Supplement

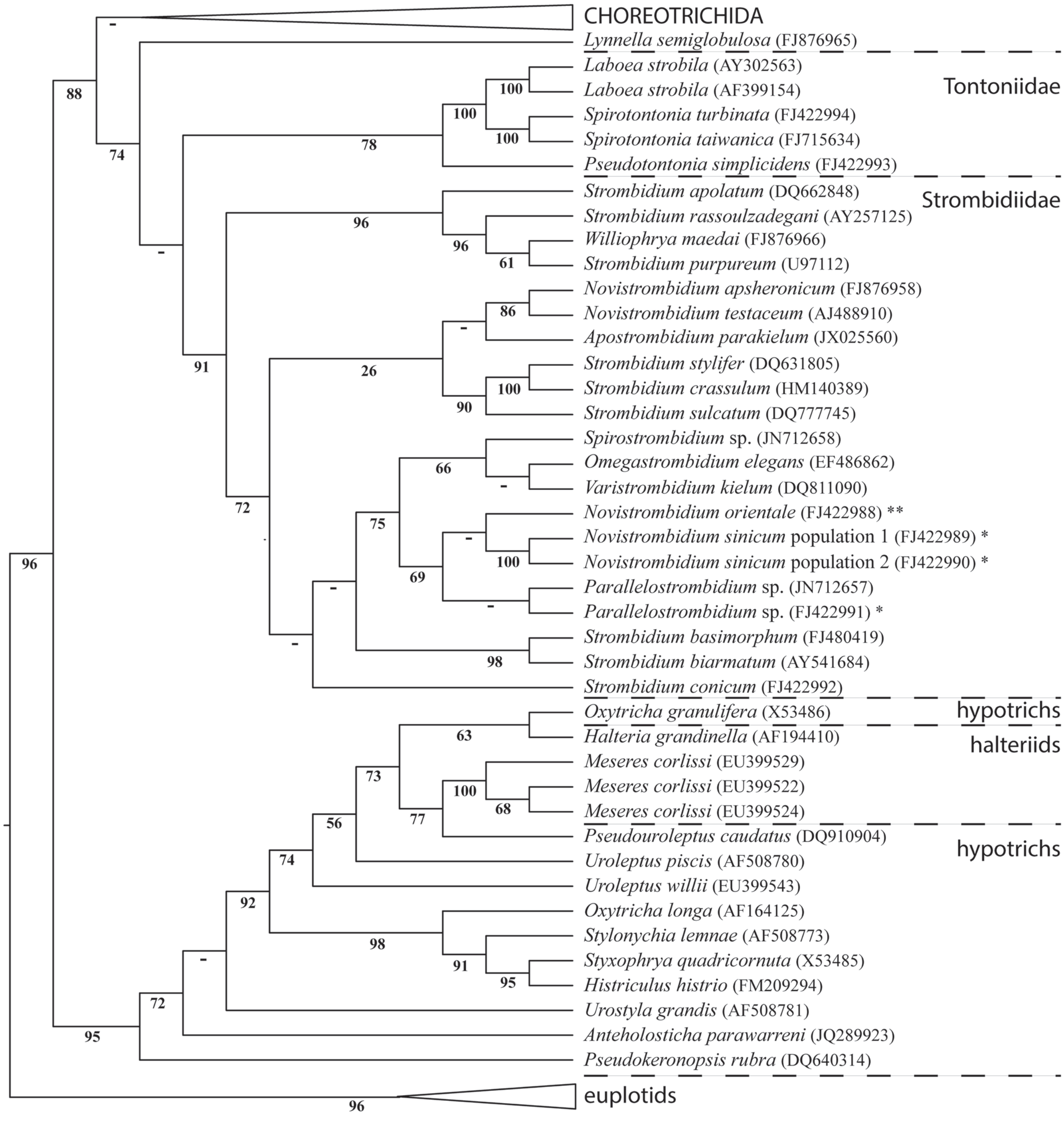


Fig. S1. Profile Neighbor Joining tree of the Oligotrichida inferred from small subunit ribosomal RNA (SSU rRNA) gene sequences (66 taxa and 1823 nucleotide positions) aligned with the Muscle algorithm (Edgar 2004) implemented in MEGA ver. 5.1 (Tamura *et al.* 2011). The tree was computed with ProfDistS (Wolf *et al.* 2008). Support values are listed at the nodes. Values below 50% are represented by dashes. * – initially published as *Spirostrombidium* sp.; ** – initially published as *Parallelostrombidium* sp.

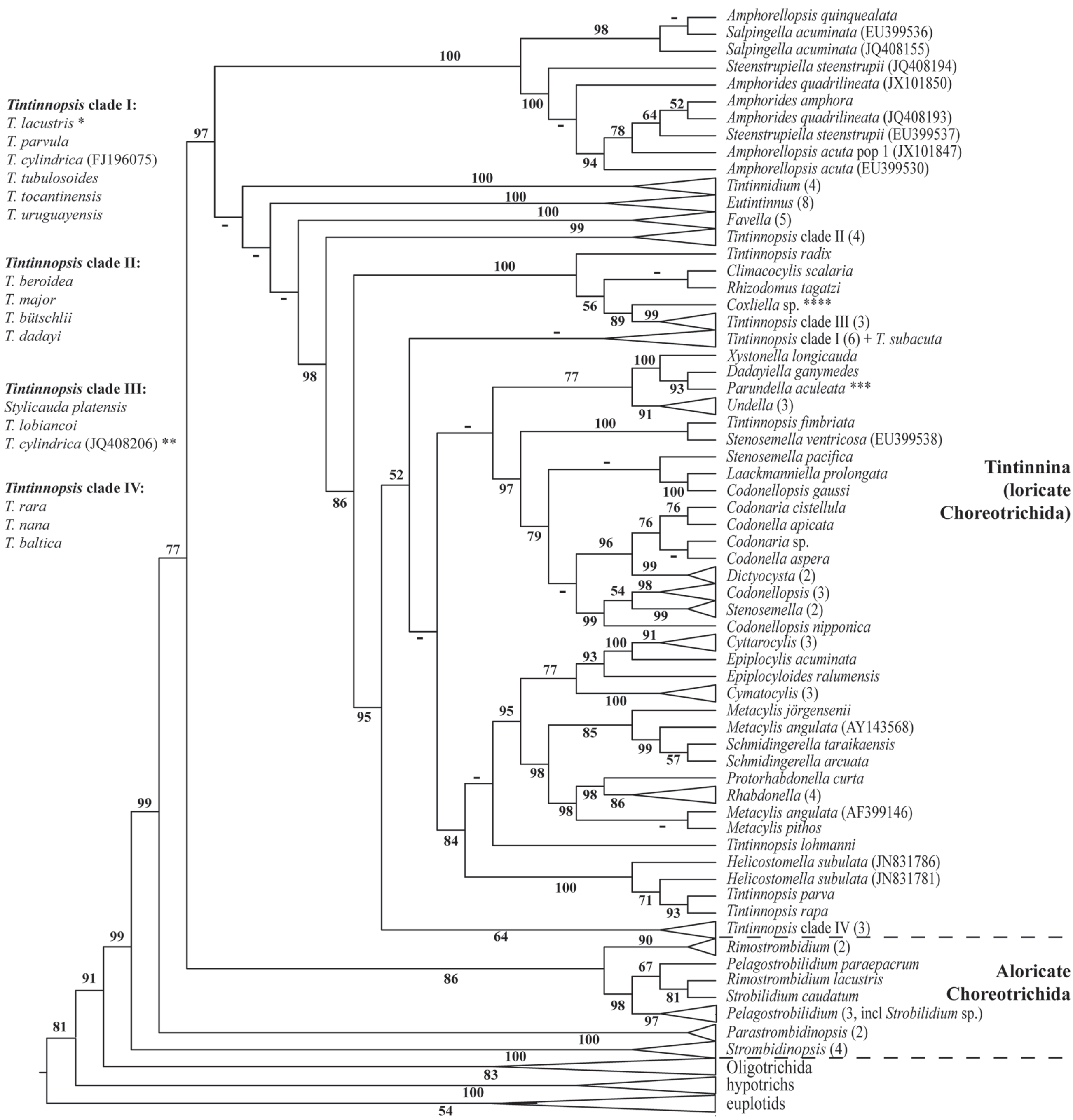


Fig. S2. Profile Neighbor Joining tree of the Choreotrichida inferred from small subunit ribosomal RNA (SSU rRNA) gene sequences (138 taxa and 1859 nucleotide positions) aligned with the Muscle algorithm (Edgar 2004) implemented in MEGA ver. 5.1 (Tamura *et al.* 2011). The tree was computed with ProfDistS (Wolf *et al.* 2008). Support values are listed at the nodes. Values below 50% are represented by dashes. Branches with unambiguously clustered taxa are collapsed, species of the genus *Tintinnopsis* grouped in 5 different clades numbered I–V. * – after Kofoid and Campbell (1929) a synonym of *Codonella cratera*; ** – does not correspond with the redescription of Agatha and Riedel-Lorjé (2006); *** – possibly incorrectly identified, might be *Dadayiella acutiformis*; **** – invalid taxon, very likely a replacement lorica (see text).

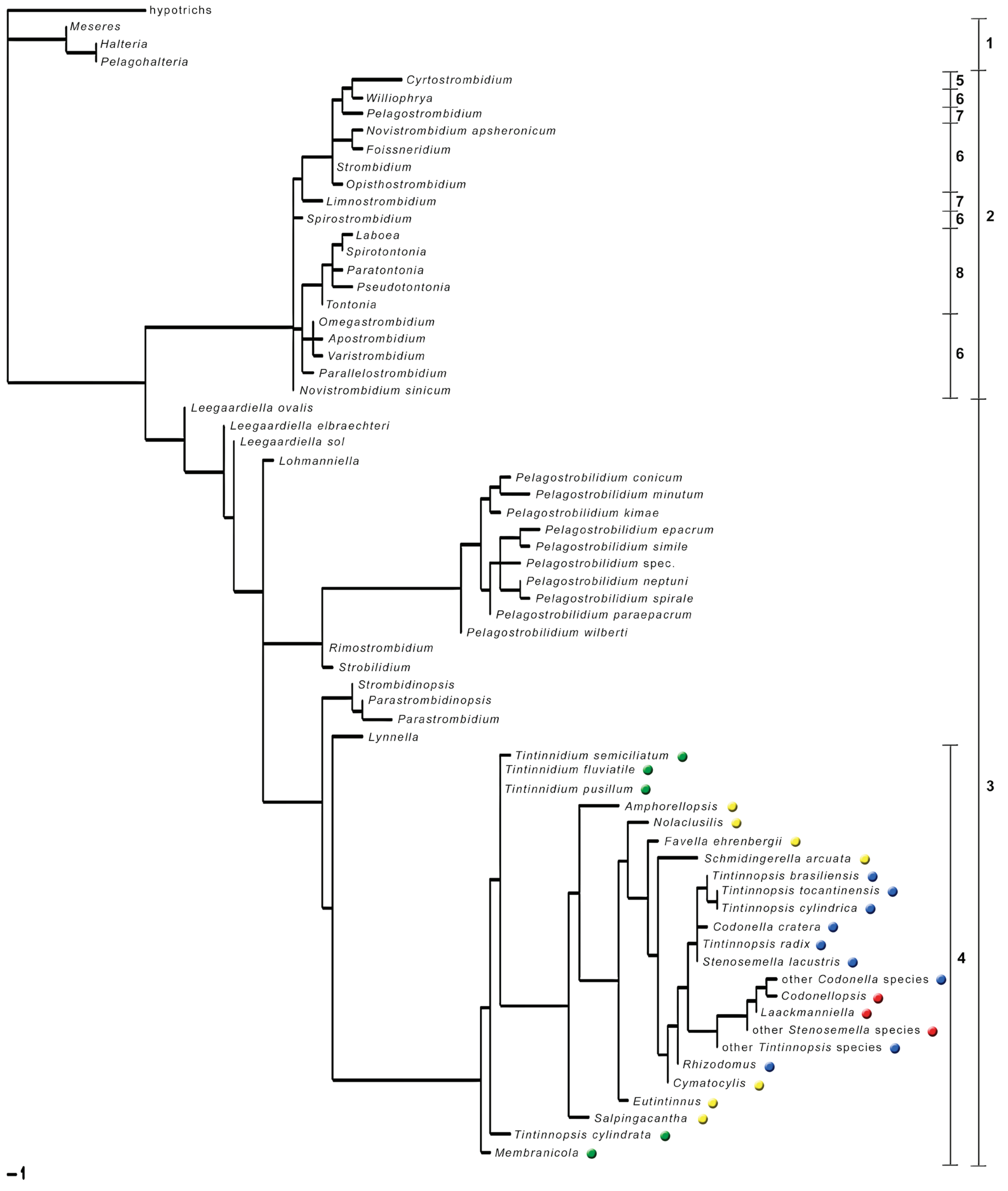


Fig. S3. Maximum parsimony tree calculated with PAUP* vers. 4.0b10 (Swofford 2002), equally weighted morphologic characters (Tables S1, S2), and hypotrichs as outgroup. 83 out of 94 characters parsimony-informative, tree length 227, consistency index 0.71, homoplasy index 0.29, retention index 0.95. 1 – halteriids, 2 – oligotrichids, 3 – choreotrichids, 4 – tintinnids, 5 – Cyrtostrombidiidae, 6 – Strombidiidae, 7 – Pelagostrombidiidae, 8 – Tontoniidae. Most common lorica structures: green – flexible, agglomerated, blue – hard, agglomerated, yellow – hard, entirely hyaline, red – hard, composed of hyaline collar and agglomerated bowl. *Pelagostrobilidium* spec. sensu Ota and Taniguchi (2003).

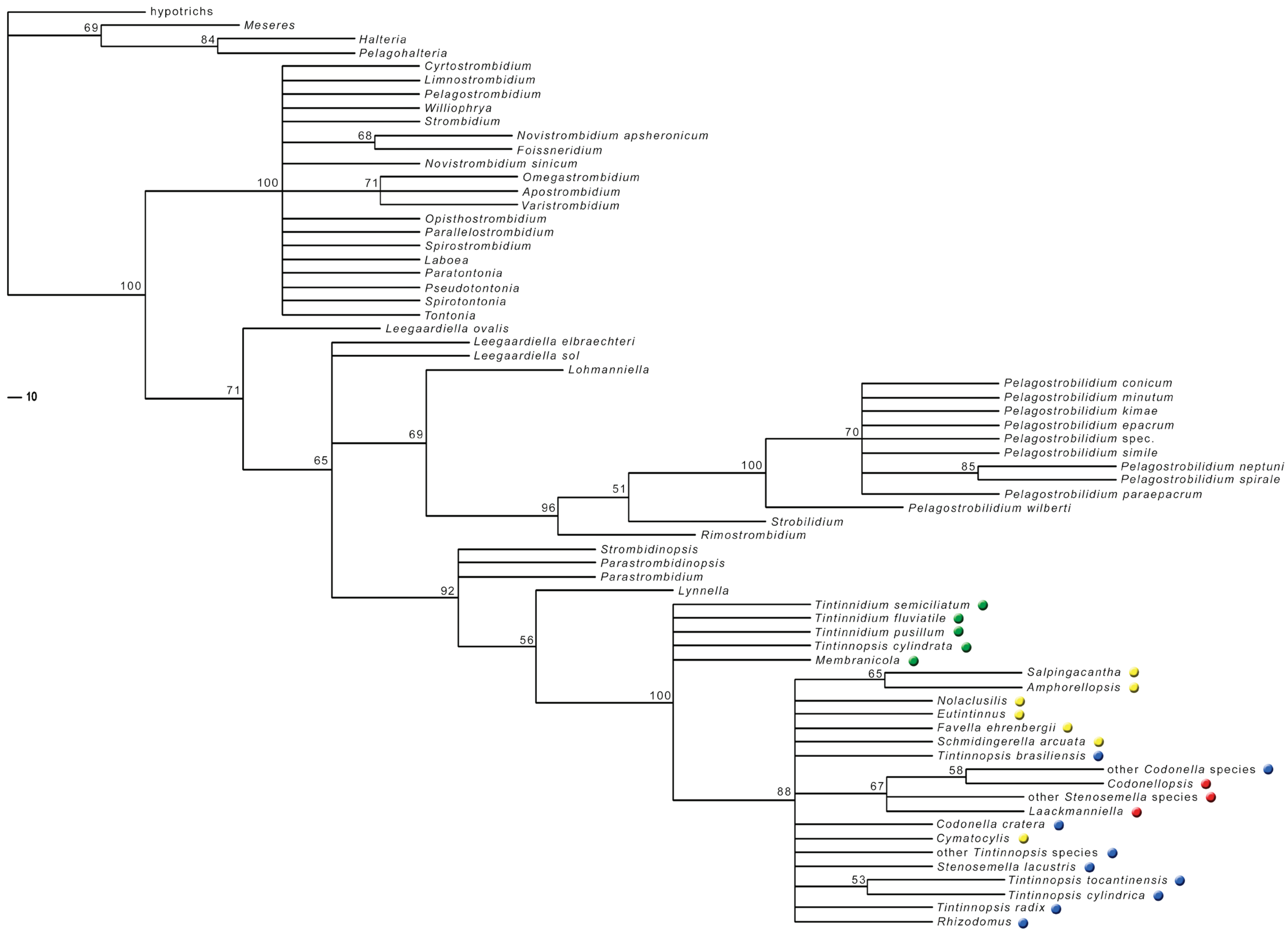


Fig. S4. Bootstrap 50% majority-rule consensus parsimony tree inferred from morphologic data of the Oligotrichea (Tables S1, S2), using PAUP* ver. 4.0b10 (Swofford 2002) and the hypotrichs as outgroup. 83 out of 94 characters were parsimony-informative. The bootstrap method with heuristic search included 100 replicates. 1 – halteriids, 2 – oligotrichids, 3 – choreotrichids, 4 – tintinnids, 5 – Cyrtostrombidiidae, 6 – Strombidiidae, 7 – Pelagostrombidiidae, 8 – Tontoniidae. Most common lorica structures: green – flexible, agglomerated, blue – hard, agglomerated, yellow – hard, entirely hyaline, red – hard, composed of hyaline collar and agglomerated bowl. *Pelagostrobilidium* spec. sensu Ota and Taniguchi (2003).

Fig. S5. Strict consensus tree of the Oligotrichea calculated with the computer program Hennig86 by a heuristic analysis of equally weighted morphologic characters (Tables S1, S2) and the branch-swapping algorithm, using the hypotrichs as outgroup. It has a length of 180, a consistency index of 66, and a retention index of 90. 1 – halteriids, 2 – oligotrichids, 3 – choreotrichids, 4 – tintinnids, 5 – Cyrtostrombidiidae, 6 – Strombidiidae, 7 – Pelagostrombidiidae, 8 – Tontoniidae. Most common lorica structures: green – flexible, agglomerated, blue – hard, agglomerated, yellow – hard, entirely hyaline, red – hard, composed of hyaline collar and agglomerated bowl. *Pelagostrobilidium* spec. sensu Ota and Taniguchi (2003).

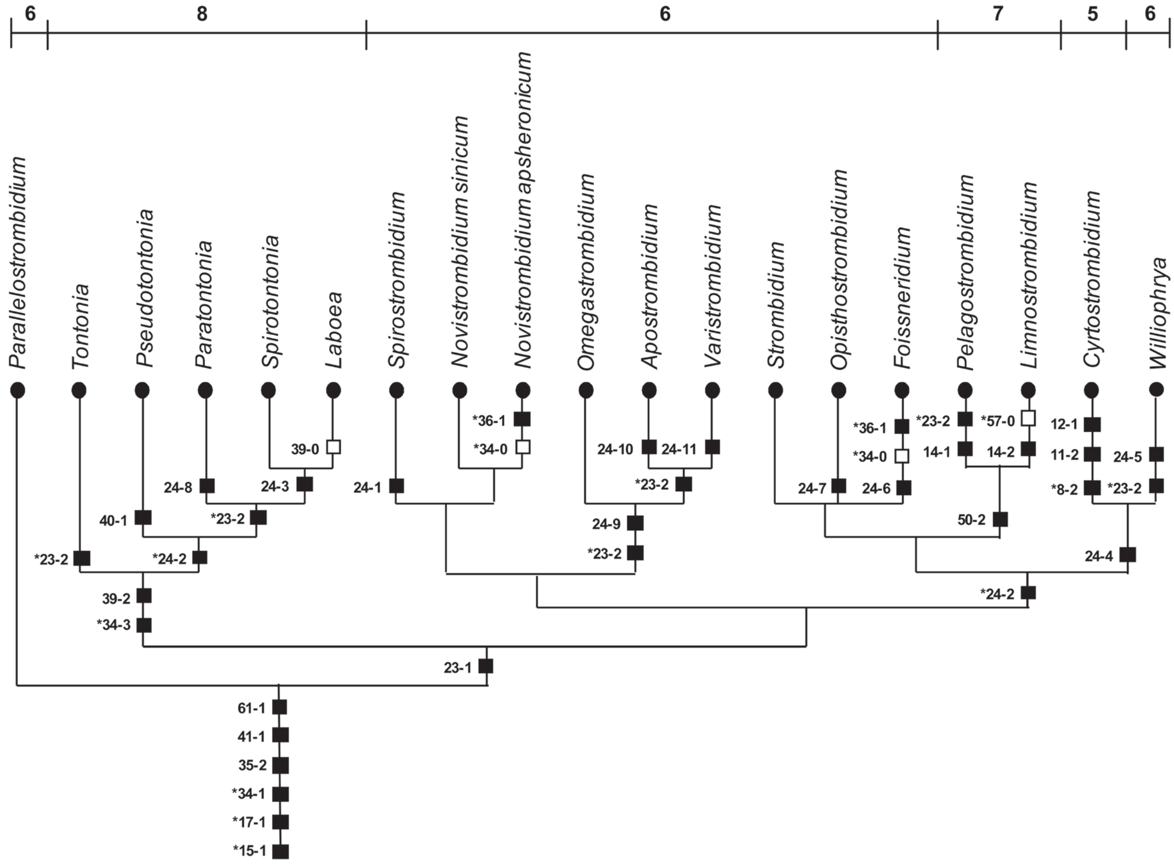
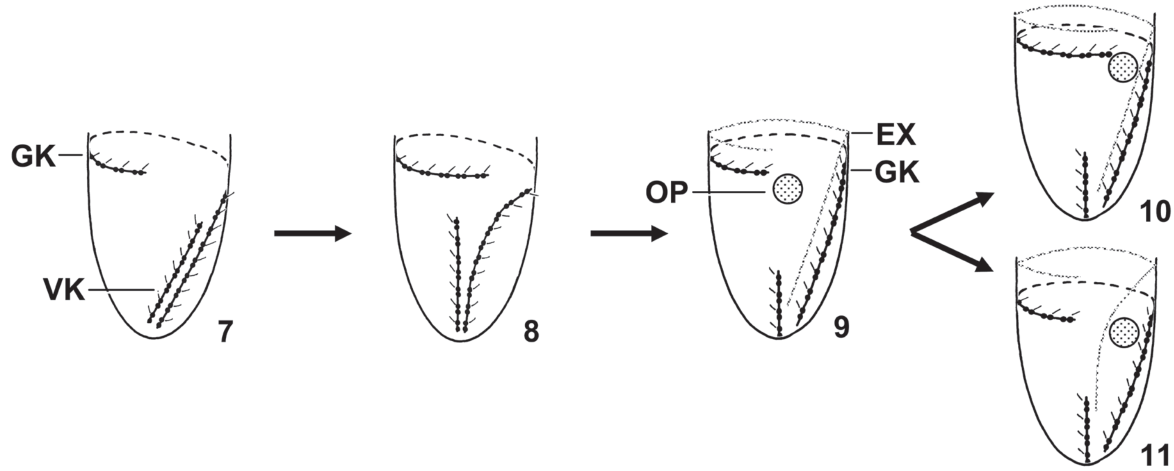
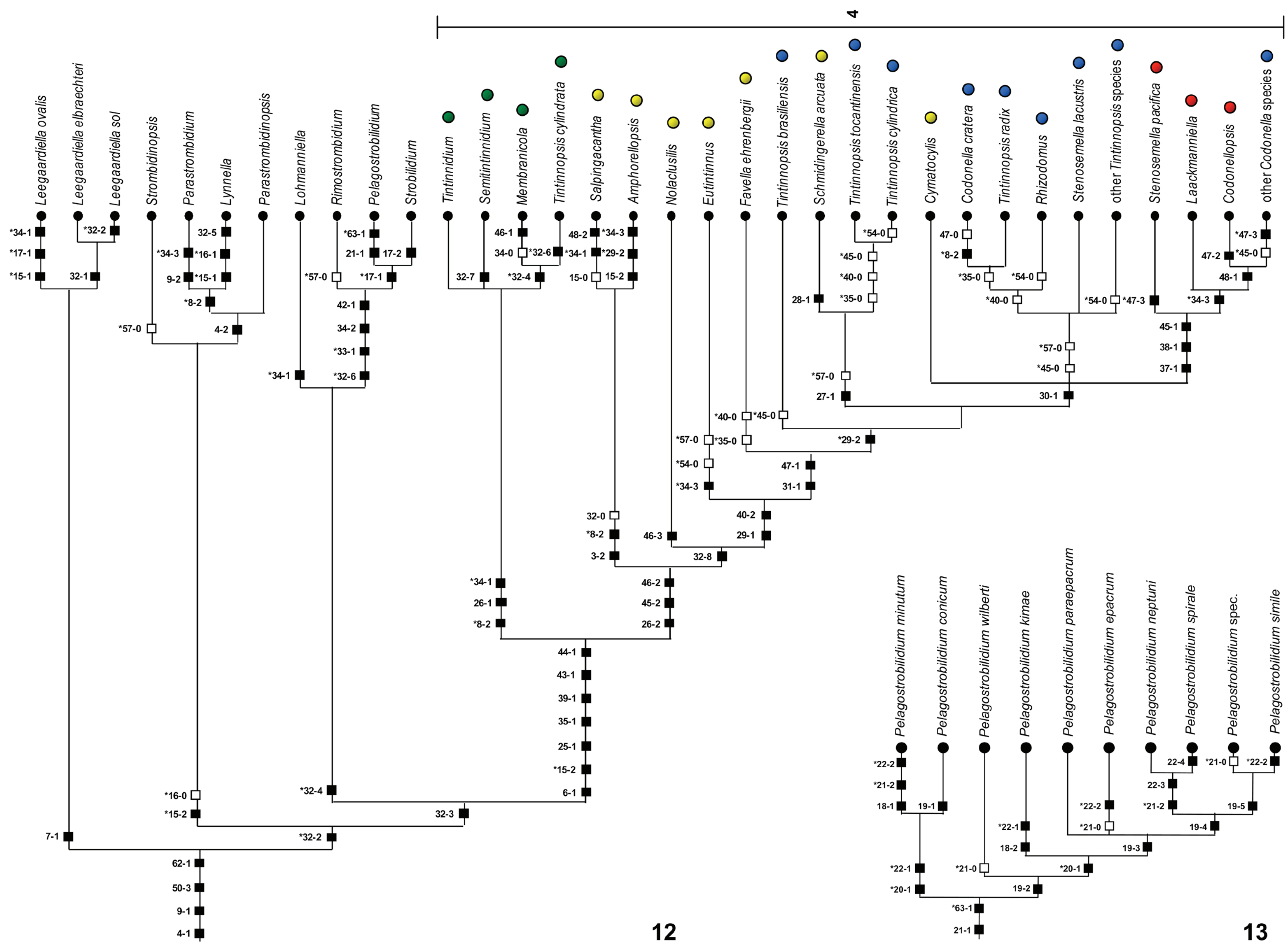


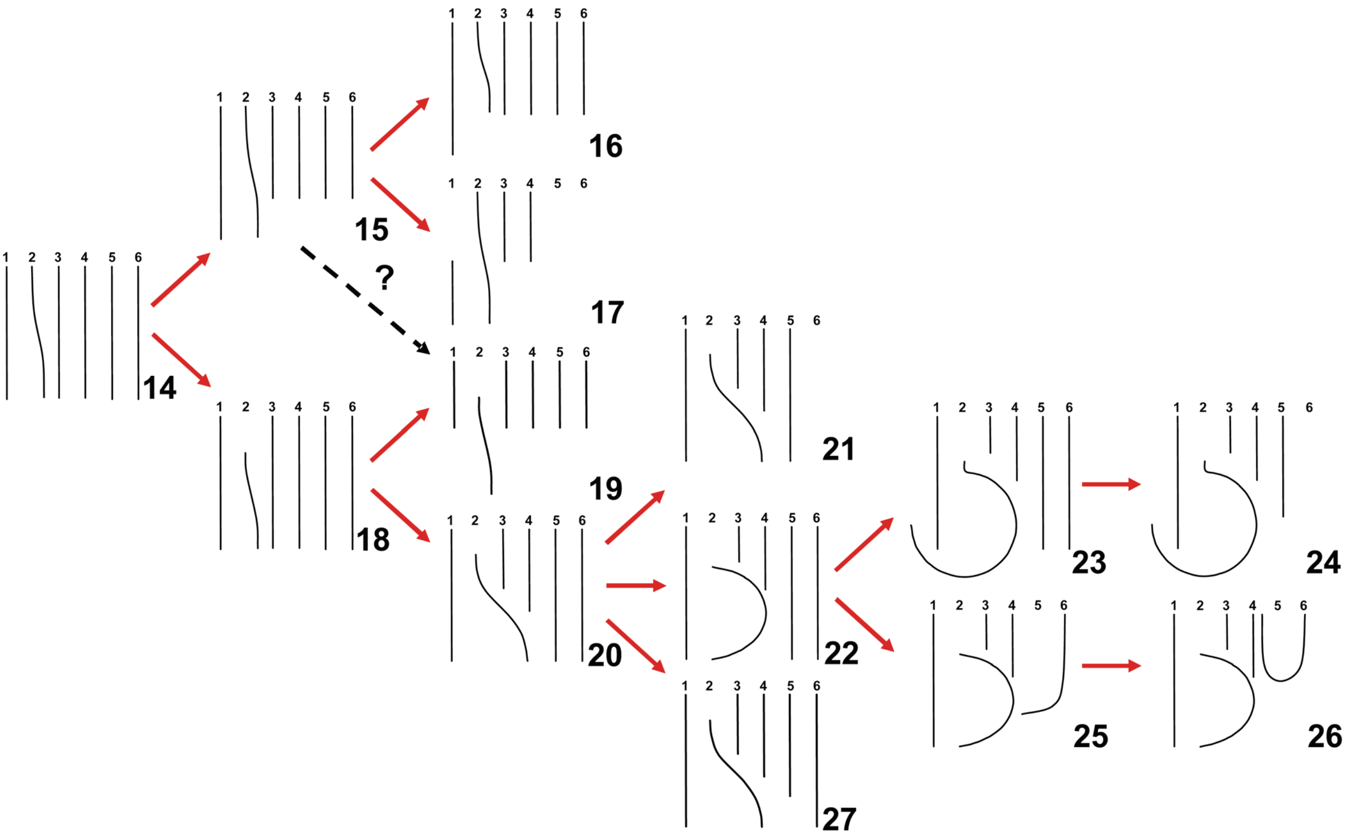
Fig. S6. Monophyletic oligotrichid ciliates in the maximum parsimony tree of the Oligotrichea generated by the Hennigian argumentation method. For character coding, see Table S1. Black squares mark apomorphies, open squares denote reversals to plesiomorphic states, and asterisks mark homoplasies. 5 – Cyrtostrombidiidae, 6 – Strombidiidae, 7 – Pelagostrombidiidae, 8 – Tontoniidae.



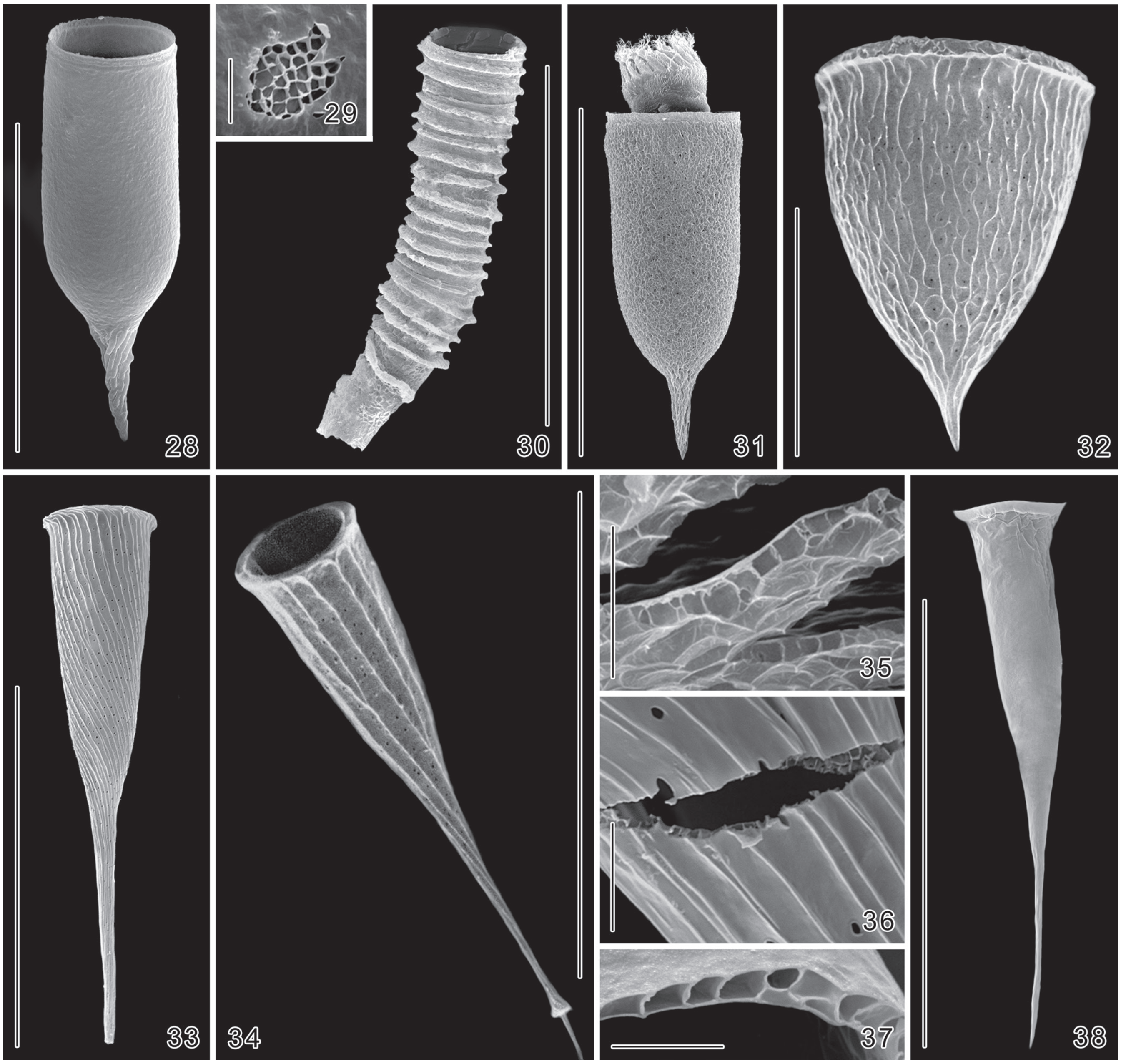
Figs S7–S11. Evolution of somatic ciliary patterns in the genera *Parallelostrombidium* and *Novistrombidium* [originals based on illustrations of Montagnes and Taylor 1994 (7), Xu *et al.* 2006 (8), Liu *et al.* 2009 (10), and Agatha 2003 (11); protargol impregnation]. The pattern of *Parallelostrombidium* (*Parallelostrombidium*) *siculum* (7) probably gave rise to the pattern of *Parallelostrombidium* (*Asymptokinetum*) *paralatum* (8), which possibly represents the transition stage to the genus *Novistrombidium* (9). The hypothetic ancestor of that genus had the stripe of extrusome attachment sites associated with the girdle kinety as usual, and both structures are posterior to the oral primordium. It represents the origin of the subgenus *Propecingulum* (10; with *N. ioanum* nov. comb., *N. orientale*, *N. platum* nov. comb., and *N. sinicum*) and the subgenus *Novistrombidium* (11; with *N. apsheronicum* and *N. testaceum*). EX – extrusome attachment sites, GK – girdle kinety, OP – oral primordium, VK – ventral kinety.



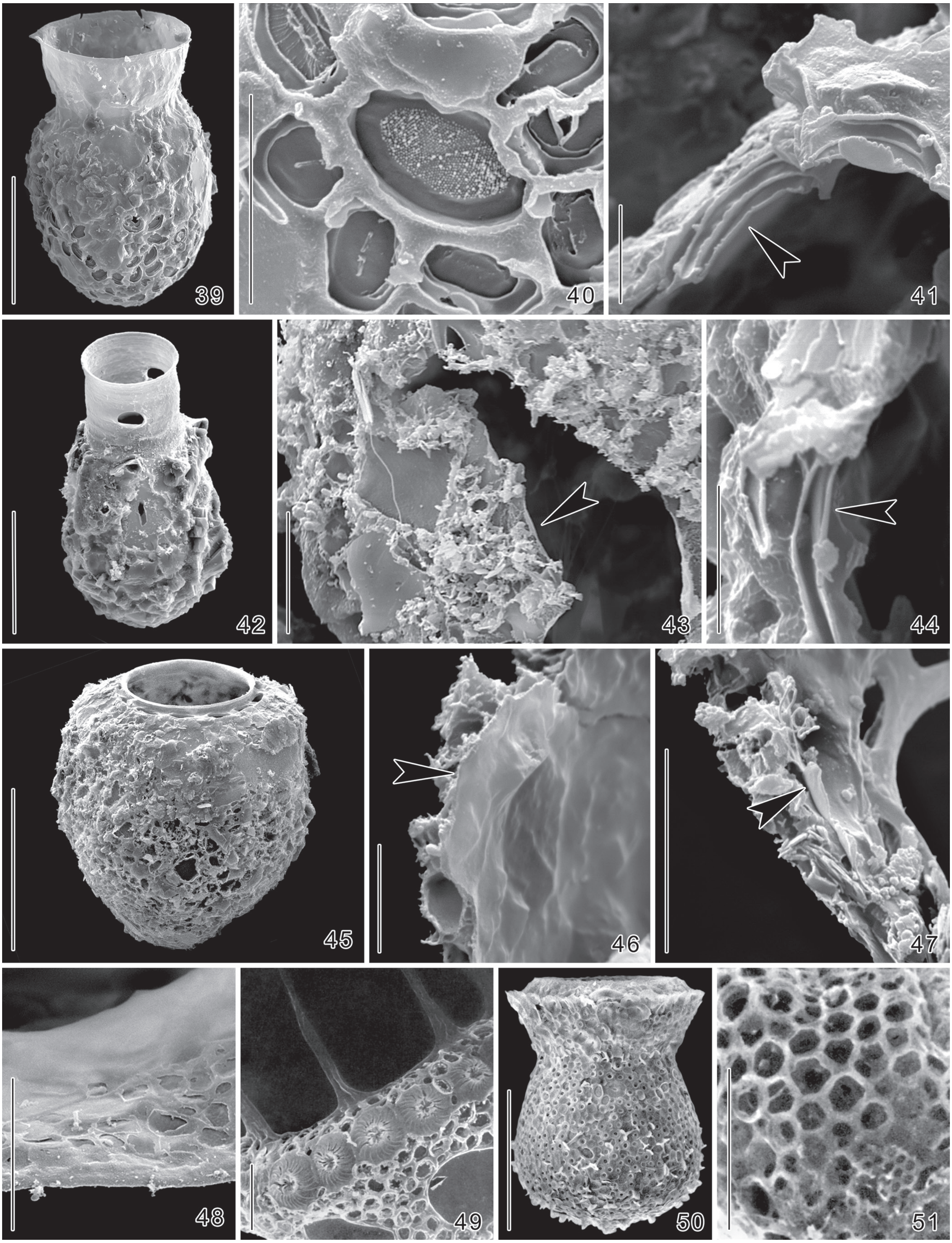
Figs S12, S13. Monophyletic choreotrichid ciliates (12) and monophyletic genus *Pelagostrobilidium* (13) in the maximum parsimony tree of the Oligotrichea generated by the Hennigian argumentation method. For character coding, see Table S1. Black squares mark apomorphies, open squares denote reversals to plesiomorphic states, and asterisks mark homoplasies. 4 – tintinnids, *Semitintinnidium* – subgenus of the genus *Tintinnidium*, *Tintinnidium* – subgenus of the identically named genus. Most common lorica structures: green – flexible, agglomerated, blue – hard, agglomerated, yellow – hard, entirely hyaline, red – hard, composed of hyaline collar and agglomerated bowl.



Figs S14–S27. Evolution of somatic ciliary patterns in choreotrichid genus *Pelagostrobilidium* [originals based on Lynn and Montagnes 1988 (21, 26), Montagnes and Taylor 1994 (25), Agatha and Riedel-Lorjé 1998 (16), Song and Bradbury 1998 (24), Ota and Taniguchi 2003 (23), Küppers *et al.* 2006 (18), Lee *et al.* 2011 (19), Liu *et al.* 2012 (17, 27); protargol impregnation]. **14** – Hypothetic *Rimostrombidium*-like ancestor; **15, 20, 22** – hypothetic intermediate states; **16** – *P. conicum*; **17** – *P. minutum*; **18** – *P. wilberti*; **19** – *P. kimae* nov. spec.; **21** – *P. epacrum*; **23 – *Pelagostrobilidium*** spec.; **24** – *P. simile*; **25** – *P. neptuni*; **26** – *P. spirale*; **27 –** *P. paraepacrum*. 1–5 – somatic kineties 1–5.



Figs S28–S38. Structure and texture of hyaline loricae [28–31, 33, 35–38, originals from specimens collected at the U.S. east coast (28, 29, 31, 35) and in the Mediterranean Sea (30, 33, 36–38); 32, after Abboud-Abi Saab 2008; 34, after Gold and Morales 1977; scanning electron micrographs]. **28, 29** – *Favella panamensis*, lateral view of lorica (28) and lorica wall with removed outer surface (29) showing the monolaminar texture with alveoli; **30** – *Climacocylis* sp., lateral view of lorica. The monolaminar texture with alveoli is recognizable in the posterior portion of the lorica, where the surface layer has been removed; **31, 35** – *Schmidingerella arcuata*, lateral view of lorica (31) and fracture of lorica wall (35). The lorica wall has minute pores and reticulate ridges on the outer surface; **32** – *Epiplocyloides*, lateral view of lorica. The wall has minute pores and reticulate ridges; **33, 34, 36 –** *Rhabdonella spiralis* (33, 36) and *Rhabdonellopsis apophysata* (34), lateral views of loricae (33, 34) and fracture of lorica wall (36). The walls have minute pores and spiralled, anastomosing ridges; **37, 38** – *Xystonella longicauda*, lateral view of lorica (38) and fracture of lorica wall (37). Scale bars: 200 µm (28, 30, 31, 33, 34, 38), 50 µm (32), and 5 µm (29, 35–37).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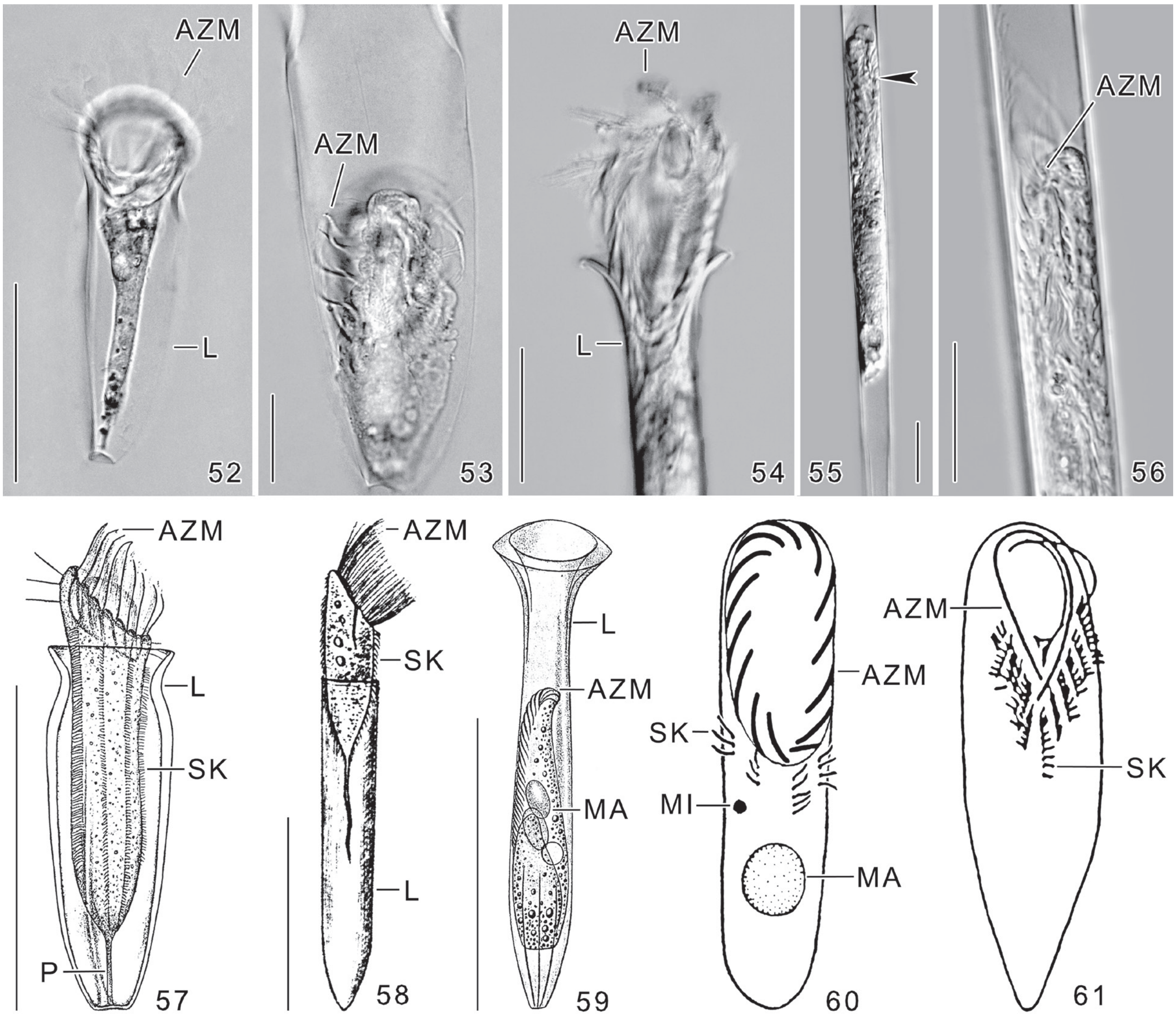

Figs S52–S61. Obliquely orientated adoral zones of membranelles in tintinnids (52–56, originals from specimens collected in the Mediterranean Sea; 57, from Fauré-Fremiet 1924; 58, redrawn by Kent 1880–1882; 59, from Entz 1884; 60, 61, from Small and Lynn 1985; 52–59, from life; 60, 61, protargol impregnation). **52, 53, 57** – *Amphorides quadrilineata*, extended (52, 57) and contracted (53) specimens; **54–56** – *Salpingella attenuata*, just extending (54) and contracted specimens (55, 56). Arrowhead marks oblique adoral zone (55); **58** – *Bursaopsis obliqua*, extending specimen. Size taken from Kent (1881–1882); **59** – *Steenstrupiella entzi*. Entz (1884) and Kofoid and Campbell (1929) identified the cell in the lorica with a hypotrich ciliate, possibly based on the oblique and thus untypical orientation of the adoral zone; **60** – *Salpingacantha* sp., contracted specimen without lorica (size not mentioned); **61** – *Amphorellopsis acuta*, contracted specimen without lorica (size not mentioned). Scale bars: 100 µm (52, 57–59) and 20 µm (53–56). AZM – adoral zone of membranelles, L – lorica, MA – macronucleus, MI – micronucleus, P – peduncle, SK – somatic kineties.

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Figs S39–S51. Structure and texture of agglomerated loricae (39–48, originals from specimens collected in the Mediterranean Sea; 49, after Burns 1983; 50, 51, after Gold and Morales 1977; scanning electron micrographs). **39–41, 48** – *Codonella aspera*, lateral view of lorica (39), detail of outer bowl surface with impressions of formerly incrustrated coccoliths (40), fracture surface of bowl (41), and inner collar surface (48). The wall seems to be composed of compact matrix material, in which particles are/were embedded, and an inner layer (arrowhead); **42–44** – *Codonellopsis schabi*, lateral view of lorica (42) and surfaces and fracture surfaces of bowl (43, 44). Apparently, the agglomerated particles are embedded into compact matrix material and an inner layer (arrowheads) lines the bowl; **45–47** – *Stenosemella ventricosa*, lateral view of lorica (45) and fracture surfaces of bowls (46, 47) showing compact matrix material, in which particle are embedded, and a continuous inner layer (arrowheads); **49** – *Dictyocysta reticulata*, transition zone between collar and bowl. The impressions of the formerly embedded coccoliths strongly resemble those in *Codonella* (Figs S39, S40); accordingly, we assume a similar wall texture; **50, 51** – *Codonaria oceanica*, lateral view of lorica (50) and lorica matrix (51) after hydrochloric acid treatment that removed the coccoliths. The impressions of the formerly embedded coccoliths strongly resemble those in *Codonella* (Figs S39, 40); thus, a similar wall texture is supposed. Scale bars: 50 µm (50), 40 µm (39, 42, 45), 10 µm (40, 43, 47–49, 51), and 4 µm (41, 44, 46).

Table S1. Character states and coding used for construction of a cladogram with the Hennigian argumentation method (first or only code; Figs. S6, S12, S13) and for computer analyses (only or second code; Figs. S3–S5). The coding is mainly based on outgroup comparison with the hypotrichs. If not stated otherwise, the characters are ordered/additive (the states have a certain sequence; Wagner/Farris optimisation).

	Characters	
	Apomorphic states	Plesiomorphic states
1	Cell usually globular to obconical (coded 1)	Cell usually distinctly dorsoventrally flattened (coded 0)
2	Usually planktonic (coded 1)	Usually benthic (coded 0)
3	Adoral zone of membranelles mainly apical (coded 1) or secondarily ventral in contracted specimens (coded 2)	Adoral zone of membranelles mainly ventral (coded 0)
4	Adoral zone of membranelles circular (coded 1) or secondarily with minute ventral gap (coded 2)	Adoral zone of membranelles C-shaped (coded 0)
5	30–50% (coded 1) or 0% (coded 2) of adoral polykinetids composed of four rows of basal bodies	> 90% of adoral polykinetids composed of four rows of basal bodies (coded 0)
6	Postciliary and transverse microtubules absent in adoral membranelles (coded 1)	Postciliary and transverse microtubules present in adoral membranelles (coded 0)
7	Collar polykinetids bipartite (coded 1)	Collar polykinetids continuous (coded 0)
8	Adoral zone bipartite, i.e., composed of buccal membranelles with small polykinetids and short cilia and collar membranelles with broad polykinetids and long cilia (coded 1), buccal membranelles absent (coded 2)	Adoral zone not bipartite, i.e., polykinetids and cilia of membranelles gradually decrease in size towards the cytostome (coded 0)
9	Last collar membranelles with proximally elongated polykinetids (coded 1) or proximally and distally elongated polykinetids (coded 2)	All collar membranelles with similar-sized polykinetids (coded 0)
10	Undulating membrane(s) often diplostichomonad (two parallel rows of basal bodies) or polystichomonad (more than two parallel rows of basal bodies; coded 1)	Undulating membrane(s) monostichomonad (single row of basal bodies; coded 0)
11	Paroral membrane absent (coded 1), paroral and endoral membranes absent (coded 2)	Usually endoral and paroral membranes present (coded 0)
12	Cyrtos-like (conspicuously strong) pharyngeal fibres (coded 1)	Common pharyngeal fibres (coded 0)
13	Cirri absent (coded 1)	Cirri present (coded 0)
14 [a]	Somatic kinetids unciliated (coded 1) or with clavate cilia (coded 2)	Somatic kinetids with rod-shaped or fusiform cilia (coded 0)
15 [a]	Usually one or two somatic kineties (coded 1), usually ten or more somatic kineties (coded 2)	Usually 3–9 somatic kineties (coded 0)
16	≥ 40% of unspecialised somatic kineties shortened or entirely reduced (coded 1)	Unspecialised somatic kineties extend from adoral zone of membranelles to posterior cell end (coded 0)
17 [a]	Some unspecialised somatic kineties curved (coded 1) or forming a posterior spiral (coded 2)	Unspecialised somatic kineties longitudinal (coded 0)
18 [a]	*Pelagostrobilidium* – somatic kinety 1: anteriorly (coded 1) or posteriorly shortened (coded 2)	*Pelagostrobilidium* – somatic kinety 1: unshortened (coded 0)
19 [b]	*Pelagostrobilidium* – somatic kinety 2: posteriorly shortened (coded 1; coded 10000); anteriorly shortened (coded 2; coded 01000); distinctly sigmoidal (coded 3; coded 01100); semicircular (coded 4; coded 01110); or performs ~ 270° curvature (coded 5; coded 01111)	*Pelagostrobilidium*: somatic kinety 2 unshortened and slightly sigmoidal (coded 0; coded 00000)
20	*Pelagostrobilidium* – somatic kineties 3 and 4: posteriorly shortened (coded 1)	*Pelagostrobilidium* – somatic kineties 3 and 4: unshortened (coded 0)
21	*Pelagostrobilidium* – somatic kinety 5: posteriorly shortened (coded 1) or absent (coded 2)	*Pelagostrobilidium* – somatic kinety 5: unshortened (coded 0)
22 [b]	*Pelagostrobilidium* – somatic kinety 6: posteriorly shortened (coded 1; coded 1000); absent (coded 2; coded 1100); L-shaped (coded 3; coded 0010); or U-shaped (coded 4; coded 0011)	*Pelagostrobilidium* – somatic kinety 6: longitudinal and unshortened (coded 0)
23 [a]	Oligotrichid ventral kinety erected (coded 1), usually indistinct or absent (coded 2)	Oligotrichid ventral kinety dextrally spiralled (coded 0)

	Characters	
	Apomorphic states	Plesiomorphic states
24 [b]	Oligotrichid girdle kinety: dextrally spiralled with posterior end inversely orientated (coded 1; coded 10000000000); horizontally orientated anterior to oral primordium (coded 2; coded 01000000000); sinistrally spiralled (coded 3; coded 01100000000); horizontally orientated anterior to oral primordium with dorsal gap (coded 4; coded 01010000000); horizontally orientated at level of oral primordium, with dorsal gap (coded 5; coded 01011000000); horizontally orientated posterior to oral primordium and separate from extrusome attachment sites (coded 6; coded 01000100000); horizontally orientated posterior to oral primordium together with extrusome attachment sites (coded 7; coded 01000010000); Ω-shaped anterior to oral primordium (coded 8; coded 01000001000); Ω-shaped posterior to oral primordium (coded 9; coded 00000000100); extends to posterior cell end on ventral and dorsal sides, in two or three fragments (coded 10; coded 00000000110); in several mostly clockwise inclined fragments (coded 11; coded 00000000101)	Oligotrichid girdle kinety dextrally spiralled (coded 0; coded 00000000000)
25	Somatic kineties arranged in a right and left ciliary field (coded 1)	Somatic kineties more or less equidistantly arranged (coded 0)
26 [a]	Two ventral organelles (coded 1) or one specialised tintinnid ventral kinety (coded 2)	Specialised ventral organelles or tintinnid ventral kinety absent (coded 0)
27	Tintinnid ventral kinety composed of a monokinetidal anterior and a dikinetidal posterior portion (coded 1)	Tintinnid ventral kinety monokinetidal (coded 0)
28	Right ciliary field and tintinnid ventral kinety separated by a broad unciliated stripe (coded 1)	Right ciliary field abuts on ventral kinety (coded 0)
29	Two dorsal kineties (coded 1) or one dorsal kinety (coded 2)	Specialised dorsal kinety/kineties absent (coded 0)
30	Posterior kinety present (coded 1)	Specialised posterior kinety absent (coded 0)
31	Lateral ciliary field present (coded 1)	Lateral ciliary field absent (coded 0)
32 [b]	Unspecialised somatic kineties: some dikinetids with cilia only at the anterior basal bodies, other dikinetids with two cilia (coded 1; coded 10000000); all dikinetids with two cilia (coded 2; coded 11000000); most dikinetids with cilia only at the posterior basal bodies, few dikinetids with two cilia (coded 3; coded 11100000); all dikinetids with cilia only at the posterior basal bodies (coded 4; coded 11110000); some dikinetids with cilia only at the posterior basal bodies, some ciliated monokinetids (coded 5; coded 11111000); ciliated monokinetids (coded 6; coded 11111100); mostly ciliated monokinetids, some dikinetids with two cilia, some dikinetids with cilia only at the posterior basal bodies (coded 7; coded 11100010); mostly ciliated monokinetids, some dikinetids with two cilia (coded 8; coded 11100011)	Unspecialised somatic kineties composed of dikinetids, each has a distinct cilium associated only with the anterior basal body (coded 0; coded 00000000)
33	Somatic kinetids condensed (coded 1)	Somatic kinetids distinctly separate (coded 0)
34 [a]	Majority of members with one ellipsoidal macronucleus nodule (coded 1), one C-shaped macronucleus (coded 2), or more than two macronucleus nodules (coded 3)	Majority of members with two macronucleus nodules (coded 0)
35 [a]	Tintinnid extrusomes (capsules) and/or structures usually associated with tintinnid extrusomes (coded 1) or oligotrichid extrusomes (trichites; coded 2) present	Extrusomes absent (coded 0)
36	Stripe of extrusome (trichite) attachment sites distinctly apart from oligotrichid girdle kinety (coded 1)	Stripe of extrusome (trichite) attachment sites directly anterior to oligotrichid girdle kinety (coded 0)
37 [a]	Capsule Type II (coded 1)	Capsule Type I (coded 0)
38	Mucocyst Type A (coded 1)	Mucocysts absent (coded 0)
39 [a]	Contractility of peduncle (coded 1) or tail (coded 2)	Posterior cell portion acontractile (coded 0)
40 [a]	Anterior cell portion with contractile tentacles (coded 1) or tentaculoids (coded 2)	Anterior cell portion without cytoplasmic appendages (coded 0)
41	Polysaccharidic cortical platelets (coded 1)	Cortical platelets absent (coded 0)
42	Kinetal lips covering bases of somatic cilia present (coded 1)	Kinetal lips covering bases of somatic cilia absent (coded 0)

	Characters	
	Apomorphic states	Plesiomorphic states
43	Vesicular reticulum present (coded 1)	Vesicular reticulum absent (coded 0)
44	Lorica present (coded 1)	Lorica absent (coded 0)
45 [a]	Lorica types: bowl agglomerated, collar hyaline (coded 1); entirely hyaline (coded 2)	Lorica entirely agglomerated (coded 0)
46 [b]	Lorica flexible with subterminal membrane (coded 1; coded 010), hard (coded 2; coded 100), or hard and collapsible (coded 3; coded 101)	Lorica flexible (coded 0; coded 000)
47 [a]	Texture of lorica wall: monolaminar alveolar (coded 1); collar monolaminar alveolar, bowl bilaminar (coded 2); or collar monolaminar compact, bowl bilaminar (coded 3)	Texture of lorica wall monolaminar compact (coded 0)
48 [a]	Closing apparatus: foldable with lorica sac (coded 1) or diaphragm-like without lorica sac (coded 2)	Lorica sac and closing apparatus absent (coded 0)
49	Enantiotropy (coded 1)	Homeotropy (coded 0)
50 [b]	Stomatogenesis hypoapokinetal in transient tube (coded 1; coded 100), in permanent tube (coded 2; coded 110), or in transient pouch (coded 3; coded 101)	Stomatogenesis epiapokinetal (coded 0; coded 000)
51	Undulating membranes originate de novo (coded 1)	Undulating membranes originate from oral primordium or cirral anlagen (coded 0)
52	Unspecialised somatic kineties originate de novo (coded 1)	Unspecialised somatic kineties originate usually by intrakinetal proliferation of basal bodies (coded 0)
53	Reorganisation of somatic kineties present (coded 1)	Reorganisation of somatic kineties absent (coded 0)
54	Preformed emergence pore of resting cyst closed with a plug (coded 1)	Preformed emergence pore and plug absent in resting cyst (coded 0)
55	Ectocyst (outer cyst layer) bipartite and granular (coded 1)	Ectocyst comprises a single microfibrillar or membranous layer (coded 0)
56	Wall of resting cyst with inorganic layers (coded 1)	Wall of resting cyst without inorganic layers (coded 0)
57 [a]	Lepidosome structure tubular (coded 1) or fibrous (coded 2)	Lepidosomes absent (coded 0)
58	Lepidosome shape conical/spine-like (coded 1)	Lepidosomes globular (coded 0)
59	"Curious structures" in cytoplasm of resting cyst present (coded 1)	"Curious structures" in cytoplasm of resting cyst absent (coded 0)
60	Cyst wall precursors of halteriid type (coded 1)	Cyst wall precursors of hypotrich type (coded 0)
61	Inner cyst membrane that encloses the ciliate emerging from the cyst absent (coded 1)	Inner cyst membrane that encloses the ciliate emerging from the cyst present (coded 0)
62	Pycnosis of vegetative macronucleus without fragmentation (coded 1)	Fragmentation of vegetative macronucleus prior to pycnosis (coded 0)
63 [a]	Interlocking arrangement (coded 1) or oblique arrangement (coded 2) of conjugants	Parallel arrangement of conjugants (coded 0)
64	Transient dimorphism of conjugants (coded 1)	Isomorphic conjugants (coded 0)
65	Conjugants share membranelles (coded 1)	Conjugants do not share membranelles (coded 0)
66	Single derivative of first maturation division performs second division (coded 1)	All derivatives of first maturation division participate in second division (coded 0)

[a] Non-additive (unordered) character states, i.e., each state can change into any other state by one step.
[b] Binary coding of character state trees (first code for Hennigian argumentation scheme; second code for computer analyses).

Table S2. Distribution of character states over the taxa cladistically analysed with the computer programs PAUP* and Hennig86 (Figs S3–S5). Note that the character state trees of Characters 19, 22, 24, 32, 46, and 50 (Table S1) were converted into additive binary coding. Shades of grey mark the most common (in ≥ 50% of species) character state in a polymorphic taxon and the presumed character state of a taxon adopted from the state in its closest relatives.

	Characters									
Taxon[a]	10	20	30	40	50	60	70	80	90	
Hypo	00000000-1	0000000---	----------	----------	--------00	000000000-	--000000--	----000000	1000100000	2110
Mese	1110100100	0010000---	----------	----------	--------00	000000010-	--000000--	----100011	1010201100	?111
Halt	1110100100	0010010---	----------	----------	--------00	000000110-	--000000--	----100011	1010211?0	1111
Phal	1110100100	0010010---	----------	----------	--------00	000000110-	--000000--	----100011	10?0??11?0	?111
Cyrt	111020020-	2110111---	---------1	0101000000	0-------00	0000000120	--001000--	----110010	01?1?1????	000?
Will	1110200100	1010111---	---------2	0101100000	0-------00	0000000120	--00?000--	----110010	01?1??????	000?
Plst	1110200100	1011111---	---------2	0100000000	0-------00	0000000120	--001000--	----111010	011121??1?	000?
Limn	1110200100	1012111---	---------1	0100000000	0-------00	0000000120	--001000--	----111010	01?10-????	000?
Labo	1110200100	1010111---	---------2	0110000000	0-------00	0000000320	--001000--	----110010	01?1??????	000?
Noap	1110200100	1010111---	---------1	0000000000	0-------00	0000000021	--001000--	----110010	01?1??????	000?
Nosi	1110200100	1010111---	---------1	0000000000	0-------00	0000000120	--001000--	----110010	01?1??????	000?
Omeg	1110200100	1010111---	---------2	0000000010	0-------00	0000000120	--001000--	----110010	01?1??????	000?
Opis	1110200100	1010111---	---------1	0100001000	0-------00	0000000120	--001000--	----110010	01?1??????	000?
Fois	1110200100	1010111---	---------1	0100010000	0-------00	0000000021	--001000--	----110010	01?1??????	000?
Plle	1110200100	1010111---	---------0	0000000000	0-------00	0000000120	--001000--	----110010	01?1??????	000?
Spir	1110200100	1010111---	---------1	1000000000	0-------00	0000000120	--001000--	----110010	01?1??????	000?
Stro	1110200100	1010111---	---------1	0100000000	0-------00	0000000120	--001000--	----110010	01?121??1?	000?
Pato	1110200100	1010111---	---------2	0100000100	0-------00	0000000320	--201000--	----110010	01?1??????	000?
Psto	1110200100	1010111---	---------1	0100000000	0-------00	0000000320	--211000--	----110010	01?1??????	000?
Spto	1110200100	1010111---	---------2	0110000000	0-------00	0000000320	--201000--	----110010	01?1??????	000?
Tont	1110200100	1010111---	---------2	0000000000	0-------00	0000000320	--201000--	----110010	01?1??????	000?
Apos	1110200100	1010111---	---------2	0000000011	0-------00	0000000120	--00?000--	----110010	01?1??????	000?
Vari	1110200100	1010111---	---------2	0000000010	1-------00	0000000120	--00?000--	----110010	01?1??????	000?
Lova	1111201110	1010111---	----------	----------	--------00	000000010-	--000000--	----110110	01?1?????1	?000
Lelb	1111201110	1010010---	----------	----------	--------10	000000000-	--000000--	----110110	01?1?????1	?000
Lsol	1111201110	1010010---	----------	----------	--------11	000000000-	--000000--	----110110	01?1?????1	?000
Lohm	1111200110	1010010---	----------	----------	--------11	110000010-	--000000--	----110110	01?1?????1	?000
Pcon	1111200110	1010011010	000111000-	----------	--------11	111100120-	--000100--	----110110	01?1?????1	1000
Pmin	1111200110	1010011100	000121100-	----------	--------11	111100120-	--000100--	----110110	01?1?????1	1000
Pwil	1111200110	1010011001	000000000-	----------	--------11	111100120-	--000100--	----110110	01?1?????1	1000
Pkim	1111200110	1010011201	000111000-	----------	--------11	111100120-	--000100--	----110110	01?1?????1	1000
Pepa	1111200110	1010011001	100101100-	----------	--------11	111100120-	--000100--	----110110	01?1?????1	1000
Pota	1111200110	1010011001	111100000-	----------	--------11	111100120-	--000100--	----110110	01?1?????1	1000
Psim	1111200110	1010011001	111111100-	----------	--------11	111100120-	--000100--	----110110	01?1?????1	1000
Pnep	1111200110	1010011001	110120010-	----------	--------11	111100120-	--000100--	----110110	01?1?????1	1000
Pspi	1111200110	1010011001	110120011-	----------	--------11	111100120-	--000100--	----110110	01?1?????1	1000
Ppep	1111200110	1010011001	100110000-	----------	--------11	111100120-	--000100--	----110110	01?1?????1	1000
Rimo	1111200110	1010010---	----------	----------	--------11	111100120-	--000100--	----110110	01?10-???1	?000

	Characters									
Taxon[a]	10	20	30	40	50	60	70	80	90	
Strb	1111200110	1010012---	----------	----------	--------11	111100120-	--000100--	----110110	01?1?????1	?000
Spsi	1111200110	1010200---	----------	----------	-00--00011	000000000-	--000000--	----110110	01?10-???1	?000
Parp	1112200110	1010200---	----------	----------	-00--00011	000000000-	--000000--	----110110	01?1?????1	?000
Parb	1112200220	1010200---	----------	----------	-00--00011	000000030-	--000000--	----110110	01?1?????1	?000
Lynn	1112200210	1010110---	----------	----------	-00--00011	111000000-	--000000--	----110110	01?1?????1	?000
semi	1111210210	1010210---	----------	----------	-11--00011	100010011-	??10001100	0000110110	0????????1	0000
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pusi	1111210210	1010210---	----------	----------	-11--00011	100000011-	??10001100	0000110110	0????????1	0000
cyda	1111210210	1010210---	----------	----------	-11--00011	111100011-	??10001100	0000110110	0????????1	0000
Memb	1111210210	1010210---	----------	----------	-11--00011	11000000?-	??10001100	1000110110	0????????1	0000
Amph	112121021?	?010210---	----------	----------	-2?020000	00000003?-	??1?001121	00001101?0	0????????1	0000
Scan	112121021?	?010010---	----------	----------	-2?0?00??	??????01?-	??1?001121	00021101?0	0????????1	0000
Nola	1111210110	1010210---	----------	----------	-20000011	100011001-	??1?001121	0100110110	0????????1	0000
Euti	1111210110	1010210---	----------	----------	-20010011	100011031-	??12001121	0000110110	00??0-???1	0000
Fehr	1111210110	1010210---	----------	----------	-20010111	100011000-	-?10001121	0010110110	0????????1	0000
Schm	1111210110	1010210---	----------	----------	-21120111	100011001-	??12001121	0010110110	01??0-???1	0000
bras	1111210?10	1010210---	----------	----------	-20020111	10001100?-	??1?001101	00?0110110	0????????1	0000
Ocod	1111210110	1010210---	----------	----------	-20021111	100011031-	1112001101	0031110110	0????????1	0000
Ccra	1111210210	1010210---	----------	----------	-20021111	100011000-	-?10001101	0000110110	0????????1	0000
Cpsi	1111210110	1010210---	----------	----------	-20021111	100011031-	1112001111	0021110110	0????????1	0000
Cyma	1111210110	1010210---	----------	----------	-20021111	100011001-	??1?001121	0010110110	0????????1	0000
Otsp	1111210110	1010210---	----------	----------	-20021111	100011001-	0012001101	00?0110110	00??0-???1	0000
lacu	1111210110	1010210---	----------	----------	-20021111	10001100?-	??1?001101	00?0110110	0????????1	0000
Oste	1111210110	1010210---	----------	----------	-20021111	100011001-	1112001111	0030110110	0????????1	0000
toca	1111210110	1010210---	----------	----------	-21020111	100011000-	-?10001101	00?0110110	0???0-???1	0000
radi	1111210110	1010210---	----------	----------	-20021111	100011000-	-?10001101	00?0110110	0???0-???1	0000
cyli	1111210110	1010210---	----------	----------	-21020111	100011000-	-?10001101	00?0110110	00??0-???1	0000
Rhiz	1111210110	1010210---	----------	----------	-20021111	100011001-	??10001101	0010110110	00??0-???1	0000
Laac	1111210110	1010210---	----------	----------	-20021111	10001103?-	??1?001111	00?0110110	0????????1	0000

[a] *Amph – Amphorellopsis*, *Apos – Apostrombidium*, *bras – Tintinnopsis brasiliensis*, *Ccra – Codonella cratera*, *Cpsi – Codonellopsis*, *cyda – Tintinnopsis cylindrata*, *cyli – Tintinnopsis cylindrica*, *Cyma – Cymatocylis*, *Cyrt – Cyrtostrombidium*, *Euti – Eutintinnus*, *Fehr – Favella ehrenbergii*, *fluv – Tintinnidium fluviatile* of subgenus *Tintinnidium*, *Fois – Foissneridium*, *Halt – Halteria*, Hypo – hypotrichs, *Laac – Laackmanniella*, *Labo – Laboea*, *lacu – Stenosemella lacustris*, *Lelb – Leegaardiella elbraechteri*, *Limn – Limnostrombidium*, *Lohm – Lohmanniella*, *Lova – Leegaardiella ovalis*, *Lsol – Leegaardiella sol*, *Lynn – Lynnella*, *Memb – Membranicola*, *Mese – Meseres*, *Noap – Novistrombidium apsheronicum*, *Nola – Nolaclusilis*, *Nosi – Novistrombidium sinicum*, Ocod – other *Codonella* species, *Omeg – Omegastrombidium*, *Opis – Opisthostrombidium*, Oste – other *Stenosemella* species, Otsp – other *Tintinnopsis* species, *Parb – Parastrombidium*, *Parp – Parastrombidinopsis*, *Pato – Paratontonia*, *Pcon – Pelagostrobilidium conicum*, *Pepa – Pelagostrobilidium epacrum*, *Phal – Pelagohalteria*, *Pkim – Pelagostrobilidium kimae*, *Plle – Parallelostrombidium*, *Plst – Pelagostrombidium*, *Pmin – Pelagostrobilidium minutum*, *Pnep – Pelagostrobilidium neptuni*, *Pota – Pelagostrobilidium* studied by Ota and Taniguchi (2003), *Ppep – Pelagostrobilidium paraepacrum*, *Psim – Pelagostrobilidium simile*, *Pspi – Pelagostrobilidium spirale*, *Psto – Pseudotontonia*, *pusi – Tintinnidium pusillum* of subgenus *Tintinnidium*, *Pwil – Pelagostrobilidium wilberti*, *radi – Tintinnopsis radix*, *Rhiz – Rhizodomus*, *Rimo – Rimostrombidium*, *Scan – Salpingacantha*, *Schm – Schmidingerella arcuata*, *semi – Tintinnidium semiciliatum* of subgenus *Semitintinnidium*, *Spir – Spirostrombidium*, *Spsi – Strombidinopsis*, *Spto – Spirotontonia*, *Strb – Strobilidium*, *Stro – Strombidium*, *toca – Tintinnopsis tocantinensis*, *Tont – Tontonia*, *Vari – Varistrombidium*, *Will – Williophrya*.

Table S3. Alphabetical list of all sequences used in the phylogenetic analyses of this study: genus and species name, isolate or strain designation if necessary, and GenBank Accession Number.

Taxa	Accession numbers
Amphorellopsis acuta	EU399530
Amphorellopsis acuta	JX101847
Amphorellopsis quinquealata	JQ924058
Amphorides amphora	JX101849
Amphorides quadrilineata	JQ408193
Amphorides quadrilineata	JX101850
Anteholosticha parawarreni	JQ289923
Apostrombidium parakielum	JX025560
Aspidisca steinii	AF305625
Climacocylis scalaria	JQ408213
Codonaria cistellula	JQ408202
Codonaria sp.	JQ408172
Codonella apicata	EU399531
Codonella aspera	JQ408179
Codonellopsis americana	AY143571
Codonellopsis gaussi	JQ924053
Codonellopsis morchella	JQ408173
Codonellopsis nipponica	FJ196072
Codonellopsis orthoceras	JQ408180
Coxliella sp.	JX101851
Cymatocylis calyciformis	JQ924046
Cymatocylis convallaria	JQ924050
Cymatocylis drygalskii	JQ924052
Cyttarocylis ampulla (formerly *Petalotricha ampulla*)	JQ408168
Cyttarocylis cassis	JQ408203
Cyttarocylis eucecryphalus	JQ408169
Dadayiella ganymedes	JX101852
Dictyocysta lepida	JQ408188
Dictyocysta reticulata	EU399532
Diophrys appendiculata	AY004773
Epiplocylis acuminata	JQ715615
Epiplocyloides ralumensis	JX101854
Euplotes aediculatus	X03949
Eutintinnus apertus	JQ408195
Eutintinnus fraknoi	EU399534
Eutintinnus lusus-undae (agglomerated-form)	JX101858
Eutintinnus pectinis	AY143570
Eutintinnus stramentus	JX101859
Eutintinnus tenuis	JN871721
Eutintinnus tubulosus (agglomerated-form)	JX101856
Eutintinnus tubulosus	JQ408187
Favella adriatica	JQ408215

Taxa	Accession numbers
Favella campanula	FJ422984
Favella ehrenbergii	GU574767
Favella markusovszkyi	JN871725
Favella panamensis	AY143572
Halteria grandinella	AF194410
Helicostomella subulata	JN831781
Helicostomella subulata	JN831786
Histriculus histrio	FM209294
Laackmanniella prolongata	JQ924056
Laboea strobila	AF399154
Laboea strobila	AY302563
Lynnella semiglobulosa	FJ876965
Meseres corlissi (strain AU5)	EU399524
Meseres corlissi (strain CHI)	EU399529
Meseres corlissi (strain DR)	EU399522
Metacylis angulata	AF399146
Metacylis angulata	AY143568
Metacylis jörgensenii	JQ408183
Metacylis pithos	JX101862
Moneuplotes crassus	AJ310492
Novistrombidium orientale	FJ422988
Novistrombidium sinicum population 1	FJ422989
Novistrombidium sinicum population 2	FJ422990
Novistrombidium apsheronicum	FJ876958
Novistrombidium testaceum	AJ488910
Omegastrombidium elegans	EF486862
Oxytricha granulifera	X53486
Oxytricha longa	AF164125
Parallelostrombidium sp. (3-GD-08040807)	FJ422991
Parallelostrombidium sp. (WS-2012)	JN712657
Parastrombidinopsis minima	DQ393786
Parastrombidinopsis shimi	AJ786648
Parundella aculeata	JQ408204
Pelagostrobilidium minutum	FJ876959
Pelagostrobilidium neptuni	AY541683
Pelagostrobilidium paraepacrum	FJ876963
Protorhabdonella curta	JX101863
Pseudokeronopsis rubra	DQ640314
Pseudotontonia simplicidens	FJ422993
Pseudouroleptus caudatus	DQ910904
Rhabdonella elegans	JQ408175
Rhabdonella hebe	AY143566

Taxa	Accession numbers
Rhabdonella poculum	JX101864
Rhabdonella spiralis	JQ408158
Rhizodomus tagatzi	JQ392572
Rimostrombidium lacustris	DQ986131
Rimostrombidium sp.	EU024986
Rimostrombidium veniliae	FJ876964
Salpingella acuminata	JQ408155
Salpingella acuminata	EU399536
Schmidingerella arcuata	JQ837816
Schmidingerella taraikaensis	FJ196073
Spirostrombidium sp.	JN712658
Spirotontonia taiwanica	FJ715634
Spirotontonia turbinata	FJ422994
Steenstrupiella steenstrupii	JQ408194
Steenstrupiella steenstrupii	EU399537
Stenosemella nivalis	FJ196074
Stenosemella pacifica	JN831792
Stenosemella ventricosa	JQ408170
Stenosemella ventricosa	EU399538
Strobilidium caudatum	AY143573
Strobilidium sp.	AF399124
Strombidinopsis acuminatum	AJ877014
Strombidinopsis jeokjo	AJ628250
Strombidinopsis sp. (LFS-2012b)	JQ028734
Strombidinopsis sp.	AM412524
Strombidium apolatum	DQ662848
Strombidium biarmatum	AY541684
Strombidium basimorphum	FJ480419
Strombidium conicum	FJ422992
Strombidium crassulum	HM140389
Strombidium purpureum	U97112
Strombidium rassoulzadegani	AY257125
Strombidium stylifer	DQ631805
Strombidium sulcatum	DQ777745
Stylonychia lemnae	AF508773
Styxophrya quadricornuta	X53485

Taxa	Accession numbers
Tintinnidium balechi	JN831797
Tintinnidium fluviatile	JQ408163
Tintinnidium mucicola	AY143563
Tintinnidium pusillum	DQ487200
Tintinnopsis baltica	JN831805
Tintinnopsis beroidea	EF123709
Tintinnopsis bütschlii	JN831810
Tintinnopsis cylindrica	FJ196075
Tintinnopsis cylindrica	JQ408206
Tintinnopsis dadayi	AY143562
Tintinnopsis fimbriata	AY143560
Tintinnopsis lacustris	JQ408161
Tintinnopsis lobiancoi	JN831814
Tintinnopsis lohmanni	FJ196076
Tintinnopsis major	JN831816
Tintinnopsis nana	JN831821
Tintinnopsis parva	JN831824
Tintinnopsis parvula	JN831830
Stylicauda platensis (as *Tintinnopsis*)	JN831832
Tintinnopsis radix	EU399540
Tintinnopsis rapa	JN831834
Tintinnopsis rara	JQ408200
Tintinnopsis subacuta	EU399541
Tintinnopsis tocantinensis	AY143561
Tintinnopsis tubulosoides	AF399109
Tintinnopsis uruguayensis	EU399542
Undella claparedei	JQ408164
Undella hyalina	JQ408171
Undella marsupialis	JQ408190
Uroleptus piscis	AF508780
Uroleptus willii	EU399543
Uronychia transfuga	AF260120
Urostyla grandis	AF508781
Varistrombidium kielum	DQ811090
Williophrya maedai	FJ876966
Xystonella longicauda	JQ408160

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