

Table 1: Results of the evolutionary analyses for positively selected sites for Spike ali nucl-VIRULIGN. P-values were achieved by performing chi-squared tests on twice the difference of the computed log likelihood values of the models disallowing (M7) or allowing (M8) $dN/dS > 1$. The BEB column lists rapidly evolving sites with a $dN/dS > 1$ and a posterior probability > 0.95 , determined by the Bayes Empirical Bayes implemented in **Codem1**. Amino acids refer to *SARS-CoV—GenBank:AY278741*. Note that INDELs and the stop codon were removed from the alignment prior to evolutionary analysis, so shown positions are based on the **alignment without gaps**. Fragments arising from insignificant breakpoints (adjusted p-value > 0.1) are marked with an asterisk.

Region	M7 vs M8 (χ^2)	M7 vs M8 p-value	% sites with $\omega > 1$	avg(ω)	M8 BEB ($PP > 0.95/ > 0.99$)
F61					
full (aa 1–1219)	8.51	0.014	4.13	1.0	none
frag1 (aa 1–842)	4.66	0.097	0.91	1.96	none
frag2* (aa 843–1219)	0.0	0.999	NA	NA	NA
F1X4					
full (aa 1–1219)	12.24	0.002	2.41	1.0	none
frag1 (aa 1–842)	10.21	0.006	1.21	1.5	none
frag2* (aa 843–1219)	0.0	0.999	NA	NA	NA
F3X4					
full (aa 1–1219)	18.62	< 0.001	2.16	1.0	none
frag1 (aa 1–842)	27.92	< 0.001	1.89	1.15	none
frag2* (aa 843–1219)	0.0	0.999	NA	NA	NA