

The evolution of traits and functions in herbivorous coral reef fishes through space and time

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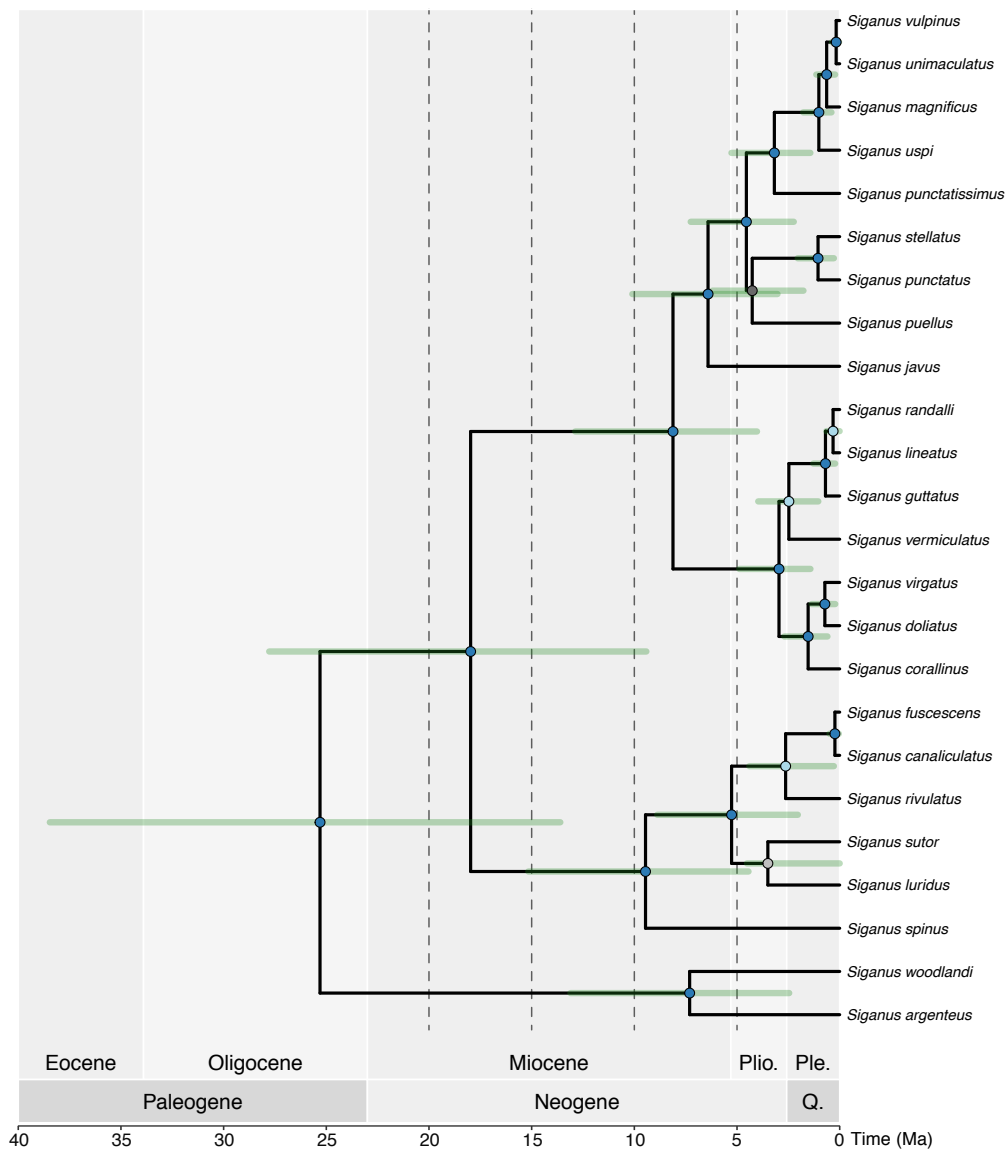
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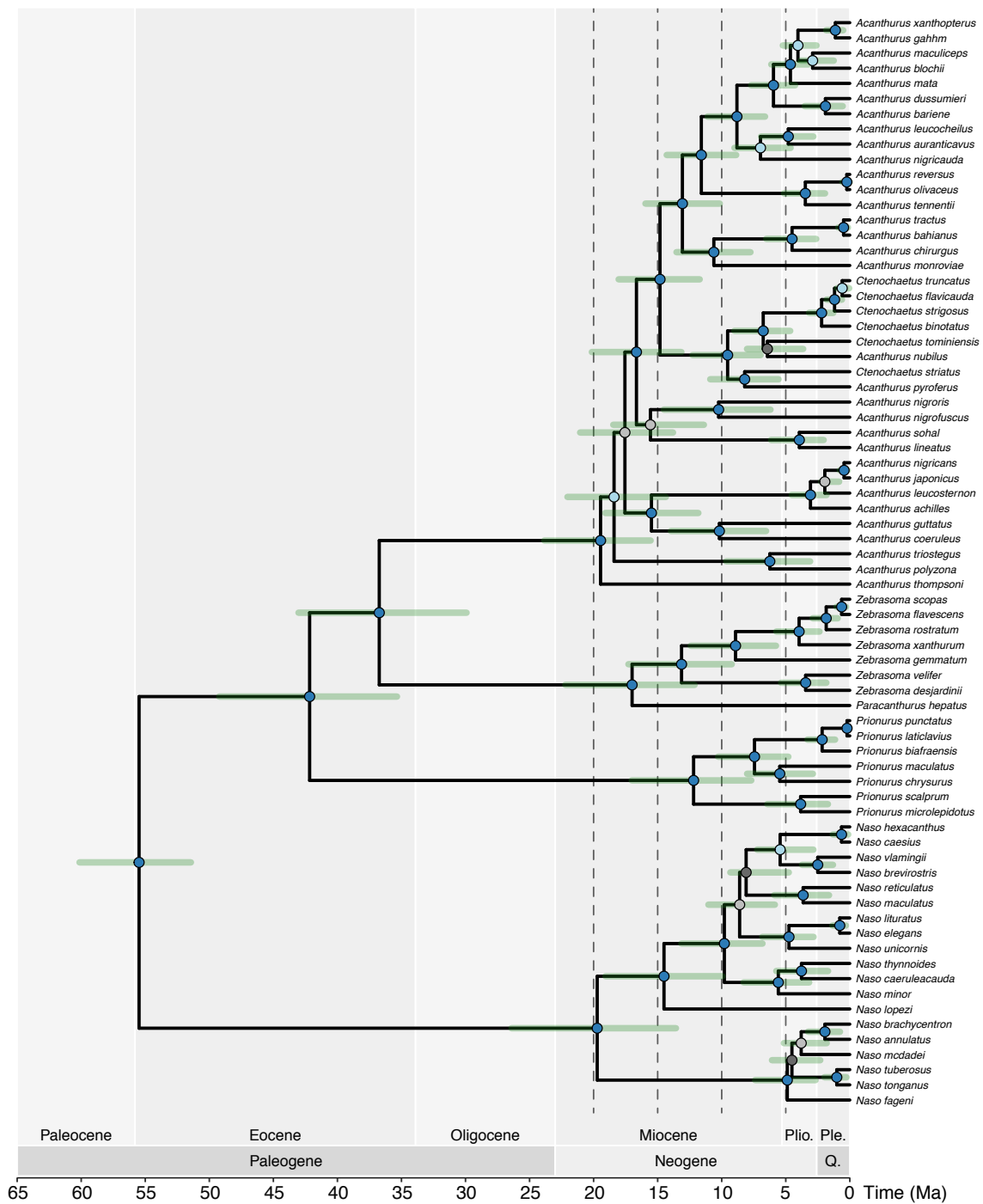
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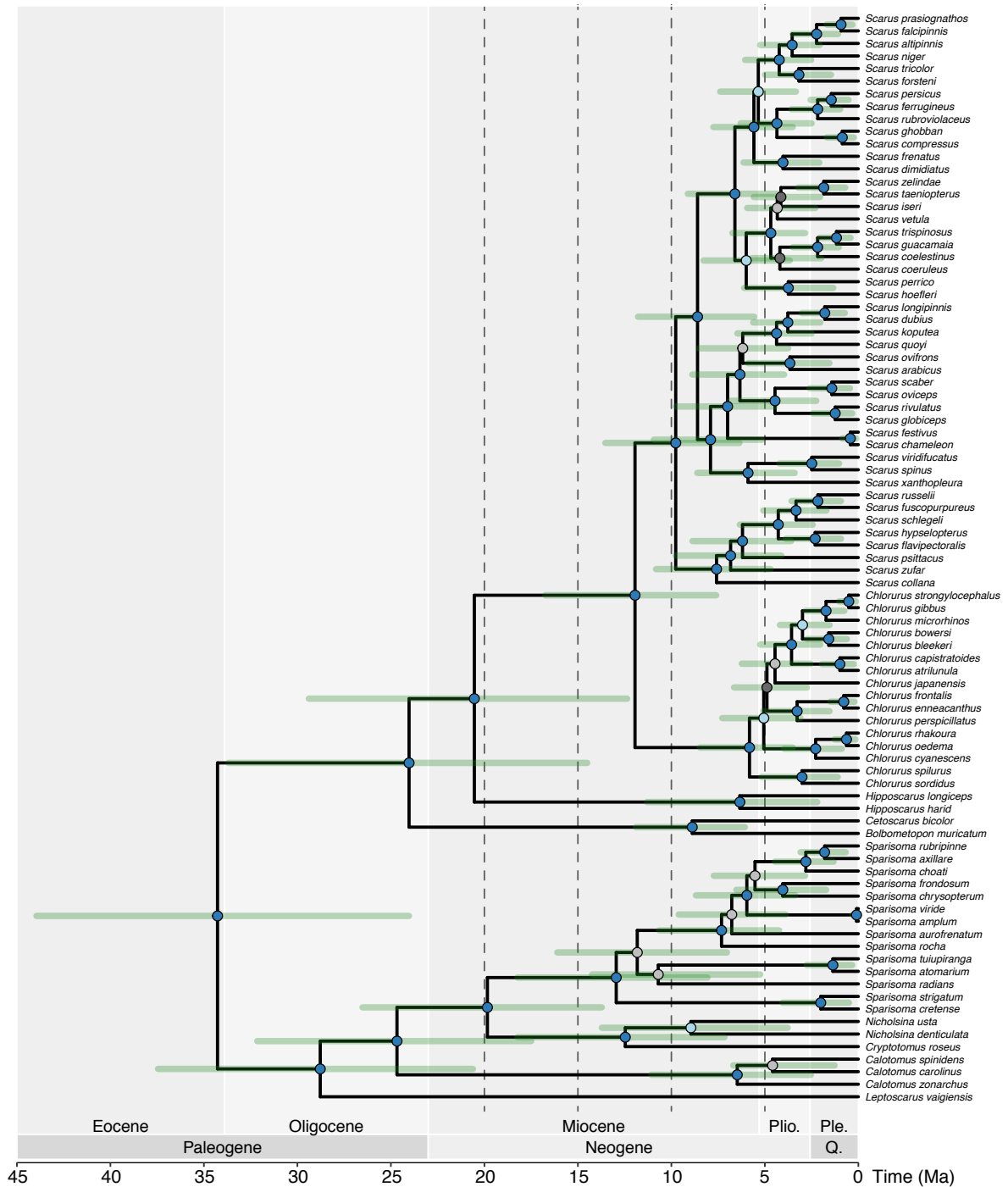
Supplementary figures



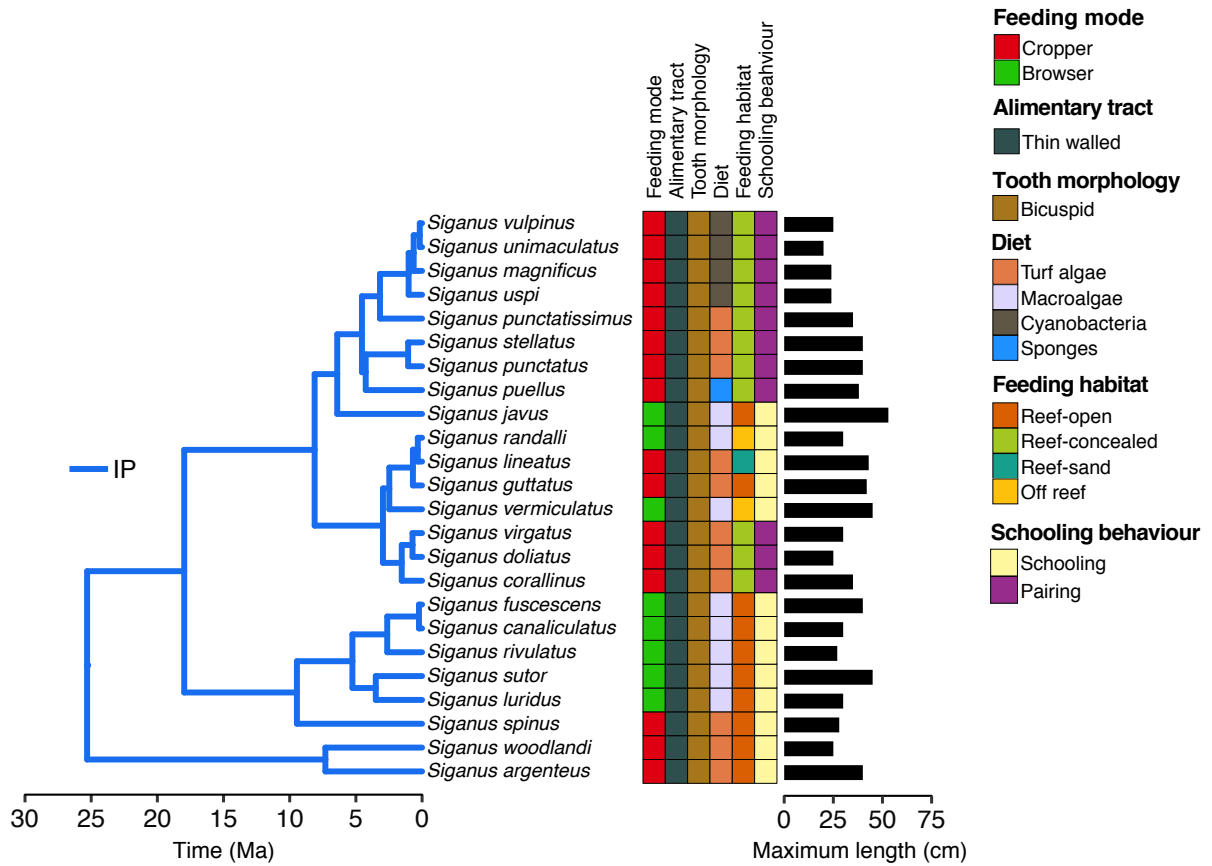
Supplementary figure 1. Maximum Clade Credibility (MCC) tree resulting from the Bayesian Inferences for Siganidae. Node colours represent posterior support values: ≥ 0.9 (dark blue); $< 0.9 - \geq 0.7$ (light blue); $< 0.7 - \geq 0.5$ (light grey); ≤ 0.5 (dark grey). Highest Posterior Density intervals for node ages are shown in green. Dashed lines represent the time-slices used to retrieve ancestral states.



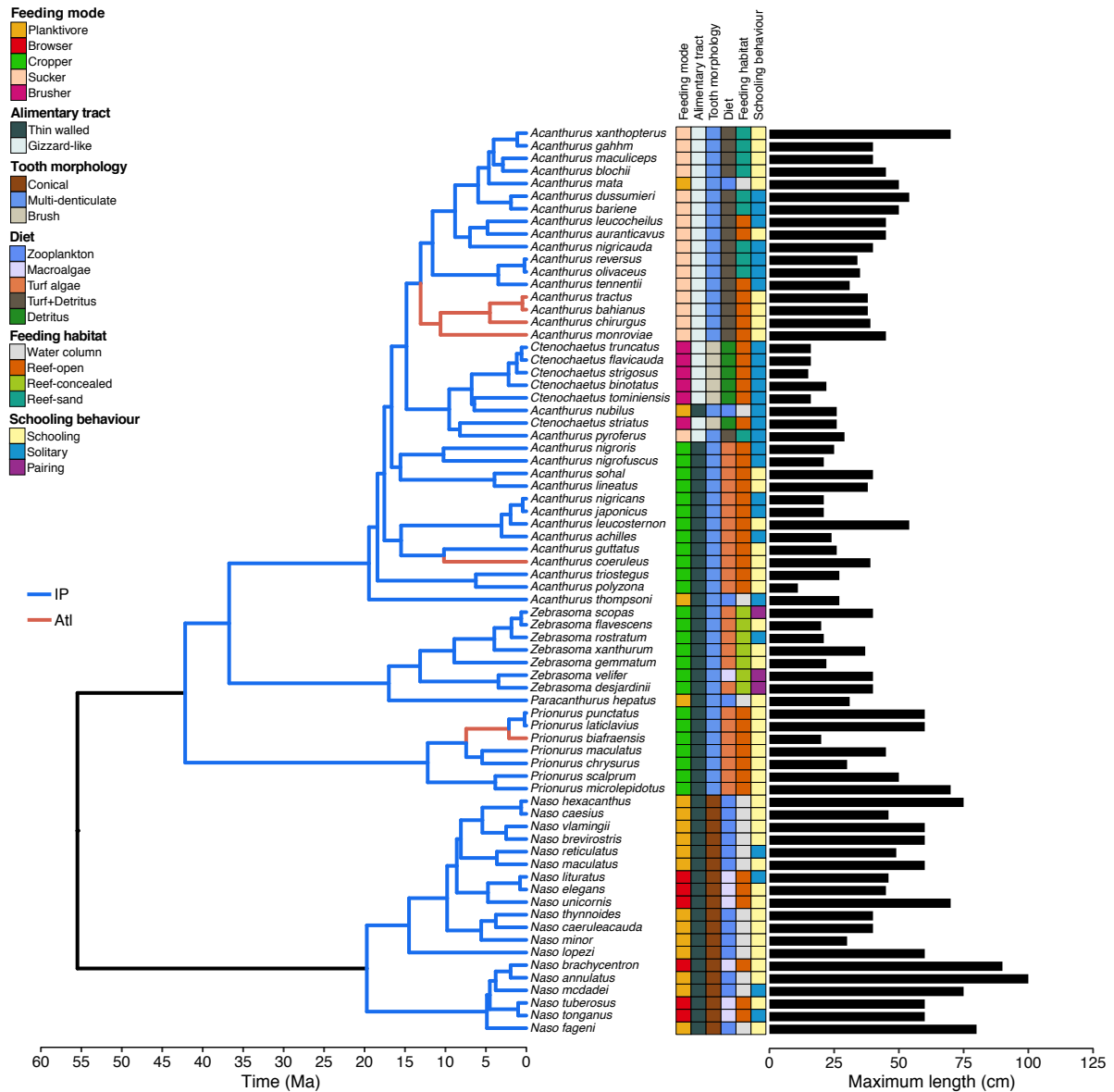
Supplementary figure 2. Maximum Clade Credibility (MCC) tree resulting from the Bayesian Inferences for Acanthuridae. Node colours represent posterior support values: ≥ 0.9 (dark blue); $< 0.9 - \geq 0.7$ (light blue); $< 0.7 - \geq 0.5$ (light grey); ≤ 0.5 (dark grey). Highest Posterior Density intervals for node ages are shown in green. Dashed lines represent the time-slices used to retrieve ancestral states.



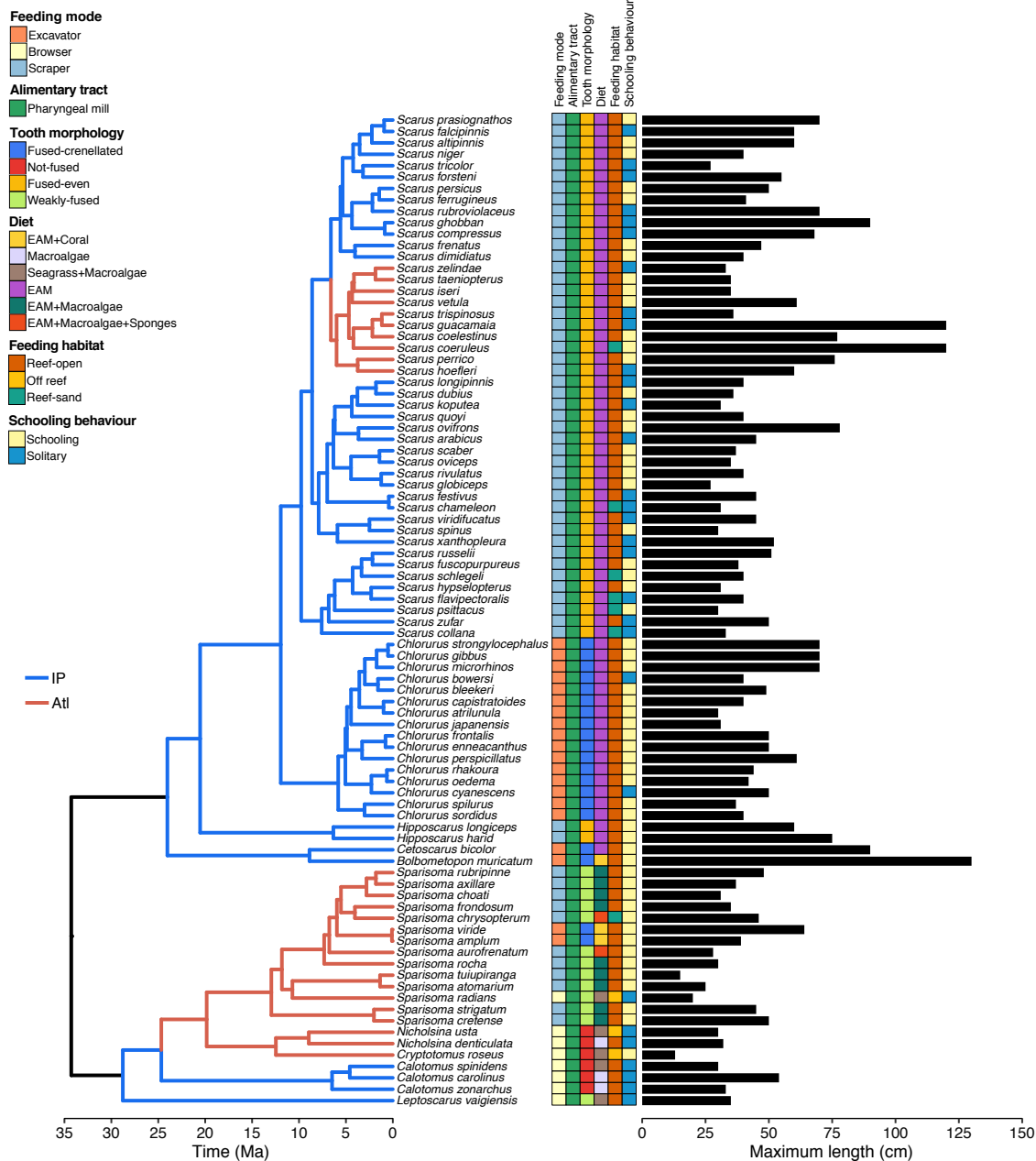
Supplementary figure 3. Maximum Clade Credibility (MCC) tree resulting from the Bayesian Inferences for Scarini. Node colours represent posterior support values: ≥ 0.9 (dark blue); $< 0.9 - \geq 0.7$ (light blue); $< 0.7 - \geq 0.5$ (light grey); ≤ 0.5 (dark grey). Highest Posterior Density intervals for node ages are shown in green. Dashed lines represent the time-slices used to retrieve ancestral states.



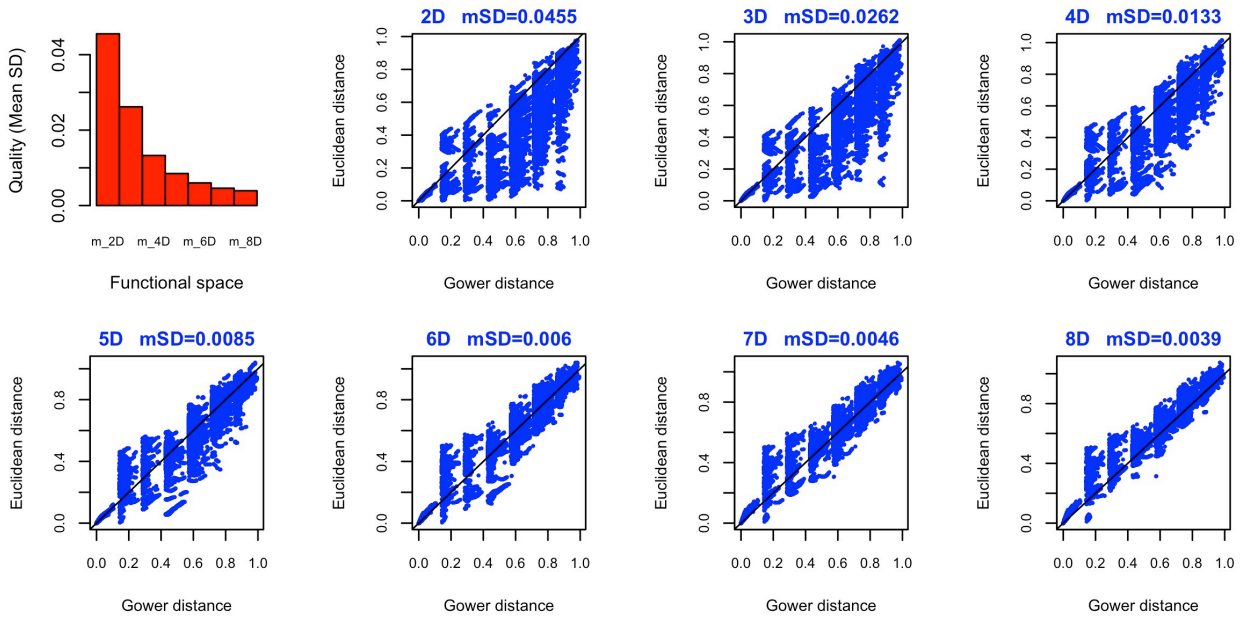
Supplementary figure 4. Trait state distribution for Siganidae species ordered according the phylogeny. Branches are coloured according the results from the best ancestral range reconstruction model for the group (DEC; Supplementary table 1), from which we split between areas present in the Indo-Pacific (IP) and Atlantic (Atl).



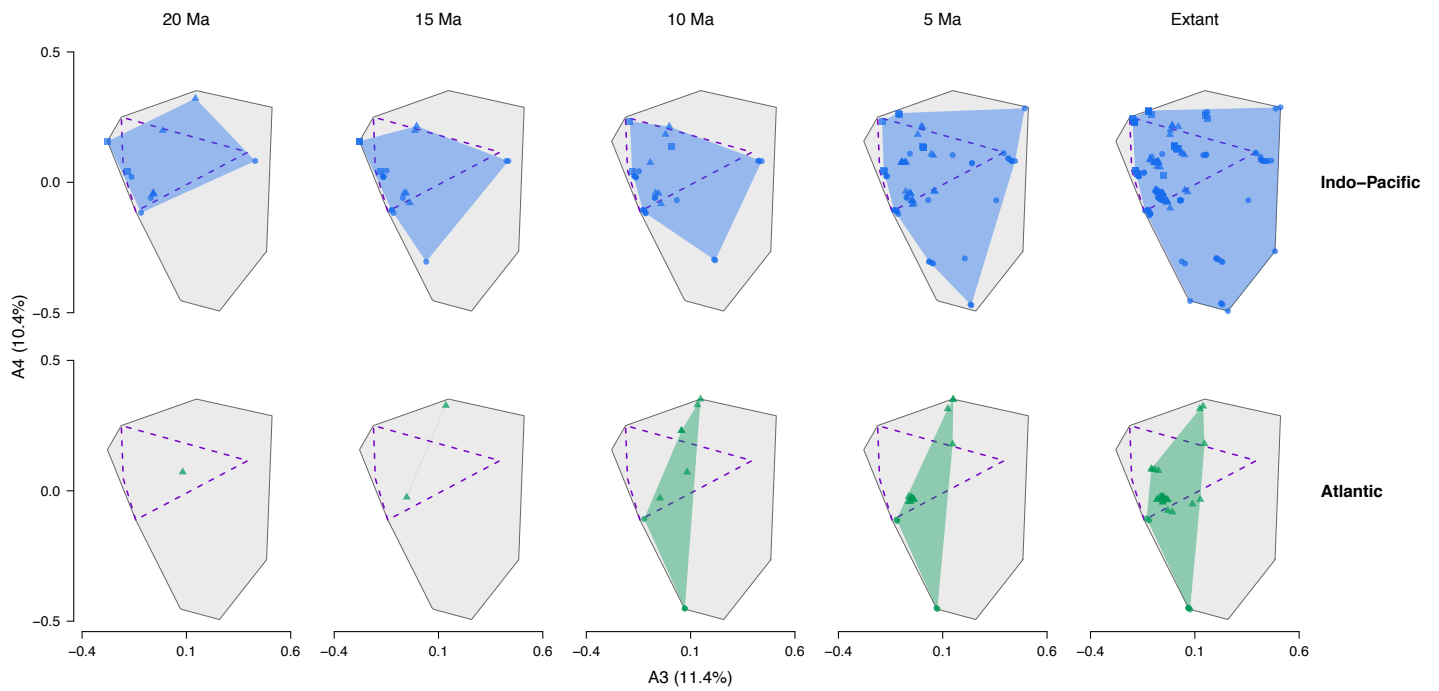
Supplementary figure 5. Trait state distribution for Acanthuridae species ordered according the phylogeny. Branches are coloured according the results from the best ancestral range reconstruction model for the group (BAYAREALIKE+J+W; Supplementary table 2), from which we split between areas present in the Indo-Pacific (IP) and Atlantic (Atl). Black branches represent ancestral lineages that were likely restricted to the Tethyan marine biodiversity hotspot (see Supplementary methods).



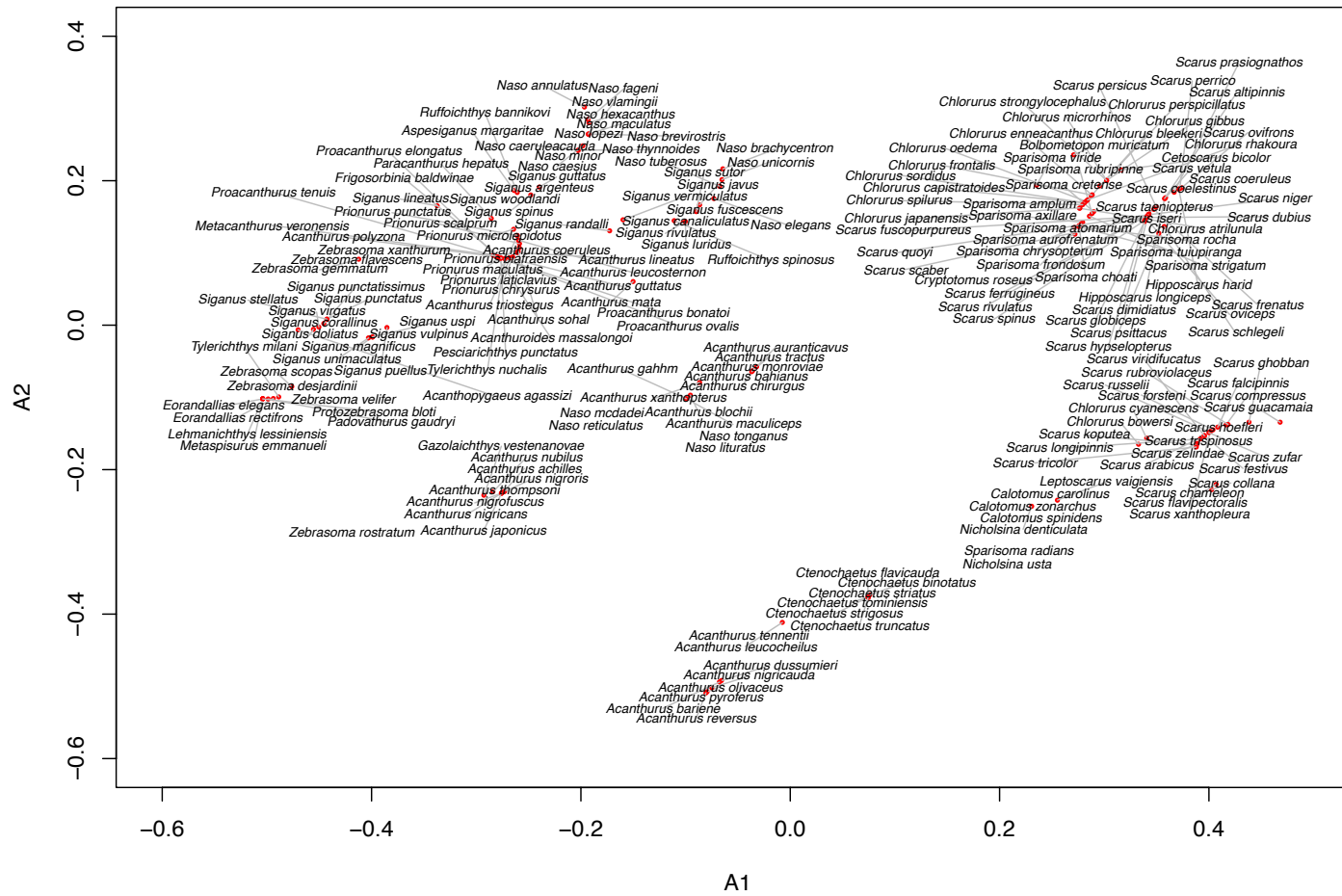
Supplementary figure 6. Trait state distribution for Scarini species ordered according the phylogeny. Branches are coloured according the results from the best ancestral range reconstruction model for the group (DEC+J+W; Supplementary table 3), from which we split between areas present in the Indo-Pacific (IP) and Atlantic (Atl). Black branches represent ancestral lineages that were likely restricted to the Tethyan marine biodiversity hotspot (see Supplementary methods).



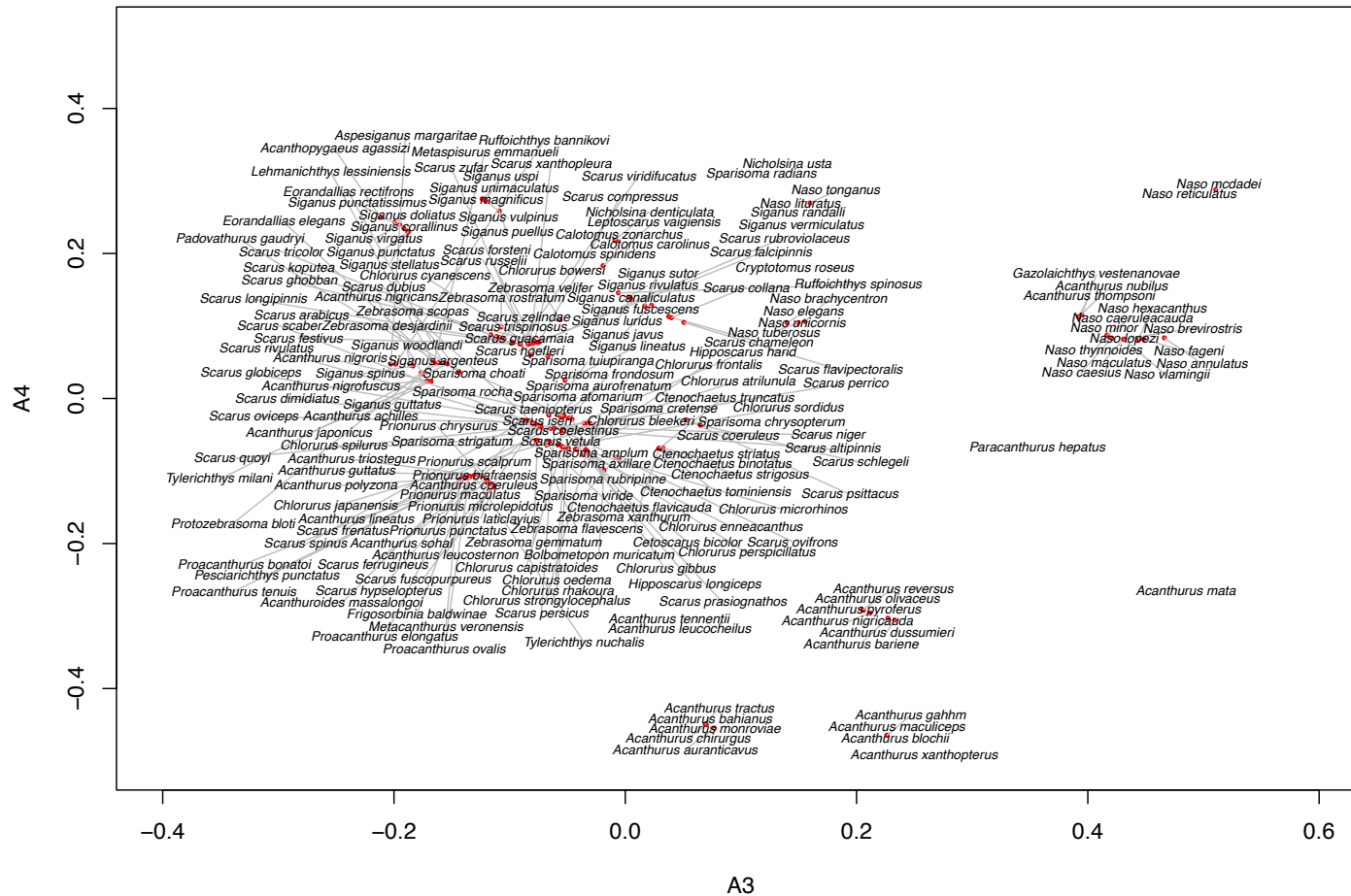
Supplementary figure 7. Quality of representation of the multidimensional space for trait combinations in surgeonfishes, parrotfishes and rabbitfishes. Output from the ‘*quality_funct_space*’ R function, showing an increase in quality (lower mSD values) with concomitant increase in the number of axes.



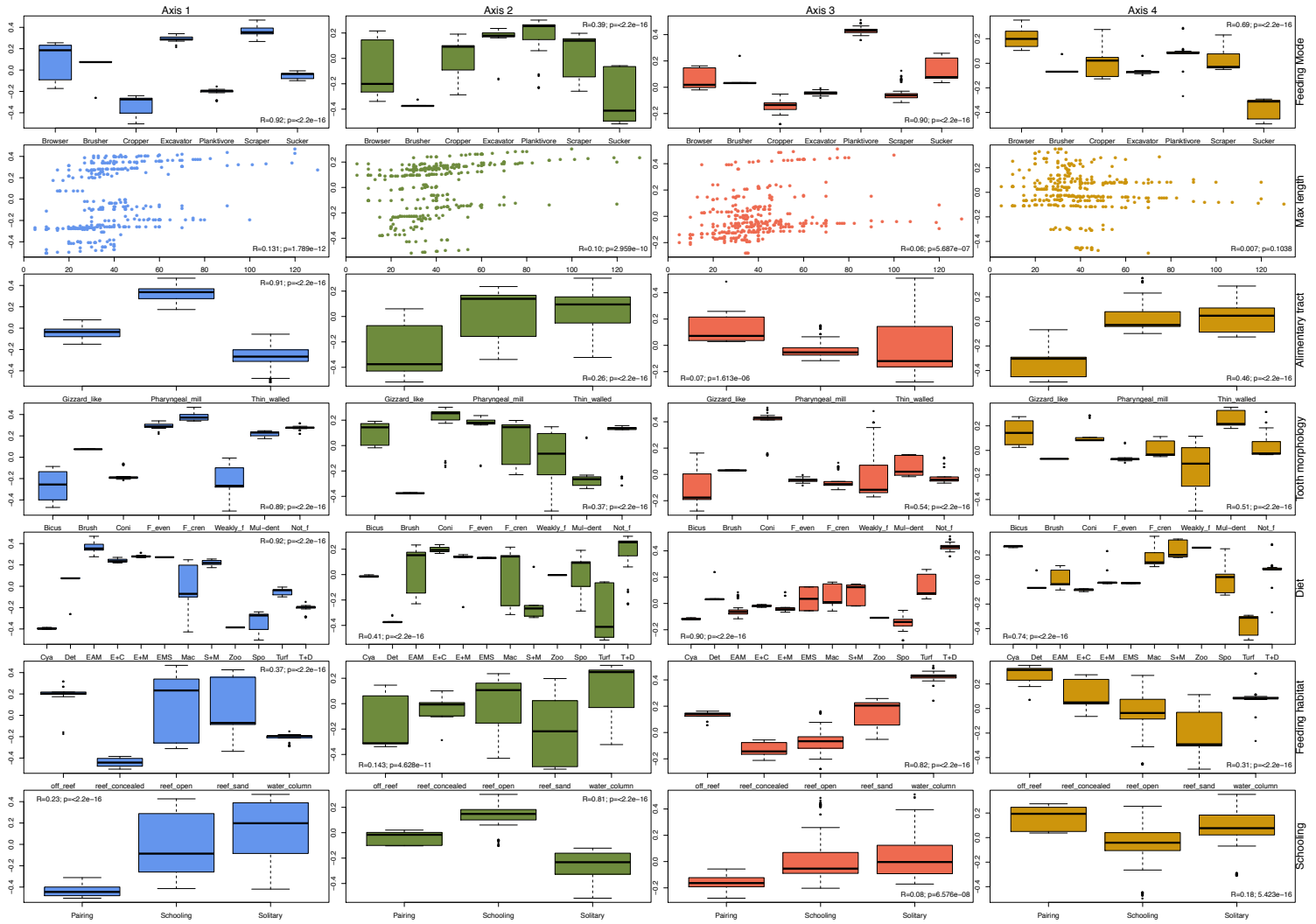
Supplementary figure 8. Multidimensional trait space occupied by surgeonfish (circles), rabbitfish (squares) and parrotfish (triangles) lineages in two biogeographic regions through time. Plots show the third and fourth axes (A3-A4) derived from a principal coordinate analysis (PCoA) performed on seven traits related to feeding. Each column represents a time-slice (20-5 Ma) in which we assessed the traits through ancestral reconstructions. The Extant column represents trait space of extant species. Background grey area shows the total space occupied combining fossils, time-slices and extant species. Convex hulls represent space occupied by Atlantic (green), Indo-Pacific (blue) and Tethys (50 Ma; purple dashed line) lineages. Symbols represent lineages present in each point in time.



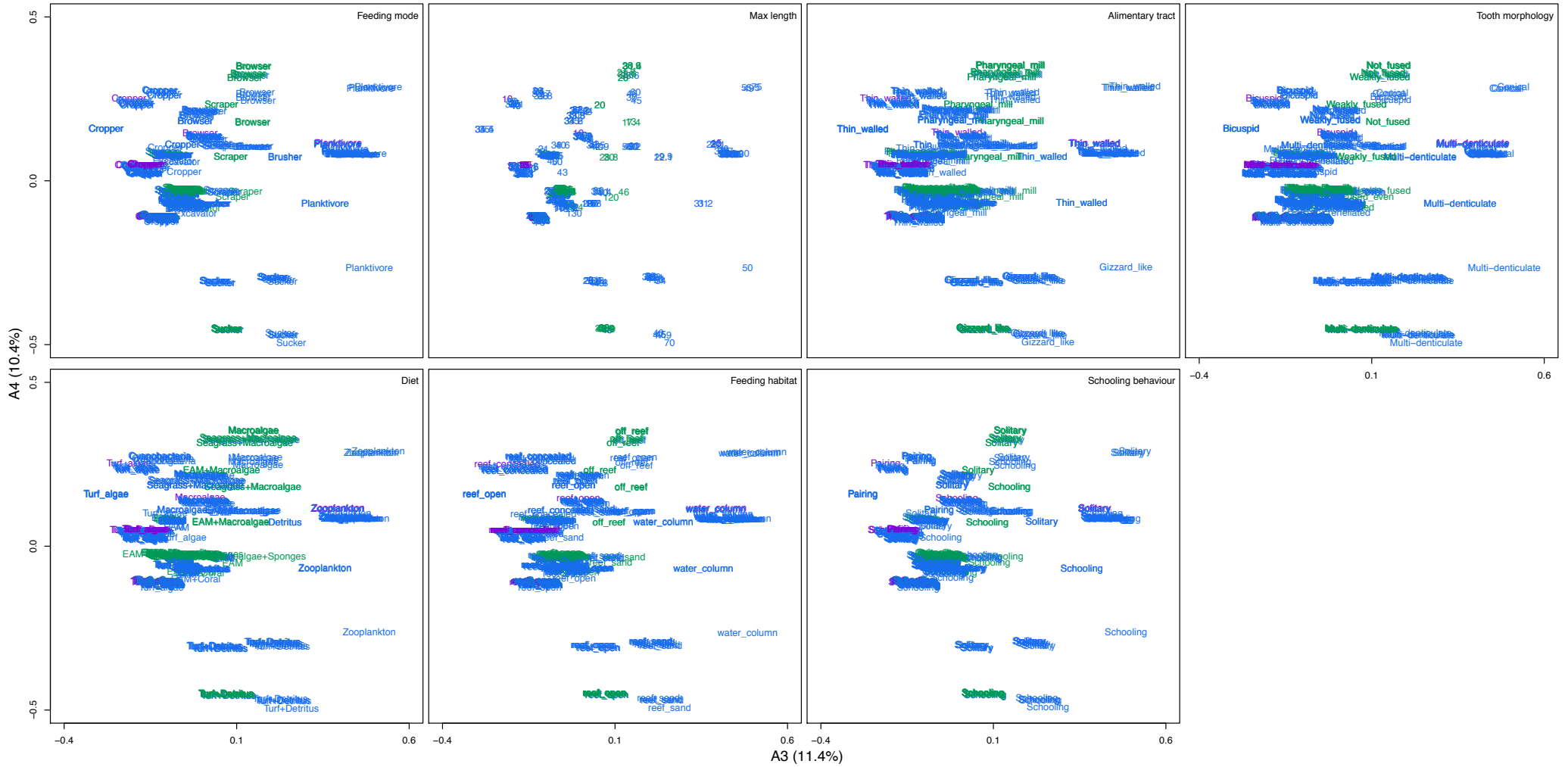
Supplementary figure 9. Species' positions in multidimensional space for axes 1 and 2 derived from the PCoA performed on seven traits related to feeding of extant surgeonfishes, rabbitfishes and parrotfishes present in the phylogenies, and known herbivorous fish fossils from Monte Bolca.



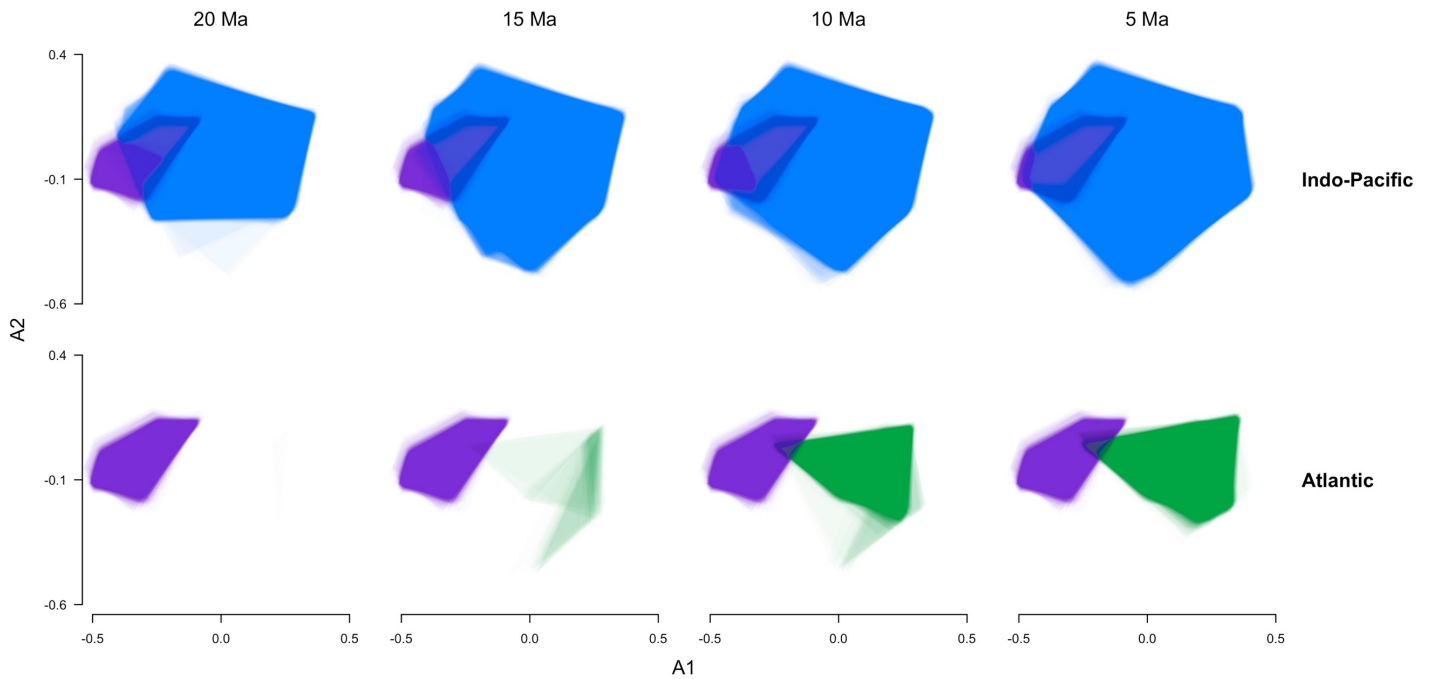
Supplementary figure 10. Species' positions in multidimensional space for axes 3 and 4 derived from the PCoA performed on seven traits related to feeding of extant surgeonfishes, rabbitfishes and parrotfishes present in the phylogenies, and known herbivorous fish fossils from Monte Bolca.



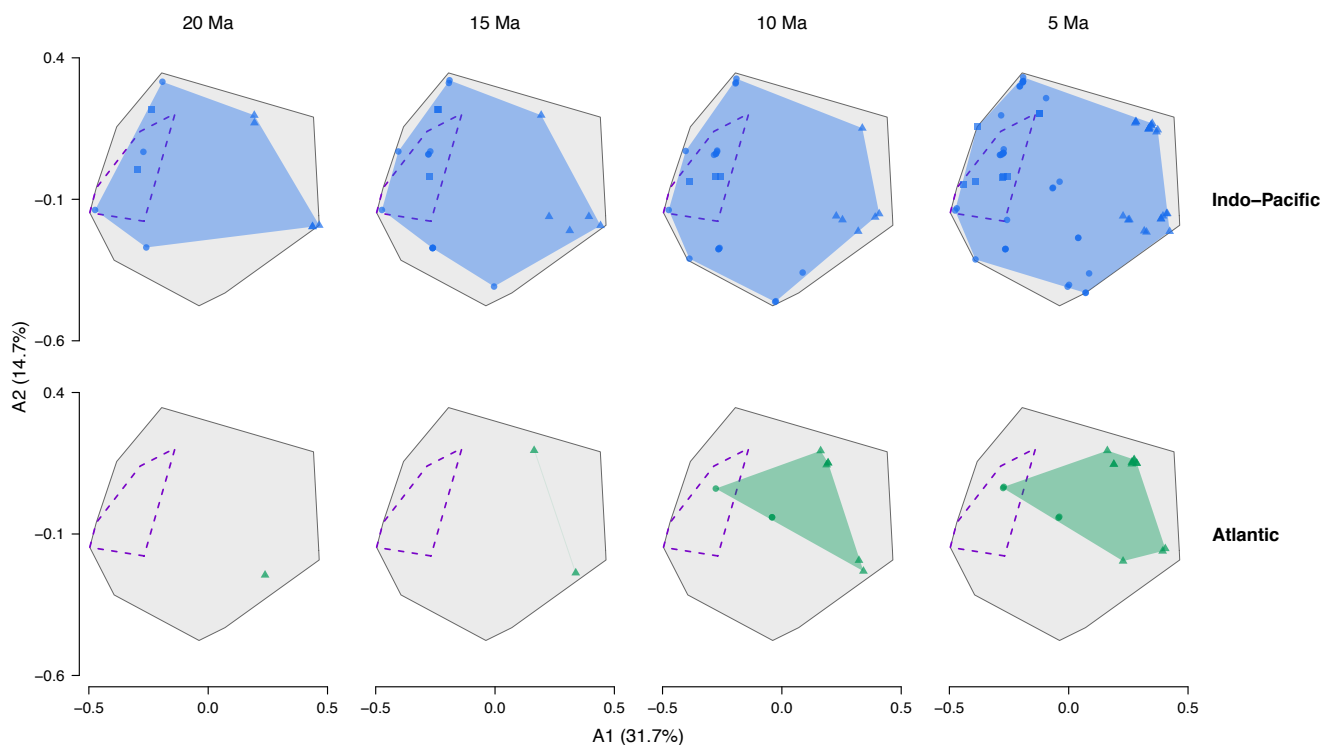
Supplementary figure 11. Correlation between PCoA axes and traits categorized for herbivorous fishes, assessed using linear models. The different states in each trait are explained in the Supplementary methods. Abbreviations in Tooth morphology: Bicus - Bicuspid; Coni - Conical; F_even - Fused-even; F_cren - Fused-crenelated; Weakly_f - Weakly fused; Mul-dent - Multi-denticulate; Not_f - Not fused. Abbreviations in Diet: Cya - Cyanobacteria; Det - Detritus; E+C - EAM + Coral; E+M - EAM + Macroalgae; EMS - EAM + Macroalgae + Sponges; Mac - Macroalgae; S+M - Seagrass + Macroalgae; Zoo - Zooplankton; Spo - Sponges; T+D - Turf + Detritus.



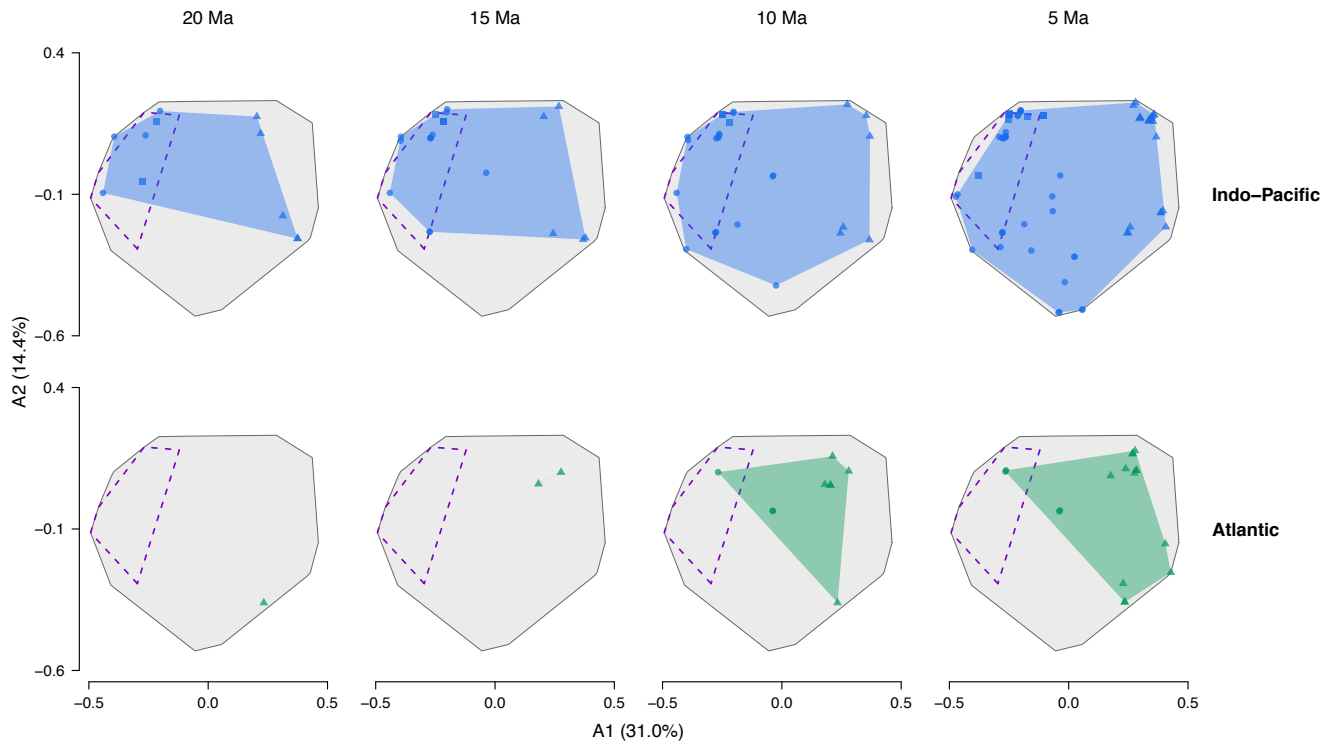
Supplementary figure 13. Trait distribution in multidimensional space for axes 3 and 4 derived from the PCoA performed on seven traits related to feeding of extant surgeonfishes, rabbitfishes and parrotfishes present in the phylogenies, and known herbivorous fish fossils from Monte Bolca.



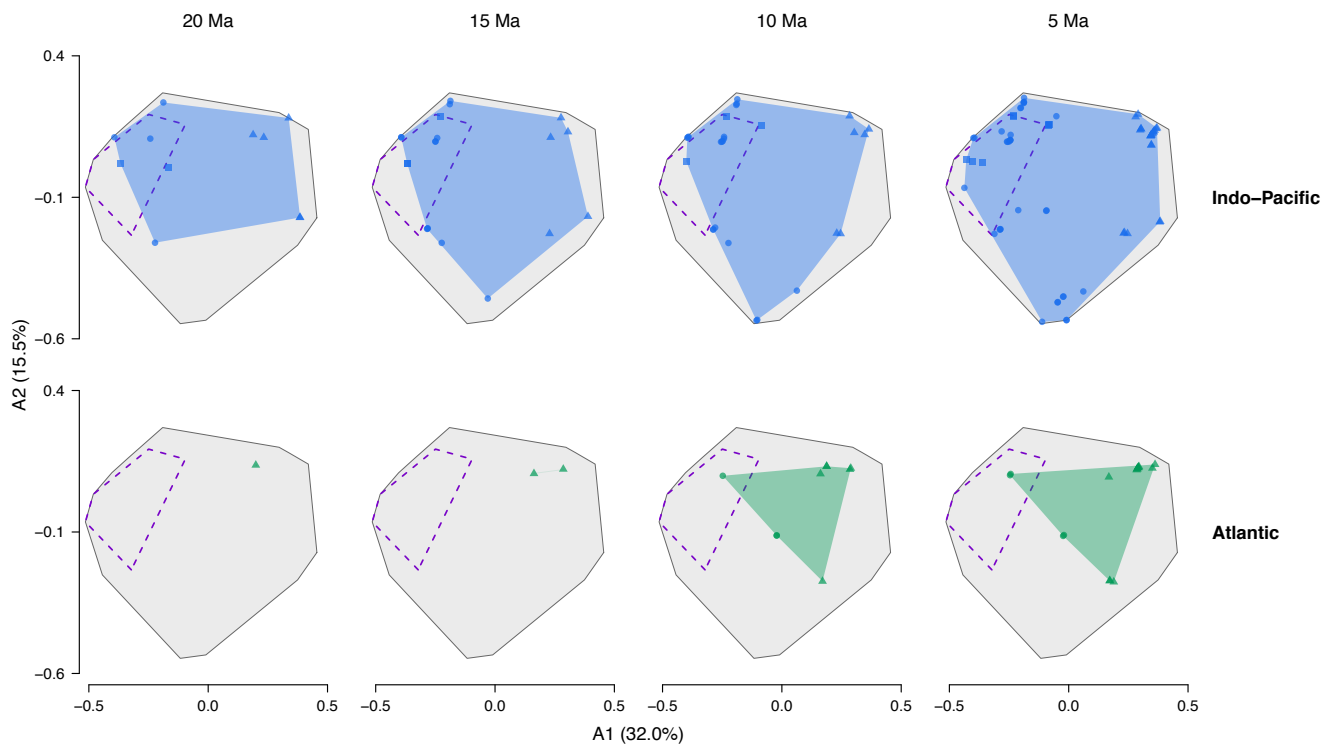
Supplementary figure 14. Overlapped convex hulls of 1000 PCoAs performed on seven traits related to feeding of surgeonfishes, rabbitfishes and parrotfishes. Each polygon results from a sample of three phylogenies (one per herbivorous group) from the posterior distribution derived from the Bayesian inferences (see Supplementary methods). Each column represents a time-slice (20-5 Ma) in which we assessed the traits through ancestral reconstructions. Convex hulls represent space occupied by Atlantic (green), Indo-Pacific (blue) and Tethys (50 Ma; purple) lineages.



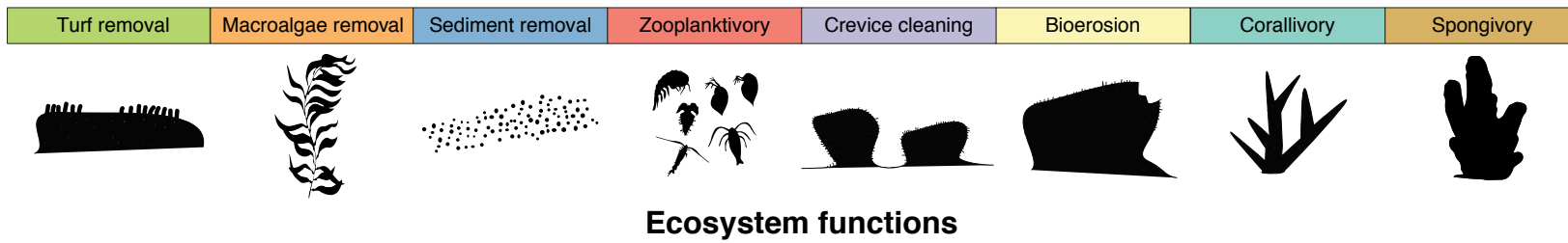
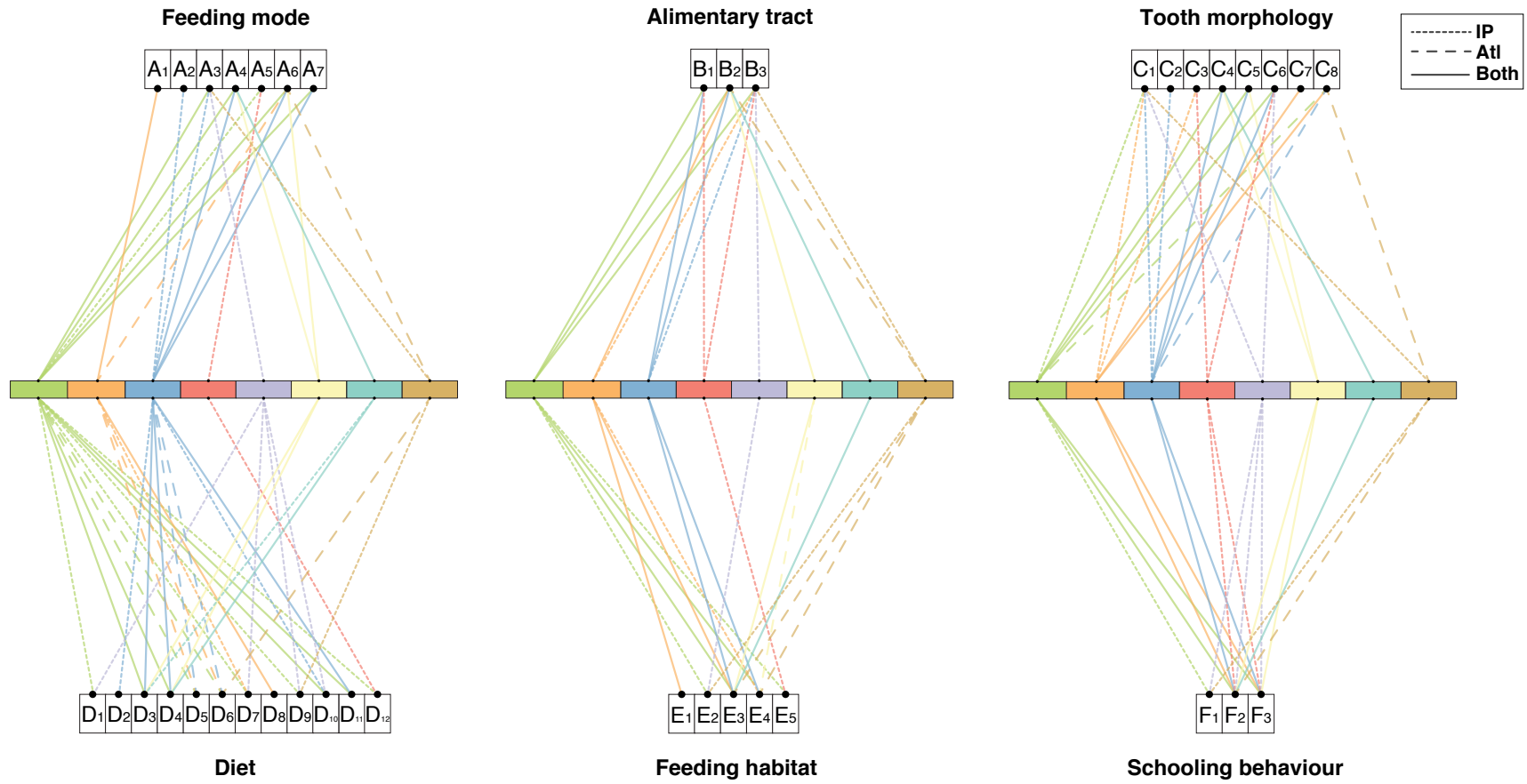
Supplementary figure 15. Multidimensional trait space occupied by surgeonfish (circles), rabbitfish (squares) and parrotfish (triangles) lineages in two biogeographic regions through time. Plots show the two first axes (A1-A2) derived from a PCoA performed on seven traits related to feeding. Each column represents a time-slice (20-5 Ma) in which we assessed the traits through ancestral reconstructions. Nodes that had the posterior probability for the highest state below 0.67 were classified with the second most likely state (see Supplementary methods). The Extant column represents trait space of extant species. Background grey area shows the total space occupied combining fossils, time-slices and extant species. Convex hulls represent space occupied by Atlantic (green), Indo-Pacific (blue) and Tethys (50 Ma; purple dashed line) lineages. Symbols represent lineages present in each point in time.



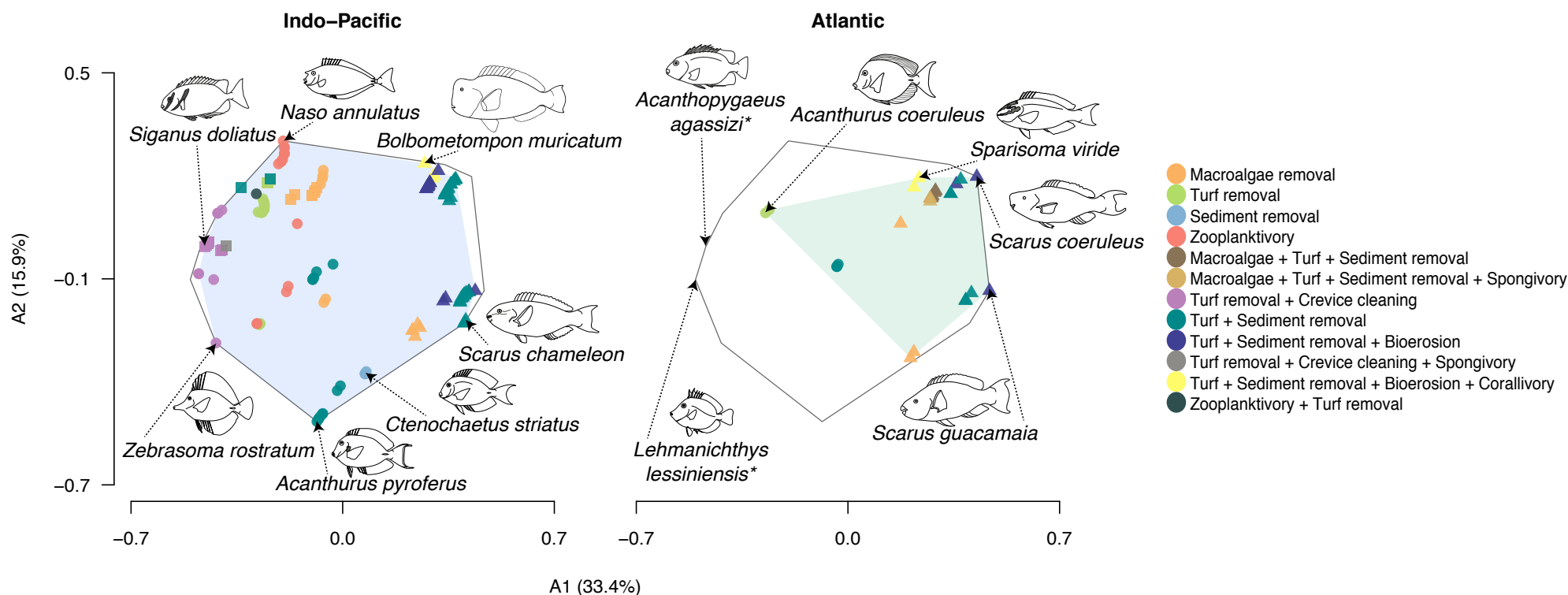
Supplementary figure 16. Multidimensional trait space occupied by surgeonfish (circles), rabbitfish (squares) and parrotfish (triangles) lineages in two biogeographic regions through time. Plots show the two first axes (A1-A2) derived from a PCoA performed on seven traits related to feeding. Each column represents a time-slice (20-5 Ma) in which we assessed the traits through ancestral reconstructions. Nodes that had less than 95% of the higher posterior probabilities associated with the best-supported were classified with the second most likely state (see Supplementary methods). The Extant column represents trait space of extant species. Background grey area shows the total space occupied combining fossils, time-slices and extant species. Convex hulls represent space occupied by Atlantic (green), Indo-Pacific (blue) and Tethys (50 Ma; purple dashed line) lineages. Symbols represent lineages present in each point in time.



Supplementary figure 17. Multidimensional trait space occupied by surgeonfish (circles), rabbitfish (squares) and parrotfish (triangles) lineages in two biogeographic regions through time. Plots show the two first axes (A1-A2) derived from a PCoA performed on seven traits related to feeding. Each column represents a time-slice (20-5 Ma) in which we assessed the traits through ancestral reconstructions using hidden Markov models (see Supplementary methods). The Extant column represents trait space of extant species. Background grey area shows the total space occupied combining fossils, time-slices and extant species. Convex hulls represent space occupied by Atlantic (green), Indo-Pacific (blue) and Tethys (50 Ma; purple dashed line) lineages. Symbols represent lineages present in each point in time.



Supplementary figure 18. Trait states of herbivorous coral reef fishes mapped with their respective ecosystem functions. Trait coding: Feeding mode (A1 - Browser; A2 - Brusher; A3 - Cropper; A4 - Excavator; A5 -Planktivore; A6 - Scraper; A7 - Sucker) ; Alimentary tract (B1 - Gizzard-like; B2 - Pharyngeal mill; B3 - Thin-walled); Tooth morphology (C1 - Bicuspid; C2 - Brush; C3 - Conical; C4 - Fused-crenelated; C5 -Fused-even; C6 - Multi-denticulate; C7 - Not fused; C8 - Weakly fused); Diet (D1 - Cyanobacteria; D2 -Detritus; D3 - EAM; D4 - EAM + Coral; D5 -EAM + Macroalgae; D6 - EAM + Macroalgae + Sponges; D7 - Macroalgae; D8 - Seagrass + Macroalgae; D9 - Sponges; D10 - Turf-algae; D11 -Turf + Detritus; D12 - Zooplankton); Feeding habitat (E1 - off-reef; E2 - reef-concealed; E3 - reef-open; E4 - reef-sand; E5 - water column); Schooling behaviour (F1 - Pairing; F2 - Schooling; F3 - Solitary).



Supplementary figure 19. Multidimensional trait space occupied by extant surgeonfish (circles), rabbitfish (squares) and parrotfish (triangles) species in two biogeographic regions. Plots show the first two axes (A1-A2) derived from a principal coordinate analysis (PCoA) performed on seven traits related to feeding. Points are coloured according to the ecosystem functions performed by each species. Grey contour shows the total space occupied combining fossils, time-slices and extant species. Convex hulls represent space occupied by Indo-Pacific (blue) and Atlantic (green) species. Illustrations show representatives from each biogeographical realm and two fossil species (*).

Supplementary tables

Supplementary table 1. Biogeographical model comparison for Siganidae ordered according to lowest AICc. LnL: log-likelihood; d: dispersal; e: extinction; j: founder-speciation event parameter; w: dispersal multiplier matrix power exponential parameter; AICc: Akaike Information Criteria corrected for sample size; AIC_wt: Akaike Information Criteria weight.

Models	LnL	params	d	e	j	w	AICc	AICc wt
DEC	-67.9	2	0.16	0.042	0	1	140.3	0.62
DEC+J	-67.9	3	0.16	0.042	1.00E-05	1	142.9	0.17
DEC+W	-68.31	3	0.15	0.047	0	0.68	143.7	0.11
DEC+J+W	-67.86	4	0.16	0.042	1.00E-05	1.11	145.6	0.044
DIVALIKE	-71.57	2	0.18	0.046	0	1	147.7	0.016
BAYAREALIKE+J	-70.59	3	0.11	0.061	0.13	1	148.3	0.012
BAYAREALIKE	-72.63	2	0.13	0.083	0	1	149.8	0.0055
DIVALIKE+J	-71.49	3	0.21	0.052	1.00E-05	1	150.1	0.0048
DIVALIKE+W	-71.95	3	0.18	0.057	0	0.76	151	0.003
BAYAREALIKE+J+W	-70.58	4	0.11	0.061	0.13	1.08	151.1	0.0029
DIVALIKE+J+W	-71.55	4	0.2	0.051	1.00E-05	0.93	153	0.0011
BAYAREALIKE+W	-75.38	3	0.14	0.094	0	0.16	157.9	9.70E-05

Supplementary table 2. Biogeographical model comparison for Acanthuridae ordered according to lowest AICc. LnL: log-likelihood; d: dispersal; e: extinction; j: founder-speciation event parameter; w: dispersal multiplier matrix power exponential parameter; AICc: Akaike Information Criteria corrected for sample size; AIC_wt: Akaike Information Criteria weight.

Models	LnL	params	d	e	j	w	AICc	AICc wt
BAYAREALIKE+J+W	-201.9	4	0.11	0.045	0.33	0.63	412.4	0.58
BAYAREALIKE+J	-203.4	3	0.13	0.051	0.35	1	413.1	0.41
DEC+J+W	-206	4	0.22	0.036	0.095	0.57	420.6	0.0097
DEC+J	-211	3	0.26	0.04	0.14	1	428.3	0.0002
DEC	-212.5	2	0.22	0.025	0	1	429.1	0.0001
DIVALIKE+W	-213.7	3	0.3	0.051	0	0.6	433.8	1.30E-05
DIVALIKE+J+W	-213.9	4	0.29	0.05	0.11	0.62	436.3	3.70E-06
DIVALIKE+J	-217.7	3	0.33	0.052	0.036	1	441.7	2.50E-07
DEC+W	-218.2	3	0.15	0.032	0	0.0049	442.7	1.60E-07
DIVALIKE	-223.3	2	0.2	0.032	0	1	450.7	2.80E-09
BAYAREALIKE	-224	2	0.26	0.13	0	1	452.3	1.30E-09
BAYAREALIKE+W	-228	3	0.13	0.099	0	0.17	462.4	8.00E-12

Supplementary table 3. Biogeographical model comparison for Scarini ordered according to lowest AICc. LnL: log-likelihood; d: dispersal; e: extinction; j: founder-speciation event parameter; w: dispersal multiplier matrix power exponential parameter; AICc: Akaike Information Criteria corrected for sample size; AIC_wt: Akaike Information Criteria weight.

Models	LnL	params	d	e	j	w	AICc	AICc_wt
DEC+J+W	-197.5	4	0.091	0.0087	0.06	0.46	403.5	0.48
DEC+J	-199	3	0.098	0.0087	0.057	1	404.3	0.32
DEC	-200.6	2	0.12	0.014	0	1	405.3	0.2
BAYAREALIKE+J+W	-202	4	0.051	0.023	0.19	0.51	412.5	0.0054
BAYAREALIKE+J	-204.3	3	0.056	0.027	0.2	1	415	0.0015
DEC+W	-204.5	3	0.093	0.018	0	0.0014	415.2	0.0014
DIVALIKE+J+W	-206.4	4	0.11	0.0075	0.065	0.48	421.3	6.40E-05
DIVALIKE+J	-209.6	3	0.12	0.0078	0.079	1	425.5	7.80E-06
DIVALIKE+W	-212.8	3	0.092	0.0097	0	0.05	431.9	3.30E-07
DIVALIKE	-215.7	2	0.094	0.018	0	1	435.5	5.30E-08
BAYAREALIKE	-224.9	2	0.13	0.12	0	1	454	5.10E-12
BAYAREALIKE+W	-232.9	3	0.059	0.076	0	0.012	472.1	6.20E-16

Supplementary table 4. Genetic accession numbers used to build the Siganidae phylogeny.

Species	16s	Cytb	ITS1
<i>Siganus argenteus</i>	DQ898097	AB276803	AB276971
<i>Siganus canaliculatus</i>	EF210164	AB276851	AB276988
<i>Siganus corallinus</i>	DQ898105	AB276936	AB277043
<i>Siganus doliatus</i>	DQ898107	AB276957	AB277054
<i>Siganus fuscescens</i>	DQ898101	AB276831	AB276981
<i>Siganus guttatus</i>	DQ898108	AB276913	AB277025
<i>Siganus javus</i>	DQ898109	AB276852	AB276995
<i>Siganus lineatus</i>		AB276918	AB277034
<i>Siganus luridus</i>	DQ898111	AM949027	
<i>Siganus magnificus</i>		AB276882	AB277005
<i>Siganus puellus</i>	DQ898112	AB276867	AB276997
<i>Siganus punctatissimus</i>		AB276872	AB276999
<i>Siganus punctatus</i>	DQ898113	AB276879	AB277001
<i>Siganus randalli</i>		EF210188	
<i>Siganus rivulatus</i>	JX026505	EU601390	
<i>Siganus spinus</i>	DQ898117	AB276818	AB276975
<i>Siganus unimaculatus</i>	EF210170	AB276889	AB277010
<i>Siganus uspi</i>		AB276881	AB277003
<i>Siganus vermiculatus</i>	DQ898118	AB276904	AB277021
<i>Siganus virgatus</i>	EF210171	AB276949	
<i>Siganus vulpinus</i>	DQ898119	AB276902	AB277051
<i>Siganus woodlandi</i>	DQ898120	AB276793	AB276968
<i>Siganus stellatus</i>	DQ532960	KT953191	
<i>Siganus sutor</i>		MF326167	
<i>Prionurus scalprum</i>	AY264591	AB276963	AB277066
<i>Zanclus cornutus</i>	AY057282	AB276965	AB375558

Supplementary table 5. Genetic accession numbers used to build the Acanthuridae phylogeny.

Species	Cox1	Cytb	ENC1	ETS2	myh6	plagl2	Rag1	Rh	zic1
<i>Acanthurus achilles</i>	KC623654	KC623692	KC623730		KC623763	KC623798	KC623828	KC623863	KC623902
<i>Acanthurus auranticavus</i>	KC623655	KC623693	KC623731		KC623764	KC623799	KC623829	KC623864	KC623903
<i>Acanthurus bahianus</i>		FJ905179			JX189759	JX189441	JX189919		JX189146
<i>Acanthurus bariene</i>	KC623657	KC623695	KC623733		KC623766	KC623801	KC623831	KC623866	KC623905
<i>Acanthurus blochii</i>	HM034180	AY264632	KC623734	AY264685	KC623767	KC623802	KC623832	KC623867	KC623906
<i>Acanthurus chirurgus</i>	KC623658	KC623696	KC623735		KC623768	KC623803	KC623833	KC623868	KC623907
<i>Acanthurus coeruleus</i>	KC623659	KC623697	KC623736		KC623769	KC623804	KC623834	KC623869	KC623908
<i>Acanthurus dussumieri</i>		AY264633		AY264686					
<i>Acanthurus gahhm</i>		KT953166		KT953202					
<i>Acanthurus guttatus</i>	KC623660	KC623698	EF539241		EF536294	EF536256	EF530094	KC623870	EF533917
<i>Acanthurus japonicus</i>	KC623661	KC623699	KC623737		KC623770	KC623805	KC623835	KC623871	KC623909
<i>Acanthurus leucocheilus</i>	KC623662	KC623700				KC623806	KC623836	KC623872	KC623910
<i>Acanthurus leucosternon</i>	KC623663	EU136032	KC623738		KC623771	KC623807	KC623837	KC623873	KC623911
<i>Acanthurus lineatus</i>	KC623664	EU273284	KC623739		KC623772	KC623808	KC623838	KC623874	KC623912
<i>Acanthurus maculiceps</i>	KY683548								
<i>Acanthurus mata</i>	KC623665	KC623701	KC623740		KC623773	KC623809	KC623839	KC623875	KC623913
<i>Acanthurus monroviae</i>	KC623666	KC623702	KC623741		KC623774	KC623810	KC623840	KC623876	KC623914
<i>Acanthurus nigricans</i>	KC623667	KC623703	KC623742	AY264687	KC623775	KC623811	KC623841	KC623877	KC623915
<i>Acanthurus nigricauda</i>	HM034189	KC623704	KC623743		KC623776	KC623812	KC623842	KC623878	KC623916
<i>Acanthurus nigrofuscus</i>	KC623668	KC623705	KC623744	AY264688	KC623777	KC623813	KC623843	KC623879	KC623917
<i>Acanthurus nigroris</i>		KC623706							
<i>Acanthurus nubilus</i>	HM034193	AY264636		AY264689					
<i>Acanthurus olivaceus</i>	KC623669	KC623707	KC623745	AY264690	KC623778	KC623814	KC623844	KC623880	KC623918
<i>Acanthurus polyzona</i>	JQ349664								
<i>Acanthurus pyroferus</i>	KC623670	KC623708	KC623746	AY264691	KC623779	KC623815	KC623845	KC623881	KC623919
<i>Acanthurus reversus</i>	KY683549								
<i>Acanthurus sohal</i>	MF123727	KT953172		KT953208					
<i>Acanthurus tennentii</i>	KC623671	KC623709	KC623747		KC623780	KC623816	KC623846	KC623882	KC623920
<i>Acanthurus thompsoni</i>	KC623672	KC623710	KC623748		KC623781	KC623817	KC623847	KC623883	KC623921
<i>Acanthurus tractus</i>	KC623673	KC623694	KC623732		KC623765	KC623800	KC623830	KC623865	KC623904
<i>Acanthurus triostegus</i>	KC623673	KC623711	EF539242	AY264692	EF536295	EF536257	EF530095	KC623884	EF533918
<i>Acanthurus xanthopterus</i>	KC623674	KC623712	KC623749	AY264693	KC623782	KC623818	KC623848	KC623885	KC623922
<i>Ctenochaetus binotatus</i>		KC623713	KC623750	AY264694	KC623783		KC623849	KC623886	KC623923
<i>Ctenochaetus flavicauda</i>	HM034209								
<i>Ctenochaetus striatus</i>	KC623675	KC623714	EF539243	AY264695	EF536296	EF536258	EF530096		EF533919
<i>Ctenochaetus strigosus</i>	KC623676	FJ376811	KC623751		KC623784	KC623819	KC623850	KC623887	KC623924
<i>Ctenochaetus tominiensis</i>	KC623677	KC623715	KC623752		KC623785	KC623820	KC623851		KC623925
<i>Ctenochaetus truncatus</i>	KC623678	KC623716	KC623753		KC623786	KC623821	KC623852	KC623888	KC623926
<i>Naso annulatus</i>	HM034155	AY264643		AY264696					
<i>Naso brachycentron</i>		AY264644		AY264697					
<i>Naso brevirostris</i>	KC623679	KC623717	EF539240	AY264698	EF536293	EF536255	EF530093	KC623889	EF533916
<i>Naso caeruleacauda</i>		AY264646		AY264699					
<i>Naso caesius</i>		AY264647		AY264700					
<i>Naso elegans</i>	KC623680	KC623718	KC623754	AY264701			KC623853	KC623890	
<i>Naso fageni</i>		AY264649		AY264702					
<i>Naso hexacanthus</i>		AY264650		AY264703					
<i>Naso lituratus</i>	HM034247	AY264651	EF539239	AY264704	EF536292	EF536254	EF530092	EU637984	EF533915
<i>Naso lopezi</i>	AP009163	AY264652		AY264705					
<i>Naso maculatus</i>		AY264653		AY264706					
<i>Naso mcdadei</i>		AY264654		AY264707					
<i>Naso minor</i>		AY264655		AY264708					
<i>Naso reticulatus</i>		AY264656		AY264709					
<i>Naso thynnoides</i>		AY264657		AY264710					
<i>Naso tonganus</i>		AY264658		AY264711					
<i>Naso tuberosus</i>		AY264659		AY264712					
<i>Naso unicornis</i>	KC623681	KC623719	KC623755	AY264713	KC623787	KC623822	KC623854	KC623891	KC623927
<i>Naso vlamingii</i>	KC623682	KC623720	KC623756	AY264714	KC623788	KC623823	KC623855	KC623892	KC623928

Species	Cox1	Cytb	ENC1	ETS2	myh6	plag12	Rag1	Rh	zic1
<i>Paracanthurus hepatus</i>	KC623683	KC623721	EF539244	AY264680	EF536297	EF536259	EF530097	KC623893	EF533920
<i>Prionurus biafraensis</i>	KC623684	KC623722	KC623757		KC623789	KC623824	KC623856	KC623894	KP280517
<i>Prionurus chrysurus</i>	KP280488						KP280510		KP280518
<i>Prionurus laticlavus</i>	KC623685	KC623723	KC623758		KC623790	KC623825	KC623857	KC623895	KP280519
<i>Prionurus maculatus</i>	KC623687	KC623725			KC623792			KC623897	KC623932
<i>Prionurus microlepidotus</i>		KC623726		AY264681	KC623793	EF536260	KC623859		EF533921
<i>Prionurus punctatus</i>	KC623686	KC623724	KC623759		KC623791		KC623858	KC623896	KC623931
<i>Prionurus scalprum</i>		AY264629		AY264682					
<i>Zebrasoma desjardini</i>	KC623688	KC623727	KC623760		KC623794		KC623860	KC623898	KC623934
<i>Zebrasoma flavescens</i>	KC623689	AP006032	KC623761		KC623795	KC623827	KC623861	KC623899	KC623935
<i>Zebrasoma gemmatum</i>	JF494799								
<i>Zebrasoma rostratum</i>	HM034282						KF141385		KF140659
<i>Zebrasoma scopas</i>	KC623690	KC623728	EF539238	AY264683	KC623796	EF536253	AY308776	KC623900	KC623936
<i>Zebrasoma velifer</i>	KC623691	KC623729	KC623762	AY264684	KC623797		KC623862	KC623901	KC623937
<i>Zebrasoma xanthurum</i>	MF124084	KT953199		KT953235					
<i>Zanclus cornutus</i>	KC623652	AY264626	EF539247	AY264679	EF536300	EF536262	EF530100		EF533923
<i>Luvarus imperialis</i>	KC623653	AY264625	EF539246	AY264678	EF536299	EF536261	EF530099	EU637975	EF533922

Supplementary table 6. Genetic accession numbers used to build the Scarini phylogeny.

Species	12s	16s	Bmp4	Control region	Cox1	Cytb	Dlx2	Otx1	Rag2	S711	Tmo-4C4
<i>Bolbometapon muricatum</i>	EU601178	AY081091	EU601456		NC033901	NC033901	EU601506	EU601406	EU601307	JX026592	AY081108
<i>Calotomus carolinus</i>	EU601179	AY081092	EU601457		JQ349815	EU601358	EU601507	EU601407	EU601308		AY081109
<i>Calotomus spinidens</i>	EU601180	EU601228	EU601458		KJ202134	EU601359	EU601508	EU601408	EU601309		EU601265
<i>Calotomus zonarchus</i>					DQ521016						
<i>Cetoscarus bicolor</i>	EU601181	EU601229	EU601459		JQ349874	EU601360	EU601509	EU601409	EU601310	JX026593	AY081105
<i>Chlorurus atrilunula</i>		JX026457		JX026525						JX026596	
<i>Chlorurus bleekeri</i>	EU601182	EU601230	EU601460	JX026526		EU601361	EU601510	EU601410	EU601311	JX026597	EU601267
<i>Chlorurus bowersi</i>	EU601183	EU601231	EU601461	JX026527		EU601362	EU601511	EU601411	EU601312	JX026598	EU601268
<i>Chlorurus capistratoides</i>	EU601184	EU601232	EU601462	JX026528		EU601363	EU601512	EU601412	EU601313	JX026599	EU601269
<i>Chlorurus cyanescens</i>		JX026461		JX026529						JX026600	
<i>Chlorurus enneacanthus</i>		JX026462		JX026530						JX026601	
<i>Chlorurus frontalis</i>	AB974582	JX026463		JX026531	JQ431620	LC068812				JX026602	
<i>Chlorurus gibbus</i>		JX026464		JX026532							
<i>Chlorurus japonensis</i>	EU601209	EU601250	EU601487	JX026533		EU601388	EU601537	EU601437	EU601338	JX026603	EU601288
<i>Chlorurus microrhinos</i>	EU601185	EU601233	EU601463	JX026534		EU601364	EU601513	EU601413	EU601314	JX026604	EU601270
<i>Chlorurus oedema</i>	EU601186	EU601234	EU601464	JX026535		EU601365	EU601514	EU601414	EU601315	JX026605	AY081107
<i>Chlorurus perspicillatus</i>		JX026468		JX026536		KF809191				JX026606	
<i>Chlorurus rhakoura</i>		JX026469		JX026537						JX026607	
<i>Chlorurus sordidus</i>			EU601465	JX026539	EU601367	NC006355		EU601415		JX026609	AY081106
<i>Chlorurus spilurus</i>		JX026470		JX026538						JX026608	
<i>Chlorurus strongylocephalus</i>		JX026472		JX026540						JX026610	
<i>Cryptotomus roseus</i>	AY279592	AY279695	EU601466		JQ839422	EU601367	EU601516	EU601416	AY279901		AY279798
<i>Hipposcarus harid</i>		JX026455		JX026523						JX026594	
<i>Hipposcarus longiceps</i>	EU601189	AY081093	EU601467	JX026524	KF929973	EU885924	EU601517	EU885926	EU601318	JX026595	AY081110
<i>Leptoscarus vaigiensis</i>	EU601190	AY081094	EU601468		FJ237788	EU601369		EU601418	EU601319		AY081111
<i>Nicholsina denticulata</i>	U95761	U95762				DQ457021					
<i>Nicholsina usta</i>			EU601469			DQ457023		EU601419	AY279933		AY081112
<i>Scarus altipinnis</i>	EU601192	EU601237	EU601470	JX026541	JQ432095	EU601371	EU601520	EU601420	EU601321	JX026611	EU601273
<i>Scarus arabicus</i>		JX026474		JX026542						JX026612	
<i>Scarus chameleon</i>	EU601193	EU601238	EU601471	JX026613	FJ237917	EU601372	EU601521	EU601421	EU601322	JX026613	EU601274
<i>Scarus coelestinus</i>	EU601194	AY081084	EU601472	JX026544		EU601373	EU601522	EU601422	EU601323	JX026614	AY081101
<i>Scarus coeruleus</i>		JX026476		JX026545						JX026615	
<i>Scarus collana</i>			KY815801	JX026546						JX026616	KY815559
<i>Scarus compressus</i>		JX026478		JX026547						JX026617	
<i>Scarus dimidiatus</i>	AY279642	AY279745	EU601473	JX026548		EU601374	EU601523	EU601423	AY279951	JX026618	AY279848
<i>Scarus dubius</i>		JX026480		JX026549		KF809216				JX026619	
<i>Scarus falcipinnis</i>		JX026481		JX026550						JX026620	
<i>Scarus ferrugineus</i>			KY815802	JX026551						JX026621	KU862922
<i>Scarus festivus</i>	EU601196	EU601239	EU601474	JX026552		EU601375	EU601524	EU601424	EU601325	JX026622	EU601276
<i>Scarus flavipectoralis</i>	EU601197	AY081086	EU601475	JX026553	KP194579	EU601376	EU601525	EU601425	EU601326	JX026623	AY081103
<i>Scarus forsteni</i>	EU601198	EU601240	EU601476	JX026554	NC011928	NC011928	EU601526	EU601426	EU601327	JX026624	EU601278
<i>Scarus frenatus</i>	AY279643	AY279746	EU601477	JX026555	KP194827	EU601378	EU601527	EU601427	AY279952	JX026625	AY081104
<i>Scarus fuscopurpureus</i>		JX026487		JX026556						JX026626	KU862923
<i>Scarus ghobban</i>	EU601200	EU601241	EU601478	JX026558	NC011599	NC011599	EU601528	EU601428	EU601329	JX026628	KU862921
<i>Scarus globiceps</i>	EU601201	EU601242	EU601479	JX026561	JQ432103	EU601380	EU601529	EU601429	EU601330	JX026631	EU601280
<i>Scarus guacamaia</i>	EU601202	EU601243	EU601480	JX026562	JQ843039	EU601381	EU601530	EU601430	EU601331	JX026632	AY081102
<i>Scarus hoefleri</i>	AY141393	JX026493		JX026563						JX026633	

Species	12s	16s	Bmp4	Control region	Cox1	Cytb	Dlx2	Otx1	Rag2	S711	Tmo-4C4
<i>Scarus hypselopterus</i>	EU601204	EU601245	EU601482			EU601383	EU601532	EU601432	EU601333		EU601283
<i>Scarus iseri</i>	EU601203	EU601244	EU601481	JX026564	JQ842671	EU601382	EU601531	EU601431	EU601332	JX026634	EU601282
<i>Scarus koputea</i>		JX026495		JX026565						JX026635	
<i>Scarus longipinnis</i>		JX026496		JX026566						JX026636	
<i>Scarus niger</i>	EU601205	JX026497	EU601483	JX026567	KP194654	KT953190	EU601533	EU601433	EU601334	JX026637	KU862926
<i>Scarus oviceps</i>	EU601206	EU601247	EU601484	JX026568	JQ432106	EU601385	EU601534	EU601434	EU601335	JX026638	EU601285
<i>Scarus ovifrons</i>	LC092086	JX026499		JX026569		LC068811				JX026639	
<i>Scarus perrico</i>		JX026500		JX026570						JX026640	
<i>Scarus persicus</i>		JX026501		JX026571						JX026641	
<i>Scarus prasiognathos</i>	EU601207	EU601248	EU601485	JX026572		EU601386	EU601535	EU601435	EU601336	JX026642	EU601286
<i>Scarus psittacus</i>	EU601208	EU601249	EU601486	JX026573	JQ432113	EU601387	EU601536	EU601436	EU601337	JX026643	KU862925
<i>Scarus quoyi</i>	EU601210	EU601251	EU601488	JX026574	KF930376	EU601389	EU601538	EU601438	EU601339	JX026644	EU601289
<i>Scarus rivalatus</i>	EU601211	EU601252	EU601489	JX026575		EU601390	EU601539	EU601439	EU601340	JX026645	EU601290
<i>Scarus rubroviolaceus</i>	EU601212	EU601253	EU601490	JX026577	NC011343	NC011343	EU601540	EU601440	EU601341	JX026647	EU601291
<i>Scarus russelii</i>		JX026510		JX026580	KF489744					JX026650	KU862927
<i>Scarus scaber</i>		JX026511		JX026581	JQ350333					JX026651	
<i>Scarus schlegeli</i>	EU601213	EU601254	EU601491	JX026582	NC011936	NC011936	EU601541	EU601441	EU601342	JX026652	EU601292
<i>Scarus spinus</i>	EU601214	EU601255	EU601492	JX026583	KP193990	EU601393	EU601542	EU601442	EU601343	JX026653	EU601293
<i>Scarus taeniopterus</i>	EU601215	EU601256	EU601493	JX026584	JQ842301	EU601394	EU601543	EU601443	EU601344	JX026654	EU601294
<i>Scarus tricolor</i>	EU601216	EU601257	EU601494	JX026585	JQ350335	EU601395	EU601544	EU601444	EU601345	JX026655	EU601295
<i>Scarus trispinosus</i>		JX026516		JX026586						JX026656	
<i>Scarus vetula</i>				JX026587	FJ584083					JX026657	KY815561
<i>Scarus viridifucatus</i>		JX026518		JX026588						JX026658	
<i>Scarus xanthopleura</i>		JX026519		JX026589		LC068816				JX026659	
<i>Scarus zelindae</i>		JX026520		JX026590						JX026660	
<i>Scarus zufar</i>		JX026521		JX026591						JX026661	
<i>Sparisoma amplum</i>						DQ457024					
<i>Sparisoma atomarium</i>	U95767	U95768			JQ840703	DQ457029					
<i>Sparisoma aurofrenatum</i>	EU601217	U95766	EU601495		JQ839898	DQ457031	EU601545	EU601445	EU601346		AY081099
<i>Sparisoma axillare</i>	KC526954	KC526953				DQ457034					
<i>Sparisoma choati</i>	AF114483	AF115312				DQ457036					
<i>Sparisoma chrysopterum</i>	AY279645	AY279748	EU601496		GU225439	DQ457033	EU601546	EU601446	AY279954		AY081100
<i>Sparisoma cretense</i>	U95777	AF517578			KC501534	DQ457026					
<i>Sparisoma frondosum</i>	JX645341	JX645342				DQ457032					
<i>Sparisoma radians</i>	U95771	U95772				DQ457028					
<i>Sparisoma rocha</i>	GU985521	GU985520									
<i>Sparisoma rubripinne</i>	KY815337	U95774			GU225443	DQ457035					
<i>Sparisoma strigatum</i>						DQ457027					
<i>Sparisoma tuliupiranga</i>						DQ457030					
<i>Sparisoma viride</i>	EU601219	AY081081	EU601497	AF370453	JQ841013	DQ457025	EU601547	EU601447	EU601348		AY081098
<i>Achoerodus viridis</i>	AY279574	AY279677	KY815674		EF609278		KY816077	KY815925	AY279883		AY279780
<i>Cheilinus abudjubbe</i>						KY815828			KY815584		KY815482
<i>Cheilinus chlorourus</i>			KY815691		KP194859	KY815829	KY816088	KY815941	KY815585		KY815483
<i>Cheilinus fasciatus</i>	AY279580	AY279683	KY815692		KP194612	KY815830	KY816089	KY815942	AY279889		AY279786
<i>Cheilinus lunulatus</i>						KY815831			KY815586		KY815484
<i>Cheilinus oxycephalus</i>	AY279581	AY279684	KY815693		KF929730	KY815832		KY815943	AY279890		AY279787
<i>Cheilinus trilobatus</i>			KY815694		KP194018	KY815833	KY816090	KY815944	KY815587		KY815485
<i>Cheilinus undulatus</i>	AY279582	AY279685	EU601498		KM461717	KM461717	EU601548	EU601448	AY279891		AY279788
<i>Lachnolaimus maximus</i>	AY279618	AY279721	EU601503		GU224537	EU601404	EU601553	EU601453	AY279927		AY279824

Supplementary table 7. Best gene partitioning scheme resulting from PartitionFinder for Siganidae.

Subset	Model	#sites	Genes
1	SYM+I+G	512	16s
2	GTR+I+G+X	1140	Cytb
3	TRN+G+X	1349	ITS1

Supplementary table 8. Best gene partitioning scheme resulting from PartitionFinder for Acanthuridae.

Subset	Model	#sites	Genes
1	GTR+I+G+X	651	Cox1
2	GTR+I+G+X	1047	Cytb
3	TRN+I+G+X	1498	ENC1, Myh6
4	HKY+G+X	422	ETS2
5	GTR+G+X	567	Plagl2
6	SYM+I+G	1556	Rag1
7	GTR+I+G+X	798	Rh
8	HKY+I+X	690	Zic1

Supplementary table 9. Best gene partitioning scheme resulting from PartitionFinder for Scarini.

Subset	Model	#sites	Genes
1	GTR+I+G+X	935	12s
2	GTR+I+G+X	503	16s
3	GTR+I+G+X	1005	Cox1, Cytb
4	HKY+I+G+X	433	Control region
5	HKY+I+G+X	480	Bmp4
6	HKY+G+X	516	Dlx2
7	GTR+I+G+X	669	Otx1
8	SYM+I+G	714	Rag2
9	GTR+G+X	618	S7I1
10	GTR+I+G+X	423	Tmo-4C4

Supplementary table 10. Summary of BayesTraits model results for discrete traits for Siganidae. Posterior Modal values (lower; upper - Highest Density Interval) of Lh: likelihood; q: transition rates between states; #Br: number of branch lengths scaled using variable rates; #Nd: number of nodes scaled using variable rates. Trait states: Diet (0 - Cyanobacteria; 1 - Macroalgae; 2 - Sponges; 3 - Turf algae); Feeding Mode (0 - Browser; 1 - Cropper); Feeding Habitat (0 - off reef; 1 - reef-concealed; 2 - reef-open; 3 - reef-sand); Schooling behaviour (0 - Pairing; 1 - Schooling).

Traits	Lh	q01	q02	q03	q10	q12	q13	q20	q21	q23	q30	q31	q32	#Br	#Nd
Diet	-21.68 (-24.65; -17.97)	0.09 (0.006; 0.09)	0.07 (0.006; 0.09)	0.09 (0.01; 0.09)	0.01 (3e-5; 0.08)	0.01 (1e-4; 0.08)	0.09 (0.008; 0.09)	0.08 (0.006; 0.09)	0.09 (0.007; 0.09)	0.08 (0.01; 0.09)	0.02 (1e-4; 0.07)	0.05 (0.01; 0.09)	0.01 (1e-4; 0.08)	2 (0; 4)	0 (0; 2)
Feeding Mode	-13.02 (-14.38; -9.11)	0.08 (0.02; 0.10)	-	-	0.04 (0.01; 0.10)	-	-	-	-	-	-	-	-	2 (0; 5)	1 (0; 3)
Feeding Habitat	-15.10 (-20.82; -12.54)	0.02 (9e-4; 0.02)	0.02 (0.002; 0.02)	0.02 (0.001; 0.02)	0.01 (9e-6; 0.02)	0.02 (0.002; 0.02)	0.005 (2e-6; 0.02)	0.004 (4e-4; 0.02)	0.006 (2e-4; 0.02)	0.003 (1e-5; 0.02)	0.02 (0.003; 0.02)	0.01 (8e-4; 0.02)	0.02 (0.001; 0.02)	1 (0; 4)	1 (0; 3)
Schooling	-8.59 (-56.40; -41.87)	0.07 (9e-4; 0.009)	-	-	0.02 (1e-6; 0.005)	-	-	-	-	-	-	-	-	1 (2; 11)	0 (2; 8)

Supplementary table 11. Summary of BayesTraits model results for discrete traits for Acanthuridae. Posterior Modal values (lower; upper - Highest Density Interval) of Lh: likelihood; q: transition rates between states; #Br: number of branch lengths scaled using variable rates; #Nd: number of nodes scaled using variable rates. Trait states: Diet (0 - Detritus; 1 - Macroalgae; 2 - Turf algae; 3 - Turf+Detritus; 4 - Zooplankton); Feeding Mode (0 - Browser; 1 - Brusher; 2 - Cropper; 3 - Planktivore; 4 - Sucker); Feeding Habitat (0 - reef-concealed; 1 - reef-open; 2 - reef-sand; 3 - water column); Tooth morphology (0 - Brush; 1 - Conical; 2 - Multi-denticulate); Alimentary tract (0 - Gizzard-like; 1 - Thin walled); Schooling behaviour (0 - Pairing; 1 - Schooling; 2 - Solitary).

Traits	Lh	q01	q02	q03	q04	q10	q12	q13	q14	q20	q21	q23	q24
Diet	-48.67 (-54.50; -40.55)	1e-5 (40.55; 9e-4)	1e-5 (1e-8; 9e-4)	8e-4 (1e-8; 9e-4)	8e-4 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	8e-4 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	8e-4 (1e-8; 9e-4)	8e-4 (1e-8; 9e-4)	9e-4 (2e-4; 0.001)
Feeding Mode	-42.93 (-50.26; -35.12)	1e-5 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	8e-4 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	8e-4 (1e-8; 9e-4)	8e-4 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	8e-4 (1e-8; 9e-4)	9e-4 (3e-4; 9e-4)	8e-4 (1e-8; 9e-4)
Feeding Habitat	-46.13 (-52.53; -39.84)	5e-4 (1e-8; 9e-4)	3e-4 (1e-8; 9e-4)	8e-4 (7e-5; 9e-4)	-	9e-5 (1e-8; 8e-4)	8e-4 (1e-4; 0.001)	8e-4 (1e-4; 9e-4)	-	9e-5 (1e-8; 9e-4)	7e-4 (5e-5; 9e-4)	8e-4 (8e-5; 9e-4)	-
Tooth Morphology	-11.71 (-16.71; -8.44)	1e-4 (6e-6; 9e-4)	7e-4 (7e-5; 9e-4)	-	-	3e-4 (1e-5; 9e-4)	8e-4 (6e-5; 9e-4)	-	-	8e-4 (1e-4; 0.001)	2e-4 (6e-6; 9e-4)	-	-
Alimentary tract	-10.15 (-13.62; -5.64)	5e-4 (6e-5; 9e-4)	-	-	-	7e-4 (1e-4; 0.001)	-	-	-	-	-	-	-
Schooling	-48.26 (-56.40; -41.87)	0.008 (9e-4; 0.009)	0.005 (1e-4; 0.009)	-	-	7e-4 (1e-6; 0.005)	0.008 (0.001; 0.009)	-	-	8e-8 (1e-6; 0.007)	0.009 (0.003; 0.009)	-	-

Supplementary table 11. Continuation.

Traits	q30	q31	q32	q34	q40	q41	q42	q43	#Br	#Nd
Diet	8e-4 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	8e-4 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	8e-4 (3e-4; 0.001)	1e-5 (0; 9e-4)	1e-5 (1e-8; 9e-4)	7 (1; 10)	4 (2; 7)
Feeding Mode	8e-4 (3e-4; 9e-4)	1e-5 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	8e-4 (1e-8; 9e-4)	1e-5 (1e-8; 9e-4)	8e-4 (1e-8; 9e-4)	5 (2; 11)	4 (2; 8)
Feeding Habitat	2e-4 (2e-6; 9e-4)	9e-4 (4e-4; 0.001)	1e-4 (7e-6; 9e-4)	-	-	-	-	-	6 (1; 10)	4 (2; 7)
Tooth Morphology	-	-	-	-	-	-	-	-	5 (1; 10)	3 (1; 6)
Alimentary tract	-	-	-	-	-	-	-	-	5 (2; 10)	3 (0; 6)
Schooling	-	-	-	-	-	-	-	-	5 (2; 11)	5 (2; 8)

Supplementary table 12. Summary of BayesTraits model results for discrete traits for Scarini. Posterior Modal values (lower; upper - Highest Density Interval) of Lh: likelihood; q: transition rates between states; #Br: number of branch lengths scaled using variable rates; #Nd: number of nodes scaled using variable rates. Trait states: Diet (0 - EAM; 1 - EAM+Coral; 2 - EAM+Macroalgae; 3 - EAM+Macroalgae+Sponges; 4 - Macroalgae Seagrass+Macroalgae); Feeding Mode (0 - Browser; 1 - Excavator; 2 - Scraper); Feeding Habitat (0 - off reef; 1 - reef-open; 2 - reef-sand); Tooth morphology (0 - Fused-crenellated; 1 - Fused-even; 2 - Not-fused; 3 - Weakly-fused); Schooling behaviour (0 - Schooling; 1 - Solitary).

Traits	Lh	q01	q02	q03	q04	q05	q10	q12	q13	q14	q15	q20	q21	q23	q24	q25
Diet	-35.19 (-40.93; -30.20)	6e-04 (1e-8; 0.009)	2e-04 (1e-8; 0.008)	1e-04 (1e-8; 0.008)	1e-04 (1e-8; 0.008)	3e-04 (1e-8; 0.009)	3e-04 (1e-8; 0.009)	4e-04 (1e-8; 0.009)	4e-04 (1e-8; 0.009)	3e-04 (1e-8; 0.009)	4e-04 (1e-8; 0.009)	2e-04 (1e-8; 0.009)	5e-04 (1e-8; 0.009)	1e-04 (1e-8; 0.009)	2e-04 (1e-8; 0.009)	5e-04 (1e-8; 0.009)
Feeding Mode	-22.08 (-27.66; -18.12)	0.006 (5e-5; 0.06)	0.008 (5e-5; 0.07)	-	-	-	0.01 (2e-5; 0.09)	0.07 (0.002; 0.09)	-	-	-	0.006 (4e-6; 0.06)	0.01 (9e-5; 0.07)	-	-	-
Feeding Habitat	-35.02 (-39.19; -31.72)	0.08 (0.01; 0.09)	0.01 (0.003; 0.09)	-	-	-	0.001 (1e-6; 0.01)	0.01 (0.002; 0.03)	-	-	-	0.01 (0.002; 0.09)	0.09 (0.02; 0.09)	-	-	-
Tooth Morphology	-22.44 (-26.21; -18.56)	0.005 (1e-4; 0.009)	0.002 (1e-5; 0.009)	0.001 (1e-5; 0.009)	-	-	0.003 (8e-6; 0.009)	9e-4 (5e-6; 0.008)	8e-4 (8e-6; 0.008)	-	-	0.007 (9e-6; 0.009)	0.002 (1e-4; 0.009)	0.008 (0.001; 0.009)	-	-
Schooling	-52.48 (-55.78; -47.87)	0.03 (0.01; 0.14)	-	-	-	-	0.04 (0.02; 0.19)	-	-	-	-	-	-	-	-	-

Supplementary table 12. Continuation.

Traits	q30	q31	q32	q34	q35	q40	q41	q42	q43	q45	q50	q51	q52	q53	q54	#Br	#Nd
Diet	3e-04 (1e-8; 0.009)	4e-04 (1e-8; 0.009)	5e-04 (1e-8; 0.009)	3e-04 (1e-8; 0.009)	4e-04 (1e-8; 0.009)	2e-04 (1e-8; 0.009)	3e-04 (1e-8; 0.009)	3e-04 (1e-8; 0.009)	3e-04 (1e-8; 0.009)	0.008 (1e-8; 0.009)	2e-04 (1e-8; 0.009)	2e-04 (1e-8; 0.009)	4e-04 (1e-8; 0.009)	2e-04 (1e-8; 0.009)	9e-04 (1e-8; 0.009)	8 (2; 12)	3 (1; 7)
Feeding Mode	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6 (1; 11)	3 (1; 6)
Feeding Habitat	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7 (2; 12)	3 (0; 6)
Tooth Morphology	0.006 (0.001; 0.009)	0.001 (2e-5; 0.009)	0.006 (5e-4; 0.009)	-	-	-	-	-	-	-	-	-	-	-	-	7 (2; 12)	2 (0; 5)
Schooling	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7 (2; 12)	4 (1; 7)

Supplementary table 13. Summary of BayesTraits model results for the continuous trait (maximum length). Posterior Modal values (lower; upper - Highest Density Interval) of Lh: likelihood; Alpha: phylogenetic mean of the trait; Sigma: Brownian motion variance for the trait; #Br: number of branch lengths scaled using variable rates; #Nd: number of nodes scaled using variable rates.

Taxa	Lh	Alpha	Sigma	#Br	#Nd
Siganidae	-85.83 (-89.84; -82.91)	34.44 (28.86; 40.85)	89.37 (18.78; 99.97)	2 (0; 4)	0 (0; 2)
Acanthuridae	-279.42 (-290.64; -268.81)	36.54 (26.82; 63.32)	87.22 (15.24; 99.97)	7 (3; 12)	3 (0; 6)
Scarini	-366.91 (-373.74; -356.92)	44.95 (15.46; 80.45)	29.76 (14.20; 47.13)	7 (3; 12)	4 (1; 7)

Supplementary table 14. Summary of BayesTraits model results for ecosystem functions. Posterior Modal values (lower; upper - Highest Density Interval) of Lh: likelihood; q: transition rates between states; #Br: number of branch lengths scaled using variable rates; #Nd: number of nodes scaled using variable rates. States: Siganidae (0 - Macroalgae removal; 1 - Turf removal; 2 - Turf removal + Crevice cleaning; 3 - Turf removal + Crevice cleaning+Spongivory; 4 - Turf + Sediment removal); Acanthuridae (0 - Macroalgae removal; 1 - Sediment removal; 2 - Turf removal; 3 - Turf removal + Crevice cleaning; 4 - Turf + Sediment removal; 5 - Zooplanktivory; 6 - Zooplanktivory + Turf removal); Scarini (0 - Macroalgae removal; 1 - Macroalgae + Turf+Sediment removal; 2 - Macroalgae + Turf+Sediment removal + Spongivory; 3 - Turf + Sediment removal; 4 - Turf + Sediment removal + Bioerosion; 5 - Turf + Sediment removal + Bioerosion + Corallivory).

Taxa	Lh	q01	q02	q03	q04	q05	q06	q10	q12	q13	q14	q15	q16	q20	q21	q23	q24	q25	
Siganidae	-22.24 (-27.39; -18.90)	0.01 (1e-8; 0.01)	0.01 (1e-8; 0.01)	2e-4 (1e-8; 0.01)	0.01 (1e-8; 0.01)	-	-	0.01 (1e-8; 0.01)	0.01 (1e-8; 0.01)	2e-4 (1e-8; 0.01)	2e-4 (1e-8; 0.01)	-	-	0.01 (1e-8; 0.01)	2e-4 (1e-8; 0.01)	0.01 (1e-8; 0.01)	2e-4 (1e-8; 0.01)	-	
Acanthuridae	-50.73 (-56.92; -44.30)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	
Scarini	-58.69 (-66.58; -49.15)	0.006 (1e-8; 0.006)	2e-4 (1e-8; 0.006)	2e-4 (1e-8; 0.006)	1e-4 (1e-8; 0.006)	2e-4 (1e-8; 0.006)	-	3e-4 (1e-8; 0.006)	0.006 (1e-8; 0.006)	1e-4 (1e-8; 0.006)	1e-4 (1e-8; 0.006)	3e-4 (1e-8; 0.006)	-	1e-4 (1e-8; 0.006)	2e-4 (1e-8; 0.006)	2e-4 (1e-8; 0.006)	2e-4 (1e-8; 0.006)	2e-4 (1e-8; 0.006)	2e-4 (1e-8; 0.006)

Traits	q26	q30	q31	q32	q34	q35	q36	q40	q41	q42	q43	q45	q46	q50	q51	q52	q53	q54
Siganidae	-	0.01 (1e-8; 0.01)	0.01 (1e-8; 0.01)	2e-4 (1e-8; 0.01)	0.01 (1e-8; 0.01)	-	-	0.01 (1e-8; 0.01)	3e-4 (1e-8; 0.01)	3e-4 (1e-8; 0.01)	2e-4 (1e-8; 0.01)	-	-	-	-	-	-	-
Acanthuridae	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)
Scarini	-	2e-5 (1e-8; 0.006)	1e-5 (1e-8; 0.006)	2e-5 (1e-8; 0.006)	0.006 (1e-8; 0.006)	2e-5 (1e-8; 0.006)	-	1e-4 (1e-8; 0.006)	1e-4 (1e-8; 0.006)	1e-4 (1e-8; 0.006)	2e-4 (1e-8; 0.006)	0.006 (1e-8; 0.006)	-	2e-4 (1e-8; 0.006)	2e-4 (1e-8; 0.006)	2e-4 (1e-8; 0.006)	1e-4 (1e-8; 0.006)	3e-4 (1e-8; 0.006)

Supplementary table 14. Continuation.

Traits	q56	q60	q61	q62	q63	q64	q65	#Br	#Nd
Siganidae	-	-	-	-	-	-	-	1 (0; 5)	1 (0; 3)
Acanthuridae	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	0.002 (1e-8; 0.002)	5 (2; 11)	3 (0; 5)
Scarini	-	-	-	-	-	-	-	7 (3; 12)	4 (1; 7)