**Supplementary Table S1. Trinotate report of transcripts used in heatmaps for the enriched gene ontologies of digestion, proteolysis, lipid hydroxylation, and immune response in *Totoaba macdonaldi* juveniles fed with experimental prebiotic diets.**

| **Transcript ID** | **Protein Name** | **Similarity** | **E-value** |
| --- | --- | --- | --- |
| **Digestion** |  |  |  |
| Tmac.NODE\_11622\_length\_1029\_cov\_173421.856855\_g10268\_i0.p1 | Chymotrypsin A, a | 0.87 | E:7.85e-154 |
| Tmac.R728798.p1 | Chymotrypsin A, b | 0.87 | E:7.85e-154 |
| Tmac.TRINITY\_DN12700\_c2\_g1\_i1.p1 | Trypsin-1, a | 0.84 | E:8.81e-114 |
| Tmac.NODE\_26480\_length\_306\_cov\_538452.304833\_g24578\_i0.p1 | Trypsin-1, b | 0.93 | E:5.68e-43 |
| Tmac.TRINITY\_DN12541\_c7\_g3\_i1.p1 | Trypsin-1, c | 0.89 | E:2.75e-37 |
| Tmac.R728796.p2 | Trypsin-1, d | 0.90 | E:1.34e-164 |
| Tmac.TRINITY\_DN12616\_c2\_g1\_i1.p2 | Trypsin-3, a | 0.85 | E:4.38e-63 |
| Tmac.NODE\_12891\_length\_919\_cov\_681.620181\_g11412\_i0.p1 | Trypsin-3, b | 0.70 | E:3.7e-120 |
| **Proteolysis** |  |  |  |
| Tmac.TRINITY\_DN12353\_c1\_g1\_i1.p1 | 72 kDa type IV collagenase | 0.49 | E:0 |
| Tmac.NODE\_3114\_length\_2360\_cov\_21.388291\_g2780\_i0.p1 | Calpain-5, a | 0.58 | E:0 |
| Tmac.R773547.p1 | Calpain-5, b | 0.50 | E:4.94e-67 |
| Tmac.NODE\_2451\_length\_2596\_cov\_9.080500\_g2189\_i0.p1 | Carboxypeptidase E | 0.96 | E:0 |
| Tmac.NODE\_10592\_length\_1123\_cov\_8.339779\_g9348\_i0.p1 | Caspase-3 | 0.36 | E:2.13e-40 |
| Tmac.NODE\_8412\_length\_1361\_cov\_18.538520\_g7418\_i0.p1 | Cathepsin L, a | 0.55 | E:5.27e-122 |
| Tmac.TRINITY\_DN2676\_c0\_g1\_i2.p1 | Cathepsin L, b | 0.55 | E:5.27e-122 |
| Tmac.NODE\_5441\_length\_1815\_cov\_21.768279\_g4806\_i0.p1 | Collagenase 3 | 0.42 | E:1.77e-139 |
| Tmac.NODE\_5949\_length\_1727\_cov\_6.062130\_g5247\_i0.p1 | Disintegrin and metalloproteinase  domain-containing protein 10 | 0.47 | E:1.05e-134 |
| Tmac.NODE\_8925\_length\_1299\_cov\_16.238510\_g7877\_i0.p1 | Mast cell protease 1A | 0.47 | E:2.13e-59 |
| Tmac.J731958.p1 | Matrix metalloproteinase-9 | 0.55 | E:1.12e-69 |
| Tmac.TRINITY\_DN12172\_c4\_g3\_i1.p1 | Polyserase-2 | 0.34 | E:1.62e-70 |
| Tmac.TRINITY\_DN14625\_c0\_g1\_i1.p1 | Procollagen C-endopeptidase enhancer 1 | 0.57 | E:1.2e-110 |
| Tmac.NODE\_9022\_length\_1288\_cov\_104.575540\_g7964\_i0.p1 | Serine protease 27, a | 0.45 | E:7.75e-69 |
| Tmac.NODE\_5434\_length\_1816\_cov\_17.679595\_g4801\_i0.p1 | Serine protease 27, b | 0.42 | E:2.37e-62 |
| Tmac.NODE\_6330\_length\_1662\_cov\_12.095385\_g5590\_i0.p1 | Serine protease 27, c | 0.41 | E:7.91e-55 |
| Tmac.NODE\_6555\_length\_1625\_cov\_4.666877\_g5784\_i0.p1 | Serine protease HTRA1A | 0.81 | E:0 |
| Tmac.NODE\_5066\_length\_1886\_cov\_9.503515\_g4490\_i0.p1 | Sonic hedgehog protein A | 0.78 | E:0 |
| Tmac.NODE\_3620\_length\_2222\_cov\_16.778490\_g3211\_i0.p1 | Suppressor of tumorigenicity 14 protein, a | 0.55 | E:0 |
| Tmac.NODE\_7220\_length\_1525\_cov\_5.366263\_g6362\_i0.p1 | Suppressor of tumorigenicity 14 protein, b | 0.56 | E:3.13e-130 |
| Tmac.NODE\_2867\_length\_2448\_cov\_10.731232\_g2561\_i0.p1 | Transmembrane protease serine 13 | 0.40 | E:1e-35 |
| Tmac.NODE\_2363\_length\_2627\_cov\_7.336293\_g2113\_i0.p1 | Urokinase-type plasminogen activator | 0.41 | E:1.2e-93 |
| **Lipid Hydroxylation** |  |  |  |
| Tmac.NODE\_22628\_length\_402\_cov\_50.789041\_g20730\_i0.p1 | Cytochrome P450 2M1 | 0.50 | E:2.76e-06 |
| Tmac.NODE\_2612\_length\_2536\_cov\_18.096439\_g2331\_i0.p1 | Cytochrome P450 2K1 | 0.61 | E:0 |
| Tmac.NODE\_3512\_length\_2247\_cov\_63.409955\_g3118\_i0.p1 | Cytochrome P450 2K1 | 0.70 | E:0 |
| Tmac.NODE\_4052\_length\_2109\_cov\_68.261583\_g3118\_i1.p1 | Cytochrome P450 2K1 | 0.70 | E:0 |
| Tmac.NODE\_7075\_length\_1546\_cov\_2095.720345\_g6232\_i0.p1 | Cytochrome P450 2K1 | 0.77 | E:1.1e-123 |
| Tmac.TRINITY\_DN12603\_c1\_g1\_i1.p1 | Cytochrome P450 2K1 | 0.69 | E:0 |
| Tmac.TRINITY\_DN12603\_c1\_g1\_i5.p1 | Cytochrome P450 2K1 | 0.70 | E:0 |
| Tmac.TRINITY\_DN12603\_c1\_g1\_i6.p1 | Cytochrome P450 2K1 | 0.71 | E:0 |
| **Immune Response** |  |  |  |
| Tmac.R729490.p1 | Complement C3, a | 0.60 | E:0 |
| Tmac.NODE\_1083\_length\_3372\_cov\_476.333133\_g64\_i4.p1 | Complement C3, b | 0.60 | E:0 |
| Tmac.NODE\_935\_length\_3486\_cov\_392.088141\_g850\_i0.p1 | Complement factor B | 0.43 | E:9.88e-23 |
| Tmac.TRINITY\_DN12608\_c10\_g1\_i2.p1 | Complement factor H | 0.32 | E:3.47e-60 |
| Tmac.NODE\_3531\_length\_2243\_cov\_216.176791\_g3135\_i0.p1 | Early growth response protein 1, a | 0.54 | E:4.58e-89 |
| Tmac.NODE\_4109\_length\_2097\_cov\_193.091262\_g3135\_i1.p1 | Early growth response protein 1, b | 0.67 | E:1.62e-81 |
| Tmac.J735183.p1 | Early growth response protein 1, c | 0.53 | E:1.52e-21 |
| Tmac.NODE\_4617\_length\_1974\_cov\_272.224058\_g4095\_i0.p1 | Ig heavy chain Mem5 | 0.43 | E:1.46e-44 |
| Tmac.R735652.p1 | Immunoglobulin gamma-1 heavy chain | 0.44 | E:2.14e-35 |
| Tmac.TRINITY\_DN12087\_c1\_g1\_i6.p1 | Immunoglobulin kappa light chain | 0.44 | E:4.63e-34 |
| Tmac.NODE\_11821\_length\_1011\_cov\_571.072895\_g7850\_i2.p1 | Immunoglobulin lambda-1 light chain, a | 0.46 | E:2.3e-39 |
| Tmac.NODE\_9498\_length\_1237\_cov\_503.171667\_g7850\_i1.p1 | Immunoglobulin lambda-1 light chain, b | 0.44 | E:2.81e-43 |
| Tmac.NODE\_16427\_length\_674\_cov\_134.356358\_g14677\_i0.p1 | Immunoglobulin mu heavy chain | 0.33 | E:2.3e-30 |
| Tmac.NODE\_147\_length\_5137\_cov\_11.629020\_g140\_i0.p1 | Integrin alpha-4, a | 0.45 | E:0 |
| Tmac.TRINITY\_DN12469\_c3\_g1\_i2.p1 | Integrin alpha-4, b | 0.45 | E:0 |
| Tmac.TRINITY\_DN12443\_c4\_g7\_i2.p1 | Nephronectin, a | 0.71 | E:1.63e-148 |
| Tmac.TRINITY\_DN12443\_c4\_g7\_i3.p1 | Nephronectin, b | 0.67 | E:3.17e-144 |
| Tmac.NODE\_5427\_length\_1817\_cov\_8.530899\_g4795\_i0.p1 | Tyrosine-protein kinase Tec | 0.71 | E:3.12e-139 |