

**Table 1. Summary of the next-generation sequencing assemblies for nine copepod and three additional crustacean species**

| Order and Family        | Species names                  | Source                   | Assemblies <sup>a</sup> (range; N50)                                      |
|-------------------------|--------------------------------|--------------------------|---------------------------------------------------------------------------|
| Siphonostomatoida       |                                |                          |                                                                           |
| Caligidae               | <i>Lepeophtheirus salmonis</i> | Genome                   | 10,615 (300 – 827 bps; 366)                                               |
| Caligidae               | <i>Caligus rogercresseyi</i>   | Transcriptome            | 76,788 (301 – 9,505 bps; 1,414)                                           |
| Cyclopoida              |                                |                          |                                                                           |
| Cyclopidae              | <i>Mesocyclops edax</i>        | Genome                   | 25,442 (300 – 1,275 bps; 401)                                             |
| Lernaeidae              | <i>Lernaea cyprinacea</i>      | Transcriptome            | 271,824 (301 – 22,442 bps; 2,266)                                         |
| Harpacticoida           |                                |                          |                                                                           |
| Harpacticidae           | <i>Tigriopus californicus</i>  | Genome and Transcriptome | 60,840 (301 – 8,614 bps; 1,510)                                           |
| Calanoida               |                                |                          |                                                                           |
| Calanidae               | <i>Calanus sinicus</i>         | Transcriptome            | 29,458 (301 – 3,923 bps; 513)                                             |
| Calanidae               | <i>Calanus finmarchicus</i>    | Genome                   | 8,629 (300 – 1,067 bps; 347)                                              |
| Acartiidae              | <i>Acartia fossae</i>          | Transcriptome            | 100,383 (301 – 8,174 bps; 769)                                            |
| Temoridae               | <i>Eurytemora affinis</i>      | Genome and Transcriptome | 118,299 (99 – 26,685 bps; 2,271),<br>6,899 (604 – 7,289,689 bps; 862,645) |
| Branchiopoda, Anostraca |                                |                          |                                                                           |
| Artemiidae              | <i>Artemia franciscana</i>     | Transcriptome            | 59,654 (301 – 48,245 bps; 1,747)                                          |
| Malacostraca, Decapoda  |                                |                          |                                                                           |
| Penaeidae               | <i>Penaeus monodon</i>         | Transcriptome            | 94,814 (301 – 17,471 bps; 2,473)                                          |
| Thecostraca, Sessilia   |                                |                          |                                                                           |
| Balanidae               | <i>Amphibalanus amphitrite</i> | Transcriptome            | 80,455 (301 – 8,040 bps; 857)                                             |

<sup>a</sup>The number of contigs (> 300 bps) except for the *Eurytemora affinis* transcriptome. The NCBI accession numbers and sequencing platforms were summarized in supplementary tables S1 and S2. The transcriptomes and the genomes were assembled using the software package Trinity and Velvet, respectively (more details in Materials and Methods).