**Table S1**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Database | Score ≥ 200 | similarity ≥ 40% | e-value ≤ e-20 | combined |
| UniprotKB/swissprot (selected species) | 11% | 70% | 19% | 7% |
| UniprotKB/swissprot (*Crustacea)* | 2% | 73% | 6% | 1% |
| Refseq protein (selected species) | 24% | 64% | 37% | 21% |
| Refseq protein (*Crustacea*) | 0% | 36% | 0% | 0% |
| OrthoDB BUSCO (*Arthropoda*) | 14% | 57% | 24% | 11% |

**Database search on DE genes from the transcriptome.** DE genes from the transcriptome were blasted against several databases implemented in NCBI and OrthoDB. The organisms used in these databases were either *Arthropoda*, *Crustacea* in general or a set of selected arthropod species (*Daphnia pulex*, *Drosophila melanogaster*, *Tribolium castaneum*, *Ixodes scapularis* and *Apis mellifera*).

**Table S2**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Sample | Total Reads | Aligned | Singletons | Multihits Pairs | Multihits  Singletons | Spliced |
| ChlamyI | 6228000 | 5700046 | 403164 | 19782 | 3743 | 410356 |
| ChlamyII | 6808720 | 6150057 | 494795 | 29395 | 4753 | 447923 |
| ChlamyIII | 6888926 | 6224503 | 512171 | 25317 | 4585 | 457462 |
| MutI | 16046218 | 14547750 | 1050674 | 73593 | 64896 | 1058632 |
| MutII | 8310712 | 7523658 | 588210 | 34313 | 5153 | 556872 |
| MutIV | 7863126 | 7100179 | 581189 | 29004 | 4259 | 513200 |
| WTI | 11248752 | 10354425 | 653893 | 33845 | 4818 | 669711 |
| WTII | 10934860 | 10018107 | 648919 | 39781 | 5099 | 682411 |
| WTIII | 13483832 | 12247852 | 861428 | 56841 | 6042 | 848300 |

**TopHat Alignment Statistics.** Chlamy: *D. magna* fed with 100% *Chlamydomonas klinobasis*, Mut: *D. magna* fed with 90% *C. klinobasis* and 10% of the microcystin-free mutant strain of *M. aeruginosa* PCC7806, WT: *D. magna* fed with 90% *C. klinobasis* and 10% of the WT strain of *M. aeruginosa* PCC7806.