## Supplementary materials

**Table S1. Summary of functional annotation for R. gigas reference transcriptome.** Results of automated annotation of R. gigas transcripts coding protein (n=61,983) against several databases. For each database, name and ID and database description are listed. Three databases (PANTHER, HMAP SFLD and TIGRFAM) for which the annotation was <3% are not included in the Table.

| **Database name (ID)** | **Database description** | **Annotation (%)** |
|---|---|---|
| SwissProt | Protein database | 55.2 |
| INTERPRO | Protein sequence analysis & classification | 57.8 |
| GO | Gene Ontology | 39.4 |
| SUPERFAMILY | Structural and functional annotation for all proteins and genomes | 46.3 |
| PRINTS | Protein families | 83 |
| PFAM | Protein families | 49.4 |
| CDD | Protein conserved domain | 16.9 |
| GENE3 | CATH domain families from 3D-structures | 48.2 |
| SMART | Protein domain | 23.4 |
| PATHWAYS | Metabolic pathways from KEGG, REACTOME and METACYC databases | 9.2 |
| EC NUMBER | KEGG Enzyme commission number | 18.6 |
| PROSITEPATTERNS | Protein database using patterns as motif descriptors | 13.2 |
| PROSITEPROFILES | Protein database using profiles as motif descriptors | 29.6 |

**Table S2: List of R. gigas transcripts encoding enzymes involved in the glutathione metabolism pathway.** Transcripts have been annotated against KEGG pathway database and represent the "expected" enzymes using D. melanogaster as reference organism. Enzymes are ordered following the KEGG hierarchy (3 networks). In each network, the R. gigas transcripts, with protein length (description and bp), annotation E value and top blast hit (NCBI Accession number) are listed**.**

| | **Protein length (complete, I=internal, P=partial)** | **Protein length (bp)** | **Evalue annotation** | **Topblast Accesion #** | |
|---|---|---|---|---|---|
| **Network 1: GSH biosynthesis** | | | | | |
| **3.5.2.9-5-Oxoprolinase** | | | | | |
| TRINITY_DN18491_c0_g1_i1 | complete | 1282 | 0.0 | O14841 | OPLA_HUMAN |
| TRINITY_DN18491_c0_g1_i2 | complete | 850 | 0.0 | P97608 | OPLA_RAT |
| TRINITY_DN18491_c0_g1_i3 | complete | 1282 | 0.0 | O14841 | OPLA_HUMAN |
| **6.3.2.2-Gamma-glutamylcysteine synthetase** | | | | | |
| TRINITY_DN21557_c0_g1_i1 | internal | 553 | 0.0 | P48506 | GSH1_HUMAN |
| TRINITY_DN21557_c1_g1_i1 | complete | 636 | 0.0 | P48506 | GSH1_HUMAN |
| **6.3.2.3-Glutathione synthetase (GSH synthetase)** | | | | | |
| TRINITY_DN14939_c0_g1_i1 | prime_partial | 495 | 2.77e-119 | P35668 | GSHB_XENLA |
| TRINITY_DN19928_c0_g2_i1 | complete | 502 | 1.31e-129 | P35668 | GSHB_XENLA |
| TRINITY_DN19928_c0_g2_i2 | complete | 520 | 2.40e-125 | P35668 | GSHB_XENLA |
| | | | | | |
| **1.11.1.12-Phospholipid hydroperoxide glutathione peroxidase** | | | | | |
| TRINITY_DN18436_c1_g2_i1 | complete | 129 | 1.05e-34 | Q9N2J2 | GPX4_BOVIN |
| TRINITY_DN18436_c1_g2_i3 | complete | 114 | 5.29e-41 | Q9N2J2 | GPX4_BOVIN |
| TRINITY_DN18436_c1_g2_i4 | complete | 120 | 1.00e-39 | Q9N2J2 | GPX4_BOVIN |
| TRINITY_DN18436_c1_g2_i7 | complete | 114 | 1.74e-39 | Q9N2J2 | GPX4_BOVIN |
| **1.11.1.9-Glutathione peroxidase** | | | | | |
| TRINITY_DN19336_c0_g1_i10 | complete | 106 | 9.25e-18 | G9JJU2 | GPX_PROCL |
| TRINITY_DN19336_c0_g1_i4 | 5prime_partial | 127 | 7.13e-22 | G9JJU2 | GPX_PROCL |
| TRINITY_DN19336_c0_g1_i5 | complete | 106 | 9.25e-18 | G9JJU2 | GPX_PROCL |

| | | | | | |
|---|---|---|---|---|---|
| TRINITY_DN19336_c0_g1_i6 | complete | 106 | 2.84e-18 | G9JJU2 | GPX_PROCL |
| TRINITY_DN19336_c0_g1_i7 | complete | 106 | 1.48e-17 | G9JJU2 | GPX_PROCL |
| TRINITY_DN19336_c0_g1_i9 | 5prime_partial | 127 | 5.68e-24 | G9JJU2 | GPX_PROCL |
| TRINITY_DN19336_c0_g1_i3 | 5prime_partial | 147 | 2.06e-25 | G9JJU2 | GPX_PROCL |
| TRINITY_DN21001_c0_g1_i1 | complete | 107 | 9.02e-19 | G9JJU2 | GPX_PROCL |
| TRINITY_DN21001_c0_g1_i10 | complete | 108 | 9.02e-19 | G9JJU2 | GPX_PROCL |
| TRINITY_DN21001_c0_g1_i12 | complete | 108 | 5.89e-19 | G9JJU2 | GPX_PROCL |
| TRINITY_DN21001_c0_g1_i3 | complete | 108 | 5.89e-19 | G9JJU2 | GPX_PROCL |
| TRINITY_DN21001_c0_g1_i4 | complete | 108 | 5.89e-19 | G9JJU2 | GPX_PROCL |
| TRINITY_DN21001_c0_g1_i6 | complete | 108 | 5.29e-19 | G9JJU2 | GPX_PROCL |
| TRINITY_DN21001_c0_g1_i7 | complete | 108 | 5.29e-19 | G9JJU2 | GPX_PROCL |
| TRINITY_DN21001_c0_g1_i8 | 5prime_partial | 108 | 9.45e-19 | G9JJU2 | GPX_PROCL |
| TRINITY_DN21001_c0_g1_i9 | 5prime_partial | 158 | 1.45e-38 | G9JJU2 | GPX_PROCL |
| TRINITY_DN19460_c0_g1_i1 | complete | 147 | 2.50e-41 | Q4AEI2 | GPX1_HYLLA |
| TRINITY_DN19460_c0_g1_i4 | complete | 140 | 1.06e-55 | Q4AEI2 | GPX1_HYLLA |
| TRINITY_DN19460_c0_g1_i5 | complete | 147 | 2.29e-41 | Q4AEI2 | GPX1_HYLLA |
| TRINITY_DN19460_c0_g1_i6 | 3prime_partial | 113 | 1.74e-43 | Q4AEI2 | GPX1_HYLLA |
| TRINITY_DN19460_c0_g1_i8 | complete | 140 | 7.34e-57 | Q4AEI2 | GPX1_HYLLA |
| TRINITY_DN19460_c0_g1_i9 | complete | 140 | 1.02e-55 | Q4AEI2 | GPX1_HYLLA |
| TRINITY_DN15942_c0_g1_i1 | complete | 147 | 2.18e-49 | P11352 | GPX1_MOUSE |
| TRINITY_DN14552_c0_g1_i4 | complete | 140 | 7.38e-54 | A6QLY2 | GPX7_BOVIN |
| **Network 2:Glutathione reduction** | | | | | |
| **1.8.1.7-Glutathione reductase(GR)** | | | | | |
| TRINITY_DN19043_c0_g1_i1 | complete | 507 | 2.28e-173 | P47791 | GSHR_MOUSE |
| **Network 3:NADP+ reduction** | | | | | |
| **1.1.1.42-Isocitrate dehydrogenase [NADP]** | | | | | |
| TRINITY_DN22501_c0_g1_i1 | complete | 737 | 0.0 | P16100 | IDH_AZOVI |
| TRINITY_DN22501_c0_g1_i2 | internal | 112 | 1.97e-33 | P50216 | IDH_CORGL |
| TRINITY_DN22667_c0_g1_i1 | complete | 759 | 0.0 | P16100 | IDH_AZOVI |
| TRINITY_DN22667_c0_g1_i3 | 3prime_partial | 582 | 0.0 | P41561 | IDH2_COLMA |
| TRINITY_DN22667_c0_g1_i2 | 3prime_partial | 416 | 4.19e-147 | P16100 | IDH_AZOVI |

| | | | | | |
|---|---|---|---|---|---|
| **1.1.1.44-6-phosphogluconate dehydrogenase** | | | | | |
| TRINITY_DN14414_c0_g1_i1 | 3prime_partial | 103 | 1.86e-51 | Q9DCD0 | 6PGD_MOUSE |
| TRINITY_DN15592_c0_g1_i1 | internal | 119 | 1.09e-61 | P00349 | 6PGD_SHEEP |
| TRINITY_DN15592_c0_g1_i2 | internal | 112 | 9.87e-56 | P00349 | 6PGD_SHEEP |
| TRINITY_DN15592_c0_g1_i3 | internal | 119 | 3.13e-61 | P00349 | 6PGD_SHEEP |
| TRINITY_DN15592_c0_g1_i4 | internal | 112 | 1.08e-54 | P00349 | 6PGD_SHEEP |
| TRINITY_DN15592_c0_g1_i5 | internal | 119 | 6.97e-61 | P00349 | 6PGD_SHEEP |
| TRINITY_DN23631_c3_g1_i1 | internal | 183 | 2.93e-85 | Q17761 | 6PGD_CAEEL |
| TRINITY_DN23631_c3_g1_i2 | complete | 487 | 0.0 | P52209 | 6PGD_HUMAN |
| TRINITY_DN23631_c3_g1_i3 | complete | 487 | 0.0 | P52209 | 6PGD_HUMAN |
| **1.1.1.49-Glucose-6-phosphate 1-dehydrogenase (G6PD)** | | | | | |
| TRINITY_DN21382_c0_g3_i2 | internal | 184 | 1.37e-96 | Q27638 | G6PD_DROYA |
| TRINITY_DN7346_c0_g1_i1 | internal | 117 | 1.17e-48 | Q27638 | G6PD_DROYA |
| TRINITY_DN21382_c0_g1_i1 | internal | 466 | 0.0 | P12646 | G6PD_DROME |
| TRINITY_DN21382_c0_g1_i2 | internal | 424 | 0.0 | P12646 | G6PD_DROME |
| TRINITY_DN21382_c0_g3_i1 | 5prime_partial | 525 | 0.0 | P12646 | G6PD_DROME |
| TRINITY_DN21382_c0_g3_i3 | 5prime_partial | 525 | 0.0 | P12646 | G6PD_DROME |

**Table S3. List of the R. gigas transcripts encoding antifreeze proteins (AFPs).** Transcripts have been annotated against SwissProtein database. For each R. gigas transcript, transcript ID, protein length (description and bp), annotation E value and top blast hit (NCBI Accession number, organism) are listed.

| Transcripts encoding R. gigas antifreeze proteins | Annotation | Protein length (complete, internal, partial) | Protein length (bp) | Evalue annotation | Topblast Accesion # | |
|---|---|---|---|---|---|---|
| TRINITY_DN19051_c0_g1_i1 | Type-2 ice-structuring protein (Type II antifreeze protein) (AFP) | 5prime_partial | 207 | 2.25e-09 | P05140 | *Hemitripterus americanus* |
| TRINITY_DN20104_c0_g1_i1 | Type-2 ice-structuring protein (Type II antifreeze protein) (AFP) | internal | 229 | 9.87e-16 | Q01758 | *Osmerus mordax* |
| TRINITY_DN20104_c0_g1_i13 | Type-2 ice-structuring protein (Type II antifreeze protein) (AFP) | 3prime_partial | 141 | 1.08e-16 | Q01758 | *Osmerus mordax* |
| TRINITY_DN20104_c0_g1_i3 | Type-2 ice-structuring protein (Type II antifreeze protein) (AFP) | internal | 240 | 4.73e-15 | Q01758 | *Osmerus mordax* |
| TRINITY_DN20104_c0_g1_i5 | Type-2 ice-structuring protein (Type II antifreeze protein) (AFP) | internal | 290 | 5.40e-15 | Q01758 | *Osmerus mordax* |
| TRINITY_DN21643_c1_g1_i1 | Type-2 ice-structuring protein (Type II | internal | 184 | 6.83e-12 | P05140 | *Hemitripterus americanus* |

| | | | | | | |
|---|---|---|---|---|---|---|
| | antifreeze protein) (AFP) | | | | | |
| TRINITY_DN21643_c1_g1_i3 | Type-2 ice-structuring protein (Type II antifreeze protein) (AFP) | internal | 163 | 1.04e-12 | P05140 | *Hemitripterus americanus* |