATCTAGG ACTACTTACT -459
ATGTCCTTAG CCTGTCTTT GTTTAATGTA GCACCTTGAT CCTGGAGAAA CGTCGTCTCA TTTCACCTTG TACTGTAACA GCTATATATG GTTAAAATGA -359
CAATAAAAGC TTCTTGACTT GACTTGAAAA AGGTTTCTCT GACAGGGGTC AGGAGTAGCG CGACACAGGC ACTGGTCTCA AATCGGTCAT TAACACTTTA -259
                                         AP1
CCAAGCAATA CTAAGTAATT AGAAATGTGT GATAATGATA TAGTCCCTGT CAGATGAATC CTTACATTCC TTCATCAATC AAATAAGGGA AATAAGAGAA -159
AGGAAATAAG AATAGAGTTA CATCGTCTGG CTTAAT CTCA GCCCAGGGA GGGAGAAAG TCACATGAC AGTTTAGTCA CGAGGGATCG TTTTTTTTTT -59
                                         CCAAT-box  SREBP1  SP1          SREBP1
TTAAAGGTCA CCCACACACA AGTCGCTCCA CATCTGCACA CACCCAAGAG CCAAGTTCA TTTCTCGGTG TAAAGTACCG CTTACGTGC GCGCCGCTAG +41
TATA-box          MRE          TSS
CCGTCAGGAC CTCGTC +57

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Figure S1. Nucleotide sequence of yellow catfish *ctr1* promoter. Numbers are relative to the transcription start site (TSS) (+1). The putative transcription factor binding sites are underlined. The highlighted sequences show putative transcription factor binding sites of NRF2 and SREBP1.

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CCCAACGCA ATTAAAAATG TTGAGTTAG TGTGAAAAA CCCTTAAGTT TGACATTTTA TCTTTCTCC TGTAAACAC TATTGTAATG CTGCGTTCAT -1742
GCTACCTAGT AACAGGAGC AGGAGTTATA AACTCAAAAT AGCAAGGAGT ATAGCTGGTG TATTAGATCG AACTAAATAC TGCTGTGATA ATAACGTATC -1642
TAAAACGAAT ACTGTTAGAA ACTAATTTAA AAGTAGAGAA GGGGACTTT AGTCCATTTT TCACTGGGTG TGACCAAGAG GATTTGACGT CACTCTGTAC -1542
                                     KLF4                                     MAC1
TCAGGGAAGG AGCTGGTAGC GCCAATGACT ACCTCAAGAA GCTAGCAGGT CAAAATTACT AGTTAAAGTG AGGTCCACT GTGTGTGTA GTGTGTGTGT -1442
TGTTTTTTTT CAGTAATAGC GCAATTACAT GTTCGCCTCG AAAACAAGAG CACAAAGAAC ATCACCTTGT GATGTCAGTG ACATACTTCT CACAGGAATA -1342
                                     MAC1                                     CREB1
ACAAATGTAC ATCACTAAAA ATGAATTAAA CCCCAAATAG ATGGAAGACA ACATGTTTTT TTTTCAATA TATATTTAAA GCTGTTCAAT CAGAGGCTGG -1242
                                     SP1
ATGTTAATTA ATGTGTTTTT ATTAACATAT TTTACTTCTT GATACTGCCA TGGTCTATA GCTGTGAACA GACTGATGAG GCTCATGGGG CTCAGTTTGT -1142
AATCGAATGA TACTAAATAA AAAATAGTGA TGGATACAAA AGTACCTGAT TTGGACTTT TCCTCAGCAG ACATCATCTG GCCATTTTGA TCAGCAATCT -1042
                                     PPARy                                     SREBP1
CACACAAAAT GCCACTAAGT AGCACACAGC GCAGCAGCAC CATAACGAG CAGCTGAAGC AGGGACTCTT CTCTGCTCTT ACACCTATTT TACCCATTAA -942
AACTAGATTT TTCCCCCTAC TGATCGTGAA AGGAAAACGA CTTTTTTTCC TTCCAAGAGA TCCTGAACGT TCTTTAATTA AAGTACACGT AAACAGTTAA -842
                                     STAT4
AGCATGATAG TAAACCTCCT CCTGTCAGTC AAGGAACAAT TAATAACAA CACGGAATA AACACCACA AGCTTTGAAT AGCCAAATAT TTTAAACGAC -742
TCAACAATTT AGTGTAATTT ACGACAGSTA GATAACAGT ATATCTAACC TCGCCTAAGC TAAACAGAAA GCTAGTTAGT TTAGTCAAGT TTAGCTTCGA -642
GCATGACGT TAGCTTAGTT GCTAAACCGG TAGCCGGCTA AGCTAATAC TTCATAGCTA ACACAAGAAA AGAGAAAAGT CCTTCTTGGA TAAATATTC -542
SREBP1
AGAAAATGTT CCCTGGAGGA GTCAAATTGC CGAAATACTC CATTTCACAC CGTCTCAGA TGTACATATT TTCGTGAAGG CTCATCTAAA CCCAGCGACT -442
STAT3
CCTCGCCGCC TCCTGCTTAA TCAAAACACC AAAATATTCA CATATTTACA TTGACGCCAT CTTTCTTTAC ACTCGACAA GCCGGAAGTA GAATTAATAA -342
SP1                                     AP1
TAATATATAT TTTTATGATT TTTAAACACA CGATAAAGG CATTTTCATG TCACATTACA TTTCATGTCA CATTTTATA TTATTATGTT ATATAAAG -242
ATTTATATAT ATAAAAAAA TAAAAAGTA CTGTATGAGT AACCAATGAC AGCTCAAAAT TGAGTCAGTG TGACGTATTT TAACGGACGA ATCCAAATAT -142
                                     CCAAT-box                                     CREB1
CACTTTAGTG CACTAGGTAG GGTACAGGAG AAGCTTTTGG TTATTCATA CCTGGTAGAG CTAGCTAGG GAGTAGGAA CAATTTGGTT TTTACTGCAT -42
PPARy
TTGCACGTTT ACTTATATAG CTTGTTTCCC TTTGTGAAC CTAGGAG CAGGAGGACA AAGCTGTAGC TGGATTATAT AATAA +43
TATA-box                                     TSS

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Figure S2. Nucleotide sequence of yellow catfish *ctr2* promoter. Numbers are relative to the transcription start site (TSS) (+1). The putative transcription factor binding sites are underlined. The highlighted sequences show putative transcription factor binding sites of SREBP1.

TACAAATATT AACCAAGTATT TATATGACAG TGGGTGGGT CCCTGGTGGT CCAATAGCAG GATCTCACTG CCACAGTCAG GGTTCGATTC CCAGGCAGGG -1725
 SP1
 AACAACTCA GACACTGAGG GGTTCATTGC TGGTCCTTAG GAAGGGAATC CAGCATAAAA CCTGCGCCAA ATTAAATATA GGTGGATCGA ATGATTGCT -1625
 AP1
 GTGGTGAAAG AGGCAAGAGC AATATTCATA TGACAGAAAG TTGGATCAAA ATATATCACA AATCTTATCT AGTATTTTCA AATAAAAAACA GCTCTGTAT -1525
 MAC1
 CAATGCATGA CTTCCCTAAA TGACTCTAAG CATTTACTGA AGGCTATTTA AACATCTACA ATTAACCTGT TGAACATATG GATATACATG TCATCATGAG -1425
 CREB1
 TGATTACAGT ACAATTGTGT TGCTTTTTTC AGGGCGTAAA AGGCATACGT TAACCATGAA ATTGTGCAAG TGAAATTAAA AATTACATAT GTAAAAATATG -1325
 TTATGCAACA GTTAAAAAAT ATGAGGTTTT TTTTGTGTTT GTTTTTTGCC ATGCACTACA AGAAACTGCT GATCACTGTG GCTTCTGAG ACAGCATATA -1225
 NRF2
 AACAGTTTCT TCCATGACTG ACGTTTTTCG CCATGACATA ACTATGTTTA ATGAAAAAAA TCTTCTCTTT CATTCGAAGG ATGATGAATC CAACGCTTTC -1125
 CREB1
 TTTACAGTGA AAACAACAGC ACATTAACAC ATTCAGATCA TTGACCTGCA TATGGTTTAT GTTCTGTGT TTTCAACAT CTACCATCTA CAGTTATTAT -1025
 TATTATACTA TTATTATTAG TTTGAATACG TTCCACAAA ATAATGAGTC GCTCTTATTT CTGAAGGCA TCAGTAAATA AACCGGATCT TACTGTGAAA -925
 AP1
 CCTGCATTGA TTATATCAGA CTTACCAAGG CCGAGAGCAG CTGTAGTCCA ATCTTATTAT GTAACAGTCT TCAAAATATG CAGAAAACTG CACATTTTTA -825
 CATGCATTGT TAATCAGATG TTGTTTTATT AAAACCCCTGA ACGCTGACCA TCTCATTCCA CTACGAGCCC TTGTCTTTTC CTCCTTATGC TTTTCCTGTT -725
 KLF4
 TAGTCTTCTT GTAGCGGTC ACATGAT TTA CTCGGTCAGC TGTGTAACCT ACCAGGGAGC GTCTGTGTAA AACCTGTCAG CTAGTTCAGC GTGCAGATT -625
 SREBP1
 GTTGACTATA TGCTTCCAAA ATACTTCGGA ACTCAAGTGT TTCAGTGGT TTTGGATAAT AAAAAATAAA ACGCAAACGT GTAATGCTGT ACAAATGTGT -525
 GACAACAACA ACAACAACA AAAATGAGTT AAAATGACAT TTATAGTGAA TTGTTTTTAT TGAATCGACT CGTAAATATG GAGGATTGTG TTGTGGTTGT -425
 TGTGTTTTGCC AGTGAAACTA TTTAGAACAT GTTCTTATAC GCAAACAAAC CGCTGTTTCC GCTATAGTTT GTGCTTCTGT GAACCGAATC GTACACAAAG -325
 AP1 NRF2
CGSTGCCAC AGGCAACGGA GCTTCAACGT CATTGGTCAC GTGTTTATG CAGAACGAAT CAAGCGCCTA GGCAGTGTTA CGAATTAAG TGATTTTCT -225
 CCAAT-box SP1 SREBP1
 TCACACAGTA TAAATGATAA CATATAATGT GTCAATTTAT GCCTGAAAAAT ATCTAAAATT ACCGTTTCATC AATAATACTT ATATAATAAG CCTAATATTC -125
 STAT3 TATA-box
 ATGTAAACTA AAACATGTTT CTGTTTTTCAT AAACGCTTTT GAAAAGTTCT GGGAATTTAA CGATCATCCC TAAGTCAG CACTGAGTCAC CGGCTACAGT -25
 STAT4 NRF2
 CAGTTCAAAG TGACAGAGTT TGTTCATCAT TTGTGTGTTT TAGCCGAGTG TCTTTTTTTC TCTTCTT +43
 TSS

Figure S3. Nucleotide sequence of yellow catfish *atox1* promoter. Numbers are relative to the transcription start site (TSS) (+1). The putative transcription factor binding sites are underlined. The highlighted sequences show putative transcription factor binding sites of NRF2 and SREBP1.