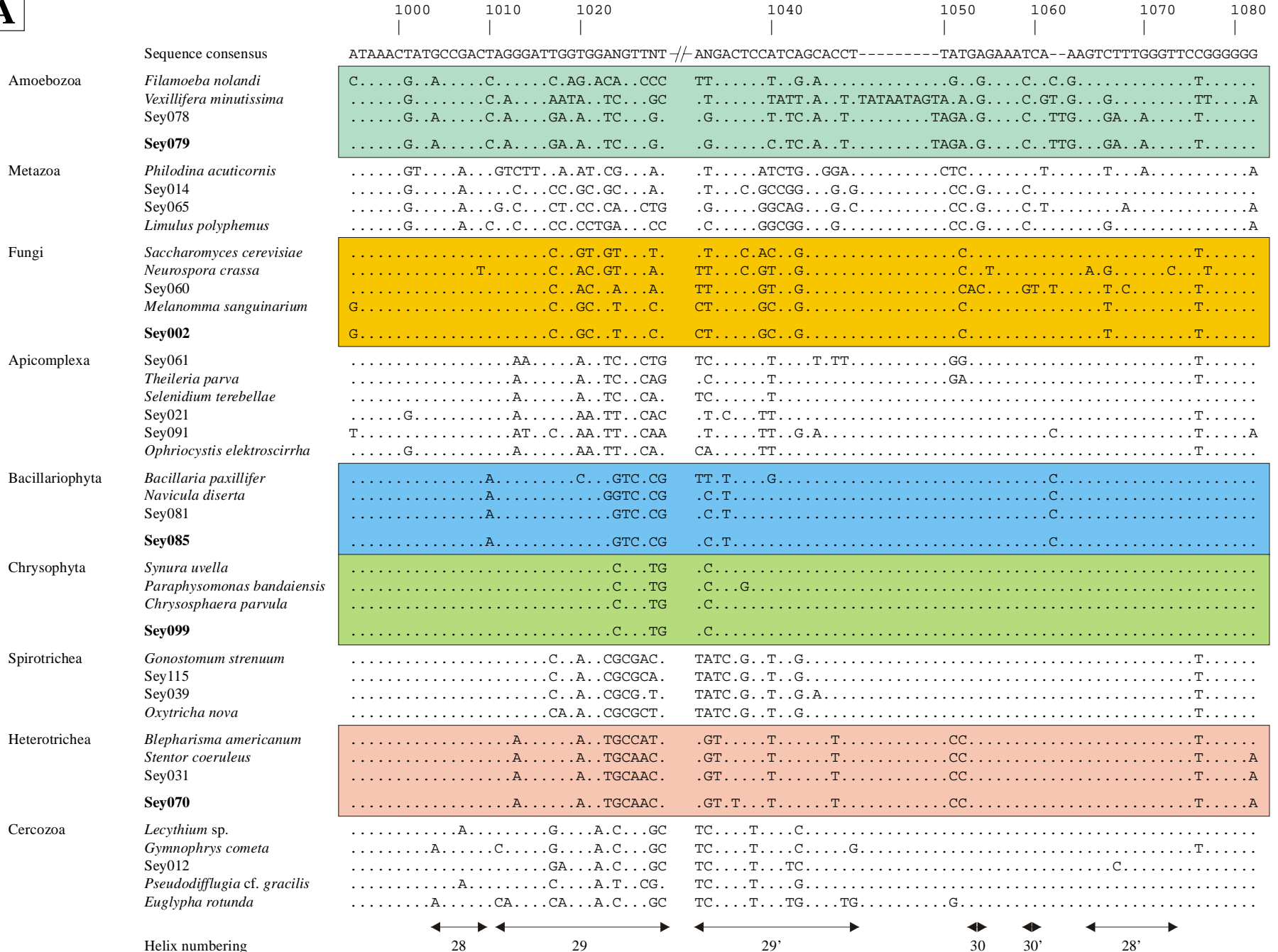


Additional File 1 : Supplementary Figure 1.

Illustration of the methods we used for the detection of chimeric sequences.

Visual screening of partial alignments of the V5 region (**A**) and the V9 region (**B**) of the SSU rRNA gene, including 17 sequences from our EES of the river Seymaz, strongly suggests the presence among them of 5 chimeric sequences (indicated in bold), because different regions of the same sequence contain rare substitutions and/or indels that are specific for different lineages of eukaryotes. Helices are numbered according to the secondary structure model proposed by Wuyts et al. [45] and the numbers at the top of the alignment refer to the sequence of the red alga *Palmaria palmata* (GenBank accession number X53500). The different colored boxes highlight the taxonomic lineage to which each part of the chimera belongs. The V5 region of sequence Sey079 is almost identical to that of sequence Sey078 (Amoebozoa), while its V9 region is identical to that of the rotifer *Philodina acuticornis* (Metazoa). The V5 region of sequence Sey002 is identical to that of the ascomycete *Melanomma sanguinarium* (Fungi), while its V9 region is identical to that of sequence Sey061 (Apicomplexa). The V5 region of sequence Sey085 is identical to that of sequence Sey081 (Bacillariophyta), while its V9 region possesses all characteristic features of the chrysophytes. The V5 region of sequence Sey099 is identical to that of the chrysophyte *Chryso-sphaera parvula*, while its V9 region possesses all characteristic features of the spirotrich ciliates. Finally, the V5 region of sequence Sey070 is almost identical to that of sequence Sey031 and the heterorich ciliate *Stentor coeruleus*, while its V9 region is identical to that of *Lecythium* sp. (Cercozoa). These observations are confirmed by partial treeing analysis [12], i.e. distance analyses based on different subsets of unambiguously aligned regions. For this example, analyses were based on (**C**) the first 150 sites at the 5' end of the partial alignment (helices 27 to 50) used for Figure 1, and (**D**) the last 425 sites at the 3' end of the same alignment. Colored boxes highlight the change of position of each chimeric sequence (indicated in bold), depending on the region analyzed. In both trees, all branches are drawn to scale.



B

		1610	1620	1630	1640	1650	1690	1700	1710	1720	1730	
	Sequence consensus	CCGTCGCTCCTACCGATT--GAATGGTCCGGTGAATCTTCGGANTGNNN--					TNNNGNGAAGTTGATTAAACCTTATCATTTAGAGGAAGGAGAAGTCG					
Amoebozoa	<i>Filamoeba nolandi</i>C.....A...TATTGG					.CGATA.....G.....CTG.....					
	<i>Vexillifera minutissima</i>T.....A.....A...AA..G...T.ATAA					.TGTA...A...C...AT.....G.....					
	Sey078-.....AT...A...C.A..G...ACTGTC					GATT.CC..C.CT.G...T...T.....					
	Sey079A.....T.TTA...G.....CT..GTT					.ATC.AA...A..C.C...TGG.....T.A.....					
Metazoa	<i>Philodina acuticornis</i>A.....T.TTA...G.....CT..GTT					.ATC.AA...A..C.C...TGG.....T.A.....					
	Sey014A.....G.....TTA...GG..C...TC.GCC					CGCC.A...AC...C...T.G.CT..C...T.A.....					
	Sey065A.....TTA.C.G..TC...T..GGC					GTCT.A...AAAC.C.G.T.G.....T.A.....					
	<i>Limulus polyphemus</i>A.....A.TTA...GG.....C..GCT					.GCC.AA...A...CC...T.G.....T.A.....					
Fungi	<i>Saccharomyces cerevisiae</i>AG.....CTTA...GGC..CA...TCTGCT					AGCG.A...T...GAC...T.GG.....CT.A.....					
	<i>Neurospora crassa</i>A.....CT.A...GGCT.C...C..GCC					GGCC.GA...C.ATCC...TCGG.....T.A.....					
	Sey060A.....CT.A...GGCT.C...C..GCC					GGCC.GA...ATCC...TCGG.....T.A...A					
	<i>Melanomma sanguinarium</i>A.....CT.A...GGC.....C..GCT					AGCC.GA...CG.C...TCGG.....T.A.....					
Apicomplexa	Sey002GG..A.....T.AC...C.TGTG					ATCA.G..G...TTG.G.....C.....					
	Sey061GG..A.....T.AC...C.TGTG					ATCA.G..G...TTG.G.....C.....					
	<i>Theileria parva</i>C...G..A.....T.A...CC.TGA					.CTA.G...TTG.G.....C..A.....					
	<i>Selenidium terebellae</i>GG..A.TA...T.A...CCACAC					.CGT.G...CTTG.G...C..G.C.....					
	Sey021CT.A.T...C...G.C.A...TGAC...C..GAA					.GCT.GA...TTG.G...AC..G.C.GA..A.T.AGA.....					
	Sey091AT.A.T...G..A.T...TGA...T..ATT					AATT.A...TTG...CA..C.C.GT..TCT.ATC.....					
Bacillariophyta	<i>Ophriocystis elektrosirra</i>CT.A.T...C...G..A...T.A...CC.ACT					AGAC.A...TTA.G...AA...C.GA..A.T.AGA...C					
	<i>Bacillaria paxillifer</i>A.....GC...CG...T..TGG					.CGC.A...C...TC.....T.....					
	<i>Navicula diserta</i>A.....GC...CG...T..CGA					.TGT.A...C...TC.....T.....					
Chrysophyta	Sey081A.....GC...G...T..TGA					.TGT.A...C...TC.....T.....					
	Sey085A.....C.....T.....AT..A..CCTAGG					CCAG.GA...AT.....C.....T.....					
	<i>Synura uvella</i>A.....A.T...AT.CT...C..TGG					CTAT.G...AT.....C.....T.....					
	<i>Paraphysomonas bandaiensis</i>A.....T...AT...CC.CGG					CTGT.GA...T...C.....T.....					
Spirotrichea	<i>Chrysophaera parvula</i>A.....A.T...CTC...CC.ACG					CATT.G...AT.....A.....T.....					
	Sey099TC..G.....CCT..T...CC.TAC					GTGT.G...A.CA.G...A...C.....					
	<i>Gonostomum strenuum</i>TC..G..T.....CCT...CC.CGC					GTGT.G...CA.G...A..A..C.....					
	Sey115TC..G.....CCT..T...C..TGC					GCGT.GA..A.CA.G...A...C.....					
Heterotrichea	Sey039TC..G..A.....CCT..T...C..CGT					GTGC.GA..A.CA.G...A...C.....					
	<i>Oxytricha nova</i>TC..G..A.....CCA..T...CC.CGG					CTGT.GA..A.CT.G...A...C.....					
	<i>Blepharisma americanum</i>TC..G..A.GA...TC..C...C..CAC					GTGT.G.....G.....C.....					
Cercozoa	<i>Stentor coeruleus</i>TC..G..A.GA...CC..C...C..TGC					CGTT.G.....G.....C.....					
	Sey031TC..G..A.GA...CC..C...C..TGC					CGTT.G.....G.....C.....					
	Sey070A.....CTTA...GC...CT...C..TTG					AAAT.G...GA...C...T.G.....T.A.....					
	<i>Lecythium</i> sp.A.....CTTA...GC...CT...C..TTG					AAAT.G...GA...C...T.G.....T.A.....					
	<i>Gymnophrys cometa</i>A.....AC.TA...GT.TCA...T..TTG					CAGT.A...GA..C...T.G.....T.A.....					
Sey012A.....ATTA...GC.TCA...T..TTG					CAAC.A...GA..C...T.GC.....T.A.....						
<i>Pseudodifflugia</i> cf. <i>gracilis</i>A.....CTTA...GC..A...C..CGT					ATGC.G...A...C...T.G.....T.A.....						
<i>Euglypha rotunda</i>A.....G...TTA...GG.TCA...C..TTG					ATACTG...GACCC...T.G...C.....T.A.....						
Helix numbering		←-----→					←-----→					
		49					49'					

