**Table S1**. **Summary of transcriptomic resources *in silico* mined in the study.** Each dataset has a description of the Order, Family and species of interest as well as the NCBI Bioproject accession number. Sequencing platform (all paired end-PE), assembly software and number of assembled transcripts are listed.

| **Order** | **Calanoida** | | | | **Harpacticoida** | **Cyclopoida** | **Siphonostomatoida** | |
|---|---|---|---|---|---|---|---|---|
| **Family** | Calanidae | | | Pseudodiaptomidae | Harpacticidae | Cyclopettidae | Caligidae | |
| **Species** | *Calanus helgolandicus* | *Calanus glacialis* | *Acartia tonsa* | *Pseudodiaptomus annandalei* | *Tigriopus californicus* | *Paracyclopina nana* | *Caligus rogercresseyi* | *Lepeophtheirus salmonis* |
| **Bioproject** | PRJNA640515 | PRJNA237014 | PRJEB20069 | PRJNA558682 | PRJNA237968 | PRJNA268783 | PRJNA234316 | PRJNA73431 |
| **RNA-Seq** | Illumina Hi-Seq 2000 | IonTorrent | Illumina NextSeq | Illumina NextSeq | Illumina; PacBio RSII | Illumina HiSeq | Illumina PET 100bp | Sanger ESTs and Illumina |
| **Assembly** | Trinity r2013-02 | Trinity r2013_08_14 | Trinity 2.2.0 | Trinity 2.8.4 | HiRise 2017-07 | Trinity r2013_08_14 | Trinity r2013-02-25 | SOAPdenovo |
| **#transcripts** | 30,339 | 36,888 | 119,439 | 183,458 | 15,557 * | 60,687 | 44,089 | Not provided |

* number of deduced proteins sequences from the *T. californicus* genome