**S4 Table. Key genes associated with stress adaptation for the hydrothermal vent environment in transcriptomes of *Austinograea alayseae*.**

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| --- | --- | --- | --- | --- |
| **Gene category**  | **Unigene ID** | **Annotation** | **Matched Organism** | **E-value** |
| **Hypoxia and Oxidative stress** |
| *Hemocyanin* | AUS|c562859\_g1 | hemocyanin  | *Portunus pelagicus* | 5.93E-81 |
|  | AUS|c562824\_g1 | hemocyanin subunit  | *Callinectes sapidus* | 1.01E-31 |
|  | AUS|c558281\_g2 | hemocyanin subunit 1  | *Metacarcinus magister* | 1.03E-148 |
|  | AUS|c357597\_g1 | hemocyanin 2  | *Pacifastacus leniusculus* | 6.22E-109 |
|  | AUS|c516811\_g1 | hemocyanin subunit 3  | *Metacarcinus magister* | 5.48E-66 |
|  | AUS|c562859\_g3 | hemocyanin subunit 6  | *Eriocheir sinensis* | 0 |
| *Catalase* | AUS|c745874\_g1 | catalase | *Haliotis discus discus* | 1.83E-103 |
|  | AUS|c653336\_g1 | catalase  | *Haliotis discus discus* | 1.19E-40 |
| *Dual oxidase* | AUS|c559068\_g1 | dual oxidase 2  | *Zootermopsis nevadensis* | 0 |
|  | AUS|c807569\_g1 | dual oxidase 2-like | *Strongylocentrotus purpuratus* | 1.27E-08 |
| *GPx* | AUS|c533274\_g1 | glutathione peroxidase | *Metapenaeus ensis* |  |
|  | AUS|c529506\_g1 | glutathione peroxidase | *Procambarus clarkii* |  |
|  | AUS|c543665\_g1 | selenium-dependent glutathione peroxidase | *Scylla paramamosain* |  |
|  | AUS|c523008\_g1 | phospholipid glutathione peroxidase | *Macrophthalmus japonicas* |  |
| *SOD* | AUS|c63709\_g1 | superoxide dismutase, putative | *Ichthyophthirius multifiliis* | 4.55E-62 |
|  | AUS|c574623\_g1 | superoxide dismutase | Aplysia californica | 3.84E-50 |
|  | AUS|c622390\_g1 | extracellular copper-zinc superoxide dismutase | *Portunus trituberculatus* | 4.50E-57 |
|  | AUS|c93835\_g1 | copper/zinc superoxide dismutase CuZnSODb | *Anemonia viridis* | 7.70E-37 |
|  | AUS|c89729\_g1 | copper/zinc superoxide dismutase | *Eriocheir sinensis* | 2.97E-27 |
|  | AUS|c809777\_g1 | superoxide dismutase [Cu-Zn], partial | *Stegodyphus mimosarum* | 7.31E-41 |
|  | AUS|c551942\_g1 | copper zinc superoxide dismutase  | *Callinectes sapidus* | 4.29E-81 |
|  | AUS|c546265\_g1 | copper/zinc superoxide dismutase isoform 2 | *Marsupenaeus japonicus* | 2.08E-66 |
|  | AUS|c791847\_g1 | Cu-Zn superoxide dismutase | *Apostichopus japonicus* | 4.51E-35 |
|  | AUS|c535132\_g1 | extracellular Cu, Zn-superoxide dismutase | *Callinectes sapidus* | 8.61E-64 |
|  | AUS|c594053\_g1 | copper zinc superoxide dismutase  | *Callinectes sapidus* | 7.14E-56 |
|  | AUS|c786861\_g1 | superoxide dismutase [Mn], mitochondrial-like | *Amphimedon queenslandica* | 5.88E-40 |
|  | AUS|c679503\_g1 | superoxide dismutase [Mn], mitochondrial  | *Calypte anna* | 2.21E-34 |
|  | AUS|c577856\_g1 | Mn-superoxide dismutase | *Haliotis rufescens* | 3.00E-45 |
|  | AUS|c755058\_g1 | manganese superoxide dismutase | *Chironomus riparius* | 3.11E-38 |
|  | AUS|c679719\_g1 | manganese superoxide dismutase | *Hypophthalmichthys molitrix* | 1.33E-30 |
|  | AUS|c543594\_g2 | cytoplasmic manganese superoxide dismutase | *Segonzacia mesatlantica* | 0 |
|  | AUS|c59753\_g1 | superoxide dismutase, Fe-Mn family  | *Strigomonas culicis* | 8.47E-43 |
|  | AUS|c17187\_g1 | superoxide dismutase [Fe]-like | *Ceratitis capitata* | 2.14E-76 |
| *Selenoprotein W* | AUS|c676372\_g1 | selenoprotein W | *Astyanax mexicanus* | 8.25E-13 |
|  | AUS|c672387\_g1 | selenoprotein W-like | *Python bivittatus* | 2.41E-08 |
|  | AUS|c800914\_g1 | selenoprotein W-like  | *Python bivittatus* | 2.17E-11 |
|  | AUaS|c586830\_g1 | selenoprotein W2 | *Artemia franciscana* | 4.94E-17 |
|  | AUS|c105444\_g1 | selenoprotein W2 | *Artemia franciscana* | 1.99E-08 |
| *Thioredoxin* | AUS|c210857\_g1 | thioredoxin-like, thioredoxin 1 | *Amphimedon queenslandica* | 3.71E-26 |
|  | AUS|c517941\_g1 | thioredoxin 2  | *Portunus trituberculatus* | 1.02E-67 |
| **Chemical stress** |
| *Metallothionein* | AUS|c525976\_g1 | mt gene for metallothionein (MT-1) | *Cyanagraea praedator* | 9.14E-170 |
|  | AUS|c422670\_g1 | copper-specific metallothionein-2 (MT-Cu) | *Callinectes sapidus* | 8.10E-12 |
|  | AUS|c534743\_g1 | metallothionein (MT-2) | *Haliotis diversicolor supertexta* | 6.35E-06 |
| *Ferritin* | AUS|c31576\_g1 | ferritin 1  | *Eriocheir sinensis* | 2.56E-54 |
|  | AUS|c557662\_g1 | ferritin 2  | *Eriocheir sinensis* | 3.72E-94 |
|  | AUS|c509576\_g1 | ferritin  | *Haliotis discus hannai* | 4.76E-123 |
|  | AUS|c44954\_g1 | ferritin  | *Haliotis rufescens* | 8.12E-123 |
| **Pathogenic microorganism stress** |
| *Prophenoloxidase-activating system* |
| *Serine protease* | AUS|c554340\_g1 | serine protease  | *Fenneropenaeus chinensis* | 2.54E-22 |
|  | AUS|c543493\_g1 | serine protease  | *Scylla paramamosain* | 4.11E-63 |
|  | AUS|c428045\_g1 | serine protease | *Scylla paramamosain* | 1.51E-33 |
|  | AUS|c517161\_g1 | serine protease  | *Penaeus monodon* | 8.11E-39 |
|  | AUS|c515713\_g1 | serine protease like protein  | *Cephonodes hylas* | 3.53E-13 |
|  | AUS|c532579\_g1 | serine protease 1  | *Litopenaeus vannamei* | 6.99E-119 |
|  | AUS|c202394\_g1 | serine protease H51  | *Tribolium castaneum* | 9.70E-13 |
|  | AUS|c470504\_g1 | serine proteinase inhibitor  | *Pacifastacus leniusculus* | 6.71E-17 |
|  | AUS|c795406\_g1 | Kazal-type serine protease inhibitor  | *Pinctada fucata* | 3.07E-06 |
|  | AUS|c520773\_g1 | Kazal-like serine protease inhibitor-like protein  | *Scylla paramamosain* | 3.33E-09 |
| *Pacifastin* | AUS|c747984\_g1 | pacifastin heavy chain precursor | *Scylla paramamosain* | 9.01E-40 |
|  | AUS|c744585\_g1 | pacifastin heavy chain precursor  | *Pacifastacus leniusculus* | 1.84E-123 |
|  | AUS|c610778\_g1 | pacifastin heavy chain  | *Macrobrachium rosenbergii* | 3.74E-46 |
|  | AUS|c562054\_g1 | pacifastin-related serine protease inhibitor  | *Portunus trituberculatus* | 1.36E-129 |
|  | AUS|c533678\_g2 | pacifastin-related serine protease inhibitor  | *Portunus trituberculatus* | 6.46E-06 |
| *Prophenoloxidase* | AUS|c551199\_g1 | prophenoloxidase  | *Cancer pagurus* | 0 |
|  | AUS|c86352\_g1 | prophenoloxidase-activating factor  | *Eriocheir sinensis* | 2.91E-76 |
|  | AUS|c553174\_g3 | prophenoloxidase activating enzyme III | *Callinectes sapidus* | 4.73E-165 |
|  | AUS|c68584\_g1 | prophenoloxidase activating factor serine proteinase | *Scylla serrata* | 3.68E-59 |
|  | AUS|c717233\_g1 | phenoloxidase activating factor | *Portunus trituberculatus* | 2.43E-29 |
| *Serpin* | AUS|c409015\_g1 | serpin B13  | *Ornithorhynchus anatinus* | 8.02E-09 |
| *Antimicrobial peptides* |
| *ALF* | AUS|c570416\_g1 | anti-lipopolysaccharide factor 3 | *Eriocheir sinensis* | 2.23E-56 |
| AUS|c470637\_g1 | anti-lipopolysaccharide factor | *Eriocheir sinensis* | 2.42E-70 |
| AUS|c454934\_g1 | anti-lipopolysaccharide factor | *Portunus trituberculatus* | 1.67 E-8 |
| AUS|c41256\_g1 | anti-lipopolysaccharide factor isoform 3 | *Portunus trituberculatus* | 4.98E-33 |
| AUS|c117300\_g1 | anti-lipopolysaccharide factor isoform 6  | *Portunus trituberculatus* | 1.19E-64 |
| *Crustin* | AUS|c718485\_g1 | crustin | *Scylla tranquebarica* | 5.9E-34 |
| AUS|c541271\_g2 | crustin 3 | *Panulirus japonicus* | 6.27E-16 |
| AUS|c535665\_g1 | crustin-2 | *Eriocheir sinensis* | 6.93E-33 |
| AUS|c521157\_g1 | crustin 2 | *Portunus trituberculatus* | 7.83E-14 |
| AUS|c497789\_g1 | crustin 3  | *Portunus trituberculatus* | 4.65E-23 |
| AUS|c433370\_g1 | crustin-like peptide type 5 | *Marsupenaeus japonicus* | 6.62E-7 |
| AUS|c758128\_g1 | crustin antimicrobial peptide | *Portunus trituberculatus* | 1.45E-48 |