Figure S1. Maximum likelihood phylogenetic tree of the Stylommatophora based on concatenated sequences of 5782 unambiguously aligned nucleotides from the combined dataset of the LSU (and 5.8S) gene, the SSU gene, the H3 gene and the 1st and 2nd codon positions of the CO1 gene. The optimal model GTR+Γ was used. The phylogeny is rooted on the siphonariid *Siphonaria pectinata*. Values on the nodes represent bootstrap support (1000 replicates). Bootstrap support values less than 50% are not shown. The scale bar represents 1 substitutional change per 100 nucleotide positions.
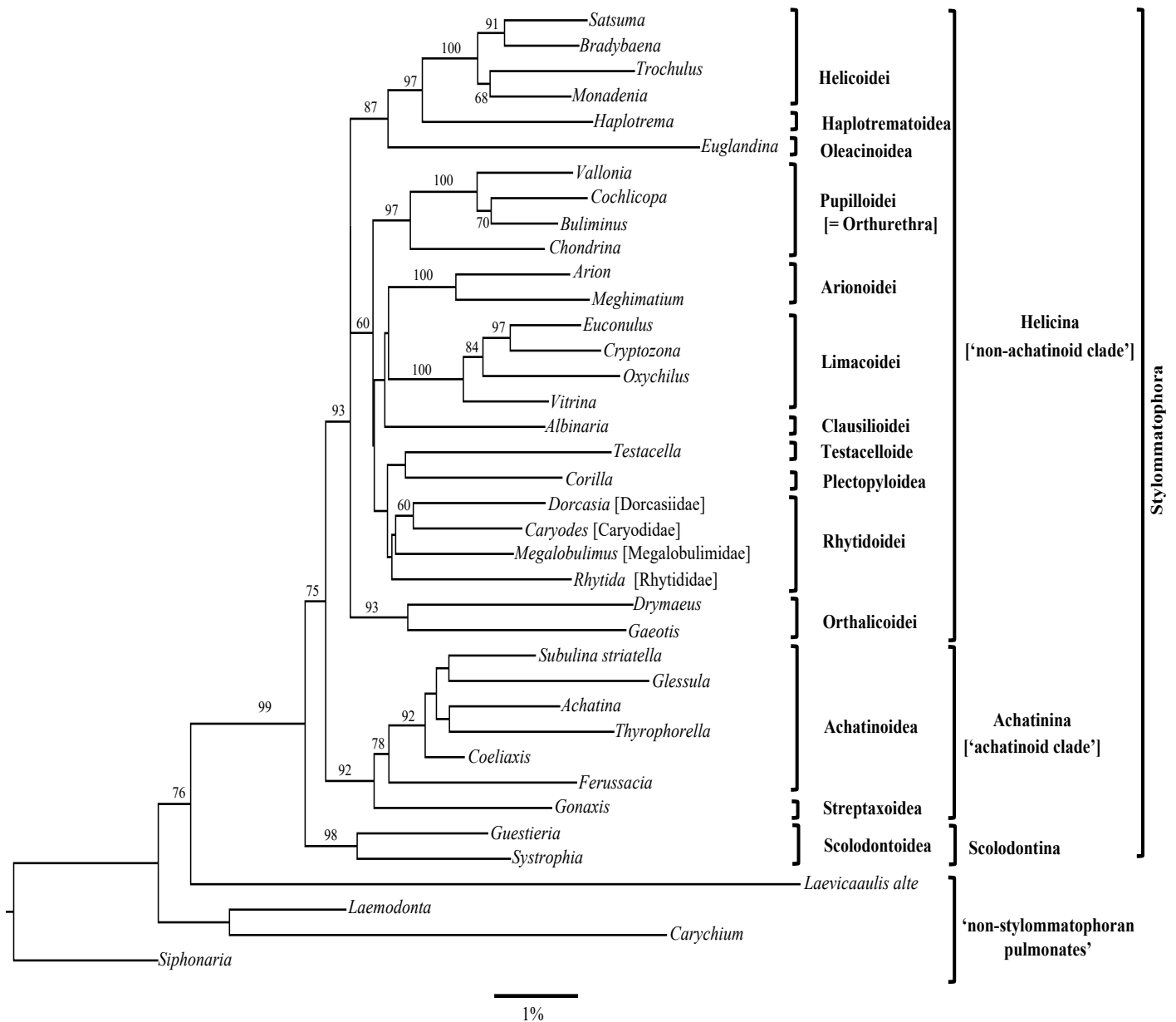
Figure S2. Neighbor-joining phylogenetic tree of the Stylommatophora based on concatenated sequences of 5782 unambiguously aligned nucleotides from the combined dataset of the LSU (and 5.8S) gene, the SSU gene, the H3 gene and the 1st and 2nd codon positions of the CO1 gene. The phylogeny is rooted on the siphonariid *Siphonaria pectinata*. Values on the nodes represent bootstrap support (1000 replicates). Bootstrap support values less than 50% are not shown. The scale bar represents 1 substitutional change per 100 nucleotide positions.
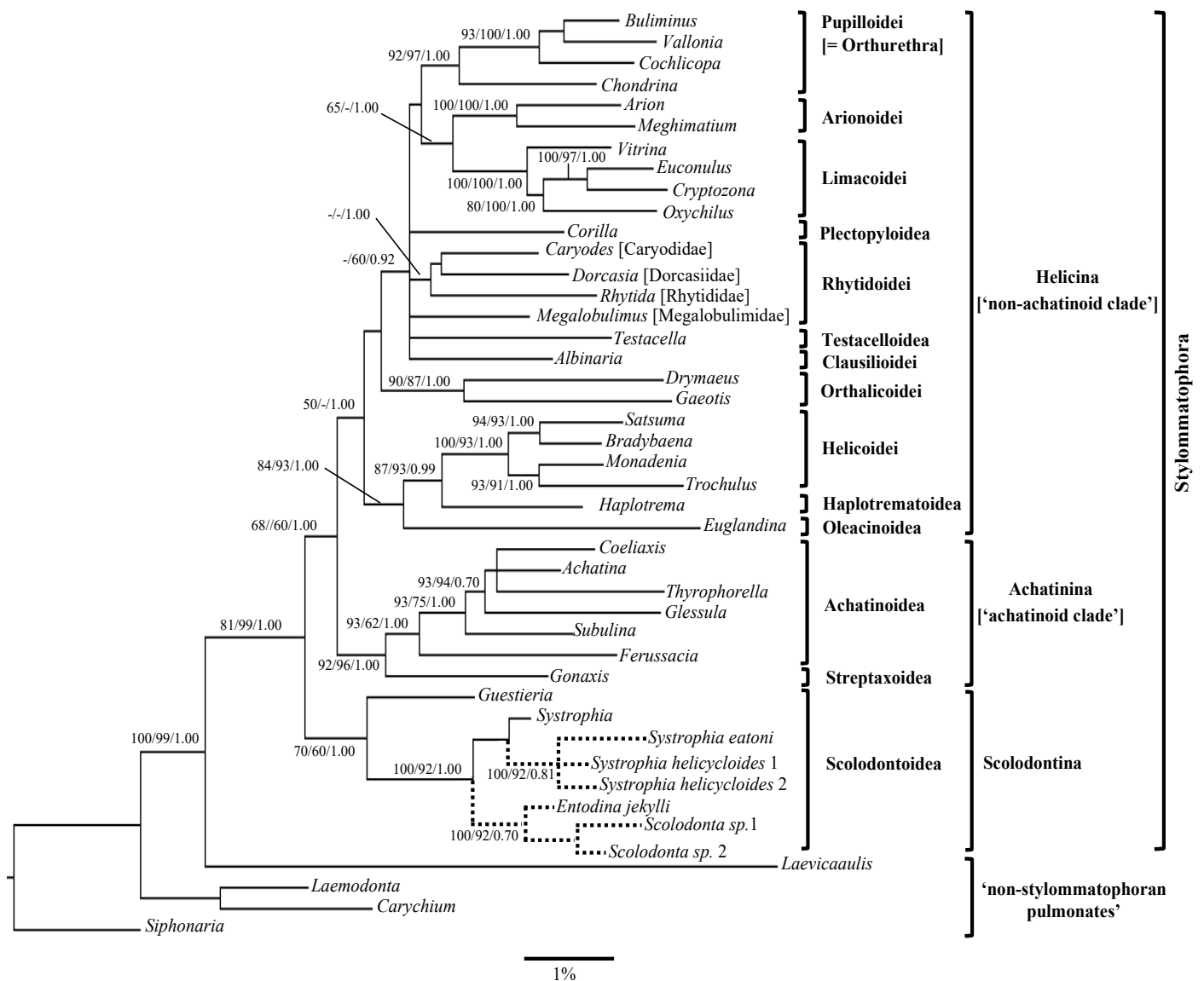
2

Figure S3. Bayesian phylogenetic tree of the Stylommatophora based on concatenated sequences of 5782 unambiguously aligned nucleotides from the combined dataset of the LSU (and 5.8S) gene, the SSU gene, the H3 gene and the 1st and 2nd codon positions of the CO1 gene. The phylogeny also incorporates all published partial rRNA sequences (431bp) of the Scolodontidae from Ramirez et al. (2012) shown as dotted lines. The accession numbers of the published taxa are (*Systrophia eatoni* = HM067823.1, *Systrophia helicycloides* 1= JN604723.1, *Systrophia helicycloides* 2= JN604724.1, *Entodina jekylli* = HM067824.1, *Scolodonta sp.* = HM067825.1 and *Scolodonta sp.* 2 =HM116227.1). The optimal model GTR+Γ was used. The phylogeny is rooted on the siphonariid *Siphonaria pectinata*. Values on the nodes represent bootstrap support (1000 replicates) for ML, NJ and posterior probabilities for BI (based on last 75% of trees), respectively. Bootstrap support values less than 50% and posterior probabilities less than 0.7 are not shown. The scale bar represents 1 substitutional change per 100 nucleotide positions.
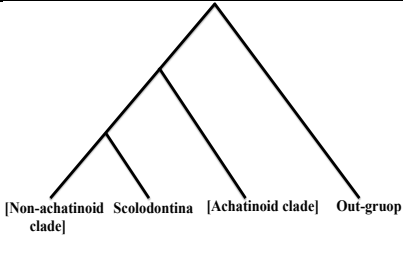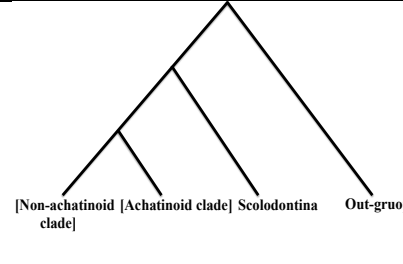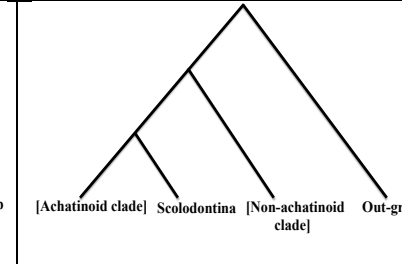
Table S1: Genbank sequence accessions of all sequences used in this study.

Taxa	LSU rRNA gene (also incorporating partial 5.8S and complete ITS-2)	SSU rRNA	H3	CO1
Ferussacia foilliculus	MF444871[1]	MN022689	MF415338[1]	MF415348[1]
Subulina striatella	MF444888 [1]	MN022690	MF415330[I]	MF415358[1]
Glessula ceylanica	MF444872[1]-MF444873[1]	MN022691	MF415337[1]	MF415347[1]
Lissachatina fulica [= *Achatina fulica*]	MF444864[1]	MN022692	MF415320[1]	MF41534[1]
Coeliaxis blandii	MF444867[1]- MF444868[1]	MN022693	MF415335 [1]	MF415345[1]
Thyrophorella thomensis	MF444891[1]	MN022694	MF415339[1]	MF415349[1]
Gonaxis quadrilateralis	MF444893[1]	MN022697	MN022760	MN022729
Cochlicopa lubrica	KU341313 [2]	MN022682	MN022751	MN022720
Vallonia excentrica	MN022656	MN022683	MN022752	MN022721
Chondrina clienta	MN022657	MN022684	MN022753	MN022722
Buliminus labrosus	MN022658	MN022685	MN022754	MN022723
Albinaria xantostoma	MN022659	MN022686	MN022755	MN022724
Drymaeus discrepans	MN022660	MN022687	MN022756	MN022725
Gaeotis nigrolineata	MN022661	MN022688	MN022757	MN022726
Euglandina rosea	MN022662	MN022695	MN022758	MN022727
Haplotrema vancouverense	MN022668	MN022702	MN022765	MN022734
Rhytida stephenensis	MN022667	MN022701	MN022764	MN022733
Megalobulimus oblongus	MN022664	MN022698	MN022761	MN022730
Dorcasia alexandri	MN022665	MN022699	MN022762	MN022731
Caryodes dufresnii	MN022666	MN022700	MN022763	MN022732
Euconulus fulvus	MN022670	MN022704	MN022767	MN022736
Cryptozona bistrialis	AY014106[3] & MN022671	MN022705	MN022768	MN022737
Vitrina pellucida	MN022672	MN022706	MN022769	MN022738
Oxychilus alliarius	MN022673	MN022707	MN022770	MN022739
Satsuma japonica	MN022674	MN022708	MN022771	MN022740
Trochulus striolata	MN022675	MN022709	MN022772	MN022741
Bradybaena similaris	MN022676	MN022710	MN022773	MN022742
Monadenia fidelis	MN022677	MN022711	MN022774	MN022743
Arion hortensis	KU341315[2]	MN022712	MN022775	MN022744
Meghimatium bilineatum	MN022678	MN022713	MN022776	MN022745
Testacella scutulum	MN022663	MN022696	MN022759	MN022728
Corilla adamsi	AY014091[3] & MN022669	MN022703	MN022766	MN022735
Guestieria sp.	MN022679	MN022714	MN022777	MN022746
Systrophia sp.	MN022680 & MN022681	MN022715	MN022778	MN022747
Laemodonta sp.	KU341316[2]	MN022716	MN022779	KM281112[4]
Carychium tridentatum	KU341318[2]	MN022717	MN022780	MN022748
Laevicaulis alte	KU341319[2]	MN022718	MN022781	MN022749
Siphonaria pectinata	AY014149[3] & KU341320[2]	MN022719	MN022782	MN022750

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2. Davison, A., McDowell, G.S., Holden, J.M., Johnson, H.F., Koutsovoulos, G.D., Liu, M.M., Hulpiau, P., Van Roy, F., Wade, C.M., Banerjee, R. and Yang, F., 2016. Formin is associated with left-right asymmetry in the pond snail and the frog. Curr. Biol. 26, 654-660.

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Table S2: Three possible alternative phylogenetic trees showing the possible position of the Scolodontina within the Stylommatophora (tree one: 'non-achatinoid clade' clusters with Scolodontina, tree two: 'non-achatinoid clade' clusters with 'achatinoid clade' with Scolodontina falling as a sister group to both clades, tree three: 'achatinoid clade' clusters with Scolodontina. The reliability of the inferred trees was tested by bootstrap resampling of maximum likelihood (ML), neighbor-joining (NJ), minimum-evolution (ME), Fitch-Margoliash (FM) and differences in the number of supporting parsimony informative sites. The number of supporting parsimony informative sites were calculated based on four taxon trees incorporating *Siphonaria pectinata*, *Guestieria sp.*, *Lissachatina fulica* and *Monadenia fidelis*.

	Tree1	Tree 2	Tree 3
ML bootstrap	3	93	4
NJ bootstrap	22	75	3
ME bootstrap	8	88	4
FM bootstrap	5	84	11
Parsimony informative sites	11	22	11
Parsimony transversion/ sites	0	10	2