**Supplemental Table 1** Feed formulation and proximate analysis of experimental diets

| | M-Se | A-Se | E-Se |
|---|---|---|---|
| Ingredients (g/kg) | | | |
| Casein | 420 | 420 | 420 |
| Gelatin | 20 | 20 | 20 |
| Fish oil | 30 | 30 | 30 |
| Corn oil | 30 | 30 | 30 |
| Wheat flour | 250 | 250 | 250 |
| Ascorbyl-2-polyphosphate | 10 | 10 | 10 |
| NaCl | 10 | 10 | 10 |
| $Ca(H_2PO_4)_2 \cdot H_2O$ | 10 | 10 | 10 |
| Vitamin premix [1] | 5 | 5 | 5 |
| Mineral premix [1] | 5 | 5 | 5 |
| Betaine | 10 | 10 | 10 |
| Cellulose | 200 | 199.9995 | 199.986 |
| $Na_2SeO_3$ | 0 | 0.0005 | 0.014 |
| *Proximate analysis (*g/kg *dry matter basis)* | | | |
| Moisture | 70.5 | 69.2 | 68.8 |
| Crude protein | 397.5 | 398.2 | 398.8 |
| Lipid | 96.2 | 97.4 | 98.0 |
| Ash | 58.9 | 59.2 | 59.7 |
| Se | 0.00003 | 0.00025 | 0.00639 |

[1] Vitamin premix mg provided/kg diet: retinyl acetate 3; cholecalciferol 0.025; dl-α-tocopheryl acetate 30; menadione nicotinamide bisulfite 7; thiamine hydrochloride 6; riboflavin 3; pyridoxine hydrochloride 12; D-calcium pantothenate 30; niacin 50; biotin 1; folic acid 6; cyanocobalamine 0.03. Trace mineral premix mg provided/kg diet: $Ca(H_2PO_3)_2 \cdot H_2O$, 1000; $FeSO_4 \cdot 7H_2O$ 40; $ZnSO_4 \cdot H_2O$ 100; $MnSO_4 \cdot H_2O$ 40; $CuSO_4 \cdot 5H_2O$ 2; $CaIO_3 \cdot 6H_2O$ 3.

**Supplemental Table 2** Primers used for the analysis of the regions of *selenos,selenom* and *selenon* promoter

| Primers | Forward primer (5'-3') | Reverse primer (5'-3') |
|---|---|---|
| *selenos* pGl3-1236/+75 | ctatcgataggtaccgagctcG TGCTCGCTGATCCA GTCACC | cagtaccggaatgccaagcttGCCT AGAACCCGATAATTTGCT A |
| *selenos* Mut1-SREBP1c | CATCtcgtaagacgATCA TCATCACATCACATC ATCACC | TGATcgtcttacgaGATGTGAT GGTGTAATGCTGATATGT |
| *selenos* Mut2- SREBP1c | CTAAtcgcaaagtgGAC AATTTAAAGGAAAC AGGTGATAAA | TGTCcactttgcgaTTAGTGA GTTTCTCATGCAGAGTCT G |
| *selenos* Mut1-PPARγ | Gtagccatgtctactg CTAT CAGTGTTATCTTATG GAAGTGAAAAC | Gcagtagacatggcta CAGATGT TGTTCTACAAATTTGTTC TACA |
| *selenos* Mut2-PPARγ | GcgcctatgcttagagACAC TGTCACTGTCCATTA TGTAACCA | TctctaagcataggcgCACTGTG TAAGGCAGCTCTTACAG A |
| *selenom* pGl3-521/+83 | ctatcgataggtaccgagctcA GCATCTGACTACAT TTTTTTAGCCT | cagtaccggaatgccaagcttTACT CGCGCACTAAACAGTAC ACA |
| *selenom* Mut-SREBP1c | CGGTtcagatatgaCAAT GAGCCATTTGAGAA TTGGA | ATTGtcatatctgaACCGAAAT CTGTGACCTATCGTATG |
| *selenon* pGl3-1561/+54 | ctatcgataggtaccgagctcA GTACTCGCACCTAC AAATATTAGCC | cagtaccggaatgccaagcttACGT GCCCTACGGAGACATTA A |
| *selenon* Mut-SREBP1c | GAGTTGTtcatatctgaG ATGATGATAAGTTAC CTGTCAATCAAA | CtcagatatgaACAACTCAGG CATTTCATCACTATCA |
| *selenon* Mut-PPARγ | Acatggaagagatgac GTT CACAGGCCTCGGGT CC | Cgtcatctcttccatg TCCAAGG AAACTCGGACACG |
| pcDNA3.1-SREBP1c | ctagcgtttaaacttaagcttAT GGATTACAAGGATG ACGACGA | aacgggccctctagactcgagCTAC AGAGCCATCCGTGAGCG |
| *selenos* biotin-probe-SREBP1c | ACTAAATCACCCAA TGACAA | TTGTCATTGGGTGATTTA GT |
| *selenos* mut-competitor-SREBP1c | ACTAACCGCAAAGT GGACAA | TTGTCCACTTTGCGGTTA GT |
| *selenom* biotin-probe- | TCGGTGTCACACCA | CATTGCTGGTGTGACAC |

| | | |
|---|---|---|
| SREBP1c | GCAATG | CGA |
| *selenom* mut-competitor-SREBP1c | TCGGTCCAGTTATGACAATG | CATTGTCATAACTGGACCGA |
| *selenon* biotin-probe-SREBP1c | GTTGTGTAGTGTGATGATGA | TCATCATCACACTACACAAC |
| *selenon* mut-competitor-SREBP1c | GTTGTCCTGAACTCGGATGA | TCATCCGAGTTCAGGACAAC |

**Supplemental Table 3** Primers used for real-time quantitative PCR analysis

| Genes | Forward primer (5'-3') | Reverse primer (5'-3') | Accession no. |
|---|---|---|---|
| *6pgd* | GCTCTGATGTGGCGAGGTGG | CGTAGAAGGACAGTGCAGTGG | JX992745 |
| *g6pd* | CAGGAATGAACGCTGGGATG | TCTGCTACGGTAGGTCAGGTCC | JX992744 |
| *fas* | AACTAAAGGCTGCTGGTTGCTA | CACCTTCCCGTCACAAACCTC | JN579124 |
| *accα* | GGGGTTTTCACGCTGCTTC | GGTTCTGATTGGGTCGTCCTG | JX992746 |
| *dgat1* | CACGCTGACCTCTATGACCC | CTGATCTCCCGGCACCATTT | XM_027155099.1 |
| *dgat2* | ACATCTTCGGTTATCATCCTCACG | ACGATGACCACAGCGTTTCC | XM_027158632.1 |
| *gpat3* | AACTGGAGCTGAGCCCTATGT | TGTAGAAGCCCTTGAGTGAGATG | XM_027139963.1 |
| *atgl* | CACTGGTGGCTGGATAAGCA | AGACCGGAGATCTGAGCCAT | XM_027151136.1 |
| *srebp1c* | CTGGGTCATCGCTTCTTTGTG | TCCTTCGTTGGAGCTTTTGTCT | JX992742 |
| *pparα* | AGGCTTCCACTATGGTGTGC | TGGCACTTGTTCCGGTTCTT | KF614122.1 |
| *grp78* | GCTCCACTCGTATCCCCAA | TCCGTAAGCCACAGCCTCA | KM114873 |
| *crt* | CACCCACCTGTACACGCTAA | TGGGGGCAAAAAGTCCCAAT | XM_027166562.1 |
| *perk* | GCTGGTTGGAGGAAAATCGC | GGTCTCCTCCTCTCCCCAAT | XM_027142084.1 |
| *eif2α* | AGGATGTGGTGATGGTGAA | CGATGCGGATAAGTTTGTT | KR231690.1 |
| *atf4* | AGTGGATGCGTTTTCAGG | TGATGGGAATGGGAGTGG | KY963823 |
| *ddit3* | ACTGTCCCAAACTCATCCCC | ACTTCCTTCCCGTAACCCCT | MG685920 |
| *ire1a* | CCTACTTCACATCCCGCTT | AGTTCGCTTGACTTTGCTC | KP687345 |
| *xbp1* | GGTGGAAGTGGAAACCGTCT | GACCGCGATAGAGTCGTTGT | XM_027162925.1 |
| *insig1* | TGCCAAGCTGGACTTTGTGA | CGTAGCCCAACTGAGGAGAC | KR231693.1 |
| *ip3r1* | ACGCCCCTTTCCGCCATAT | CCACCTCAAACCGTGACAACA | XM_027160476.1 |

| | | | |
|---|---|---|---|
| *ip3r2* | TCGCGGTAGCCATAAGCA | AGAAGAACTCGTGGACAAACAGA | XM_027161418.1 |
| *ip3r3* | ATGTCCTACGCAAACCCTCAA | CATCCGTGGGAACCAATCC | XM_027166762.1 |
| *ryr2* | AGCGGTAAGGGATGACAATAAG | TTTCGTCCAGAAGAGCATAAGG | XM_027132735.1 |
| *gpx1* | CTCTCTGAGGCATGACGGTC | CCCAGGACGCACATACTTCA | MN062284 |
| *gpx2* | TTGAAGCACGTACGACCAGG | AGACAGGATGCACGTTAGCC | XM_027172340.1 |
| *gpx3* | ATCTGGGTCTCTGTCCTGCT | TGACGGAAGGGAATGTGCAA | MN062285 |
| *gpx4* | CTTGGGCAGAGCAATGTGTG | CTGCTCAGTGTACGTGGTGT | MN062286 |
| *gpx6* | ATCACTGCTGATGGGTTGCC | GGAGTGCAGCTACGTCTCTC | XM_027132802.1 |
| *gpx7* | GTGGATCGGTCTCCTTGGTG | TGGCCGAACTGATTACAGGG | XM_027139892.1 |
| *gpx8* | TCACTTCACCGTGTTGGCTT | TCCACCTCTGACCCCATGAT | XM_027140322.1 |
| *txnrd2* | GGCACTACATGGGGTATCGG | ACTCTGTGGCCCCAATTCAG | MN062290 |
| *txnrd3* | AGACAAGGCTGGGGTGATTG | GACCGCAGCTACCATACTCC | MN062291 |
| *dio2* | TCTCTCTGGAAGTCGCCTGA | CGAAGTGCAATGCTCGGTTT | XM_027157036.1 |
| *msrb1* | TCTGAATGACGGACCCAAGC | ACTCTACTGTCCATCTGCCTCT | XM_027141750.1 |
| *selenof* | GGCTTTTACCGTTGCTTCAGT | ACCTCCCCAATTTTCATCCA | XM_027150758.1 |
| *selenok* | ACAGTAGGACACAGTCGCCA | GCTTGACGAGGGTCTGAAAGA | XM_027166810.1 |
| *selenom* | GCTGCGTTTCTTCCATGCTT | TCCTCCACAACTCTCCACCT | XM_027145607.1 |
| *selenon* | CCGCATCTGGGCTTTATTC | GCGACGCCTGTGAGTTTCT | XM_027143731.1 |
| *selenos* | TCCGTGGTAATGCGTCAGG | TTTGTCCGTCTTGGGCTTC | XM_027163809.1 |
| *selenot* | CCCTCTGCCTATTTACCGGC | CCAAACAGCATGAACGGGTC | XM_027156829.1 |
| *selenoh* | GCGTGAGGCTCTCTTCTCTG | TTTACGGGGAGGACCCTTCT | XM_027154592.1 |
| *selenoe* | GGGAAAACTGATGGCTC | GCCCAATGCTCCATGA | XM_0271 |

| | | | |
|---|---|---|---|
| | CCA | GGAA | 62931.1 |
| *selenoi* | TGGGTTGTCTGTTTGCC | AGGCCTCGTACACAGA | XM_0271 |
| | GTA | GCTA | 45083.1 |
| *selenoo* | GCTTCATGGACCGCTTT | CCAGGTTCCAGCGACA | XM_0271 |
| | GAC | GATT | 61831.1 |
| *selenop* | TGTGGAAGGTCGGTGAT | TTGCTAAGCCTGCATCC | XM_0271 |
| *1* | GTG | TCC | 71023.1 |
| *selenop* | GGGACACGCTACAGGGA | CCTCCACGTACGGATA | XM_0271 |
| *2* | GAT | GTGC | 42616.1 |
| *seleno* | GTACAGGCCCAAGTTCA | TCCCCGTTCTTCTTCGA | MN06228 |
| *w1* | CCA | GTG | 8 |
| *seleno* | AGGTATCTGGCTTCGTTG | ATCGTGGGCTTTCTGGA | XM_0271 |
| *w2a* | GC | TGG | 41504.1 |
| *selenou* | CGTGTACACCCTGCGTC | CTGCAGAGCAGAGAA | XM_0271 |
| | ATT | AGTGC | 41798.1 |
| *sephs2* | GTCCCTGATCCAGACTA | TGTCACAGAAGTGCCT | XM_0271 |
| | CAGATTT | CCCTC | 70772.1 |
| *sbp2* | AGCTTGCGTTATTTGTGT | AGAGGACTGGCTCTGT | XM_0271 |
| | GGT | CGAT | 38387.1 |
| *b2m* | GCTGATCTGCCATGTGA | TGTCTGACACTGCAGC | KP938520 |
| | GTG | TGTA | .1 |
| *gapdh* | GCCTCCTGCACCAC | GGACCATCCACGGT | KP893555 |
| | AAACT | CTTCT | |
| *rpl7* | GCGCCAGATCTTCAATG | CTCATTCTGCCATGACC | KP893557 |
| | GAG | ACG | |
| *tbp* | AGCAAAGAGTGAGGAG | ACTGCTGATGGGTGAG | KP938525 |
| | CAGT | AACA | |
| *18srRN* | TCATTCCGATAACGAAC | GGACATCTAAGGGCAT | KP893562 |
| *A* | GAG | CACA | |
| *elfa* | GTCTGGAGATGCTGCCA | AGCCTTCTTCTCAACG | KU88630 |
| | TTG | CTCT | 7.1 |
| *hprt* | CCTCTCCGACTCACAGC | GTCGCCATCTTCACC | KP893556 |
| | TAG | TCAAC | |
| *ubce* | GCCCGTGGAAGGATTCA | AAGGCAGGTGGAGAGT | KP893560 |
| | AAA | ATGG | |
| *tuba* | CACTTCCCTCTTGCCACC | ACGGTACAGGAGACAA | KP893558 |
| | TA | CAGG | |

Abbreviations: *6pgd*, 6-phosphogluconate dehydrogenase; *accα*, acetyl-CoA carboxylase *α*; *atf4*, activating transcription factor 4; *atgl*, adipose triglyceride lipase; *b2m*, beta-2-microglobulin; *crt*, calreticulin; *ddit3*, DNA damage inducible transcript 3, *dgat*, diacylgycerol acyltransferase; *dio2*, deiodinase 2; *eif2α,* eukaryotic initiation

factor 2*α*; *elfa*, translation elongation factor; *fas*, fatty acid synthase; *g6pd*, glucose 6-phosphate dehydrogenase; *gapdh*, glyceraldehyde-3-phosphate dehydrogenase; *gpat3*, glycerol-3-phosphate acyltransferase 3; *gpx*, glutathione peroxidase; *grp78*, glucose-regulated protein 78; *hprt*, hypoxanthine-guanine phosphoribosyltransferase; *insig1*, insulin-induced gene 1; *ire1α*, inositol-requiring enzyme 1α; *ip3r*, inositol 1,4,5-triphosphate receptor; *msrb1*, methionine sulfoxide reductase b1; *perk*, protein kinase R like endoplasmic reticulum kinase; *pparα*, peroxisome proliferators-activated receptor *α*; *rpl7*, ribosomal protein L7; *ryr2*, ryanodine receptor 2; *sbp2*, SECIS binding protein 2, *selenof*, *k*, *m*, *n*, *s*, *t*, *h*, *e*, *i*, *o*, *p1*, *p2*, *w1*, *w2a*, *u*, selenoprotein f, k, m, n, s, t, h, e, i, o, p1, p2, w1, w2a, u; *sephs2*, selenophosphate synthetase 2; *srebp1c*, sterol regulatory element binding proteins 1c; *tbp*, TATA-box-binding protein; *tuba*, tubulin alpha chain; *txnrd*, thioredoxin reductase; *ubce*, ubiquitin-conjugating enzyme.

**Supplemental Table 4** Correlation between the mRNA levels of ER stress genes and lipogenic genes in the AI of yellow catfish fed diets varying in Se level for 12 wk

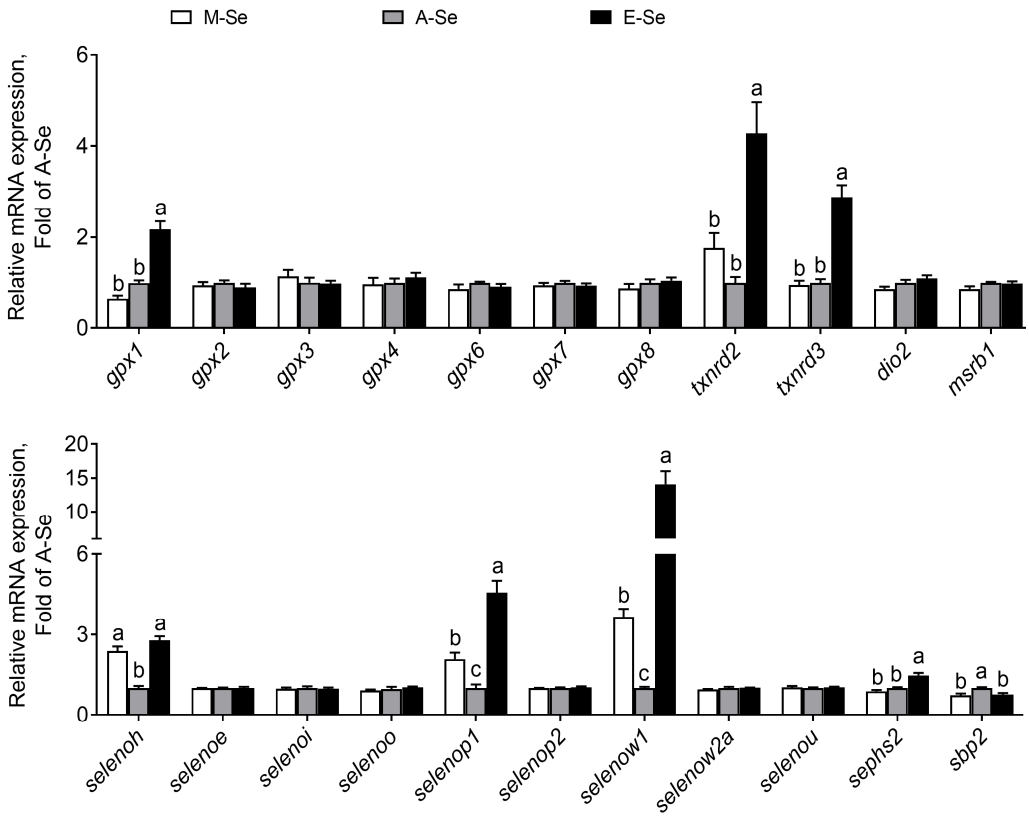
| genes | *6pgd* | *g6pd* | *fas* | *accα* | *dgat1* | *dgat2* | *gpat3* | *srebp1c* |
|---|---|---|---|---|---|---|---|---|
| *grp78* | 0.658 | 0.587 | 0.748* | 0.955** | 0.776* | 0.864** | 0.895** | 0.837** |
| *crt* | 0.762* | 0.226 | 0.918** | 0.737* | 0.468 | 0.395 | 0.655 | 0.839** |
| *perk* | 0.61 | 0.585 | 0.734* | 0.951** | 0.796* | 0.776* | 0.804** | 0.817** |
| *eif2α* | 0.718* | 0.599 | 0.878** | 0.926** | 0.690* | 0.621 | 0.868** | 0.931** |
| *atf4* | 0.746* | 0.513 | 0.790* | 0.990** | 0.886** | 0.837** | 0.787* | 0.838** |
| *ddit3* | 0.353 | 0.313 | 0.295 | 0.581 | 0.752* | 0.442 | 0.141 | 0.248 |
| *ire1α* | 0.21 | 0.317 | 0.364 | 0.5 | 0.382 | 0.487 | 0.672* | 0.544 |
| *xbp1* | 0.734* | 0.509 | 0.838** | 0.962** | 0.839** | 0.690* | 0.760* | 0.871** |
| *insig1* | -0.887** | -0.239 | -0.957** | -.829** | -0.61 | -0.556 | -0.837** | -0.943** |
| *ip3r1* | 0.737* | -0.174 | 0.708* | 0.443 | 0.302 | 0.071 | 0.416 | 0.702* |
| *ip3r2* | 0.793* | 0.213 | 0.503 | 0.536 | 0.745* | 0.48 | 0.199 | 0.404 |
| *ip3r3* | 0.645 | -0.065 | 0.606 | 0.343 | 0.214 | 0.162 | 0.504 | 0.675* |
| *ryr2* | 0.685* | 0.052 | .766* | 0.576 | 0.284 | 0.423 | 0.706* | 0.748* |

Value represents for Pearson correlation coefficient. * $P < 0.05$, ** $P < 0.01$. *6pgd*, 6-phosphogluconate dehydrogenase; *accα*, acetyl-CoA carboxylase *α*; *atf4*, activating transcription factor 4; *crt*, calreticulin; *ddit3*, DNA damage inducible transcript 3, *dgat*, diacylgycerol acyltransferase; *eif2α,* eukaryotic initiation factor 2*α*; *fas*, fatty acid synthase; *g6pd*, glucose 6-phosphate dehydrogenase; *gpat3*, glycerol-3-phosphate acyltransferase 3; *grp78*, glucose-regulated protein 78; *insig1*, insulin-induced gene 1; *ire1α*, inositol-requiring enzyme 1α; *ip3r*, inositol 1,4,5-triphosphate receptor; *perk*, protein kinase R like endoplasmic reticulum kinase; *ryr2*, ryanodine receptor 2; *srebp1c*, sterol regulatory element binding proteins 1c.

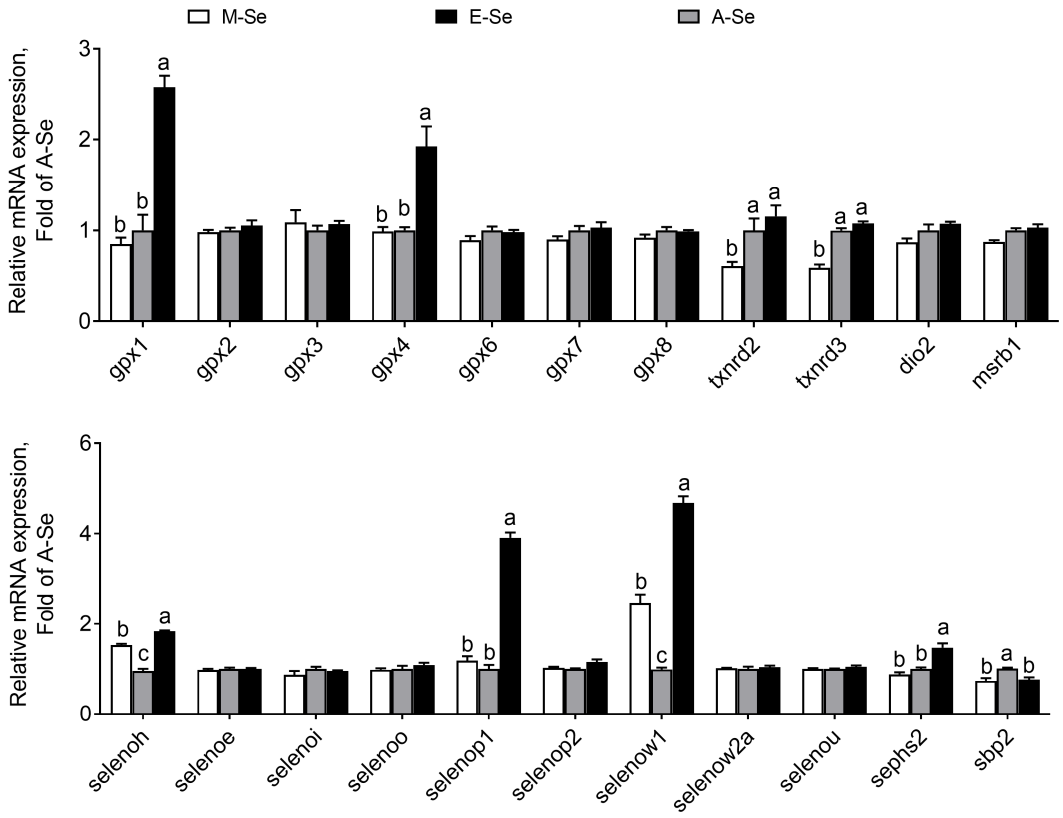
**Supplemental Table 5** Correlation between the mRNA levels of ER stress genes and lipogenic genes in the MI of yellow catfish fed diets varying in Se level for 12 wk

| *genes* | *6pgd* | *g6pd* | *fas* | *accα* | *dgat1* | *dgat2* | *gpat3* | *srebp1c* |
|---|---|---|---|---|---|---|---|---|
| *grp78* | 0.309 | -0.022 | 0.334 | -0.767* | -.727* | -.871** | -0.497 | -0.828** |
| *crt* | 0.109 | -0.103 | 0.184 | -0.794* | -0.688* | -0.894** | -0.525 | -0.709* |
| *perk* | -0.506 | -0.583 | 0.852** | 0.117 | -0.417 | -0.497 | 0.524 | -0.516 |
| *eif2α* | -0.38 | -0.518 | 0.417 | 0.457 | -0.116 | 0.038 | 0.471 | 0.07 |
| *atf4* | -0.352 | -0.219 | 0.177 | 0.837** | 0.591 | 0.644 | 0.737* | 0.481 |
| *ddit3* | 0.201 | -0.009 | -0.185 | 0.633 | 0.765* | 0.780* | 0.382 | 0.627 |
| *ire1α* | 0.202 | 0.322 | 0.296 | 0.015 | 0.185 | -0.111 | 0.018 | -0.057 |
| *xbp1* | -0.009 | 0.265 | -0.227 | 0.523 | 0.654 | 0.585 | 0.231 | 0.850** |
| *insig1* | 0.597 | 0.469 | -0.563 | -0.64 | -0.024 | -0.199 | -0.820** | 0.037 |
| *ip3r1* | -0.445 | -0.599 | 0.903** | 0.109 | -0.41 | -0.489 | 0.58 | -0.504 |
| *ip3r2* | -0.251 | 0.355 | 0.555 | 0.606 | 0.375 | 0.171 | 0.529 | 0.264 |
| *ip3r3* | -0.032 | -0.371 | -0.481 | 0.252 | -0.017 | 0.584 | 0.105 | 0.25 |
| *ryr2* | -0.485 | -0.493 | 0.843** | 0.273 | -0.233 | -0.325 | 0.625 | -0.399 |

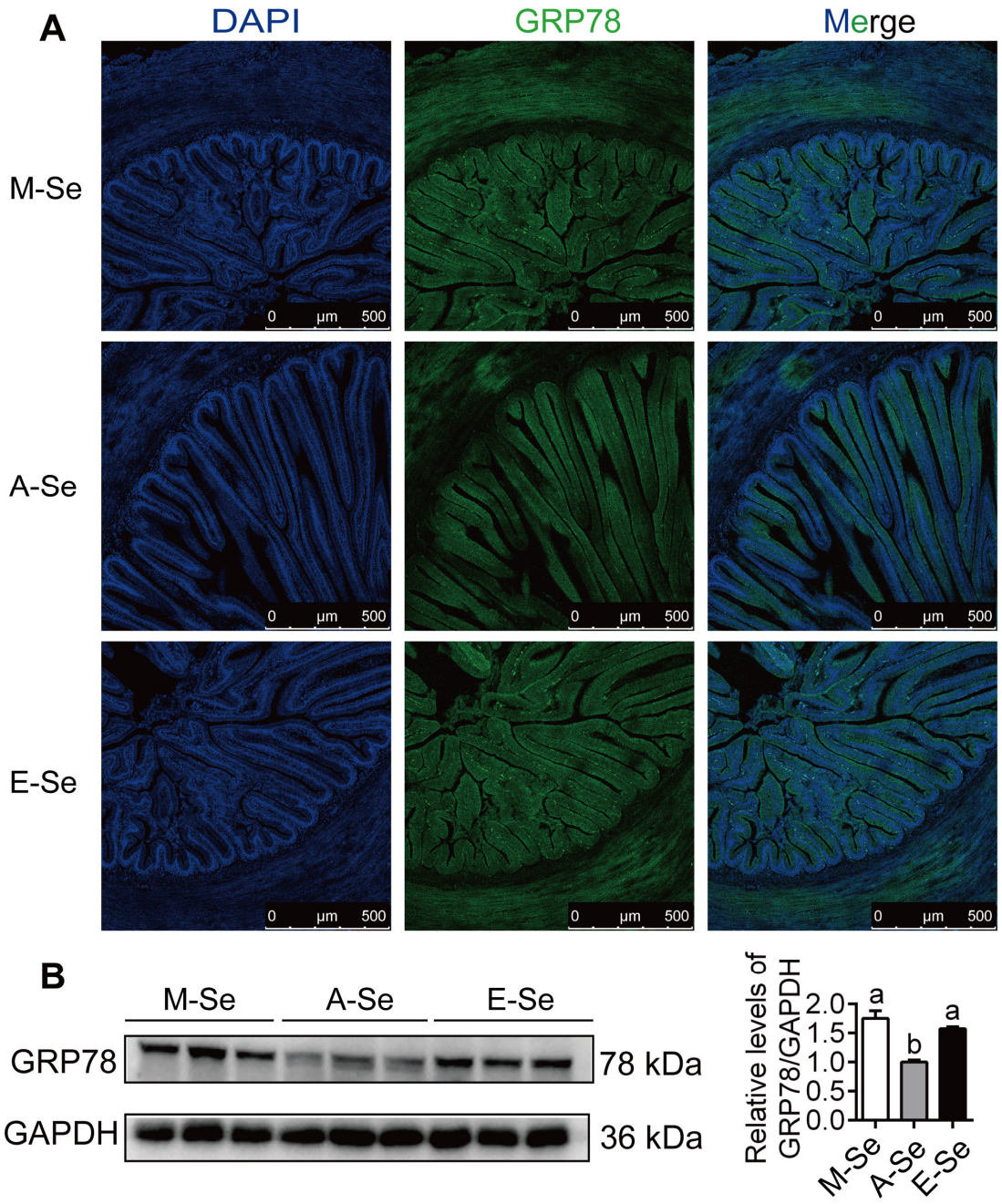
Value represents for Pearson correlation coefficient. * $P < 0.05$, ** $P < 0.01$. *6pgd*, 6-phosphogluconate dehydrogenase; *accα*, acetyl-CoA carboxylase *α*; *atf4*, activating transcription factor 4; *crt*, calreticulin; *ddit3*, DNA damage inducible transcript 3, *dgat*, diacylgycerol acyltransferase; *eif2α,* eukaryotic initiation factor 2*α*; *fas*, fatty acid synthase; *g6pd*, glucose 6-phosphate dehydrogenase; *gpat3*, glycerol-3-phosphate acyltransferase 3; *grp78*, glucose-regulated protein 78; *insig1*, insulin-induced gene 1; *ire1α*, inositol-requiring enzyme 1α; *ip3r*, inositol 1,4,5-triphosphate receptor; *perk*, protein kinase R like endoplasmic reticulum kinase; *ryr2*, ryanodine receptor 2; *srebp1c*, sterol regulatory element binding proteins 1c.




**Supplemental Figure 1** The relative mRNA levels of 22 selenoproteins (excluding six ER-resident selenoproteins) in the AI of yellow catfish fed diets varying in Se level for 12 wk (Expt. 1). AI, anterior intestine; *dio2*, deiodinase 2; *gpx*, glutathione peroxidase; *msrb1*, methionine sulfoxide reductase b1; *sbp2*, SECIS binding protein 2, *selenoh*, *e*, *i*, *o*, *p1*, *p2*, *w1*, *w2a*, *u*, selenoprotein f, k, m, n, s, t, h, e, i, o, p1, p2, w1, w2a, u; *sephs2*, selenophosphate synthetase 2; *txnrd*, thioredoxin reductase




**Supplemental Figure 2** The relative mRNA levels of 22 selenoproteins (excluding six ER-resident selenoproteins) in the MI of yellow catfish fed diets varying in Se level for 12 wk (Expt. 1). *dio2*, deiodinase 2; *gpx*, glutathione peroxidase; MI, middle intestine; *msrb1*, methionine sulfoxide reductase b1; *sbp2*, SECIS binding protein 2, *selenoh*, *e*, *i*, *o*, *p1*, *p2*, *w1*, *w2a*, *u*, selenoprotein f, k, m, n, s, t, h, e, i, o, p1, p2, w1, w2a, u; *sephs2*, selenophosphate synthetase 2; *txnrd*, thioredoxin reductase.




**Supplemental Figure 3** Anterior intestine (AI) GRP78 immunofluorescence (A) and protein expression (B) of yellow catfish fed diets varying in Se level for 12 wk. Values are means ± SEMs, n = 3 (replicates of 3 fish). Labeled means without a common letter differ, $P < 0.05$ (1-factor ANOVA, Duncan post hoc test). DAPI, 4',6-diamidino-2-phenylindole; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; GRP78, glucose regulated protein 78.


**Supplemental Figure 4** Nucleotide sequence of yellow catfish *selenos* promoter. The highlighted sequences indicate the binding sites of putative transcription factors.

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TTCAATCTAA GTACTGGAAC AGAATAAATC AGCACCCCCA GCTCTAGACA AATATGGGTA TGTCTTTTTA TTGTACTGAA CGCATAGGTT TGTTCTATGA  -2001
GTTTGACATA TAAAAATAAA TGCTGAAAAA TAACTAAGAC GTTATATGAT AGCAGAGTAC CCTATTTAAA ATCCTTAAAA TCCTCAAGCA CCATGTCTCC  -1901
CTCTAGAGGA CAAGTTTATG AAGCAATTGA ATCAAAAAGC ATACTGTATA TTTTCTAGTC GACAAAGACC AAATAATTTA ATGCCTTTTA GTAAAAAATG  -1801
TTTTCTGTCG CAAAAGAGTC GAGTCCTTGA GTCGATTCTC CCTAGGTGAC CCTTATGAAT CCAACTATAT AATTTTTACA CTGATGGCCT GTCATTTTTG  -1701
TGCTTAAGTG AATTAGTAGT ATTAATTTAA ACTTTTAATT TTTTAGCATT GATAAAAACA AAATTCCTTC ATTTCTGAAA TCTTAGTAAC GGTTTCAAAT  -1601
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AATCTTGTTG CGAGAACGCG CCAAGCGCCG TGAACGTTAC ATTCAACGCG CGTGCCGTCG TGCTGCAAAG AAACAGTTGC ATGCGCATTG AACTAAAGAC  -1301
TCATTTACAG TACTTAAAAA AACAAAGCTA TTCAAATGCT TTTGCATTCT GTTTTCTTGA TTGCTTTTTT TTAACTACCC TGAAAGTCAT TTATTAATTA  -1201
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GGTGACCGTG CTGTAAGTTT GTTTCTGTTG ACATGAGACC CAAATCCTTT TCAGGATATA CTATAGAGGG TGTTAGGCAT CACCAGAGTG AATATGGAGA  -801
ACATTCAATT CAATTCGGTG TGAAATAGAG GGAGGTAACG GATTCTGATA ACCTGTAATG CCTTATCATA TTTTGTGACC GTGCTGTAAG TTTGTTTAAT  -701
TCAAATTTGT AATAATAATA ATAATAATAA TAATAATAAT AATAATAATA ATAATAATAA TAATAATAAT AATAAGCATC AGCATCTGAC TACATTTTTT  -601
TAGCCTTAAT TAATAAATGA CTTTCAGGGT AGTTAAAAAA AGCAATCAAG AAAACAGAAT GCAAAAGCAT TTGAATAGCT TTGTTTTTTT AAGTACTGTA  -501
AATGAGTCTT TAGTTCAATG CGCATGCAAC TGTTTCTTTG CAGCACGACG GCACGCGCGT TGAATGTAAC GTTCACGGCG CTTGGCGCGT TCTCGCAACA  -401
AGATTTACGC AAGATTTTGC ATTTACTCTG TTACGTAGCG AACGTCTCTA GACGACCTAT TTTAAGCTGC ATTTTAGCCA CAGCGCCCTC TAAGGTCACA  -301
ACATACGATA GGTCACAGAT TTCGGTGTCA CACCAGCAAT GAGCCATTTG AGAATTGGAA GAGTCGACTC TTATTGTTCA GCTGAAAAAT TCTCATCACT  -201
                    SREBP1c
AGCCTGTCGC AGAGATCGAC TGCGCATGCG AGTAATCATC CAATAAGCTT CTAGATCTGA AATTACTCTT GCCTGGTTCC TCCTCCTTAA AGAGGAACTC  -101
G                                                                                                             -1
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**Supplemental Figure 5** Nucleotide sequence of yellow catfish *selenom* promoter. The highlighted sequences indicate the binding sites of putative transcription factors.

TAAAAGACGG TGAGTCTCTT ATTGACATTA ATATTAACTG ACCGCCCAGA AGCCCTGCTC ACTTTTCTTG ATGTAGCTTA GATTCTTTCC ACTCTCCAAA -2001

CAGAGATCCA ACGTAGTCCC CGAGCCGTTC GATTCGACCG CACTATAAAG TGAAAAACAC TCGATCAATG ATGGATTGTC AACCTGCCAA CACACACCAC -1901

TGCTATTAAT ATTGGAGAGG CTTCTCTTTT GATTTGGATT CGCAGGTTGA AGCAGCTGAG AGAGGAGCCG TACACTCAGG CTGAGGCGGA GCGAGCGGCA -1801

GGGATGGGCT CGTACGTCCC TCCTAAAAAA GTCGAGGTGC ACACACAGCA GGTGGAGGAG GACATGGAGT GAACGCTGTA CGTCATCTCG ACACTACTGT -1701

AGCCTGAAGA TCACTTTCAA GCACAGTGTC TCACCCTCCG AGTACTCGCA CCTACAAATA TTAGCCCCCG ACGTGTCCGA GTTTCCTTGG A**TGCCTTTTC** -1601
PPARG

**CCTGAC**GTTC ACAGGCCTCG GGTCCTCAGA AGGTTTACAC ACAAACGTGT ATTCAGGATC CAGATAATTA ACCTCTTGAA TTAAAACCGT GCGTTTTATT -1501

CCTTTTATTT GTGTTGAAGC ACTACAGGGG GTTTGATCAG GTGTCTGATA GTGATGAAAT GCCTGAGTTG T**GTAGTGTGA T**GATGATGAT AAGTTACCTG -1401
SREBP1c

TCAATCAAAT CCCACAGTAA CACACTGATG TGTGTTGGTT TATTGTGTGT TAGGATTTGA CTGGACTGTG ACCACATATG GCTTCATGTG TAAATTCATA -1301

TGTAAATAAA TTGTGAAATC AGAATGTTGT GCACATGCAG TTCTGTAAAA GTGTGTGTGT GTGAGAGAGA GAGAGAGAAG AGAGAGTGTG TGTGTGTGTG -1201

TGAGTGAGAG AGAGAGTGTG TGTGTGAGAG AGAGAGAGAG AGTGTGTGTG TGTGTGCGGC CGGCCCCGAG AGATAGTGTG GGGAGCGAGA GAGTGCCTGT -1101

GTGAGGCGAC CCGATGTGTG GTGTTTAGGC GAGAGCTGTG GCGAGAGCCC GTGTGTGTGT TGTGCCCTCG CCGTGCGTTG TGTGTAGAGT GAGAGAGCCA -1001

GTGTGTGGGT GTGTGTGTGA GTGTGCAGAA GTGCGTGTGA GCGCGCTGTG TGTGGTGCGT GCGCTTCTCG ACGTGCGTGT GGAGCGAGAG AGTGTGTGTG -901

TGTGAGAGAG AGAGAGAGAG AGAGTGTGTC GTTCCTTTGA GAGAGAGTGT GTGTGTTGTG TGTGTGCGTG TGTGAGAGAG AGTGAGTGTG TGTGCGTGTG -801

TGTGAGAGAG AGTGTGTGTG AGAGTGTGTG TGTGTGTGTG TGTGTGTGTG TGCTCTCTTT TCCCTACATT AATAAAACCA GCTGTATTAA AACTAAGACT -701

GTTAACTAGA CGTGTCTCTG GTGATCAAAT ACATTTTAAT GAAGTGTAAA AATGCACATT AAGTACGTGT CTAAGATTAG CCTTAAATTG TAGGTTTAAT -601

TAAAACCCCT AATGGAGCAA CAAAAACTCC CTTTTTATGT AGTCATGAAT ATACAGTAAA CAAACAGTCT AATTCTAACA CCACATGTTT GTTCACTTTG -501

CTTTATTGTG TTTAACTTTA CTGTTTGTTT TATTGGACTC AGTTTATTTT ATTCATAGAA ACGTGCAAAA GTGCTTTTTA ACACTCTGAG TGAATATGAA -401

TCTTACTGAA TCGAAGAGTT GAATCGGGAG CCGAGTCATG CGATGAAGAA AATAAAGCAT TTTGGAAAAC TTTTATATAT CAGTGCACTA AGAATAATCT -301

GCTGTTGTCC TTTGAGGTAA AAAAAAAAAG TTATCGAAAC ACGATTTTTC GTGTAGACGT GCTTATATTA GCACAACAAC AACCCGGTTA TTGAATGAAT -201

CAGTGAGTCG AATCTTTTTG GATGATTCGA AATTAATACC GTTATTTTAA TTTAAAATAA AAAAAAAGGT GTACTGTGGC TTTAAGAGTG AAACCTTTCC -101

T -1

**Supplemental Figure 6** Nucleotide sequence of yellow catfish *selenon* promoter. The highlighted sequences indicate the binding sites of putative transcription factors.