Supplementary Table S2. Complete gene ontology (GO) enrichment report for differentially expressed genes (DEGs) detected in the liver of *Totoaba macdonaldi* juveniles, including all the treatments together. Annotated: indicates the number of transcripts from the reference transcriptome included in each GO category. Significant: indicates the number of DEGs detected in each GO category. Expected: indicates the number of DEGs per category expected by the Fisher Exact Test. The P-values from the Fisher Exact Test were adjusted after Benjamini-Hochberg procedure (BH).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| GO.ID | Term | Annotated | Significant | Expected | BH adjusted P-value |
| GO:0007586 | digestion | 111 | 46 | 13.88 | 0 |
| GO:0061436 | establishment of skin barrier | 49 | 29 | 6.13 | 0 |
| GO:0006508 | proteolysis | 1925 | 279 | 240.72 | 0 |
| GO:0098609 | cell-cell adhesion | 800 | 165 | 100.04 | 0 |
| GO:0030198 | extracellular matrix organization | 380 | 104 | 47.52 | 0.000005 |
| GO:0043049 | otic placode formation | 19 | 13 | 2.38 | 0.000054 |
| GO:0007155 | cell adhesion | 1592 | 329 | 199.08 | 0.000058 |
| GO:0014021 | secondary neural tube formation | 8 | 8 | 1 | 0.000104 |
| GO:0070268 | cornification | 49 | 21 | 6.13 | 0.000187 |
| GO:0033564 | anterior/posterior axon guidance | 13 | 11 | 1.63 | 0.000449 |
| GO:0098968 | neurotransmitter receptor transport postsynaptic membrane to endosome | 9 | 8 | 1.13 | 0.0006 |
| GO:0021902 | commitment of neuronal cell to specific neuron type in forebrain | 14 | 10 | 1.75 | 0.000667 |
| GO:0031069 | hair follicle morphogenesis | 27 | 14 | 3.38 | 0.000908 |
| GO:0009887 | animal organ morphogenesis | 1147 | 237 | 143.43 | 0.000908 |
| GO:0048252 | lauric acid metabolic process | 12 | 9 | 1.5 | 0.000908 |
| GO:0002933 | lipid hydroxylation | 12 | 9 | 1.5 | 0.000908 |
| GO:0050904 | diapedesis | 12 | 9 | 1.5 | 0.000908 |
| GO:0001736 | establishment of planar polarity | 86 | 19 | 10.75 | 0.000936 |
| GO:0070293 | renal absorption | 34 | 16 | 4.25 | 0.001108 |
| GO:1905123 | regulation of glucosylceramidase activity | 10 | 8 | 1.25 | 0.001404 |
| GO:0015917 | aminophospholipid transport | 10 | 8 | 1.25 | 0.001404 |
| GO:0097475 | motor neuron migration | 25 | 13 | 3.13 | 0.001909 |
| GO:0043589 | skin morphogenesis | 19 | 11 | 2.38 | 0.001909 |
| GO:0090673 | endothelial cell-matrix adhesion | 8 | 7 | 1 | 0.001909 |
| GO:0072011 | glomerular endothelium development | 8 | 7 | 1 | 0.001909 |
| GO:0007160 | cell-matrix adhesion | 299 | 76 | 37.39 | 0.003068 |
| GO:0001763 | morphogenesis of a branching structure | 233 | 60 | 29.14 | 0.003068 |
| GO:2000178 | negative regulation of neural precursor cell proliferation | 44 | 18 | 5.5 | 0.00351 |
| GO:0043113 | receptor clustering | 64 | 20 | 8 | 0.004841 |
| GO:0021514 | ventral spinal cord interneuron differentiation | 28 | 11 | 3.5 | 0.00702 |
| GO:0048752 | semicircular canal morphogenesis | 19 | 10 | 2.38 | 0.007898 |
| GO:0035089 | establishment of apical/basal cell polarity | 35 | 13 | 4.38 | 0.007898 |
| GO:0097150 | neuronal stem cell population maintenance | 22 | 11 | 2.75 | 0.008672 |
| GO:0071679 | commissural neuron axon guidance | 22 | 11 | 2.75 | 0.008672 |
| GO:0001944 | vasculature development | 975 | 180 | 121.92 | 0.008867 |
| GO:2000977 | regulation of forebrain neuron differentiation | 13 | 10 | 1.63 | 0.008867 |
| GO:0035854 | eosinophil fate commitment | 7 | 6 | 0.88 | 0.008867 |
| GO:0010482 | regulation of epidermal cell division | 7 | 6 | 0.88 | 0.008867 |
| GO:0030203 | glycosaminoglycan metabolic process | 128 | 24 | 16.01 | 0.010029 |
| GO:0007499 | ectoderm and mesoderm interaction | 5 | 5 | 0.63 | 0.010029 |
| GO:1904674 | positive regulation of somatic stem cell population maintenance | 5 | 5 | 0.63 | 0.010029 |
| GO:0060529 | squamous basal epithelial stem cell differentiation involved in prostate gland acinus development | 5 | 5 | 0.63 | 0.010029 |
| GO:0016338 | calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules | 39 | 15 | 4.88 | 0.011487 |
| GO:0007182 | common-partner SMAD protein phosphorylation | 23 | 11 | 2.88 | 0.011487 |
| GO:0021983 | pituitary gland development | 27 | 12 | 3.38 | 0.011544 |
| GO:0009953 | dorsal/ventral pattern formation | 117 | 22 | 14.63 | 0.012514 |
| GO:0008361 | regulation of cell size | 496 | 93 | 62.02 | 0.016088 |
| GO:0071709 | membrane assembly | 58 | 21 | 7.25 | 0.016088 |
| GO:0050918 | positive chemotaxis | 54 | 17 | 6.75 | 0.016905 |
| GO:0060059 | embryonic retina morphogenesis in camera-type eye | 32 | 13 | 4 | 0.017129 |
| GO:0042060 | wound healing | 580 | 118 | 72.53 | 0.01782 |
| GO:1903729 | regulation of plasma membrane organization | 164 | 39 | 20.51 | 0.01782 |
| GO:0001655 | urogenital system development | 386 | 89 | 48.27 | 0.020398 |
| GO:0033631 | cell-cell adhesion mediated by integrin | 15 | 7 | 1.88 | 0.021698 |
| GO:0010725 | regulation of primitive erythrocyte differentiation | 8 | 6 | 1 | 0.021698 |
| GO:2000353 | positive regulation of endothelial cell apoptotic process | 25 | 11 | 3.13 | 0.023567 |
| GO:0071773 | cellular response to BMP stimulus | 171 | 38 | 21.38 | 0.023646 |
| GO:0001886 | endothelial cell morphogenesis | 30 | 12 | 3.75 | 0.033528 |
| GO:0030335 | positive regulation of cell migration | 684 | 130 | 85.53 | 0.033528 |
| GO:0033278 | cell proliferation in midbrain | 7 | 6 | 0.88 | 0.033528 |
| GO:0060513 | prostatic bud formation | 12 | 6 | 1.5 | 0.033528 |
| GO:0060197 | cloacal septation | 6 | 5 | 0.75 | 0.033528 |
| GO:0048807 | female genitalia morphogenesis | 6 | 5 | 0.75 | 0.033528 |
| GO:0071918 | urea transmembrane transport | 6 | 5 | 0.75 | 0.033528 |
| GO:0035469 | determination of pancreatic left/right asymmetry | 6 | 5 | 0.75 | 0.033528 |
| GO:0070830 | bicellular tight junction assembly | 88 | 23 | 11 | 0.033528 |
| GO:0006957 | complement activation, alternative pathway | 59 | 19 | 7.38 | 0.033528 |
| GO:0043471 | regulation of cellular carbohydrate catabolic process | 15 | 8 | 1.88 | 0.0351 |
| GO:0051016 | barbed-end actin filament capping | 41 | 15 | 5.13 | 0.036626 |
| GO:0043001 | Golgi to plasma membrane protein transport | 72 | 20 | 9 | 0.040114 |
| GO:0035696 | monocyte extravasation | 12 | 7 | 1.5 | 0.04095 |
| GO:0010838 | positive regulation of keratinocyte proliferation | 12 | 7 | 1.5 | 0.04095 |
| GO:0019628 | urate catabolic process | 9 | 6 | 1.13 | 0.044236 |
| GO:0019481 | L-alanine catabolic process, by transamination | 4 | 4 | 0.5 | 0.044337 |
| GO:0019101 | female somatic sex determination | 4 | 4 | 0.5 | 0.044337 |
| GO:0099173 | postsynapse organization | 193 | 27 | 24.13 | 0.044337 |