

Expanded View Figures

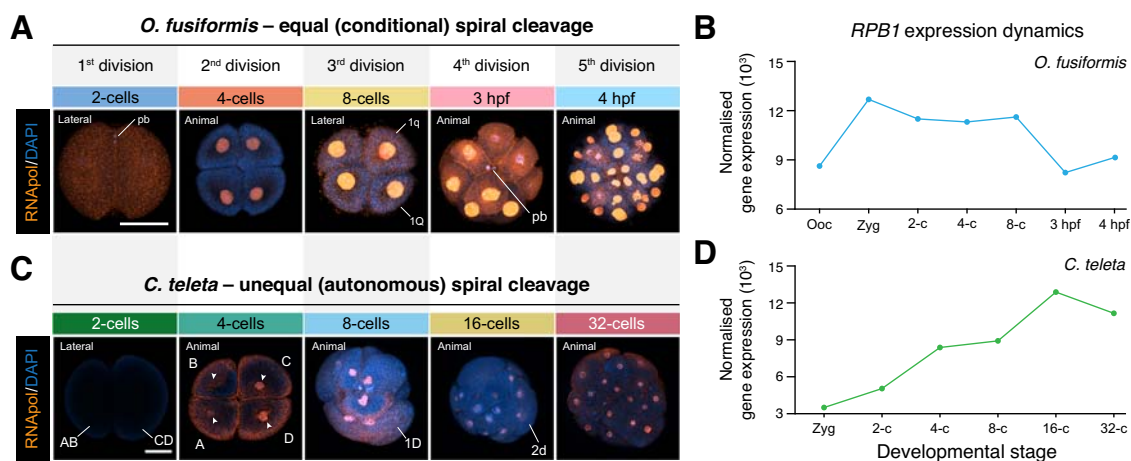


Figure EV1. Dynamics of RNA polymerase II nuclearisation during spiral cleavage.

(A, C) Z-projections of confocal stacks of embryos of *O. fusiformis* (A) and *C. teleta* (C) from the 2-cell stage to 4 h post-fertilisation (hpf) or the 32-cell stage. RNA polymerase II localises to the nuclei from the 4-cell stage onwards in both annelids. In *C. teleta*, the nuclearisation is more intense in the C and D blastomeres than in the A and B cells. (B, D) Expression dynamics of the *RPB1* gene (largest subunit of the RNA polymerase II, recognised by the antibody used in A and C) in *O. fusiformis* (B) and *C. teleta* (D). In the two annelids, RPB1 is a highly abundant maternal gene. Gene expression values are the average of two biological replicates.

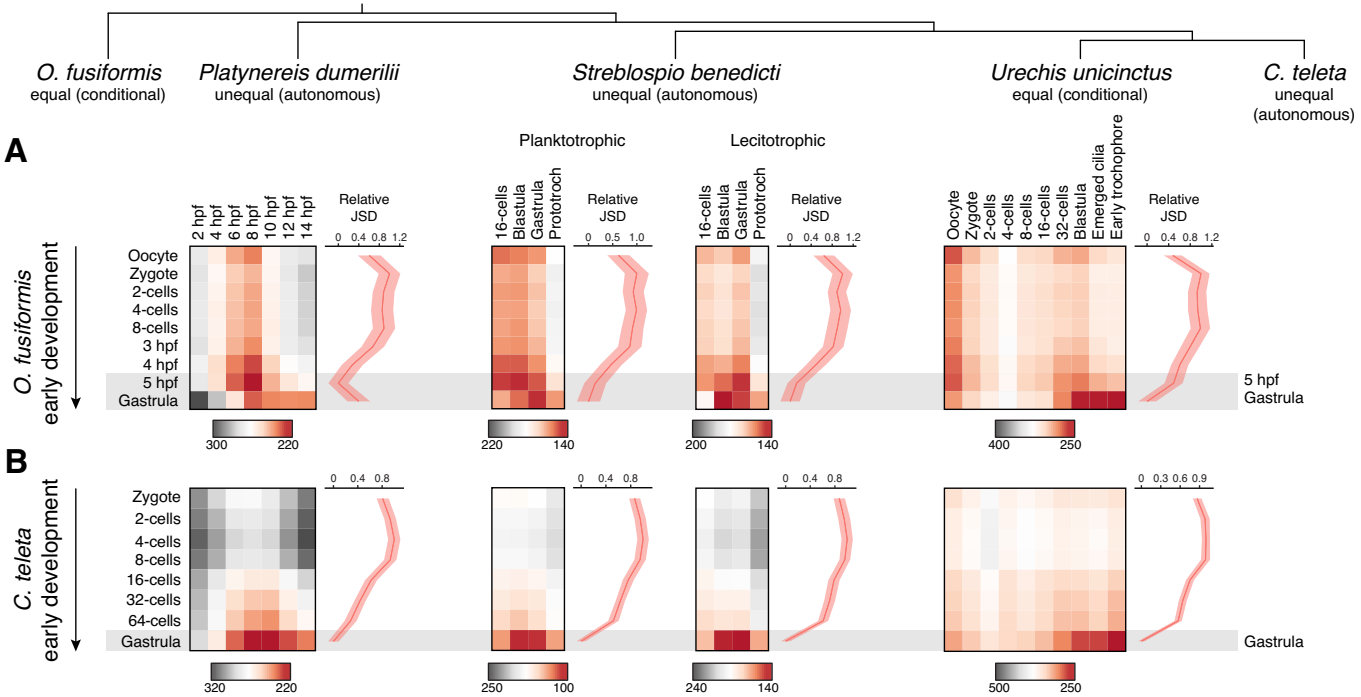


Figure EV2. Transcriptomic dynamics during spiral cleavage in Annelida.

(A, B) Jensen-Shannon transcriptomic divergence during the spiral cleavage between *O. fusiformis* (A) and *C. teleta* (B) and four other annelid species with publicly available transcriptomic resources covering at least one cleavage stage and the gastrula stage. In all cases, the point of maximal transcriptomic similarity occurs at the late cleavage and gastrulation (grey horizontal bar).

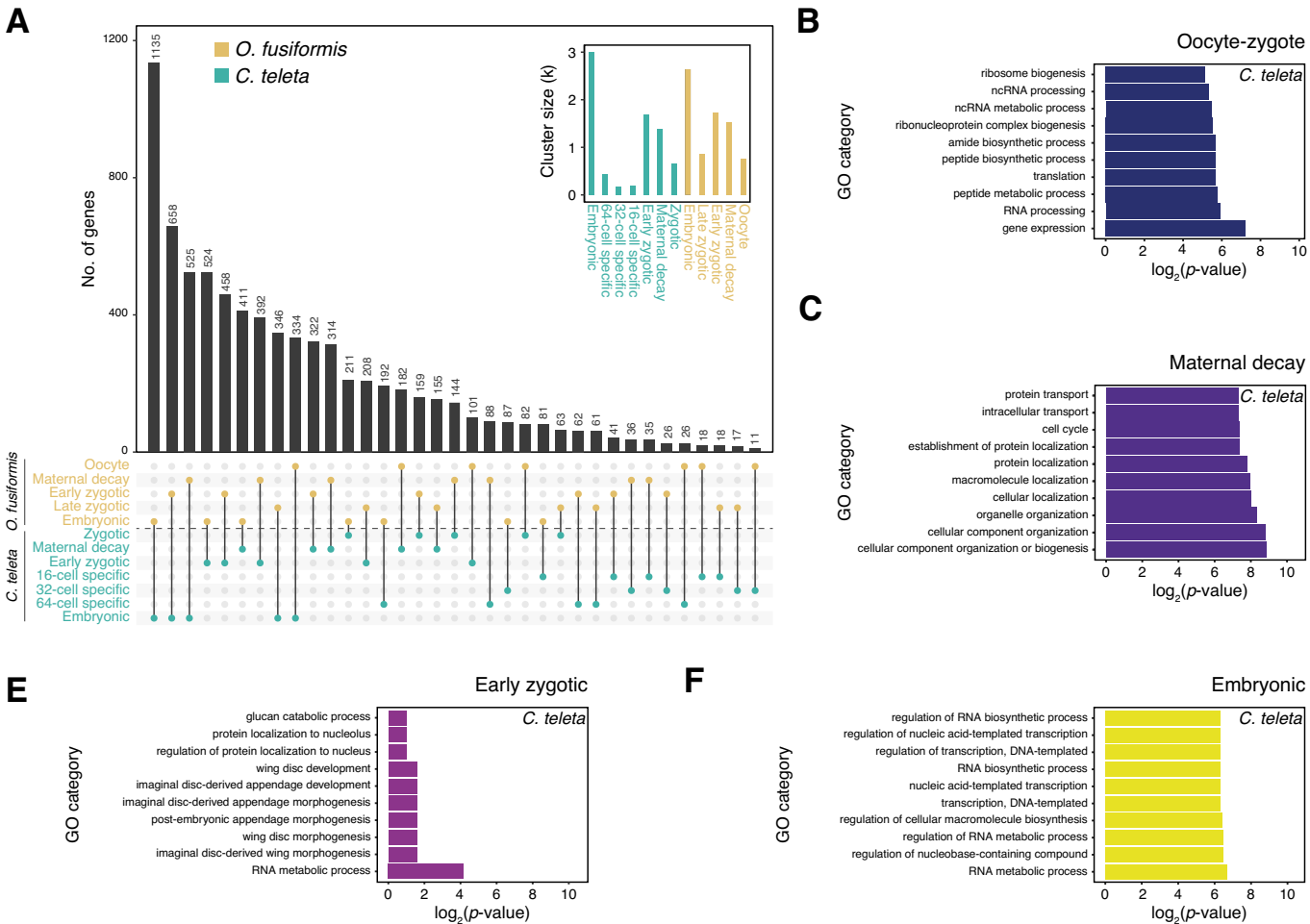


Figure EV3. The comparison of clusters of temporally coregulated genes between conditional and autonomous spiral cleavage.

(A) Upset plot indicating the number of shared one-to-one orthologs between clusters of temporally coregulated genes. The inset indicates the total number of genes in each cluster. (B–F) Bar plots indicating the top ten Gene Ontology (GO) categories amongst shared orthologous genes in the oocyte/zygote, maternal decay, early zygotic, and embryonic clusters, according to the GO annotation for the *C. teleta* ortholog. *P* values were computed from upper-tail Fisher's exact tests.

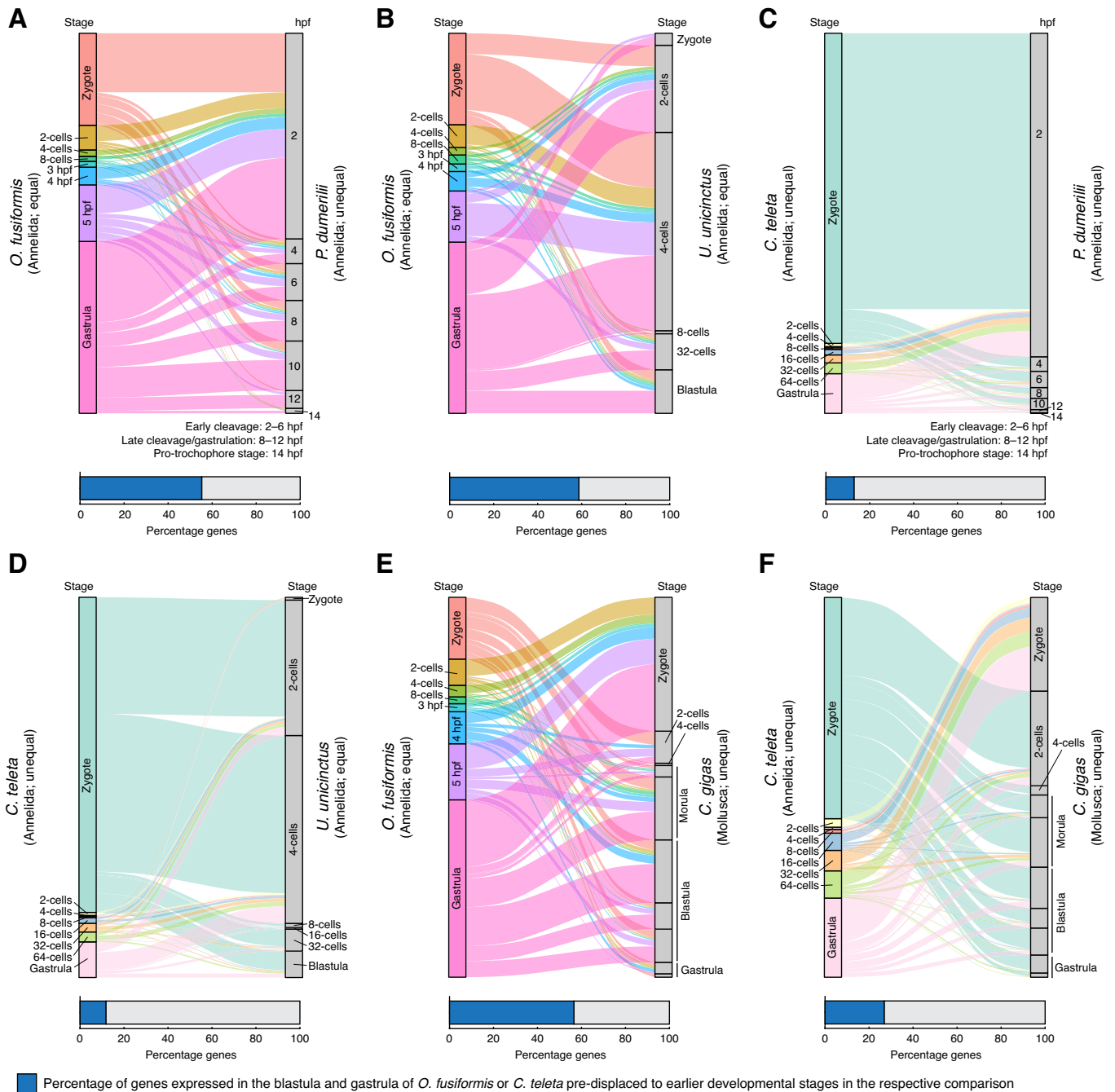


Figure EV4. Heterochronic shifts in gene expression between selected molluscan and annelid species.

(A–F) Alluvial plots depicting the comparative deployment of one-to-one orthologs exhibiting shifts in temporal activation during spiral cleavage between *O. fusiformis* and *P. dumerilii* (A), *O. fusiformis* and *U. unicinctus* (B), *C. teleta* and *P. dumerilii* (C), *C. teleta* and *U. unicinctus* (D), *O. fusiformis* and *C. gigas* (E), and *C. teleta* and *C. gigas* (F). Generally, more genes shift from late cleavage stages in *O. fusiformis* to early stages in other species than when *C. teleta* is included in equivalent comparisons.

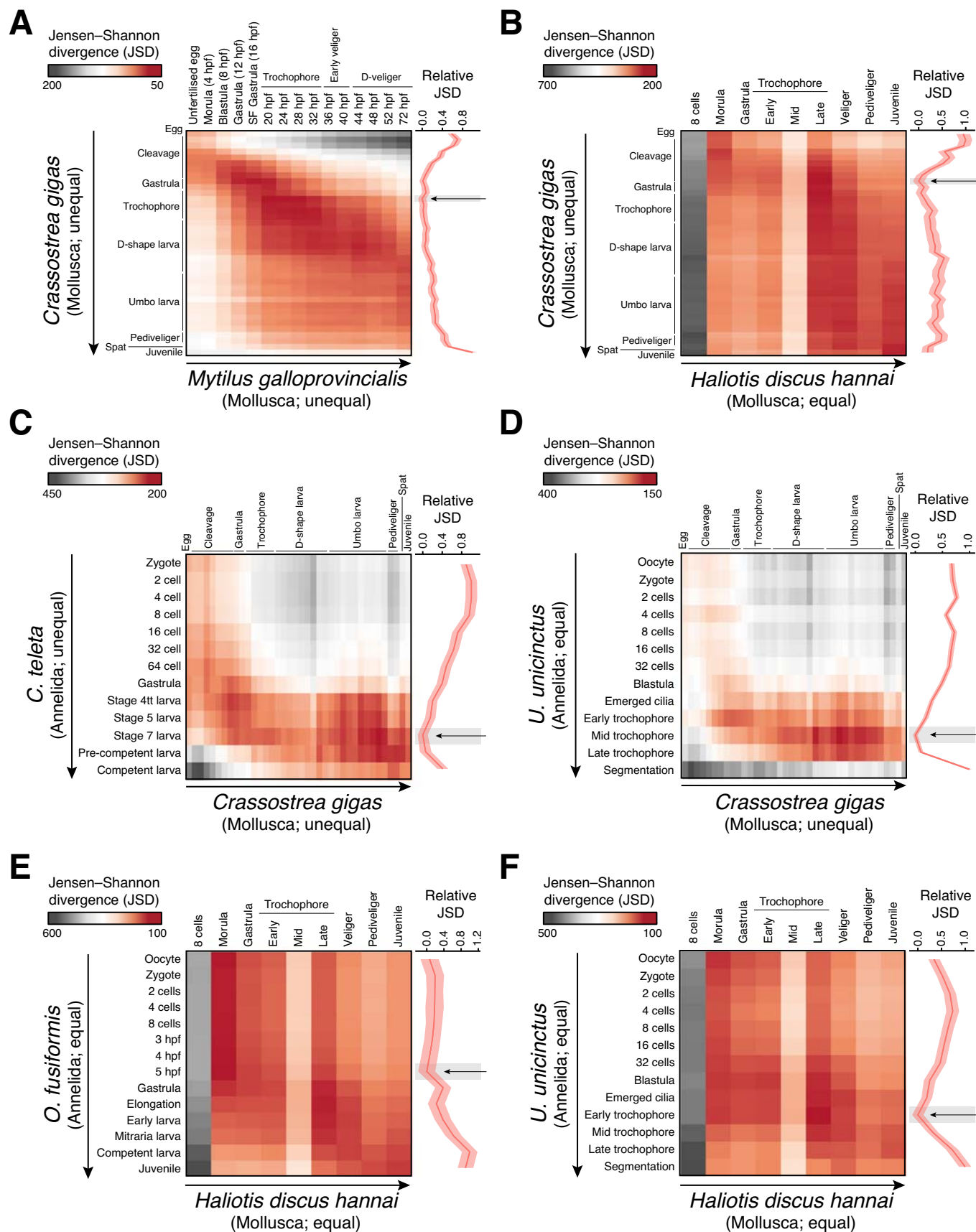


Figure EV5. Transcriptional similarity between Molluscan and Annelid development.

(A–F) Jensen-Shannon transcriptomic divergence between all possible inter-species pairwise comparisons during the entire life cycle, from oocyte or cleavage to juvenile or competent larva, between molluscan and annelid species with a high-resolution time course. In intra-phylum comparisons, the stages of maximal similarity are at or around gastrulation. In contrast, in inter-phylum comparisons, the larval stages are more transcriptionally similar (except for the *O. fusiformis* versus *Haliotis discus hannai* comparisons, which might be due to the poor quality of the molluscan dataset).