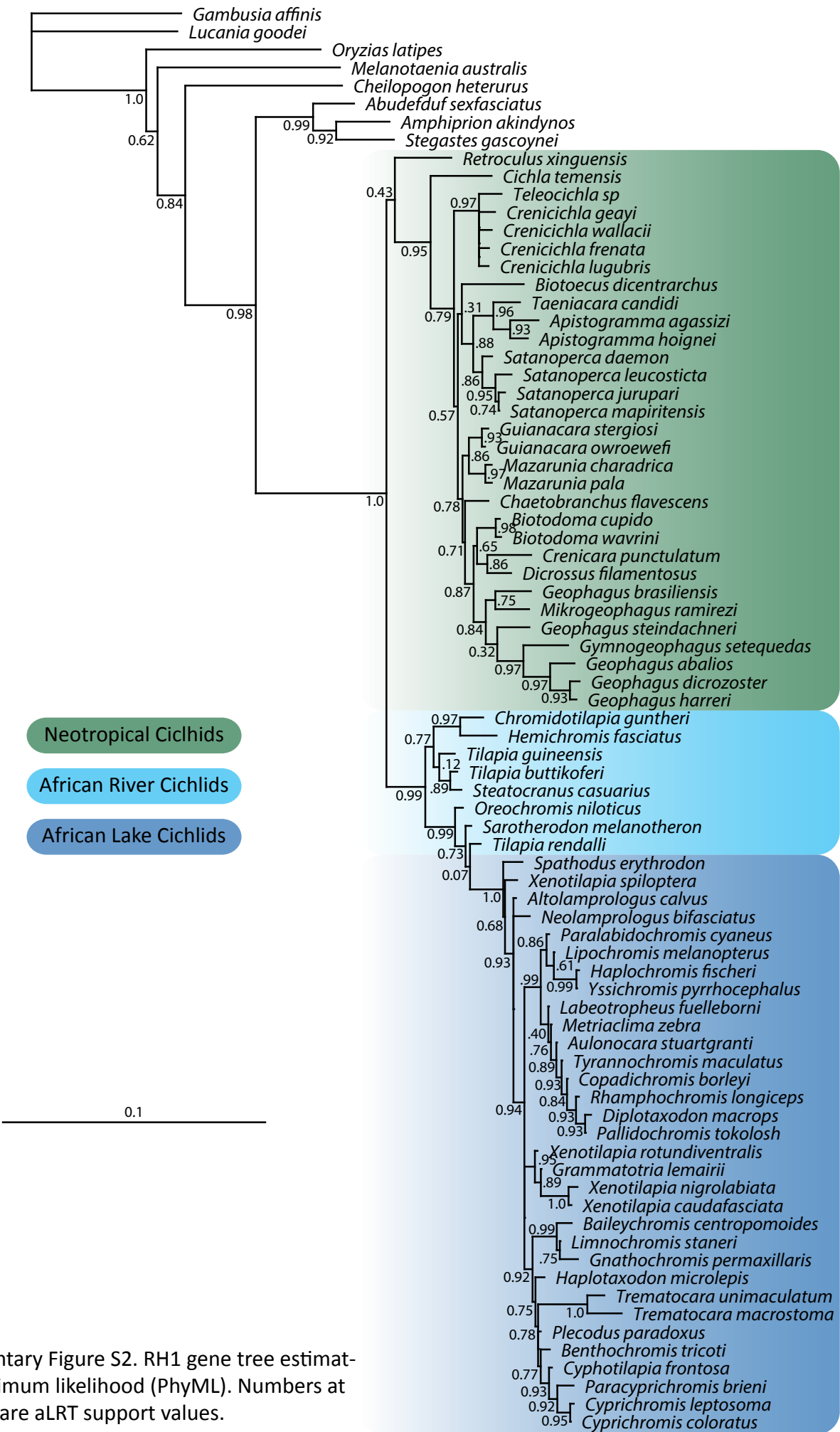
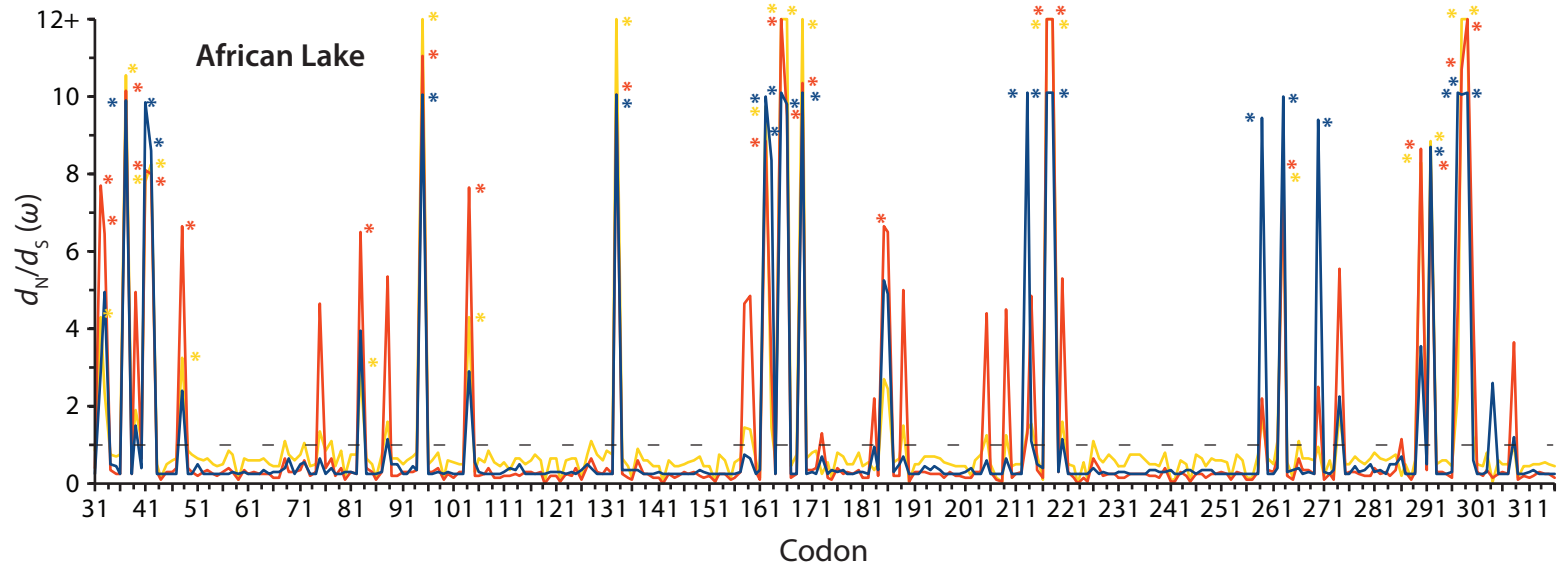
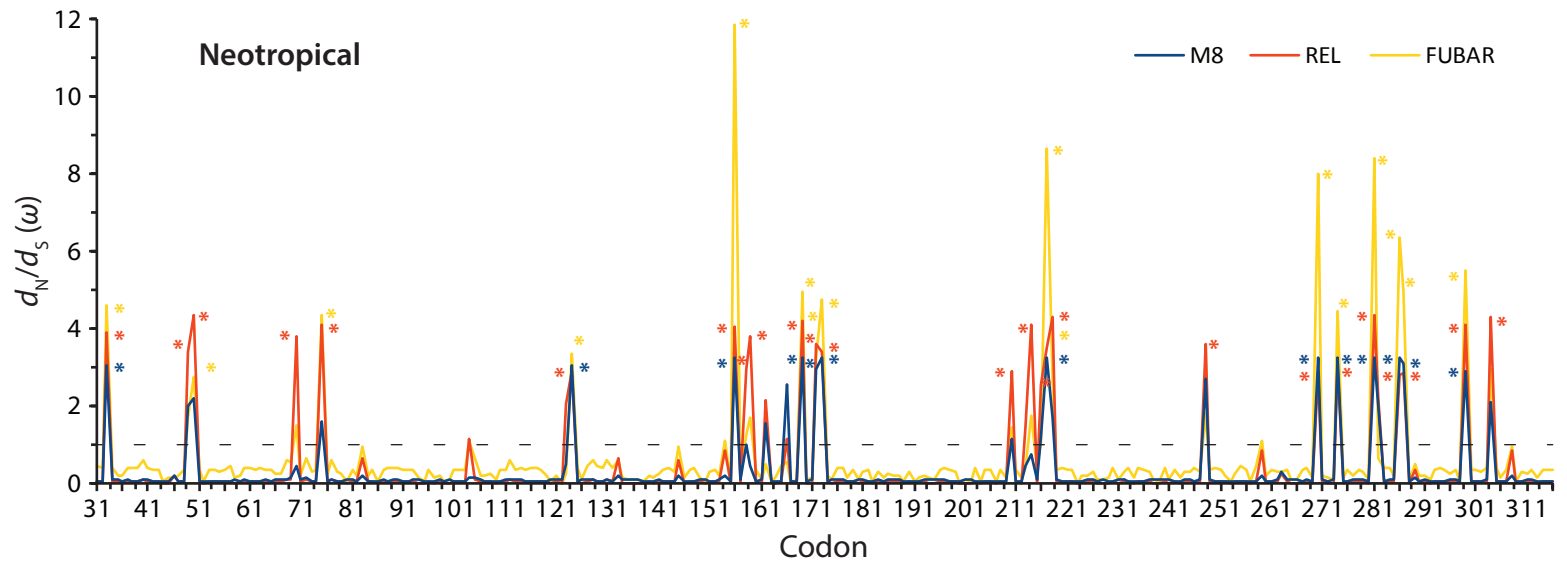


Supplementary Figure S1. RH1 gene tree estimated by Bayesian inference (MrBayes). Numbers at the nodes are posterior probabilities.



Supplementary Figure S2. RH1 gene tree estimated by maximum likelihood (PhyML). Numbers at the nodes are aLRT support values.



Supplementary Figure S3. Line graphs depicting $d_N/d_S (\omega)$ across sites as estimated by the M8 (PAML) and REL and FUBAR (HYPHY) models for Neotropical and African lake cichlids using the Bayesian gene tree. Values greater than one with 80% or higher posterior probability are indicated with an asterisk. The ω values for African lake cichlids are cut off at 12 to facilitate comparison with Neotropicals cichlids. Actual values range between 12 and 31.5 and can be found in Supplementary Tables S11, S12.

Supplementary Table S1. List of taxa used in this study.

Group	Species	Catalogue Number	Origin of Tissue	Accession Number	Reference
Outgroup	<i>Gambusia affinis</i>	N/A	N/A	Y11146.1	Archer and Hirano 1997
Outgroup	<i>Lucania goodei</i>	N/A	N/A	AY296738.1	Unpublished
Outgroup	<i>Oryzias latipes</i>	N/A	N/A	AB180742.1	Kawamura et al. 2005
Outgroup	<i>Melanotaenia australis</i>	N/A	N/A	FJ940704.1	Unpublished
Outgroup	<i>Cheilopogon heterurus</i>	N/A	N/A	EU637950.1	Li et al. 2009
Outgroup	<i>Abudefduf sexfasciatus</i>	N/A	N/A	HQ286548.1	Hofmann et al. 2012
Outgroup	<i>Stegastes gascoynei</i>	N/A	N/A	HQ286557.1	Hofmann et al. 2012
Outgroup	<i>Amphiprion akindynos</i>	N/A	N/A	HQ286549.1	Hofmann et al. 2012
Neotropical	<i>Retroculus xinguensis</i>	T15042	Iri River, tributary of Xingu River, Brazil	JX576463	This study
Neotropical	<i>Cichla temensis</i>	T11604, T11623	Cinaruco River, Venezuela	JX576464	This study
Neotropical	<i>Biotococcus dicentrarchus</i>	T11618	Cinaruco River, Venezuela	JX576465	This study
Neotropical	<i>Chaetobranchius flavescens</i>	ANSP2186	Rupununi River tributary, Guyana	JX576466	This study
Neotropical	<i>Mazarunia charadrica</i>	T06044	Philipai, Kukui River, Mazaruni	JX576467	This study
Neotropical	<i>Mazarunia pala</i>	T06235	Mazaruni River, tributary of Essequibo River, Guyana	JX576468	This study
Neotropical	<i>Guianacara owroewefi</i>	ANSP1018	Lawa River, Suriname	JX576469	This study
Neotropical	<i>Guianacara stergiosi</i>	T11668	Claro River, Venezuela	JX576470	This study
Neotropical	<i>Crenicichla lugubris</i>	T06671	Pirara River, Rupununi	JX576471	This study
Neotropical	<i>Crenicichla geayi</i>	T11561	Las Marias River, Venezuela	JX576472	This study
Neotropical	<i>Crenicichla wallacii</i>	T11611	Cinaruco River, Venezuela	JX576474	This study
Neotropical	<i>Crenicichla frenata</i>	N/A	N/A	JN990733	Weadick et al. 2012
Neotropical	<i>Teleocichla preta</i>	T15170	Iri River, tributary of Xingu River, Brazil	JX576473	This study
Neotropical	<i>Taeniacara candidi</i>	T11695	Aquarium trade	JX576475	This study
Neotropical	<i>Apistogramma agassizi</i>	T11548, T11550	Orosa River, Peru	JX576476	This study
Neotropical	<i>Apistogramma hoignei</i>	T11566, T11568,	Cano Maporal, Venezuela	JX576477	This study

T11585

Neotropical	<i>Satanoperca daemon</i>	T11607, T11633	Cinaruco River, Venezuela	JX576478	This study
Neotropical	<i>Satanoperca leucosticta</i>	ANSP2376	Pirara River, Guyana	JX576479	This study
Neotropical	<i>Satanoperca mapiritensis</i>	T11660, T11675	Morichal Largo River, Venezuela	JX576480	This study
Neotropical	<i>Satanoperca jurupari</i>	T11727	Nanay River, Peru	JX576481	This study
Neotropical	<i>Crenicara punctulatum</i>	T11825	Aquarium trade	JX576482	This study
Neotropical	<i>Dicrossus filamentosus</i>	T11686	Aquarium trade	JX576483	This study
Neotropical	<i>Biotodoma cupido</i>	T11544, T11546	Orosa River, Peru	JX576484	This study
Neotropical	<i>Biotodoma wavrini</i>	T11556, T11594	Cinaruco River, Venezuela	JX576485	This study
Neotropical	<i>Mikrogeophagus ramirezi</i>	T11580	Cano Maporal, Venezuela	JX576486	This study
Neotropical	' <i>Geophagus</i> ' <i>brasiliensis</i>	T11688, H5987	Aquarium trade	JX576487	This study
Neotropical	' <i>Geophagus</i> ' <i>steindachneri</i>	H5988	Aquarium trade	JX576488	This study
Neotropical	<i>Gymnogeophagus setequedas</i>	T11845	Aquarium trade	JX576489	This study
Neotropical	<i>Geophagus abalios</i>	T11631, T08707	Cinaruco River, Venezuela & Rupununi River, Guyana	JX576490	This study
Neotropical	<i>Geophagus dicrozoster</i>	T11626, T11627	Cinaruco River, Venezuela	JX576491	This study
Neotropical	<i>Geophagus harreri</i>	T11820	Antecume Pata, French Guiana	JX576492	This study
African river	<i>Oreochromis niloticus</i>	N/A	N/A	XM_00343900 5	NCBI Reference Sequence
African river	<i>Hemichromis fasciatus</i>	T17720	Lake Nokue Market, Benin	JX576461	This study
African river	<i>Chromidotilapia guntheri</i>	T11699	Beffa River, Benin	JX576462	This study
African river	<i>Sarotherodon melanotheron</i>	N/A	N/A	AB084940.1	Sugawara et al. 2005
African river	<i>Steatocranus casuarius</i>	N/A	N/A	AB084942.1	Sugawara et al. 2005
African river	<i>Tilapia buttikoferi</i>	N/A	N/A	AB084943.1	Sugawara et al. 2005
African river	<i>Tilapia rendalli</i>	N/A	N/A	AB084944.1	Sugawara et al. 2005
African river	<i>Tilapia guineensis</i>	N/A	N/A	GQ409803.1	Timelthaler and Spaethe, unpublished
African lake	<i>Aulonocara stuartgranti</i>	N/A	N/A	AB185215.1	Sugawara et al. 2005
African lake	<i>Diplotaxodon macrops</i>	N/A	N/A	AB185220.1	Sugawara et al. 2005
African lake	<i>Metriaclima zebra</i>	N/A	N/A	AB185235.1	Sugawara et al. 2005
African lake	<i>Pallidochromis tokolosh</i>	N/A	N/A	AB185229.1	Sugawara et al. 2005
African lake	<i>Rhamphochromis longiceps</i>	N/A	N/A	AB196147.1	Sugawara et al. 2005
African lake	<i>Copadichromis borleyi</i>	N/A	N/A	AY775121.1	Spady et al. 2005

African lake	<i>Labeotropheus fuelleborni</i>	N/A	N/A	AY775113.1	Spady et al. 2005
African lake	<i>Tyrannochromis maculatus</i>	N/A	N/A	AY775117.1	Spady et al. 2005
African lake	<i>Baileychromis centropomoides</i>	N/A	N/A	AB185217.1	Spady et al. 2005
African lake	<i>Xenotilapia nigrolabiata</i>	N/A	N/A	AB185241.1	Sugawara et al. 2005
African lake	<i>Xenotilapia caudafasciata</i>	N/A	N/A	AB185239.1	Sugawara et al. 2005
African lake	<i>Cyphotilapia frontosa</i>	N/A	N/A	AB084929.1	Sugawara et al. 2005
African lake	<i>Cyprichromis leptosoma</i>	N/A	N/A	AB084930.1	Sugawara et al. 2005
African lake	<i>Haplotaxodon microlepis</i>	N/A	N/A	AB185390.1	Sugawara et al. 2005
African lake	<i>Limnochromis staneri</i>	N/A	N/A	AB185225.1	Sugawara et al. 2005
African lake	<i>Spathodus erythrodon</i>	N/A	N/A	AB084941.1	Sugawara et al. 2005
African lake	<i>Trematocara macrostoma</i>	N/A	N/A	AB084945.1	Sugawara et al. 2005
African lake	<i>Trematocara unimaculatum</i>	N/A	N/A	AB185238.1	Sugawara et al. 2005
African lake	<i>Xenotilapia spiloptera</i>	N/A	N/A	AB185242.1	Sugawara et al. 2005
African lake	<i>Neolamprologus bifasciatus</i>	N/A	N/A	AB458135.1	Nagai et al. 2011
African lake	<i>Altolamprologus calvus</i>	N/A	N/A	AB458132.1	Nagai et al. 2011
African lake	<i>Plecodus paradoxus</i>	N/A	N/A	AB588119.1	Nagai et al. 2011
African lake	<i>Benthochromis tricoti</i>	N/A	N/A	AB457852.1	Nagai et al. 2011
African lake	<i>Paracyprichromis brienii</i>	N/A	N/A	AB458121.1	Nagai et al. 2011
African lake	<i>Cyprichromis coloratus</i>	N/A	N/A	AB588118.1	Nagai et al. 2011
African lake	<i>Xenotilapia rotundiventralis</i>	N/A	N/A	AB458123.1	Nagai et al. 2011
African lake	<i>Grammatotria lemairii</i>	N/A	N/A	AB457989.1	Nagai et al. 2011
African lake	<i>Gnathochromis permaxillaris</i>	N/A	N/A	AB084932.1	Sugawara et al. 2002
African lake	<i>Paralabidochromis cyaneus</i>	N/A	N/A	AY673747.1	Hofmann et al. 2009
African lake	<i>Lipochromis melanopterus</i>	N/A	N/A	AY673743.1	Hofmann et al. 2009
African lake	<i>Haplochromis fischeri</i>	N/A	N/A	AB667606.1	Miyagi et al. 2012
African lake	<i>Yssichromis pyrrocephalus</i>	N/A	N/A	AB667170.1	Miyagi et al. 2012

Supplementary Table S2. Results of random sites (PAML) analyses on various subsets of the cichlid RH1 Bayesian gene tree.

Tree ¹	Model	np	lnL	K	Parameters ²			Null	LRT	df	P
					ω_0/p	ω_1/q	ω_2/ω_p				
C+OG	M0	146	-6589.94	2.42	0.25			n/a			
	M1a	147	-6239.50	2.24	0.03 (81.3%)	1 (18.7%)		M0	700.87	1	0.0000
	M2a	149	-6186.53	2.46	0.04 (80.1%)	1 (16.6%)	4.27 (3.3%)	M1a	105.95	2	0.0000
	M3	150	-6179.99	2.39	0.01 (72.0%)	0.51 (21.5%)	2.68 (6.5%)	M0	819.90	4	0.0000
	M7	147	-6227.38	2.17	0.08	0.35		n/a			
	M8a	148	-6221.35	2.17	0.15	2.13	1 (13.0%)	n/a			
	M8	149	-6172.68	2.38	0.10	0.49	3.71 (3.7%)	M7	109.40	2	0.0000
	M8a							M8a	97.34	1	0.0000
Cichlid	M0	130	-4815.73	2.73	0.38			n/a			
	M1a	131	-4559.93	2.27	0.02 (80.7%)	1 (19.3%)		M0	511.60	1	0.0000
	M2a	133	-4503.54	2.58	0.02 (79.8%)	1 (13.7%)	3.98 (6.6%)	M1a	112.77	2	0.0000
	M3	135	-4503.54	2.58	0.02 (79.7%)	0.99 (13.7%)	3.96 (6.6%)	M0	624.38	5	0.0000
	M7	131	-4560.92	2.26	0.01	0.03		n/a			
	M8a	132	-4559.28	2.25	0.20	7.01	1 (18.0%)	n/a			
	M8	133	-4504.29	2.56	0.06	0.36	3.73 (7.2%)	M7	113.26	2	0.0000
	M8a							M8a	109.99	1	0.0000
Af	M0	74	-2749.25	2.62	0.64			n/a			
	M1a							M0	178.75	1	0.0000
	M2a	77	-2591.21	2.34	0.01 (72.4%)	1 (21.9%)	9.48 (5.7%)	M1a	137.33	2	0.0000
	M3	78	-2591.17	2.33	0 (69.9%)	0.91 (24.3%)	9.35 (5.8%)	M0	316.15	4	0.0000
	M7	75	-2660.31	1.97	0.01	0.03		n/a			
	M8a	76	-2659.89	1.99	1.67	99	1 (22.1%)	n/a			
	M8	77	-2591.23	2.33	0.01	0.04	9.30 (5.8%)	M7	138.16	2	0.0000
	M8a							M8a	137.31	1	0.0000

¹The complete alignment and gene tree (C+OG) and datasets pruned to contain only cichlids and African river cichlid (AfR) were analyzed.

² ω values of each site class are shown for models M0-M3 (ω_0 – ω_2) with the proportion of each site class in parentheses. For M7-M8, the shape parameters, p and q, which describe the beta distribution are listed. In addition, the ω value for the positively selected site class (ω_p , with the proportion of sites in parentheses) is shown for M8a (where ω_p is constrained to equal one) and M8.

Abbreviations—**np**, number of parameters; **lnL**, ln Likelihood; **K**, transition/transversion ratio; **LRT**, likelihood ratio test statistic; **df**, degrees of freedom; **P**, P-value; **n/a**, not applicable.

Supplementary Table S3. Results of random sites (PAML) analyses on various subsets of the cichlid RH1 maximum likelihood gene tree.

Tree ¹	Model	np	lnL	K	Parameters ²			Null	LRT	df	P
					ω_0/p	ω_1/q	ω_2/ω_p				
C+OG	M0	157	-6586.94	2.43	0.26			n/a			
	M1a	158	-6236.58	2.24	0.03 (81.3%)	1 (18.7%)		M0	700.72	1	0.0000
	M2a	160	-6182.58	2.48	0.04 (80.0%)	1 (16.6%)	4.26 (3.4%)	M1a	108.01	2	0.0000
	M3	161	-6175.11	2.40	0.01 (71.9%)	0.51 (21.7%)	2.71 (6.5%)	M0	823.65	4	0.0000
	M7	158	-6224.00	2.17	0.08	0.35		n/a			
	M8a	159	-6228.95	2.21	0.01	0.03	1 (6.9%)	n/a			
	M8	149	-6168.32	2.39	0.10	0.50	3.71 (3.8%)	M7	111.35	2	0.0000
	M8a							M8a	121.25	1	0.0000
Cichlid	M0	141	-4812.26	2.73	0.38			n/a			
	M1a	142	-4557.22	2.27	0.02 (80.7%)	1 (19.3%)		M0	510.08	1	0.0000
	M2a	144	-4498.30	2.59	0.02 (79.6%)	1 (13.9%)	4.08 (6.5%)	M1a	117.84	2	0.0000
	M3	145	-4498.30	2.59	0.02 (79.6%)	1 (13.9%)	4.08 (6.5%)	M0	627.92	4	0.0000
	M7	142	-4558.17	2.26	0.01	0.03		n/a			
	M8a	143	-4556.84	2.25	0.20	6.76	1 (18.1%)	n/a			
	M8	144	-4499.02	2.57	0.06	0.35	3.83 (7.1%)	M7	118.30	2	0.0000
	M8a							M8a	115.62	1	0.0000
Neo	M0	61	-3068.88	2.76	0.25			n/a			
	M1a	62	-2936.62	2.40	0.01 (84.6%)	1 (15.4%)		M0	264.52	1	0.0000
	M2a	64	-2916.61	2.71	0.01 (85.1%)	1 (10.1%)	3.72 (4.8%)	M1a	40.03	2	0.0000
	M3	65	-2916.56	2.72	0.01 (86.7%)	1.37 (10.4%)	4.77 (2.9%)	M0	304.65	4	0.0000
	M7	62	-2938.96	2.35	0.01	0.08		n/a			
	M8a	63	-2936.63	2.40	0.54	99	1 (15.4%)	n/a			
	M8	64	-2916.61	2.71	0.01	0.08	3.66 (4.9%)	M7	44.72	2	0.0000
	M8a							M8a	40.05	1	0.0000
Af	M0	79	-2753.01	2.68	0.65			n/a			
	M1a	80	-2663.48	2.02	0.02 (77.9%)	1 (22.1%)		M0	179.08	1	0.0000
	M2a	82	-2590.93	2.43	0 (71.0%)	1 (23.7%)	10.19 (5.4%)	M1a	145.10	2	0.0000
	M3	83	-2590.92	2.43	0.01 (72.9%)	1.07 (21.8%)	10.29 (5.3%)	M0	324.19	4	0.0000
	M7	80	-2663.98	2.01	0.01	0.03		n/a			
	M8a	81	-2663.49	2.02	1.65	99	1 (22.1%)	n/a			
	M8	82	-2591.07	2.41	0.02	0.05	9.87 (5.5%)	M7	145.83	2	0.0000
	M8a							M8a	144.84	1	0.0000
AfR	M0	15	-1553.24	2.81	0.16			n/a			
	M1a	16	-1540.26	2.53	0 (87.5%)	1 (12.5%)		M0	25.95	1	0.0000

M2a	18	-1536.92	2.65	0 (93.1%)	1 (0%)	3.07 (6.9%)	M1a	6.68	2	0.0355
M3	19	-1536.92	2.65	0 (92.7%)	0 (0.3%)	3.07 (6.9%)	M0	32.63	4	0.0000
M7	16	-1540.56	2.45	0.01	0.05		n/a			
M8a	17	-1540.26	2.53	0.01	2.80	1 (12.5%)	n/a			
M8	18	-1536.92	2.65	0.01	81.7	3.07 (6.9%)	M7	7.28	2	0.0263
							M8a	6.68	1	0.0098
AfL	M0	63	-2238.27	2.71	1.24		n/a			
M1a	64	-2192.05	1.91	0 (72.1%)	1 (27.9%)		M0	92.43	1	0.0000
M2a	66	-2123.09	2.36	0 (62.3%)	1 (31.1%)	14.98 (6.6%)	M1a	137.93	2	0.0000
M3	67	-2121.36	2.43	0.08 (80.1%)	2.93 (14.8%)	19.54 (5.1%)	M0	233.81	4	0.0000
M7	64	-2192.24	1.93	0.01	0.01		n/a			
M8a	65	-2192.05	1.91	0.01	2.56	1 (27.9%)	n/a			
M8	66	-2123.19	2.34	0.01	0.01	14.37 (6.6%)	M7	138.10	2	0.0000
							M8a	137.72	1	0.0000

¹The complete gene tree and RH1 alignment and those pruned to contain only cichlids (C), Neotropical cichlids (Neo), African cichlids (Af), African river cichlids (AfR), and African lake cichlids (AfL) were analyzed.

² ω values of each site class are shown for models M0-M3 (ω_0 – ω_2) with the proportion of each site class in parentheses. For M7-M8, the shape parameters, p and q, which describe the beta distribution are listed. In addition, the ω value for the positively selected site class (ω_p , with the proportion of sites in parentheses) is shown for M8a (where ω_p is constrained to equal one) and M8.

Abbreviations—**np**, number of parameters; **lnL**, *ln* Likelihood; **K**, transition/transversion ratio; **LRT**, likelihood ratio test statistic; **df**, degrees of freedom; **P**, *P*-value; **n/a**, not applicable.

Supplementary Table S4. Results of PARRIS analyses on various subsets of the cichlid RH1 Bayesian gene tree.

Tree ¹	Model	lnL	d_s (prob.)					ω (prob.)					LRT	P
			1	2	3	Mean	STDV	1	2	3	Mean	STDV		
C	Null	-4468.9	0.27 (0.50)	1.10 (0.34)	3.12 (0.16)	1	0.99	0 (0.69)	1 (0.31)	–	0.31	0.46		
	Alt	-4445.5	0.31 (0.52)	1.26 (0.45)	7.28 (0.04)	1	1.34	0 (0.74)	1 (0.13)	2.90 (0.14)	0.53	1.00	46.7	0.000
Neo	Null	-2901.4	0.33 (0.66)	1.56 (0.33)	20.39 (0.01)	1	2.29	0 (0.81)	1 (0.19)	–	0.19	0.39		
	Alt	-2897.7	0.56 (0.91)	2.67 (0.08)	22.05 (0.01)	1	2.45	0 (0.84)	1 (0.11)	4.01 (0.05)	0.32	0.94	7.5	0.023
Af	Null	-2571.8	0.34 (0.80)	3.35 (0.20)	13.6 (0.01)	1	1.53	0 (0.59)	1 (0.41)	–	0.41	0.49		
	Alt	-2560.9	0.27 (0.63)	1.77 (0.32)	5.24 (0.05)	1	1.19	0 (0.67)	1 (0.21)	4.52 (0.11)	0.72	1.41	21.9	0.000
AfR	Null	-1533.4	0 (0.56)	0.05 (0)	2.28 (0.44)	1	1.13	0 (0.81)	1 (0.19)	–	0.19	0.39		
	Alt	-1533.4	0 (0.55)	0 (0)	2.24 (0.45)	1	1.11	0 (0.82)	1 (0.13)	1.25 (0.05)	0.20	0.42	0	0.986
AfL	Null	-2103.9	0.11 (0.77)	3.54 (0.22)	21.19 (0.01)	1	2.11	0.02 (0.37)	1 (0.63)	–	0.64	0.47		
	Alt	-2093.8	0 (0.54)	1.78 (0.45)	10.83 (0.02)	1	1.63	0.14 (0.68)	1 (0.08)	4.10 (0.24)	1.15	1.67	20.1	0.000

¹The complete gene tree and RH1 alignment and those pruned to contain only cichlids (C), Neotropical cichlids (Neo), African cichlids (Af), African river cichlids (AfR), and African lake cichlids (AfL) were analyzed.

Supplementary Table S5. Results of PARRIS analyses on various subsets of the cichlid RH1 ML gene tree.

Tree ¹	Model	lnL	dS (prob.)					ω (prob.)					LRT	P
			1	2	3	Mean	STDV	1	2	3	Mean	STDV		
C	Null	-4462.3	0.41 (0.70)	2.05 (0.28)	8.18 (0.02)	1	1.20	0 (0.71)	1 (0.29)	–	0.30	0.45		
	Alt	-4442.5	0.30 (0.51)	1.27 (0.46)	7.81 (0.03)	1	1.35	0 (0.73)	1 (0.14)	2.97 (0.13)	0.53	1.00	39.5	0.000
Neo	Null	-2911.2	0.18 (0.45)	1.28 (0.47)	4.05 (0.08)	1	1.03	0 (0.77)	1 (0.23)	–	0.23	0.42		
	Alt	-2896.8	0.10 (0.28)	1.02 (0.70)	12.09 (0.02)	1	1.68	0 (0.81)	1 (0.12)	3.52 (0.07)	0.38	0.94	28.9	0.000
Af	Null	-2571.8	0.34 (0.80)	3.35 (0.20)	13.59 (0.01)	1	1.53	0 (0.59)	1 (0.41)	–	0.41	0.49		
	Alt	-2560.9	0.27 (0.63)	1.77 (0.32)	5.23 (0.05)	1	1.19	0 (0.67)	1 (0.21)	4.52 (0.11)	0.72	1.41	21.9	0.000
AfR	Null	-1533.1	0 (0.39)	0 (0.17)	2.27 (0.44)	1	1.13	0 (0.81)	1 (0.19)	–	0.19	0.39		
	Alt	-1532.7	0 (0.46)	0 (0.06)	2.09 (0.48)	1	1.04	0.04 (0.90)	1 (0)	1.78 (0.10)	0.22	0.53	0.6	0.728
AfL	Null	-2104.4	0.11 (0.76)	3.41 (0.23)	20.72 (0.01)	1	2.13	0 (0.35)	1 (0.65)	–	0.65	0.48		
	Alt	-2097.4	0.53 (0.78)	1.81 (0.19)	8.18 (0.03)	1	1.36	0.07 (0.83)	1 (0)	6.85 (0.17)	1.22	2.54	14.1	0.001

¹The complete gene tree and RH1 alignment and those pruned to contain only cichlids (C), Neotropical cichlids (Neo), African cichlids (Af), African river cichlids (AfR), and African lake cichlids (AfL) were analyzed.

Supplementary Table S6. Results of branch-site (BrS) and clade model C (CmC) analyses on the RH1 cichlid gene tree highlighting the branch leading to cichlids, Neotropical cichlids, and African cichlids.

Branch ¹	Model	np	lnL	K	Parameters ²				ΔAIC	Null	LRT	df	P
					ω ₀	ω ₁	ω _{2a}	ω _{2b}					
None	M2a_rel	149	-6186.5	2.5	0.04 (80.1%)	1 (16.6%)	4.27 (3.3%)		0	n/a			
	BrS_Null	148	-6239.5	2.2	B: 0.03 F: 0.03 (81.3%)	B: 1 F: 1 (18.7%)	B: 0.03 F: 1 (0%)	B: 1 F: 1 (0%)	103.9	n/a			
Cichlid	BrS_Alt	149	-6239.5	2.2	B: 0.03 F: 0.03 (81.3%)	B: 1 F: 1 (18.7%)	B: 0.03 F: 2.35 (0%)	B: 1 F: 2.35 (0%)	105.9	BrS_Null	0	1	n/a
	CmC	150	-6186.3	2.5	B: 0.04 F: 0.04 (80.1%)	B: 1 F: 1 (16.6%)	B: 4.19 F: 6.45 (3.4%)		1.6	M2a_rel	0.4	1	0.542
Af	BrS_Null	148	-6239.5	2.2	B: 0.03 F: 0 (81.0%)	B: 1 F: 1 (18.7%)	B: 0.03 F: 1 (0%)	B: 1 F: 1 (0%)	103.9	n/a			
	BrS_Alt	149	-6237.5	2.2	B: 0.04 F: 0.04 (81.2%)	B: 1 F: 1 (18.1%)	B: 0.04 F: 65.47 (0.6%)	B: 1 F: 65.47 (0.1%)	102	BrS_Null	4.0	1	0.046
	CmC	150	-6185.8	2.5	B: 0.04 F: 0.04 (80.1%)	B: 1 F: 1 (16.7%)	B: 4.23 F: 11.30 (3.3%)		0.5	M2a_rel	1.5	1	0.226
Neo	BrS_Null	148	-6237.7	2.2	B: 0.03 F: 0.03 (0%)	B: 1 F: 1 (0%)	B: 0.03 F: 1 (81.2%)	B: 1 F: 1 (18.8%)	100.3	n/a			
	BrS_Alt	149	-6237.4	2.2	B: 0.03 F: 0.03 (0%)	B: 1 F: 1 (0%)	B: 0.03 F: 999 (81.2%)	B: 1 F: 999 (18.8%)	101.7	BrS_Null	0.7	1	0.410
	CmC	150	-6186.5	2.5	B: 0.04 F: 0.04 (80.0%)	B: 1 F: 1 (16.6%)	B: 4.25 F: 10.35 (3.0%)		1.9	M2a_rel	0.1	150	1.000

¹Branches leading to each of the major clades, cichlids, African cichlids (Af), and Neotropical cichlids (Neo), were individually highlighted as the foreground.

²ω values of each site class are shown with the proportion of each site class in parentheses. B and F refer to the background and foreground partitions using the Branch-site terminology.

Abbreviations—**np**, number of parameters; **lnL**, ln Likelihood; **K**, transition/transversion ratio; **LRT**, likelihood ratio test statistic; **df**, degrees of freedom; **P**, P-value; **n/a**, not applicable.

Supplementary Table S7. Results of Clade Model C (CmC, PAML) analyses on the RH1 cichlid ML gene tree.

Model & Partition ¹	np	lnL	K	Parameters ²			Δ AIC ³	Null	LRT	df	P
				ω_0	ω_1	ω_2/ω_d					
M1a	158	-6236.58	2.24	0.03 (81.3%)	1 (18.7%)		160.49	n/a			
M2a	160	-6182.58	2.48	0.04 (80.0%)	1 (16.6%)	4.26 (3.4%)	56.48	M1a	108.01	2	0.0000
M2a_rel	160	-6182.35	2.48	0.04 (80.0%)	1 (16.6%)	4.30 (3.4%)	56.03	M1a	108.46	2	0.0000
Cichlid	161	-6173.76	2.45	0.04 (80.2%)	1 (14.4%)	1.34 (5.4%) Cichlid: 4.40	40.86	M2a_rel	17.17	1	0.0000
Neo	161	-6174.12	2.50	0.04 (79.9%)	1 (16.5%)	6.18 (3.6%) Neo: 2.30	41.56	M2a_rel	16.47	1	0.0000
Af	161	-6158.88	2.42	0.04 (80.2%)	1 (15.2%)	1.94 (4.7%) Af: 8.92	11.08	M2a_rel	46.95	1	0.0000
AfR	161	-6182.26	2.48	0.04 (80.0%)	1 (16.7%)	4.41 (3.3%) AfR: 3.66	57.85	M2a_rel	0.19	1	0.6665
AfL	161	-6154.46	2.41	0.04 (80.5%)	1 (14.3%)	1.71 (5.2%) AfL: 12.49	2.26	M2a_rel	55.77	1	0.0000
Neo/Af	162	-6158.31	2.42	0.04 (80.2%)	1 (15.1%)	1.67 (4.7%) Neo: 8.89 Af: 2.21	11.95	M2a_rel	48.08 1.13	2 1	0.0000 0.2881
R/L	162	-6152.33	2.41	0.04 (80.6%)	1 (13.7%)	1.19 (5.8%) R: 2.02 L: 12.16	0	M2a_rel Af AfL	60.03 13.08 4.26	2 1 1	0.0000 0.0003 0.0391
Neo/AfR/AfL	163	-6151.32	2.41	0.04 (80.7%)	1 (13.2%)	1.20 (6.1%) Neo: 1.54 AfR: 3.24 AfL: 12.21	-0.02	M2a_rel AfL R+L	62.05 6.28 2.02	3 2 1	0.0000 0.0433 0.1552

¹Partitions listed are explained in Figure 1. In all cases an additional partition exists that contains the remaining taxa (e.g., outgroups).

² ω values of each site class are shown with the proportion of each site class in parentheses. ω_d is divergent site class that has a separate value for each partition.

Abbreviations—**np**, number of parameters; **lnL**, ln Likelihood; **K**, transition/transversion ratio; **LRT**, likelihood ratio test statistic; **df**, degrees of freedom; **P**, P-value; **n/a**, not applicable.

³The difference in AIC values were calculated compared to the overall best-fitting model, R/L, with an AIC of 12628.67.

Supplementary Table S8. Restricted clade model C (CmC) analyses testing for the presence of significant positive selection in each partition using the Bayesian gene tree.

Partition ¹	Model ²	np	lnL	K	Null	LRT	df	P
Cichlid	C_Res	149	-6216.38	2.18	Res	74.32	1	0.0000
	Alt	150	-6179.22	2.44				
Neo	Neo_Res	149	-6184.90	2.43	Res	11.22	1	0.0008
	Alt	150	-6179.29	2.49				
Af	Af_Res	149	-6211.54	2.18	Res	91.73	1	0.0000
	Alt	150	-6165.68	2.41				
AfR	AfR_Res	149	-6187.59	2.46	Res	54.54	1	0.0000
	Alt	150	-6160.32	2.40				
AfL	AfL_Res	149	-6201.14	2.18	Res	29.58	1	0.0000
	Alt	150	-6186.35	2.47				
Neo/Af	Neo_Res	150	-6169.01	2.36	Neo_Res Af_Res	7.825 92.46	1	0.0052 0.0000
	Af_Res	150	-6211.33	2.30				
	Alt	151	-6165.10	2.41				
R/L	R_Res	150	-6163.29	2.33	R_Res L_Res	118.12	1	0.0012 0.0000
	L_Res	150	-6217.13	2.31				
	Alt	151	-6158.07	2.40				
Neo/AfR/AfL	Neo_Res	151	-6159.10	2.36	Neo_Res AfR_Res AfL_Res	3.24 10.16 106.72	1	0.0720 0.0014 0.0000
	AfR_Res	151	-6162.56	2.37				
	AfL_Res	151	-6210.84	2.30				
	Alt	152	-6157.48	2.40				

¹Partitions listed are explained in Figure 1. In all cases an additional partition exists that contains the remaining taxa (e.g., outgroups).

²Listed partitions were restricted (Res) so that the ω value of the divergent site class was constrained to equal one.

Abbreviations—**np**, number of parameters; **lnL**, ln Likelihood; **K**, transition/transversion ratio; **LRT**, likelihood ratio test statistic; **df**, degrees of freedom; **P**, P-value; **n/a**, not applicable.

Supplementary Table S9. Results of branch-site (BrS, PAML) analyses on the RH1 cichlid gene tree highlighting clades, in comparison to the CmC results.

Partition ¹	Model	np	lnL	K	Parameters ²				Δ AIC ³	Null	LRT	df	P
					ω_0	ω_1	ω_{2a}	ω_{2b}					
n/a	M2a_rel	149	-6186.5	2.5	0.04 (80.1%)	1 (16.6%)	4.27 (3.3%)		50	n/a			
	BrS_Null	148	-6221.5	2.2	B: 0.03 F: 0.03 (77.8%)	B: 1 F: 1 (14.7%)	B: 0.03 F: 1 (6.3%)	B: 1 F: 1 (1.2%)	118	n/a			
Af	BrS_Alt	149	-6172.0	2.3	B: 0.04 F: 0.04 (77.7%)	B: 1 F: 1 (15.2%)	B: 0.04 F: 7.07 (6.0%)	B: 1 F: 7.07 (1.2%)	21	BrS_Null	99.0	1	0.000
	CmC	150	-6165.7	2.4	B: 0.04 F: 0.04 (80.3%)	B: 1 F: 1 (14.8%)	B: 1.90 F: 8.41 (4.9%)		11	M2a_rel	41.7	1	0.000
	BrS_Null	148	-6239.5	2.2	B: 0.03 F: 0.03 (81.3%)	B: 1 F: 1 (18.7%)	B: 0.03 F: 1 (0%)	B: 1 F: 1 (0%)	154	n/a			
AfR	BrS_Alt	149	-6235.4	2.2	B: 0.03 F: 0.03 (80.9%)	B: 1 F: 1 (18.7%)	B: 0.03 F: 38.22 (0.29%)	B: 1 F: 38.22 (0.07%)	148	BrS_Null	8.3	1	0.004
	CmC	150	-6186.4	2.5	B: 0.04 F: 0.04 (80.1%)	B: 1 F: 1 (16.7%)	B: 4.40 F: 3.34 (3.3%)		52	M2a_rel	0.4	1	0.553

¹Partitions listed are explained in Figure 1. In all cases an additional partition exists that contains the remaining taxa (referred to as the background in the branch-site model).

² ω values of each site class are shown with the proportion of each site class in parentheses. B and F refer to the background and foreground partitions using the Branch-site terminology.

³Minimum overall AIC (African Lake partition of CmC; 12620.6) was used for all comparisons.

Abbreviations—**np**, number of parameters; **lnL**, ln Likelihood; **K**, transition/transversion ratio; **LRT**, likelihood ratio test statistic; **df**, degrees of freedom; **P**, P-value; **n/a**, not applicable.

Supplementary Table S11. List of positively selected sites found by the M2a and M8 BEB and the REL, FEL, and FUBAR HYPHY analyses for Neotropical cichlids. Sites were included if they had a posterior probability (Pr) of being positively selected of at least 80% for one of the models.

Bovine	M2a (Pr)	M8 (Pr)	REL (Pr)	FUBAR (Pr)	FEL (P)
33	0.746	0.928	0.960	0.935	0.096
49	0.365	0.540	0.923	0.666	0.571
50	0.437	0.623	0.987	0.827	0.091
70	0.036	0.035	0.898	0.664	0.252
75	0.203	0.394	0.973	0.911	0.076
124	0.727	0.920	0.872	0.872	0.433
156	0.993	0.999	0.970	0.995	0.010
158	0.115	0.182	0.874	0.592	0.824
159	0.030	0.028	0.930	0.686	0.253
169	0.969	0.992	0.981	0.929	0.051
172	0.709	0.891	0.939	0.853	0.283
173	0.940	0.990	0.925	0.941	0.161
210	0.154	0.242	0.868	0.628	0.735
214	0.115	0.125	0.943	0.702	0.173
217	1.000	1.000	0.932	0.994	0.032
218	0.288	0.442	0.984	0.814	0.098
248	0.617	0.791	0.939	0.738	0.308
270	0.995	0.999	0.867	0.964	0.162
274	0.992	0.999	0.904	0.942	0.284
281	0.977	0.996	0.988	0.988	0.015
286	0.968	0.996	0.856	0.965	0.158
287	0.778	0.951	0.864	0.931	0.285
299	0.627	0.873	0.974	0.953	0.057
304	0.504	0.590	0.977	0.797	0.095

Supplementary Table S12. List of positively selected sites found by the M2a and M8 BEB and the REL, FEL, and FUBAR HYPHY analyses for African lake cichlids. Sites were included if they had a posterior probability (Pr) of being positively selected of at least 80% for one of the models.

Codon	M2a (Pr)	M8 (Pr)	REL (Pr)	FUBAR (Pr)	FEL (P)
32	0.212	0.247	0.996	0.837	0.281
33	0.432	0.465	0.990	0.777	0.487
37	0.970	0.980	0.998	0.961	0.162
41	0.966	0.977	0.999	0.936	0.203
42	0.797	0.844	0.999	0.945	0.201
48	0.162	0.195	0.993	0.817	0.416
83	0.323	0.358	0.992	0.803	0.458
95	0.992	0.996	0.999	0.979	0.120
104	0.208	0.244	0.996	0.837	0.287
133	0.990	0.994	0.998	0.976	0.14
162	0.987	0.991	0.999	0.955	0.143
163	0.800	0.819	0.986	0.600	0.938
165	1.000	1.000	0.999	0.997	0.016
166	0.953	0.968	0.999	0.970	0.118
169	0.999	0.999	0.999	0.982	0.091
185	0.462	0.495	0.992	0.792	0.443
213	1.000	1.000	0.266	0.545	0.596
217	1.000	1.000	0.999	0.992	0.052
218	1.000	1.000	0.999	0.994	0.034
259	0.906	0.932	0.946	0.686	0.967
263	0.983	0.989	0.999	0.942	0.197
270	0.915	0.926	0.972	0.523	0.800
290	0.278	0.314	0.997	0.911	0.199
292	0.807	0.853	0.999	0.950	0.182
297	1.000	1.000	0.949	0.770	0.629
298	0.995	0.997	0.999	0.986	0.090
299	1.000	1.000	0.999	0.992	0.031

Supplementary Table S13. List of positively selected sites found by the M2a and M8 BEB and the REL, FEL, and FUBAR HYPHY analyses for African riverine cichlids. Sites were included if they had a posterior probability (Pr) of being positively selected of at least 80% for one of the models.

Codon	M2a (Pr)	M8 (Pr)	REL (Pr)	FUBAR (Pr)	FEL (P)
49	0.801	0.870	1.000	0.8610	0.128
50	0.254	0.322	0.998	0.644	0.311
133	0.771	0.851	1.000	0.861	0.144
162	0.974	0.987	1.000	0.887	0.392
166	0.278	0.345	0.998	0.641	0.321
169	0.500	0.546	0.998	0.646	0.334
173	0.195	0.257	0.995	0.343	0.796
218	0.233	0.299	0.998	0.660	0.283
260	0.661	0.778	1.000	0.827	0.217
263	0.351	0.415	0.997	0.599	0.526
282	0.377	0.439	0.998	0.602	0.504
297	0.760	0.845	1.000	0.946	0.141
298	0.160	0.219	0.993	0.295	0.600
304	0.528	0.578	0.997	0.520	0.990

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