

**TABLE S1. Bayes factor comparisons of generalized coalescent models for H4 and H6 viruses from the North American gene pool**

Dataset	Null model (H <sub>0</sub> )	- log Likelihood (95% HPD)	Alternative model (H <sub>1</sub> )		
			Constant	Expansion	Exponential
H6	<b>Constant</b> <b>(Strong)</b> <sup>1</sup>	- 9521.497 (-9541.201; -9501.84)	-9541.837 ± 0.364 <sup>2</sup>	5.8 <sup>3</sup>	6.1
	Expansion	-9528.081 (-9548.169; -9508.855)		-9548.846 ± 0.398	0.3
	Exponential	-9528.041 (-9546.856; -9507.31)			-9548.501 ± 0.403
H6 lineage A	<b>Constant</b> <b>(Strong)</b>	-4824.563 (-4836.73; -4813.123)	-4836.026 ± 0.247	0.416	5.728
	<b>Expansion</b> <b>(Strong)</b>	-4824.642 (-4837.14; -4813.266)		-4838.890 ± 0.245	5.312
	Exponential	-4827.551 (-4839.336; -4815.882)			-4836.234 ± 0.225
H6 lineage B	Constant	-4952.56 (-4968.847; -4936.281)	-4969.414 ± 0.327	-0.830	0.878
	Expansion	-4952.017 (-4969.139; -4936.457)		-4969.853 ± 0.295	1.708
	Exponential	-4953.365 (-4969.491; -4937.661)			-4968.999 ± 0.286
H4	<b>Constant</b>	-10140 (-10150; -10120)	-10155.57 ± 0.362	2.486	1.796
	Expansion	-10140 (-10160; -10120)		-10156.81 ± 0.412	-0.688
	Exponential	-10140 (-10150; -10120)			-10156.47 ± 0.421

<sup>1</sup> Bold model names indicate which coalescent model fits the data in the comparison. Evidence against H<sub>0</sub> is assessed in the following way:  $2 \leq 2 \times \text{Bayes factor} \leq 6$  indicates positive evidence for the null model;  $6 \leq 2 \times \text{Bayes factor} \leq 10$  indicates strong evidence for the null model;  $2 \times \text{Bayes factor} > 10$  indicates very strong evidence for the null model.

<sup>2</sup> Bayes factors were estimated comparing the approximate marginal likelihoods of different models. Bayes factor is the difference (in log<sub>e</sub> space) of the marginal likelihood of null (H<sub>0</sub>) and the alternative (H<sub>1</sub>) coalescent model. Numbers shown are  $2 \times \text{Bayes factor}$

<sup>3</sup> Marginal likelihoods are contained in diagonal boxes of each dataset comparison (i.e. constant vs. constant). Marginal likelihoods were calculated using the harmonic mean of the sampled likelihoods.