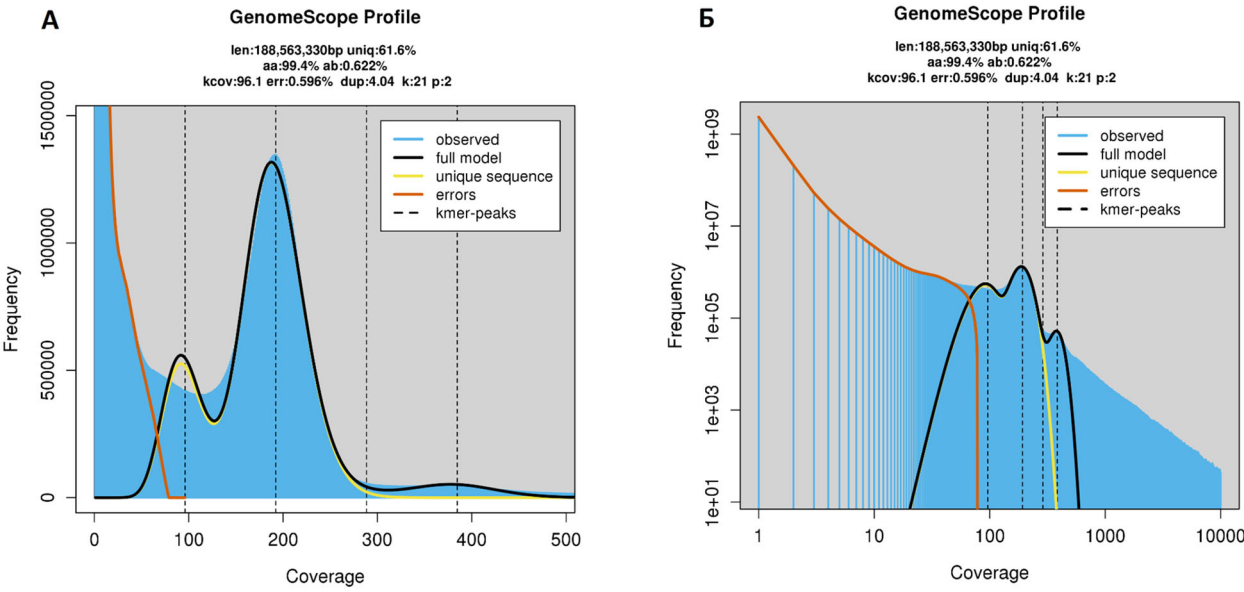
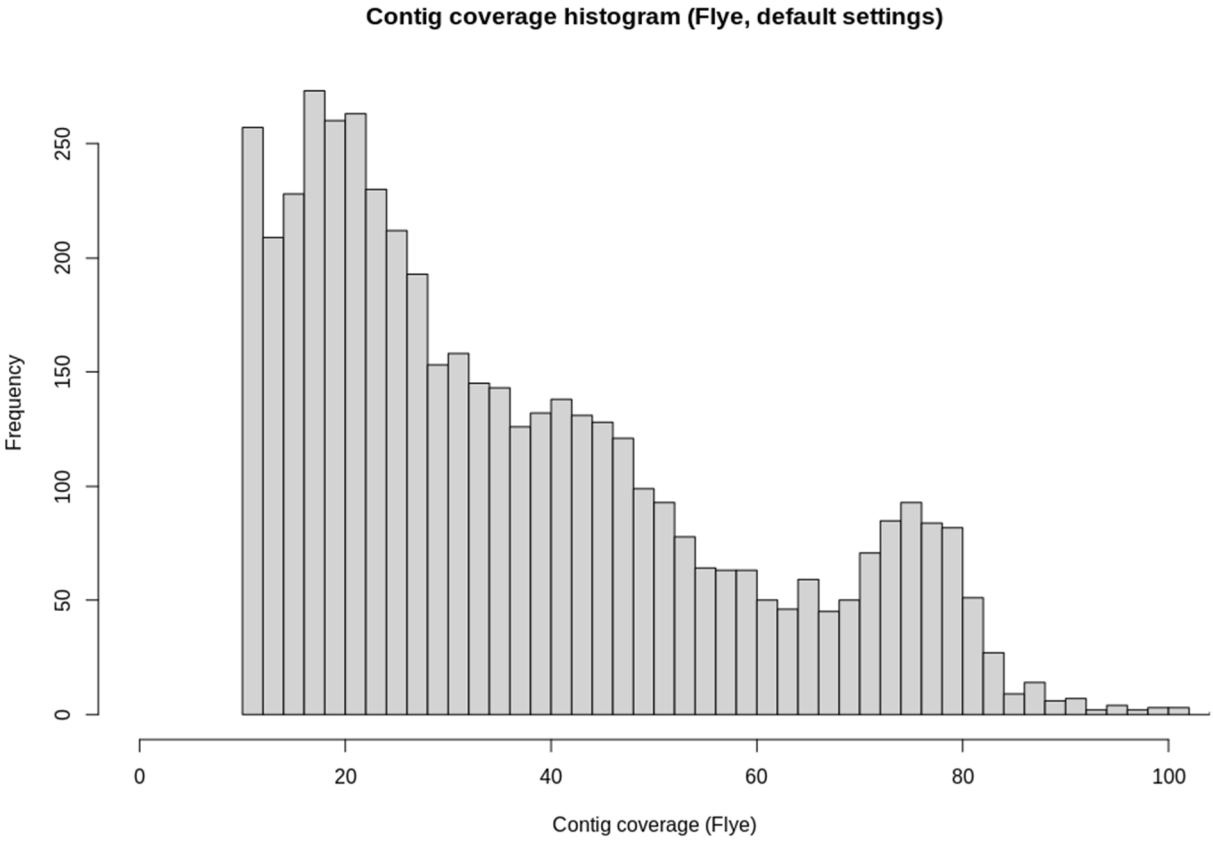


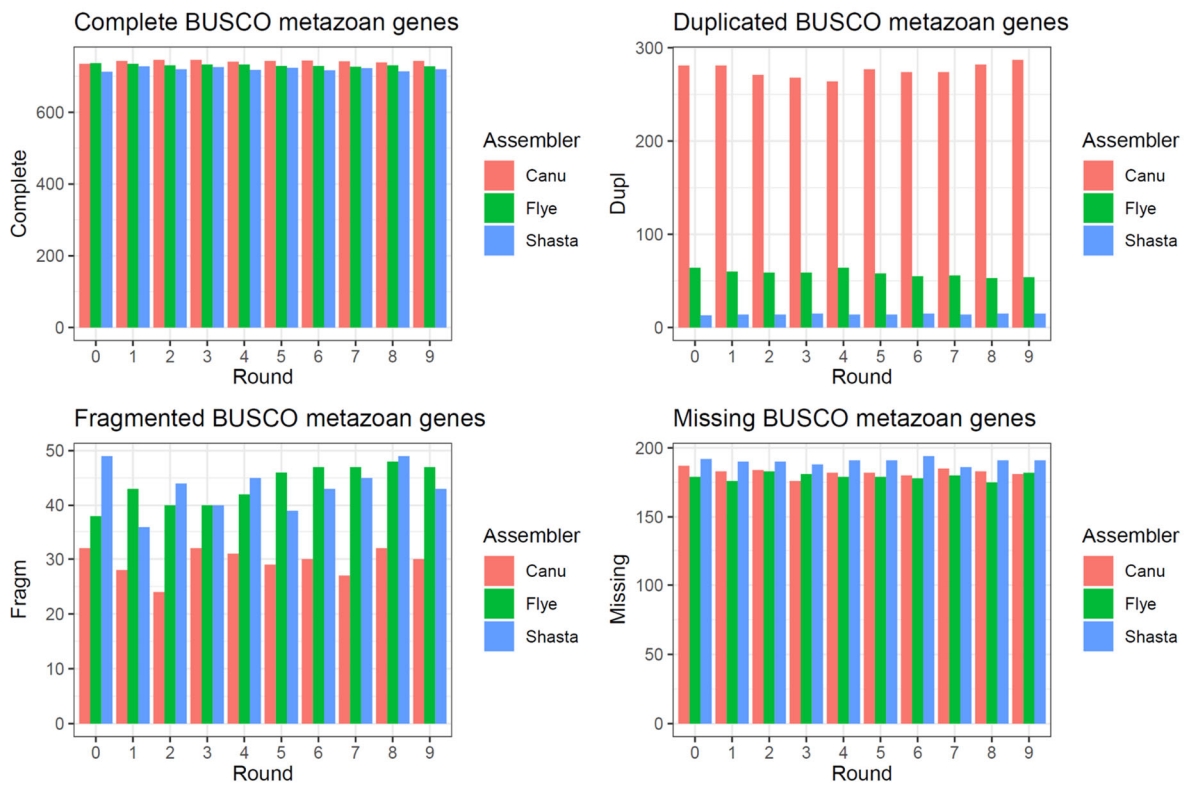
Supplementary Figure S1. Frequency spectra of k-mer (k=21) in natural (A) and logarithmic (B) scales, and the results of modeling the observed k-mer frequency distribution. The peak of the distribution with a coverage of about 200 corresponds to the haploid genome. The k-mer counting was performed using the jellyfish v2.3.0.



Supplementary Figure S2. Histogram of coverages of individual contigs by reads obtained by Flye assembler.

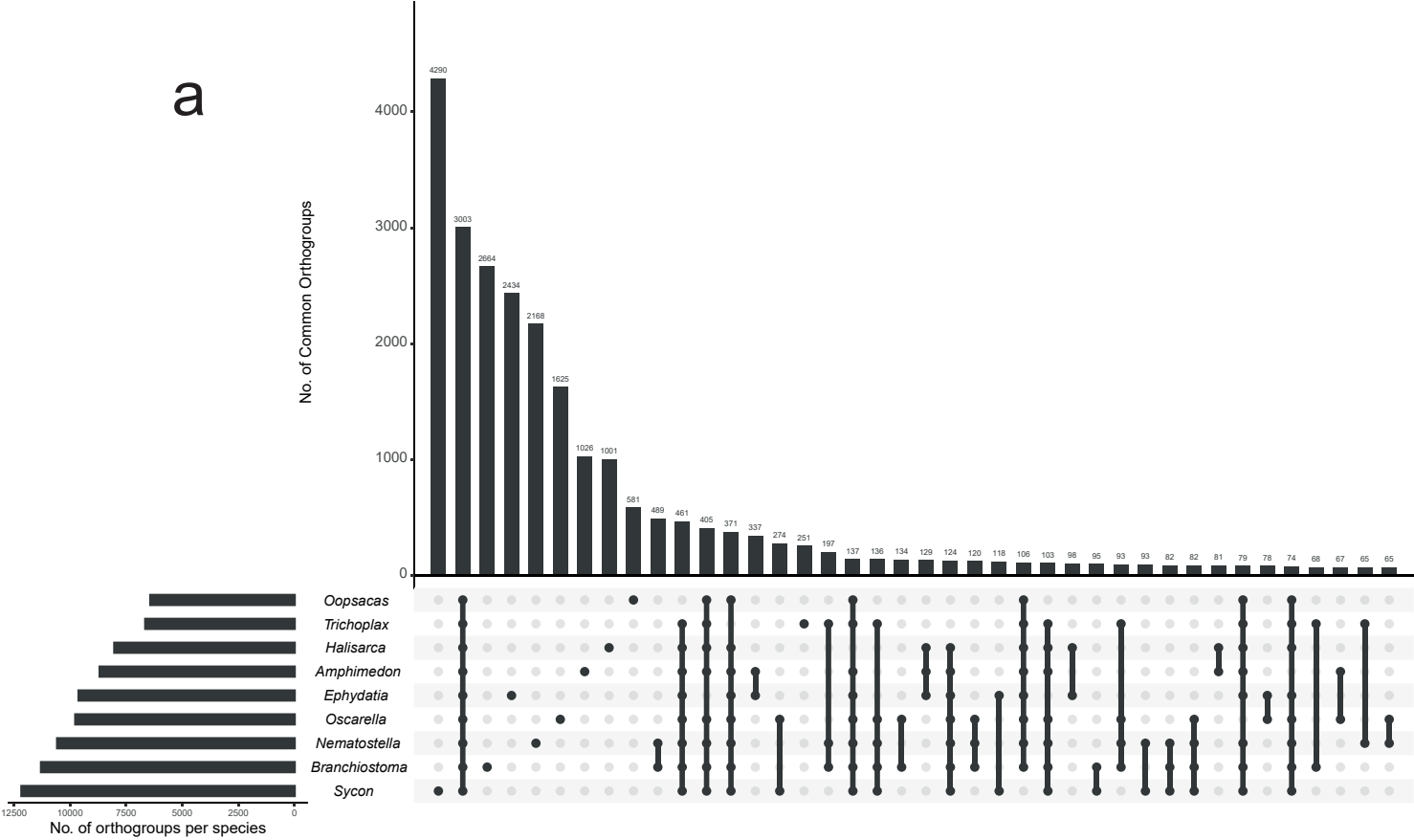


Supplementary Figure S3. Results of polishing genomic assemblies using long reads and the Racon software.



Supplementary Figure S4. (a) Orthology analysis performed on sponges, cnidarians, placozoans and Deuterostomia. (b) GO enrichment of sequences unique for *H. dujardinii*. GO terms in category “Cell compartment” are indicated inside cells, and cell square proportional to p-value.

a



b

