

Supplementary table S3. Likelihood values and parameter estimates for mammalian rhodopsin genes

Model code (a)	$\ell$ (b)	$P$ (c)	Parameter estimates
<b>Dataset I: all mammals</b>			
<i>Branch Models</i>			
A1: One-ratio	-9008.20	118	$\omega=0.040$
B1: Free-ratio	-8843.40	233	variable $\omega$ by branch
C1: Two-ratio: AFM branch, background	-9006.28	119	$\omega_0=0.039, \omega_1=0.104$
D1: Two-ratio: Middle East blind mole rat branch, background	-9007.92	119	$\omega_0=0.040, \omega_1=0.055$
E1: Two-ratio: Hottentot golden mole branch, background	-9008.20	119	$\omega_0=0.040, \omega_1=0.038$
F1: Two-ratio: CET branch, background	-9004.02	119	$\omega_0=0.039, \omega_1=0.202$
G1: Two-ratio: PIN branch, background	-9007.87	119	$\omega_0=0.040, \omega_1=0.000$
H1: Two-ratio: West Indian manatee branch, background	-9005.33	119	$\omega_0=0.041, \omega_1=0.009$
I1: Two-ratio: sea otter branch, background	-9008.15	119	$\omega_0=0.040, \omega_1=0.034$
J1: Two-ratio: BAT branch, background	-9008.20	119	$\omega_0=0.040, \omega_1=0.038$
<i>Site Models</i>			
K1: M1a: nearly neutral	-8857.65	119	$\rho_0=0.936$ ( $\rho_1=0.064$ ) $\omega_0=0.025$ ( $\omega_1=1.000$ )
L1: M2a: positive selection	-8857.65	121	$\rho_0=0.936, \rho_1=0.064$ ( $\rho_2=0.000$ ) $\omega_0=0.025, \omega_1=1.000$ ( $\omega_2=75.307$ )
M1: M8a: $\beta$ & $\omega=1$	-8663.43	119	$p=0.127, q=1.984$
N1: M8: $\beta$ & $\omega$	-8663.44	121	$\rho_0=1.000, p=0.127, q=1.984$ $\rho_1=0.000, \omega=2.724$
<i>Clade Models</i>			
O1: Model C: all African mole-rats	-8676.08	122	$\omega_0=0.005, \rho_0=0.816; \omega_1=1, \rho_1=0.010$ $\omega_2=0.199, \omega_3=0.298$ ( $\rho_2=0.174$ )
P1: Model C: all pinnipeds	-8658.42	122	$\omega_0=0.006, \rho_0=0.820; \omega_1=1, \rho_1=0.004$ $\omega_2=0.197, \omega_3=1.262$ ( $\rho_2=0.177$ )
Q1: Model C: all cetaceans	-8660.95	122	$\omega_0=0.005, \rho_0=0.811; \omega_1=1, \rho_1=0.015$ $\omega_2=0.180, \omega_3=1.205$ ( $\rho_2=0.174$ )
R1: Model C: all bats	-8668.22	122	$\omega_0=0.005, \rho_0=0.815; \omega_1=1, \rho_1=0.007$ $\omega_2=0.236, \omega_3=0.102$ ( $\rho_2=0.178$ )
<b>Dataset II: bats only</b>			
<i>Branch Models</i>			
A2: One-ratio	-2963.02	29	$\omega=0.023$
B2: Free-ratio	-2945.07	55	variable $\omega$ by branch
C2: Two-ratio: OWF branch, background	-2962.76	30	$\omega_0=0.022, \omega_1=0.035$
D2: Two-ratio: HDC branch, background	-2961.85	30	$\omega_0=0.022, \omega_1=\infty$
E2: Two-ratio: YAN branch, background	-2960.73	30	$\omega_0=0.024, \omega_1=0.001$
<i>Site Models</i>			
F2: M1a: nearly neutral	-2954.28	30	$\rho_0=0.978$ ( $\rho_1=0.022$ ) $\omega_0=0.015$ ( $\omega_1=1.000$ )
G2: M2a: positive selection	-2954.29	32	$\rho_0=0.978, \rho_1=0.022$ ( $\rho_2=0.000$ ) $\omega_0=0.015, \omega_1=1.000$ ( $\omega_2=45.178$ )
H2: M8a: $\beta$ & $\omega=1$	-2949.45	30	$p=0.101, q=3.231$
I2: M8: $\beta$ & $\omega$	-2949.45	32	$\rho_0=1.000, p=0.101, q=3.231$ $\rho_1=0, \omega=1.000$
<i>Clade Models</i>			
J2: Model C: all Old World fruit bats	-2948.75	33	$\omega_0=0.009, \rho_0=0.936; \omega_1=1, \rho_1=0$ $\omega_2=0.297, \omega_3=0.267$ ( $\rho_2=0.064$ )
K2: Model C: all high-duty-cycle bats	-2948.73	33	$\omega_0=0.009, \rho_0=0.935; \omega_1=1, \rho_1=0$ $\omega_2=0.273, \omega_3=0.339$ ( $\rho_2=0.065$ )
L2: Model C: all Yangochiroptera	-2948.53	33	$\omega_0=0.009, \rho_0=0.944; \omega_1=1, \rho_1=0$ $\omega_2=0.368, \omega_3=0.263$ ( $\rho_2=0.056$ )

(a) Codes for focal branches (e.g. AFM) are given in fig. 1; (b) Likelihood values; (c) Number of parameters