

Supplemental Figure S3. PLK4 and ZYG-1 phylogeny. Maximum likelihood and Bayesian trees were produced for PLKs (pink), including PLK4 (blue), and ZYG-1 (green). Topology support for nodes is indicated (maximum likelihood bootstrap values/posterior probability). For phylogenetic inference, amino acid sequence alignments were produced using MAFFT and trimmed to remove poorly aligned positions. MrBayes v3.1.2 was used to infer Bayesian trees (random start tree, 4 chains of temperature 0.2, WAG substitution matrices, 4 discrete categories of gamma distribution substitution rate, 250,000 generations). Maximum likelihood bootstrap values were produced using PHYMLv2.4.4 (100 replicates, WAG matrix, 4 gamma categories, alpha parameter re-estimation for each replicate). Ap=*Apis mellifera*, Ci=*Ciona intestinalis*, Ce=*Caenorhabditis elegans*, Cm=*Cyanidioschyzon merolae*, Cs=*Capitella* sp., Dd=*Dictyostelium discoideum*, Dm=*Drosophila melanogaster*, Dr=*Danio rerio*, Ec=*Encephalitozoon cuniculi*, Gg=*Gallus gallus*, Hs=*Homo sapiens*, Lg=*Lottia gigantea*, Lm=*Leishmania major*, Mb=*Monosiga brevicollis*, Nc=*Neurospora crassa*, Ng=*Naegleria gruberi*, Nv=*Nematostella vectensis*, Ot=*Ostreococcus tauri*, Pt=*Paramecium tetraurelia*, Sc=*Saccharomyces cerevisiae*, Spo=*Schizosaccharomyces pombe*, Spu=*Strongylocentrotus purpuratus*, Ta=*Trichoplax adhaerens*, Tb=*Trypanosoma brucei*, Th=*Tetrahymena thermophila*, Tr=*Takifugu rubripes*, Um=*Ustilago maydis*.

Figure S3. PLK4 and ZYG-1 phylogeny.

