A. Log Likelihood Scores and Parameter Estimates for Four Models of Variable ω's Among Sites Assuming the F3x4 Model of Codon Frequencies

Model	Parameter Estimates	Sites* with $\omega > 1$	λ
M0: one ratio	average dN/dS for each branch = 1.316		**-4209.047**
Site models			
M1: neutral	$(\omega = 0)$ $f = 0.3275$ $(\omega = 1)$ $(f = 0.6275)$ average dN/dS for each branch = 0.6725	Not allowed	**-4171.503**
M2: selection	$(\omega = 0)$ $f = 0.292$ $(\omega = 1)$ $f = 0.379$ **$\omega = 3.777$**$(f = 0.329)$ average dN/dS for each branch = 1.6203	8, 13, 14, 29, **59**, 61, 69, 102, 169, 187, 196, 200, **213**, 248, **249**, **274**, **276**, 303, 330, **344**, 365	**-4136.417**
M3:discrete	$\omega = 0.00001$ $f = 0.31982$ **$\omega = 1.305$ $(f = 0.4178)$** **$\omega = 4.189$ $(f = 0.2624)$** average dN/dS for each branch = 1.6444	Too many to list	**-4136.302**
M7:Beta	$p = 0.00397$ $q = 0.00186$ average dN/dS for each branch = 0.7000	Not allowed	**-4171.826**
M8:Beta&ω	$p = 0.02755$ $q = 0.02328$ $f = 0.658$ **$\omega = 3.702$ $(f = 0.342)$** average dN/dS for each branch = 1.6169	8, 13, 14, 29, **59**, 61, 69, 99, 102, 169, 176, 187, 196, 200, **213**, 248, **249**, **274**, **276**, 303, 330, **344**, 362, 365	**-4136.495**

B. Log Likelihood Scores and Parameter Estimates for Four Models of Variable ω's Among Sites Assuming the F61 Model of Codon Frequencies

Model	Parameter Estimates	Sites* with $\omega > 1$	λ
M0: one ratio	average dN/dS for each branch = 1.3078		**-4152.141**
Site models			
M1: neutral	$(\omega = 0)$ $f = 0.31758$ $(\omega = 1)$ $(f = 0.68242)$ average dN/dS for each branch = 0.6824	Not allowed	**-4116.327**
M2: selection	$(\omega = 0)$ $f = 0.27762$ $(\omega = 1)$ $f = 0.40166$ **$\omega = 3.745$**$(f = 0.3207)$ average dN/dS for each branch = 1.6029	5, 8, 13, 14, 29, **59**, 61, 102, 169, 187, 196, 200, **213**, 248, 249, **274**, **276**, 303, 330, **344**	**-4084.584**
M3:discrete	$\omega = 0.00001$ $f = 0.3048$ **$\omega = 1.292$ $(f = 0.44)$** **$\omega = 4.184$ $(f = 0.255)$** average dN/dS for each branch = 1.6366	Too many to list	**-4084.419**
M7:Beta	$p = 0.00289$ $q = 0.00106$ average dN/dS for each branch = 0.7	Not allowed	**-4116.456**
M8:Beta&ω	$p = 0.00223$ $q = 0.00136$ $f = 0.6835$ **$\omega = 4.43$ $(f = 0.3165)$** average dN/dS for each branch = 1.606	5, 8, 13, 14, 29, **59**, 61, 102, 169, 187, 196, 200, **213**, 248, 249, **274**, **276**, 303, 330, **344**	**-4084.590**

Note: p and q are parameters of the beta distribution. f is the proportion of sites assigned to an individual ω category or to a beta distribution with shape parameters p and q. The proportion f in parentheses is not a free parameter. Sites assigned to ω are those with posterior probabilities $(P) > 0.95$, and those with $P > 0.99$ are in bold. Note: analyses conducted using κ as a free parameter.

*Codon positions listed have been adjusted to correspond to the human Apobec3G sequence, not to the multiple alignment where small gapped regions had to be removed prior to performing this analysis. Note that the species-specific residue (128) does not show up as being under positive selection. This is because it has not repeatedly changed.

C. Likelihood ratio test statistics (2δ) for models of variable selective pressure among sites.

	2δ	df	P-value
F3x4			
One ratio vs. M3 ($k = 3$)	145.49	4	**$P < 0.0001$**
M1 vs. M2	70.172	2	**$P < 0.0001$**
M7 vs. M8	70.662	2	**$P < 0.0001$**
F61			
One ratio vs. M3 ($k = 3$)	135.444	4	**$P < 0.0001$**
M1 vs. M2	63.486	2	**$P < 0.0001$**
M7 vs. M8	63.732	2	**$P < 0.0001$**

Figure S1
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