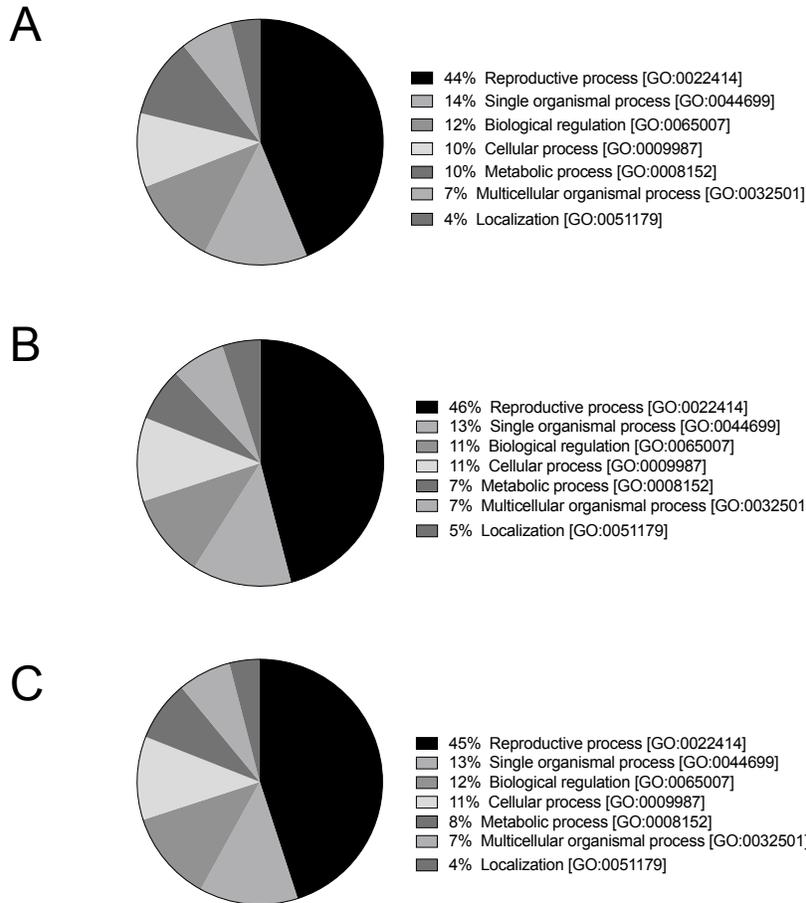


## Supplementary materials



### Supplementary Figure 1. Gene ontology annotation of *Neocalanus flemingeri* adult females.

Pie charts show proportion of GO terms represented: A) *N. flemingeri* reference transcriptome (Roncalli et al., 2018a); B) among the DEGs identified in pairwise comparisons between diapausing females (Cluster 1) and post-diapausing females (all other clusters); and C) among the DEGs identified using the generalized linear model comparing the three post-diapausing females clusters (CL2-CL4). For B and C, DEGs from in each pairwise analysis were independent annotated. Annotation results for these DEGs were similar across all pairwise comparisons thus were averaged for the pie chart (B,C). For each GO term the percentage refers to the ratio between the total number of DEGs annotated within the term and the total number of annotated DEGs obtained for each paired comparison.