**Table S1: Statistics assessing whether time-trending substitution could have resulted from inheritance.**

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| --- | --- |
| **Substitution** | ***P* value** |
| 6E | 0.9984 |
| 11D | 1 |
| 72V | 0.0274 |
| 101I | 1 |
| 122I | 1 |
| 135V | 1 |
| 154I | 0 |
| 165I | 0 |
| 201I | 1 |
| 256E | 1 |
| 265V | 0 |

Small *P* values indicate that substitutions are significantly more closely related than random, i.e. they are clustered in the phylogenetic tree and there is evidence for inheritance. *P* values were calculated against a null model. For a particular substitution, we drew N random sequences, matching the number of sequences bearing the particular time-trending substitution. For these N random sequences, we computed the mean patristic distance μrand. The procedure was repeated M=10000 times to obtain a statistic for the mean patristic distance of N random sequences. We then computed the patristic distance of sequences harbouring the time-trending substitution μsubst. To compute a *P* value assessing whether the mean patristic distance of sequences with the time-trending substitution was smaller than the mean patristic distance of the random sequences (H0: μsubst ≥ μrand; H1: μsubst < μrand), we counted *P* = (#μsubst ≥ μrand)/M, where ‘#μsubst ≥ μrand’ denotes the number of times where the null hypothesis was true.