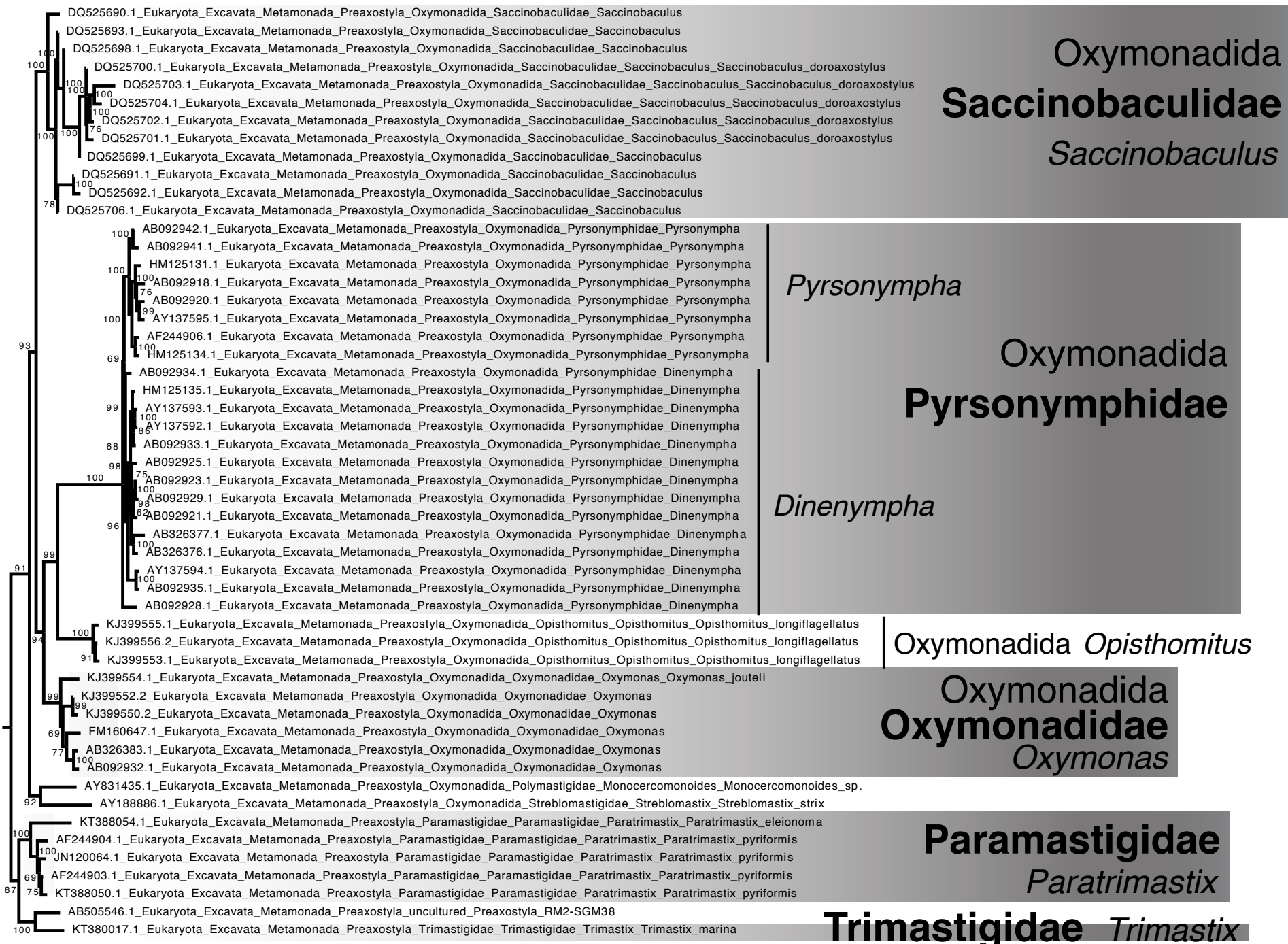


Figures S1 – S9. Maximum likelihood phylogenetic trees for each specific EukRef database constructed in RAxML using GTRCAT model. Statistical support is derived from 100 bootstrap replicates. Euglenida and Glycomonada datasets were each split into two separate tree figures as they both contain very large number of sequences. Trees are outgroup rooted. Tip labels are the final classification in the databases.

Figure S1
Preaxostyla



Oxymonadida
Saccinobaculidae
Saccinobaculus

Pyrsonympha

Oxymonadida
Pyrsonymphidae

Dinenympha

Oxymonadida *Opisthomitus*

Oxymonadida
Oxymonadidae
Oxymonas

Paramastigidae
Paratrimastix

Trimastigidae *Trimastix*

0.5
2120 positions

Figure S2
Fornicata

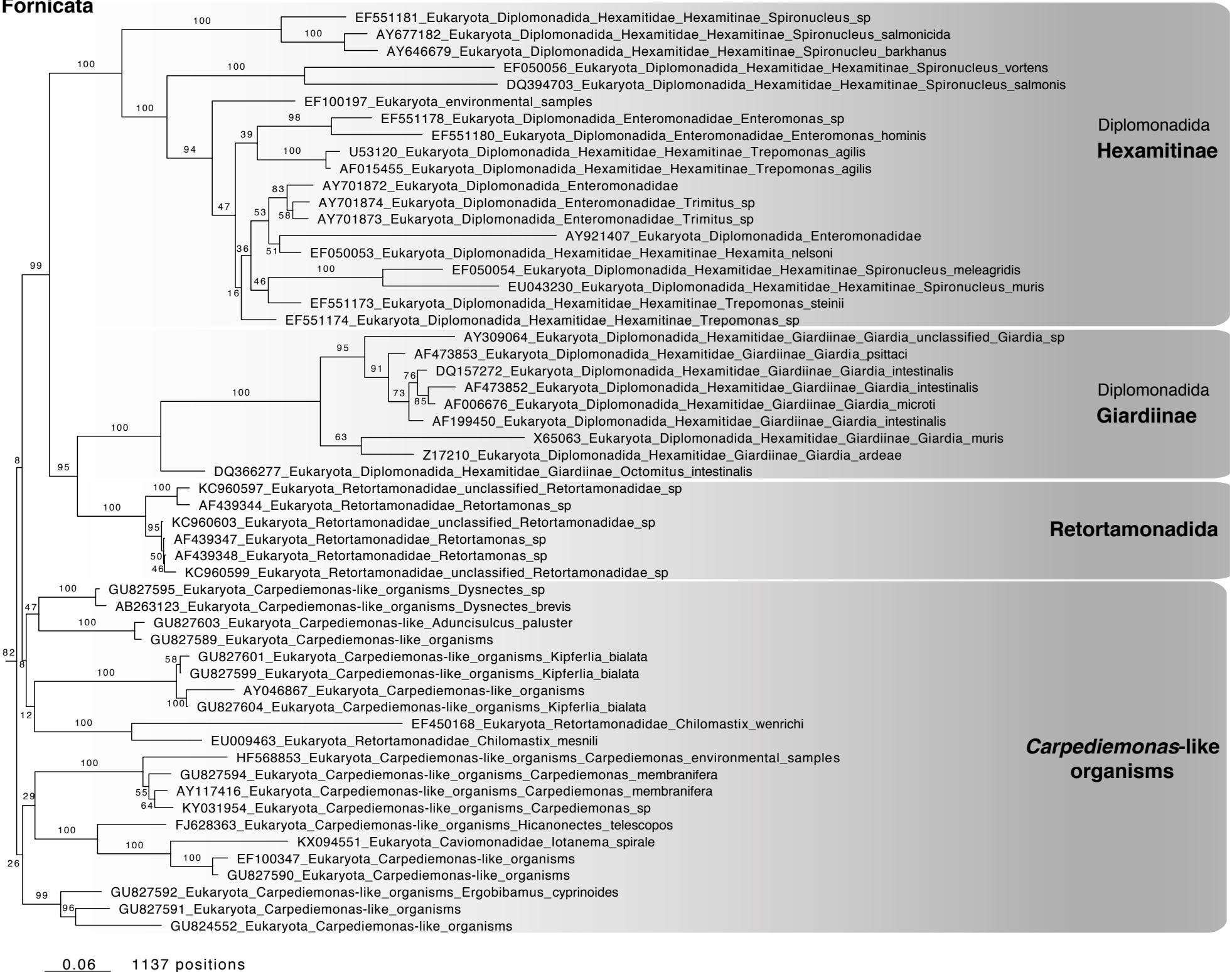


Figure S3
Parabasalia

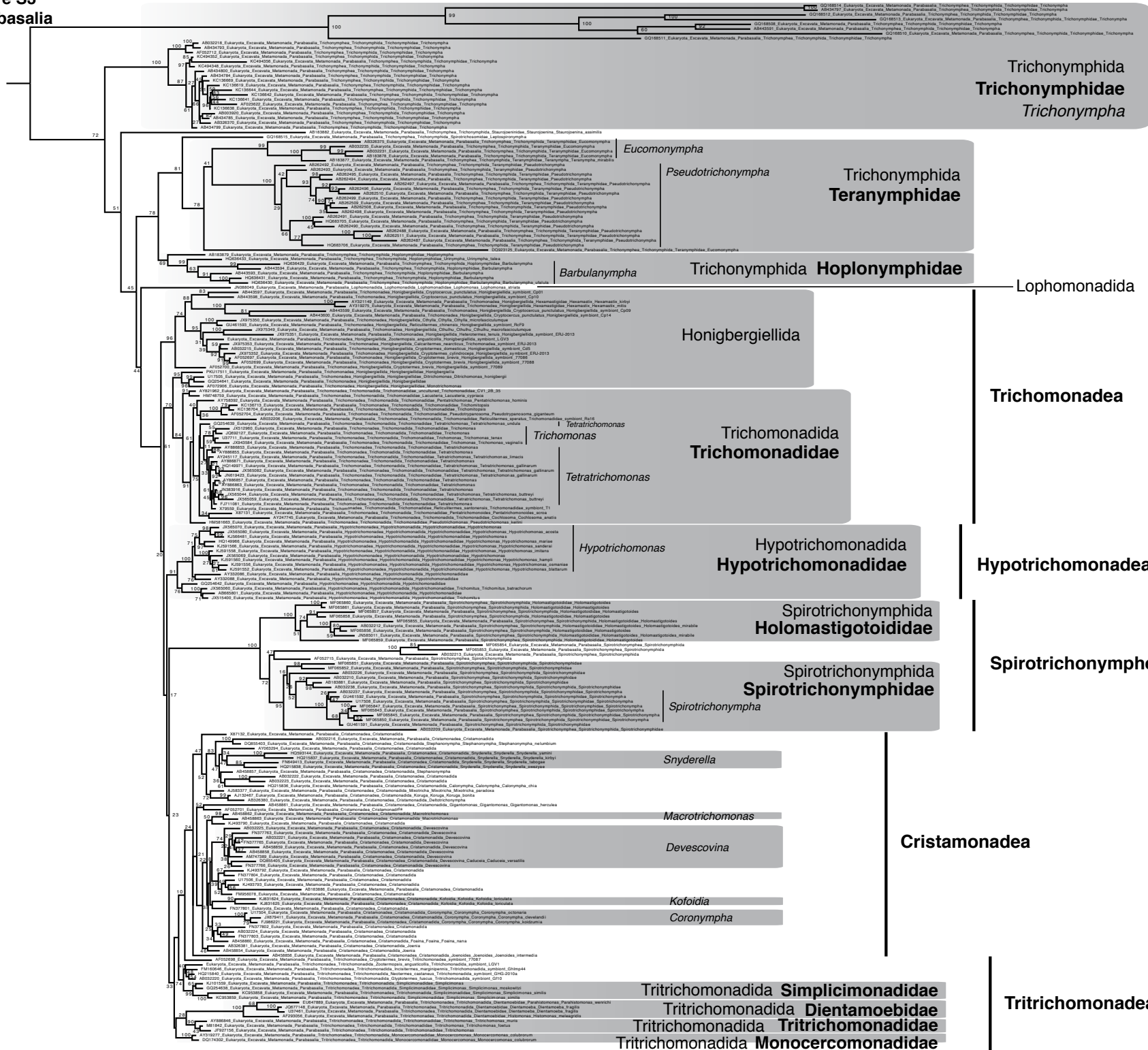


Figure S4
Jakobida

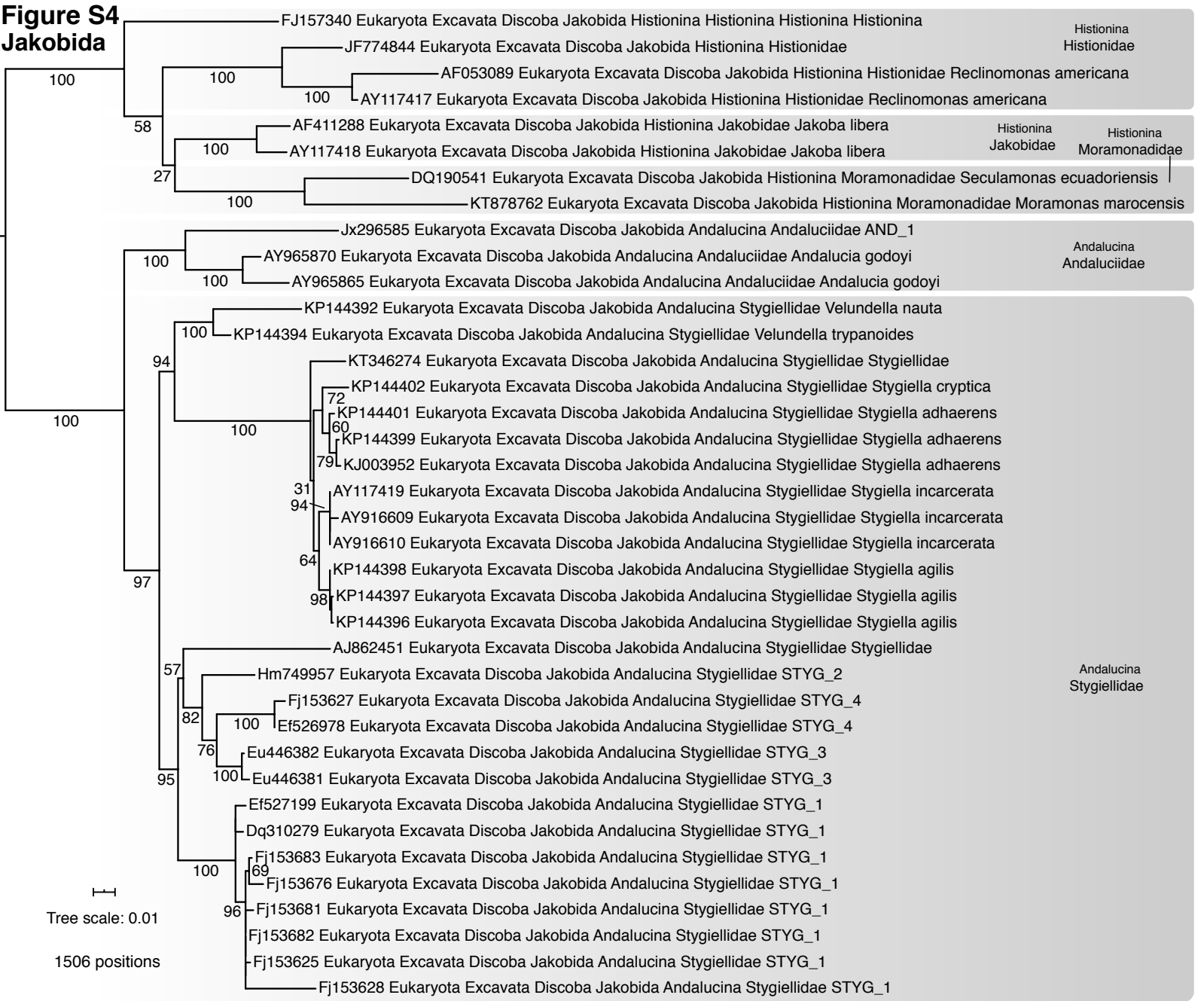


Figure S5

Heterolobosea



Figure S6
Euglenida 1

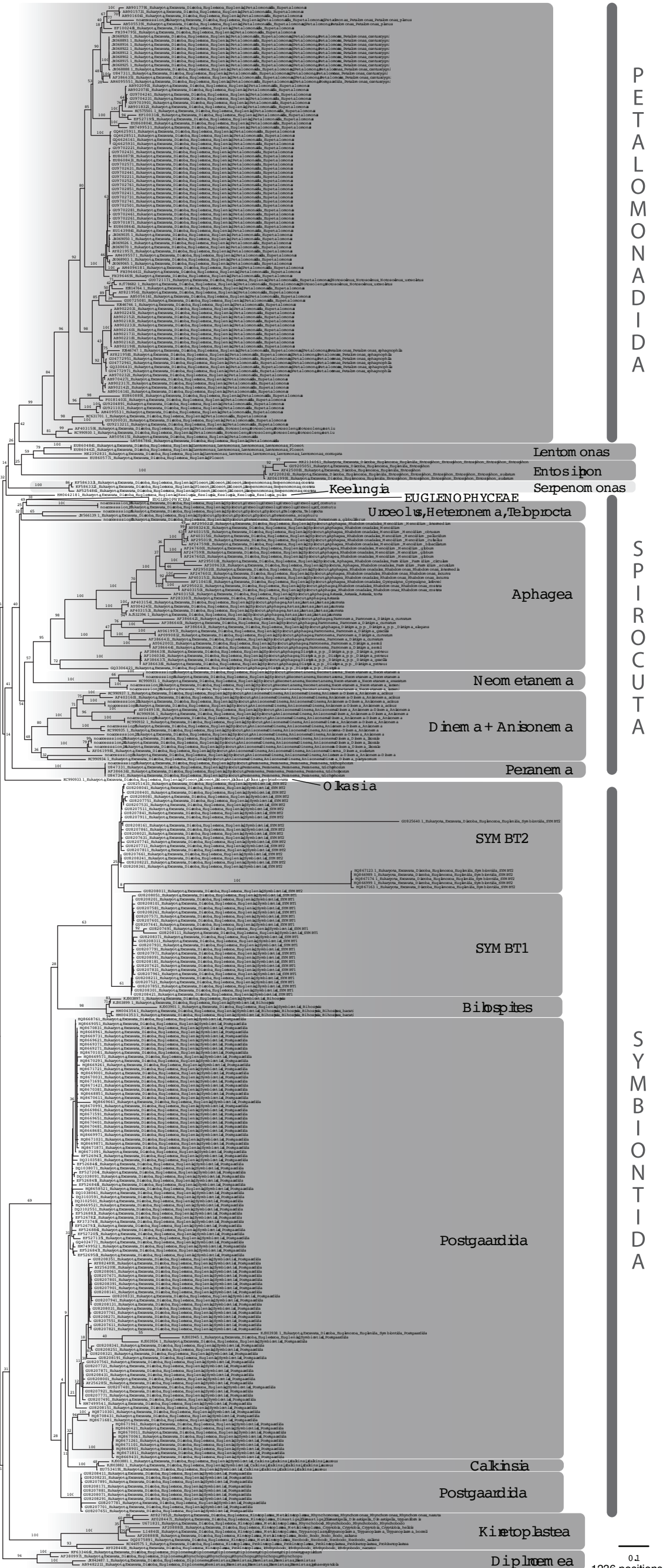
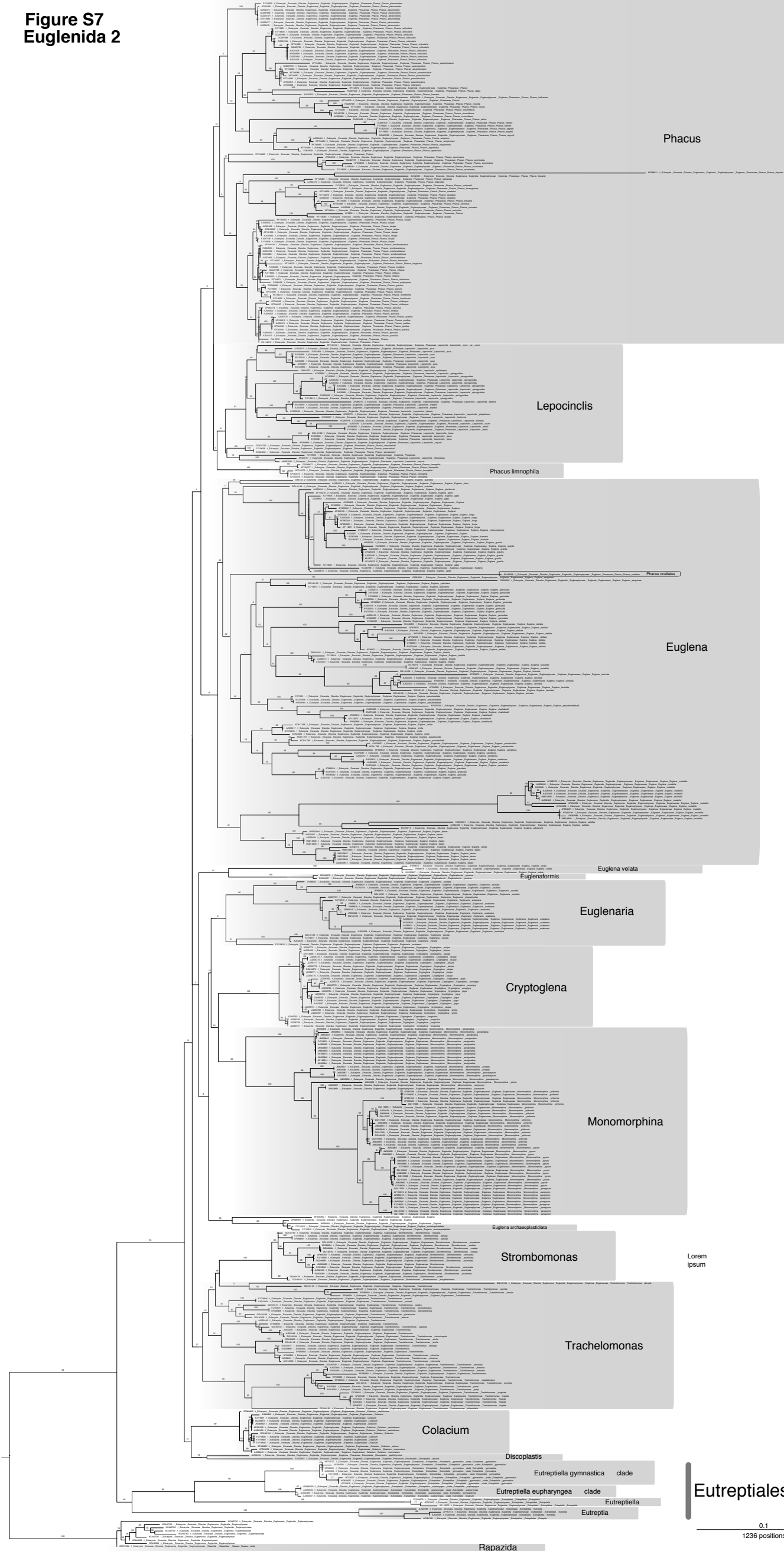


Figure S7
Euglenida 2

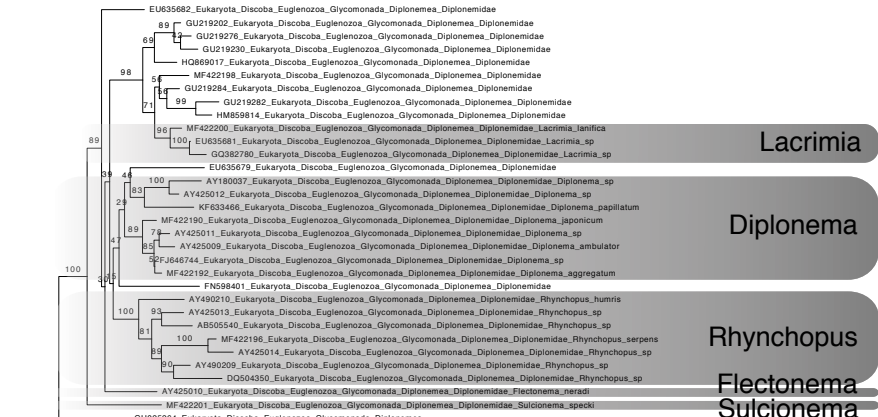


EUGLENA

Eutreptiales

0.1
1236 positions

Figure S8
Diplonemea



Diplonemidae

Rhynchopus

Flectonema

Sulcionema

Hemistasiidae

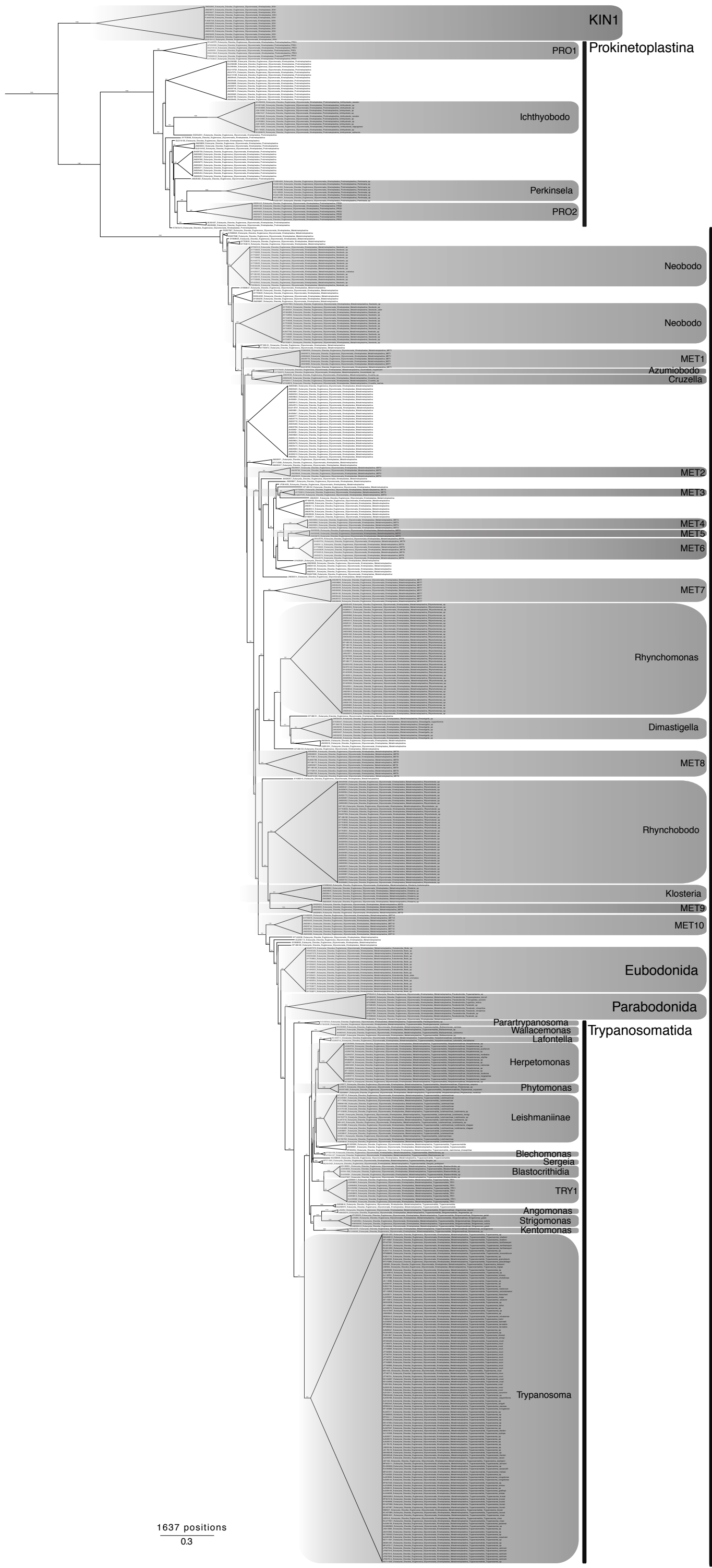
DSPDII

Eupelagonemidae

0.3

1637 positions

Figure S9
Kinetoplastea



Metakinetoplastina

KIN1

PRO1

Ichthyobodo

Perkinsela

PRO2

Neobodo

Neobodo

MET1

Azumiobodo

Cruzella

MET2

MET3

MET4

MET5

MET6

MET7

Rhynchomonas

Dimastigella

MET8

Rhynchobodo

Klosteria

MET9

MET10

Eubodonida

Parabodonida

Paratrypanosoma

Wallacemonas

Lafontella

Herpetomonas

Phytomonas

Leishmaniinae

Blechomonas

Sergeia

Blastocrithidia

TRY1

Angomonas

Strigomonas

Kentomonas

Trypanosoma

Prokinetoplastina

Trypanosomatida