

Table S1. Key features of 72 myxomycete S1389 group I introns included in this work.

Host species	Acc No	Isolate	Size ¹	Insert ²	P5d ³	P7 ⁴
Order Physarales						
<i>Diderma fallax</i> ⁵	MZ313547	It-K52	532 bp	-	-	A1
<i>D. globosum</i>	DQ903677	AMFD110	722 bp	-	-	A1
<i>D. meyerae</i>	HE614614	It-K61	735 bp	-	-	A2
<i>D. meyerae</i> ⁵	MZ313546	It-K68	921 bp	-	-	A2
<i>D. niveum</i> ⁵	MZ313548	Fr-M26	749 bp	-	-	A1
<i>D. niveum</i>	AM231291	Fr-K10	682 bp	-	-	A1
<i>D. niveum</i>	HE614616	It-K66	683 bp	-	-	A1
<i>D. niveum</i>	HE614617	Uk-K79	683 bp	-	-	A1
<i>D. saundersii</i> ⁵	MZ313549	Mx-K30	532 bp	-	-	A1
<i>D. testeceum</i>	AM231292	Pr3-1	529 bp	-	-	G1
<i>Didymium iridis</i>	AJ938151	CR19-1	523 bp	-	-	A1
<i>D. iridis</i>	AJ938150	CUR1-4	637 bp	-	-	A1
<i>D. nigripes</i>	AF239230	-	654 bp	-	-	A1
<i>D. squamulosum</i>	AM231293	CR10	792 bp	-	-	U1
<i>Fuligo leviderma</i>	DQ903676	AMFD130	517 bp	-	-	A1
<i>Lepidoderma carestianum</i>	HE614618	It-K71	393 bp	-	-	A2
<i>L. crustaceum</i>	HE614619	It-K62	396 bp	-	-	A2
<i>L. peyerimhoffii</i> ⁵	MZ313552	It-K63	388 bp	-	+	A2
<i>L. tigrinum</i>	DQ903678	AMFD192	785 bp	-	-	A1
<i>Mucilago crustacea</i> ⁵	MZ313554	No-K94	1274 bp	DR-P9	-	A1
Order Stemonitales						
<i>Brefeldia maxima</i>	JQ031957	MM24519	1304 bp	HEG-P1	+	A3
<i>Colloderma oculatum</i>	JQ031959	HS2885	421 bp	-	+	A3
<i>C. robustum</i>	JQ031960	AMFD270	384 bp	-	+	A1
<i>Comatricha nigra</i>	DQ903683	AMFD155	788 bp	-	+	A1
<i>C. pseudoalpina</i>	DQ903673	MM23892	815 bp	-	+	U1
<i>Diacheopsis pauxilla</i>	JQ031966	MM29883	628 bp	-	-	A1
<i>Diachea subsessilis</i>	JQ031964	MM24463	919 bp	-	-	U1
<i>Lamproderma aeneum</i>	JQ031969	MM36255	545 bp	-	-	A3
<i>L. arcyrioides</i>	JQ031973	MM37005	1006 bp	DR-P9	+	A2
<i>L. cacographicum</i>	JQ031976	AMFD310	957 bp	DR-P9	-	A1
<i>L. columbinum</i>	HQ687204	F2	503 bp	-	-	A2
<i>L. columbinum</i>	HQ687196	106	563 bp	-	-	U2
<i>L. columbinum</i>	HQ687197	63b	474 bp	-	-	A2
<i>L. columbinum</i>	HQ687200	132	480 bp	-	+	A3
<i>L. disseminatum</i>	JQ031978	AMFD38	498 bp	-	-	A1
<i>L. echinosporum</i>	JQ031980	AMFD136	486 bp	-	+	A3
<i>L. echinosporum</i>	JQ031979	AK06016	481 bp	-	+	A3
<i>L. pseudomaculatum</i>	JQ031985	MM37354	411 bp	-	-	A3
<i>L. puncticulatum</i>	HQ687194	172	514 bp	-	+	A2
<i>L. puncticulatum</i>	HQ687202	162	511 bp	-	+	A1
<i>L. puncticulatum</i>	HQ687195	3	517 bp	-	+	A1
<i>L. sauteri</i>	DQ903674	AMFD208	543 bp	-	+	A1
<i>L. zonatum</i>	DQ903672	MM21644	434 bp	-	-	A1
<i>Meriderma carestiae</i>	JQ031999	MM35985	566 bp	-	-	A1
<i>M. carestiae</i>	DQ903671	AMFD173	566 bp	-	-	A1
<i>M. cribariooides</i>	JQ032000	MM37106	538 bp	-	-	A1
Order Liceales						
<i>Licea marginata</i>	JX481296	DWM7368	455 bp	-	+	A3
Order Trichiales						
<i>Calomyxa metallica</i>	JX481284	AMFD483	532 bp	-	-	A3
<i>Trichia varia</i>	KM494993	sc22370	1531 bp	HEG-P1	-	A3
<i>T. varia</i>	KM494994	LE259268	586 bp	-	-	A3
<i>T. varia</i>	KM494995	LE259461	586 bp	-	-	A3
<i>T. varia</i>	KM494996	JVR848	1531 bp	HEG-P1	-	A3
<i>T. varia</i>	KM494997	sc22386	559 bp	-	-	A1
<i>T. varia</i>	KM494998	sc22408	559 bp	-	-	A1
<i>T. varia</i>	KM494999	sc22409	559 bp	-	-	A1
<i>T. varia</i>	KM495003	sc22442	559 bp	-	-	A1
<i>T. varia</i>	KM495005	sc22517	559 bp	-	-	A1
<i>T. varia</i>	KM495006	sc27697	559 bp	-	-	A1

<i>T. varia</i>	KM495009	sc27742	559 bp	-	-	A1
<i>T. varia</i>	KM495010	sc27839	559 bp	-	-	A1
<i>T. varia</i>	KM495018	KRAM M-1585	559 bp	-	-	A1
<i>T. varia</i>	KM495019	sc27686	559 bp	-	-	A1
<i>T. varia</i>	KM495020	sc27737	559 bp	-	-	A1
<i>T. varia</i>	KM495021	sc27850c1	559 bp	-	-	A1
<i>T. varia</i>	KM495022	sc27860c4	559 bp	-	-	A1
<i>T. varia</i>	KM495023	sc27507	559 bp	-	-	A1
<i>T. varia</i>	KM495024	sc27648c1	559 bp	-	-	A1
<i>T. varia</i>	KM495026	sc27667c1	559 bp	-	-	A1
<i>T. varia</i>	KM495027	sc27667c2	559 bp	-	-	A1
<i>T. varia</i>	KM495028	sc27772c2	559 bp	-	-	A1
<i>T. varia</i>	KM495029	sc27850c2	559 bo	-	-	A1
<i>T. varia</i>	KM495030	LE254838	1544 bp	HEG-P1	-	A1

Host species	Acc No	Isolate	Size	Insert	P5d	P7
--------------	--------	---------	------	--------	-----	----

Notes:

¹ Size in base pairs of the S1389 group I intron insertion.

² Type of large insertions in group I ribozyme paired segment P1 or P9. HEG, homing endonuclease gene; DR, direct repeat motifs.

³ Presence or absence of the optional paired segment P5d.

⁴ G-binding sequence variants in segment P7, as indicated in Figure 3.

⁵ This work.

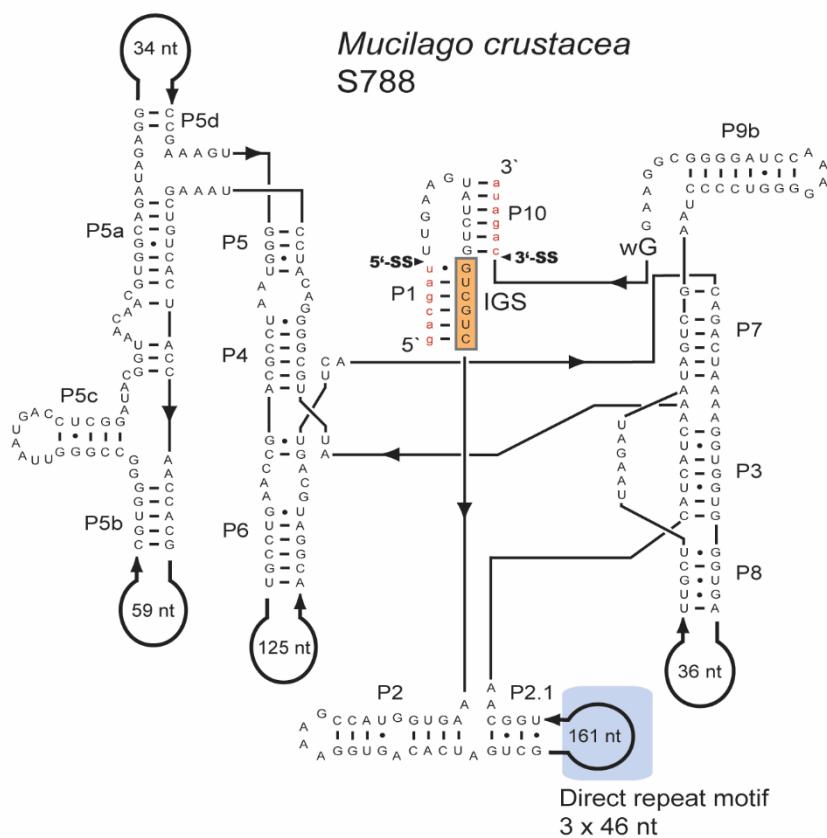
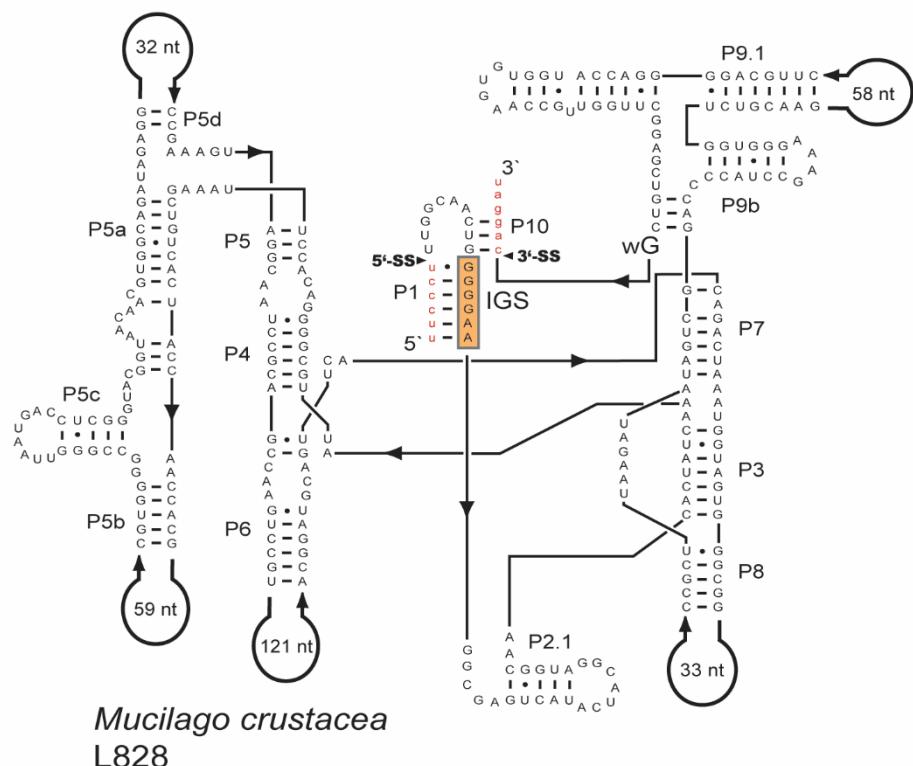
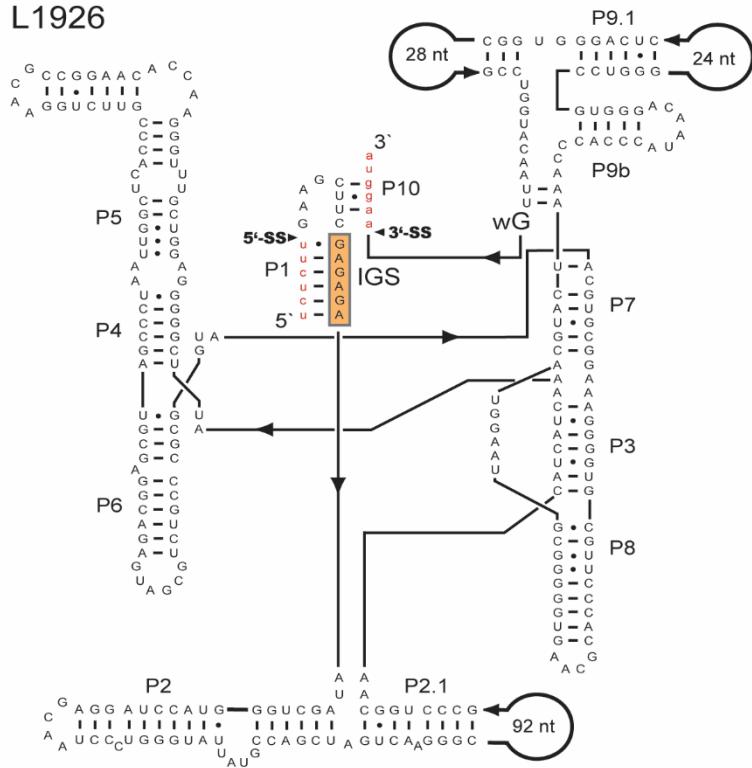
a**b**

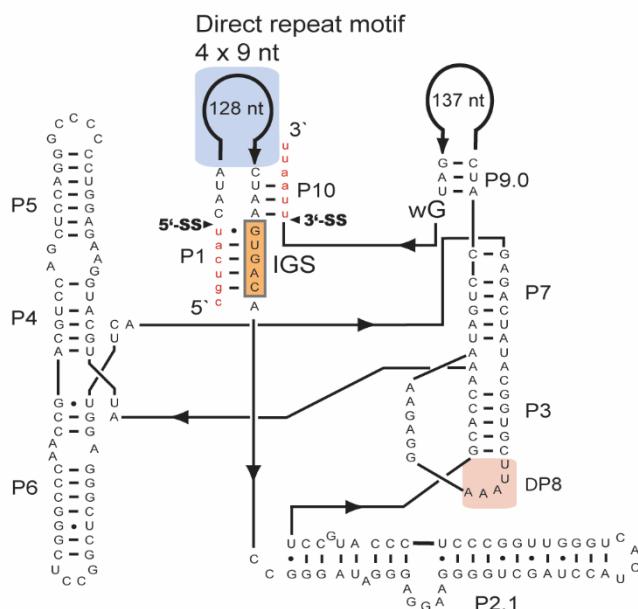
Figure S1 (a&b)

C

Mucilago crustacea
L1926



d

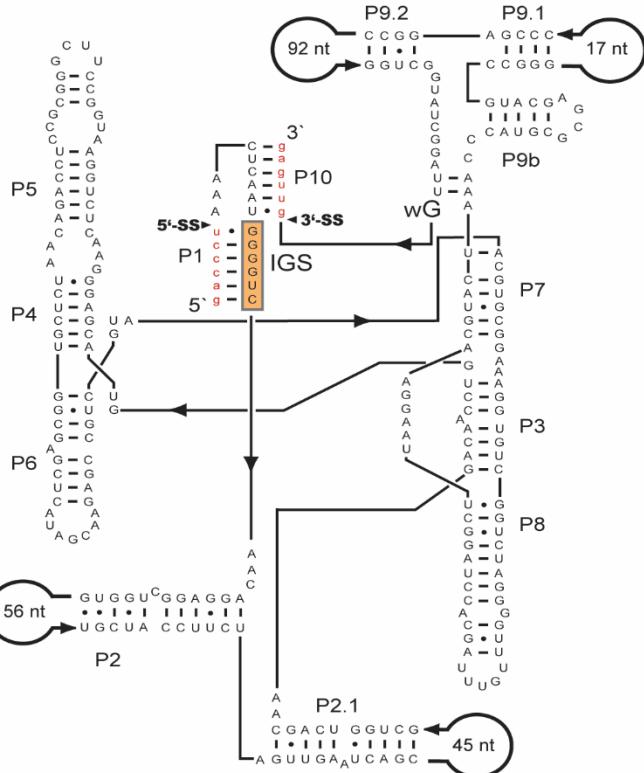


Mucilago crustacea
L1949

Figure S1 (c&d)

e

Mucilago crustacea
L2066



f

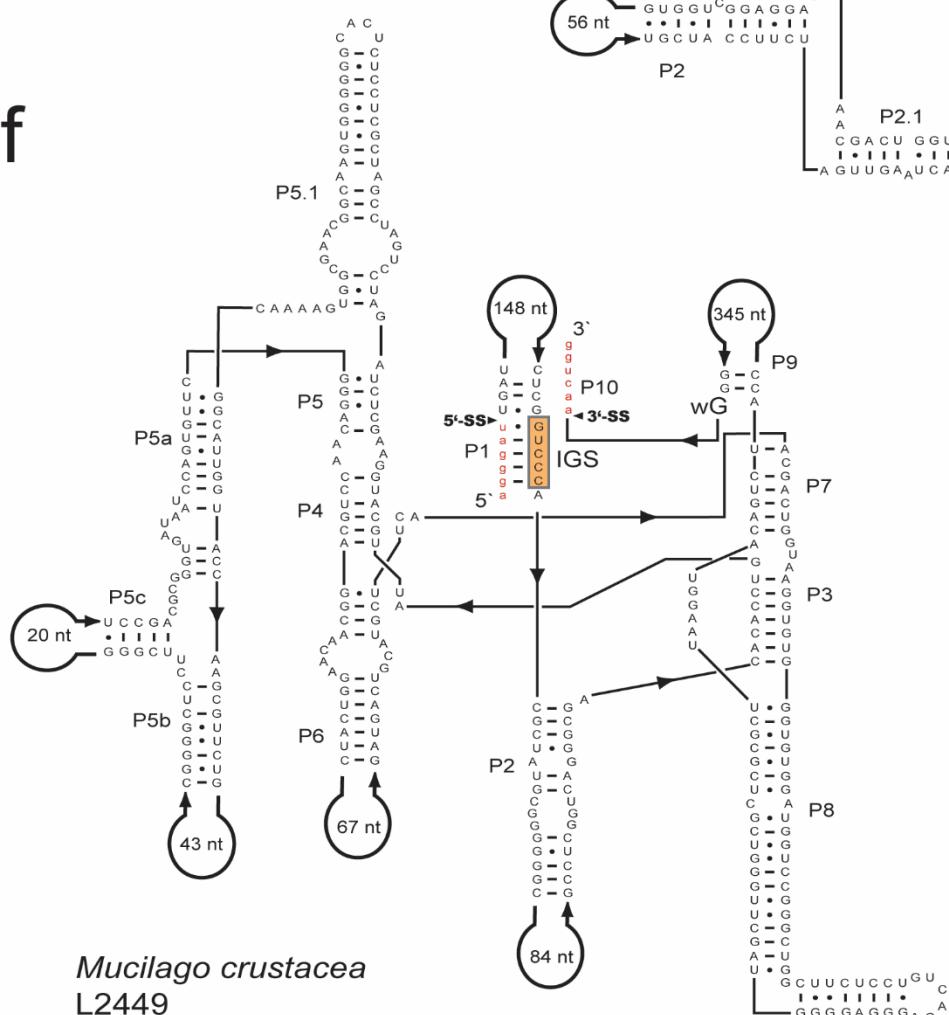


Figure S1 (e&f)

Figure S1: Secondary structure diagrams of the *Mucilago crustacea* rDNA group I introns. (a) S788 is a group IC1 intron in the SSU rRNA gene. Note that segment P2.1 (blue box) contains a 46-nt direct repeat motif. (b) L828 is a group IC1 intron in

the LSU rRNA gene. (c) L1926 is a group IE intron in the LSU rRNA gene. (d) L1949 is an unclassified group I intron in the LSU rRNA gene. Note that the P8 segment of the catalytic core is missing (pink box), and that segment P1 (blue box) contains a 9-nt direct repeat motif. (e) L2066 is a group IE intron in the LSU rRNA gene. (f) L2449 is a group IC1 intron in the LSU rRNA gene. Note that P1 and P9 contain extension sequences, but with no reading frame or direct repeat features. Common note to all intron diagrams: P1-P10, paired RNA segments; 5' SS and 3'SS, exon-intron splice sites; IGS, internal guide sequence; ωG, last nucleotide residue of intron; red lowercase letters, exon sequences.

<<P1>> <<P1>> <<P3>> <<P4>> <<P5>> <<<P5a>>>>> <<<P5a>>>>>>>

MZ313554 gccuuGAAGGGGCGUACACUG-ACAAAAAU-G-CGGGAAGGGUCGGUAAAAGGAA-GCCA-CAACAAGUAUGGUACAGC-UGC-U-UCCUA
MZ313547 guccuGAAGGGGCGGACACCG-ACAAAAA-G-CGGGAAAGGCCU-UAGA-AGCA-UCGGUAACCAAGUACGGUAGAACG-CCGA-UAGC-AU
MZ313549 gccuguGAAGGGGCGGACACCG-ACAAAAA-G-CGGGAAAGGCCU-UAGA-AGCA-UCGGUAACCAAGUACGGUAGAACG-CCGA-UAGC-AU
MZ313548 gccuguGAAGGGGCGGACACUA-ACCAAGUAG-CGGGAAUCUCCU-UAAA-AGCA-CUGGUAACCAAGUAGGUGUAAGAACGCG-GAGC-AU
MZ313546 gccuUAAGGGGCGGACACUA-ACCAAGUAG-CGGGAAUCUCCU-UAAA-AGCA-CUGGUAACCAAGUAGGUGUAAGAACGCG-GAGC-AU
DQ903677 gccuguGAAGGGGCGGACACUA-ACCAAGUAG-CGGGAAUCUCCU-UAAA-AGCA-CUGGUAACCAAGUAGGUGUAAGAACGCG-GAGC-AU
HE614614 gccuGAAGGGGCGGACACUA-ACCAAGUAG-CGGGAAUCUCCU-UAAA-AGCA-CUGGUAACCAAGUAGGUGUAAGAACGCG-GAGC-AU
AM231291 gccuguGAAGGGGCGGACACUA-ACCAAGUAG-CGGGAAUCUCCU-UAAA-AGCA-CUGGUAACCAAGUAGGUGUAAGAACGCG-GAGC-AU
HE614616 gccuguGAAGGGGCGGACACUA-ACCAAGUAG-CGGGAAUCUCCU-UAAA-AGCA-CUGGUAACCAAGUAGGUGUAAGAACGCG-GAGC-AU
HE614617 gccuguGAAGGGGCGGACACUA-ACCAAGUAG-CGGGAAUCUCCU-UAAA-AGCA-CUGGUAACCAAGUAGGUGUAAGAACGCG-GAGC-AU
AM231292 gccuguGAAGGGGCGGACACUA-ACCAAGUAG-CGGGAAUCUCCU-UAAA-AGCA-CUGGUAACCAAGUAGGUGUAAGAACGCG-GAGC-AU
AJ938151 gccuACAGGGGCGGACACUAUG-GUAAAUC-G-CGGUGA-CUCCU-UCUU-GCAUAGGA-UACCAGUAGGUGUACAC-UCCU-U-GC-AU
AJ938150 gccuUAGGGGGCGUAUCAUUG-GCAAAAU-G-CGGGAAAGGCCACCAAGCUCUCAUC-UCCAAGUACGGUAUAC-GGUG-U-CG-UA
AF239230 gccuUAGGGGGCGGACACCG-GCAAAAU-G-CGGGAAAGGCCUCAACCGCUCUCAUC-UCCAAGUACGGUAUAC-GGUG-U-CG-UA
AM231293 gccuUAGGGGGCGGACACCA-GCAAAACU-G-CGGGAAAGGCCUCAACCGCUCUCAUC-UCCAAGUACGGUAUAC-GGUG-G-GUAGC
HE614618 gccuUAGGGGGCGGACACCA-GCAAAACU-G-CGGGAAAGGCCUCAACCGCUCUCAUC-UCCAAGUACGGUAUAC-GGUG-G-CAG-AU
HE614619 gccuUAGGGGGCGGACACCA-GCAAAACU-G-CGGGAAAGGCCUCAACCGCUCUCAUC-UCCAAGUACGGUAUAC-GGUG-CAG-AU
MZ313552 gccuUAGGGGGCGGACACCG-ACAAAAAU-G-CGGGAAUCUCCU-UAAA-GCUG-GCCC-UACCAAGUACGGUAUACAU-GGGC-CAG-AU
DQ903678 gccuAAAGGGGCGGACACUG-AACAAAGUAG-CGGGAAUCUCCU-UAAA-GCUG-GCCC-UACCAAGUACGGUAUACAU-GGGC-G-GU-AU
DQ903676 gccuUAGGGGGCGGACACUG-CAAAAUU-G-CGGGAAACACCC-UAAA-GCUA-UCAC-UACAGCUAGUAUUAAC-GUGA-U-AG-AU
JQ031957 gccuUUGGGGGCGGACACUG-CAAAAUU-G-CAGGAAACACCC-UAAA-GAUU-CAGC-UACCAAGUACGGUAUAAU-GCUG-A-AU-AU
JQ031959 gccuUUGGGGGCGGACACUA-CAAAAUU-G-CAGGAAACACCC-UAAA-GAUU-CAGC-UACCAAGUACGGUAUAAU-GGUG-G-GU-AU
JQ031960 gcccuCAGGGGGCGGACACUA-CAAAAUU-G-CAGGAAACACCC-UAAA-GAUU-CAGC-UACCAAGUACGGUAUAAU-GGUG-G-GU-AU
DQ903683 gccuUGAACAGGGGCGGACACUAU-G-UUACAA-C-G-CAGGAAUCUCCU-CAAAAUU-GGCC-UACCCAGGGAGUACAGC-UUUU-G-GG-AU
DQ903673 gccuUAGGGGGCGGACACUA-CAAAAUU-G-CGGGAAACACCC-UAAA-GAUU-CAGC-UACCAAGUACGGUAUACAU-GUGC-A-AG-CAU
JQ031966 gccuUAGGGGGCGGACACUG-CAAAAUU-G-CGGGAAACACCC-UAAA-GAUU-CAGC-UACCAAGUACGGUAUACAU-GGCC-A-GG-AU
JQ031964 gccuUAGGGGGCGGACACUGCAACAU-U-G-CAGGAA-GUCCUUCAUAGCAG-G-AUCCAGUAUACGGUACAC-GGCUUC-GU-CGG
JQ031969 gccuUAGGGGGCGGACACUG-CAAAAUU-GA-CGGGAA-GUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAA-GGAU-G-GG-AU
JQ031973 gccuUGGGGGCGGACACCA-UCAAAAUU-GA-CAGGAA-GUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAGU-GCUG-A-GU-AU
JQ031976 gccuUUGGGGGCGGACACUA-CAAAAUU-G-CGGGAA-GUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAUACGGUC-U-GG-AU
H0687204 gccuUAGGGGGCGGACACCA-UCAAAAUU-G-CGGGAA-GUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAUACGGU-U-GG-AU
H0687196 gccuUAGGGGGCGGACACCU-UCAAAAUU-G-CAGGAA-GUCCU-UAGA-GCUU-AAACCUACCAAGUACGGUAUAAAAGGGU-U-A-G-AU
HQ687197 gccuUUAAGGGGCGGACACCCA-UCAAAAUU-GA-CGGGAA-GUCCU-UAGA-GCUU-AAACCUACCAAGUACGGUAUAAAAGGGUUA-A-G-AU
H0687200 gccuUAGGGGGCGGACACUG-CAAAAUU-G-CGGGAA-GUCCU-UAGA-GCUU-AAACCUACCAAGUACGGUAUAAAAGGGUUA-A-G-AU
JQ031978 gccuUAGGGGGCGGACACUG-CAAAAUU-G-CGGGAA-GUCCU-UAGA-GCUU-AAACCUACCAAGUACGGUAUAAAAGGGUUA-A-G-AU
JQ031980 gccuUAGGGGGCGGACACUG-CAAAAUU-GA-CAGGAA-GUCCU-UAGA-GCUU-AAACCUACCAAGUACGGUAUAAAAGGGUUA-A-G-AU
JQ031979 gccuCCGGGGGUGAACACUG-UCAAAAUU-GA-CAGGAA-GUCCU-UAGA-GCUU-AAACCUACCAAGUACGGUAUAAAAGGGUUA-A-G-AU
JQ031985 gccuUUAAGGGGGCGGACACUG-ACAAAAUU-G-CGGGAA-GUCCU-UAGA-GCUU-AAACCUACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
H0687194 gccuUAGGGGGCGGACACCA-UCAAAAUU-G-CGGGAAACACCC-UAAA-GGGU-CUGGUUACCAAGUAGGGGUUAACAU-CUGGU-A-UC-AU
H0687202 gccuUCCCGUGCGGACACCA-UCAAAAUU-G-CGGGAAACCCUU-AGGU-GGGU-CUGGUUACCAAGUAGGGGUUAACAU-CUGGU-A-UC-AU
HQ687195 gccuUCGAGGGGGCGGACACCA-UCAAAAUU-G-CGGGAAACCCAC-UAAA-GGGU-CUGGUUACCAAGUAGGGGUUAACAU-CUGGU-A-UC-AU
DQ903674 gccuUAGGGGGCGGACACUA-CAAAAUU-G-CGGGAAACCCCC-UAAA-GAUU-UCAGCUACUAAGUACAGCU-CGU-AU
DQ903672 gccuUAGGGGGCGGACACU-UAGA-GCGU-CUCC-UACCAAGUACGGUAUAAAAGGGUUA-A-GAG-C-AU
JQ031999 gccuUAGGGGGCGGACACUA-CAAAAUU-G-CGGGAAACCCCC-UAAA-GAUU-UCAGCUACUAAGUACAGCU-CGU-AU
DQ903671 gccuUAGGGGGCGGACACUA-CAAAAUU-G-CGGGAAAGCCCCUACAGAGCUU-GAUC-UACCAAGUACGGUAACAC-GAUC-A-GGCCAG
JQ032000 gccuUAGGGGGCGGACACUA-CAAAAUU-G-CGGGAAAGCCCC-UAAA-GAUU-UCAGCUACUAAGUACGGUAUAAAAGGGUUA-A-G-G-GAU
JX481296 gcuuCUGGGGAGCGGACACCA-CAAAAUU-G-CGGGAAACACCC-UAAA-GAUU-UCAGCUACUAAGUACGGUAUAAAAGGGUUA-A-G-G-GAU
KM494993 gcuuUUUUGGGAGCGGACACCG-UCAAAAUU-GAUCCGGAAAGUCCU-UAGA-GCUU-GCAC-UACCAAGUACGGUAUACAC-GUGC-A-GG-AU
KM494994 gcuuUUUUGGGAGCGGACACCG-UCAAAAUU-GAUCCGGAAAGUCCU-UAGA-GCUU-GCAC-UACCAAGUACGGUAUACAC-GUGCUA-GG-AU
KM494995 gcuuUUUUGGGAGCGGACACCG-UCAAAAUU-GAUCCGGAAAGUCCU-UAGA-GCUU-GCAC-UACCAAGUACGGUAUACAC-GUGCUA-GG-AU
KM494996 gcuuUUUUGGGAGCGGACACCG-UCAAAAUU-GAUCCGGAAAGUCCU-UAGA-GCUU-GCAC-UACCAAGUACGGUAUACAC-GUGC-A-GG-AU
KM494997 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM494998 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM494999 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495003 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495005 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495006 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495009 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495010 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495018 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495019 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495020 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495021 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495022 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495023 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495024 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495026 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495027 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495028 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495029 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
KM495030 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
JX481284 gcuuUUUUGGGAGCGGACACCA-UCAAAAUU-GC-CGGGAAAGUCCU-UAGA-GCCC-AUCC-UACCAAGUACGGUAUAAAAGGGUUA-G-G-GAU
V01416 ucucuAUUUGGGAGCGGACACCA-UCAAAAUU-G-CGGGAAACAUCC-UAAA-GCUG-UCAC-UACCAAUACGGUAACAC-GUGG-CAG-AU
MZ313554* acgauUUUGGUUGCGGACACUA-UCAAAAUU-G-CGGGAAACAUCC-UAAA-GCUG-UCAC-UACCAAUACGGUAACAC-GUGG-CAG-AU

<<P5>> <<<P4>>><<<P6>>>><<<P6>>>><<P7>>> <<P3>>><<P8>><P8>> <<P7>> *
 GGUC-AACU-CGCAGCCAAGUCCUAGGGGAUGCAGUUCACAGACCAAACGUCAGUGGGUGGCCCUAAGAGAUGGUCGGUCGuugua
 MZ313547 GGUACGAC-CGGCGCCAAGCCCCUAGGGGUGCAGGCCAACAGACCAAACGUCAGGGUGGCCAUAGACAAUGGUCGUAGCGuugua
 MZ313549 GGUACGAC-UCCGCGCCAAGCCCCUAGGGGUGCAGGCCAACAGACCAAACGUCAGGGCAACAGGUAGGGUGGCCUUAAGAUAGGUCGACCGuugua
 MZ313548 GGGC-AACC-UGCGGCCAACGCCGUAGGGGUGCAGCUACAGACCAAACGUCAGGGCAACAGGUAGGGUGGCCUUAAGAUAGGUCGACCGuugua
 MZ313546 GGGGCAAC-UCCGCGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGGCAACAGGUAGGGUGGCCUUAAGAUAGGUCGACCGuugua
 DQ903677 GGGC-AACC-UGCGGCCAACGCCGUAGGGGUGCAGCUACAGACCAAACGUCAGGGCAACAGGUAGGGUGGCCUUAAGAUAGGUCGACCCGuugua
 HE614614 GGGGCAAC-UCCGCGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGGCAACAGGUAGGGUGGCCUUAAGAUAGGUCGACCCGuugua
 HE614616 AM231291 GGGAUAAAC-UCCGCGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAGGUCGACCCGuugua
 HE614617 GGGAUAAAC-UCCGCGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAGGUCGACCCGuugua
 AM231292 GUGU-AACC-UGCGGCCAACCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAGGUCGACCCGuugua
 AJ938151 GGUUCACU-UCCGCUCCAAACCCGUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAGGUCGACCCGuugua
 AJ938150 GGGC-UACU-UGCAACCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAGGUCGACCCGuugua
 AF239230 GGGC-AACC-UGCAGCCAACUCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAGGUCGACCCGuugua
 AM231293 GGAU-UAC-UGCAGCCAACUCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAGGUCGACCCGuugua
 HE614618 HE614619 GGGU-UAC-UGCAGCUAACCCCACUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAGGUCGACCCGuugua
 MZ313552 GGGU-UAC-UGCAGCCAACCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAGGUCGACCCGuugua
 DQ903678 GGGC-AACC-UGCGGCCAACGCCGUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAGGUCGACCCGuugua
 DQ903676 GGGC-AACC-UGCAGCCAACGCCGUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAGGUCGACCCGuugua
 JQ031957 JQ031959 GGGC-AACC-UGCAGCCAACGCCGUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 JQ031960 JQ031968 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 DQ903673 GAGU-AACU-UGCGGCCAACGUUACAGGGACGGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 JQ031966 GGGC-AACU-UGCAGCCAACCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 JQ031964 JQ031969 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 JQ031973 JQ031976 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 HQ687204 HQ687196 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 HQ687197 HQ687200 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 JQ031978 JQ031980 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 JQ031979 JQ031985 GGGC-AACC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 HQ687194 HQ687202 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 HQ687195 HQ687200 GGGC-AACC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 DQ903674 DQ903672 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 JQ031999 DQ903671 GGGU-UAC-UGCAGCCAACACCCACCGGGGCCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 JQ032000 JX481296 GGGU-UAC-UGCAGCCAACACCCACCGGGGCCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 KM494993 KM494994 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 KM494995 KM494996 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 KM494997 KM494998 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 KM494999 KM495003 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 KM495005 KM495006 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 KM495009 KM495010 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 KM495018 KM495019 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 KM495020 KM495021 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 KM495022 KM495023 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 KM495024 KM495026 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 KM495027 KM495028 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 KM495029 KM495030 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 JX481284 V01416 GGGU-UAC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua
 MZ313554* GGGU-AAUC-UGCAGCCAAGCCCCUAGGGGUGCAGCUACAGACCAAACGUCAGGUAGGGUGGCCUUAAGAUAUAGCCGAAAGGuugua

Figure S2: Sequence alignment of core structure nucleotides of myxomycete S1389 group I intron. Dashes correspond to deleted positions. Secondary structure paired segments (P1-P8) are shown above the alignment. Intron sequences are indicated by GenBank accession numbers. V01416 and MZ313554* correspond to the out-group *Tetrahymena* intron Tth.L1925 and *Mucilago* intron Mr.S788, respectively.

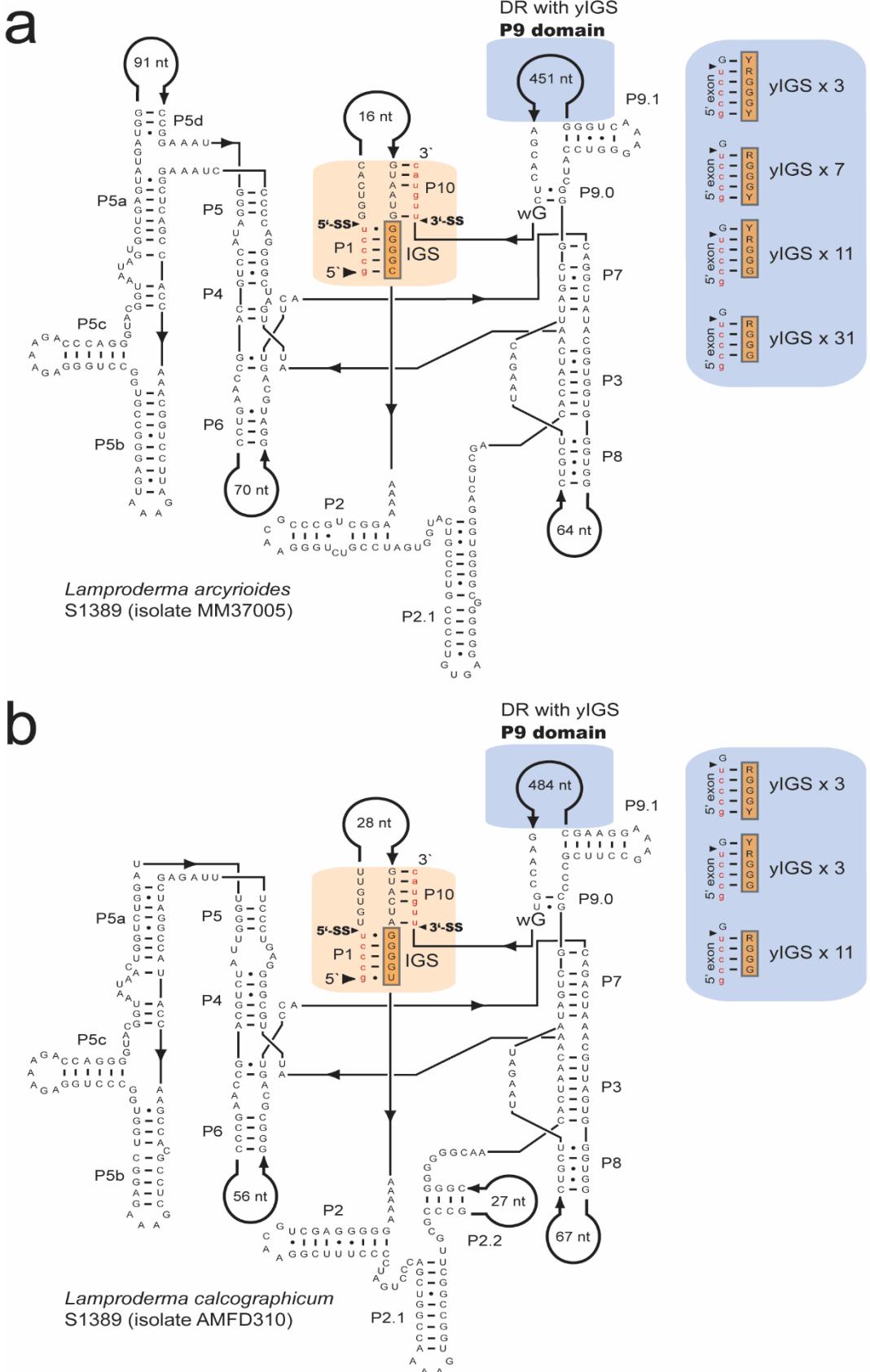


Figure S3

Figure S3: Secondary structure diagrams of (a) *Lamproderma arcyrioides* and (b) *Lamproderma arcyrioides* S1389 group I intron. P1-P10, paired RNA segments; 5' SS and 3'SS, exon-intron splice sites; IGS, internal guide sequence. The introns contain large extensions in P9 that contains direct repeat motifs (blue box) with ΨIGS sequences motifs.

a

His-Cys Box homing endonuclease (KM494996)

MPPKESKAEEKMREHRNETKRRSRAKIKRDQDEKRRKLGLPPPERGAT SANRAARLGLLCATDAGLLEM RGSQSGEVTHGTCVYVPRLL
MHKRMVDKARLEVYREVRET VELMGEDEKVQAHHVQMILDDRERVGRWYDHLKARAA ALANGEAGNLPDV TGSHTCRKELFMQLS GGER
ARYRDYTCAAFHCPFDYHSHNLAQKCPQS QHFRVAGALYRADCTCRAPCVL SDNQVIDLKPE (244 amino acids)

His-Cys Box homing endonuclease (KM495030)

MPRHTEETEEALERAKAKNKRASRATLKLQREKGSEKPAKKARGATAENKANRLRLVLCQTDLLKLLRAAAVKTGVEFGPCLYAPRVR
LSKDKTVWDIERMKRGFVTRETVALGEDEKEVQAHHVQMVLDDRVREEWYDRLVSRAAISKGDAEVPPDTYGSHTCRKEAFRQLSDPK
EQAKYRDHTCTAQFHCPVPLHVSNLAKQDCPSKHFRLLNGEIYRAECQCSVRCVPQTNTTSLVKE (247 amino acids)

b

Homing endonuclease gene (KM494996)

AUGCCGCCUAAGGAAAGCAAGCAGAGAAAAAAUAGGGAGCAUAGGAUAGAGACUAACGCAGAACGCCGGCAAAGAUCAAGCAGAGACCAAGAUGAGAAAAGGCCGAAGCUAGGGUUC
CCCCCCCUCGAGGGGGGCCACUCGGCUCAAGCGGCCUAUGUUCGGCCUUCUUCGUCGCCAGACUGUUCGGCCUUCUUAJAGAUUCGCCAGGCCAGGGGAAGUACCCAC
GCCACAUAGCUUAJAGUUCUCCUCGUUAAGUACAGGUAGGGCGGUUAGGGCCGGCCACCCGGCUGUAAGUCAACAAAGCAGCAGGUUGUUAAGGUUCUCCUGGUAGUACCCGG
AGGUACGGGAAACCGUJAGUAGCAUAGGGCAGAAGUAGAGGUACAGGCAGCACCGUAGUACAUAGUACUAGUACUGUAGCAGGUUGGGCGCUGGUAGUACCAUCUAAAAGCCGGG
CUGUCGCCUUCGUUAAGGCCUJAGCAGGAGAAAGGUACUGGUACUCCGGCCAGAGGAGCUCUAGGCGGGGGGGAGGGCCGAUACAGG
GACUJAACUUCGUUAAGGCCUJAGCAGGAGAAAGGUACUGGUACUCCGGCCAGAGGAGCUCUAGGCGGGGGGGAGGGCCGAUACAGG
UGCACGUUGCAGAGGCCUGGUAUAAAAGCAUAACAUAGGUAGCUCUAAACCCGAAUAAAAAAACU

Homing endonuclease gene (KM495030)

AUGCCAAGACACAACAGAAGAACACAGAAGGAGCCCUUGGAAGCUAAGGUCAAAAGCAAGCGUCAUCAGGCCAAGGGCAAGCJUGAAGCUGCAGAGGGAGAAAGGCUCUGAAAAG
CCUCCCAAGAACAGCAGGGGCGUACGCGCCAGAACAGGCCAAUJAGCCGUCGUUCGUCCUAUAGCAGGCCCUAAGCJUGAAGCUGCAGGGGAGAAAGGCUCUGAAAAG
GAGUUGGUCCGGCCUUUAAGCAGGGCUCGUJUGAGGUACAUAGGUAUGAUGGGGUUGGGGUUUUCUGACGUAUCCUGGUAGUAJAGACUGCCUGGUUGGUAGUAUCG
AGGCCAAUAGAAAGGUUUGGUUGGUACAGCGGAAACGUCCUGGUCCUGGGAGAACAGGAGAACAGGUACAGGCCUCAAUAGGUACAGGUACGUCCGGUAGGAGGUUG
AUGCGGUUAGUAJUCAAGCGGCCGCGUCUGAACACAGCAAAAGCGGUACUGAAGGUCCCCCCACUACAGGGGUUCCACAAAGCUGGGAAAGGGCJUUIJAGGCAGGCCUGGUACCG
AGCGGCCAAUAGCAAGGGGUACUCCUAGCGGCCGUUCCAGGUUCCGUUJUGACGUUAGGUACAGGGGUUCCACAAAGCAGGUUCCUJUAAUAGGGG
AAUAGGUACCGGGGAAUCCGUAGGUUCCGUUCCGUUJUGACGUUAGGUACAGGGGUUCCACAAAGCAGGUUCCUJUAAUAGGGGAAUAGGUACAGGG
AAUAGGUACCGGGGAAUCCGUAGGUUCCGUUCCGUUJUGACGUUAGGUACAGGGGUUCCACAAAGCAGGUUCCUJUAAUAGGGGAAUAGGUACAGGG

C

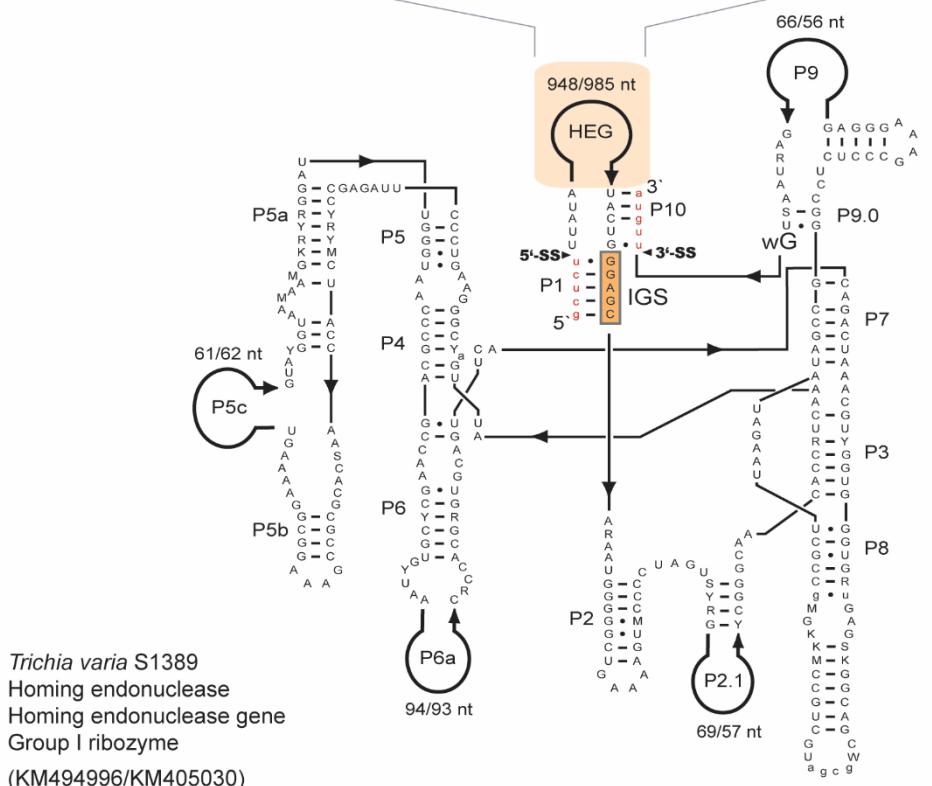


Figure S4

Figure S4: Sequence features in *Trichia varia* S1389 group I introns. (a) Amino acid sequence of *T. varia* homing endonucleases, including His-Cys box motifs (green letters). (b) Nucleotide sequence of *T. varia* homing endonuclease genes, including spliceosomal introns (red letters). Start codon (AUG) and stop codon (UAA) are indicated by green letters. Polyadenylation signal (AAUAAA) is indicated as bold underlined letters at the 3' end of sequence. (c) Secondary structure

diagram of *T. varia* group I introns (KM494996 and KM495030). Homing endonuclease gene (HEG) insertions are located in segment P1. P1-P10, paired RNA segments; 5' SS and 3'SS, exon-intron splice sites; IGS, internal guide sequence; ωG, last nucleotide residue of intron; red lowercase letters, exon sequences; black lowercase letters, nucleotide positions only present in one of the introns. R represents A or G (purine); Y represents C or U (pyrimidine); K represents G or U; M represents A or C; S represents C or G; W represents A or U.

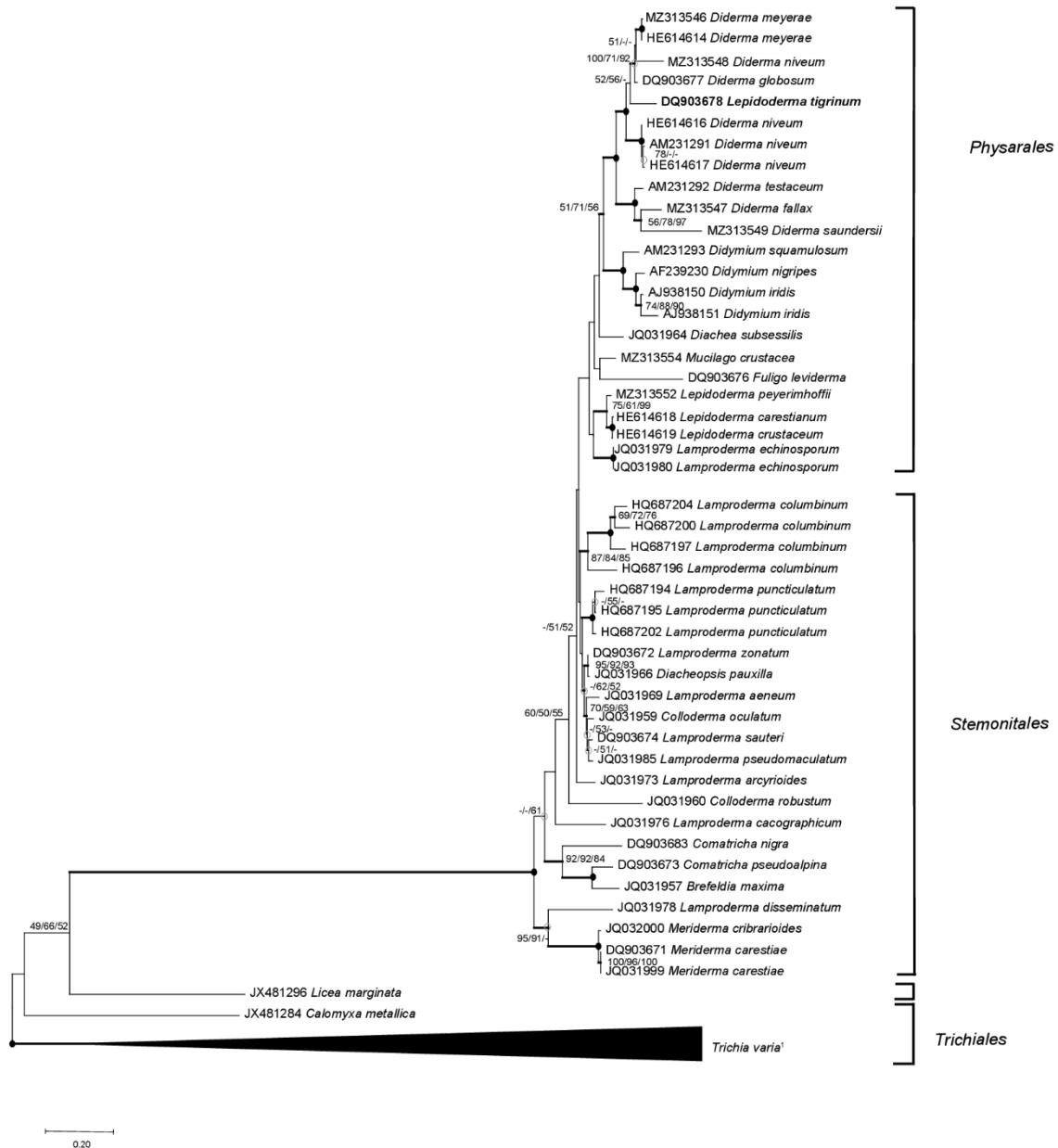


Figure S5: Molecular phylogeny of myxomycete taxa based SSU rDNA sequences. The SSU topology is obtained by neighbor-joining (NJ) analysis of 72 taxa and 1,575 nt aligned positions (SSU dataset 1; Table S1). The tree is rooted with the *T. varia* SSU rDNA sequence. The NJ, maximum likelihood (ML), and maximum parsimony (MP) bootstrap replicates ($\geq 50\%$) are given at each node. Bayesian posterior (BI) probabilities (≥ 0.95) are shown in bold branches. Black dots at branch points; maximum support in NJ, ML, and MP ($\geq 97\%$). The scale bar indicates the fraction of substitutions per site.

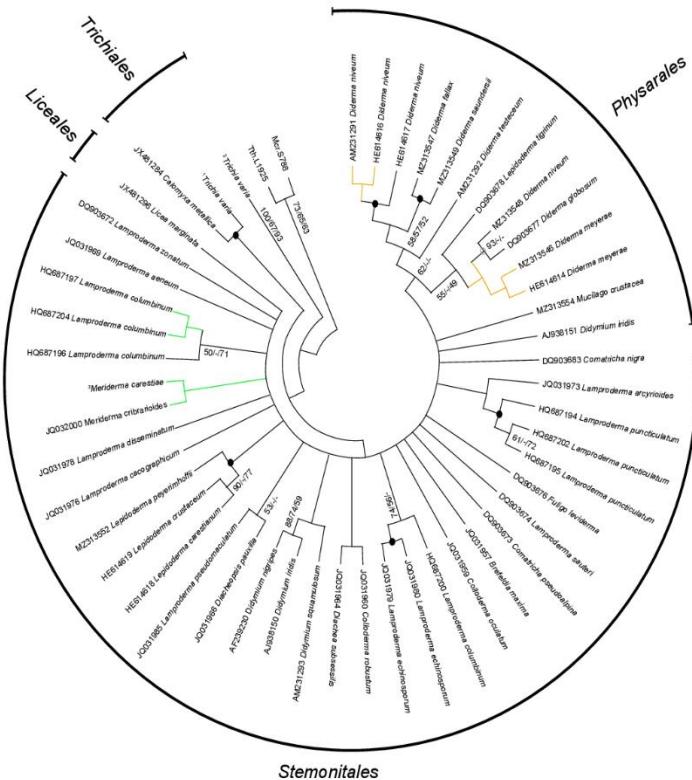


Figure S6: Molecular phylogeny of myxomycete S1389 group I introns. The intron topology is obtained by neighbor-joining (NJ) analysis of 74 taxa (including group introns from *Tetrahymena* (Tth.1925) and *Mucilago* (Mcr.S788), and 166 nt aligned positions (intron dataset 2; Table S1). The NJ-, maximum likelihood (ML), and maximum parsimony (MP) bootstrap replicates ($\geq 50\%$) are given for each node. Bayesian posterior (BI) probabilities (≥ 0.95) are shown in bold branches. Black dots at branch site indicate maximum support in NJ, ML, and MP ($\geq 98\%$). Green line indicates maximum support in NJ, ML and MP ($\geq 90\%$). Orange line indicates maximum support in NJ, ML, and MP ($\geq 70\%$). Gray circles indicate alternative topologies in NJ, ML, and MP. ¹ *Tricia varia* clade is composed of four *T. varia* isolates (KM494993-6). ² *Tricia varia* clade is composed of twenty *T. varia* isolates (KM494997-9, KM495003, KM495005, KM495006, KM495009, KM495010, KM495018-30). ³ *Meriderma carestiae* clade is composed of two *M. carestiae* isolates (JQ031999 and DQ903671). The scale bar indicates the fraction of substitutions per site.