Table S3: Available molecular substitution rates for converged and best replicate lineages and clades with at least 50 sequences and evidence of ongoing circulation

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Lineage/clade | Sample size | Subsampled? | Likelihood | Substitution ratea | 1,2, sub. rateb | 3 sub. ratec |
| Classical lineage | 3064 | Y (n=750) | -30634.3 | 3.69E-03 | 2.07E-03 | 6.94E-03 |
| N1.C.2 | 109 | N | -6167.2 | 2.76E-03 | 1.27E-03 | 5.74E-03 |
| N1.C.2.1 | 122 | N | -5650.4 | 4.25E-03 | 2.27E-03 | 8.20E-03 |
| N1.C.3 | 1230 | Y (n=750) | -19641.9 | 4.22E-03 | 2.51E-03 | 7.65E-03 |
| N1.C.3.1 | 711 | N | -14511.8 | 3.73E-03 | 1.98E-03 | 7.22E-03 |
| N1.C.3.2 | 543 | N | -11980.8 | 4.12E-03 | 2.25E-03 | 7.86E-03 |
| N1.P | 629 | N | -18897.1 | 4.72E-03 | 2.90E-03 | 8.36E-03 |

athe general molecular substitution rate

bthe absolute molecular substitution rate for the first and second base pairs in each codon

cthe absolute molecular substitution rate for the third base pair in each codon