**Table S5. Tumor necrosis factor (TNF) and Cytochrome P450 (CYP) downregulated transcripts** (3 and 19 total respectively) in the oil-dispersant treatment (OD) detected by DESeq2 (and thus upregulated in the negative control). These features were not detected by edgeR. Transcripts blasted to the same GO molecular functions, for TNF: receptor binding, and for CYP: Heme binding, iron ion binding, monooxygenase activity, and oxydoreductase activity. Organism Uniprot identity: Kuruma prawn – PENJP (*Penaeus japonicus*), fruit fly - DROME (*Drosophila melanogaster*), house mouse - MOUSE (*Mus musculus*), and tropical cockroach - BLADI (*Blaberus discoidalis*). For full annotations see DS1, and DS4-5.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Transcript ID** | **SwissProt Top BLASTX Hit** | **ID %**  **(E-value)** | **GO BLAST cellular component** | **GO BLAST biological process** |
| TNFs |  |  |  |  |
| TR124428|c0\_g1\_i1 | PENJP  Tumor necrosis factor 2 homolog | 60.00%  (1e-31) | Integral component of membrane | Immune response |
| TR124428|c0\_g1\_i2 | PENJP  Tumor necrosis factor 2 ligand | 44.54%  (1e-53) | Integral component of membrane | Immune response |
| TR124428|c0\_g1\_i3 | PENJP  Tumor necrosis factor 2 homolog | 53.75%  (2e-52) | Integral component of membrane | Immune response |
| CYPs |  |  |  |  |
| TR86989|c3\_g1\_i2 | DROME Cytochrome P450 18a1 | 63.12%  (3e-58) | Integral component of membrane | Metamorphosis |
| TR86989|c3\_g1\_i1 | DROME Cytochrome P450 18a1 | 56.97%  (2e-59) | Integral component of membrane | Metamorphosis |
| TR70835|c0\_g1\_i1 | DROME Cytochrome P450 18a1 | 42.00%  (2e-25) | Integral component of membrane | Metamorphosis |
| TR175617|c0\_g1\_i2 | MOUSE  Cytochrome P450 2J6 | 27.18%  (2e-18) | Endoplasmic reticulum membrane | Response to organic cyclic compound |
| TR175617|c0\_g1\_i6 | MOUSE  Cytochrome P450 2J6 | 33.19%  (3e-74) | Endoplasmic reticulum membrane | Response to organic cyclic compound |
| TR175617|c0\_g1\_i4 | MOUSE  Cytochrome P450 2J6 | 33.68%  (9e-17) | Endoplasmic reticulum membrane | Response to organic cyclic compound |
| TR237724|c0\_g1\_i1 | DROME Cytochrome P450 301a1 | 33.94%  (9e-06) | Mitochondrial membrane | Tergite morphogenesis |
| TR78968|c0\_g1\_i3 | BLADI Cytochrome P450 4C1 | 51.86%  (3e-147) | Endoplasmic reticulum membrane | Oxidation-reduction process |
| TR78968|c0\_g1\_i5 | BLADI Cytochrome P450 4C1 | 51.86%  (3e-147) | Endoplasmic reticulum membrane | Oxidation-reduction process |
| TR78968|c0\_g1\_i11 | DROME Cytochrome P450 4C3 | 38.89%  (3e-07) | Endoplasmic reticulum membrane | Oxidation-reduction process |
| TR78968|c0\_g1\_i7 | DROME Cytochrome P450 4C3 | 48.54%  (3e-70) | Endoplasmic reticulum membrane | Oxidation-reduction process |
| TR78968|c0\_g1\_i1 | DROME Cytochrome P450 4C3 | 38.89%  (3e-07) | Endoplasmic reticulum membrane | Oxidation-reduction process |
| TR78968|c0\_g1\_i8 | DROME Cytochrome P450 4C3 | 48.54%  (4e-70) | Endoplasmic reticulum membrane | Oxidation-reduction process |
| TR78968|c0\_g1\_i6 | DROME Cytochrome P450 4C3 | 51.91%  (1e-58) | Endoplasmic reticulum membrane | Oxidation-reduction process |
| TR78968|c0\_g1\_i2 | DROME Cytochrome P450 4C3 | 50.00%  (2e-61) | Endoplasmic reticulum membrane | Oxidation-reduction process |
| TR78968|c0\_g1\_i10 | DROME Cytochrome P450 4C3 | 38.67%  (9e-6) | Endoplasmic reticulum membrane | Oxidation-reduction process |
| TR230432|c0\_g1\_i2 | DROME Cytochrome P450 4C3 | 57.87%  (8e-87) | Endoplasmic reticulum membrane | Oxidation-reduction process |
| TR230432|c0\_g1\_i1 | DROME Cytochrome P450 4C3 | 51.81%  (1e-19) | Endoplasmic reticulum membrane | Oxidation-reduction process |
| TR230432|c0\_g1\_i3 | DROME Cytochrome P450 4C3 | 73.44%  (3e-27) | Endoplasmic reticulum membrane | Oxidation-reduction process |