

**Table S4. Model fit for comparative TMCRA estimates of 229E, NL63, OC43, and HKU1 hCoV**

hCoV type	Clock model	Demographic model	Log marginal likelihood	MCMC chain
229E WG	Strict	Constant	-42436.48	200 mil
229E WG	Strict	Exponential	1711388.9	200 mil
229E WG	Strict	Skyline	1141416.68	100 mil
229E WG	UCLN	Constant	-42878.79	100 mil
229E WG	UCLN	Exponential	-42879.04	100 mil
229E WG	UCLN	Skyline	-42873.31	200 mil
229E RBD S1 gene	UCLN	Skyline	–	600 mil
229E S gene	UCLN	Skyline	–	600 mil
229E N gene	UCLN	Skyline	–	600 mil
229E N and S gene	UCLN	Skyline	–	600 mil
OC43 WG <sup>a</sup>	Strict	Constant	-59899.62	600 mil
OC43 WG <sup>a</sup>	Strict	Exponential	-59895.68	600 mil
OC43 WG <sup>a</sup>	Strict	Skyline	-59881.69	600 mil
OC43 WG <sup>a</sup>	UCLN	Constant	-59863.16	600 mil
OC43 WG <sup>a</sup>	UCLN	Exponential	-59866.145	600 mil
OC43 WG <sup>a</sup>	UCLN	Skyline	-59851.46	600 mil
NL63 WG <sup>a</sup>	Strict	Constant	-42203	600 mil
NL63 WG <sup>a</sup>	Strict	Exponential	-42206.51	600 mil
NL63 WG <sup>a</sup>	Strict	Skyline	-42203.81	600 mil
NL63 WG <sup>a</sup>	UCLN	Constant	-42194.37	600 mil
NL63 WG <sup>a</sup>	UCLN	Exponential	-42199.37	600 mil
NL63 WG <sup>a</sup>	UCLN	Skyline	-42188.97	600 mil
NL63 <sup>b</sup>	Strict	Constant	-11745.53	600 mil
NL63 <sup>b</sup>	Strict	Exponential	-11747.46	600 mil
NL63 <sup>b</sup>	Strict	Skyline	-11746.42	600 mil
NL63 <sup>b</sup>	UCLN	Constant	infinity	600 mil

NL63 <sup>b</sup>	UCLN	Exponential	infinity	600 mil
NL63 <sup>b</sup>	UCLN	Skyline	-11743.43	600 mil
HKU1 WG <sup>a</sup>	Strict	Constant	-51641.8511	600 mil
HKU1 WG <sup>a</sup>	Strict	Exponential	-51641.6057	600 mil
HKU1 WG <sup>a</sup>	Strict	Skyline	-51523.685	600 mil
HKU1 WG <sup>a</sup>	UCLN	Constant	-51496.93	600 mil
HKU1 WG <sup>a</sup>	UCLN	Exponential	-51498.577	600 mil
HKU1 WG <sup>a</sup>	UCLN	Skyline	-51495.71	600 mil

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UCLN = uncorrelated lognormal (relaxed clock)

WG = whole genome

<sup>a</sup>Recombinant genomes removed

<sup>b</sup>Recombinant section removed