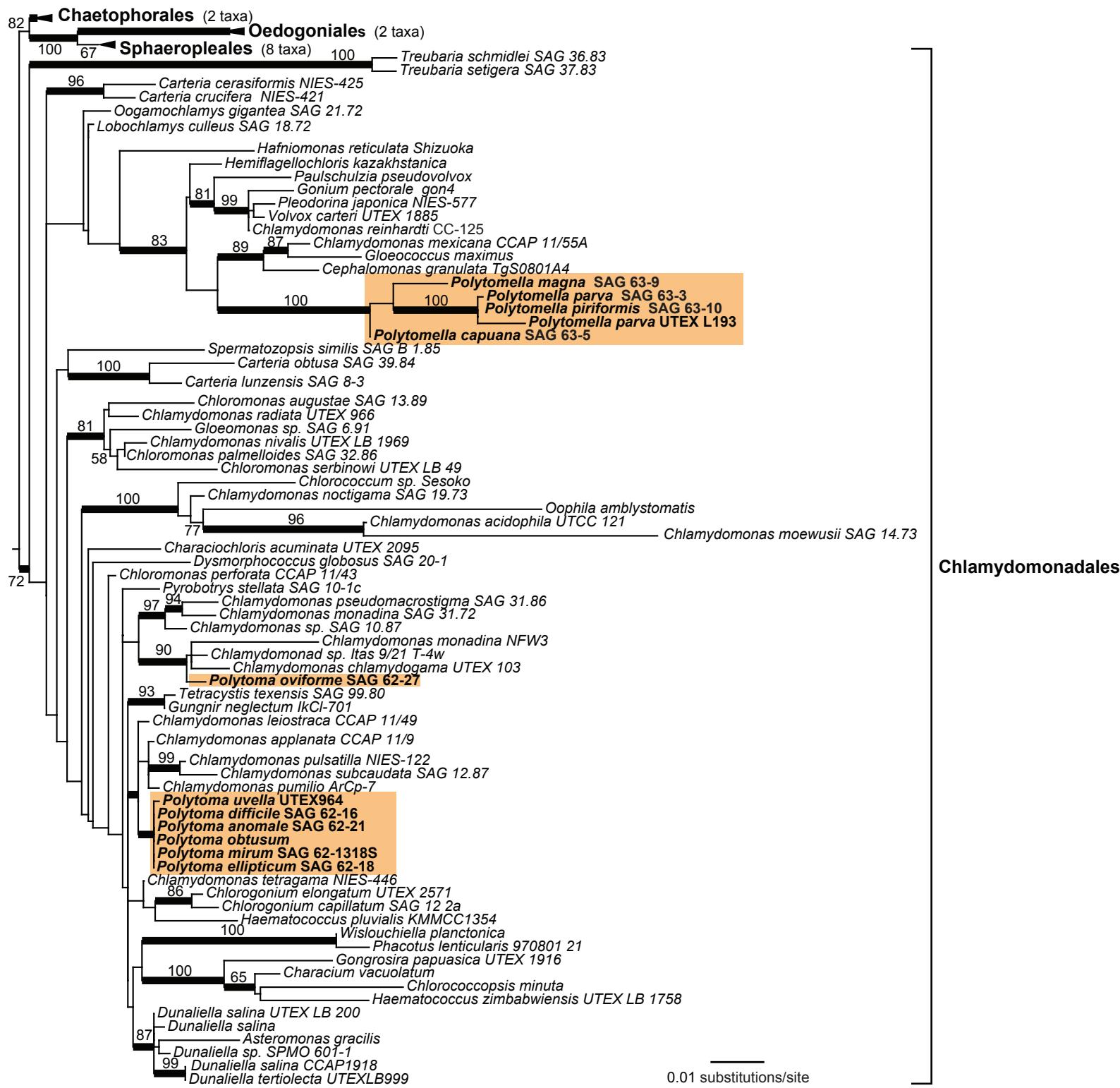


# Figure S2



**Figure S2.** Maximum Likelihood tree of estimated from 18S rRNA (*rrnL*) sequences. Numbers near branches represent RAxML (GTRGAMMA substitution model) bootstrap values >50%. Thick branches are supported by posterior probabilities  $\geq 0.95$ . Branch lengths are proportional to the number of substitutions per site. Rectangular boxes highlight nonphotosynthetic lineages.