Supplementary File 1: Biological function, annotation, blast top hit species, contig number and primer sequence of the selected candidate genes

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| Biological function | Annotation | BlastX top hit species  | BlastX *e*value | Contig number | Primer |
| Calcification process | Voltage-gated calcium channel | *Brugia malayi* | 3.9E-13 | Locus\_51519\_Transcript\_1 | F: attggtatgcacggacgaagR: tccattccagttgtctccag |
| Sodium calcium exchanger | *Nematostella vectensis* | 5.7E-31 | transcripts\_v2\_44780 | F: agcaagtcagcccaaatgagR: atccattccagcaccaagac |
| Plasma membrane calcium ATPase | *Stylophora pistillata* | 1.2E-41 | Locus\_55224\_Transcript\_1 | F: gcaacagccatctgttctgR: ctgtccttgttttggcacttc |
| HCO3- exchanger 3 | *Nematostella vectensis* | 1.8E-10 | Locus\_72394\_Transcript\_1 | F: aaagtaccccggtcatttcgR: tcaatcctggaggcatgaac |
| Sodium bicarbonate cotransporter 1 | *Oreochromis mossambicus* | 1.1E-10 | Locus\_38592\_Transcript\_1 | F: accaccataccttgcacagtcR: ttgcatgatagcccagtgac |
| Sodium bicarbonate cotransporter | *Strongylocentrotus purpuratus* | 1.8E-11 | Locus\_62347\_Transcript\_1 | F: atcatggagatccggcaacR: agccctgacgatgattttg |
| Na-dependent Cl/HCO3 exchanger | *Loligo pealei* | 2.7E-41 | Locus\_57537\_Transcript\_1 | F: ggtttgatgggcacaaagacR: aaacggaacggcatgtagtc |
| Sodium bicarbonate cotransporter | *Homo sapiens* | 2.6 E-103 | Locus\_20518\_Transcript\_1 | F: cggcttactccaacgatttcR: caccatcattgccaacagac |
| Sodium bicarbonate cotransporter | *Taenuipygia guttata* | 4.8E-60 | transcripts\_v2\_1213 | F: tggtgaagatgcaggaagtgR: tctgcatcaccaggagtttg |
| Carbonic anhydrase I | *Stylophora pistillata* | 1.2 E-9 | Locus\_42936\_Transcript\_1 | F: aactagccaaggaaaacagatcc R: atcgcagctaaactggcttg |
| Carbonic anhydrase II | *Stylophora pistillata* | 9.3E-113 | transcripts\_v2\_567 | F: tccatagtcttggcacatggR: tccatagtcttggcacatgg |
| Galaxin-like1-like1 | *Acropora millepora* | 1.0 E-8 | Locus\_74336\_Transcript\_1 |

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| F: aagtgctgctacaacagagtgg |
| R: acttgtgagtccacggattg |

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| Galaxin-like1-like2 | *Acropora millepora* | 3.0E-16 | transcripts\_v2\_46613 |

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| F: atatgcatcttgccctcgtc |
| R: tacgcagtattccgtggatg |

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| Galaxin-like | *Galaxea fascicularis* | 4.3 E-4 | Locus\_74019\_Transcript\_1 |

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| F: cgacgcaaagtttgatatgtg |
| R: agacgatgttaccaccacagc |

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| Bone morphogenetic protein 1 | *Branchostoma floridae* | 4.6 E-6 | Locus\_69171\_Transcript\_1 | F: tcgttttcacctgctaccaa R: cccaattttcccgacaacta |
| Bone morphogenetic protein 7 | *Nematostella vectensis* | 3.2E-10 | Locus\_21318\_Transcript\_1 | F: tggaactaaacgcctcaagcR: gtcagtttctgttcgccatc |
| Photosynthesis | Light-harvesting protein | *Symbiodinium sp* | 1.4 E-26 | Locus\_72480\_Transcript\_1 | F: catggacgtgtctccatgttR: cacgtcggtgaacttgatct |
| Plasma membrane proton efflux p-type ATPase-like | *Aureococcus anophagefferens* | 3.6 E-14 | Locus\_68104\_Transcript\_1 | F: cagccacttgatggtcgtaaR: ctctcggcgtatcttcaagc |
| Photosystem II protein L | *Heterocapsa triquetra* | 2.7 E-17 | Locus\_64216\_Transcript\_1 | F: gagaacagcaccgagaggacR: actggcaacagcttggagat |
| Photosystem I subunit IV | *Heterocapsa triquetra* | 1.2 E-25 | Locus\_62203\_Transcript\_1 | F: cttcgacccgagtcctactgR: caaagccatttgtgttcacg |
| Photosystem I subunit XI | *Heterocapsa triquetra* | 1.2E-104 | transcripts\_v2\_34789 | F: gtggtgcaggagaaggagagR: ccatacacctccgcaaaagt |
| Photosystem I subunit III | *Symbiodinium sp* | 4.7E-61 | Locus\_56575\_Transcript\_1 | F: cacattccactcacctgtggR: aagaaggttgcccagatcaa |
| Photosystem II cp43 protein | *Symbiodinium sp* | 9.6E-44 | transcripts\_v2\_6035 | F: cttgagaggcttctgctgctR: tcagccgtagctttatgtgc |
| Photosystem I P700 chlorophyll a apoprotein A2 | *Akashiwo sanquinea* | 3.6E-22 | transcripts\_v2\_26768 | F: aattcgcggttattctgcacR: cctgccagtaacctctccaa |
| Glycolysis | Hexokinase | *Nematostella vectensis* | 3.1 E-10 | Locus\_9609\_Transcript\_1 | F: aggttttgcagcgagtttgtR: aggcttccatcaacagcaat |
| Aldolase | *Nematostella vectensis* | 4.6E-141 | Locus\_6992\_Transcript\_1 | F: acgagtgactgagcgaggttR: atagtgcccgtgctttcatc |
| Glyceraldehyde-3-phosphate dehydrogenase | *Nematostella vectensis* | 8.6E-147 | transcripts\_v2\_13354 | F: cgcttgaagacaccaactgaR: ccagctttggcatcaaaaat |
| Enolase | *Nematostella vectensis* | 0.0E0 | transcripts\_v2\_65585 | F: atttgcaaagcaggagcagtR: tttattcccagcatggcttc |
| Krebbs cycle | Citrate synthase | *Nematostella vectensis* | 6.7E-178 | transcripts\_v2\_34322 | F: acaaggtgggtggtatgagcR: cagtggatccaggcaaagat |
| Aconitate hydratase | *Nematostella vectensis* | 2.4E-103 | Locus\_3922\_Transcript\_1 | F: gtttggccagtcttcagctcR: cagggtgttagagcggtgat |
| Isocitrate dehydrogenase | *Nematostella vectensis* | 1.7E-170 | transcripts\_v2\_70609 | F: gtcgtcaatggaccaggagtR: gtgacacctccagtccctgt |
| Oxoglutarate dehydrogenase | *Anolis carolinensis* | 0.0E0 | Locus\_409\_Transcript\_1 | F: ggactttcagccatcgtcatR: catgctgaaaccaagctcaa |
| ATP-citrate synthase | *Nematostella vectensis* | 1.6E-25 | Locus\_29110\_Transcript\_1 | F: ctcctccaacacccatgtctR: caaaccctcctcattcatgtc |
| Succinate dehydrogenase | *Mus musculus* | 1.4E-18 | Locus\_26352\_Transcript\_1 | F: aaattcccttggccacttttR: tggactgggctctagcagtt |
| Fumarase | *Nematostella vectensis* | 1.9E-39 | Locus\_6324\_Transcript\_1 | F: tcaagtcatgggcaatcaaaR: tacacaggcatctcccatca |
| Malate dehydrogenase | *Nematostella vectensis* | 5.3E-131 | Locus\_5898\_Transcript\_1 | F: gccatttggctttgtacgatR: ggactcctgcagggataaca |
| Oxidative phosphorylation | NADH dehydrogenase | *Nematostella vectensis* | 2.3E-16 | Locus\_46943\_Transcript\_1 | F: gacgaaggaaagcaagcaacR: cggcaataaccaaattcctg |
| Succinate dehydrogenase | *Mus musculus* | 1.4E-18 | Locus\_26352\_Transcript\_1 | F: aaattcccttggccacttttR: tggactgggctctagcagtt |
| Ubiquinol-cytochrome C reductase complex | *Nematostella vectensis* | 1.8E-93 | Locus\_8844\_Transcript\_2 | F: aatgaatggcgaaagtcaggR: aacatcaccaatggctgaca |
| ATP synthase subunit beta | *Tribolium castaneum* | 0.0E0 | transcripts\_v2\_425 | F: ggtcgagggtagatcaccaaR: agtgtttctggacccacagg |
| Lipolysis and beta oxidation | Triglyceride lipase | *Acropora millepora* | 5.4E-10 | Locus\_27044\_Transcript\_1 | F: ttgaattctccctccatccaR: ggttctggggaagttgatga |
| Acyl-CoA dehydrogenase | *Nematostella vectensis* | 7.8E-30 | Locus\_67964\_Transcript\_1 | F: gatgtgggctgttttggtct R: cagtgcatttggtgtgttga |
| Hydroxyacyl-CoA dehydrogenase/3-Ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein) | *Nematostella vectensis* | 0.0E0 | transcripts\_v2\_23540 | F: gtcaatatgggctggttgctR: ttgcatgcctatcatgtgg |
| Hydroxyacyl-CoA dehydrogenase | *Nematostella vectensis* | 1.1E-107 | transcripts\_v2\_1920 | F: gcaacaagcttgggagaaagR: atgggccaatcagatgtttc |
| Kinase activity | Tyrosine kinase | *Nasonia vitripensis* | 6.5E-8 | Locus\_25628\_Transcript\_1 | F: ctcaaggctggtctattgc R:ttcttcaacaagtccagctc |
| Serine/Threonine-protein kinase H1 | *Nematostella vectensis* | 2.4E-18 | Locus\_62445\_Transcript\_1 | F: atgcgatccaagagttcaccR: tgaagcacgattacattgttca |
| Tyrosine-protein kinase | *Trobolium castaneum* | 1.9E-7 | Locus\_20203\_Transcript\_1 | F: gtcccttcgcgagtagactgR: gggatttttccattcccttt |
| Serine/threonine-proteine kinase TBK1 | *Nematostella vectensis* | 5.0E-8 | transcripts\_v2\_25678 | F: atcgctcaggacaaccaactR: acaccgatgaccagtccttc |