

1 **Supplementary Figures and Tables**

2 **Supplementary Table 1. Model comparison for phylogenetic and molecular evolutionary**

3 **analyses using Akaike's Information Criterion through MCMC (AICM)**

Overall RSV-A (with global reference strains)	Name of model(s)	AICM (\pm SE) ^a
Clock model(s)	Strict clock	10461.762 (\pm 0.624)
	Uncorrelated lognormal relaxed clock	10395.818 (\pm 1.089)
	Uncorrelated exponential relaxed clock	10365.190 (\pm 0.738)
	Random local clock	10358.855 (\pm1.137)
Demographic model(s)	Constant size	10557.787 (\pm 2.106)
	Exponential growth	10396.908 (\pm0.682)
	Logistic growth	10465.181 (\pm 0.135)
	Expansion growth	10484.369 (\pm 0.142)
RSV-A genotype ON1 (with global reference strains)		
Clock model(s)	Strict clock	4600.323 (\pm0.258)
	Uncorrelated lognormal relaxed clock	4666.472 (\pm 0.302)
	Uncorrelated exponential relaxed clock	4613.886 (\pm 0.319)
	Random local clock	4620.186 (\pm 0.409)
Demographic model(s)	Constant size	4647.206 (\pm 0.305)
	Exponential growth	4551.228 (\pm0.199)
	Logistic growth	4586.247 (\pm 0.242)
	Expansion growth	4571.183 (\pm 0.521)
RSV-A genotype ON1 (only from central Vietnam)		
Clock model(s)	Strict clock	1930.269 (\pm0.079)
	Uncorrelated lognormal relaxed clock	1948.648 (\pm 0.084)
	Uncorrelated exponential relaxed clock	1931.584 (\pm 0.052)
	Random local clock	1953.300 (\pm 0.131)
Demographic model(s)	Constant size	1923.068 (\pm0.087)
	Exponential growth	1925.873 (\pm 0.109)
	Logistic growth	1954.706 (\pm 0.146)
	Expansion growth	1957.218 (\pm 0.118)
RSV-A genotype NA1 (only from central Vietnam)		
Clock model(s)	Strict clock	2072.666 (\pm 0.073)
	Uncorrelated lognormal relaxed clock	2094.742 (\pm 0.082)
	Uncorrelated exponential relaxed clock	2069.993 (\pm 0.086)
	Random local clock	2049.950 (\pm0.068)
Demographic model(s)	Constant size	2068.713 (\pm 0.135)
	Exponential growth	2064.947 (\pm 0.107)
	Logistic growth	2064.890 (\pm 0.092)
	Expansion growth	2062.951 (\pm0.169)
Overall RSV-A (ON1 & NA1) (only from central Vietnam)		
Clock model(s)	Strict clock	3318.706 (\pm 0.151)
	Uncorrelated lognormal relaxed clock	3314.696 (\pm 0.181)
	Uncorrelated exponential relaxed clock	3292.572 (\pm 0.263)
	Random local clock	3292.009 (\pm0.169)
Demographic model(s)	Constant size	3368.231 (\pm 0.170)
	Exponential growth	3344.131 (\pm0.146)
	Logistic growth	3372.944 (\pm 0.190)
	Expansion growth	3368.190 (\pm 0.268)

^a Models with the lowest AICM values were indicated as bold style.

5 **Supplementary Table 2. Conditions of Bayesian Markov Chain Monte Carlo (MCMC) for molecular evolutionary and Bayesian Skyline**

6 **Plot (BSP) analyses**

7

Phylogenetic and molecular evolutionary analyses	No. of strains (n)	Nucleotide substitution model(s) ^d	Clock model(s)	Demographic model(s)
Overall RSV-A (with global reference strains) ^a	312	GTR-gamma	Random local clock	Exponential growth
Overall RSV-A (only from central Vietnam) ^b	89	HKY85-gamma	Random local clock	Exponential growth
Genotype ON1 (with global reference strains) ^c	121	HKY85-gamma	Strict clock	Exponential growth
Genotype ON1 (only from central Vietnam)	42	HKY85-gamma	Strict clock	Constant growth
Genotype NA1 (only from central Vietnam)	47	HKY85-gamma	Random local clock	Expansion growth
Bayesian Skyline Plot (BSP) analysis				
Overall RSV-A (only from central Vietnam) ^b	89	HKY85-gamma	Uncorrelated exponential relaxed clock	Bayesian Skyline Plot

^a Total number of 29 RSV-A ON1, 47 NA1 strains from central Vietnam and 236 RSV-A global reference strains (Hirano et al., 2014) were included in the analysis.

^b For overall RSV-A (only from central Vietnam), the total number of 89 (42 ON1 and 47 NA1 strains) were included in the analysis.

^c Total number of 29 RSV-A ON1 from central Vietnam and 93 ON1 global reference strains (Hirano et al., 2014) were included in the analysis.

^d GTR stands for General Time Reversible model, and HKY85 stands for Hasegawa, Kishino and Yano 1985 model.

8

9 **Supplementary Table 3. Model comparison for Bayesian Skyline Plot (BSP) analysis using**
 10 **Akaike's Information Criterion through MCMC (AICM)**

11

Overall RSV-A (only from central Vietnam)	Name of clock model(s)	AICM (\pm SE) ^a
Clock model(s)	Strict clock	3378.591 (\pm 0.198)
	Uncorrelated lognormal relaxed clock	3344.084 (\pm 0.179)
	Uncorrelated exponential relaxed clock	3330.608 (\pm0.222)
	Random local clock	3330.637 (\pm 0.177)

^a Model with the lowest AICM value was indicated as bold style.

12

13 **Supplementary Table 4. Lineage-specific N-glycosylation pattern of central Vietnam RSV-A**
 14 **genotype NA1 strains G gene hypervariable region**

15

RSV-A NA1 lineage(s)	(Overall: Lineage 1 - 4)	Lineage 1	Lineage 2	Lineage 3	Lineage 4
Number of strains (n)	(n=136)	(n=32)	(n=65)	(n=11)	(n=28)
N-glycosylation site(s)	n (%)				
237-240 (NTTK)	33 (24.3%)	31 (96.9%)	0	2 (18.2%)	0
251-254 (NTTG)	124 (91.2%)	32 (100%)	64 (98.5%)	0	28 (100%)
273-276 (NLSP)	79 (58.1%)	0	49 (75.4%)	5 (45.5%)	25 (89.3%)
299-302 (NLSQ)	1 (0.7%)	0	0	1 (9.1%)	0
318-321 (NTTK / NTTE)	63 (46.3%)	32 (100%)	1 (1.5%)	2 (18.2%)	28 (100%)

16

17 **Supplementary Table 5. Negatively selected amino acid substitutions of central Vietnam RSV-A**
 18 **strains G gene hypervariable region**

19

Selection model(s)	Negatively selected amino acid substitution site(s)
SLAC ^a , FEL ^b , IFEL ^c	I236, T245, T246, T249, E263, S317

^a SLAC: Single Likelihood Ancestor Counting

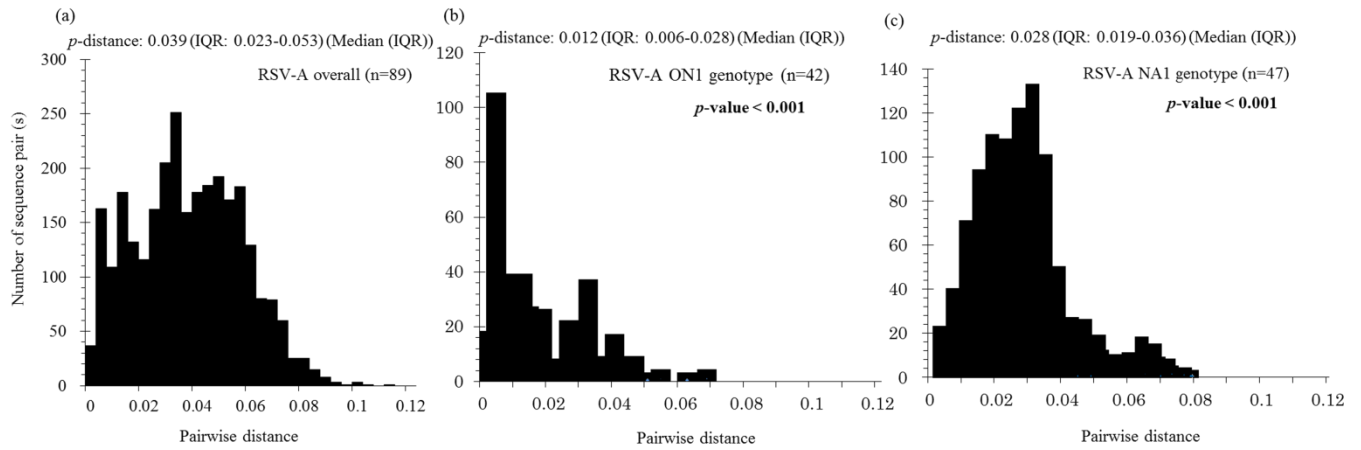
^b FEL: Fixed Effects Likelihood.

^c IFEL: Internal Fixed Effects Likelihood.

20

21 **Supplementary Figure 1 (a), (b) and (c). Pairwise distance (*p*-distance) frequency distributions**
22 **of central Vietnam RSV-A (a), ON1 (b) and NA1 (c) strains *G* gene hypervariable region**

23



24

25

26 The values of median *p*-distance between central Vietnam RSV-A genotypes (a) ON1 and (b) NA1
27 strains were compared using Mann-Whitney U test. The value of *p*-value less than 0.05 was
28 considered to be statistically significant and indicated as bold style.

29