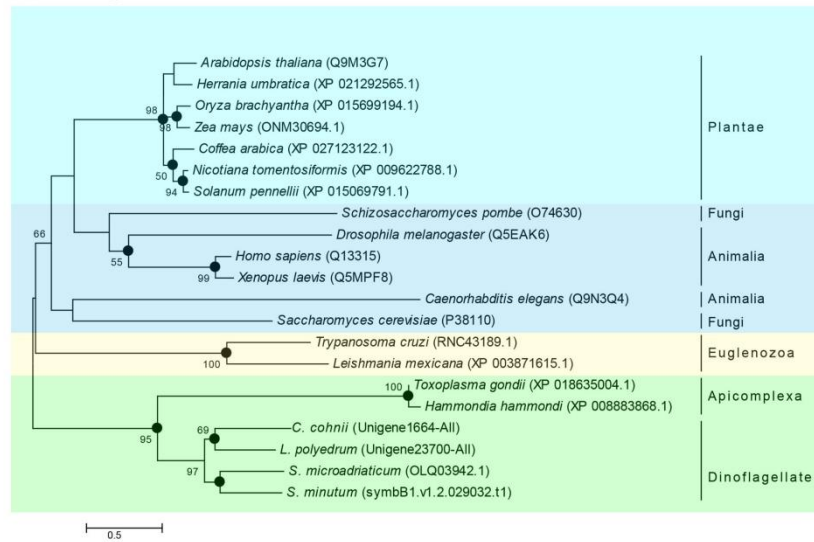
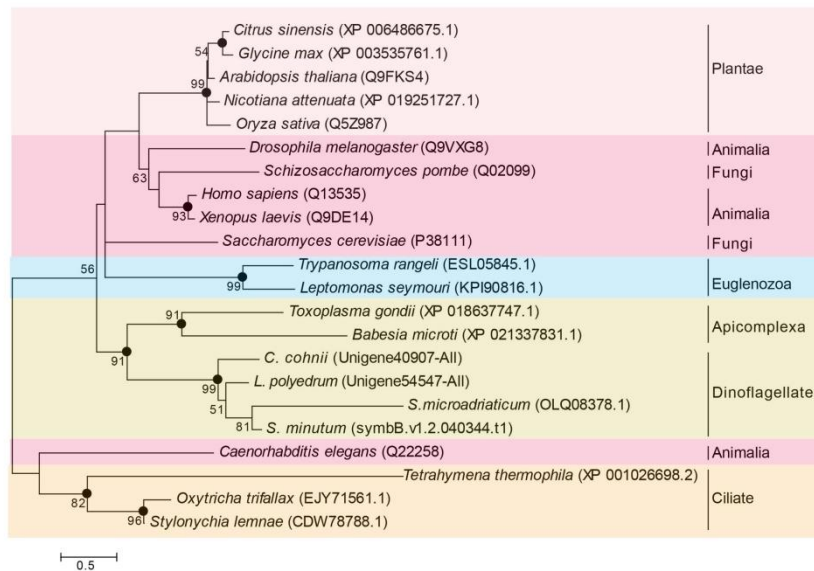


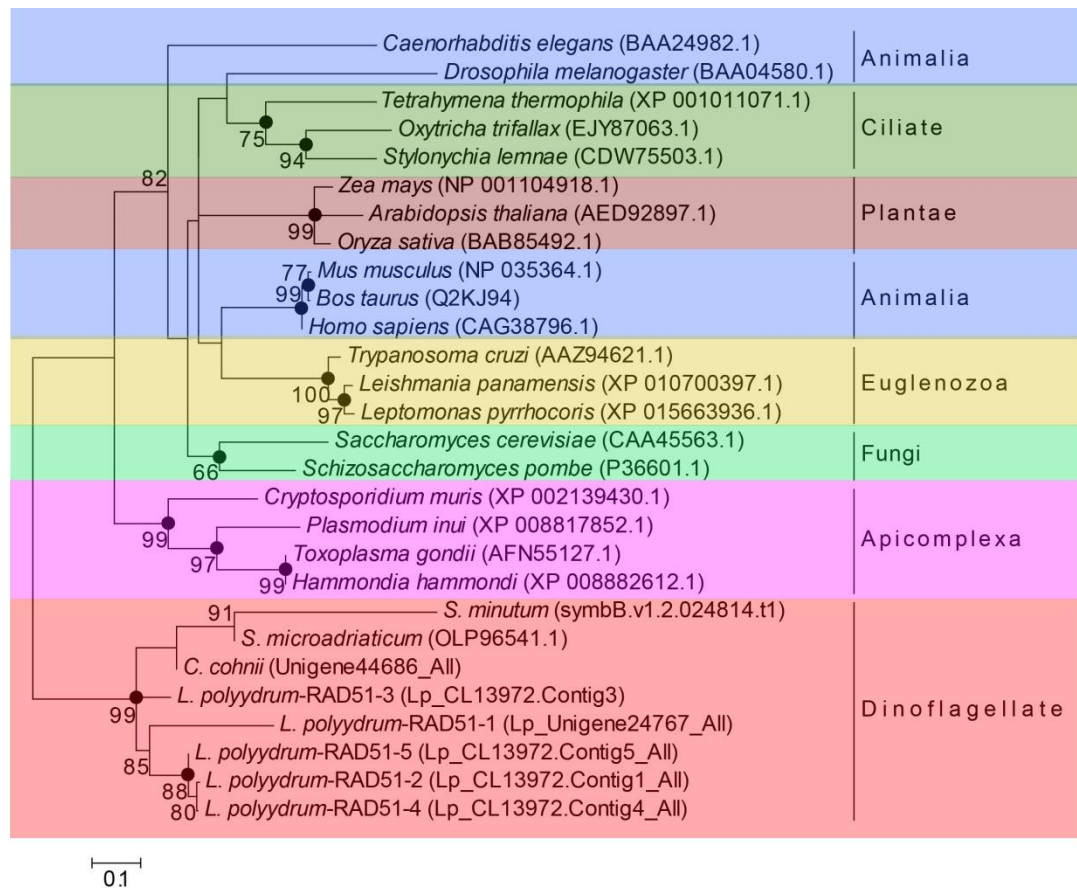
(A) ATM protein



(B) ATR ptotein



**Figure S1.** Phylogenetic analysis of dinoflagellate central checkpoint kinases ATM and ATR. (A) Maximum-likelihood phylogenetic tree based on the analysis of dinoflagellate and representative eukaryotes ATM sequences; (B) Maximum-likelihood phylogenetic tree based on the analysis of dinoflagellate and representative eukaryote ATR sequences. Bootstrap values (>50%, with 1000 replications of resampling analysis) are shown at branch points. Filled circles indicate that the nodes were also recovered by trees generated using the neighbour-joining method. GenBank accession numbers and dinoflagellate protein ID numbers are included in the bracket.



**Figure S2.** Phylogenetic analysis of dinoflagellates Rad51 proteins. Maximum-likelihood phylogenetic tree based on the analysis of dinoflagellate and representative eukaryotes Rad51 protein sequences. Bootstrap values (>50%, with 1000 replications of resampling analysis) are shown at branch points. Filled circles mean that the nodes were also recovered by trees generated using the neighbour-joining method. GenBank accession numbers and dinoflagellate protein ID numbers are included in the bracket.