

Table E4: Parameter estimates and likelihood scores under models of variable ω ratios among sites for HIV-2 *nef* genes.

Nested model pairs	d_N/d_S ^b	Parameter estimates ^c	PSS ^d	ℓ
M0: one-ratio (1) ^a	?	$\omega = ?$	N.A.	?
M3: discrete (5)	?	$p_0 = ?, p_1 = ?, (p_2 = ?)$ $\omega_0 = ?, \omega_1 = ?, \omega_2 = ?$? (?)	?
M1: neutral (1)	?	$p_0 = ?, (p_1 = ?)$ $\omega_0 = ?, (\omega_1 = 1)$	N.A.	?
M2: selection (3)	?	$p_0 = ?, p_1 = ?, (p_2 = ?)$ $\omega_0 = ?, (\omega_1 = 1), \omega_2 = ?$? (?)	?
M7: beta (2)	?	$p = ?, q = ?$	N.A.	?
M8: beta& ω (4)	?	$p_0 = ? (p_1 = ?)$ $p = ?, q = ?, \omega = ?$? (?)	?

^a The number after the model code, in parentheses, is the number of free parameters in the ω distribution.

^b This d_N/d_S ratio is an average over all sites in the HIV-2 *nef* gene alignment.

^c Parameters in parentheses are not free parameters.

^d PSS is the number of positive selection sites (NEB). The first number is the PSS with posterior probabilities > 50%. The second number (in parentheses) is the PSS with posterior probabilities > 95%.

NOTE: Codeml now implements models M1a and M2a !