Supporting Information for:

Phylogeny of parasitic Parabasalia and free-living relatives inferred from conventional markers *vs. Rpb1,* a single-copy gene

(*PLOS One,* 2011. doi:10.1371/journal.pone.0020774)

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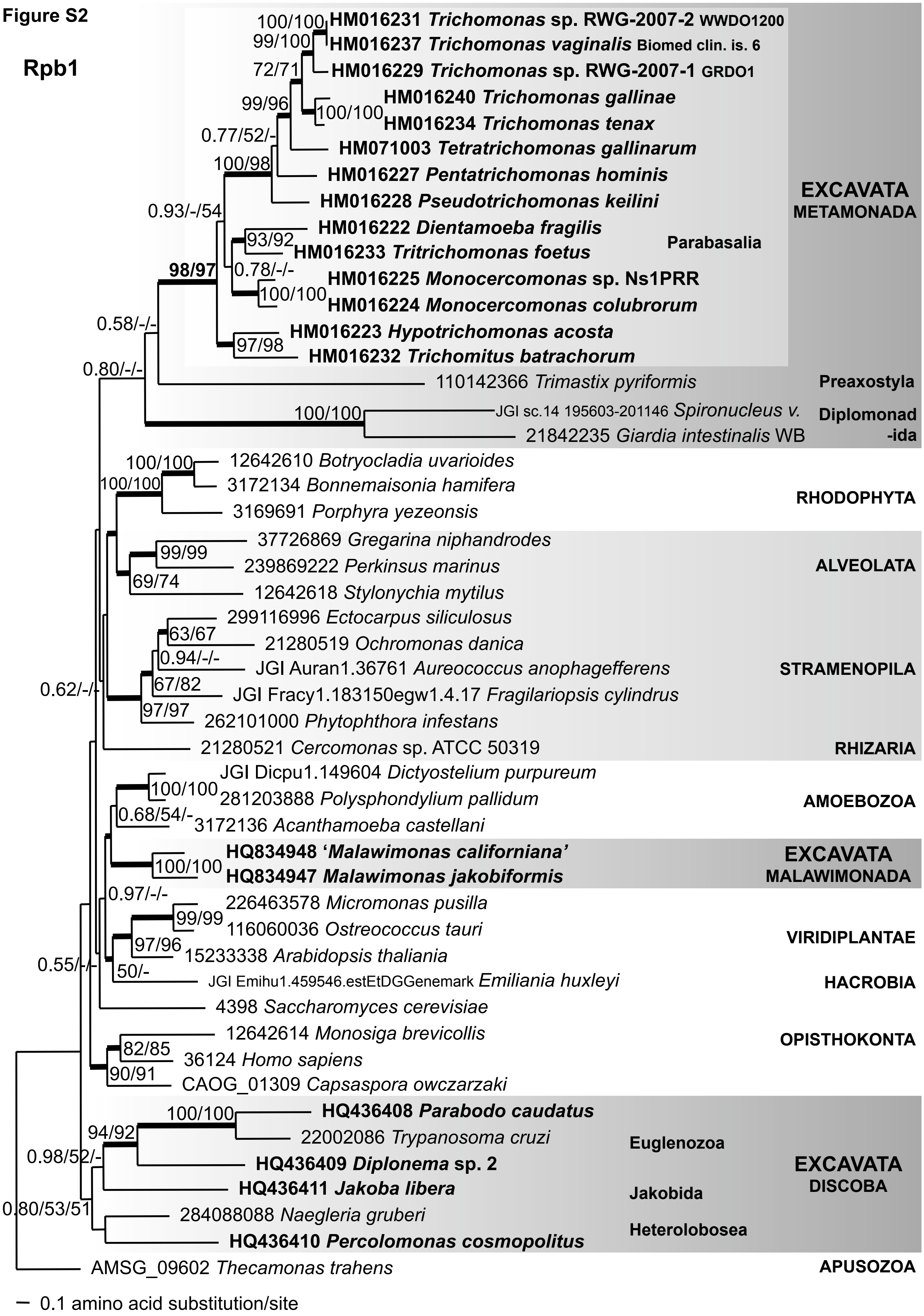
Figure S2: Rooted eukaryotic Rpb1 phylogeny with constant sites removed recovers monophyletic Metamonada topology.
New sequences from this study are indicated in bold type. This tree topology was calculated by RAxML 7.2.7 from 857 unambiguously aligned amino acids spanning conserved regions A to G of Rpb1, with constant sites removed. Thickened lines indicate the nodes supported by a Bayesian posterior probability of 1.00. Numbers at the nodes correspond to Bayesian posterior probabilities from the best post burn-in 1500 trees (chains run for 2×10^6 generations), followed by percent bootstrap support $\geq 50\%$ given by PhyML (100 replicates) and RAxML (1000 replicates). LnL = – 56091.16, $\alpha = 1.33$, pI= 0.0013. Scale bar represents 0.1 amino acid substitution per site. The alignment is provided in the **Supporting Information Dataset S8**. GenBank accession numbers, Joint Genome Institute or Broad Institute locus IDs are shown at the left for each taxon.

Figure S2


Rpb1
100/100 HM016231 Trichomonas sp. RWG-2007-2 WWDO1200
99/100 HM016237 Trichomonas vaginalis Biomed clin. is. 6
72/71 HM016229 Trichomonas sp. RWG-2007-1 GRDO1
99/96 HM016240 Trichomonas gallinae
100/100 HM016234 Trichomonas tenax
0.77/52/- HM071003 Tetratrichomonas gallinarum
100/98 HM016227 Pentatrichomonas hominis
HM016228 Pseudotrichomonas keilini
0.93/-/54 HM016222 Dientamoeba fragilis
93/92 HM016233 Tritrichomonas foetus
98/97 0.78/-/- HM016225 Monocercomonas sp. Ns1PRR
100/100 HM016224 Monocercomonas colubrorum
0.58/-/- HM016223 Hypotrichomonas acosta
97/98 HM016232 Trichomitus batrachorum
0.80/-/- 110142366 Trimastix pyriformis
100/100 JGI sc.14 195603-201146 Spironucleus v.
21842235 Giardia intestinalis WB
Parabasalia
EXCAVATA
METAMONADA
Preaxostyla
Diplomonad-ida
100/100 12642610 Botryocladia uvarioides
100/100 3172134 Bonnemaisonia hamifera
3169691 Porphyra yezeonsis
RHODOPHYTA
37726869 Gregarina niphandrodes
99/99 239869222 Perkinsus marinus
69/74 12642618 Stylonychia mytilus
ALVEOLATA
299116996 Ectocarpus siliculosus
63/67 21280519 Ochromonas danica
0.94/-/- JGI Auran1.36761 Aureococcus anophagefferens
67/82 JGI Fracy1.183150egw1.4.17 Fragilariopsis cylindrus
0.62/-/- 97/97 262101000 Phytophthora infestans
STRAMENOPILA
21280521 Cercomonas sp. ATCC 50319
RHIZARIA
JGI Dicpu1.149604 Dictyostelium purpureum
100/100 281203888 Polysphondylium pallidum
0.68/54/- 3172136 Acanthamoeba castellani
AMOEBOZOA
HQ834948 'Malawimonas californiana'
100/100 HQ834947 Malawimonas jakobiformis
EXCAVATA
MALAWIMONADA
0.97/-/- 226463578 Micromonas pusilla
99/99 116060036 Ostreococcus tauri
97/96 15233338 Arabidopsis thaliania
VIRIDIPLANTAE
0.55/-/- 50/- JGI Emihu1.459546.estEtDGGenemark Emiliania huxleyi
HACROBIA
4398 Saccharomyces cerevisiae
12642614 Monosiga brevicollis
82/85 36124 Homo sapiens
90/91 CAOG_01309 Capsaspora owczarzaki
OPISTHOKONTA
100/100 HQ436408 Parabodo caudatus
94/92 22002086 Trypanosoma cruzi
0.98/52/- HQ436409 Diplonema sp. 2
Euglenozoa
HQ436411 Jakoba libera
Jakobida
0.80/53/51 284088088 Naegleria gruberi
HQ436410 Percolomonas cosmopolitus
Heterolobosea
EXCAVATA
DISCOBA
AMSG_09602 Thecamonas trahens
APUSOZOA
0.1 amino acid substitution/site