



Figure S1. Date-randomization test (DRT) of genogroup 1 IPNV strains.

Table S1 Marginal likelihoods of different combinations of clock model and tree prior, estimators of the marginal likelihood—path sampling (PS)

| Molecular clock model | Coalescent tree prior | Log marginal likelihood |
|--|-------------------------|-------------------------|
| Strict clock | Bayesian skyline | -4171.045 |
| Strict clock | Exponential growth | -4189.685 |
| Strict clock | Constant size | -4188.345 |
| *Uncorrelated lognormal relaxed clock | Bayesian skyline | -4157.578 |
| Uncorrelated lognormal relaxed clock | Exponential growth | -4174.000 |
| Uncorrelated lognormal relaxed clock | Constant size | -4169.600 |

*the combination of clock model and tree prior that best fit our sequences data in this study.

Table S2 Marginal likelihoods of different combinations of clock model and tree prior, stepping-stone (SS) sampling

| Molecular clock model | Coalescent tree prior | Log marginal likelihood |
|--|-------------------------|-------------------------|
| Strict clock | Bayesian skyline | -4172.473 |
| Strict clock | Exponential growth | -4191.000 |
| Strict clock | Constant size | -4188.846 |
| *Uncorrelated lognormal relaxed clock | Bayesian skyline | -4158.026 |
| Uncorrelated lognormal relaxed clock | Exponential growth | -4175.153 |
| Uncorrelated lognormal relaxed clock | Constant size | -4170.961 |

*the combination of clock model and tree prior that best fit our sequences data in this study.