**Supplementary Table S1.** GenBank accession numbers for sequences from simian foamy virus.

|  |  |
| --- | --- |
| **GenBank accession** | **Host species** |
| JQ867466.1 | *Cercopithecus nictitans* |
| JQ867464.1 | *Gorilla gorilla* |
| JQ867462.1 | *Pan troglodytes troglodytes* |
| JQ867465.1 | *Gorilla gorilla* |
| JQ867463.1 | *Pan troglodytes troglodytes* |
| NC\_010820.1 | *Chlorocebus sabaeus* |
| NC\_010819.1 | *Simia inuus* |
| NC\_001364.1 | *Pan troglodytes troglodytes* |
| U04327.1 | *Pan troglodytes troglodytes* |
| JN801175.1 | *Simia inuus* |
| HM245790.1 | *Gorilla gorilla* |
| U21247.1 | *Homo sapiens* |
| GU356394.1 | *Simia sciureus* |
| GU356395.1 | *Callithrix jacchus* |
| AF232918.1 | *Pan troglodytes troglodytes* |
| AF232917.1 | *Homo sapiens* |
| AF033816.1 | *Homo sapiens* |
| EU010385.1 | *Simia paniscus* |
| Y07725.1 | *Homo sapiens* |
| AJ544579.1 | *Pongo pygmaeus pygmaeus* |
| X54482.1 | *Simia inuus* |
| X05592.1 | *Homo sapiens* |
| X05591.1 | *Homo sapiens* |

**Supplementary Table S2.** Bayes factors for lognormal and exponential clock models for the analysis of simian foamy virus with different calibrating nodes.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Calibrating node** | **Log(Likelihood)** | | **Log(Bayes factor)** | |
| **Exponential clock** | **Lognormal clock** | **Exponential vs lognormal** | **Standard error** |
| Cercopithecidae-Hominidae split | -125699.3 | -125699.2 | 0.15 | 0.06 |
| Cercopithecidae | -125699.6 | -125699.2 | 0.42 | 0.07 |
| Hominidae | -125699.1 | -125777.0 | 77.91 | 0.95 |
| *Pan/Homo*-*Gorilla* split | -125699.2 | -125699.6 | 0.42 | 0.18 |
| *Pan* | -125701.3 | -125706.0 | 4.73 | 0.17 |

**Supplementary Table S3.** Spearman’s correlation coefficient (*ρ*) for error and precision scores among estimates of parameters of interest for all analyses of the position of calibrating nodes.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Precision** | | | |
| Error | Substitution rate | 0.99 | 0.99 | 0.99 |
| 0.79 | Root node age | 0.99 | 0.99 |
| 0.85 | 0.97 | Median node age | 0.99 |
| 0.72 | 0.95 | 0.94 | Shallowest node age |

**Supplementary Table S4.** Maximum a posteriori (MAP) clock model for ten replicates of simulations with different settings.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Simulation parameters** | | | | **Number of simulations with correct MAP model selection[[1]](#footnote-1)** |
| **Clock model** | **Mean rate** | **Standard deviation of rate** | **Number of calibrations** |
| Lognormal | 0.01 | 0.001 | 1 | 3 |
| Lognormal | 0.01 | 0.005 | 1 | 1 |
| Exponential | 0.01 | 0.01 | 1 | 9 |
| Exponential | 0.001 | 0.001 | 1 | 8 |
| Lognormal | 0.01 | 0.001 | 2 | 0 |
| Lognormal | 0.01 | 0.005 | 2 | 0 |
| Exponential | 0.01 | 0.01 | 2 | 8 |
| Exponential | 0.001 | 0.001 | 2 | 10 |
| Lognormal | 0.01 | 0.001 | 5 | 4 |
| Lognormal | 0.01 | 0.005 | 5 | 3 |
| Exponential | 0.01 | 0.01 | 5 | 9 |
| Exponential | 0.001 | 0.001 | 5 | 8 |
| Lognormal | 0.01 | 0.001 | 10 | 6 |
| Lognormal | 0.01 | 0.005 | 10 | 4 |
| Exponential | 0.01 | 0.01 | 10 | 7 |
| Exponential | 0.001 | 0.001 | 10 | 8 |
| Lognormal | 0.01 | 0.001 | 20 | 1 |
| Lognormal | 0.01 | 0.005 | 20 | 1 |
| Exponential | 0.01 | 0.01 | 20 | 8 |
| Exponential | 0.001 | 0.001 | 20 | 10 |
| Lognormal | 0.01 | 0.001 | 30 | 1 |
| Lognormal | 0.01 | 0.005 | 30 | 1 |
| Exponential | 0.01 | 0.01 | 30 | 10 |
| Exponential | 0.001 | 0.001 | 30 | 7 |
| Lognormal | 0.01 | 0.001 | 40 | 3 |
| Lognormal | 0.01 | 0.005 | 40 | 4 |
| Exponential | 0.01 | 0.01 | 40 | 10 |
| Exponential | 0.001 | 0.001 | 40 | 9 |
| Lognormal | 0.01 | 0.001 | 49 | 5 |
| Lognormal | 0.01 | 0.005 | 49 | 4 |
| Exponential | 0.01 | 0.01 | 49 | 9 |
| Exponential | 0.001 | 0.001 | 49 | 9 |

**Supplementary Table S5.** Correlations *ρ* for error and precision scores of the estimates of the five nodes with known ages and the substitution rate in the analysis of simian foamy virus. The *ρ* values correspond to estimates with the exponential and lognormal clock models.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Error** | | **Precision** | |
| **Node age estimated** | **Lognormal clock** | **Exponential clock** | **Lognormal clock** | **Exponential clock** |
| Cercopithecidae-Hominidae | -0.90 | -0.81 | 0.06 | 0.06 |
| Crown Cercopithecidae | -0.80 | -0.81 | 0.06 | 0.06 |
| Crown Hominidae | -0.94 | -0.81 | 0.06 | 0.06 |
| *Pan/Homo-Gorilla* | -0.99 | -0.73 | 0.06 | 0.06 |
| Crown *Pan* | 0.58 | 0.59 | 0.06 | 0.06 |
| Substitution rate | - | - | -0.73 | -0.74 |

1. The numbers reported correspond to the simulations where the correct clock model was selected with MAP. The total number of simulations per set of settings was ten. [↑](#footnote-ref-1)