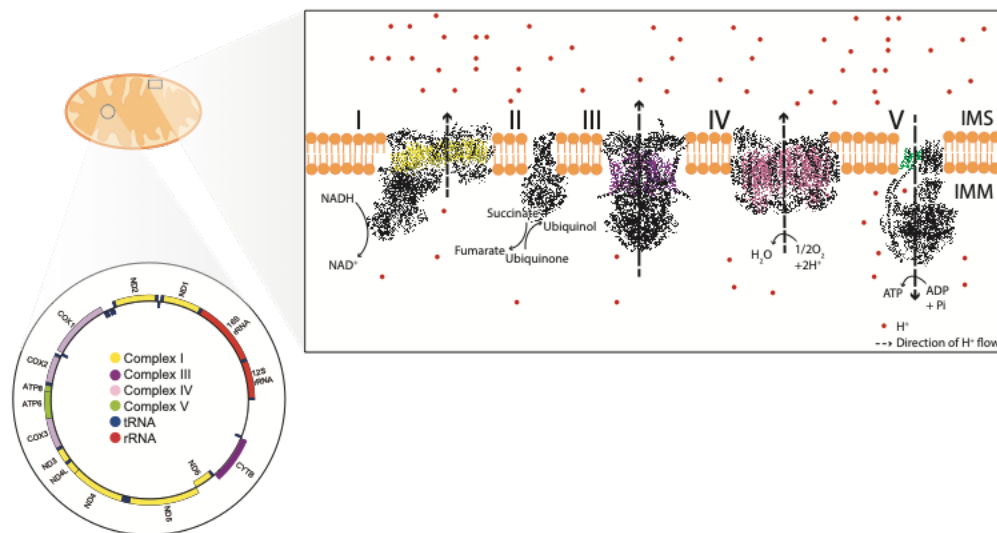
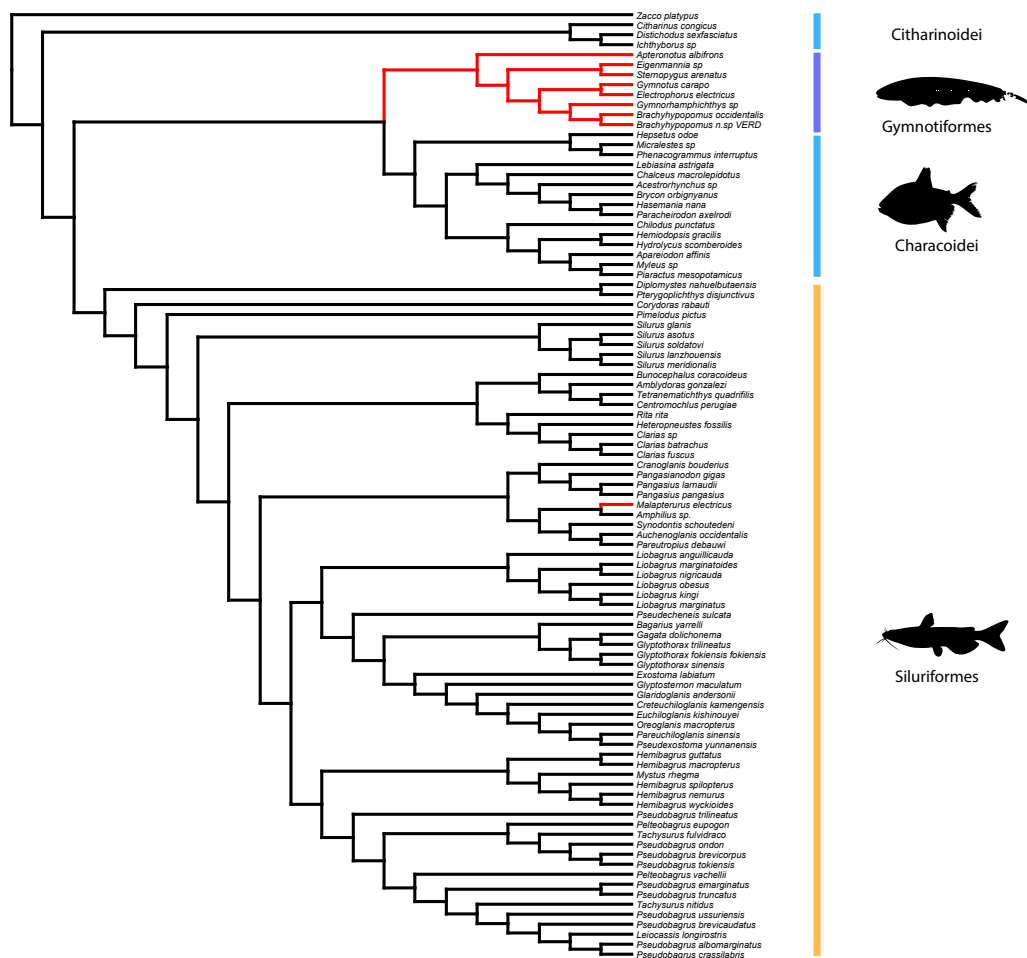
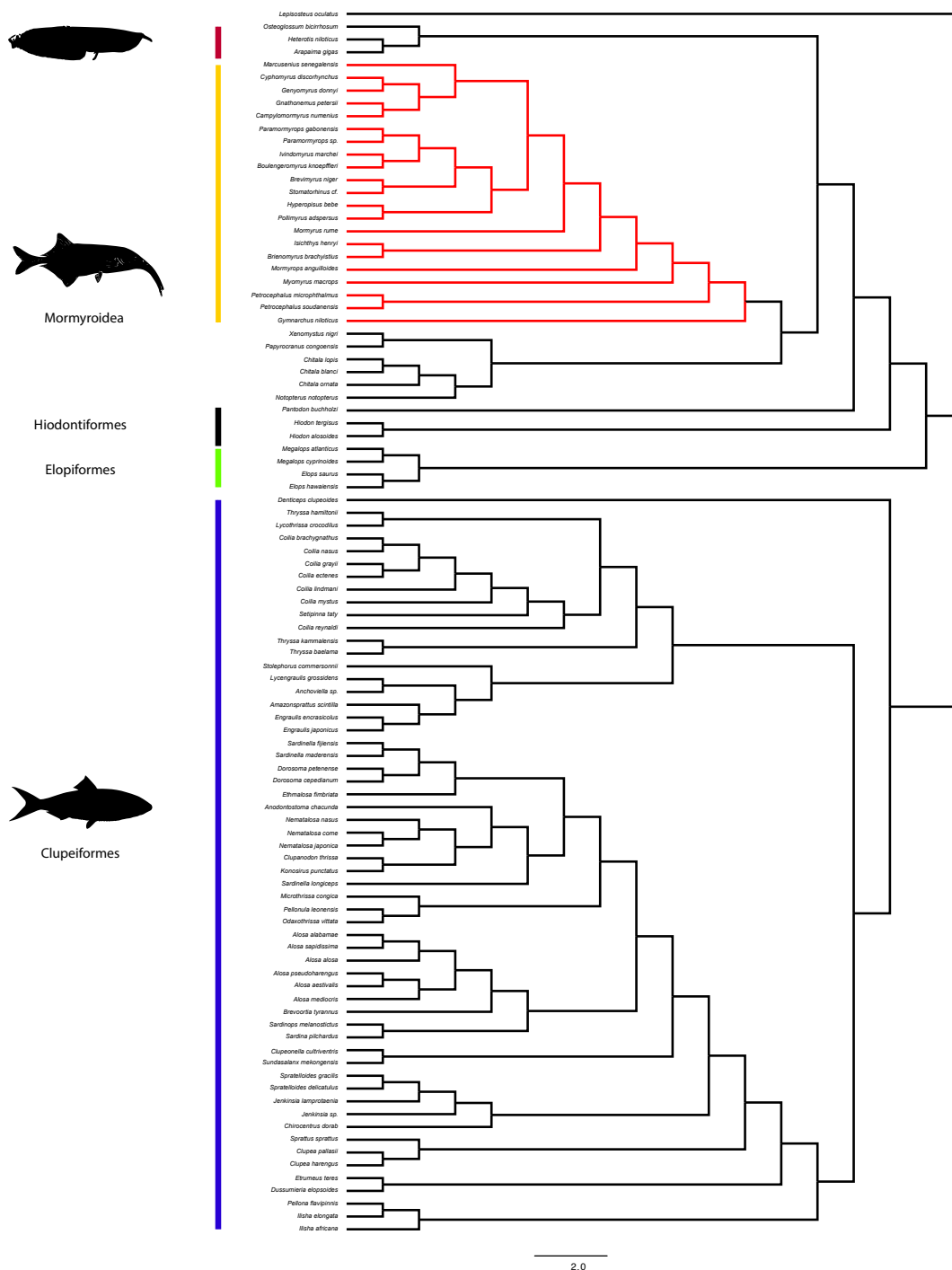




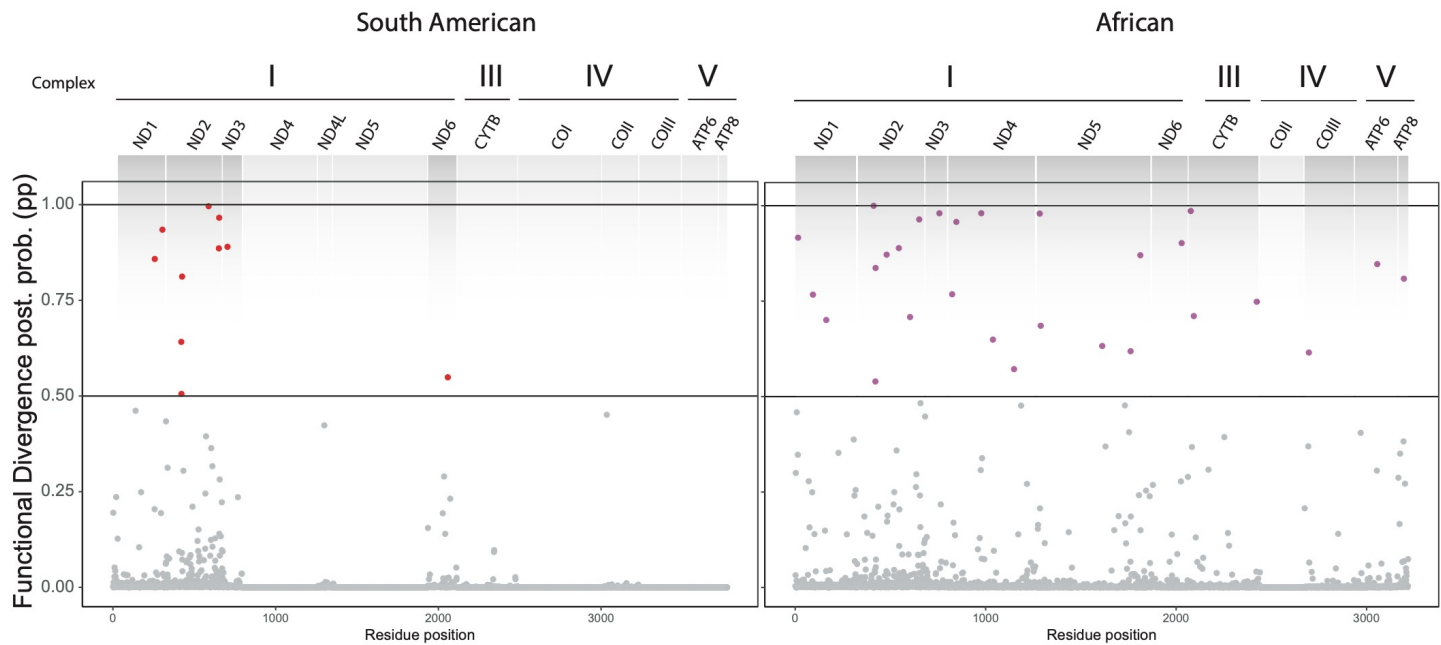
Supplementary Figure 1 – Schematic representation of mitochondrial genomes and their contribution to OXPHOS complexes. Left inset shows mitochondrial genomes presented in their circular orientation, with genes ordered to represent the typical vertebrate gene order and coloured according to the respiratory complex they encode. Right inset shows mitochondrial complexes roles in oxidative phosphorylation and ATP generation. Nuclear-encoded subunits are shown in black, while mitochondrial subunits are shown in yellow (complex I), purple (complex III), pink (complex IV) and green (complex V). Proton molecules are represented by red circles, and direction of proton flow during oxidative phosphorylation is indicated by black dashed arrows. IMS, inter-membrane space; IMM, inner mitochondrial membrane.



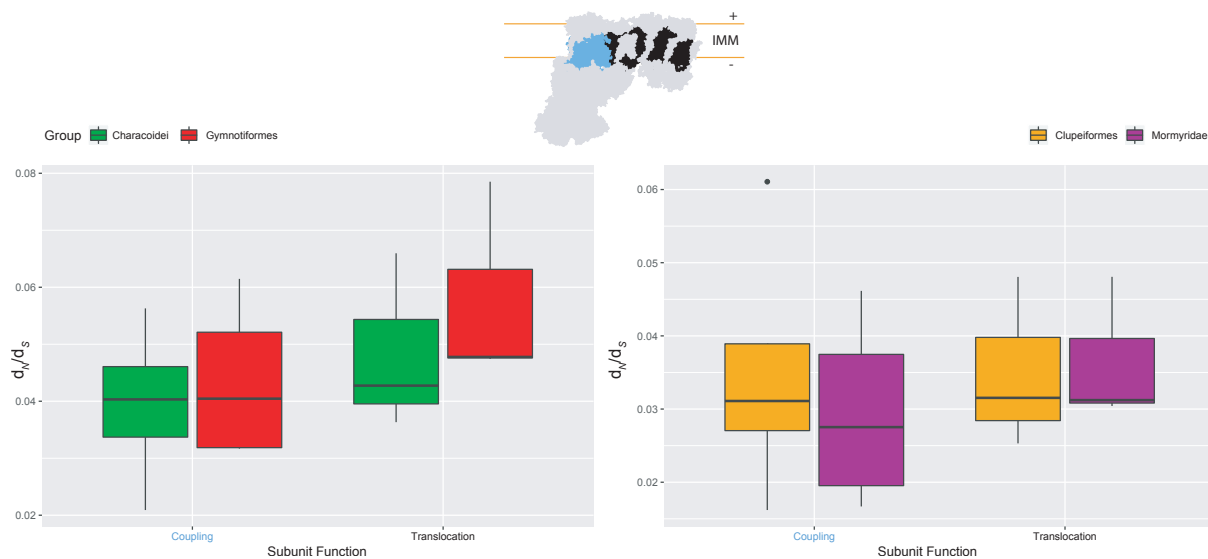
Supplementary Figure 2 – molecular phylogeny of the South American dataset. A maximum likelihood phylogenetic inference of the relationships between the species included in the South American dataset, generated using IQ-Tree. Electrogenic group coloured in red. Adapted from [1].



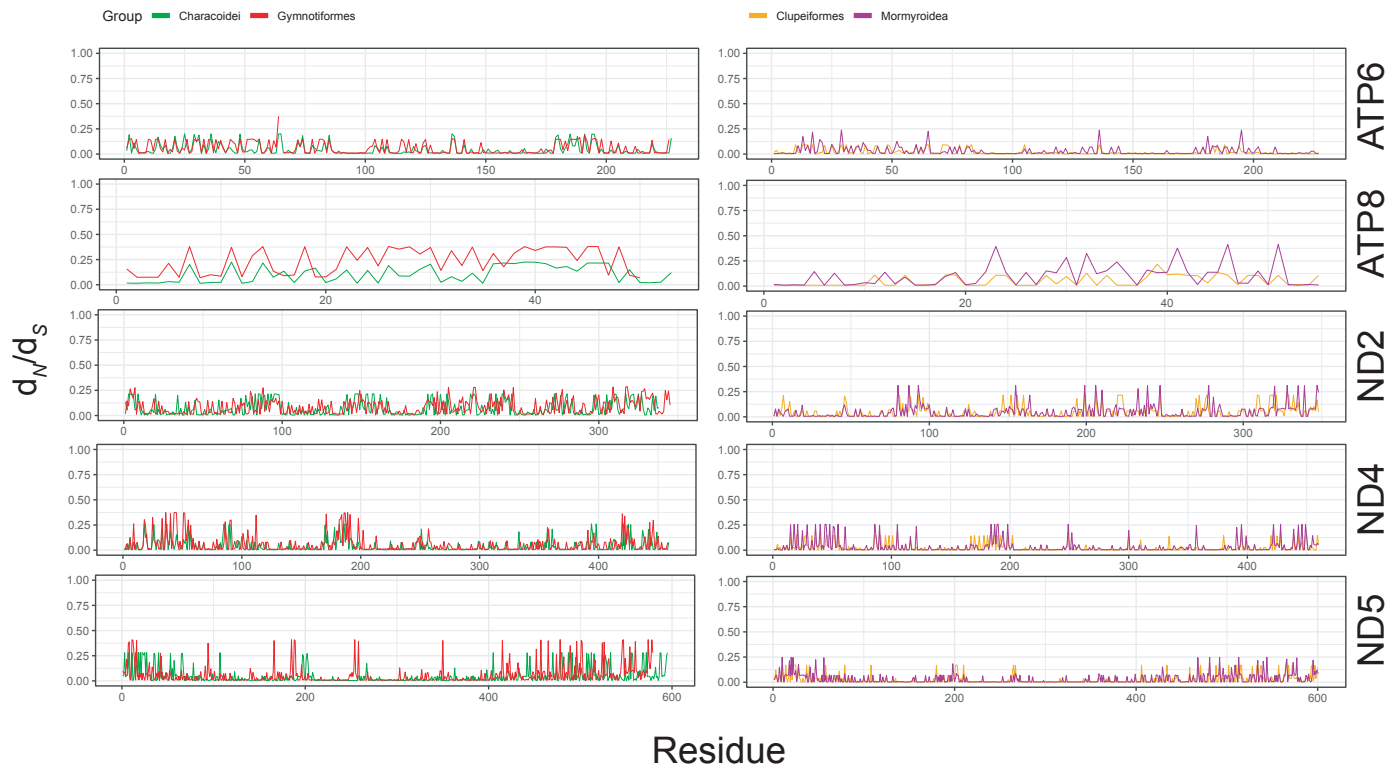
Supplementary Figure 3 – molecular phylogeny of the African dataset. A maximum likelihood reconstruction of the relationships of species included in the African dataset, based on complete mitochondrial genomes and using IQ-Tree program. Electrogenic group is highlighted with red branches.



Supplementary Figure 5 – functional divergence of OXPHOS sites between electric fishes and non-electric relatives. Sites with posterior probability, of being in the divergent class, above 0.5 are shown in red (South American dataset) and purple (African dataset). Genes with darker shades have at least one residue with evidence of functional divergence.



Supplementary Figure 5 – functional constraint on complex I subunits evolution. Rates of non-synonymous to synonymous substitutions estimated across genes (model M0) based on their involvement in either proton translocation (black) or coupling (cornflower blue). Schematic on the top shows the location of both types of subunits within complex I (PDB:5LNK).



Supplementary Figure 6 – Omega estimates across sites in complex I and V. For each gene, mean omega estimate across sites in the electric fishes and non-electric relative is plotted show peaks of elevated d_N/d_S .

Supplementary Table 1 - Taxa used in this study.

Order	Species	Genbank Accession
Gymnotiformes	<i>Gymnorhamphichthys sp.</i>	NC_015754.1
Gymnotiformes	<i>Electrophorus electricus</i>	KX058572
Gymnotiformes	<i>Brachyhypopomus occidentalis</i>	AP011570
Gymnotiformes	<i>Eigenmannia sp.</i>	NC_004701.1
Gymnotiformes	<i>Brachyhypopomus sp. n. VERD</i>	KX058570
Gymnotiformes	<i>Apteronotus albifrons</i>	NC_004692.1
Characiformes	<i>Hepsetus odoe</i>	NC_015819.1
Characiformes	<i>Citharinus congicus</i>	NC_015805.1
Characiformes	<i>Distichodus sexfasciatus</i>	NC_015836.1
Characiformes	<i>Ichthyborus sp.</i>	NC_015752.1
Characiformes	<i>Chalceus macrolepidotus</i>	NC_004700.1
Characiformes	<i>Hemiodopsis gracilis</i>	NC_015816.1
Characiformes	<i>Myleus sp.</i>	NC_015751.1
Characiformes	<i>Piaractus mesopotamicus</i>	NC_024940.1
Characiformes	<i>Apareiodon affinis</i>	NC_015834.1
Characiformes	<i>Chilodus punctatus</i>	NC_015801.1
Characiformes	<i>Lebiasina astrigata</i>	NC_015750.1
Characiformes	<i>Hydrolycus scomberoides</i>	NC_015813.1
Siluriformes	<i>Amphilius sp.</i>	NC_015746.1
Siluriformes	<i>Amblydoras gonzalezi</i>	NC_015745.1
Siluriformes	<i>Tetranematichthys quadrifilis</i>	NC_015743.1
Siluriformes	<i>Centromochlus perugiae</i>	NC_015748.1
Siluriformes	<i>Synodontis schoutedeni</i>	NC_015808.1
Siluriformes	<i>Pangasianodon gigas</i>	NC_006381.1
Siluriformes	<i>Pangasius larnaudii</i>	NC_015839.1
Siluriformes	<i>Pangasius pangasius</i>	NC_023924.1
Siluriformes	<i>Auchenoglanis occidentalis</i>	NC_015809.1
Siluriformes	<i>Cranoglanis boudierius</i>	NC_008280.1
Siluriformes	<i>Pareutropius debauwi</i>	NC_015837.1
Siluriformes	<i>Heteropneustes fossilis</i>	NC_015827.1
Siluriformes	<i>Clarias sp.</i>	NC_015749.1
Siluriformes	<i>Clarias batrachus</i>	NC_023923.1
Siluriformes	<i>Clarias fuscus</i>	NC_023941.1
Siluriformes	<i>Pseudobagrus ussuriensis</i>	NC_020344.1
Siluriformes	<i>Leiocassis longirostris</i>	NC_014586.1
Siluriformes	<i>Pseudobagrus albomarginatus</i>	NC_022726.1
Siluriformes	<i>Pseudobagrus crassilabris</i>	NC_021394.1
Siluriformes	<i>Pseudobagrus brevicaudatus</i>	NC_021393.1

Siluriformes	<i>Tachysurus nitidus</i>	NC_024456.1
Siluriformes	<i>Pseudobagrus truncatus</i>	NC_021395.1
Siluriformes	<i>Pseudobagrus emarginatus</i>	NC_024279.1
Siluriformes	<i>Pelteobagrus vachellii</i>	NC_014862.1
Siluriformes	<i>Pseudobagrus tokiensis</i>	NC_004697.1
Siluriformes	<i>Pseudobagrus brevicorpus</i>	NC_015625.1
Siluriformes	<i>Pseudobagrus ondon</i>	NC_022725.1
Siluriformes	<i>Tachysurus fulvidraco</i>	NC_023767.1
Siluriformes	<i>Pelteobagrus eupogon</i>	NC_018768.1
Siluriformes	<i>Pseudobagrus trilineatus</i>	NC_022705.1
Siluriformes	<i>Hemibagrus macropterus</i>	NC_019592.1
Siluriformes	<i>Hemibagrus guttatus</i>	NC_023976.1
Siluriformes	<i>Hemibagrus spilopterus</i>	NC_023222.1
Siluriformes	<i>Hemibagrus nemurus</i>	NC_024273.1
Siluriformes	<i>Hemibagrus wyckioides</i>	NC_024278.1
Siluriformes	<i>Mystus rhegma</i>	NC_023223.1
Siluriformes	<i>Silurus glanis</i>	NC_014261.1
Siluriformes	<i>Silurus asotus</i>	NC_015806.1
Siluriformes	<i>Silurus soldatovi</i>	NC_022723.1
Siluriformes	<i>Silurus lanzhouensis</i>	NC_015650.1
Siluriformes	<i>Silurus meridionalis</i>	NC_014866.1
Siluriformes	<i>Rita rita</i>	NC_023376.1
Siluriformes	<i>Liobagrus kingi</i>	NC_020337.1
Siluriformes	<i>Liobagrus marginatus</i>	NC_022923.1
Siluriformes	<i>Liobagrus marginatoides</i>	NC_021122.1
Siluriformes	<i>Liobagrus nigricauda</i>	NC_021407.1
Siluriformes	<i>Liobagrus anguillicauda</i>	NC_021602.1
Siluriformes	<i>Liobagrus obesus</i>	NC_008232.1
Siluriformes	<i>Glyptothorax fokiensis fokiensis</i>	NC_018769.1
Siluriformes	<i>Glyptothorax sinensis</i>	NC_024672.1
Siluriformes	<i>Gagata dolichonema</i>	NC_021596.1
Siluriformes	<i>Glyptothorax trilineatus</i>	NC_021608.1
Siluriformes	<i>Bagarius yarrelli</i>	NC_021606.1
Siluriformes	<i>Glaridoglanis andersonii</i>	NC_021600.1
Siluriformes	<i>Glyptosternon maculatum</i>	NC_021597.1
Siluriformes	<i>Creteuchiloglanis kamengensis</i>	NC_021599.1
Siluriformes	<i>Pseudexostoma yunnanensis</i>	NC_021604.1
Siluriformes	<i>Pareuchiloglanis sinensis</i>	NC_024434.1
Siluriformes	<i>Oreoglanis macropterus</i>	NC_021607.1
Siluriformes	<i>Euchiloglanis kishinouyei</i>	NC_021598.1
Siluriformes	<i>Pseudecheneis sulcata</i>	NC_021605.1
Siluriformes	<i>Exostoma labiatum</i>	NC_021601.1
Siluriformes	<i>Pimelodus pictus</i>	NC_015797.1

Siluriformes	<i>Malapterurus electricus</i>	NC_015833.1
Siluriformes	<i>Diplomystes nahuelbutaensis</i>	NC_015823.1
Siluriformes	<i>Pterygoplichthys disjunctivus</i>	NC_015747.1
Siluriformes	<i>Bunocephalus coracoideus</i>	NC_015811.1
Siluriformes	<i>Corydoras rabauti</i>	NC_004698.1
Characiformes	<i>Phenacogrammus interruptus</i>	NC_004699.1
Characiformes	<i>Micralestes sp.</i>	NC_015753.1
Characiformes	<i>Acestrorhynchus sp.</i>	NC_015755.1
Cypriniformes	<i>Zacco platypus</i>	NC_023105.1
Characiformes	<i>Brycon orbignyanus</i>	NC_024938.1
Characiformes	<i>Hasemania nana</i>	NC_022724.1
Characiformes	<i>Paracheirodon axelrodi</i>	NC_023270.1
Gymnotiformes	<i>Sternopygus arenatus</i>	KX058571
Lepisosteiformes	<i>Lepisosteus oculatus</i>	NC_004744
Osteoglossiformes	<i>Osteoglossum bicirrhosum</i>	AB043025.1
Osteoglossiformes	<i>Osteoglossum bicirrhosum</i>	NC_003095.1
Osteoglossiformes	<i>Heterotis niloticus</i>	AP009498.1
Osteoglossiformes	<i>Arapaima gigas</i>	AP009497.1
Osteoglossiformes	<i>Marcusenius senegalensis</i>	AP011575.1
Osteoglossiformes	<i>Cyphomyrus discorhynchus</i>	AP009613.1
Osteoglossiformes	<i>Genyomys donnyi</i>	AP009500.1
Osteoglossiformes	<i>Gnathonemus petersii</i>	AP009611.1
Osteoglossiformes	<i>Gnathonemus petersii</i>	AP008928.2
Osteoglossiformes	<i>Campylomormyrus numenius</i>	AP011571.1
Osteoglossiformes	<i>Paramormyrops gabonensis</i>	AP009614.1
Osteoglossiformes	<i>Paramormyrops sp.</i>	AP011581.1
Osteoglossiformes	<i>Paramormyrops sp.</i>	AP011580.1
Osteoglossiformes	<i>Paramormyrops sp.</i>	AP011579.1
Osteoglossiformes	<i>Paramormyrops sp.</i>	AP011578.1
Osteoglossiformes	<i>Ivindomyrus marchei</i>	AP011574.1
Osteoglossiformes	<i>Boulengeromyrus knoepffleri</i>	AP011568.1
Osteoglossiformes	<i>Brevimyrus niger</i>	AP009612.1
Osteoglossiformes	<i>Brienomyrus niger</i>	AP008929.1
Osteoglossiformes	<i>Hyperopisus bebe</i>	AP011572.1
Osteoglossiformes	<i>Mormyrops anguilloides</i>	AP011576.1
Osteoglossiformes	<i>Pollimyrus adspersus</i>	AP011582.1
Osteoglossiformes	<i>Stomatorhinus cf.</i>	AP011583.1
Osteoglossiformes	<i>Isichthys henryi</i>	AP011573.1
Osteoglossiformes	<i>Brienomyrus brachyistius</i>	AP011569.1
Osteoglossiformes	<i>Mormyrus rume</i>	AP011577.1
Osteoglossiformes	<i>Myomyrus macrops</i>	AP009501.1
Osteoglossiformes	<i>Petrocephalus microphthalmus</i>	AP009609.1
Osteoglossiformes	<i>Petrocephalus soudanensis</i>	AP009502.1

Osteoglossiformes	<i>Gymnarchus niloticus</i>	AP009610.1
Osteoglossiformes	<i>Gymnarchus niloticus</i>	AP008930.1
Osteoglossiformes	<i>Xenomystus nigri</i>	AP009503.1
Osteoglossiformes	<i>Xenomystus nigri</i>	AP008927.1
Osteoglossiformes	<i>Papyrocranus congoensis</i>	AP008926.1
Osteoglossiformes	<i>Chitala lopis</i>	AP008922.1
Osteoglossiformes	<i>Chitala blanci</i>	AP008921.1
Osteoglossiformes	<i>Chitala ornata</i>	AP008923.1
Osteoglossiformes	<i>Notopterus notopterus</i>	AP008925.1
Osteoglossiformes	<i>Notopterus notopterus</i>	AP008924.1
Osteoglossiformes	<i>Pantodon buchholzi</i>	AB043068.1
Osteoglossiformes	<i>Pantodon buchholzi</i>	NC_003096.1
Osteoglossiformes	<i>Pantodon buchholzi</i>	AP011564.1
Elopiformes	<i>Megalops atlanticus</i>	NC_005804.1
Elopiformes	<i>Megalops cyprinoides</i>	NC_005799.1
Elopiformes	<i>Elops saurus</i>	NC_005803.1
Elopiformes	<i>Elops hawaiiensis</i>	NC_005798.1
Hiodontiformes	<i>Hiodon tergisus</i>	AP009499.1
Hiodontiformes	<i>Hiodon alosoides</i>	AP004356.2
Clupeiformes	<i>Denticeps clupeoides</i>	NC_007889.1
Clupeiformes	<i>Thryssa hamiltonii</i>	NC_036672.1
Clupeiformes	<i>Thryssa kammalensis</i>	NC_029940.1
Clupeiformes	<i>Coilia brachygnathus</i>	NC_026912.1
Clupeiformes	<i>Coilia nasus</i>	KM257636.1
Clupeiformes	<i>Coilia grayii</i>	NC_023538.1
Clupeiformes	<i>Coilia ectenes</i>	NC_019625.1
Clupeiformes	<i>Coilia lindmani</i>	NC_014271.1
Clupeiformes	<i>Coilia mystus</i>	NC_019644.1
Clupeiformes	<i>Setipinna taty</i>	NC_020468.1
Clupeiformes	<i>Coilia reynaldi</i>	NC_014276.1
Clupeiformes	<i>Thryssa baelama</i>	NC_014264.1
Clupeiformes	<i>Lycothrissa crocodilus</i>	NC_014277.1
Clupeiformes	<i>Stolephorus commersonnii</i>	NC_033521.1
Clupeiformes	<i>Lycengraulis grossidens</i>	NC_014279.1
Clupeiformes	<i>Anchoviella sp.</i>	NC_014269.1
Clupeiformes	<i>Amazonsprattus scintilla</i>	NC_014265.1
Clupeiformes	<i>Engraulis encrasicolus</i>	NC_009581.1
Clupeiformes	<i>Engraulis japonicus</i>	NC_003097.1
Clupeiformes	<i>Sardinella fijiensis</i>	NC_035874.1
Clupeiformes	<i>Sardinella maderensis</i>	NC_009587.1
Clupeiformes	<i>Dorosoma petenense</i>	NC_009580.1
Clupeiformes	<i>Dorosoma cepedianum</i>	MG570429.1
Clupeiformes	<i>Ethmalosa fimbriata</i>	NC_009582.1

Clupeiformes	<i>Microthrissa congica</i>	NC_016695.1
Clupeiformes	<i>Pellonula leonensis</i>	NC_009591.1
Clupeiformes	<i>Odaxothrissa vittata</i>	NC_009590.1
Clupeiformes	<i>Anodontostoma chacunda</i>	NC_021446.1
Clupeiformes	<i>Nematalosa nasus</i>	NC_023824.1
Clupeiformes	<i>Nematalosa come</i>	NC_021447.1
Clupeiformes	<i>Nematalosa japonica</i>	NC_009586.1
Clupeiformes	<i>Clupanodon thrissa</i>	NC_018600.1
Clupeiformes	<i>Konosirus punctatus</i>	JQ753955.1
Clupeiformes	<i>Alosa alabamae</i>	NC_028275.1
Clupeiformes	<i>Alosa sapidissima</i>	KY769128.1
Clupeiformes	<i>Alosa alosa</i>	NC_009575.1
Clupeiformes	<i>Alosa pseudoharengus</i>	NC_009576.1
Clupeiformes	<i>Alosa aestivalis</i>	MG570463.1
Clupeiformes	<i>Alosa mediocris</i>	MG570462.1
Clupeiformes	<i>Brevoortia tyrannus</i>	NC_014266.1
Clupeiformes	<i>Sardinops melanostictus</i>	NC_002616.1
Clupeiformes	<i>Sardinella longiceps</i>	NC_033407.1
Clupeiformes	<i>Clupeonella cultriventris</i>	NC_015109.1
Clupeiformes	<i>Sprattus sprattus</i>	NC_009593.1
Clupeiformes	<i>Clupea pallasii</i>	NC_009578.1
Clupeiformes	<i>Clupea harengus</i>	NC_009577.1
Clupeiformes	<i>Sardina pilchardus</i>	NC_009592.1
Clupeiformes	<i>Pellona flavipinnis</i>	NC_014268.1
Clupeiformes	<i>Ilisha elongata</i>	NC_009585.1
Clupeiformes	<i>Ilisha africana</i>	NC_009584.1
Clupeiformes	<i>Etrumeus teres</i>	NC_009583.1
Clupeiformes	<i>Sundasalanx mekongensis</i>	NC_006919.1
Clupeiformes	<i>Spratelloides gracilis</i>	NC_009589.1
Clupeiformes	<i>Spratelloides delicatulus</i>	NC_009588.1
Clupeiformes	<i>Jenkinsia lamprotaenia</i>	NC_006917.1
Clupeiformes	<i>Dussumieria elopsoidea</i>	NC_035063.1
Clupeiformes	<i>Chirocentrus dorab</i>	NC_006913.1
Clupeiformes	<i>Jenkinsia sp.</i>	NC_015076.1

Supplementary Table 2 - Random site analysis of the protein coding mitochondrial genes of South American dataset. Np, number of paramteres; k is the kappa estimate; df is degrees of freedom; p is the p-value using chi distribution; AIC is the Akaike Information Criterion; ns, non-significant

Gene	Complex	Model	np	ln L	κ	Parameters ^a			Null	LRT	df	p	AIC
						ω_0 (Perco) or p	ω_1 (prop ₁) or q	ω_2 (prop ₂) or ω_p					
ND1	I	M0	189	-30657.79865	5.1857	0.02317							61693.5973
		M1a	190	-30614.65322	5.04242	0.02261 (99.0%)	1.0000 (1.0%)						61609.30644
		M2a	192	-30614.65322	5.04241	0.02261 (99.0%)	1.0000 (0.4%)	1.0000 (0.6%)	M1a	0	2	1	61613.30644
		M3	193	-29654.69242	5.24566	0.00170 (58.6%)	0.02769 (30.0%)	0.12430 (11.3%)	M0	2006.212464	4	0	59695.38484
									M2a	1919.921604	1	0	
		M7	190	-29631.76332	5.24249	p = 0.25404	q = 8.72239						59643.52664
		M8	192	-29631.76636	5.24257	p = 0.25404	q = 8.72244	1.0000 (0%)	M7	-0.00608	2	ns	59647.53272
0													
ND2	I	M0	189	-39056.80908	4.46779	0.05068							78491.61815
		M1a	190	-38684.10183	4.61345	0.04648 (94.6%)	1.0000 (5.4%)						77748.20366
		M2a	192	-38684.10183	4.61328	0.04648 (94.6%)	1.0000 (5.4%)	17.94018 (0%)	M1a	0	2	1	77752.20366
		M3	193	-37444.4727	4.71766	0.00530 (49.8%)	0.06028 (36.6%)	0.21272 (13.6%)	M0	3224.672758	4	0	75274.94539
									M2a	2479.258264	1	0	
		M7	190	-37350.29501	4.76955	p = 0.37732	q = 4.89105						75080.59002
		M8	192	-37350.29828	4.76956	p = 0.37732	q = 4.89094	1.00000 (0%)	M7	-0.006548	2	ns	75084.59657
0													
ND3	I	M0	189	-12713.01323	4.22514	0.04684							25804.02646
		M1a	190	-12473.69538	4.13086	0.02991 (86.7%)	1.0000 (13.3%)						25327.39077
		M2a	192	-12473.69538	4.13086	0.02991 (86.7%)	1.0000 (0.2%)	1.0000 (13.1%)	M1a	0	2	1	25331.39077
		M3	193	-12053.18052	4.351	0.00514 (69.0%)	0.07732 (17.7%)	0.26694 (13.3%)	M0	1319.66542	4	0	24492.36104
									M2a	841.029726	1	0	
		M7	190	-12038.6984	4.48102	p = 0.23018	q = 2.78520						24457.39681
		M8	192	-12038.69953	4.48102	p = 0.23018	q = 2.78521	1.79134 (0%)	M7	-0.00226	2	ns	24461.39907
0													
ND4	I	M0	189	-47682.46601	4.30728	0.03463							95742.93202
		M1a	190	-47407.16812	4.37746	0.03139 (96.0%)	1.0000 (4.0%)						95194.33624
		M2a	192	-47407.16812	4.37747	0.03139 (96.0%)	1.0000 (0.2%)	1.0000 (3.8%)	M1a	0	2	1	95198.33624
		M3	193	-45895.14863	4.37496	0.00396 (64.5%)	0.05400 (23.4%)	0.18294 (12.1%)	M0	3574.634756	4	0	92176.29727
									M2a	3024.038972	1	0	
		M7	190	-45839.3084	4.39962	p = 0.26221	q = 4.90001						92058.61679
		M8	192	-45832.91643	4.42848	p = 0.27371	q = 5.90539	1.0000 (0.4%)	M7	12.783928	2	0.00167	92049.83286
0													
ND4L	I	M0	189	-9579.580687	5.37352	0.0323							19537.16137
		M1a	190	-9579.581667	5.37352	0.03230 (100%)	1.0000 (0%)						19539.16333
		M2a	192	-9579.580687	5.37352	0.0323 (100%)	1.0000 (0%)	1.0000 (0%)	M1a	0.00196	2	0.99902	19543.16137

ND5	I	M3	193	-9383.798437	5.41133	0.00650 (64.7%)	0.05454 (25.6%)	0.14571 (9.7%)	M0	391.5645	4	0	19153.59687
										M2a	391.5645	1	0
		M7	190	-9382.032981	5.40989	p = 0.41951	q = 11.14882	19144.06596					
		M8	192	-9382.03396	5.41001	p = 0.41954	q = 11.14995	1.0000 (0%)	M7	-0.001958	2	ns	19148.06792
		0											
		M0	189	-65760.79795	3.87461	0.04452	131899.5959						
		M1a	190	-65204.30578	4.05128	0.03936 (94.0%)	1.00000 (6.0%)	130788.6116					
		M2a	192	-65204.30578	4.05126	0.03936 (94.0%)	1.00000 (0.1%)	1.00000 (5.9%)	M1a	-2E-06	2	ns	130792.6116
		M3	193	-62985.44635	4.08736	0.00426 (56.3%)	0.05384 (29.5%)	0.20687 (14.2%)	M0	5550.70321	4	0	126356.8927
										M2a	4437.71887	1	0
ND6	I	M7	190	-62895.06542	4.13608	p = 0.31598	q = 4.71588	126170.1308					
		M8	192	-62895.06968	4.1361	p = 0.31599	q = 4.71627	1.00000 (0%)	M7	-0.008528	2	ns	126174.1394
		0											
		M0	189	-19173.44218	5.80276	0.04983	38724.88437						
		M1a	190	-19095.2088	6.39772	0.04788 (96.3%)	1.00000 (3.7%)	38570.41761					
		M2a	192	-19095.2088	6.39769	0.04788 (96.3%)	1.00000 (1.5%)	1.00000 (2.2%)	M1a	0	2	1	38574.41761
		M3	193	-18528.96331	6.49906	0.00554 (42.5%)	0.03793 (31.6%)	0.15813 (25.9%)	M0	1288.957754	4	0	37443.92661
										M2a	1132.490994	1	0
		M7	190	-18513.73709	6.66572	p = 0.49380	q = 7.43407	37407.47417					
		M8	192	-18513.73881	6.66574	p = 0.49380	q = 7.43407	1.00000 (0%)	M7	-0.00345	2	ns	37411.47762
Cytb	III	0											
		M0	189	-34464.69401	4.67992	0.02399	69307.38802						
		M1a	190	-34300.21571	4.35716	0.02219 (96.2%)	1.00000 (3.8%)	68980.43142					
		M2a	192	-34300.21571	4.35715	0.02219 (96.2%)	1.00000 (0.1%)	1.00000 (3.7%)	M1a	0	2	1	68984.43142
		M3	193	-32980.22552	4.73681	0.00162 (65.7%)	0.03495 (23.8%)	0.15708 (10.5%)	M0	2968.936976	4	0	66346.45105
										M2a	2639.980372	1	0
		M7	190	-32947.48439	4.72998	p = 0.18912	q = 5.63044	66274.96877					
		M8	192	-32947.4879	4.72996	p = 0.18912	q = 5.63042	1.00000 (0%)	M7	-0.00702	2	ns	66278.97579
COI	IV	0											
		M0	189	-41296.68133	4.24903	0.01182	82971.36266						
		M1a	190	-41211.62667	4.25935	0.01072/0.99411	1.0000/0.00589	82803.25334					
		M2a	192	-41211.62667	4.25934	0.01072 (99.4%)	1.0000 (0.1%)	1.0000 (0.5%)	M1a	0	2	1	82807.25334
		M3	193	-40696.86569	4.22563	0.00133 (77.8%)	0.02783 (17.4%)	0.04827 (12.2%)	M0	1199.631284	4	0	81779.73137
										M2a	1029.521966	1	0
		M7	190	-40705.03319	4.22743	p = 0.14750	q = 7.29379	81790.06638					
		M8	192	-40705.03821	4.22745	p = 0.14749	q = 7.29337	1.0000 (0%)	M7	-0.01004	2	ns	81794.07642
COII	IV	0											
		M0	189	-17711.72612	3.97043	0.02582	35801.45225						
		M1a	190	-17623.78921	3.97235	0.02288 (98.7%)	1.0000 (1.3%)	35627.57843					
		M2a	192	-17623.78921	3.97238	0.02288 (98.7%)	1.0000 (0.2%)	1.00000 (1.1%)	M1a	0	2	1	35631.57843
		M3	193	-17308.92809	3.95641	0.00522 (73.8%)	0.0583 (22.4%)	0.22433 (3.8%)	M0	805.596078	4	0	35003.85617
										M2a	629.722258	1	0

COIII	IV	M7	190	-17304.77943	3.95318	p = 0.25947	q = 6.01003						
		M8	192	-17295.82325	3.95485	p = 0.29636	q = 9.40877	1.0000 (0.4%)	M7	17.91236	2	0.00013	34975.64649
		0											
		M0	189	-21536.94963	3.97274	0.02199							43451.89926
		M1a	190	-21485.7016	3.97948	0.01897 (98.0%)	1.0000 (2.0%)						
		M2a	192	-21485.70159	3.98007	0.01897 (98.0%)	1.0000 (0.5%)	1.00000 (1.4%)	M1a	3.8E-05	2	0.99998	43355.40317
		M3	193	-21039.66195	3.97342	0.00488 (77.3%)	0.04708 (15.9%)	0.16379 (6.8%)	M0	994.575374	4	0	42465.32389
								M2a		892.07928	1	0	
		M7	190	-21056.21886	3.97343	p = 0.28454	q = 8.04947						
		M8	192	-21056.22139	3.97322	p = 0.28464	q = 8.05411	1.00001 (0%)	M7	-0.005064	2	ns	42496.44279
ATP6	V	0											
		M0	189	-24014.26324	4.43053	0.03661							48406.52647
		M1a	190	-23826.77997	4.56831	0.03318 (95.6%)	1.0000 (4.4%)						
		M2a	192	-23826.78258	4.59338	0.03306 (95.6%)	1.0000 (3.3%)	1.0000 (1.2%)	M1a	-0.005214	2	ns	48037.56516
		M3	193	-23247.85238	4.59212	0.00470 (60.7%)	0.06100 (31.7%)	0.23803 (7.6%)	M0	1532.821714	4	0	46881.70476
								M2a		1157.860398	1	0	
		M7	190	-23215.67119	4.54438	p = 0.27882	q = 4.48612						
		M8	192	-23218.42518	4.5358	p = 0.27256	q = 3.96319	1.0000 (0%)	M7	-5.507984	2	ns	46820.85037
ATP8	V	M0	189	-4751.951078	3.63263	0.11782							9881.902156
		M1a	190	-4696.529282	3.79772	0.10633 (88.1%)	1.00000 (11.9%)						
		M2a	192	-4696.529282	3.79772	0.10633 (88.1%)	1.00000 (10.9%)	1.00000 (1.0%)	M1a	0	2	1	9777.058564
		M3	193	-4583.717207	3.60262	0.01173 (37.8%)	0.13154 (49.5%)	0.43251 (12.6%)	M0	336.467742	4	0	9553.434414
								M2a		225.62415	1	0	
		M7	190	-4583.407345	3.61239	p = 0.56417	q = 3.92647						
		M8	192	-4583.407824	3.61239	p = 0.56417	q = 3.92647	1.15342 (0%)	M7	-0.000958	2	ns	9550.815648
		0											

Supplementary Table 3 - Likelihood ratio tests for random-sites models (PAML) of the mitochondrial protein-coding genes of African dataset. Np, number of paramteres; k is the kappa estimate; df is degrees of freedom; p is the p-value using chi distribution; AIC is the Akaike Information Criterion; ns, non-significant

Gene	Complex	Model	np	ln L	κ	Parameters ^a			Null	LRT	df	p	AIC
						ω_0 (<i>prop</i> ₀) or <i>p</i>	ω_1 (<i>prop</i> ₁) or <i>q</i>	ω_2 (<i>prop</i> ₂) or ω_p					
ND1	I	M0	213	-35224.04365	4.66396	0.02272							70874.08729
		M1a	214	-35169.84224	4.6958	0.02146 (98.1%)	1.0000 (1.9%)						70767.68447
		M2a	216	-35169.84224	4.6958	0.02146 (98.1%)	1.0000 (1.8%)	1.0000 (0.1%)	M1a	0	2	1	70771.68447
		M3	217	-34243.95583	4.69627	0.00156 (63.8%)	0.0361 (26.5%)	0.12897 (9.7%)	M0	1960.175636	4	0	68921.91166
									M2a	1851.772816	1	0	
		M7	214	-34227.03988	4.73417	p = 0.22572	q = 6.93456						68882.07977
		M8	216	-34227.04312	4.73417	p = 0.22572	q = 6.93457	1.0000 (0%)	M7	-0.00648	2	ns	68886.08625
0													
ND2	I	M0	213	-45412.11501	4.06095	0.05566							91250.23003
		M1a	214	-45251.7562	4.16148	0.05333 (95.8%)	1.0000 (4.2%)						90931.5124
		M2a	216	-45251.7562	4.16148	0.05333 (95.8%)	1.0000 (3.9%)	17.94018 (0.3%)	M1a	0	2	1	90935.5124
		M3	217	-43956.26871	4.19856	0.00436 (44.1%)	0.0513 (33.2%)	0.16454 (22.7%)	M0	2911.692608	4	0	88346.53742
									M2a	2590.974984	1	0	
		M7	214	-43872.68033	4.26169	p = 0.41017	q = 6.06572						88173.36066
		M8	216	-43872.6838	4.26169	p = 0.41017	q = 6.06571	1.00000 (0%)	M7	-0.006932	2	ns	88177.36759
0													
ND3	I	M0	213	-13773.41678	4.90619	0.03663							27972.83355
		M1a	214	-13693.80805	4.89356	0.03118 (91.4%)	1.0000 (8.6%)						27815.61611
		M2a	216	-13693.80805	4.89357	0.03118 (91.4%)	1.0000 (8.2%)	1.0000 (0.4%)	M1a	0	2	1	27819.61611
		M3	217	-13140.97914	5.17597	0.00238 (62.7%)	0.04671 (22.3%)	0.17576 (15.0%)	M0	1264.875264	4	0	26715.95829
									M2a	1105.657818	1	0	
		M7	214	-13126.57476	5.227	p = 0.22700	q = 5.38231						26681.14952
		M8	216	-13126.57592	5.227	p = 0.22700	q = 5.38230	1.0000 (0%)	M7	-0.00232	2	ns	26685.15184
0													
ND4	I	M0	213	-52822.0422	4.29891	0.03129							106070.0844
		M1a	214	-52566.3819	4.38911	0.02761 (96.7%)	1.0000 (3.3%)						105560.7638
		M2a	216	-52566.3819	4.3891	0.02761 (96.7%)	1.0000 (2.9%)	1.0000 (0.4%)	M1a	0	2	1	105564.7638
		M3	217	-51017.02916	4.42707	0.00263 (59.4%)	0.03703 (27.7%)	0.1561 (12.9%)	M0	3610.026074	4	0	102468.0583
									M2a	3098.70548	1	0	
		M7	214	-50955.98124	4.47306	p = 0.26478	q = 5.60178						102339.9625
		M8	216	-50955.98584	4.47307	p = 0.26478	q = 5.60180	1.0000 (0%)	M7	-0.0092	2	ns	102343.9717
0													
ND4L	I	M0	213	-10318.57133	5.53842	0.02898							21063.14266
		M1a	214	-10318.57231	5.53842	0.02898 (100.0%)	1.0000 (0%)						21065.14462
		M2a	216	-10317.45609	5.56808	0.02887 (100.0%)	1.0000 (0%)	999.000 (0%)	M1a	2.232444	2	0.32751	21066.91217
		M3	217	-10084.63541	5.87429	0.00394 (59.8%)	0.03912 (23.4%)	0.10277 (16.8%)	M0	467.871842	4	0	20603.27081

		M8	216	-18439.64995	4.38638	p = 0.27179	q = 14.59493	2.00239 (0%)	M7	-0.0046	2	ns	37311.2999
		0											
COIII	IV	M0	213	-22437.91077	4.26021	0.01656							45301.82154
		M1a	214	-22420.22949	4.26523	0.01529 (98.9%)	1.0000 (1.1%)						45268.45898
		M2a	216	-22420.22949	4.26523	0.01529 (98.9%)	1.0000 (0.5%)	1.00000 (0.6%)	M1a	0	2	1	45272.45898
		M3	217	-21853.32876	4.25283	0.00076 (75.0%)	0.03207 (15.3%)	0.12356 (9.7%)	M0	1169.164022	4	0	44140.65752
									M2a	1133.801462	1	0	
		M7	214	-21849.93925	4.24891	p = 0.13230	q = 5.59197						44127.8785
		M8	216	-21849.94186	4.24892	p = 0.13230	q = 5.59205	2.01136 (0%)	M7	-0.00522	2	ns	44131.88372
		0											
ATP6	V	M0	213	-25093.10846	4.60925	0.02334							50612.21692
		M1a	214	-25093.11073	4.60929	0.02334 (100.0%)	1.0000 (0%)						50614.22146
		M2a	216	-25093.10846	4.60925	0.02334 (100.0%)	1.0000 (0%)	1.0000 (0%)	M1a	0.00454	2	0.99773	50618.21692
		M3	217	-24549.57586	4.72297	0.00150 (50.7%)	0.02057 (30.7%)	0.08814 (18.6%)	M0	1087.065194	4	0	49533.15172
									M2a	1087.065194	1	0	
		M7	214	-24538.8149	4.76052	p = 0.33219	q = 11.77892						46811.34238
		M8	216	-24538.81717	4.76052	p = 0.33219	q = 11.77895	1.0000 (0%)	M7	-0.00454	2	ns	49509.63435
		0											
ATP8	V	M0	213	-5780.629912	4.77949	0.07771							11987.25982
		M1a	214	-5780.630462	4.77952	0.07771 (100.0%)	1.00000 (0%)						11989.26092
		M2a	216	-5780.629912	4.77949	0.07771 (100.0%)	1.00000 (0%)	1.00000 (0%)	M1a	0.0011	2	0.99945	11993.25982
		M3	217	-5621.925806	5.09675	0.00744 (39.6%)	0.07873 (34.8%)	0.19538 (25.5%)	M0	317.408212	4	0	11677.85161
									M2a	317.408212	1	0	
		M7	214	-5621.842447	5.1594	p = 0.58625	q = 7.68718						9546.81469
		M8	216	-5621.842997	5.1594	p = 0.58625	q = 7.68717	2.19493 (0%)	M7	-0.0011	2	ns	11675.68599
		0											

Supplementary Table 4 – Random-site likelihood ratio tests for random-sites models (PAML) of the independent clades. Gymn, Gymnotiformes only dataset; Charac, Characoidei only dataset; Morm, Mormyroidea only dataset; Clupe, Clupeiformes only dataset.

Gene	Model	np	ln L	κ	Parameters ^a			Null	LRT	df	p
					ω_0/p	ω_1/q	ω_2/ω_p				
Gymn ATP6	M0	16	-3641.42	2.77045	0.05357						
	M3	20	-3566.98	2.95321	0.00548 (58.4%)	0.11412 (35.9%)	0.28940 (5.8%)	M0	148.8767	4	0
Gymn ATP8	M0	16	-960.93	2.92573	0.22725						
	M3	20	-952.734	3.1314	0.06458 (41.1%)	0.39467 (25.7%)	0.39467 (33.3%)	M0	16.39274	4	0.00254
Gymn COI	M0	16	-6167.86	3.10002	0.0124						
	M3	20	-6125.31	3.03813	0.00001 (71.9%)	0.03004 (23.4%)	0.13497 (4.7%)	M0	85.09226	4	0
Gymn COII	M0	16	-3085.92	3.0664	0.04392						
	M3	20	-3052.26	3.07948	0.00000 (44.9%)	0.05812 (45.8%)	0.18327 (9.3%)	M0	67.31411	4	0
Gymn COIII	M0	16	-3211.12	3.08523	0.02842						
	M3	20	-3175	3.06573	0.00000 (65.3%)	0.07088 (31.0%)	0.24404 (3.7%)	M0	72.24241	4	0
Gymn CYTB	M0	16	-5180.29	3.70993	0.02629						
	M3	20	-5074.4	4.01799	0.00000 (40.7%)	0.01504 (40.8%)	0.11773 (18.4%)	M0	211.7719	4	0
Gymn ND1	M0	16	-4584.07	4.64259	0.03191						
	M3	20	-4504.76	4.98183	0.00000 (53.5%)	0.05606 (40.8%)	0.21714 (5.7%)	M0	158.6147	4	0
Gymn ND2	M0	16	-6072.52	2.6095	0.07852						
	M3	20	-5957.82	2.81775	0.01215 (51.4%)	0.12695 (40.3%)	0.29681 (8.3%)	M0	229.3847	4	0
Gymn ND3	M0	16	-1911.42	2.69619	0.06147						
	M3	20	-1847.85	3.06738	0.00000 (52.9%)	0.09290 (35.8%)	0.38500 (11.2%)	M0	127.143	4	0
Gymn ND4	M0	16	-7083.68	3.14867	0.04777						
	M3	20	-6911.27	3.44741	0.00143 (50.9%)	0.06622 (40.7%)	0.35446 (8.4%)	M0	344.816	4	0
Gymn ND4L	M0	16	-1483.89	5.88689	0.03169						
	M3	20	-1463.42	6.28033	0.00844 (74.7%)	0.10413 (10.6%)	0.10413 (14.8%)	M0	40.93118	4	0
Gymn ND5	M0	16	-9121.84	2.94278	0.04743						
	M3	20	-8865.62	3.15319	0.00590 (62.5%)	0.08244 (28.1%)	0.37209 (9.4%)	M0	512.4464	4	0
Gymn ND6	M0	16	-2787.93	3.32951	0.04899						
	M3	20	-2728.03	4.17696	0.00578 (47.7%)	0.05589 (38.3%)	0.25631 (14.1%)	M0	119.8003	4	0
Charac ATP6	M0	29	-5798.06	2.99678	0.04027						
	M3	33	-5667.81	2.99309	0.00491 (58.2%)	0.05706 (29.3%)	0.28940 (5.8%)	M0	260.5005	4	0
Charac ATP8	M0	29	-1442.11	3.69051	0.10061						
	M3	33	-1407.25	3.67211	0.01396 (42.5%)	0.10019 (24.6%)	0.22728 (32.9%)	M0	69.71498	4	0
Charac COI	M0	29	-9942.78	3.67161	0.01213						
	M3	33	-9802.6	3.63449	0.00064 (84.5%)	0.05180 (12.5%)	0.19125 (3.1%)	M0	280.3627	4	0
Charac COII	M0	29	-4446.27	3.74345	0.02661						
	M3	33	-4377.31	3.69873	0.00597 (79.5%)	0.09907 (19.3%)	0.34893 (1.2%)	M0	137.9079	4	0
Charac	M0	29	-5206.77	2.94498	0.01674						

COIII	M3	33	-5169.95	3.00346	0.00599 (80.0%)	0.05377 (19.5%)	0.38437 (0.5%)	M0	73.62768	4	0
	M0	29	-7909.7	3.52718	0.02534						
Charac CYTB	M3	33	-7621.84	3.59699	0.00165 (71.5%)	0.05394 (22.3%)	0.26642 (6.3%)	M0	575.7063	4	0
	M0	29	-7168.14	4.58791	0.02091						
Charac ND1	M3	33	-6994.24	4.56179	0.00317 (75.5%)	0.06026 (19.5%)	0.16816 (5.0%)	M0	347.7908	4	0
	M0	29	-10098.8	2.80312	0.06596						
Charac ND2	M3	33	-9764.78	2.88207	0.00297 (38.4%)	0.05580 (38.5%)	0.21542 (23.0%)	M0	667.9682	4	0
	M0	29	-2835.36	3.56083	0.04267						
Charac ND3	M3	33	-2734.91	3.59353	0.00094 (60.2%)	0.05947 (29.0%)	0.29632 (10.8%)	M0	200.9025	4	0
	M0	29	-11146.9	3.44173	0.03633						
Charac ND4	M3	33	-10821	3.55098	0.00364 (67.6%)	0.07591 (25.1%)	0.26059 (7.3%)	M0	651.8642	4	0
	M0	29	-2340.34	5.86618	0.03797						
Charac ND4L	M3	33	-2295.43	5.96939	0.00540 (67.4%)	0.08876 (30.1%)	0.34320 (2.5%)	M0	89.81815	4	0
	M0	29	-15446.9	2.67729	0.04274						
Charac ND5	M3	33	-14928.9	2.88888	0.00320 (53.4%)	0.04762 (36.9%)	0.28052 (9.7%)	M0	1036.078	4	0
	M0	29	-4969.27	3.32299	0.05629						
Charac ND6	M3	33	-4769.2	4.10706	0.00218 (41.1%)	0.06807 (42.3%)	0.21191 (16.6%)	M0	400.1426	4	0
Morm ATP6	M0	55	-7188.76	6.52273	0.02745						
	M3	59	-7050.75	7.05078	0.0433 (71.0%)	0.07008 (25.3%)	0.24159 (3.7%)	M0	276.0278	4	0
Morm ATP8	M0	55	-1812.72	6.39377	0.09484						
	M3	59	-1758.87	7.88508	0.00919 (47.9%)	0.13155 (41.3%)	0.41545 (10.8%)	M0	107.6871	4	0
Morm COI	M0	55	-12982.2	5.4923	0.00823						
	M3	59	-12860	5.54809	0.00000 (77.3%)	0.02533 (21.0%)	0.19026 (1.6%)	M0	244.4144	4	0
Morm COII	M0	55	-5339.79	6.53611	0.01509						
	M3	59	-5276.26	6.60956	0.00000 (51.9%)	0.01651 (40.1%)	0.11734 (8.0%)	M0	127.0529	4	0
Morm COIII	M0	55	-6535.79	5.36063	0.02096						
	M3	59	-6344.97	5.41863	0.00000 (78.5%)	0.07933 (18.7%)	0.32431 (2.8%)	M0	381.6354	4	0
Morm CYTB	M0	55	-10366.5	6.39386	0.01883						
	M3	59	-10093	6.53981	0.00000 (61.7%)	0.02284 (27.6%)	0.12325 (10.6%)	M0	547.0882	4	0
Morm ND1	M0	55	-9371.54	5.91441	0.01669						
	M3	59	-9191.92	6.17638	0.00000 (53.5%)	0.01627 (30.8%)	0.07742 (15.7%)	M0	359.2413	4	0
Morm ND2	M0	55	-11321.4	5.26914	0.04807						
	M3	59	-10985.5	5.54386	0.00403 (56.8%)	0.07811 (37.0%)	0.31273 (6.2%)	M0	671.9298	4	0
Morm ND3	M0	55	-3909.48	6.66134	0.03458						
	M3	59	-3766.68	7.3023	0.00000 (47.5%)	0.02188 (35.2%)	0.17196 (17.3%)	M0	285.5845	4	0
Morm ND4	M0	55	-14590.8	6.06355	0.03122						
	M3	59	-14140.4	6.39522	0.00244 (65.3%)	0.04918 (26.5%)	0.25728 (8.2%)	M0	900.6552	4	0
Morm ND4L	M0	55	-2882.78	6.92015	0.02048						
	M3	59	-2844.4	7.36025	0.00000 (42.3%)	0.01976 (50.6%)	0.16517 (7.2%)	M0	76.75393	4	0
Morm ND5	M0	55	-18415.1	5.72727	0.03042						
	M3	59	-17851.4	6.03656	0.00200 (65.2%)	0.06842 (30.8%)	0.24786 (4.0%)	M0	1127.396	4	0
Morm ND6	M0	55	-5397.21	7.25336	0.04615						
	M3	59	-5248.21	8.68757	0.00514 (57.6%)	0.08052 (38.6%)	0.53480 (3.8%)	M0	297.9879	4	0

	M0	115	-14770.8	4.2861	0.0192						
Clupei ATP6	M3	119	-14494.2	4.34603	0.00004 (49.2%)	0.01536 (35.8%)	0.09203 (15.0%)	M0	553.1381	4	0
	M0	115	-3072.08	4.38044	0.05136						
Clupei ATP8	M3	119	-3002.45	4.44387	0.00824 (59.2%)	0.10556 (37.8%)	0.22893 (3.0%)	M0	139.2567	4	0
	M0	115	-25579.2	3.94091	0.00638						
Clupei COI	M3	119	-25430.7	3.92246	0.00113 (85.8%)	0.02763 (13.1%)	0.14658 (1.1%)	M0	297.0871	4	0
	M0	115	-11130.6	3.88962	0.01276						
Clupei COII	M3	119	-10997.3	3.86601	0.00294 (83.6%)	0.05563 (15.9%)	0.36160 (0.4%)	M0	266.6692	4	0
	M0	115	-13454.6	4.34276	0.01131						
Clupei COIII	M3	119	-13168.5	4.38325	0.00099 (86.0%)	0.05229 (11.1%)	0.19843 (2.9%)	M0	572.191	4	0
	M0	115	-22090.2	3.74164	0.01483						
Clupei CYTB	M3	119	-21639	3.73096	0.00110 (75.0%)	0.02993 (18.1%)	0.13314 (6.8%)	M0	902.2545	4	0
	M0	115	-21478.7	5.59896	0.0162						
Clupei ND1	M3	119	-20990.3	5.70695	0.00165 (72.8%)	0.03598 (21.4%)	0.12598 (5.9%)	M0	976.7363	4	0
	M0	115	-28437.5	4.20765	0.04806						
Clupei ND2	M3	119	-27556.2	4.51347	0.00457 (49.7%)	0.05838 (39.2%)	0.21535 (11.0%)	M0	1762.644	4	0
	M0	115	-8141.29	4.98023	0.03067						
Clupei ND3	M3	119	-7791.77	5.37017	0.00114 (66.0%)	0.05355 (22.4%)	0.17241 (11.6%)	M0	699.0489	4	0
	M0	115	-31874.5	4.29799	0.02531						
Clupei ND4	M3	119	-30848.8	4.524	0.00146 (62.6%)	0.02962 (26.6%)	0.14542 (11.2%)	M0	2051.381	4	0
	M0	115	-6198.73	5.39936	0.03153						
Clupei ND4L	M3	119	-6086.66	5.6652	0.00006 (31.3%)	0.01470 (36.2%)	0.07879 (32.5%)	M0	224.1264	4	0
	M0	115	-40347.2	4.36211	0.02526						
Clupei ND5	M3	119	-38957.3	4.55562	0.00158 (64.8%)	0.03823 (26.2%)	0.17005 (9.0%)	M0	2779.812	4	0
	M0	115	-15892.1	4.30808	0.06107						
Clupei ND6	M3	119	-15420.2	4.80591	0.00534 (30.3%)	0.03690 (35.6%)	0.14467 (34.1%)	M0	943.8119	4	0

Supplementary Table 5 - Clade model analyses of the South American dataset. Np, number of parameters; LRT is likelihood ratio test; p is the p-value of significance; ns denotes those with negative LRTs. Foreground omega estimates labelled F, and background estimates labelled B.

Gene	Complex	Model	np	ln L	κ	Parameters ^b			Null	LRT	df	p
						ω_0	ω_1	ω_2/ω_4				
<u>ND1</u>	I	M2a_rel	192	-29788.47877	5.23087	0.09171 (19.8%)	1.0000 (0%)	0.00648 (80.2%)				
		CmC_Alt	193	-29788.43056	5.22811	0.00649 (80.2%)	1.0000 (0%)	0.09135 (19.8%)	M2a_rel	0.10	1	0.756
								F: 0.09497				
		M3	193	-29654.69242	5.24566	0.00170 (58.6%)	0.02769 (30.0%)	0.12430 (11.3%)	M2a_rel	267.57	1	0.000
		CmD_Alt	194	-29654.69204	5.24585	0.02769 (30.0%)	0.00170 (58.6%)	B: 0.12435 (11.3%)	M3	0.00	1	0.978
								F: 0.12386				
<u>ND2</u>	I	M2a_rel	192	-37647.16431	4.58039	0.10606 (39.3%)	1.0000 (2.4%)	0.00989 (58.3%)				
		CmC_Alt	193	-37632.03531	4.58299	0.11973 (34.1%)	1.00000 (2.4%)	B: 0.01091 (63.5%)	M2a_rel	30.26	1	0.000
								F: 0.02339				
		M3	193	-37444.4727	4.71766	0.00530 (49.8%)	0.06028 (36.6%)	0.21272 (13.6%)	M2a_rel	405.38	1	0.000
		CmD_Alt	194	-37435.19616	4.6614	0.00531 (49.0%)	0.20346 (15.6%)	B: 0.05400 (35.3%)	M3	18.55	1	0.000
								F: 0.08892				
<u>ND3</u>	I	M2a_rel	192	-12121.08627	4.26827	0.16158 (27.1%)	1.0000 (0.7%)	0.00671 (72.2%)				
		CmC_Alt	193	-12120.53711	4.25529	0.00684 (72.2%)	1.00000 (0.8%)	B: 0.15884 (27.0%)	M2a_rel	1.10	1	0.295
								F: 0.19197				
		M3	193	-12053.18052	4.351	0.00514 (69.0%)	0.07732 (17.7%)	0.26694 (13.3%)	M2a_rel	135.81	1	0.000
		CmD_Alt	194	-12051.76689	4.33813	0.00518 (68.8%)	0.26942 (13.2%)	B: 0.07293 (17.9%)	M3	2.83	1	0.093
								F: 0.10371				
<u>ND4</u>	I	M2a_rel	192	-46044.18884	4.41331	0.10731 (28.0%)	1.0000 (0.5%)	0.00631 (71.5%)				
		CmC_Alt	193	-46041.99601	4.40111	0.00638 (71.4%)	1.0000 (0.5%)	B: 0.10473 (28.0%)	M2a_rel	4.39	1	0.036
								F: 0.12775				
		M3	193	-45895.14863	4.37496	0.00396 (64.5%)	0.05400 (23.4%)	0.18294 (12.1%)	M2a_rel	298.08	1	0.000
		CmD_Alt	194	-45894.75161	4.35193	0.05492 (23.5%)	0.00401 (64.6%)	B: 0.18254 (11.9%)	M3	0.79	1	0.373
								F: 0.20276				
<u>ND4L</u>	I	M2a_rel	192	-9399.676672	5.39418	0.00790 (69.7%)	1.0000 (0%)	0.08782 (30.3%)				
		CmC_Alt	193	-9399.665489	5.39032	0.00792 (69.7%)	1.0000 (0%)	B: 0.08746 (30.3%)	M2a_rel	0.02	1	0.881
								F: 0.09027				
		M3	193	-9383.798437	5.41133	0.00650 (64.7%)	0.05454 (25.6%)	0.14571 (9.7%)	M2a_rel	31.76	1	0.000
		CmD_Alt	194	-9383.266763	5.40507	0.00652 (65.1%)	0.05528 (25.5%)	B: 0.15421 (9.3%)	M3	1.06	1	0.302
								F: 0.11397				
<u>ND5</u>	I	M2a_rel	192	-63341.12628	4.10121	0.11727 (32.7%)	1.0000 (1.1%)	0.0082 (66.1%)				
		CmC_Alt	193	-63340.84953	4.09677	0.00823 (66.1%)	1.00000 (1.1%)	B: 0.1166 (32.7%)	M2a_rel	0.55	1	0.457
								F: 0.12364				
		M3	193	-62985.44635	4.08736	0.00426 (56.3%)	0.05384 (29.5%)	0.20687 (14.2%)	M2a_rel	711.36	1	0.000
		CmD_Alt	194	-63198.08393	4.04675	0.00702 (63.0%)	0.50000 (4.6%)	B: 0.09786 (32.4%)	M3	-425.28	1	#NUM!
								F: 0.13536				
<u>ND6</u>	I	M2a_rel	192	-18592.85375	6.74474	0.13064 (33.5%)	1.0000 (0.9%)	0.01403 (65.5%)				

			CmC_Alt	193	-18592.84114	6.74598	0.01403 (65.6%)	1.0000 (0.9%)	B: 0.1307 (33.5%)	M2a_rel	0.03	1	0.874
			F: 0.11552										
			M3	193	-18528.96331	6.49906	0.00554 (42.5%)	0.03793 (31.6%)	0.15813 (25.9%)	M2a_rel	127.78	1	0.000
			CmD_Alt	194	-18574.6769	6.91106	0.01377 (65.1%)	0.50000 (2.8%)	B: 0.12202 (32.1%)	M3	-91.43	1	#NUM!
			F: 0.11973										
	CYTB	III	M2a_rel	192	-33172.21124	4.72806	0.10446 (20.4%)	1.0000 (0%)	0.00500 (79.6%)				
			CmC_Alt	193	-33169.50293	4.76485	0.00507 (80.1%)	1.0000 (0%)	B: 0.10935 (19.9%)	M2a_rel	5.42	1	0.020
			F: 0.08110										
			M3	193	-32980.22552	4.73681	0.00162 (65.7%)	0.03495 (23.8%)	0.15708 (10.5%)	M2a_rel	383.97	1	0.000
			CmD_Alt	194	-34834.90037	4.71921	0.03447 (24.4%)	0.15724 (10.6%)	B: 0.00107 (65.0%)	M3	-3709.35	1	#NUM!
			F: 0.00378										
	COI	IV	M2a_rel	192	-40751.73338	4.22016	0.06333 (13.8%)	1.0000 (0.2%)	0.00265 (86.0%)				
			CmC_Alt	193	-40749.96187	4.21119	0.00265 (86.0%)	1.0000 (0.2%)	B: 0.06069 (13.9%)	M2a_rel	3.54	1	0.060
			F: 0.07847										
			M3	193	-40696.86569	4.22563	0.00133 (77.8%)	0.02783 (17.4%)	0.04827 (12.2%)	M2a_rel	-109.74	1	#NUM!
			CmD_Alt	194	-40696.86464	4.22557	0.00133 (77.8%)	0.02784 (17.4%)	B: 0.1225 (4.8%)	M3	0.00	1	0.964
			F: 0.12149										
	COII	IV	M2a_rel	192	-17332.87637	3.93379	0.08417 (21.9%)	1.0000 (0.4%)	0.00633 (77.6%)				
			CmC_Alt	193	-17331.17535	3.92931	0.00646 (77.4%)	1.0000 (0.4%)	B: 0.08003 (22.2%)	M2a_rel	3.40	1	0.065
			F: 0.10719										
			M3	193	-17308.92809	3.95641	0.00522 (73.8%)	0.05832 (22.4%)	0.22433 (3.8%)	M2a_rel	47.90	1	0.000
			CmD_Alt	194	-17303.2793	3.94545	0.00522 (72.2%)	0.22573 (3.9%)	B: 0.05037 (23.9%)	M3	11.30	1	0.001
			F: 0.09212										
	COIII	IV	M2a_rel	192	-21086.51885	3.94968	0.10026 (16.7%)	1.0000 (0%)	0.00661 (83.3%)				
			CmC_Alt	193	-21083.34997	3.9417	0.00653 (83.0%)	1.0000/0%	B: 0.09413 (17.0%)	M2a_rel	6.34	1	0.012
			F: 0.13763										
			M3	193	-21039.66195	3.97342	0.00488 (77.3%)	0.04708 (15.9%)	0.16379 (6.8%)	M2a_rel	93.71	1	0.000
			CmD_Alt	194	-21039.45949	3.97137	0.00485 (77.1%)	0.04623 (15.8%)	B: 0.15922 (7.1%)	M3	0.40	1	0.525
			F: 0.17991										
	ATP6	V	M2a_rel	192	-23367.26063	4.41468	0.0962 (32.7%)	1.0000 (1.3%)	0.00679 (66.0%)				
			CmC_Alt	193	-23360.61019	4.39782	0.00689 (65.7%)	1.000 (1.3%)	B: 0.09033 (32.9%)	M2a_rel	13.30	1	0.000
			F: 0.14265										
			M3	193	-23247.85238	4.59212	0.00470 (60.7%)	0.06100 (31.7%)	0.23803 (7.6%)	M2a_rel	238.82	1	0.000
			CmD_Alt	194	-23234.22358	4.54349	0.00444 (59.0%)	0.22564 (8.8%)	B: 0.05077 (32.3%)	M3	27.26	1	0.000
			F: 0.10499										
	ATP8	V	M2a_rel	192	-4612.110298	3.64021	0.01508 (38.1%)	1.0000 (10.3%)	0.17179 (51.6%)				
			CmC_Alt	193	-4609.379669	3.61657	0.01516 (37.6%)	1.0000 (10.4%)	B: 0.1598 (52.0%)	M2a_rel	5.46	1	0.019
			F: 0.27603										
			M3	193	-4583.717207	3.60262	0.01173 (37.8%)	0.13154 (49.5%)	0.43251 (12.6%)	M2a_rel	56.79	1	0.000
			CmD_Alt	194	-4581.970191	3.59987	0.01202 (37.5%)	0.44103 (12.8%)	B: 0.12454 (49.7%)	M3	3.49	1	0.062
			F: 0.19799										

Supplementary Table 6 - Clade model analyses of the African dataset. Np, number of parameters; LRT is likelihood ratio test; p is the p-value of significance; ns denotes those with negative LRTs. Foreground omega estimates labelled F, and background estimates labelled B.

Gene	Complex	Model	np	ln L	α	Parameters ^b			Null	LRT	df	p
						ω_0	ω_1	ω_2/ω_4				
<u>ND1</u>	I	M2a_rel	216	-34370.0585	4.66	0.00309 (70.6%)	1.000 (0.0%)	0.06966 (29.4%)				
		CmC_Alt	217	-34369.1683	4.67	0.00307 (70.6%)	1.000 (0.0%)	B: 0.06794 (29.4%)	M2a_rel	1.78	1	0.182
								F: 0.07825				
		M3	217	-34243.9558	4.7	0.00156 (63.8%)	0.03610 (26.5%)	0.12897 (9.7%)	M2a_rel	252.21	1	0.000
		CmD_Alt	218	-34243.9305	4.7	0.00156 (63.8%)	0.03610 (26.5%)	B: 0.12953 (9.7%)	M3	0.05	1	0.822
								F: 0.12556				
<u>ND2</u>	I	M2a_rel	216	-44151.4153	4.11	0.01044 (56.7%)	1.000 (0.9%)	0.11146 (42.5%)				
		CmC_Alt	217	-44138.0783	4.13	0.01018 (56.9%)	1.000 (0.8%)	B: 0.10272 (42.2%)	M2a_rel	26.67	1	0.000
								F: 0.15086				
		M3	217	-43956.2687	4.2	0.00436 (44.1%)	0.05130 (33.2%)	0.16454 (22.7%)	M2a_rel	390.29	1	0.000
		CmD_Alt	218	-43943.1118	4.2	0.04575 (32.0%)	0.00382 (42.9%)	B: 0.14238 (25.1%)	M3	26.31	1	0.000
								F: 0.22230				
<u>ND3</u>	I	M2a_rel	216	-13207.2859	5.1	0.00572 (73.5%)	1.000 (0.0%)	0.12212 (26.5%)				
		CmC_Alt	217	-13693.8081	4.89	0.03118 (91.4%)	1.000 (8.6%)	B: 10.68443 (0.0%)	M2a_rel	-973.04	1	ns
								F: 0.00002				
		M3	217	-13140.9791	5.18	0.00238 (62.7%)	0.04671 (22.3%)	0.17576 (15.0%)	M2a_rel	132.61	1	0.000
		CmD_Alt	218	-13137.0617	5.2	0.00233 (62.8%)	0.04622 (22.4%)	B: 0.16031 (14.8%)	M3	7.83	1	0.005
								F: 0.24977				
<u>ND4</u>	I	M2a_rel	216	-51254.3201	4.45	0.09588 (26.4%)	1.000 (0.8%)	0.00659 (73.1%)				
		CmC_Alt	217	-51251.5534	4.46	0.09523 (26.1%)	1.000 (8.5%)	B: 0.00622 (73.1%)	M2a_rel	5.53	1	0.019
								F: 0.00895				
		M3	217	-51017.0292	4.43	0.00263 (59.4%)	0.03703 (27.7%)	0.1561 (12.9%)	M2a_rel	474.58	1	0.000
		CmD_Alt	218	-51001.1352	4.44	0.03600 (27.7%)	0.00255 (59.3%)	B: 0.14047 (13.0%)	M3	31.79	1	0.000
								F: 0.23149				
<u>ND4L</u>	I	M2a_rel	216	-10100.4371	5.79	0.07236 (35.1%)	1.000 (0.0%)	0.00528 (64.9%)				
		CmC_Alt	217	-10100.2584	5.77	0.00532 (64.8%)	1.000 (0.0%)	B: 0.07394 (35.2%)	M2a_rel	0.36	1	0.550
								F: 0.06590				
		M3	217	-10084.6354	5.87	0.00394 (59.8%)	0.03912 (23.4%)	0.10277 (16.8%)	M2a_rel	31.60	1	0.000
		CmD_Alt	218	-10085.5467	5.91	0.04222 (24.6%)	0.00405 (60.8%)	B: 0.10300 (14.6%)	M3	-1.82	1	ns
								F: 0.12959				
<u>ND5</u>	I	M2a_rel	216	-65535.7445	4.21	0.00543 (68.5%)	1.000 (0.2%)	0.09203 (31.3%)				
		CmC_Alt	217	-65526.7727	4.23	0.09312 (30.5%)	1.000 (0.1%)	B: 0.00515 (69.4%)	M2a_rel	17.94	1	0.000
								F: 0.00979				
		M3	217	-65172.0891	4.25	0.00219 (57.6%)	0.04133 (29.6%)	0.15643 (12.8%)	M2a_rel	727.31	1	0.000
		CmD_Alt	218	-65161.3735	4.26	0.00250 (59.4%)	0.16096 (11.8%)	B: 0.03940 (28.8%)	M3	21.43	1	0.000
								F: 0.10000				
<u>ND6</u>	I	M2a_rel	216	-23694.0201	5.12	0.01333 (52.3%)	1.000 (0.6%)	0.11560 (47.1%)				
		CmC_Alt	217	-23688.379	5.18	0.01245 (53.1%)	1.000 (0.0%)	B: 0.10546 (46.9%)	M2a_rel	11.28	1	0.001
								F: 0.16257				

		M3	217	-23604.4616	5.19	0.00708 (39.4%)	0.05304 (33.9%)	0.15809 (26.7%)	M2a_rel	179.12	1	0.000
		CmD_Alt	218	-23599.5726	5.26	0.00555 (35.8%)	0.03979 (30.0%)	B: 0.13002 (34.2%)	M3	9.78	1	0.002
								F: 0.18978				
<u>CYTb</u>	III	M2a_rel	216	-36166.0594	4.06	0.043 (89.6%)	1.000 (9.2%)	11.58 (1.3%)				
		CmC_Alt	217	-36149.9979	4.08	0.00212 (73.1%)	1.000 (0.0%)	B: 0.06083 (26.9%)	M2a_rel	32.12	1	ns
								F: 0.10361				
		M3	217	-36027.1288	4.06	0.00133 (68.3%)	0.03604 (23.5%)	0.13721 (8.2%)	M2a_rel	277.86	1	ns
		CmD_Alt	218	-36021.2876	4.06	0.00129 (68.1%)	0.03485 (23.3%)	B: 0.12255 (8.6%)	M3	11.68	1	0.001
								F: 0.18943				
<u>COI</u>	IV	M2a_rel	216	-42725.4024	3.93	0.04528 (14.2%)	1.000 (0.0%)	0.00141 (85.8%)				
		CmC_Alt	217	-42723.7671	3.94	0.04135 (14.7%)	1.000 (0.2%)	B: 0.00128 (85.1%)	M2a_rel	3.27	1	0.071
								F: 0.00152				
		M3	217	-42676.5046	3.94	0.00103 (82.8%)	0.03155 (16.0%)	0.17090 (1.2%)	M2a_rel	-97.80	1	ns
		CmD_Alt	218	-42682.2558	3.95	0.00103 (82.8%)	0.03141 (16.0%)	B: 0.14969 (1.2%)	M3	-11.50	1	ns
								F: 0.10000				
<u>COII</u>	IV	M2a_rel	216	-18462.2046	4.38	0.00352 (76.8%)	1.000 (9.2%)	0.05442 (23.2%)				
		CmC_Alt	217	-18461.0142	4.37	0.05452 (23.2%)	1.000 (0%)	B: 0.00379 (76.8%)	M2a_rel	2.38	1	0.123
								F: 0.00166				
		M3	217	-18441.5746	4.39	0.00166 (65.2%)	0.02525 (25.7%)	0.08520 (9.1%)	M2a_rel	41.26	1	0.000
		CmD_Alt	218	-18440.0775	4.4	0.00176 (66.2%)	0.02645 (25.3%)	B: 0.08105 (8.6%)	M3	2.99	1	0.084
								F: 0.12370				
<u>COIII</u>	IV	M2a_rel	216	-21891.3842	4.24	0.00208 (82.3%)	1.000 (0.0%)	0.08767 (17.7%)				
		CmC_Alt	217	-21882.7078	4.26	0.00199 (82.1%)	1.000 (0.00%)	B: 0.07767 (17.9%)	M2a_rel	17.35	1	0.000
								F: 0.13465				
		M3	217	-21853.3288	4.25	0.00076 (75.0%)	0.03207 (15.3%)	0.12356 (9.7%)	M2a_rel	76.11	1	0.000
		CmD_Alt	218	-21845.2621	4.27	0.00072 (74.7%)	0.03031 (15.2%)	B: 0.10678 (10.1%)	M3	16.13	1	0.000
								F: 0.19590	CmD_Null			
<u>ATP6</u>	V	M2a_rel	216	-24606.5837	4.72	0.00519 (71.3%)	1.000 (0.0%)	0.06809 (28.7%)				
		CmC_Alt	217	-24600.3699	4.77	0.00497 (71.4%)	1.000 (0%)	B: 0.06155 (28.6%)	M2a_rel	12.43	1	0.000
								F: 0.09600				
		M3	217	-24549.5759	4.72	0.00150 (50.7%)	0.02057 (30.7%)	0.08814 (18.6%)	M2a_rel	114.02	1	0.000
		CmD_Alt	218	-24542.6725	4.77	0.00144 (50.8%)	0.01976 (30.6%)	B: 0.07885 (18.6%)	M3	13.81	1	0.000
								F: 0.13058				
<u>ATP8</u>	V	M2a_rel	216	-5640.89266	4.99	0.01351 (47.2%)	1.000 (0.0%)	0.13869 (52.8%)				
		CmC_Alt	217	-5639.86974	4.98	0.13895 (52.5%)	1.000 (0%)	B: 0.01213 (47.5%)	M2a_rel	2.05	1	0.153
								F: 0.02221				
		M3	217	-5621.92581	5.1	0.00744 (39.6%)	0.07873 (34.8%)	0.19538 (25.5%)	M2a_rel	37.93	1	0.000
		CmD_Alt	218	-5619.59673	5.14	0.00733 (39.8%)	0.07900 (36.0%)	B: 0.18027 (24.2%)	M3	4.66	1	0.031
								F: 0.28509				

Supplementary Table 7 – Expanded Genbank clade analyses of additional partial sequences obtained from Genbank. Np, number of parameters; LRT is likelihood ratio test; p is the p-value of significance; ns denotes those with negative LRTs. Foreground omega estimates labelled F, and background estimates labelled B.

Gene	Model	np	ln L	α	Parameters ^b			Null	LRT	df	p
					ω_0	ω_1	ω_2/ω_4				
ATP6	M2a_rel	71	-10944.89611	3.62388	0.00791 (65.2%)	1.000 (0.9%)	0.10799 (33.9%)				
	CmC_Alt	72	-10943.06098	3.66166	0.00770 (64.8%)	1.000 (0.9%)	B: 0.09375 (34.3%)	M2a_rel	3.67	1	0.055
							F: 0.12065				
	M3	72	-10917.01748	3.66519	0.00508 (58.1%)	0.06456 (31.9%)	0.20579 (10.0%)				
	CmD_Alt	73	-10916.90464	3.66029	0.06470 (31.9%)	0.00509 (58.1%)	0.21462 (10.0%)	M3	0.23	1	0.635
							F: 0.19873				
ATP8	M2a_rel	73	-2839.566908	3.66059	0.02857 (45.8%)	1.000 (0%)	0.22107 (54.2%)				
	CmC_Alt	74	-2839.343233	3.60244	0.13509 (94.7%)	1.000 (5.3%)	B: 3.09769 (0%)	M2a_rel	0.45	1	0.504
							F: 2.85524				
	M3	74	-2836.600443	3.65726	0.01514 (31.5%)	0.09304 (27.3%)	0.25107 (41.2%)				
	CmD_Alt	75	-2836.308657	3.64286	0.00907 (20.4%)	0.22802 (51.2%)	0.03686 (28.4%)	M3	0.58	1	0.445
							F: 0.06868				
CYTB	M2a_rel	322	-40302.89638	5.49634	0.08584 (24.8%)	1.000 (0.3%)	0.00364 (74.9%)				
	CmC_Alt	323	-40298.89971	5.56408	0.00355 (74.8%)	1.000 (0.3%)	B: 0.06971 (24.9%)	M2a_rel	7.99	1	0.005
							F: 0.08977				
	M3	323	-40172.15146	5.54111	0.00208 (68.0%)	0.03925 (21.5%)	0.14564 (10.5%)				
	CmD_Alt	324	-40172.10928	5.54776	0.00207 (67.9%)	0.03900 (21.5%)	B: 0.14153 (10.6%)	M3	0.08	1	0.771
							F: 0.14614				
COI	M2a_rel	270	-20309.04551	5.21197	0.04587 (14.1%)	1.000 (0%)	0.00153 (85.9%)				
	CmC_Alt	271	-20305.33006	5.2457	0.00148 (85.6%)	1.0000 (0%)	0.02974 (14.4%)	M2a_rel	7.43	1	0.006
							F: 0.05149				
	M3	271	-20305.03665	5.21529	0.00090 (79.0%)	0.01723 (12.7%)	0.05874 (8.3%)				
	CmD_Alt	272	-20298.71899	5.25523	0.02264 (12.2%)	0.00104 (81.3%)	0.02808 (6.5%)	M3	12.64	1	0.000
							F: 0.07906				

Supplementary Table 8 - Branch-site analyses of the branch leading to the ancestor of the African electric fish (Morm) and South American (Gymno). Np, number of parameters; LRT, likelihood ratio test; df, degrees of freedom. Positively-selected sites above posterior probability of 0.8 in each gene of concatenated matrix are shown with numbers corresponding to sites in the following reference crystal structures from PDB: 5LNK for complex I, 5XTE for complex III, 1OCC for complex IV, 6B8H for complex V.

Model	np	ln L	κ	Parameters ^b				Null	LRT	df	p	Positively-Selected Sites
				ω_0	ω_1	ω_{2a}	ω_{2b}					
BrS_Null_Morm	215	-408493.19	3.59855	B: 0.03281 (95.4%)	B: 1.000 (4.6%)	B: 0.03281 (0%)	B: 1.000 (0%)					
						F: 1.000	F: 1.000					
BrS_Alt_Morm	216	-408457.77	3.59684	0.03269 (93.4%)	B: 1.000 (4.5%)	B: 0.03269 (2.0%)	B: 1.00000 (0.1%)	BrS_Null	70.831996	1	0.000	ATP6: V199H; ATP8: L27I, T45L; COIII: L27T; CYTB: L363I; ND2: L97T, L326T; ND4: S405A, T427Q; ND5: M42W, T547L, M548A
						F: 11.95286	F: 11.95286					
BrS_Null_Gymno	191	-363749.11	3.50523	B: 0.03565 (89.3%)	B: 1.000 (4.9%)	B: 0.03565 (5.5%)	B: 1.000 (0.3%)					
						F: 1.000	F: 1.000					
BrS_Alt_Gymno	192	-363739.35	3.50623	B: 0.03573 (94.1%)	B: 1.000 (5.2%)	B: 0.03573 (0.6%)	B: 1.000 (0.04%)	BrS_Null	19.52475	1	0.000	COI: V366S; COIII: L95A; CYTB: L372Y; ND2: T278L, L326T; ND4: K43G, K84R; ND5: S345V, G433N, P568N
						F: 61.64676	F: 61.64676					

Supplementary Table 9 - Summary of clade model analyses of the South American and African dataset. Statistically significant tests are shown with '*'

Gene	Complex	South American		African	
		CmC vs M2aREL	CmD vs M3	CmC vs M2aREL	CmD vs M3
ND1	I				
ND2	I	*	*	*	*
ND3	I				*
ND4	I	*		*	*
ND4L	I				
ND5	I			*	*
ND6	I			*	*
CYTB	III	*		*	*
COI	IV				
COII	IV		*		
COIII	IV	*		*	*
ATP6	V	*	*	*	*
ATP8	V	*			*

Supplementary Table 10 - Branch-site analyses using individual gene matrices and testing the branch leading to the ancestor of the South American electric fish. Np, number of parameters; LRT, likelihood ratio test; df, degrees of freedom.

Gene	Model	np	ln L	α	Parameters ^b				Null	LRT	df	p
					ω_0	ω_1	ω_{2a}	ω_{2b}				
ATP6	BrS_Null	191	-23826.78	4.59328	B: 0.03306 (95.6%)	B: 1.000 (4.4%)	B: 0.03306 (0%)	B: 1.000 (0%)				
							F: 1.000	F: 1.000				
ATP6	BrS_Alt	192	-23826.78	4.59328	B: 0.03306 (95.6%)	B: 1.000 (4.4%)	B: 0.03306 (0%)	B: 1.00000 (0%)	BrS_Null	2.8E-05	1	0.996
							F: 1.00000	F: 108.41187				
ATP8	BrS_Null	191	-4696.53	3.79772	B: 0.10633 (88.1%)	B: 1.000 (11.9%)	B: 0.10633 (0%)	B: 1.000 (0%)				
							F: 1.000	F: 1.000				
ATP8	BrS_Alt	192	-4696.53	3.79772	B: 0.10633 (88.1%)	B: 1.000 (11.9%)	B: 0.10633 (0%)	B: 1.000 (0%)	BrS_Null	0	1	1.000
							F: 1.00000	F: 1.00000				
COI	BrS_Null	191	-41197.92	4.25486	B: 0.01050 (90.2%)	B: 1.000 (0.5%)	B: 0.01050 (9.2%)	B: 1.000 (0.1%)				
							F: 1.000	F: 1.000				
COI	BrS_Alt	192	-41197.88	4.25465	B: 0.01050 (92.2%)	B: 1.000 (0.5%)	B: 0.01050 (7.2%)	B: 1.000 (0%)	BrS_Null	0.077116	1	0.781
							F: 1.40703	F: 1.40703				
COII	BrS_Null	191	-17622.86	3.97206	B: 0.02267 (93.2%)	B: 1.000 (1.2%)	B: 0.02267 (5.5%)	B: 1.000 (0%)				
							F: 1.000	F: 1.000				
COII	BrS_Alt	192	-17622.86	3.97205	B: 0.02267 (93.2%)	B: 1.000 (1.2%)	B: 0.02267 (5.5%)	B: 1.000 (0.1%)	BrS_Null	0	1	1.000
							F: 1.00000	F: 1.00000				
COIII	BrS_Null	191	-21478.41	3.97406	B: 0.01870 (83.9%)	B: 1.000 (1.7%)	B: 0.01870 (14.1%)	B: 1.000 (0.3%)				
							F: 1.000	F: 1.000				
COIII	BrS_Alt	192	-21477.99	3.97279	B: 0.01869 (91.6%)	B: 1.000 (1.8%)	B: 0.01869 (6.5%)	B: 1.000 (0.1%)	BrS_Null	0.84216	1	0.359
							F: 4.20347	F: 4.20347				
CYTB	BrS_Null	191	-34300.22	4.35716	B: 0.02219 (96.2%)	B: 1.000 (3.8%)	B: 0.02219 (0%)	B: 1.000 (0%)				
							F: 1.000	F: 1.000				
CYTB	BrS_Alt	192	-34293.52	4.44565	B: 0.02230 (96.0%)	B: 1.000 (2.9%)	B: 0.02230 (1.1%)	B: 1.000 (0%)	BrS_Null	13.389232	1	0.000
							F: 69.61541	F: 69.61541				
ND1	BrS_Null	191	-30613.48	5.01921	B: 0.02253 (87.7%)	B: 1.000 (0.9%)	B: 0.02253 (11.3%)	B: 1.000 (0.1%)				
							F: 1.000	F: 1.000				
ND1	BrS_Alt	192	-30613.48	5.01903	B: 0.02253 (87.5%)	B: 1.000 (0.9%)	B: 0.02253 (11.5%)	B: 1.000 (0.1%)	BrS_Null	9.8E-05	1	0.992
							F: 1.00000	F: 1.00000				
ND2	BrS_Null	191	-39148.99	4.22958	B: 0.04963 (81.9%)	B: 1.000 (5.4%)	B: 0.04963 (11.9%)	B: 1.000 (0.8%)				
							F: 1.000	F: 1.000				
ND2	BrS_Alt	192	-39147.39	4.22443	B: 0.04960 (86.7%)	B: 1.000 (5.6%)	B: 0.04960 (7.2%)	B: 1.000 (0.5%)	BrS_Null	3.20105	1	0.074
							F: 4.51440	F: 4.51440				
ND3	BrS_Null	191	-12473.21	4.13106	B: 0.02970 (79.8%)	B: 1.000 (12.2%)	B: 0.02970 (6.9%)	B: 1.000 (1.1%)				
							F: 1.000	F: 1.000				
ND3	BrS_Alt	192	-12473.21	4.13106	B: 0.02970 (79.8%)	B: 1.000 (12.2%)	B: 0.02970 (6.9%)	B: 1.000 (1.1%)	BrS_Null	0	1	1.000
							F: 1.00000	F: 1.00000				
ND4	BrS_Null	191	-47401.22	4.36865	B: 0.03127 (90.9%)	B: 1.000 (3.8%)	B: 0.03127 (5.1%)	B: 1.000 (0.2%)				
							F: 1.000	F: 1.000				
ND4	BrS_Alt	192	-47397.10	4.36145	B: 0.03125 (94.7%)	B: 1.000 (4.1%)	B: 0.03125 (1.1%)	B: 1.000 (0%)	BrS_Null	8.245906	1	0.004

							F: 117.86539	F: 117.86539				
ND4L	BrS_Null	191	-9580.98	5.38108	B: 0.03198 (0%)	B: 1.000 (0%)	B: 0.03198 (100%)	B: 1.000 (0%)				
							F: 1.000	F: 1.000				
ND4L	BrS_Alt	192	-9579.58	5.37356	B: 0.03230 (100%)	B: 1.000 (0%)	B: 0.03230 (0%)	B: 1.000 (0%)	BrS_Null	2.803302	1	0.094
							F: 1.0000	F: 1.0000				
ND5	BrS_Null	191	-56351.39	3.95964	B: 0.03370 (93.0%)	B: 1.000 (4.1%)	B: 0.02967 (2.8%)	B: 1.000 (0.1%)				
							F: 1.000	F: 1.000				
ND5	BrS_Alt	192	-56367.7	3.94275	B: 0.02972 (95.5%)	B: 1.000 (3.2%)	B: 0.02972 (1.3%)	B: 1.000 (0%)	BrS_Null	-32.637718	1	#NUM!
							F: 330.26009	F: 330.26009				
ND6	BrS_Null	191	-17149.07	6.14279	B: 0.04306 (96.8%)	B: 1.000 (3.2%)	B: 0.04306 (0%)	B: 1.000 (0%)				
							F: 1.000	F: 1.000				
ND6	BrS_Alt	192	-17149.07	6.14279	B: 0.04306 (96.8%)	B: 1.000 (3.2%)	B: 0.04306 (0%)	B: 1.000 (0%)	BrS_Null	0	1	1.000
							F: 1.0000	F: 1.0000				

Supplementary Table 11 - Branch-site analyses using individual gene matrices and testing the branch leading to the ancestor of the African electric fish (Morm). Np, number of parameters; LRT, likelihood ratio test; df, degrees of freedom.

Gene	Model	np	ln L	α	Parameters ^b				Null	LRT	df	p
					ω_0	ω_1	ω_{2a}	ω_{2b}				
ATP6	BrS_Null	215	-25092.03	4.60719	B: 0.02326 (68.1%)	B: 1.000 (0%)	B: 0.02326 (31.9%)	B: 1.000 (0%)				
							F: 1.000	F: 1.000				
ATP6	BrS_Alt	216	-25091.94	4.60688	0.02325 (70.6%)	B: 1.000 (0%)	B: 0.02325 (29.4%)	B: 1.00000 (0%)	BrS_Null	0.190586	1	0.662
							F: 108.41187	F: 108.41187				
ATP8	BrS_Null	215	-5778.54	4.76739	B: 0.07679 (81.1%)	B: 1.000 (0%)	B: 0.07679 (18.9%)	B: 1.000 (0%)				
							F: 1.000	F: 1.000				
ATP8	BrS_Alt	216	-5777.24	4.76736	B: 0.07637 (87.9%)	B: 1.000 (0%)	B: 0.07637 (12.1%)	B: 1.000 (0.04%)	BrS_Null	2.613664	1	0.106
							F: 57.03801	F: 57.03801				
COI	BrS_Null	215	-43034.61	3.96448	B: 0.00720 (0.7%)	B: 1.000 (0%)	B: 0.00720 (98.8%)	B: 1.000 (0.4%)				
							F: 1.000	F: 1.000				
COI	BrS_Alt	216	-43034.61	3.96446	B: 3.96446 (0%)	B: 1.000 (0%)	B: 0.00720 (99.6%)	B: 1.000 (0.4%)	BrS_Null	0.000726	1	0.979
							F: 1.08073	F: 1.08073				
COII	BrS_Null	215	-18702.48	4.37726	B: 0.01479 (99.3%)	B: 1.000 (0.4%)	B: 0.01479 (0.2%)	B: 1.000 (0%)				
							F: 1.000	F: 1.000				
COII	BrS_Alt	216	-18702.48	4.37727	B: 0.01479 (99.6%)	B: 1.000 (0.4%)	B: 0.01479 (0%)	B: 1.000 (0%)	BrS_Null	0	1	1.000
							F: 1.0000	F: 1.0000				
COIII	BrS_Null	215	-22418.01	4.25872	B: 0.01515 (91.9%)	B: 1.000 (1.1%)	B: 0.01515 (7.0%)	B: 1.000 (0.1%)				
							F: 1.000	F: 1.000				
COIII	BrS_Alt	216	-22417.97	4.2585	B: 0.01515 (94.6%)	B: 1.000 (1.1%)	B: 0.01515 (4.3%)	B: 1.000 (0%)	BrS_Null	0.094974	1	0.758
							F: 1.98704	F: 1.98704				
CYTB	BrS_Null	215	-37026.16	4.06098	B: 0.01844 (64.7%)	B: 1.000 (0.7%)	B: 0.01844 (34.3%)	B: 1.000 (0.4%)				
							F: 1.000	F: 1.000				
CYTB	BrS_Alt	216	-37026.15	4.06064	B: 0.01843 (0%)	B: 1.000 (0%)	B: 0.01843 (98.9%)	B: 1.000 (1.1%)	BrS_Null	0.024204	1	0.876
							F: 1.0000	F: 1.0000				
ND1	BrS_Null	215	-35166.51	4.67989	B: 0.02137 (0%)	B: 1.000 (0%)	B: 0.03565 (98.1%)	B: 1.000 (1.9%)				
							F: 1.000	F: 1.000				
ND1	BrS_Alt	216	-35166.50	4.67949	B: 0.02136 (0%)	B: 1.000 (0%)	B: 0.02136 (98.1%)	B: 1.000 (1.9%)	BrS_Null	0.024726	1	0.875
							F: 6.53311	F: 6.53311				
ND2	BrS_Null	215	-45250.31	4.15942	B: 0.05321 (92.7%)	B: 1.000 (4.1%)	B: 0.05321 (3.1%)	B: 1.000 (0.1%)				
							F: 1.000	F: 1.000				
ND2	BrS_Alt	216	-45248.94	4.16328	B: 0.05321 (94.0%)	B: 1.000 (4.2%)	B: 0.05321 (1.7%)	B: 1.000 (0.1%)	BrS_Null	2.733208	1	0.098
							F: 55.98358	F: 55.98358				
ND3	BrS_Null	215	-13693.60	4.89226	B: 0.03110 (88.2%)	B: 1.000 (8.3%)	B: 0.03110 (3.2%)	B: 1.000 (0.3%)				
							F: 1.000	F: 1.000				
ND3	BrS_Alt	216	-13692.76	4.90481	B: 0.03107 (90.2%)	B: 1.000 (8.5%)	B: 0.03107 (1.2%)	B: 1.000 (0.1%)	BrS_Null	1.669118	1	0.196
							F: 376.86835	F: 376.86835				
ND4	BrS_Null	215	-52565.10	4.38571	B: 0.02756 (94.2%)	B: 1.000 (3.2%)	B: 0.02756 (2.5%)	B: 1.000 (0.1%)				
							F: 1.000	F: 1.000				
ND4	BrS_Alt	216	-52562.47	4.38845	B: 0.02758 (95.7%)	B: 1.000 (3.2%)	B: 0.02758 (1.0%)	B: 1.000 (0.04%)	BrS_Null	5.259332	1	0.022

						F: 115.46901		F: 115.46901	
ND4L	BrS_Null	215	-10318.57	5.53844	B: 0.02898 (100%)	B: 1.000 (0%)	B: 0.02898 (0%)	B: 1.000 (0%)	
						F: 1.000		F: 1.000	
ND4L	BrS_Alt	216	-10317.43	5.56762	B: 0.02887 (100%)	B: 1.000 (0%)	B: 0.02887 (0%)	B: 1.000 (0%)	BrS_Null 2.286688 1 0.130
						F: 1.0000		F: 1.0000	
ND5	BrS_Null	215	-67426.97	4.27996	B: 0.02967 (89.8%)	B: 1.000 (3.0%)	B: 0.02967 (7.0%)	B: 1.000 (0.2%)	
						F: 1.000		F: 1.000	
ND5	BrS_Alt	216	-67422.06	4.28267	B: 0.02972 (95.5%)	B: 1.000 (3.2%)	B: 0.02972 (1.3%)	B: 1.000 (0%)	BrS_Null 9.822976 1 0.002
						F: 330.26009		F: 330.26009	
ND6	BrS_Null	215	-24315.49	4.84677	B: 0.06036 (94.3%)	B: 1.000 (3.9%)	B: 0.06036 (1.8%)	B: 1.000 (0.1%)	
						F: 1.000		F: 1.000	
ND6	BrS_Alt	216	-24314.75	4.84471	B: 0.06031 (95.0%)	B: 1.000 (3.9%)	B: 0.06031 (1.1%)	B: 1.000 (0.0%)	BrS_Null 1.475174 1 0.225
						F: 12.37209		F: 12.37209	

References

1. Elbassiouny AA, Schott RK, Waddell JC, Kolmann MA, Lehmberg ES, Van Nynatten A, Crampton WGR, Chang BSW, Lovejoy NR. 2016 Mitochondrial genomes of the South American electric knifefishes (Order Gymnotiformes). *Mitochondrial DNA Part B Resour.* **1**, 401–403. (doi:10.1080/23802359.2016.1174090)