Table S4. Variable selection pressure on the OR7D4 gene in various lineages

A. Log likelihood scores and ω estimates for one-ratio, two-ratio, and three-ratio branchspecific models using the OR7D4+OR7D1 dataset with catarrhine OR7D4, human OR7D4, and/or Great Ape OR7D4 as the foreground branches

Model	I	ω	ω _{ga}	ω _{hu}	ω _c
MO	-2861.29	0.4	N/A	N/A	N/A
Two-ratio Great Ape	-2856.99	0.3	8	N/A	N/A
Two-ratio fix ω_{ga} = 1	-2858.89	0.3	(1)	N/A	N/A
Two-ratio human	-2861.17	0.4	N/A	0.6	N/A
Two-ratio fix ω_{hu} = 1	-2861.23	0.4	N/A	(1)	N/A
two-ratio catarrhine	-2861.25	0.4	N/A	N/A	0.6
two-ratio fix $\omega_c = 1$	-2861.27	0.3	N/A	N/A	(1)
two-ratio Great Ape = human	-2858.23	0.3	8.8	8.8	N/A
two-ratio fix ω_{ga} = ω_{hu} = 1	-2858.92	0.3	(1)	(1)	N/A
three-ratio Great Ape + human	-2856.92	0.3	∞	0.5	N/A
three-ratio fix ω_{ga} = 1	-2858.79	0.3	(1)	0.5	N/A
three-ratio fix ω_{hu} = 1	-2857.10	0.3	8	(1)	N/A
two-ratio Great Ape = catarrhine	-2857.21	0.3	∞	N/A	∞
two-ratio fix ω_{ga} = ω_{c} = 1	-2858.91	0.3	(1)	N/A	(1)
three-ratio Great Ape + catarrhine	-2856.99	0.3	~	N/A	0.4
three-ratio fix ω_{ga} = 1	-2858.87	0.3	(1)	N/A	0.5
three-ratio fix ω_c = 1	-2857.06	0.3	∞	N/A	(1)

LRT	Null	2∆ <i>I</i>	Df	P value
two-ratio Great Ape vs. M0	$\omega_{ga} = \omega_0$	8.60	1	0.0034**
two-ratio Great Ape vs. two-ratio fix ω_{qa} = 1	ω _{qa} ≤ 1	3.79	1	0.0516
two-ratio human vs. M0	$\omega_{hu} = \omega_0$	0.26	1	0.6130
two-ratio Great Ape = human vs. M0	$(\omega_{ga} = \omega_{hu}) = \omega_0$	6.13	1	0.0133*
three-ratio Great Ape + human vs. two-ratio Great Ape	$\omega_{hu} = \omega_0$	0.14	1	0.7111
three-ratio Great Ape + human vs. two-ratio human	$\omega_{ga} = \omega_0$	8.48	1	0.0036**
two-ratio human vs. two-ratio fix ω_{hu} = 1	ω _{hu} < 1	0.12	1	0.7272
two-ratio Great Ape = human vs. two-ratio fix ω_{ga} = ω_{hu} = 1	$(\omega_{ga} = \omega_{hu}) \le 1$	1.37	1	0.2424
three-ratio Great Ape + human vs. three-ratio fix ω_{ga} = 1	$\omega_{ga} \leq 1$	3.74	1	0.0532
three-ratio Great Ape + human vs. three-ratio fix ω_{hu} = 1	$\omega_{hu} \leq 1$	0.35	1	0.5524
two-ratio catarrhine vs. M0	$\omega_{\rm c} = \omega_0$	0.10	1	0.7529
two-ratio Great Ape = catarrhine vs. M0	$(\omega_{ga} = \omega_c) = \omega_0$	8.17	1	0.0043**
three-ratio Great Ape + catarrhine vs. two-ratio Great Ape	$\omega_{c} = \omega_{0}$	0.01	1	0.9398
three-ratio Great Ape + catarrhine vs. two-ratio catarrhine	$\omega_{ga} = \omega_0$	8.51	1	0.0035**
two-ratio catarrhine vs. two-ratio fix ω_c = 1	$\omega_{c} \leq 1$	0.06	1	0.8126
two-ratio Great Ape = catarrhine vs. two-ratio fix ω_{ga} = ω_{c} = 1	$(\omega_{ga} = \omega_c) \leq 1$	3.39	1	0.0654
three-ratio Great Ape + catarrhine vs. three-ratio fix ω_{ga} = 1	ω _{ga} ≤ 1	3.75	1	0.0527
three-ratio Great Ape + catarrhine vs. three-ratio fix $\omega_c = 1$	$\omega_c \le 1$	0.13	1	0.7169

B. Likelihood ratio tests comparing the one-ratio, two-ratio, and three-ratio models in A

 ω_0 is the dN/dS ratio for the background branch in the model. ω_{ga} , ω_{hu} , and ω_c are the dN/dS ratios for the Great Ape OR7D4, human OR7D4, and catarrhine OR7D4 branches, respectively, when they are set as the foreground branches. ω values in the parentheses are fixed rather than estimated. OR7D4+OR7D1 dataset with the F3x4 codon frequency model is used for this analysis. LRT, likelihood ratio test. Df, degrees of freedom. null, null hypothesis tested the likelihood ratio test. *l*, log likelihood score. $2\Delta l$, twice the difference between the log likelihood scores of the two models compared. * P < 0.05, ** P < 0.01.