Table S1. Primers used for cloning and plasmids construction

|  |  |  |  |
| --- | --- | --- | --- |
| Gene | Name | Forward primer (5'-3') | Reverse primer (5'-3') |
| Primers for RLM-5’RACE |
| *srebp*-1 | RACE-outer | CATGGCTACATGCTGACAGCCTA | CCTCAACACTGCCGACTTATT |
| RACE-inner | CGCGGATCCACAGCCTACTGATGATCAGTCGATG | TGCGTTTCTCGCCTTTATG |
| *accα* | RACE-outer | CATGGCTACATGCTGACAGCCTA | CTCAGACGCCTTCACCATC |
| RACE-inner | CGCGGATCCACAGCCTACTGATGATCAGTCGATG | GTTGTTGTTTGTCCCTCCTG |
| *scd*1 | RACE-outer | CATGGCTACATGCTGACAGCCTA | GTTAATGGTGCTGTCGTAGGG |
| RACE-inner | CGCGGATCCACAGCCTACTGATGATCAGTCGATG | GTCAGGATGTTTACGGACCAA |
| *fas* | RACE-outer | CATGGCTACATGCTGACAGCCTA | TTGAGCACTGTGGCATAGATT |
| RACE-inner | CGCGGATCCACAGCCTACTGATGATCAGTCGATG | ACTGAGGTGTTGGGCTTGA |
| Promoter construct |
| *srebp*-1 | srebp1-1998 | ctatcgataggtaccgagctcGCAACAGTTCTTCTAACCCTAAT | cagtaccggaatgccaagcttACTACCTACTCGCGTTCGTT |
| *accα* | accα-2043 | ctatcgataggtaccgagctcCCAGTGCCTTGAATTTGATT | cagtaccggaatgccaagcttGTGTAGCTCCAGCCTCTTTG |
| *scd*1 | scd1-1632 | ctatcgataggtaccgagctcGGATGAGTGT GTTTCGTGTT GTG | cagtaccggaatgccaagcttGCTTATCTGATGTTCGCTTTCT |
| *fas* | fas-1889 | ctatcgataggtaccgagctcTCTCAAATGCCACTCAAACCA | cagtaccggaatgccaagcttGCAGATCCTTTGGGATAGAGTC |
| Primers for site-mutated construct of promoters |
| *srebp*-1 | srebp1-sre1 | aaataggaggccaacacttgCTTTCTGACTCCCAATTGGTTGC | cgagtgggactctatGACGTCACGTATGTGGCTCCG |
| *accα* | accα-sre1 | AacggtgagtgaccgcAACTGTGGTGTAGTTCATTTATAGCTTATATT | gtgttggcctcctatttcatGTATGTGGCTCCGTGATTACATCA |
| *scd1* | scd1-sre1 | TGggtgtttCCAACATCATGTCATGTCAATATCA | GATGTTGGaaacaccCATTAAAACCTTTGCTCTTATTTCACC |
|  | scd1-sre2 | CGGTGaaagttgagGATTTCCAGTATAAATAAGCGAACCG | ATCctcaactttCACCGGCGAGGAGTTTCTCT |
| *fas* | fas-sre1 | TGacagagaagcagcagCAGGTGTAGGATTCCGCTCCT | ctgctgcttctctgtCATTATGAGGGGCTGGACAGC |
|  | fas-sre2 | GGAGaatctcaacTGTCAGGACAACGCGATGG | GACAgttgagattCTCCTAGCAACACCCTTGCATT |
|  | fas-sre3 | AggttaaaaggCACTGGCTGCGTCTACAGCCCA | GCCAGTGccttttaaccTTCAGAGAAAAAAAAGCGTCTGAA |
|  | fas-sre4 | ggtacaaggagttctatgCATCGAGGATGTCAGACATTTAAATG | atagaactccttgtacctAGTTTGGCTCTTAGGTGCAGTCC |
| Primers for nSREBP-1 cloning and plasmid construct |
|  | nSREBP-1 cloning | TGAATCTGTCTTTTGACGACCCG | CTACTTATCGTCGTCATCCTTGTAATCCAGAGCCATGCGAGAGCG |
|  | nSREBP-1 plasmid | ctagcgtttaaacttaagcttATGAATCTGTCTTTTGACGACCCG | tgctggatatctgcagaattcCTACTTATCGTCGTCATCCTTGTAATC |
| Primers for 3’UTR of *srebp*-1 cloning and plasmid construct |
|  | 3’UTR cloning | CATCAAACTAGGCAGCGGAAC | AAAATCAAATAGAAGACAATA |
|  | pmirGLO-srebp1 | tctagttgtttaaacgagctcCCAACTACACACAACACACACACAC | caggtcgactctagactcgagTATAGGATATACTATGTGTGCGTCTGCA |
| Primers for miR-29 site-mutated construct of pmirGLO-srebp1 |
|  | pmirGLO-srebp1-miR29mut | GTCCAACGatcatgcgAATTGGACACATATTGTAGAGCATTGC | TTcgcatgatCGTTGGACCAGAATCCAGTTTAT |

Table S2 Primers used for Q-PCR analysis

|  |  |  |  |
| --- | --- | --- | --- |
| Gene | Forward primer (5'-3') | Reverse primer (5'-3') | Accession No. |
| Primers for Q-PCR genes of *Homo sapiens* |
| *18s-rRNA* | GTTCAGCCACCCGAGATTGA | TGTGTACAAAGGGCAGGGAC | M10098 |
| *β-actin* | ACCCTGAAGTACCCCATCGA | GAGGCGTACAGGGATAGCAC | NM\_001101 |
| *b2m* | TGCCGCATTTGGATTGGATG | CCCCACCTCTAAGTTGCCAG | NM\_004048 |
| *ef1α* | CATCCAGGCCAAATAAGCGC | CTCAACACACATGGGCTTGC | M29548 |
| *gapdh* | TCAGCCGCATCTTCTTTTGC | TTAAAAGCAGCCCTGGTGAC | NM\_001289745 |
| *hprt* | CCTGGCGTCGTGATTAGTGA | GGCCTCCCATCTCCTTCATC | NM\_000194 |
| Primers for Q-PCR genes of *Ctenopharyngodon idella* |  |
| *18s-rRNA* | GGCGCGCAAATTACCCATT | TCCCGAGATCCAACTACAAGC | EU047719 |
| *β-actin* | ACCCTGAAGTACCCCATCGA | CAGAGGCATACAGGGACAGC | DQ211096 |
| *b2m* | GCACTCGTCTCTTTTGCCCT | TTTCGAAGGCCAGGTCAGTC | AB128864 |
| *ef1α* | CCACCGGCCATCTGATCTAC | GTGTCCAGGGGCATCAATGA | GQ266394 |
| *gapdh* | GGGAAACTGTGGAGGGATGG | TGCAGCCTTGACCACTTTCT | GQ245759 |
| nSREBP-1 | TCACCAATCCTGACCACCTC | GATGCAAGGTGACGCTACTG | KJ162572 |
| *srebp*-1 | GAGTCTTGGGGTTGGATGGA | TGAGACACGTCCAGAGGTTC | KJ162572 |
| *accα* | GTCCTTTGCCAGTTTCCCAG | TCCATCACCACTGCCTTCAT | GU908475 |
| *scd*1 | AGCTCACATGTGGGGAATGA | TACCCTCCTGCAATCCTTGG | AJ243835 |
| *fas* | TTGTGGTCTTCTCCTCGGTC | ACGACACCCACATCTCCAAT | MK111644 |
| Primers for miR-29 of Q-PCR |
| miR-29 | GTGCAGGGTCCGAGGT | CGCCTAGCACCATTTGAAA |  |
| U6 | GGACACGGAAAGGATTGACAG | CGGAGTCTCGTTCGTTATCGG |  |

Table S3. Primers used for electrophoretic mobility-shift assay

|  |  |  |
| --- | --- | --- |
| Primers | Forward primer (5'-3') | Reverse primer (5'-3') |
| srebp1-sre1 | Biotin-probe | Biotin-GTGACGTCATATCACCCCACTCG | Biotin-CGAGTGGGGTGATATGACGTCAC |
| Mutative-competitor | ATGAAATAGGAGGCCAACACTTG | CAAGTGTTGGCCTCCTATTTCAT |
| accα-sre1 | Biotin-probe | Biotin-GCGTCACCTCACCAT | Biotin-ATGGTGAGGTGACGC |
|  | Mutative-competitor | GCGGTCACTCACCGT | ACGGTGAGTGACCGC |
| scd1-sre1 | Biotin-probe | Biotin-ATCTCACCCAACATC | Biotin-GATGTTGGGTGAGAT |
|  | Mutative-competitor | GGTGTTTCCAACATC | GATGTTGGAAACACC |
| scd1-sre2 | Biotin-probe | Biotin-CTCGCCGGTGGGGTGAGCGGATTTC | Biotin-GAAATCCGCTCACCCCACCGGCGAG |
|  | Mutative-competitor | CTCGGACCGACAAACCTCTGAGTTC | GAACTCAGAGGTTTGTCGGTCCGAG |
| fas-sre1 | Biotin-probe | Biotin-ACATCACAGCAGCAG | Biotin-CTGCTGCTGTGATGT |
|  | Mutative-competitor | ACAGAGAAGCAGCAG | CTGCTGCTTCTCTGT |
| fas-sre2 | Biotin-probe | Biotin- CCTGACAGTTGAGATTCTCCT | Biotin- CCTGACAGTTGAGATTCTCCT |
|  | Mutative-competitor | CCTGACGGAATATGGGCTCCT | AGGAGCCCATATTCCGTCAGG |
| fas-sre3 | Biotin-probe | Biotin-GTCAGCCCATGTGGCGTGGC | Biotin-GCCACGCCACATGGGCTGAC |
|  | Mutative-competitor | AGTGATGGGCTGATTTCAGA | TCTGAAATCAGCCCATCACT |
| fas-sre4 | Biotin-probe | Biotin-AGTGATGGGCTGATTTCAGA | Biotin-TCTGAAATCAGCCCATCACT |
| Mutative-competitor | AGGTACAAGGAGTTCTATG | CATAGAACTCCTTGTACCT |



Figure S1. Nucleotide sequence of the promoter region of *srebp-*1gene. +1 denotes the transcription start site (TSS) obtained from RLM-5’RACE experiment. Number on the right of the sequence means the distance to the TSS. The highlighted sequences show putative transcription factor binding sites of *srebp-*1 promoter region. Dotted box presents putative SRE element on MatInpspector, and solid box presents putative SRE element on JASPAR.



Figure S2. Nucleotide sequence of the promoter region of *accα* gene. +1 denotes the transcription start site (TSS) obtained from RLM-5’RACE experiment. Number on the right of the sequence means the distance to the TSS. The highlighted sequences show putative transcription factor binding sites of *accα* promoter region. Dotted box presents putative SRE element on MatInpspector, and solid box presents putative SRE element on JASPAR.



Figure S3. Nucleotide sequence of the promoter region of *scd*1gene. +1 denotes the transcription start site (TSS) obtained from RLM-5’RACE experiment. Number on the right of the sequence means the distance to the TSS. The highlighted sequences show putative transcription factor binding sites of *scd*1 promoter region. Dotted box presents putative SRE element on MatInpspector, and solid box presents putative SRE element on JASPAR.



Figure S4. Nucleotide sequence of the promoter region of fas gene. +1 denotes the transcription start site (TSS) obtained from RLM-5’RACE experiment. Number on the right of the sequence means the distance to the TSS. The highlighted sequences show putative transcription factor binding sites of fas promoter region. Dotted box presents putative SRE element on MatInpspector, and solid box presents putative SRE element on JASPAR.