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| Table S2. Parameters used in the Bayesian Marcov chain Monte Carlo (MCMC) analyses of the present HuNoV GII.6 strains. | | | | | | | |
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|  | Substitution Models | Ganma shape | Proportion invariant | Clock Models | Demographic Models | Chain Length | Log Every |
| All *RdRp* regions (141 strains) P6-type 15 strains;  P7-type 126 strains | SYM+G | 0.2 | - | Relaxed Clock Exponential | Coalescent Exponential Population | 400,000,000 | 8,000 |
| P6-type *RdRp* region (15 strains) | TPM2+I | - | 0.792 | Relaxed Clock Exponential | Coalescent Exponential Population | 6,000,000,000 | 40,000 |
| P7-type *RdRp* region (126 strains) | TPM2+G | 0.242 | 0.082 | Relaxed Clock Exponential | Coalescent Constant Population | 400,000,000 | 8,000 |
| ALL GII.6 *VP1* genes (141 strains) P6-type 15 strains;  P7-type 126 strains | SYM+I+G | 1.358 | 0.524 | Relaxed Clock Exponential | Coalescent Exponential Population | 400,000,000 | 8,000 |
| GII.P6-GII.6 *VP1* gene (15 strains) | SYM+G | 0.025 | - | Relaxed Clock Exponential | Coalescent Constant Population | 400,000,000 | 8,000 |
| GII. P7-GII.6 *VP1* gene (126 strains) | SYM+I+G | 1.334 | 0.518 | Relaxed Clock Exponential | Coalescent Constant Population | 400,000,000 | 8,000 |