**Supplementary Table S2**. Proteins identified in the E-C+ and the E-C- groups, GO annotations and fold-changes observed in the vitamin C deficient fish (E-C-/E-C+ transition).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Accession number** | **Protein name** | **Gene name** | **Ave E-C+, fmol** | **Fold change** |
| **Glycolysis cycle** |
| Q6DG54 | Pyruvate kinase | pkm2b | 45.29 | \*\*0.43 |
| Q6P043 | Fructose-bisphosphate aldolase | aldoab | 19.00 | \*1.57 |
| Q7ZW73 | Fructose-bisphosphate aldolase | aldob | 39.04 | 0.85 |
| Q803Q7 | Fructose-bisphosphate aldolase | aldoaa | 78.28 | 0.44 |
| Q7SXW7 | Phosphoglucomutase 1 | pgm1 | 23.81 | 0.53 |
| Q7ZV29 | Phosphoglycerate kinase | pgk1 | 27.86 | 0.85 |
| **TCA cycle** |
| Q6PEI6 | Aconitase 2, mitochondrial | aco2 | 10.48 | 1.05 |
| Q7T334 | Malate dehydrogenase | mdh2 | 28.84 | 0.77 |
| Q801E6 | Malate dehydrogenase | mdh1a | 19.01 | 1.13 |
| Q7ZUP6 | Isocitrate dehydrogenase 2 (NADP+), mitochondrial | idh2 | 37.54 | 0.73 |
| B2GTW6 | Citrate synthase | cs | 22.32 | 0.89 |
| **Glutaminolysis** |
| Q6P3L9 | Glutamate dehydrogenase 1 | glud1b | 15.59 | \*2.12 |
| Q7ZVJ4 | L-lactate dehydrogenase | ldha | 24.75 | 1.13 |
| Q803U5 | L-lactate dehydrogenase | ldhba | 13.76 | 0.97 |
| **Structural molecule activity** |
| Q8JIY5 | Glial fibrillary acidic protein | gfap | 1.19 | \*\*27.82 |
| Q90441 | Desmin | desma | 12.24 | 1.62 |
| A8WGN0 | Keratin 8 | krt8 | 36.64 | 1.72 |
| Q9PUB5 | Type II cytokeratin | krt5 | 13.41 | 0.68 |
| Q9PUB6 | Type I cytokeratin | cki | 4.75 | 1.42 |
| Q9PWD8 | Type I cytokeratin | cyt1 | 6.42 | 0.58 |
| Q1LXJ1 | Novel protein similar to type I cytokeratin, enveloping layer | krt17 | 19.37 | 2.34 |
| Q6DHB6 | Zgc:92533 | zgc:92533 | 53.76 | 0.40 |
| **ATP binding (not functional)** |
| Q9PTF5 | Nucleoside diphosphate kinase | nme2b.1 | 28.46 | 1.80 |
| Q7SXL4 | Nucleoside diphosphate kinase | nme2b.2 | 535.05 | 1.11 |
| A0JMC2 | Myhz2 protein (Fragment) | myhz2 | 2.44 | 0.73 |
| A2BGX8 | Novel protein similar to myosin heavy chain 4 (Myhc4) (Fragment) | CH211-251M3.3-001 | 4.93 | 2.95 |
| A7E2L9 | LOC100002040 protein (Fragment) | myhb | 1.93 | \*5.96 |
| A8WBZ8 | Slow myosin heavy chain 3 (Fragment) | smyhc3 | 2.98 | 1.07 |
| B6IDE1 | Slow myosin heavy chain 2 | smyhc2 | 33.18 | 1.23 |
| B8A559 | Novel myosin family protein (Fragment) | CH211-158M24.10-001 | 10.63 | \*5.90 |
| B8A561 | Novel myosin family protein | myhz1.2 | 2.42 | 4.48 |
| O93409 | Myosin light chain 2 | mylz2 | 363.78 | 1.33 |
| Q508P7 | Fast myosin heavy chain 4 | myhc4 | 65.68 | 0.25 |
| Q9I8U7 | Fast skeletal muscle myosin light polypeptide 3 | mylz3 | 89.46 | 1.56 |
| Q7T1B8 | Fast skeletal myosin heavy chain 3 (Fragment) | myhz1.2 | 4.39 | 1.30 |
| Q6P0G6 | Novel protein similar to vertebrate myosin, light chain 6, alkali, smooth muscle and non-muscle (MYL6, zgc:77231) | myl1 | 39.60 | 1.17 |
| Q9PVE1 | Ventricular myosin heavy chain | vmhc | 17.21 | \*\*4.19 |
| A7E2H1 | Zgc:152732 protein (Fragment) | vmhcl | 22.92 | 0.80 |
| A0JMP4 | ATPase, Ca++ transporting, cardiac muscle, fast twitch 1 like | atp2a1l | 29.87 | 0.82 |
| Q08BA1 | ATP synthase subunit alpha | atp5a1 | 42.54 | 0.61 |
| Q4VBK0 | ATP synthase subunit beta | atp5b | 14.01 | 1.26 |
| Q6ZM60 | Novel protein similar to vertebrate ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 (ATP2A2) | atp2a2b | 2.61 | 1.81 |
| Q7ZW18 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2a | atp2a2a | 10.65 | 0.62 |
| Q8UUJ8 | Stress protein HSP70 | hsp70 | 7.19 | 1.74 |
| Q6P3L3 | Heat shock protein 5 | hspa5 | 18.91 | 0.52 |
| Q6PGX4 | Heat shock cognate 71 kDa protein | hsc70 | 21.12 | 1.31 |
| A5WWG8 | Heat shock protein 90kDa alpha (Cytosolic), class B member 1 | hsp90ab1 | 7.55 | \*2.32 |
| A8WG05 | Bactin2 protein | bactin2 | 186.24 | 1.31 |
| Q08BV6 | Novel protein (Zgc:92079) | ckba | 10.83 | 0.15 |
| Q68EH2 | Zgc:91930 | ak1 | 35.98 | 0.51 |
| Q7T306 | Ckmb protein | ckmb | 128.37 | 1.51 |
| Q802Z4 | Zgc:66156 protein (Fragment) | zgc:66156 | 47.02 | 0.86 |
| **Cardiac muscle contraction** |
| A7E2K1 | Tropomyosin alpha-1 chain | tpm1 | 9.10 | 1.04 |
| Q5SPK5 | Alpha-tropomyosin | tpma | 3.78 | 0.94 |
| Q5SPK6 | Alpha-tropomyosin | tpma | 122.33 | 1.53 |
| Q5U3J6 | Tropomyosin 4 | tpm4 | 4.04 | 2.09 |
| Q6P0W3 | Novel protein similar to vertebrate tropomyosin 1 (Alpha) (TPM1, zgc:77592) | tpm3 | 7.72 | 1.41 |
| Q7ZVK9 | Tpm1 protein | tpm1 | 20.75 | 1.24 |
| Q7SXW1 | Zgc:63734 | tpm4b | 28.49 | 0.61 |
| Q7T3F0 | Tropomyosin 4 | tpm4 | 21.16 | 0.99 |
| Q803M1 | Novel protein similar to vertebrate tropomyosin 1 (Alpha) (TPM1, zgc:77592) | tpm3 | 23.85 | 0.40 |
| Q6IQD7 | Zgc:86810 | tpm2 | 18.26 | 0.53 |
| **Monooxygenase activity** |
| A3KNI9 | Ywhab1 protein | ywhaba | 23.26 | 1.29 |
| B8JLJ3 | Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, iota polypeptide | ywhai | 11.79 | 0.55 |
| Q5CZQ1 | Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide 2 | ywhae2 | 15.11 | 1.16 |
| Q6P102 | Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide like | ywhabl | 71.98 | 0.42 |
| Q7ZW20 | Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide 1 | ywhae1 | 22.16 | 0.47 |
| Q803M8 | Tryosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide | ywhaqb | 18.02 | 0.65 |
| **Oxidoreductase activity** |
| B0S7W4 | Aldehyde dehydrogenase 9 family, member A1 like 1 | aldh9a1a | 14.03 | 0.60 |
| Q4KME8 | Vesicle amine transport protein 1 homolog (T californica) | vat1 | 26.08 | 0.71 |
| **DNA binding** |
| A7E2M8 | Histone H2B | zgc:173585 | 67.48 | 1.85 |
| O93584 | Y box binding protein 1 | ybx1 | 12.31 | 0.75 |
| **Calcium ion binding** |
| Q2YDR5 | Actinin, alpha 2 | actn2 | 0.76 | 5.48 |
| Q7SYE2 | Actinin, alpha 4 | actn4 | 22.56 | 3.61 |
| Q8AX99 | Actn3b | actn3b | 44.21 | 0.88 |
| A2BHA3 | Creatine kinase, muscle | ckm | 54.23 | 0.47 |
| D1GJ54 | Actn1 isoform c (Fragment) | actn1 | 5.98 | 2.34 |
| Q804W0 | Parvalbumin 1 | pvalb1 | 198.64 | 0.57 |
| Q7ZT36 | Parvalbumin 3 | pvalb3 | 538.72 | 0.81 |
| Q6IMW7 | Parvalbumin 4 | pvalb4 | 39.32 | 0.39 |
| Q6XG62 | Ictacalcin | icn | 61.70 | 0.73 |
| Q9I8U8 | Fast skeletal muscle troponin C | tnnc | 31.42 | 1.14 |
| **Lipid binding** |
| B2ZHD8 | Fatty acid-binding protein 6 | fabp6 | 18.52 | 1.31 |
| Q66I80 | Fatty acid binding protein 11a | fabp11a | 19.26 | \*0.36 |
| Q9I8N9 | Brain-type fatty acid binding protein | fabp7a | 11.22 | 0.39 |
| A2BGB3 | Apolipoprotein A-I | apoa1 | 13.83 | 1.98 |
| Q567B9 | Apolipoprotein A-IV (Fragment) | apoa4 | 17.21 | 2.72 |
| **Other or unknown activity** |
| A0JMJ1 | Scinderin like a | scinla | 16.08 | 2.22 |
| B0S564 | Novel protein similar to vertebrate procollagen-proline | p4hb | 16.20 | 0.85 |
| B0UYN4 | Novel protein (Zgc:162944) | DKEY-57A22.8 | 4.02 | 2.29 |
| B3DFP9 | Zgc:193613 | apoa2 | 51.57 | \*1.72 |
| B3DG37 | Ba1 protein | ba1 | 50.50 | 1.65 |
| Q1JQ69 | Hbaa1 protein | hbaa1 | 93.74 | 0.69 |
| B7ZVL6 | Putative uncharacterized protein | tnnt3b | 79.49 | 0.58 |
| B8JL43 | Transferrin-a | tfa | 37.09 | 1.32 |
| Q32PU7 | Zgc:123194 | zgc:123194 | 21.88 | 0.96 |
| Q4JIY5 | Elongation factor 1-alpha | ef1a | 15.86 | 2.46 |
| Q503C7 | Phosphorylase | pygma | 31.55 | 0.76 |
| Q5RKM9 | Phosphorylase | pygl | 7.56 | 4.45 |
| Q8UUZ6 | Alpha A crystallin | cryaa | 13.04 | 0.93 |
| Q52JI3 | Beta B3-crystallin | crybb3 | 15.22 | 0.56 |
| Q52JI4 | Beta B2-crystallin | crybb2 | 11.43 | \*1.82 |
| Q5BJ14 | Zgc:110761 | mybpc2b | 24.50 | 1.38 |
| Q5PR62 | Zgc:103458 | tnni1b | 5.50 | 1.89 |
| Q6DHP2 | Troponin I, skeletal, fast 2b.2 | tnni2b.2 | 23.01 | 2.78 |
| Q6DHU6 | Troponin I, skeletal, fast 2a.3 | tnni2a.3 | 50.41 | 0.67 |
| Q6IQ92 | Troponin 1 | tnni1al | 4.48 | 1.27 |
| Q6PBJ8 | Peptidyl-prolyl cis-trans isomerase | fkbp1aa | 22.04 | \*\*0.19 |
| Q6PC53 | Peptidyl-prolyl cis-trans isomerase | ppial | 47.77 | 0.74 |
| Q6TLG8 | Ribosomal protein S3 | rps3 | 6.40 | 1.32 |
| Q7ZUI4 | Thioredoxin | zgc:56493 | 12.73 | 0.81 |
| Q9DDU5 | Glutathione S-transferase pi | gstp1 | 17.87 | 0.69 |

\* p-value<0.05

\*\* p-value<0.01