Table 1: Model comparison and site-level selection results for DENV-2 *NS3* and DENV-3 *E* genes using Codeml models M0, M3, M1a, M2a, M7, and M8. Positive selection was evaluated through likelihood ratio tests (LRTs) and Bayes Empirical Bayes (BEB) posterior probabilities.

Serotype/ Gene	**Model**	d_N/d_S	**Parameters**	ℓ	**Model vs.**	$\mathbf{2\Delta\ell}$	χ^2 **(0.05)**	**PSS (BEB)**
DENV-2 / NS3	M0	0.05	$\omega = 0.05$	-4713.99	M0vs.M3	53.47	9.48	Not allowed
	M3	0.04	$p_0 = 0.98$, $p_1 = 0.01$, $p_2 = 0.00$, $\omega_0 = 0.02$, $\omega_1 = 1.80$, $\omega_2 = 43.16$	-4687.26	-	-	-	14 G 1.00**, 385 L 0.96*, 418 K 0.88, 461 I 0.56, 549 K 0.99**
	M1a	0.04	$p_0 = 0.98$, $p_1 = 0.01$, $p_2 = 0.00$	-4688.26	M1vs.M2	53.47	5.99	Not allowed
	M2a	0.05	$p_0 = 0.98$, $p_1 = 0.01$, $p_2 = 0.00$, $\omega_0 = 0.02$, $\omega_1 = 1.00$, $\omega_2 = 3.74$	-4686.11	-	-	-	14 G 0.92, 385 L 0.63
	M7	0.05	$p = 0.01$, $q = 0.18$	-4691.83	M7vs.M8	53.47	5.99	Not allowed
	M8	0.04	$p_0 = 0.98$, $p_1 = 0.01$, ..., $\omega_{10} = 3.74$	-4685.61	-	-	-	14 G 0.99**, 385 L 0.77, 418 K 0.61, 549 K 0.701
DENV-3 / E	M0	0.10	$\omega = 0.10$	-3622.42	M0vs.M3	34.35	9.48	Not allowed
	M3	0.12	$p_0 = 0.96$, $p_1 = 0.03$, $p_2 = 0.00$, $\omega_0 = 0.06$, $\omega_1 = 1.00$, $\omega_2 = 6.82$	-3605.25	-	-	-	124 P 0.98*, 132 Y 0.77
	M1a	104	$p_0 = 0.96$, $p_1 = 0.03$, $p_2 = 0.00$	-3608.29	M1vs.M2	34.35	5.99	Not allowed
	M2a	0.12	$p_0 = 0.96$, $p_1 = 0.03$, $p_2 = 0.00$, $\omega_0 = 0.06$, $\omega_1 = 1.00$, $\omega_2 = 6.82$	-3605.25	-	-	-	124 P 0.89, 132 Y 0.79, 169 T 0.54, 171 A 0.54, 301 T 0.69
	M7	0.11	$p = 0.09$, $q = 0.73$	-3610.32	M7vs.M8	34.35	5.99	Not allowed
	M8	0.12	$p_0 = 0.96$, $p_1 = 0.03$,	-3605.50	-	-	-	124 P 0.98*, 132 Y 0.91, 169 T 0.66, 171 A 0.66,