



Supplementary Material

Genetic Basis of Hydrothermal Vent Adaptation in Bythograeidae Crabs: Insights from Adaptive Evolution of Mitochondrial Protein Coding Genes

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0030-9923/2019/0005-1721 \$ 9.00/0
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Supplementary Table I.- The genbank accession number of 49 species mitochondrial genome used in this study.

Species	ID	Species	ID
<i>Pyrhila pisum</i>	NC_030047	<i>Eriocheir sinensis</i>	NC_006992
<i>Scylla olivacea</i>	NC_012569	<i>Eriocheir hepuensis</i>	NC_011598
<i>Scylla serrata</i>	NC_012565	<i>Helicana wuana</i>	NC_034995
<i>Scylla paramamosain</i>	NC_012572	<i>Helice tientsinensis</i>	NC_030197
<i>Scylla tranquebarica</i>	NC_012567	<i>Ilyoplax deschampsii</i>	NC_020040
<i>Charybdis japonica</i>	NC_013246	<i>Xenograpsus testudinatus</i>	NC_013480
<i>Charybdis feriata</i>	NC_024632	<i>Parasesarma tripectinis</i>	NC_030046
<i>Callinectes sapidus</i>	NC_006281	<i>Metopaulias depressus</i>	NC_030535
<i>Portunus sanguinolentus</i>	NC_028225	<i>Clistocoeloma sinense</i>	NC_033866
<i>Portunus pelagicus</i>	NC_026209	<i>Sesarma neglectum</i>	NC_031851
<i>Portunus trituberculatus</i>	NC_005037	<i>Sesarmops sinensis</i>	NC_030196
<i>Maja squinado</i>	NC_035425	<i>Grapsus tenuicrustatus</i>	NC_029724
<i>Maja crispata</i>	NC_035424	<i>Pachygrapsus crassipes</i>	NC_021754
<i>Damithrax spinosissimus</i>	NC_025518	<i>Ocypode cordimanus</i>	NC_029725
<i>Leptodiis sanguineus</i>	NC_029726	<i>Somaniathelphusa boyangensis</i>	NC_032044
<i>Pseudocarcinus gigas</i>	NC_006891	<i>Huananpotamon lichuanense</i>	NC_031406
<i>Segonzacia mesatlantica</i>	NC_035300	<i>Sinopotamon xiushuiense</i>	NC_029226
<i>Gandalfus puia</i>	NC_027414	<i>Geothelphusa dehaani</i>	NC_007379
<i>Gandalfus yunohana</i>	NC_013713	<i>Umalia orientalis</i>	NC_026688
<i>Austinograea alayseae</i>	NC_020314	<i>Lyreidus brevifrons</i>	NC_026721
<i>Austinograea rodriguezensis</i>	NC_020312	<i>Homologenus malayensis</i>	NC_026080
<i>Macrophthalmus japonicus</i>	NC_030048	<i>Moloha majora</i>	NC_029361
<i>Mictyris longicarpus</i>	NC_025325	<i>Parasesarma pictum</i>	MG_580780
<i>Hemigrapsus sanguineus</i>	NC_035307	<i>Clibanarius infraspinus</i>	NC_025776
<i>Eriocheir japonica</i>	NC_011597		

Supplementary Table II.- Selective pressure analyses (Branch-site Model) of mitochondrial protein-encoding genes (13 genes) in Bythograeidae.

Gene	Models	lnL	2lnL	p value	Parameters	Positive selected sites
ATP8	branch i					
	ma	-519.39935			$\omega_0 = 0.052 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-519.39935	0	1	$\omega_0 = 0.052 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch b					
	ma	-519.96253			$\omega_0 = 0.06 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-519.96253	-2E-06	1	$\omega_0 = 0.06 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch f					
	ma	-519.59176			$\omega_0 = 0.049 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-519.59176	0	1	$\omega_0 = 0.049 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch c					
	ma	-519.9324			$\omega_0 = 0.054 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-519.9324	0	1	$\omega_0 = 0.054 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch g					
	ma	-519.96253			$\omega_0 = 0.06 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-519.96253	0	1	$\omega_0 = 0.06 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch e					
	ma	-519.91764			$\omega_0 = 0.057 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-519.91764	0	1	$\omega_0 = 0.057 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch d					
	ma	-519.96253			$\omega_0 = 0.06 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
ma0	-519.96253	0	1	$\omega_0 = 0.06 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
branch h						
ma	-519.96253			$\omega_0 = 0.06 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
ma0	-519.96253	0	1	$\omega_0 = 0.06 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
COX2	branch d					
	ma	-1730.9119			$\omega_0 = 0.014 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-1730.9119	0	1	$\omega_0 = 0.014 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch g					
	ma	-1730.9119			$\omega_0 = 0.014 \ \omega_1 = 1.0 \ \omega_2 = 45.234$	
	ma0	-1730.9119	0	1	$\omega_0 = 0.014 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch h					
	ma	-1730.5828			$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-1730.5828	0	1	$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch b					
	ma	-1730.912			$\omega_0 = 0.014 \ \omega_1 = 1.0 \ \omega_2 = 12.881$	
	ma0	-1728.8364	-4.15126	1	$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch f					
	ma	-1730.9119			$\omega_0 = 0.014 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-1733.2311	4.63844	0.03126341	$\omega_0 = 0.012 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch e					
	ma	-1730.8298			$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-1730.8296	-0.00036	1	$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch c					
	ma	-1728.538			$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 999.0$	
ma0	-1728.8364	0.59668	0.43984603	$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
branch i						
ma	-1730.9119			$\omega_0 = 0.014 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
ma0	-1730.9119	0	1	$\omega_0 = 0.014 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		

Gene	Models	lnL	2lnL	p value	Parameters	Positive selected sites
COX3	branch c					
	ma	-1983.9202			$\omega_0 = 0.006$ $\omega_1 = 1.0$ $\omega_2 = 50.628$	159 0.770; 222 0.552; 232 0.929
	ma0	-1985.9746	4.10866	0.04266415	$\omega_0 = 0.005$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	branch h					
	ma	-1992.2083			$\omega_0 = 0.006$ $\omega_1 = 1.0$ $\omega_2 = 3.036$	
	ma0	-1988.9104	-6.59589	1	$\omega_0 = 0.006$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	branch g					
	ma	-1988.1312			$\omega_0 = 0.005$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	ma0	-1988.0407	-0.18107	1	$\omega_0 = 0.005$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	branch e					
	ma	-1992.3106			$\omega_0 = 0.006$ $\omega_1 = 1.0$ $\omega_2 = 3.72$	
	ma0	-1992.3105	-0.00022	1	$\omega_0 = 0.006$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	branch b					
	ma	-1983.9203			$\omega_0 = 0.006$ $\omega_1 = 1.0$ $\omega_2 = 52.197$	159 0.769; 222 0.558; 232 0.931
	ma0	-1985.9746	4.10857	0.04266632	$\omega_0 = 0.005$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	branch f					
	ma	-1984.7056			$\omega_0 = 0.006$ $\omega_1 = 1.0$ $\omega_2 = 7.36$	
	ma0	-1986.1764	2.94142	0.08633491	$\omega_0 = 0.006$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
branch d						
ma	-1988.8086			$\omega_0 = 0.006$ $\omega_1 = 1.0$ $\omega_2 = 14.585$		
ma0	-1988.8938	0.17053	0.67963766	$\omega_0 = 0.006$ $\omega_1 = 1.0$ $\omega_2 = 1.0$		
branch i						
ma	-1988.591			$\omega_0 = 0.006$ $\omega_1 = 1.0$ $\omega_2 = 1.0$		
ma0	-1988.591	0	1	$\omega_0 = 0.006$ $\omega_1 = 1.0$ $\omega_2 = 1.0$		
CYTB	branch h					
	ma	-3101.8013			$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	ma0	-3101.8013	0	1	$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	branch f					
	ma	-3101.8013			$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	ma0	-3101.8013	0	1	$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	branch d					
	ma	-3101.5883			$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	ma0	-3101.5883	0	1	$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	branch g					
	ma	-3101.8013			$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	ma0	-3101.8013	0	1	$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	branch e					
	ma	-3099.6528			$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 20.715$	
	ma0	-3100.605	1.90452	0.16757326	$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
	branch i					
	ma	-3101.1581			$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 91.225$	
	ma0	-3101.663	1.00983	0.31494309	$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	
branch c						
ma	-3098.5223			$\omega_0 = 0.014$ $\omega_1 = 1.0$ $\omega_2 = 999.0$		
ma0	-3098.6698	0.29492	0.58708733	$\omega_0 = 0.014$ $\omega_1 = 1.0$ $\omega_2 = 1.0$		
branch b						
ma	-3101.8014			$\omega_0 = 0.015$ $\omega_1 = 1.0$ $\omega_2 = 7.941$		
ma0	-3098.7234	-6.156	1	$\omega_0 = 0.014$ $\omega_1 = 1.0$ $\omega_2 = 1.0$		
COX1	branch h					
	ma	-3824.9142			$\omega_0 = 0.005$ $\omega_1 = 1.0$ $\omega_2 = 2.06$	
	ma0	-3824.9388	0.04928	0.8243244	$\omega_0 = 0.005$ $\omega_1 = 1.0$ $\omega_2 = 1.0$	

Gene	Models	lnL	2lnL	p value	Parameters	Positive selected sites
COX1	branch f					
	ma	-3824.9509			$\omega_0 = 0.005 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-3824.9509	0	1	$\omega_0 = 0.005 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch b					
	ma	-3824.9508			$\omega_0 = 0.005 \ \omega_1 = 1.0 \ \omega_2 = 5.031$	
	ma0	-3822.2606	-5.38034	1	$\omega_0 = 0.004 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch e					
	ma	-3824.9509			$\omega_0 = 0.005 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-3824.9509	0	1	$\omega_0 = 0.005 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch c					
	ma	-3824.2785			$\omega_0 = 0.004 \ \omega_1 = 1.0 \ \omega_2 = 31.659$	
	ma0	-3824.2767	-0.00352	1	$\omega_0 = 0.004 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch d					
	ma	-3824.8437			$\omega_0 = 0.004 \ \omega_1 = 1.0 \ \omega_2 = 11.315$	
	ma0	-3824.9275	0.16762	0.68223392	$\omega_0 = 0.005 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch g					
ma	-3824.9509			$\omega_0 = 0.005 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
ma0	-3824.9509	0	1	$\omega_0 = 0.005 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
branch i						
ma	-3824.9509			$\omega_0 = 0.005 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
ma0	-3824.9509	0	1	$\omega_0 = 0.005 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
ATP6	branch e					
	ma	-1757.2242			$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 5.41$	
	ma0	-1757.2242	-1.2E-05	1	$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch g					
	ma	-1756.5213			$\omega_0 = 0.01 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-1756.5213	0	1	$\omega_0 = 0.01 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch b					
	ma	-1756.8898			$\omega_0 = 0.011 \ \omega_1 = 1.0 \ \omega_2 = 999.0$	
	ma0	-1757.1384	0.4971	0.4807789	$\omega_0 = 0.012 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch i					
	ma	-1756.9165			$\omega_0 = 0.011 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-1756.9165	0	1	$\omega_0 = 0.011 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch c					
	ma	-1757.2242			$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 4.543$	
	ma0	-1757.2242	-6E-06	1	$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch f					
ma	-1757.1372			$\omega_0 = 0.012 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
ma0	-1757.1372	0	1	$\omega_0 = 0.012 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
branch h						
ma	-1757.2242			$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
ma0	-1757.2242	0	1	$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
branch d						
ma	-1757.2242			$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
ma0	-1757.2242	0	1	$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
ND4L	branch e					
	ma	-752.08739			$\omega_0 = 0.008 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-752.08739	0	1	$\omega_0 = 0.008 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch i					
ma	-752.18058			$\omega_0 = 0.009 \ \omega_1 = 1.0 \ \omega_2 = 4.242$		
ma0	-752.18058	0	1	$\omega_0 = 0.009 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		

Gene	Models	lnL	2lnL	p value	Parameters	Positive selected sites
ND4L	branch g					
	ma	-752.18058			$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 1.0$	
	ma0	-752.18058	0	1	$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch c					
	ma	-752.18058			$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 2.402$	
	ma0	-752.18058	0	1	$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch b					
	ma	-751.96335			$\omega_0 = 0.008 \omega_1 = 1.0 \omega_2 = 990.136$	
	ma0	-751.96398	0.00124	0.97188676	$\omega_0 = 0.008 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch d					
	ma	-751.28556			$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 999.0$	
	ma0	-751.30177	0.03244	0.85707408	$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch f					
	ma	-751.86756			$\omega_0 = 0.006 \omega_1 = 1.0 \omega_2 = 2.783$	
ma0	-751.98839	0.24167	0.62300398	$\omega_0 = 0.007 \omega_1 = 1.0 \omega_2 = 1.0$		
branch h						
ma	-751.74273			$\omega_0 = 0.007 \omega_1 = 1.0 \omega_2 = 15.501$		
ma0	-752.18058	0.8757	0.34938213	$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 1.0$		
ND1	branch f					
	ma	-2389.8156			$\omega_0 = 0.01 \omega_1 = 1.0 \omega_2 = 1.0$	
	ma0	-2389.8156	0	1	$\omega_0 = 0.01 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch h					
	ma	-2389.8156			$\omega_0 = 0.01 \omega_1 = 1.0 \omega_2 = 1.0$	
	ma0	-2389.8156	0	1	$\omega_0 = 0.01 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch g					
	ma	-2389.3639			$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 1.0$	
	ma0	-2389.3639	0	1	$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch c					
	ma	-2387.066			$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 11.815$	
	ma0	-2387.2644	0.39688	0.52870705	$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch i					
	ma	-2389.8156			$\omega_0 = 0.01 \omega_1 = 1.0 \omega_2 = 1.0$	
ma0	-2389.8156	0	1	$\omega_0 = 0.01 \omega_1 = 1.0 \omega_2 = 1.0$		
branch b						
ma	-2387.2763			$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 1.1$		
ma0	-2387.2803	0.00801	0.92870342	$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 1.0$		
branch d						
ma	-2389.5744			$\omega_0 = 0.009 \omega_1 = 1.0 \omega_2 = 154.202$		
ma0	-2389.5778	0.00667	0.93491882	$\omega_0 = 0.01 \omega_1 = 1.0 \omega_2 = 1.0$		
branch e						
ma	-2389.8156			$\omega_0 = 0.01 \omega_1 = 1.0 \omega_2 = 1.0$		
ma0	-2389.8156	0	1	$\omega_0 = 0.01 \omega_1 = 1.0 \omega_2 = 1.0$		
ND3	branch i					
	ma	-988.79704			$\omega_0 = 0.013 \omega_1 = 1.0 \omega_2 = 1.671$	
	ma0	-988.82001	0.04594	0.8302849	$\omega_0 = 0.013 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch d					
	ma	-990.09381			$\omega_0 = 0.015 \omega_1 = 1.0 \omega_2 = 8.578$	
	ma0	-989.63221	-0.92322	1	$\omega_0 = 0.016 \omega_1 = 1.0 \omega_2 = 1.0$	
branch b						
ma	-987.60525			$\omega_0 = 0.014 \omega_1 = 1.0 \omega_2 = 1.263$		
ma0	-987.63206	0.05361	0.81690332	$\omega_0 = 0.014 \omega_1 = 1.0 \omega_2 = 1.0$		

Gene	Models	lnL	2lnL	p value	Parameters	Positive selected sites
ND3	branch h					
	ma	-989.57141			$\omega_0 = 0.015 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-989.57141	0	1	$\omega_0 = 0.015 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch g					
	ma	-989.63221			$\omega_0 = 0.016 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-989.63221	0	1	$\omega_0 = 0.016 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch c					
	ma	-987.60525			$\omega_0 = 0.014 \ \omega_1 = 1.0 \ \omega_2 = 1.263$	
	ma0	-987.63206	0.05361	0.81690332	$\omega_0 = 0.014 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch e					
	ma	-989.00946			$\omega_0 = 0.013 \ \omega_1 = 1.0 \ \omega_2 = 11.932$	
	ma0	-989.37768	0.73644	0.39080302	$\omega_0 = 0.014 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch f					
	ma	-989.63221			$\omega_0 = 0.016 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
ma0	-989.63221	0	1	$\omega_0 = 0.016 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
ND2	branch c					
	ma	-3307.378			$\omega_0 = 0.035 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-3307.378	-4E-06	1	$\omega_0 = 0.035 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch g					
	ma	-3307.378			$\omega_0 = 0.035 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-3307.378	0	1	$\omega_0 = 0.035 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch h					
	ma	-3305.5072			$\omega_0 = 0.032 \ \omega_1 = 1.0 \ \omega_2 = 2.041$	
	ma0	-3305.6093	0.20417	0.65137898	$\omega_0 = 0.032 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch d					
	ma	-3304.0371			$\omega_0 = 0.034 \ \omega_1 = 1.0 \ \omega_2 = 9.771$	81 0.828; 146 0.688; 224 0.989; 233 0.792
	ma0	-3306.0675	4.06079	0.04388986	$\omega_0 = 0.034 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch e					
	ma	-3307.3699			$\omega_0 = 0.035 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-3307.3699	0	1	$\omega_0 = 0.035 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch i					
	ma	-3306.4291			$\omega_0 = 0.032 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-3306.4291	0	1	$\omega_0 = 0.032 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch f					
	ma	-3304.5181			$\omega_0 = 0.032 \ \omega_1 = 1.0 \ \omega_2 = 3.27$	
ma0	-3305.2249	1.41347	0.23448187	$\omega_0 = 0.032 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
branch b						
ma	-3306.9645			$\omega_0 = 0.034 \ \omega_1 = 1.0 \ \omega_2 = 999.0$		
ma0	-3307.0926	0.25618	0.61275955	$\omega_0 = 0.034 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
ND5	branch d					
	ma	-4972.0567			$\omega_0 = 0.021 \ \omega_1 = 1.0 \ \omega_2 = 34.114$	187 0.597; 247 0.932; 341 0.679; 381 0.609; 541 0.627; 543 0.518
	ma0	-4974.2993	4.48505	0.03419263	$\omega_0 = 0.021 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch e					
	ma	-4975.4892			$\omega_0 = 0.022 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-4975.4892	0	1	$\omega_0 = 0.022 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch i					
ma	-4973.2687			$\omega_0 = 0.02 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		
ma0	-4973.2687	0	1	$\omega_0 = 0.02 \ \omega_1 = 1.0 \ \omega_2 = 1.0$		

Gene	Models	lnL	2lnL	p value	Parameters	Positive selected sites
ND4	branch h					
	ma	-4975.4892			$\omega_0 = 0.022 \omega_1 = 1.0 \omega_2 = 1.0$	
	ma0	-4975.4892	0	1	$\omega_0 = 0.022 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch g					
	ma	-4975.4892			$\omega_0 = 0.022 \omega_1 = 1.0 \omega_2 = 1.0$	
	ma0	-4975.4892	0	1	$\omega_0 = 0.022 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch c					
	ma	-4973.3286			$\omega_0 = 0.02 \omega_1 = 1.0 \omega_2 = 1.0$	
	ma0	-4973.3286	0	1	$\omega_0 = 0.02 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch f					
	ma	-4974.1391			$\omega_0 = 0.021 \omega_1 = 1.0 \omega_2 = 1.0$	
	ma0	-4974.1391	0	1	$\omega_0 = 0.021 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch b					
	ma	-4973.0912			$\omega_0 = 0.02 \omega_1 = 1.0 \omega_2 = 1.0$	
	ma0	-4973.0912	0	1	$\omega_0 = 0.02 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch i					
	ma	-3538.0927			$\omega_0 = 0.012 \omega_1 = 1.0 \omega_2 = 1.0$	
	ma0	-3538.0927	0	1	$\omega_0 = 0.012 \omega_1 = 1.0 \omega_2 = 1.0$	
	branch e					
	ma	-3538.3635			$\omega_0 = 0.013 \omega_1 = 1.0 \omega_2 = 1.0$	
ma0	-3538.3635	8E-06	0.99774324	$\omega_0 = 0.013 \omega_1 = 1.0 \omega_2 = 1.0$		
branch c						
ma	-3532.9609			$\omega_0 = 0.01 \omega_1 = 1.0 \omega_2 = 1.0$		
ma0	-3532.9609	0	1	$\omega_0 = 0.01 \omega_1 = 1.0 \omega_2 = 1.0$		
branch g						
ma	-3538.3635			$\omega_0 = 0.013 \omega_1 = 1.0 \omega_2 = 1.0$		
ma0	-3538.3635	0	1	$\omega_0 = 0.013 \omega_1 = 1.0 \omega_2 = 1.0$		
branch h						
ma	-3537.4516			$\omega_0 = 0.012 \omega_1 = 1.0 \omega_2 = 4.976$		
ma0	-3537.7266	0.55016	0.45825396	$\omega_0 = 0.012 \omega_1 = 1.0 \omega_2 = 1.0$		
branch f						
ma	-3538.3635			$\omega_0 = 0.013 \omega_1 = 1.0 \omega_2 = 1.0$		
ma0	-3538.3635	0	1	$\omega_0 = 0.013 \omega_1 = 1.0 \omega_2 = 1.0$		
branch d						
ma	-3538.3635			$\omega_0 = 0.013 \omega_1 = 1.0 \omega_2 = 1.0$		
ma0	-3538.3635	0	1	$\omega_0 = 0.013 \omega_1 = 1.0 \omega_2 = 1.0$		
branch b						
ma	-3531.9809			$\omega_0 = 0.01 \omega_1 = 1.0 \omega_2 = 999.0$		
ma0	-3532.415	0.8683	0.35142526	$\omega_0 = 0.01 \omega_1 = 1.0 \omega_2 = 1.0$		
branch b						
ma	-1607.3004			$\omega_0 = 0.019 \omega_1 = 1.0 \omega_2 = 1.0$		
ma0	-1607.3004	0	1	$\omega_0 = 0.019 \omega_1 = 1.0 \omega_2 = 1.0$		
branch e						
ma	-1607.3628			$\omega_0 = 0.022 \omega_1 = 1.0 \omega_2 = 3.056$		
ma0	-1607.4093	0.09303	0.76035492	$\omega_0 = 0.021 \omega_1 = 1.0 \omega_2 = 1.0$		
branch d						
ma	-1607.1562			$\omega_0 = 0.021 \omega_1 = 1.0 \omega_2 = 2.833$		
ma0	-1607.308	0.30359	0.58164176	$\omega_0 = 0.021 \omega_1 = 1.0 \omega_2 = 1.0$		
branch g						
ma	-1607.4093			$\omega_0 = 0.021 \omega_1 = 1.0 \omega_2 = 1.0$		
ma0	-1607.4093	0	1	$\omega_0 = 0.021 \omega_1 = 1.0 \omega_2 = 1.0$		

Gene	Models	lnL	2lnL	p value	Parameters	Positive selected sites
	branch i					
	ma	-1607.4093			$\omega_0 = 0.021 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-1607.4093	0	1	$\omega_0 = 0.021 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch h					
	ma	-1607.4093			$\omega_0 = 0.021 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-1607.4093	0	1	$\omega_0 = 0.021 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch f					
	ma	-1605.1961			$\omega_0 = 0.017 \ \omega_1 = 1.0 \ \omega_2 = 1.107$	
	ma0	-1605.199	0.00578	0.93939817	$\omega_0 = 0.017 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	branch c					
	ma	-1607.3694			$\omega_0 = 0.02 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	
	ma0	-1607.3694	0	1	$\omega_0 = 0.02 \ \omega_1 = 1.0 \ \omega_2 = 1.0$	

Supplementary Table III.- Selective pressure analyses (M8 vs M8a) of mitochondrial protein-encoding genes (13 genes) in Bythograeidae.

Gene	ln_M8a	ln_M8	2lnL	p value	ω
ATP6	-1757.398543	-1758.688196	-2.579306	1	353.9346
ATP8	-518.807481	-518.807481	0	1	1
COX1	-3819.887421	-3819.887421	0	1	1
COX2	-1730.067027	-1730.067027	0	1	1
COX3	-1985.381806	-1984.431818	1.899976	0.168081005	68.59952
CYTB	-3099.311704	-3101.404619	-4.18583	1	6.76675
ND1	-2379.344403	-2378.763255	1.162296	0.280989879	2.73622
ND2	-3294.029919	-3294.029919	0	1	1
ND3	-984.420618	-984.420618	0	1	1
ND4	-3519.66149	-3519.808687	-0.294394	1	16.00669
ND4L	-745.811591	-745.811591	0	1	1
ND5	-4954.521294	-4954.306385	0.429818	0.512078266	3.04222
ND6	-1601.622579	-1601.622579	0	1	1

Supplementary Table IV.- Positively selected sites of 13 mitochondrial protein-coding genes identified by PAML, DATAMONKEY and TreeSAAP (*<https://www.predictprotein.org/>).

Genes	AA Posit.	PAML Branch-Site Model (PP>0.8)	DATAMONKEY		TreeSAAP Radical changes in amino acid properties	Total	Secondary structure* (Region)
			FEL p<0.1	REL BF>50			
ATP6	64			107.515			Protein binding
	65				1	1	Protein binding
	67			208.552		1	Protein binding
	71					1	
	81					1	Helical transmembrane
	85					1	Helical transmembrane
	99					1	Helical transmembrane
	111			263.969		1	Helical transmembrane
	115					1	Helical transmembrane
	136					1	Helical transmembrane

Genes	AA Posit.	PAML Branch- Site Model (PP>0.8)	DATAMONKEY		TreeSAAP Radical changes in amino acid properties	Total	Secondary structure* (Region)
			FEL p<0.1	REL BF>50			
ATP6	159				Equilibrium constant (ionization of COOH)	1	
	177				Isoelectric point; Short and medium range non-bonded energy; Partial specific volume	3	
	184			93.809	Mean r.m.s. fluctuation displacement	1	
	188				Mean r.m.s. fluctuation displacement	1	
	206				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	216				Isoelectric point; Short and medium range non-bonded energy; Partial specific volume	3	Helical transmembrane
ATP8	1			53.689			Protein binding
	18				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	31				Equilibrium constant (ionization of COOH)	1	
	38				Equilibrium constant (ionization of COOH)	1	
	40				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	42				Equilibrium constant (ionization of COOH)	1	Helical transmembrane; Protein binding
COX1	113				Partial specific volume; Partial specific volume; Short and medium range non-bonded energy	3	Helical transmembrane
	115				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	118				Partial specific volume; Isoelectric point; Short and medium range non-bonded energy	3	
	143				Equilibrium constant (ionization of COOH)	1	
	186				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	251				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	257				Partial specific volume; Isoelectric point; Short and medium range non-bonded energy	3	
	271				Equilibrium constant (ionization of COOH)	1	
	275				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	280				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	295				Equilibrium constant (ionization of COOH)	1	
	320				Partial specific volume; Short and medium range non-bonded energy; Isoelectric point	3	Helical transmembrane
	323				Partial specific volume; Isoelectric point; Short and medium range non-bonded energy	3	
	333				Partial specific volume; Isoelectric point; Short and medium range non-bonded energy	3	
	336				Equilibrium constant (ionization of COOH)	1	
	337				Equilibrium constant (ionization of COOH)	1	
	348				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	361				Equilibrium constant (ionization of COOH)	1	
	381				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	414				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
432				Isoelectric point	1		
434				Equilibrium constant (ionization of COOH)	1		
450				Equilibrium constant (ionization of COOH)	1		
451			66.0607		Equilibrium constant (ionization of COOH)	1	
454					Equilibrium constant (ionization of COOH)	1	Helical transmembrane
465					Partial specific volume; Equilibrium constant (ionization of COOH)	2	Helical transmembrane

Genes	AA Posit.	PAML Branch-Site Model (PP>0.8)	DATAMONKEY		TreeSAAP Radical changes in amino acid properties	Total	Secondary structure* (Region)	
			FEL p<0.1	REL BF>50				
COX1	477				Partial specific volume; Isoelectric point; Molecular weight	3		
	495				Equilibrium constant (ionization of COOH); Isoelectric point	2		
	504				Equilibrium constant (ionization of COOH)	1	Protein binding region	
COX2	28				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	29				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	31				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	32				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	45				Equilibrium constant (ionization of COOH)	1		
	46				Equilibrium constant (ionization of COOH)	1		
	55				Equilibrium constant (ionization of COOH)	1		
	71				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	116				Equilibrium constant (ionization of COOH)	1		
	143				Equilibrium constant (ionization of COOH)	1		
	152				Equilibrium constant (ionization of COOH)	1		
	165				Equilibrium constant (ionization of COOH)	1		
	207				Equilibrium constant (ionization of COOH)	1		
	214				Equilibrium constant (ionization of COOH)	1		
	223				Equilibrium constant (ionization of COOH)	1		
COX3	16				Partial specific volume; Helical contact area; Isoelectric point; Short and medium range non-bonded energy	4		
	25				Partial specific volume; Helical contact area; Isoelectric point; Short and medium range non-bonded energy	4	Helical transmembrane	
	28				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	50				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	78				Equilibrium constant (ionization of COOH)	1		
	85				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	107				Partial specific volume; Helical contact area; Isoelectric point; Short and medium range non-bonded energy	4		
	112				Equilibrium constant (ionization of COOH)	1	Protein binding	
	116				Equilibrium constant (ionization of COOH)	1	Protein binding	
	159	0.770(branch c); 0.769(branch b)				Partial specific volume; Helical contact area; Isoelectric point; Short and medium range non-bonded energy	4	
	177				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	219				Equilibrium constant (ionization of COOH)	1		
	222	0.552(branch c); 0.558(branch b)				Equilibrium constant (ionization of COOH)	1	
232	0.929(branch c); 0.931(branch b)						Protein binding	
CYTB	15				Equilibrium constant (ionization of COOH)	1		
	103				Equilibrium constant (ionization of COOH)	1		
	109				Equilibrium constant (ionization of COOH)	1		
	110				Equilibrium constant (ionization of COOH)	1		
	115				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	116				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	

Genes	AA Posit.	PAML Branch- Site Model (PP>0.8)	DATAMONKEY		TreeSAAP Radical changes in amino acid properties	Total	Secondary structure* (Region)	
			FEL p<0.1	REL BF>50				
CYTB	125				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	157				Equilibrium constant (ionization of COOH)	1		
	185				Equilibrium constant (ionization of COOH)	1		
	193				Equilibrium constant (ionization of COOH)	1		
	195				Equilibrium constant (ionization of COOH)	1		
	216				Equilibrium constant (ionization of COOH)	1		
	234				Equilibrium constant (ionization of COOH)	1		
	236				Equilibrium constant (ionization of COOH)	1		
	246				Equilibrium constant (ionization of COOH)	1		
	258				Equilibrium constant (ionization of COOH)	1		
	267				Equilibrium constant (ionization of COOH)	1		
	300				Equilibrium constant (ionization of COOH)	1		
	301				Equilibrium constant (ionization of COOH)	1		
	303				Equilibrium constant (ionization of COOH)	1		
	310				Equilibrium constant (ionization of COOH)	1		
	312				Isoelectric point	1		
	321				Equilibrium constant (ionization of COOH)	1		
	324				Equilibrium constant (ionization of COOH)	1		
	330				Equilibrium constant (ionization of COOH)	1		
	358			199.547				
	364				Equilibrium constant (ionization of COOH)	1		
	365				Equilibrium constant (ionization of COOH)	1		
	370				Equilibrium constant (ionization of COOH)	1		
	371				Equilibrium constant (ionization of COOH)	1		
	376				Equilibrium constant (ionization of COOH)	1		
	ND1	1				Equilibrium constant (ionization of COOH)		1
		2				Equilibrium constant (ionization of COOH)		1
		3				Equilibrium constant (ionization of COOH)		1
		5				Equilibrium constant (ionization of COOH)		1
		12				Equilibrium constant (ionization of COOH)		1
		13				Equilibrium constant (ionization of COOH)		1
		45				Equilibrium constant (ionization of COOH)		1
		47				Equilibrium constant (ionization of COOH)		1
		66				Equilibrium constant (ionization of COOH)		1
		67				Equilibrium constant (ionization of COOH)		1
		83				Equilibrium constant (ionization of COOH)		1
		91				Equilibrium constant (ionization of COOH)		1
98					Equilibrium constant (ionization of COOH)	1		
102					Equilibrium constant (ionization of COOH)	1		
157					Equilibrium constant (ionization of COOH)	1		
173		0.646(branch a)						
174		0.705(branch a)						
177					Equilibrium constant (ionization of COOH)	1		
181					Equilibrium constant (ionization of COOH)	1		
227					Equilibrium constant (ionization of COOH)	1		
236					Equilibrium constant (ionization of COOH)	1		
238					Equilibrium constant (ionization of COOH)	1		
243					Equilibrium constant (ionization of COOH)	1		

Genes	AA Posit.	PAML Branch-Site Model (PP>0.8)	DATAMONKEY		TreeSAAP Radical changes in amino acid properties	Total	Secondary structure* (Region)
			FEL p<0.1	REL BF>50			
ND1	252	0.990(branch a)					Helical transmembrane
	253	0.572(branch a)					Helical transmembrane
	258				Average number of surrounding residues; Coil tendencies	2	Helical transmembrane
	261				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	281				Equilibrium constant (ionization of COOH)	1	
	297				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	300				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	302				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	305				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	308				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	309	0.625(branch a)			Equilibrium constant (ionization of COOH)	1	Helical transmembrane
310		0.076833				Helical transmembrane	
311	0.992(branch a)						
ND2	15				Buriedness; Polar requirement; Solvent accessible reduction ratio	3	Helical transmembrane
	16				Buriedness; Polarity	2	Helical transmembrane
	22				Solvent accessible reduction ratio	1	Helical transmembrane
	49				Solvent accessible reduction ratio	1	Protein binding
	81	0.828(branch d)					
	83				Solvent accessible reduction ratio	1	
	86				Solvent accessible reduction ratio	1	Helical transmembrane
	110				Solvent accessible reduction ratio	1	
	141				Solvent accessible reduction ratio	1	
	143				Solvent accessible reduction ratio	1	
	146	0.688(branch d)			Solvent accessible reduction ratio	1	Helical transmembrane
	156				Solvent accessible reduction ratio	1	Helical transmembrane
	165				Solvent accessible reduction ratio	1	
	191				Solvent accessible reduction ratio	1	
	201				Solvent accessible reduction ratio	1	Helical transmembrane
	214				Solvent accessible reduction ratio	1	
	224	0.989(branch d)					Protein binding
	233	0.792(branch d)			Polarity; Solvent accessible reduction ratio	1	
	290				Solvent accessible reduction ratio	1	
296				Solvent accessible reduction ratio	1		
304				Solvent accessible reduction ratio	1	Protein binding	
ND3	109				Power to be at the middle of alpha-helix	1	
ND4	10				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	11		51.0748				Helical transmembrane
	12				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	20				Mean r.m.s. fluctuation displacement	1	Helical transmembrane
	25				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	26				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	31				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	31				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	41				Short and medium range non-bonded energy	1	
	44		0.071665		Isoelectric point	1	
	48				Equilibrium constant (ionization of COOH)	1	
51				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	

Genes	AA Posit.	PAML Branch- Site Model (PP>0.8)	DATAMONKEY		TreeSAAP Radical changes in amino acid properties	Total	Secondary structure* (Region)
			FEL p<0.1	REL BF>50			
ND4	58				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	66				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	69				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	73				Isoelectric point; Helical contact area; Partial specific volume; Short and medium range non-bonded energy	4	
	98				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	112				Isoelectric point; Helical contact area; Partial specific volume; Short and medium range non-bonded energy	4	Helical transmembrane
	138				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	140				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	153				Coil tendencies; Mean r.m.s. fluctuation displacement; Solvent accessible reduction ratio	3	Helical transmembrane
	164				Isoelectric point; Helical contact area; Partial specific volume	3	
	164				Short and medium range non-bonded energy		
	170				Mean r.m.s. fluctuation displacement	1	
	172				Thermodynamic transfer hydrophobicity	1	Protein binding
	173				Equilibrium constant (ionization of COOH)	1	
	174				Short and medium range non-bonded energy	1	
	177				Isoelectric point	1	Protein binding
	179				Equilibrium constant (ionization of COOH)	1	
	181				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	182				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	187				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	236				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	237				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	240				Mean r.m.s. fluctuation displacement	1	
	241				Equilibrium constant (ionization of COOH)	1	
	248				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	250				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	251				Isoelectric point; Helical contact area; Partial specific volume; Short and medium range non-bonded energy	4	Helical transmembrane
	255				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	258				Helical contact area; Partial specific volume	2	Helical transmembrane
	261				Isoelectric point; Helical contact area; Partial specific volume; Short and medium range non-bonded energy	4	Helical transmembrane
263				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
270				Equilibrium constant (ionization of COOH)	1		
282				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
283				Isoelectric point; Helical contact area; Partial specific volume; Short and medium range non-bonded energy	4	Helical transmembrane	
290				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
298				Isoelectric point	1		
301				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	

Genes	AA Posit.	PAML Branch-Site Model (PP>0.8)	DATAMONKEY		TreeSAAP Radical changes in amino acid properties	Total	Secondary structure* (Region)	
			FEL p<0.1	REL BF>50				
ND4	304				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	332				Equilibrium constant (ionization of COOH)	1		
	340				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	342				Isoelectric point; Helical contact area; Partial specific volume; Partial specific volume	4	Helical transmembrane	
	343				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	351				Isoelectric point; Helical contact area; Partial specific volume; Short and medium range non-bonded energy	4	Helical transmembrane	
	355				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	357				Isoelectric point; Helical contact area; Partial specific volume; Short and medium range non-bonded energy	4	Helical transmembrane	
	381				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	382				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	389				Solvent accessible reduction ratio	1	Helical transmembrane	
	391				Isoelectric point; Helical contact area; Partial specific volume; Short and medium range non-bonded energy	4	Helical transmembrane	
	398				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	400				Isoelectric point; Helical contact area; Partial specific volume; Short and medium range non-bonded energy	4		
	402				Isoelectric point; Helical contact area; Partial specific volume; Short and medium range non-bonded energy	4		
	439				Isoelectric point	1	Helical transmembrane	
	443				Isoelectric point; Short and medium range non-bonded energy	2	Helical transmembrane	
	444				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	ND4L	2				Equilibrium constant (ionization of COOH)	1	Helical transmembrane region; Protein binding
		5				Partial specific volume; Helical contact area; Isoelectric point; Short and medium range non-bonded energy	4	Helical transmembrane
7					Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
9					Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
15					Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
16					Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
40					Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
41					Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
49					Partial specific volume; Helical contact area; Isoelectric point; Short and medium range non-bonded energy	4	Helical transmembrane	
50					Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
52					Equilibrium constant (ionization of COOH)	1		
54					Partial specific volume; Helical contact area; Isoelectric point; Short and medium range non-bonded energy	4	Protein binding	

Genes	AA Posit.	PAML Branch- Site Model (PP>0.8)	DATAMONKEY		TreeSAAP Radical changes in amino acid properties	Total	Secondary structure* (Region)
			FEL p<0.1	REL BF>50			
ND4L	86				Partial specific volume; Helical contact area; Isoelectric point; Short and medium range non-bonded energy	4	Protein binding
	96				Partial specific volume; Helical contact area; Isoelectric point; Short and medium range non-bonded energy	4	
	96				Short and medium range non-bonded energy	1	
ND5	97				Equilibrium constant (ionization of COOH)	1	
	7				Equilibrium constant (ionization of COOH)	1	
	10				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	12				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	20				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	24				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	27				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	27				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	28				Chromatographic index; Mean r.m.s. fluctuation displacement	1	Helical transmembrane
	31				Buriedness; Chromatographic index; Surrounding hydrophobicity; Mean r.m.s. fluctuation displacement; Solvent accessible reduction ratio	5	Helical transmembrane
	32				Hydropathy; Chromatographic index; Mean r.m.s. fluctuation displacement	3	Protein binding
	35				Equilibrium constant (ionization of COOH)	1	
	38				Equilibrium constant (ionization of COOH)	1	
	42				Equilibrium constant (ionization of COOH)	1	
	49				Normalized consensus hydrophobicity; Chromatographic index	2	
	51				Equilibrium constant (ionization of COOH)	1	
	59				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	76				Mean r.m.s. fluctuation displacement	1	Helical transmembrane
	82				Equilibrium constant (ionization of COOH)	1	
	83				Equilibrium constant (ionization of COOH)	1	Protein binding
84				Polar requirement; Power to be at the C-terminal	1	Protein binding	
88				Mean r.m.s. fluctuation displacement	1		
92				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
94				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
100				Coil tendencies; Mean r.m.s. fluctuation displacement	2	Helical transmembrane	
102				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
104				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
105				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
142				Equilibrium constant (ionization of COOH)	1		
175				Thermodynamic transfer hydrophobicity; Chromatographic index; Mean r.m.s. fluctuation displacement	3		
182				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	

Genes	AA Posit.	PAML Branch-Site Model (PP>0.8)	DATAMONKEY		TreeSAAP Radical changes in amino acid properties	Total	Secondary structure* (Region)
			FEL p<0.1	REL BF>50			
ND5	187	0.597(branch d)					Helical transmembrane
	189				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	190				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	193				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	209				Equilibrium constant (ionization of COOH)	1	
	232				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	240				Buriedness; Coil tendencies; Chromatographic index; Equilibrium constant (ionization of COOH)	1	
	243				Power to be at the C-terminal	1	
	244				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	247		0.932 (branch d)			Coil tendencies; Equilibrium constant (ionization of COOH); Mean r.m.s. fluctuation displacement	3
	250				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	251				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	254			0.095683	Chromatographic index; Equilibrium constant (ionization of COOH); Mean r.m.s. fluctuation displacement	3	Helical transmembrane
	256				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	258				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	265				Mean r.m.s. fluctuation displacement	1	Helical transmembrane
	283				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	284				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	287				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	312			Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	323			Polar requirement; Power to be at the C-terminal	1		
	330			Equilibrium constant (ionization of COOH)	1		
	335			Power to be at the C-terminal	1		
	337			Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	344			Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	347	0.679(branch d)					Helical transmembrane
	365				Equilibrium constant (ionization of COOH)	1	
	372				Equilibrium constant (ionization of COOH)	1	
	375				Equilibrium constant (ionization of COOH)	1	
	381	0.609(branch d)					
	384				Equilibrium constant (ionization of COOH)	1	
	385				Equilibrium constant (ionization of COOH)	1	
	395				Equilibrium constant (ionization of COOH)	1	
	400				Mean r.m.s. fluctuation displacement	1	
	405				Power to be at the C-terminal	1	
	409				Power to be at the C-terminal	1	Protein binding
	414				Equilibrium constant (ionization of COOH)	1	
	421			Equilibrium constant (ionization of COOH)	1		
	427			Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	437			Coil tendencies	1	Helical transmembrane	
	438			Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
	443			Equilibrium constant (ionization of COOH)	1	Helical transmembrane	

Genes	AA Posit.	PAML Branch- Site Model (PP>0.8)	DATAMONKEY		TreeSAAP Radical changes in amino acid properties	Total	Secondary structure* (Region)
			FEL p<0.1	REL BF>50			
ND5	450				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	452				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	454				Power to be at the C-terminal	1	Helical transmembrane
	463				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	466				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	469				Coil tendencies	1	Helical transmembrane
	470				Buriedness; Chromatographic index; Surrounding hydrophobicity; Equilibrium constant (ionization of COOH); Mean r.m.s. fluctuation; Solvent accessible reduction ratio displacement	6	Helical transmembrane
	474				Equilibrium constant (ionization of COOH)	1	
	476			0.083625	Buriedness	1	
	477				Equilibrium constant (ionization of COOH)	1	
	479				Buriedness; Equilibrium constant (ionization of COOH)	1	Protein binding
	480				Coil tendencies	1	
	480				Mean r.m.s. fluctuation displacement	1	
	487				Buriedness; Polarity; Polar requirement; Hydropathy; Average number of surrounding residues; Chromatographic index; Surrounding; hydrophobicity; Mean r.m.s. fluctuation displacement; Long-range non-bonded energy; Solvent accessible reduction ratio	11	
	490				Power to be at the C-terminal	1	Protein binding
	494				Equilibrium constant (ionization of COOH)	1	
	495				Equilibrium constant (ionization of COOH)	1	
	498				Equilibrium constant (ionization of COOH)	1	
	507				Thermodynamic transfer hydrophobicity; Chromatographic index; Mean r.m.s. fluctuation displacement	1	
	515				Equilibrium constant (ionization of COOH)	1	
	516				Polarity; Hydropathy; Chromatographic index; Mean r.m.s. fluctuation displacement	4	
	519				Equilibrium constant (ionization of COOH)	1	
	520				Equilibrium constant (ionization of COOH)	1	
	541		0.627(branch d)				
	543		0.518(branch d)				
	544				Equilibrium constant (ionization of COOH)	1	
	546				Polarity; Hydropathy; Chromatographic index; Mean r.m.s. fluctuation displacement	4	Protein binding
	547				Equilibrium constant (ionization of COOH)	1	
	548				Chromatographic index; Mean r.m.s. fluctuation displacement	2	
	550				Power to be at the C-terminal	1	
560				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
562				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
564				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	
565				Equilibrium constant (ionization of COOH)	1	Helical transmembrane	

Genes	AA Posit.	PAML Branch- Site Model (PP>0.8)	DATAMONKEY		TreeSAAP Radical changes in amino acid properties	Total	Secondary structure* (Region)
			FEL p<0.1	REL BF>50			
ND5	568				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	569				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	570				Buriedness	1	Helical transmembrane
	573				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	575				Buriedness; Equilibrium constant (ionization of COOH)	1	Helical transmembrane
ND6	1				Equilibrium constant (ionization of COOH)	1	Protein binding
	6				Buriedness; Thermodynamic transfer hydrophobicity; Average number of surrounding residues; Surrounding hydrophobicity; Equilibrium constant (ionization of COOH); Solvent accessible reduction ratio	6	Helical transmembrane
	9				Buriedness; Thermodynamic transfer hydrophobicity; Average number of surrounding residues; Surrounding hydrophobicity; Equilibrium constant (ionization of COOH); Solvent accessible reduction ratio	6	Helical transmembrane
	11				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	16				Thermodynamic transfer hydrophobicity; Turn tendencies	2	Helical transmembrane
	16				Mean r.m.s. fluctuation displacement	1	Helical transmembrane
	34				Average number of surrounding residues; Solvent accessible reduction ratio	2	
	35				Equilibrium constant (ionization of COOH)	1	
	56				Buriedness; Thermodynamic transfer hydrophobicity; Average number of surrounding residues; Surrounding hydrophobicity; Equilibrium constant (ionization of COOH); Solvent accessible reduction ratio	6	Helical transmembrane
	61				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	78				Turn tendencies; Surrounding hydrophobicity; Equilibrium constant (ionization of COOH); Solvent accessible reduction ratio	4	
	81				Average number of surrounding residues; Turn tendencies	2	
	82				Average number of surrounding residues; Turn tendencies; Equilibrium constant (ionization of COOH); Buriedness; Thermodynamic transfer hydrophobicity; Average number of surrounding residues	6	
	83				Surrounding hydrophobicity; Equilibrium constant (ionization of COOH); Equilibrium constant (ionization of COOH); Solvent accessible reduction ratio	4	
	85				Buriedness; Thermodynamic transfer hydrophobicity; Average number of surrounding residues; Surrounding hydrophobicity	4	

Genes	AA Posit.	PAML Branch- Site Model (PP>0.8)	DATAMONKEY		TreeSAAP Radical changes in amino acid properties	Total	Secondary structure* (Region)
			FEL p<0.1	REL BF>50			
ND6	85				Solvent accessible reduction ratio	1	Helical transmembrane
	86				Thermodynamic transfer hydrophobicity; Turn tendencies; Mean r.m.s. fluctuation displacement	1	Helical transmembrane
	88				Thermodynamic transfer hydrophobicity; Turn tendencies; Mean r.m.s. fluctuation displacement	3	Helical transmembrane
	89				Average number of surrounding residues; Turn tendencies; Equilibrium constant (ionization of COOH)	3	Helical transmembrane
	90				Buriedness; Thermodynamic transfer hydrophobicity; Average number of surrounding residues; Surrounding hydrophobicity; Equilibrium constant (ionization of COOH); Solvent accessible reduction ratio	6	Helical transmembrane
	92				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	93				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	96				Buriedness; Thermodynamic transfer hydrophobicity; Average number of surrounding residues; Surrounding hydrophobicity; Equilibrium constant (ionization of COOH); Solvent accessible reduction ratio; Equilibrium constant (ionization of COOH)	7	Helical transmembrane
	97				Buriedness; Thermodynamic transfer hydrophobicity; Average number of surrounding residues; Surrounding hydrophobicity; Equilibrium constant (ionization of COOH); Solvent accessible reduction ratio	6	Helical transmembrane
	98				Thermodynamic transfer hydrophobicity; Turn tendencies; Mean r.m.s. fluctuation displacement	3	Helical transmembrane
	100				Average number of surrounding residues	1	Helical transmembrane
	101				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	106				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	109				Thermodynamic transfer hydrophobicity; Turn tendencies; Mean r.m.s. fluctuation displacement	3	
	111				Buriedness	1	Protein binding
	112				Equilibrium constant (ionization of COOH)	1	
	117				Average number of surrounding residues; Turn tendencies; Surrounding hydrophobicity	3	
119				Average number of surrounding residues; Turn tendencies; Surrounding hydrophobicity	3	Protein binding	
121				Average number of surrounding residues; Turn tendencies; Surrounding hydrophobicity; Equilibrium constant (ionization of COOH)	4		

Genes	AA Posit.	PAML Branch- Site Model (PP>0.8)	DATAMONKEY		TreeSAAP Radical changes in amino acid properties	Total	Secondary structure* (Region)
			FEL p<0.1	REL BF>50			
ND6	124				Buriedness; Thermodynamic transfer hydrophobicity; Average number of surrounding residues; Surrounding hydrophobicity; Equilibrium constant (ionization of COOH); Mean r.m.s. fluctuation displacement; Solvent accessible reduction ratio	7	
	125				Buriedness; Thermodynamic transfer hydrophobicity; Average number of surrounding residues; Surrounding hydrophobicity; Equilibrium constant (ionization of COOH); Solvent accessible reduction ratio	6	
	127				Buriedness; Thermodynamic transfer hydrophobicity; Average number of surrounding residues; Surrounding hydrophobicity; Equilibrium constant (ionization of COOH); Solvent accessible reduction ratio	6	
	135				Turn tendencies; Surrounding hydrophobicity; Equilibrium constant (ionization of COOH); Solvent accessible reduction ratio	4	Protein binding
	136				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	144				Equilibrium constant (ionization of COOH)	1	Helical transmembrane
	167				Average number of surrounding residues; Turn tendencies	2	Polynucleotide-binding

