

Supplementary Information for
“High resolution species trees without concatenation”

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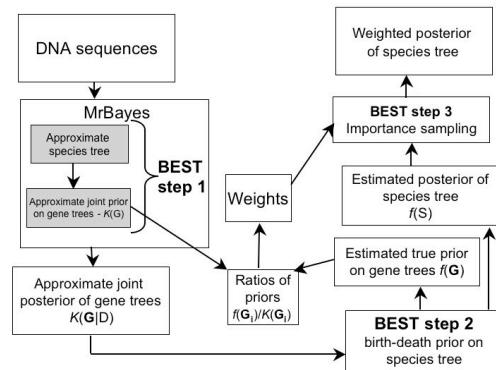
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I. Theory and Computation

A. Overview of the method

The model, which we call the BEST method (for Bayesian Estimation of Species Trees; Fig. 1) first estimates the joint posterior distribution of gene trees from DNA sequences for each locus. The joint posterior distribution is estimated by using a joint prior, which specifies the joint probability of a gene tree and coalescent times for each locus. As described in an associated technical report (1) and in a paper under review (2) coalescent theory (3) is used to model the probability distribution of gene trees given an approximation of the species tree that fulfills the constraint that all divergences of species pairs must occur after the respective gene divergences occur. The resulting approximate joint posterior distribution of gene trees, $K(\mathbf{G}|\mathbf{D})$, is used to approximate the posterior of the species tree under coalescent theory. Importance sampling is then used to align this distribution with the desired posterior under the true prior on gene trees. As currently implemented, the model can take a single sampled allele from each species, so that the number of alleles sampled per locus is equal to the number of species whose phylogenetic relationships are to be estimated.



to be estimated.

Supplementary Figure 1. Overview of Bayesian Estimation of Species Trees (BEST)

B. Estimation of posterior probability of gene trees

The species tree specifies the history of populations. In figure 1, an ancestral population 1 splits into population 2 and species C at time T1. Population 2 further splits into species A and B at time T2. Here we assume

- (i) Random mating in each population.
- (ii) No gene flow after species divergences.
- (iii) No recombination within loci.

If we sampled a copy of gene from each species, A1, B1, C1 and wanted to build a gene tree for them, according assumption (ii), the common ancestor of A1 and B1 may be in population 2 or 1. If the common ancestor is in population 2, it indicates that coalescent time t of A1 and B1 is between T1 and T2.

The branch length in gene trees is the number of mutations per site, whereas the branch length in species tree is generations (time). They are not compatible. Because the time and mutation rate are confounded in the data, we need to reparameterize population size (N_e) and speciation time (T) in the species tree by multiplying them by mutation rate μ .

Let $\theta = 4\mu N_e$ and $\tau = \mu T$. Here μ is the expected number of mutations per generation per

site.

The coalescent process in the lineages considered are conditionally independent. Rannala and Yang (3) obtained the joint probability distribution of the gene tree topology and its coalescent times $t_m, t_{m-1} \dots t_{n+1}$, for a particular population given m-n coalescent events as

$$(1) \prod_{j=n+1}^m \left[\frac{2}{\theta} \exp\left\{-\frac{j(j-1)}{\theta} t_j\right\} \right] \times \exp\left\{-\frac{n(n-1)}{\theta} (\tau - (t_m + t_{m-1} + \dots + t_{n+1}))\right\}$$

Rannala and Yang then multiply similar probabilities across all the populations to form the distribution for a single gene tree. To extend this to multiple gene trees, the assumption of independence of gene trees given the species tree is used. These joint probabilities are used repeatedly in the hierarchical Bayesian algorithm.

C. Bayesian Estimation of Species Trees (BEST) using a hierarchical model and Markov Chain Monte Carlo (MCMC)

Notations:

D_i : DNA sequences for gene i. ($i = 1, \dots, m$)

G_i : gene tree for gene i (topology and branch length). ($i = 1, \dots, m$)

\mathbf{G} : the vector of (G_1, \dots, G_m) .

S : species tree (topology, branch length and effective population size).

$\underline{\quad}$: parameters in substitution model.

There is no closed form for the posterior distribution of the species tree, because the denominator involves a complicated integral. We used MCMC to estimate the posterior distribution.

$$\begin{aligned} (2) f(S | D) &= \int_{genetree} \int_{\mu} f(S, \mathbf{G}, \mu | D) d\mathbf{G} d\mu \\ &= \frac{1}{a} \int_{genetree} \int_{\mu} f(D | \mathbf{G}, \mu) f(\mu) f(\mathbf{G} | S) f(S) d\mathbf{G} d\mu \quad (a \text{ is the normalization constant}) \\ &= \frac{1}{a} \int_{genetree} \int_{\mu} f(D | \mathbf{G}, \mu) f(\mu) \frac{f(\mathbf{G})}{f(\mathbf{G})} f(\mathbf{G} | S) f(S) d\mathbf{G} d\mu \\ &= \frac{1}{a} \int_{genetree} \int_{\mu} f(D | \mathbf{G}, \mu) f(\mu) f(\mathbf{G}) \frac{f(\mathbf{G} | S) f(S)}{f(\mathbf{G})} d\mathbf{G} d\mu \\ &= \int_{genetree} \int_{\mu} f(\mathbf{G}, \mu | D) f(S | \mathbf{G}) d\mathbf{G} d\mu. \end{aligned}$$

Because the posterior of species trees is the integral of the product of $f(\mathbf{G}, \mu | D)$ and $f(S | \mathbf{G})$, we can run a 2-step MCMC to estimate the posterior of species trees. Thus the entire BEST procedure consists of three steps:

In **step 1** (see Supplementary Fig. 1) we take advantage of MrBayes to approximate the posterior distribution of gene trees. For this we substitute an approximate gene tree prior, $K(\mathbf{G})$, into the Hastings ratio that defines the Markov chain in MrBayes. For **step 2**, this posterior distribution of gene trees from the first step forms the input of a second MCMC algorithm that assumes a birth-death prior on species trees to provide a sample from the approximate species tree posterior distribution. In **step 3** we use importance sampling to get the true posterior of gene trees and species trees simultaneously by correcting for the use of $K(\mathbf{G})$ rather than the true prior distribution $f(\mathbf{G})$ in step one:

$$\begin{aligned}
 (3) \quad f(S | D) &= \int_{genetree} \int_{\mu} f(S, \mathbf{G}, \mu | D) d\mathbf{G} d\mu \\
 &= \frac{1}{a} \int_{genetree} \int_{\mu} f(D | \mathbf{G}, \mu) f(\mu) f(\mathbf{G}) \frac{f(\mathbf{G} | S) f(S)}{f(\mathbf{G})} d\mathbf{G} d\mu \\
 &= \frac{1}{a} \int_{genetree} \int_{\mu} f(D | \mathbf{G}, \mu) f(\mu) K(\mathbf{G}) \frac{f(\mathbf{G})}{K(\mathbf{G})} \frac{f(\mathbf{G} | S) f(S)}{f(\mathbf{G})} d\mathbf{G} d\mu.
 \end{aligned}$$

In particular, the i^{th} sample from step 1 is given weight $\frac{\hat{f}(\mathbf{G}_i)}{K(\mathbf{G}_i)}$ to produce the final sample from the true posterior. Here $\hat{f}(\mathbf{G}_i)$ is the estimate of $f(\mathbf{G}_i)$ using a modification of the harmonic mean method (4).

D. Further definition of terms in equation 2:

(4) $f(D | \mathbf{G}, \mu)$

The probability distribution of DNA sequences given the gene tree and $\underline{}$, $f(D_i | G_i, \mu_i)$, is the traditional likelihood in molecular phylogenetics and can be calculated using any substitution model (5, 6). It is assumed that given the gene tree i , the probability distribution of DNA sequences D_i is independent of other genes. Therefore, the joint distribution of data given \mathbf{G} and $\underline{}$ is

$$f(D_1 \dots D_m | G_1 \dots G_m, \mu_1 \dots \mu_m) = \prod_{i=1}^m f(D_i | G_i, \mu_i)$$

(5) $f(\mu)$

There are many options for the prior of μ , $f(\mu)$ available in MrBayes (7). In our analysis of the yeast data, we used default option of Dirichlet priors for the rate parameters and the uniform prior on the gamma distribution shape parameter and the proportion of invariant sites.

(6) $f(\mathbf{G} | S)$

The probability distribution of gene trees given a species tree $f(\mathbf{G} | S)$ was specified using the extension of equation (1) following Rannala and Yang (3).

(7) $f(S)$

The second stage of the hierarchical model is the probability distribution of parameters in the species tree. We used independent gamma distributions as the prior for θ . The hyperparameters α, β defining these distributions are fixed.

A birth-death process was used to specify the prior of topologies and branch lengths for the species tree (8). The speciation rate is λ and the extinction rate is η . $\underline{_}$ is the sampling probability with $\underline{_}$ = the proportion of present day species to the total number of species in the data set (assumed to be 1 in the analysis of the yeast data). The probability that a lineage arising at time t in the past leaves at least one descendant in a present sample is then $P(0,t) = \frac{\rho(\lambda - \eta)}{\rho\lambda + (\lambda(1 - \rho) - \eta)e^{(\eta - \lambda)t}}$ while the chance that this lineage arising leaves exactly one descendant is $p_1(t) = \frac{1}{\rho}P(0,t)^2 e^{(\eta - \lambda)t}$. The joint density of a particular history $\underline{_}$ and its corresponding $s-1$ speciation times t_1, \dots, t_{s-1} is $f(\tau, t | s, t_1, \lambda, \eta) = \frac{2^{s-1}}{s!(s-1)} \prod_{j=2}^{s-1} \frac{\lambda p_1(t_j)}{\nu_{t_1}}$, where $\nu_{t_1} = 1 - \frac{1}{\rho}P(0, t_1)e^{(\eta - \lambda)t_1}$ and t_1 is the speciation time of the root.

(8) Posterior distribution $f(S | D)$:

The joint posterior distribution of gene tree, species tree and $\underline{_}$ given DNA sequences is

$$f(S, \mathbf{G}, \mu | D) \propto f(D | \mathbf{G}, \mu) f(\mu) f(\mathbf{G} | S) f(S)$$

so that

$$f(S | D) = \int_{genetree} \int_{\mu} f(S, \mathbf{G}, \mu | D) d\mathbf{G} d\mu$$

E. Relaxing the molecular clock

To relax the molecular clock during gene tree searches, we modified the acceptance scheme during MCMC searches in MrBayes. When a new gene tree is proposed by MrBayes it is accepted or rejected based on the Hastings ratio. The likelihood of the tree is first calculated without assuming a molecular clock. Then the trees are transformed to be ultrametric by an algorithm similar to that employed in Joe Felsenstein's DNAMLK algorithm in PHYLP. These 'ultrametricized trees' are then used to calculate the joint prior, $K(\mathbf{G})$.

F. Posterior distributions of gene trees

The posterior distributions of gene trees for each of the 106 genes in the yeast data set is presented below for each of the four models: 1) independent model with a molecular clock, 2) joint model with a molecular clock, 3) independent model without a clock, and

4) joint model without a clock. The values in these tables went into figures 1 and 2 of the main manuscript. The trees in the top row of each table are designated as 1 – 24 as follows:

```

1      S.cerevisiae
2      S.paradoxus,
3      S.mikatae,
4      S.kudriavzevii,
5      S.bayanus
6      S.castellii
7      S.kluyveri
8      C._albicans,

1. (8,(7,(6,(5,(4,(3,(1,2)))))));}
2. (8,(7,(6,((4,5),(3,(1,2)))))));}
3. (8,((6,7),(5,(4,(3,(1,2)))))));}
4. (8,(6,(7,(5,(4,(3,(1,2)))))));}
5. (8,(6,(7,((3,(1,2)),(4,5))))));}
6. (8,(6,(7,(3,((1,2),(4,5)))))));}
7. (8,(7,(6,(5,((3,4),(1,2)))))));}
8. (8,((3,((4,5),(1,2))), (6,7))));}
9. (8,((6,7),((3,(1,2)),(4,5)))));}
10. (8,(7,(6,(4,(5,(3,(1,2)))))));}
11. (6,(8,(7,((4,5),(3,(1,2)))))));}
12. (8,((6,7),(4,(5,(3,(1,2)))))));}
13. (8,(6,(7,(4,(5,(3,(1,2)))))));}
14. (6,(8,(7,(5,(4,(3,(1,2)))))));}
15. (8,(((1,2),(3,(4,5))), (6,7))));}
16. (8,(6,(7,((1,2),(3,(4,5)))))));}
17. (8,(7,(6,(5,(3,(4,(1,2)))))));}
18. (8,(7,(6,(3,((1,2),(4,5)))))));}
19. (8,(7,(6,((3,(4,5)),(1,2)))))));}
20. (8,(3,((4,(5,(6,7))), (1,2)))));}
21. (8,(7,(6,(2,(1,(3,(4,5)))))));}
22. (8,(7,(5,(4,(3,(2,(1,6)))))));}
23. (8,(7,(6,(1,(2,(3,(4,5)))))));}
24. (8,((6,7),(1,(2,(3,(4,5)))))));}

```

Supplementary Table 1. Independent model with a molecular clock

Topology	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	Total
Gene 1	0.147	0	0.0165	0	0	0	0	0	0	0.83	0	0.0065	0	0	0	0	0	0	0	0	0	0	0	0	1
2	0.669	0.331	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
3	0.2685	0.7305	0	0	0	0	0	0	0	0.001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
4	0.6945	0.079	0.141	0.0535	0	0	0.029	0	0	0	0	0	0	0	0	0	0.003	0	0	0	0	0	0	0	1
5	0	0	0	0	0.1995	0.0745	0	0	0	0	0	0	0	0	0.05	0.628	0	0.006	0.042	0	0	0	0	0	1
6	0.0055	0.026	0.019	0.165	0.103	0.2205	0.002	0.0145	0.0855	0	0	0.0175	0	0	0	0.0045	0	0.046	0	0	0	0	0	0	0.709
7	0	0.893	0	0	0.029	0	0	0	0.031	0	0	0	0	0	0	0	0	0.047	0	0	0	0	0	0	1
8	0.0385	0.9005	0	0	0	0	0	0	0	0.061	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
9	0.309	0.647	0	0.013	0	0	0	0	0	0.0065	0	0	0	0	0	0	0	0.0015	0.023	0	0	0	0	0	1
10	0.1915	0.6085	0	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
11	0.136	0.0805	0	0.3555	0.379	0	0	0	0	0	0	0.049	0	0	0	0	0	0	0	0	0	0	0	0	1
12	0	0.7835	0	0	0.2075	0	0	0	0.009	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
13	0.2155	0.7845	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
14	0.0885	0.8265	0	0	0	0	0	0	0	0.085	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
15	0.001	0.372	0.0045	0	0.3395	0	0	0	0.2095	0.028	0	0.0085	0.0035	0	0	0	0	0	0	0	0	0	0	0	0.9665
16	0.0815	0.9185	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
17	0.156	0.322	0	0	0	0	0	0	0.0315	0.473	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.9825
18	0.5605	0.426	0.009	0.0045	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
19	0.482	0.3145	0.028	0	0.038	0	0	0	0.0665	0.071	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
20	0.0065	0.001	0.136	0	0.002	0	0	0.0715	0.549	0	0	0.175	0	0	0.0185	0	0	0	0	0	0	0	0	0	0.9595
21	0	0.056	0	0	0.921	0	0	0	0.023	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
22	0	0.802	0	0	0	0	0	0	0.198	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
23	0.024	0.247	0.095	0.0655	0.388	0	0	0	0.096	0.022	0	0.022	0.0405	0	0	0	0	0	0	0	0	0	0	0	1
24	0.224	0.645	0	0	0	0	0	0	0	0.131	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
25	0.3745	0.2985	0.101	0.029	0.077	0	0	0	0.061	0.041	0	0.013	0.005	0	0	0	0	0	0	0	0	0	0	0	1
26	0.8865	0.036	0	0	0	0	0	0	0	0.0775	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
27	0.3445	0.541	0	0	0	0	0	0	0	0.1145	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
28	0.8375	0.1325	0	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
29	0.1705	0.0945	0.042	0.246	0.2935	0	0	0	0.0015	0.0485	0	0.023	0.0805	0	0	0	0	0	0	0	0	0	0	0	1
30	0.0235	0.8365	0	0	0	0	0	0	0	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
31	0.171	0.48	0.081	0.0235	0.0035	0	0	0	0.0975	0.0765	0	0.034	0.033	0	0	0	0	0	0	0	0	0	0	0	1
32	0	0.889	0	0	0.111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
33	0.0595	0.134	0.1095	0.0135	0.0145	0	0	0.0125	0.224	0.06	0	0.0655	0.018	0	0.203	0.014	0	0.015	0.04	0	0	0	0	0.983	
34	0.0625	0.059	0.373	0.172	0.0465	0	0	0	0.137	0.0195	0	0.09	0.019	0	0	0	0	0	0	0	0	0	0	0	0.9785
35	0	0.0965	0.001	0	0.442	0	0	0	0.456	0	0	0.0045	0	0	0	0	0	0	0	0	0	0	0	0	1
36	0.225	0.1	0.1975	0.223	0.054	0	0	0	0.1015	0.0545	0	0.022	0.0225	0	0	0	0	0	0	0	0	0	0	0	1

37	0.408	0.534	0	0	0	0	0	0	0.041	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.983	
38	0.129	0	0.6855	0.094	0	0	0.0075	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.916	
39	0	0.4765	0	0	0.134	0	0	0	0.3895	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
40	0.0015	0.0195	0.0135	0.011	0.0265	0.0985	0	0.051	0.083	0.0235	0	0.0125	0.0325	0	0.223	0.174	0	0.061	0.136	0	0	0	0	0	0	0.967	
41	0.082	0	0.0115	0	0	0	0.03	0	0	0	0	0	0	0	0	0	0	0.826	0	0	0	0	0	0	0	0.9495	
42	0.3395	0	0.364	0.263	0	0	0.0025	0	0.0015	0	0	0	0	0	0	0	0.0015	0	0	0	0	0	0	0	0	0.972	
43	0.769	0.145	0	0	0	0	0	0	0.086	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
44	0.143	0.022	0	0	0	0	0.0745	0	0	0.142	0	0	0	0	0	0	0	0.0095	0	0.272	0	0	0	0	0	0.663	
45	0.0235	0	0.68	0	0	0	0	0	0.2965	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
46	0.398	0.411	0	0.012	0	0	0.001	0	0	0.069	0	0	0	0	0	0	0	0.0385	0	0.0555	0	0	0	0	0	0.985	
47	0.016	0.9025	0.017	0.0145	0.011	0	0	0	0.025	0	0	0	0.014	0	0	0	0	0	0	0	0	0	0	0	0	1	
48	0.038	0	0.038	0.9095	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.9855	
49	0.856	0.006	0.0055	0.1325	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
50	0.2325	0.7675	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
51	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
52	0	0.1285	0	0.021	0.429	0	0	0	0.4215	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
53	0	0.0315	0.0035	0.034	0.2885	0	0	0	0.038	0.044	0	0.1045	0.448	0	0	0	0	0	0	0	0	0	0	0	0	0.992	
54	0.053	0.0395	0.2805	0.031	0.1995	0	0	0	0.2315	0	0	0.1405	0.0245	0	0	0	0	0	0	0	0	0	0	0	0	1	
55	0.36	0.5215	0.011	0.029	0.0305	0	0	0	0.027	0.0205	0	0	0.0005	0	0	0	0	0	0	0	0	0	0	0	0	1	
56	0.1865	0.14	0.079	0.2815	0.1085	0	0	0	0.0055	0.0705	0	0.001	0.1275	0	0	0	0	0	0	0	0	0	0	0	0	1	
57	0	0	0.004	0.996	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
58	0	0.953	0	0	0	0	0	0	0.047	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
59	0.516	0.4225	0	0	0	0	0	0	0	0.0615	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
60	0.0365	0.1425	0.019	0	0.001	0.009	0.02	0.0995	0.25	0	0	0	0	0	0	0.2295	0.004	0	0.0245	0.143	0	0	0	0	0	0.9785	
61	0	0.075	0	0.0605	0.5585	0.0365	0	0	0.243	0	0	0	0	0	0	0	0.0145	0	0.012	0	0	0	0	0	0	1	
62	0.7365	0.018	0.0015	0.063	0	0	0.108	0	0	0.062	0	0	0	0	0	0	0	0	0.011	0	0	0	0	0	0	1	
63	0.8765	0.1235	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
64	0.0095	0.559	0	0	0.082	0	0	0	0.219	0.106	0	0	0	0.0245	0	0	0	0	0	0	0	0	0	0	0	0	1
65	0.1605	0.547	0.003	0	0.054	0	0	0	0.2285	0.0035	0	0	0.0035	0	0	0	0	0	0	0	0	0	0	0	0	1	
66	0.096	0.536	0.0015	0.0505	0.0235	0	0	0.002	0.0655	0.032	0	0	0.003	0	0.019	0.0105	0	0.051	0.0785	0	0	0	0	0	0	0.969	
67	0.3615	0.1145	0.277	0	0.028	0	0	0	0.1965	0.0225	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
68	0.008	0	0	0.9295	0.0215	0	0	0	0	0	0	0	0.0285	0	0	0	0	0	0	0	0	0	0	0	0	0.9875	
69	0.8935	0.056	0	0	0	0	0	0	0.0505	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
70	0	0.003	0.0605	0	0.047	0	0	0	0.8895	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
71	0	0	0	0.7875	0.103	0	0	0	0	0	0	0	0.1095	0	0	0	0	0	0	0	0	0	0	0	0	1	
72	0.0585	0.7645	0.0385	0	0	0	0	0	0.108	0.017	0	0.0135	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
73	0	0	0	0.968	0.032	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
74	0.393	0	0.3745	0.124	0	0	0	0	0	0	0	0.1085	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
75	0	0.056	0.031	0	0.0175	0	0	0.047	0.6985	0	0	0.139	0.01	0	0.001	0	0	0	0	0	0	0	0	0	0	1	
76	0.8785	0	0.093	0	0	0	0	0.0005	0	0	0	0	0	0	0	0	0.028	0	0	0	0	0	0	0	0	1	

77	0.8395	0.1605	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
78	0	0.772	0	0	0.144	0	0	0	0.084	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
79	0.051	0.253	0.0045	0.05	0.49	0	0	0	0.1175	0.0235	0	0.0105	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
80	0.0725	0	0.9175	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
81	0.411	0.2315	0.087	0.0555	0.051	0	0	0	0.0385	0.094	0	0.0125	0.019	0	0	0	0	0	0	0	0	0	0	0	0	0	1		
82	0.501	0.328	0	0.0325	0.0905	0	0	0	0	0.0435	0	0.0045	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
83	0.003	0.632	0	0	0.192	0	0	0	0.173	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
84	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
85	0.5685	0.026	0.091	0.259	0	0	0	0	0.0135	0.0245	0	0	0.0175	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
86	0.0325	0.023	0.0845	0.48	0.261	0	0	0	0.0055	0.0025	0	0	0.111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
87	0.093	0.3825	0.0135	0	0.0115	0	0.003	0	0.0615	0.32	0	0.1045	0.0105	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
88	0.857	0	0	0	0	0	0	0	0	0.055	0	0	0	0	0	0	0	0.07	0	0	0	0	0	0	0	0	0	0.982	
89	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
90	0.223	0.746	0	0	0	0	0	0	0	0.031	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
91	0.405	0	0.3495	0.2455	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
92	0.13	0.3105	0.02	0.012	0.022	0	0	0	0.0795	0.1215	0	0.1245	0	0	0.021	0.01	0	0	0	0.144	0	0	0	0	0	0	0	0.995	
93	0	0.018	0.1705	0	0	0	0	0	0.8115	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
94	0.2555	0.4005	0.0815	0.041	0.1	0	0	0	0	0.0485	0	0.055	0.018	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
95	0.269	0.057	0.3875	0.1095	0.048	0	0	0	0.129	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
96	0.841	0.017	0.013	0.03	0	0	0.057	0	0	0.002	0	0	0	0	0	0	0	0.008	0	0	0	0	0	0	0	0	0.968		
97	0.088	0.6615	0	0	0	0	0	0	0	0.2105	0	0	0	0	0	0	0	0	0	0.0365	0	0	0	0	0	0	0	0.9965	
98	0.1725	0.3405	0.1545	0.0185	0.084	0	0	0	0.1055	0.0935	0	0.0095	0.0215	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
99	0	0.023	0	0.187	0.7875	0	0	0	0.0025	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
100	0.3535	0.0525	0.459	0.117	0.001	0	0	0	0.013	0.0025	0	0.0015	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
101	0.839	0.161	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
102	0.0145	0.114	0	0.0615	0.675	0	0	0	0	0.115	0	0	0	0	0	0	0	0.0075	0	0.007	0.0055	0	0	0	0	0	0	1	
103	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
104	0	0.9905	0	0	0.0095	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
105	0.9145	0	0	0.0855	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	
106	0.133	0	0.802	0.0115	0	0	0	0	0.0435	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	

Supplementary Table 2. Joint model with a molecular clock

Topology	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	Total	
Gene 1	0.451751	0.546027	0.001793	0	0.000355	0	0	0	0	0.000064	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
2	0.485632	0.511383	0	0	0	0	0	0	0	0.002975	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
3	0.001679	0.996741	0	0	0	0	0	0	0	0.00157	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
4	0.719934	0.069185	0.142395	0.056833	0.000163	0	0	0	0.009222	0.002258	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
5	0	0.001893	0	0	0	0.98849	0	0	0	0.009607	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
6	0.013688	0.022706	0.152842	0.25594	0.230699	0.000096	0	0.000012	0.28702	0.002394	0	0.026564	0.008029	0	0	0	0	0	0	0	0	0	0	0	0	0.999

7	0	0.922959	0	0	0.051621	0	0	0	0.02541	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999		
8	0.010772	0.989178	0	0	0	0	0	0	0	0.00004	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
9	0.1076	0.887889	0.000186	0.000195	0	0	0	0	0.002144	0.001976	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
10	0.264911	0.689867	0	0	0	0	0	0	0	0.045212	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
11	0.03938	0.034346	0	0.284251	0.581209	0	0	0	0	0.000285	0.014754	0	0	0	0.045765	0	0	0	0	0	0	0	0	0	0	0	0.999	
12	0	0.797455	0	0	0.164034	0	0	0	0	0.038501	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
13	0.16828	0.814165	0	0	0	0	0	0	0	0.017545	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
14	0.003492	0.932987	0	0	0.000233	0	0	0	0	0.063278	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
15	0.001674	0.085397	0	0.15266	0.718991	0	0	0	0	0.040121	0.000244	0	0	0	0.000903	0	0	0	0	0	0	0	0	0	0	0.999		
16	0.018178	0.981812	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
17	0.010315	0.987341	0	0	0	0	0	0	0	0.000035	0.002299	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
18	0.028864	0.698018	0	0.000174	0.000147	0	0	0	0.272787	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
19	0.121667	0.786722	0.023817	0.004278	0.017622	0	0	0	0	0.045221	0.000066	0	0.000007	0.000527	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
20	0.015025	0.417013	0.047788	0.000056	0.011126	0	0	0	0.474862	0.02299	0	0.010986	0.000144	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
21	0	0.320802	0	0	0.675882	0	0	0	0	0.003306	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
22	0	0.998877	0	0	0.000829	0	0	0	0	0.000284	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
23	0.000389	0.143557	0.00157	0.124478	0.70504	0	0	0	0	0.024895	0	0	0	0.000061	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
24	0.130589	0.82737	0	0	0	0	0	0	0	0.042031	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
25	0.00401	0.835729	0.012268	0.000051	0.051331	0	0	0	0	0.094123	0.001678	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
26	0.531756	0.440291	0.000169	0	0	0	0	0	0	0.027774	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
27	0.587196	0.358491	0	0	0	0	0	0	0	0.054303	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
28	0.373291	0.573164	0	0	0	0	0	0	0	0.053535	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
29	0.147421	0.562624	0.014266	0.168888	0.067257	0	0	0	0	0.007943	0.01291	0	0.005701	0.01298	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
30	0.054526	0.945464	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
31	0.018185	0.909988	0.000065	0	0.01409	0	0	0	0.054109	0.003553	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
32	0	0.849983	0	0	0.150007	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
33	0.013091	0.196404	0.116546	0.011554	0.066796	0	0	0	0	0.513651	0.049892	0	0.027369	0.004687	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
34	0.078497	0.397075	0.043432	0.026562	0.314818	0	0	0	0	0.122864	0.011384	0	0.000988	0.00437	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
35	0	0.001303	0.002171	0.003151	0.75858	0	0	0	0	0.233071	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.9982		
36	0.106164	0.094446	0.057655	0.012648	0.078808	0	0	0	0	0.530326	0.107926	0	0.00768	0.004249	0.000022	0	0	0	0	0	0	0	0	0	0	0.9999		
37	0.368782	0.631127	0	0	0	0	0	0	0	0.000081	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
38	0.150685	0.000225	0.822929	0.024712	0.000127	0	0	0	0	0.001218	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.9998		
39	0.003934	0.652404	0.005063	0.006645	0.024134	0	0	0	0	0.307399	0.00005	0	0.000323	0.000038	0	0	0	0	0	0	0	0	0	0	0	0.999		
40	0.015855	0.498758	0.003636	0.007366	0.115294	0	0	0	0	0.271299	0.000151	0	0.013915	0.07367	0	0.000046	0	0	0	0	0	0	0	0	0	0.999		
41	0.630333	0	0.076388	0.293269	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
42	0.966166	0.0018	0	0.000033	0	0	0	0	0	0	0.031991	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
43	0.563108	0.384972	0	0	0	0	0	0	0	0.05191	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
44	0.411452	0.333482	0	0	0	0	0	0	0	0.25502	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
45	0.580879	0.012335	0.012389	0.357631	0.029994	0	0	0	0	0.006762	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999		
46	0.050664	0.487559	0.000696	0	0.009121	0	0	0	0	0.001375	0.450435	0	0.000034	0.000106	0	0	0	0	0	0	0	0	0	0	0	0.999		

47	0.055118	0.935839	0	0	0.000011	0	0	0	0	0.009022	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999	
48	0.008052	0	0.001039	0.865248	0.125522	0	0	0	0	0	0	0	0	0.000129	0	0	0	0	0	0	0	0	0	0	0.999
49	0.982381	0.000172	0.000993	0.016444	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
50	0.006902	0.988713	0	0	0.001355	0	0	0	0	0.00302	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
51	0	0	0	0	0.999658	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.9996
52	0.013336	0.185463	0	0.006866	0.271167	0	0	0	0	0.214432	0.273176	0	0.012481	0.023069	0	0	0	0	0	0	0	0	0	0	0.999
53	0.011101	0.005371	0.002397	0.121776	0.366134	0	0	0	0	0.337596	0.025137	0.000052	0.034504	0.09589	0	0	0	0	0	0	0	0	0	0	0.9999
54	0.071021	0.120005	0.036612	0.044139	0.099461	0	0	0	0	0.162229	0.279975	0	0.035558	0.150945	0	0	0	0	0	0	0	0	0	0	0.999
55	0.097807	0.853488	0.009279	0.007339	0.003992	0	0	0	0	0.017318	0.010767	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
56	0.062188	0.106448	0.001168	0.211221	0.078113	0	0	0	0	0.000236	0.125189	0	0.019486	0.395941	0	0	0	0	0	0	0	0	0	0	0.999
57	0.002615	0	0.00125	0.996125	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
58	0	0.999513	0	0	0	0	0	0	0	0.000477	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
59	0.046847	0.953143	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
60	0.10542	0.387778	0.369579	0.003	0.023325	0	0	0	0	0.109884	0.000524	0	0.000276	0.000202	0	0	0	0	0	0	0	0	0	0	0.999
61	0.019769	0.278536	0.022212	0.008064	0.198209	0	0	0	0	0.370812	0.005213	0	0.003555	0.09362	0	0	0	0	0	0	0	0	0	0	0.999
62	0.965347	0.011241	0.002221	0.010981	0.000016	0	0	0	0	0.000884	0.008825	0	0	0.000475	0	0	0	0	0	0	0	0	0	0	0.999
63	0.941066	0.058924	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
64	0.005725	0.45165	0.002755	0.000054	0.277887	0	0	0	0	0.254982	0.003917	0	0.00302	0	0	0	0	0	0	0	0	0	0	0	0.999
65	0.04521	0.836414	0.049007	0.001129	0.032096	0	0	0	0	0.036099	0.000035	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
66	0.052066	0.647406	0.018376	0.006157	0.01636	0	0	0	0	0.078279	0.159297	0	0.021978	0.000071	0	0	0	0	0	0	0	0	0	0	0.999
67	0.009896	0.071327	0.1006	0.001161	0.049819	0	0	0	0	0.700508	0.002917	0	0.063675	0.000087	0	0	0	0	0	0	0	0	0	0	0.999
68	0.157712	0.000279	0.00179	0.69854	0.119749	0	0	0	0	0.000182	0	0	0	0.021738	0	0	0	0	0	0	0	0	0	0	0.999
69	0.756732	0.239213	0.00005	0	0	0	0	0	0	0.003995	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
70	0	0.094552	0.009045	0	0.000177	0	0	0	0	0.874869	0	0	0	0.021347	0	0	0	0	0	0	0	0	0	0	0.999
71	0.000054	0	0	0.376741	0.091219	0	0	0	0	0	0.280612	0	0.00462	0.229922	0	0	0	0	0	0	0	0	0	0	0.9831
72	0.066881	0.930921	0.000306	0	0.00002	0	0	0	0	0.000508	0.001354	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
73	0.012615	0.315384	0.025568	0.404649	0.131562	0	0	0	0	0.000058	0	0	0	0.110154	0	0	0	0	0	0	0	0	0	0	0.999
74	0.098554	0.004036	0.255626	0.047415	0.005216	0	0	0	0	0.431115	0.000851	0	0.154101	0.003041	0	0	0	0	0	0	0	0	0	0	0.999
75	0	0.00014	0.022134	0.000067	0.032181	0	0	0	0	0.879943	0	0	0.065525	0	0	0	0	0	0	0	0	0	0	0	0.999
76	0.998572	0.000867	0.000383	0.000168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
77	0.459719	0.496383	0	0	0	0	0	0	0	0.043888	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
78	0.003448	0.958962	0	0.000332	0.013086	0	0	0	0	0.024073	0.000089	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
79	0.00065	0.410082	0.015934	0.005099	0.43879	0	0	0	0	0.128769	0	0	0	0.000756	0	0	0	0	0	0	0	0	0	0.999	
80	0.981421	0	0.016547	0.002022	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
81	0.056782	0.745257	0.003172	0.00142	0.149256	0	0	0	0	0.040687	0.003416	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
82	0.17344	0.765267	0.002392	0.008468	0.027854	0	0	0	0	0.016827	0.005356	0	0	0.000386	0	0	0	0	0	0	0	0	0	0	0.999
83	0	0.705709	0	0	0.076872	0	0	0	0	0.2111276	0.001108	0	0.003468	0.001557	0	0	0	0	0	0	0	0	0	0	0.999
84	0.006107	0.993883	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
85	0.5975	0.115193	0.135149	0.115826	0.029023	0	0	0	0	0.004394	0.001614	0	0.0005	0.000791	0	0	0	0	0	0	0	0	0	0	0.999
86	0.023327	0.014576	0.016342	0.162636	0.7561	0	0	0	0	0.019253	0.000095	0	0	0.007661	0	0	0	0	0	0	0	0	0	0	0.999

87	0.137248	0.33024	0.035004	0	0.049693	0	0	0	0.440859	0.004293	0	0.002653	0	0	0	0	0	0	0	0	0	0	0	0.999
88	0.419596	0.447318	0	0	0	0	0	0	0	0.133076	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
89	0.991142	0.008848	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
90	0.033649	0.954501	0	0	0	0	0	0	0	0.01184	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
91	0.446829	0.00075	0.528423	0.022333	0.000287	0	0	0	0.001368	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
92	0.001476	0.653021	0.001859	0.001127	0.03929	0	0	0	0.303083	0	0	0	0	0	0	0	0	0	0.000134	0	0	0	0	0.999
93	0	0	0.033953	0	0	0	0	0	0.966037	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
94	0.07462	0.437233	0	0.004913	0.345073	0	0	0	0.002024	0.136042	0	0	0.000085	0	0	0	0	0	0	0	0	0	0	0.999
95	0.010817	0.064002	0.383576	0.033748	0.003832	0	0	0	0.502766	0.00001	0	0.001239	0	0	0	0	0	0	0	0	0	0	0	0.999
96	0.532889	0.425642	0.008576	0.012358	0.000594	0	0	0	0.010695	0.008954	0	0	0.000282	0	0	0	0	0	0	0	0	0	0	0.999
97	0.017476	0.982487	0	0	0	0	0	0	0	0.000027	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
98	0.007361	0.431195	0.016648	0.004149	0.16795	0	0	0	0.203553	0.019679	0	0.128841	0.020614	0	0	0	0	0	0	0	0	0	0	0.999
99	0.000895	0.000904	0	0.024635	0.965997	0	0	0	0.006825	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.9992
100	0.207573	0.436188	0.047062	0.016005	0.024539	0	0	0	0.252538	0.015016	0	0.000296	0.000773	0	0	0	0	0	0	0	0	0	0	0.999
101	0.836708	0.156656	0	0	0	0	0	0	0	0.006626	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
102	0.125216	0.306425	0.067012	0.120429	0.283445	0	0	0	0.097026	0	0	0.000038	0.000399	0	0	0	0	0	0	0	0	0	0	0.999
103	0	0.989076	0.000015	0	0.001978	0	0	0	0.008921	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
104	0	0.99831	0	0	0.00049	0	0	0	0.001119	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
105	0.837799	0	0.039223	0.122968	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999
106	0.039196	0.003159	0.861368	0.016337	0	0	0	0	0.079011	0.000064	0	0.000855	0	0	0	0	0	0	0	0	0	0	0	0.999

Supplementary Table 3. Independent model with a relaxed clock

Topology	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	Total	
Gene 1	0.6235	0	0.207002	0.164604	0	0	0	0	0.004988	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
	2	0.468872	0	0.04988	0.456402	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002494	0	0	0	0	0.977648	
	3	0.937744	0.054868	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007482	0	0	0	0	0	1.000094	
	4	0.94772	0	0.014964	0.03741	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
	5	0.027434	0.052374	0	0.007482	0.007482	0.017458	0	0.002494	0.002494	0.047386	0	0.002494	0	0	0.014964	0.069832	0	0.097266	0.52374	0	0.06235	0	0.047386	0	0.982636
	6	0.334196	0	0.147146	0.389064	0.002494	0.02494	0.022446	0.007482	0.002494	0	0	0	0	0	0	0	0.014964	0.002494	0	0	0	0	0	0.94772	
	7	0.002494	0.616018	0	0	0	0	0	0	0.002494	0.039904	0	0	0	0	0	0	0	0.159616	0.059856	0	0.01247	0	0.104748	0	0.9976
	8	0.082302	0.431462	0	0	0	0	0	0	0.007482	0.16211	0	0.002494	0	0	0	0	0.002494	0.077314	0	0.21199	0	0.014964	0	0.992612	
	9	0.980142	0.017458	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.002494	0	0	0	0	1.000094	
	10	0.76067	0.11223	0.029928	0	0	0	0	0	0.002494	0.089784	0	0.004988	0	0	0	0	0	0	0	0	0	0	0	1.000094	
	11	0.334196	0.029928	0.002494	0.18705	0.03741	0.004988	0	0	0.002494	0.059856	0	0	0.03741	0	0	0.027434	0	0.002494	0.044892	0	0.054868	0	0.077314	0	0.902828
	12	0.119712	0.007482	0.03741	0.154628	0.014964	0	0	0	0.23693	0	0.067338	0.359136	0	0	0	0	0	0	0	0	0	0	0	0.9976	
	13	0.314244	0.014964	0.381582	0.231942	0.014964	0	0	0.002494	0.017458	0.01247	0	0.009976	0	0	0	0	0	0	0	0	0	0	0	1.000094	
	14	0.042398	0.2494	0	0	0	0	0	0	0.002494	0	0	0	0	0	0	0	0.104748	0.391558	0	0.142158	0	0.067338	0	1.000094	
	15	0.08729	0.004988	0.02494	0.815538	0.027434	0.002494	0	0	0	0	0.01247	0	0	0	0	0	0	0	0	0.002494	0.002494	0.980142			
	16	0.004988	0	0.007482	0.987624	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	

17	0.157122	0.044892	0.034916	0.059856	0.017458	0	0	0	0.01247	0.266618	0	0.122206	0.122206	0	0	0	0	0	0	0	0	0	0	0	0.937744	
18	0.9976	0	0.002494	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
19	0.865418	0.004988	0.077314	0.052374	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
20	0	0	0.027434	0	0	0.009976	0	0.678368	0.059856	0	0	0.019952	0.002494	0	0.01247	0	0	0	0	0.002494	0	0	0	0.094772	0.907816	
21	0.114724	0.28681	0	0.002494	0.002494	0	0	0	0.002494	0.014964	0	0	0	0	0	0	0	0	0.014964	0	0.546186	0	0.007482	0	0.992612	
22	0.51127	0.481342	0	0	0	0	0	0	0.002494	0	0	0	0	0	0	0	0	0.004988	0	0	0	0	0	0	1.000094	
23	0.416498	0.09976	0.017458	0.17458	0.044892	0.007482	0	0.009976	0	0.022446	0	0	0.014964	0	0	0.002494	0	0.084796	0.02494	0	0.017458	0	0.044892	0.002494	0.98513	
24	0.304268	0.139664	0	0	0	0	0	0	0	0.543692	0	0.002494	0	0	0	0	0	0.009976	0	0	0	0	0	0	1.000094	
25	0.009976	0.004988	0	0	0.002494	0.004988	0	0.01247	0	0	0	0	0	0.017458	0.032422	0	0.042398	0.059856	0	0.009976	0	0.508776	0.119712	0.825514		
26	0.541198	0.01247	0.004988	0.032422	0	0	0	0	0	0.389064	0	0.01247	0.007482	0	0	0	0	0	0	0	0	0	0	0	1.000094	
27	0.912804	0.017458	0	0	0	0	0	0	0	0.069832	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
28	0.982636	0	0.017458	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
29	0.127194	0.007482	0.089784	0.129688	0.009976	0	0	0	0.019952	0.08729	0	0.07482	0.089784	0	0	0	0	0	0	0.082302	0	0	0	0	0.718272	
30	0.970166	0	0.007482	0.022446	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
31	0.16211	0.039904	0.251894	0.21199	0.039904	0.007482	0	0.01247	0.114724	0.042398	0	0.072326	0.03741	0	0	0	0	0.002494	0	0	0	0	0	0	0.995106	
32	0.259376	0.02494	0.01247	0.009976	0	0	0	0	0	0.017458	0	0.002494	0	0	0	0	0	0.002494	0.009976	0	0.004988	0.33669	0.154628	0.004988	0.840478	
33	0.004988	0.002494	0.029928	0.002494	0.002494	0	0	0.054868	0.032422	0.034916	0	0.244412	0.034916	0	0.002494	0	0	0.002494	0	0	0	0	0	0	0.44892	
34	0.164604	0.079808	0.007482	0.004988	0.017458	0.002494	0	0.007482	0.004988	0.014964	0	0.002494	0	0	0.019952	0.007482	0	0.034916	0.072326	0	0.082302	0	0.394052	0.032422	0.950214	
35	0.03741	0.042398	0.01247	0.04988	0.167098	0.466378	0	0.02494	0.007482	0.02494	0	0.004988	0.034916	0	0.004988	0.042398	0	0.072326	0.004988	0	0	0	0	0	0.9976	
36	0.084796	0.01247	0.104748	0.381582	0.027434	0.04988	0	0.019952	0.022446	0.004988	0	0.01247	0.064844	0	0.02494	0.084796	0	0.019952	0.022446	0	0.002494	0	0.002494	0	0.942732	
37	0.670886	0.172086	0.002494	0.022446	0.002494	0	0	0	0.002494	0.117218	0	0	0.002494	0	0	0	0	0.002494	0	0	0	0	0	0	0.995106	
38	0.531222	0	0.089784	0.3741	0	0	0.004988	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
39	0.009976	0.102254	0	0	0	0.019952	0	0.007482	0.002494	0.004988	0	0	0	0	0	0	0	0.808056	0.032422	0	0.009976	0	0.002494	0	1.000094	
40	0	0	0	0	0.002494	0.009976	0	0.244412	0	0	0	0	0	0	0.059856	0.034916	0	0	0	0.002494	0	0	0	0.04988	0.404028	
41	0.219472	0	0.381582	0.192038	0	0.004988	0.002494	0.019952	0	0	0	0	0	0	0	0	0.03741	0.009976	0	0	0	0	0	0	0.867912	
42	0.089784	0	0.007482	0.009976	0	0	0.002494	0	0	0	0	0	0	0	0	0	0	0	0.663404	0	0	0	0	0	0	0.77314
43	0.932756	0.027434	0	0	0	0	0	0	0.039904	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
44	0.179568	0	0	0	0	0	0.009976	0	0	0.603548	0	0	0.002494	0	0	0	0.01247	0.002494	0.09976	0	0	0	0.014964	0	0.925274	
45	0.184556	0	0.39904	0.416498	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
46	0.002494	0	0.004988	0.01247	0.017458	0.047386	0	0.06235	0.004988	0	0	0.017458	0.019952	0	0.052374	0.03741	0	0.002494	0.004988	0	0.082302	0.339184	0.713284			
47	0.246906	0.276834	0.004988	0.159616	0.26187	0	0	0	0.009976	0.01247	0	0	0.027434	0	0	0	0	0	0	0	0	0	0	0	1.000094	
48	0.86043	0	0.004988	0.014964	0	0	0	0	0.109736	0	0	0	0	0	0	0.009976	0	0	0	0	0	0	0	1.000094		
49	0.725754	0.004988	0.01247	0.256882	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
50	0.144652	0.371606	0.002494	0.004988	0.009976	0	0	0	0.004988	0.044892	0	0	0	0	0.004988	0.009976	0	0.06235	0.281822	0	0.009976	0	0.042398	0	0.995106	
51	0.13717	0.715778	0.002494	0.022446	0.092278	0	0	0	0	0.009976	0	0	0	0	0	0	0.004988	0.014964	0	0	0	0	0	0	1.000094	
52	0.042398	0.007482	0.02494	0.690838	0.014964	0	0	0	0	0.017458	0	0.01247	0.18705	0	0	0.002494	0	0	0	0	0	0	0	0	1.000094	
53	0.077314	0.009976	0.132182	0.072326	0.009976	0.039904	0	0.139664	0.029928	0.039904	0	0.202014	0.044892	0	0.029928	0.007482	0	0.014964	0.007482	0.002494	0	0	0.002494	0.022446	0.88537	
54	0.007482	0	0.004988	0.07482	0	0	0	0	0.039904	0	0.072326	0.79808	0	0	0	0	0	0	0	0	0	0	0	0	0.9976	
55	0.11223	0.007482	0.488824	0.28681	0.017458	0	0	0	0.02494	0.002494	0	0.014964	0.022446	0	0	0	0	0	0	0	0	0	0	0	0.977648	
56	0	0	0	0.022446	0	0	0	0	0.067338	0	0.007482	0.902828	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	

57	0.047386	0.002494	0	0.002494	0	0	0	0	0	0	0	0	0	0	0	0	0.002494	0.002494	0	0.004988	0	0.825514	0.01247	0.900334			
58	0.107242	0.354148	0	0	0	0	0	0	0	0.002494	0	0	0	0	0	0	0.421486	0.109736	0	0.002494	0	0.002494	0	1.000094			
59	1.000094	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094			
60	0.002494	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04988	0.009976	0	0.002494	0.157122	0	0.309256	0	0.246906	0.072326	0.850454		
61	0.950214	0	0.019952	0.027434	0	0	0	0	0	0.002494	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094			
62	0.675874	0.022446	0	0	0	0	0.214484	0	0	0.057362	0	0	0	0	0	0	0.004988	0	0.017458	0	0	0	0	0.992612			
63	0.980142	0.007482	0	0	0	0	0.01247	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094			
64	0.668392	0.044892	0.004988	0.007482	0	0	0	0	0	0.269352	0	0	0.004988	0	0	0	0	0.002494	0	0.004988	0.688344	0	0.02494	0	0.004988	0	1.000094
65	0	0.271846	0	0	0	0	0	0	0	0.002494	0	0	0	0	0	0.002494	0	0.004988	0	0.02494	0	0.004988	0	1.000094			
66	0.109736	0.102254	0.039904	0.019952	0.002494	0.034916	0	0.142158	0.042398	0.04988	0	0.032422	0.002494	0	0.022446	0.002494	0	0.34916	0.039904	0	0	0	0	0	0.992612		
67	0.102254	0.089784	0	0	0.002494	0	0	0	0	0.506282	0	0	0.002494	0	0.002494	0	0	0.266858	0.027434	0	0	0	0	0	1.000094		
68	0.409016	0	0.109736	0.476354	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.995106		
69	0.92278	0.009976	0	0	0	0	0	0	0	0.067338	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094		
70	0.042398	0.039904	0.06235	0.002494	0.007482	0.039904	0	0.341678	0.089784	0.02494	0	0.122206	0.009976	0	0.02494	0.007482	0	0.172086	0.01247	0	0	0	0	0	1.000094		
71	0.870406	0.064844	0	0	0	0	0	0	0	0.007482	0	0	0	0	0	0	0	0.039904	0.017458	0	0	0	0	0	1.000094		
72	0.009976	0.007482	0.533716	0	0.002494	0	0	0	0.23693	0	0	0.19952	0	0	0.002494	0	0	0	0	0	0	0	0	0	0.992612		
73	0.204508	0	0	0.793092	0	0.002494	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094		
74	0.017458	0.01247	0.039904	0.329208	0.329208	0.022446	0	0.04988	0.032422	0.007482	0	0.007482	0.147146	0	0.04988	0.002494	0	0.004988	0	0	0	0	0	0	0.962684		
75	0.01247	0.034916	0.009976	0.069832	0.104748	0.381582	0	0.022446	0.014964	0.019952	0	0.01247	0.084796	0	0.009976	0.069832	0	0.077314	0.017458	0	0.004988	0	0.01247	0.004988	0.965178		
76	0.753188	0.01247	0.03741	0.02494	0	0	0.004988	0	0.002494	0.007482	0	0.002494	0	0	0	0	0.122206	0.007482	0.002494	0	0	0	0	0	0.977648		
77	0.992612	0.002494	0	0	0	0	0	0.002494	0	0	0.002494	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094		
78	0.004988	0.379088	0	0	0	0.002494	0	0	0	0	0	0	0	0	0	0	0.002494	0	0.506282	0.104748	0	0	0	0	0	1.000094	
79	0.017458	0.002494	0.019952	0.214484	0.052374	0.017458	0	0	0	0.072326	0	0.009976	0.593572	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
80	0.825514	0	0.142158	0.032422	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
81	0.014964	0.032422	0.01247	0.209496	0.34916	0.172086	0	0.002494	0.007482	0.002494	0	0	0.032422	0	0	0.082302	0	0.017458	0.004988	0	0.002494	0	0.002494	0	0.945226		
82	0.763164	0	0.044892	0.189544	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.9976	
83	0.004988	0.019952	0.009976	0.002494	0	0	0.027434	0.032422	0.209496	0	0.618512	0.027434	0	0.014964	0	0	0.002494	0.004988	0.002494	0	0	0	0	0	0.980142		
84	0.830502	0.164604	0	0	0	0	0	0	0	0.004988	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094		
85	0.26187	0.02494	0.047386	0.022446	0.004988	0	0	0	0.4988	0	0.057362	0.082302	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
86	0.339184	0.047386	0.104748	0.117218	0.01247	0	0	0	0.014964	0.22446	0	0.052374	0.08729	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
87	0.837984	0.002494	0.119712	0.004988	0	0	0	0	0	0.029928	0	0	0	0	0	0	0	0	0.004988	0	0	0	0	0	0	1.000094	
88	0.304268	0.054868	0	0.02494	0.002494	0.009976	0.002494	0.002494	0	0.239424	0	0.007482	0.017458	0	0	0.009976	0	0.117218	0.069832	0	0.01247	0	0.072326	0.002494	0.950214		
89	1.000094	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
90	0.91031	0.002494	0.01247	0.014964	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01247	0	0	0	0	0	0.952708	
91	0.925274	0	0.032422	0.014964	0	0	0	0	0	0.02494	0	0.002494	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
92	0	0	0	0	0	0	0	0	0.36163	0	0	0	0	0	0.002494	0	0	0	0.009976	0	0	0	0	0	0.3741		
93	0.007482	0.002494	0.371606	0	0	0	0	0.401534	0.092278	0	0	0.007482	0	0	0.097266	0	0	0.01247	0.002494	0	0	0	0	0.002494	0.9976		
94	0.072326	0.009976	0.01247	0.027434	0	0.01247	0	0.004988	0	0	0	0	0	0.004988	0.027434	0	0.02494	0.064844	0	0.167098	0	0.321726	0.057362	0.808056			
95	0.06235	0	0.526234	0.069832	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.092278	0	0	0	0	0	0.750694		
96	0.054868	0.004988	0.142158	0.291798	0.014964	0.194532	0.002494	0.06235	0.004988	0	0	0.002494	0.002494	0	0.007482	0.027434	0	0.03741	0.017458	0.002494	0.009976	0.007482	0.89784				

97	0.01247	0.032422	0	0	0	0	0	0	0.004988	0	0	0	0	0.002494	0	0.204508	0.16211	0	0.042398	0	0.53621	0	0.9976		
98	0.53621	0.004988	0.192038	0.2494	0.002494	0	0	0	0.007482	0	0.002494	0	0	0	0	0	0	0	0	0	0	0	0	0.995106	
99	0.2494	0	0.394052	0.351654	0	0	0	0	0.002494	0	0.002494	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
100	0.93525	0.004988	0.019952	0.019952	0	0	0	0	0.002494	0.014964	0	0.002494	0	0	0	0	0	0	0	0	0	0	0	1.000094	
101	1.000094	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
102	0.291798	0.122206	0.027434	0.032422	0.002494	0.019952	0	0.017458	0.017458	0.027434	0	0.009976	0.002494	0	0	0.007482	0	0.36163	0.032422	0	0.014964	0	0.01247	0	1.000094
103	0.738224	0.214484	0	0	0	0	0	0	0	0.03741	0	0	0	0	0	0	0.004988	0.004988	0	0	0	0	0	1.000094	
104	0.840478	0.11223	0.014964	0.022446	0.002494	0	0	0	0.002494	0.002494	0	0	0	0	0	0.002494	0	0	0	0	0	0	0	1.000094	
105	1.000094	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.000094	
106	0.326714	0.027434	0.433956	0.064844	0.002494	0.007482	0	0.047386	0.044892	0.002494	0	0.002494	0	0	0.009976	0	0	0.029928	0	0	0	0	0	1.000094	

Supplementary Table 4. Joint model with a relaxed clock

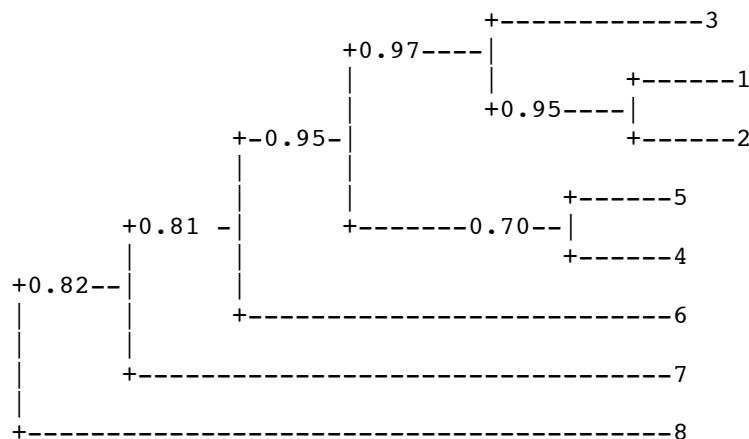
Topology	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	Total
Gene 1	0.907195	0	0.046641	0.046153	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
2	0.867158	0	0.039229	0.093602	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
3	0.999989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
4	0.930285	0	0.063039	0.066665	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
5	0.887464	0	0.10186	0.010665	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
6	0.274961	0	0.355469	0.369559	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
7	0.97086	0	0.01935	0.009763	0	0	0	0	0	0.000016	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
8	0.988346	0	0.008365	0.003278	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
9	0.999989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
10	0.998183	0	0.001806	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
11	0.324908	0	0.111997	0.563084	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
12	0.636358	0	0.122581	0.24105	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
13	0.729231	0	0.153017	0.117741	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
14	0.999989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
15	0.852462	0	0.068697	0.13883	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
16	0.000479	0	0.13653	0.86298	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
17	0.885899	0	0.096579	0.017511	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
18	0.999989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
19	0.952351	0	0.009356	0.038282	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
20	0.479043	0	0.28658	0.234366	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
21	0.995923	0	0.00122	0.002846	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
22	0.999989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
23	0.79566	0	0.039692	0.164637	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
24	0.999989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
25	0.86425	0	0.105182	0.030557	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
26	0.984017	0	0.010257	0.005715	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
27	0.999989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
28	0.905758	0	0.066935	0.027296	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
29	0.836742	0	0.024978	0.138269	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
30	0.87324	0	0.033744	0.093005	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
31	0.436193	0	0.210389	0.353407	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
32	0.825711	0	0.031628	0.14465	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
33	0.64384	0	0.174904	0.181245	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
34	0.98309	0	0.014171	0.002728	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
35	0.578004	0	0.142894	0.279091	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
36	0.431335	0	0.245045	0.323609	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
37	0.966943	0	0.000614	0.032432	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
38	0.743375	0	0.002833	0.253781	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
39	0.973332	0	0.021454	0.005203	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
40	0.067748	0	0.714237	0.218004	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
41	0.627384	0	0.234621	0.137984	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
42	0.999989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
43	0.999989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
44	0.999883	0	0.000033	0.000073	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
45	0.999989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
46	0.722876	0	0.169963	0.10715	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989

96	0.485199	0	0.20296	0.31183	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
97	0.993889	0	0.000168	0.005932	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
98	0.63181	0	0.045541	0.322638	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
99	0.17874	0	0.618456	0.202793	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
100	0.997158	0	0.000247	0.002584	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
101	0.999989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
102	0.526589	0	0.172971	0.300429	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
103	0.999989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
104	0.899979	0	0.00318	0.09683	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
105	0.999989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989
106	0.801104	0	0.039683	0.159202	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.999989

G. Posterior Distributions of Species Trees

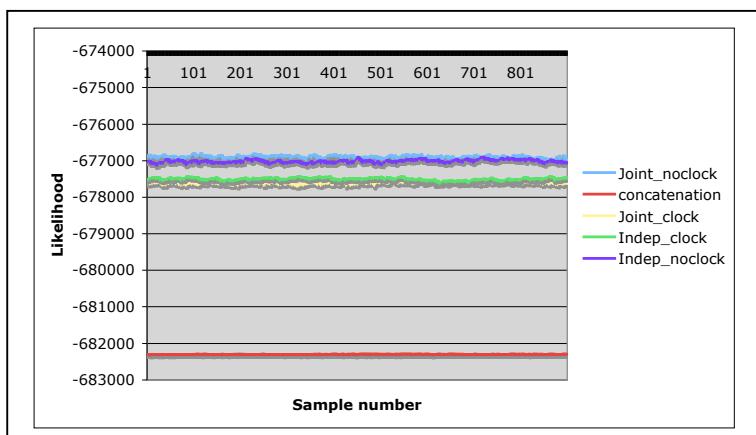
Analysis of the posterior distribution of gene trees assuming a molecular clock consistently yielded a highly resolved species tree in which *S. kudriavzevii* and *S. bayanus* form a clade (topology 2, Fig. 2 in main text), regardless of whether a joint or independent model was used. By contrast, as mentioned in the main text, with a joint model without a clock, the same tree as Rokas was obtained (tree 1 in figure 2 of main text). The model of substitution seemed only to be relevant when grossly mis-estimated – for example, when using a JC model, posterior probability values on the nodes of the species tree were generally below significance. In the case of the independent model and joint model with a clock, as well as the joint model without a clock, the species tree had posterior probability 1 on all nodes. In the case of the independent model without a molecular clock, the posterior probabilities were as follows:

Made from consensus of 20,000 trees



The estimates of the ancestral population sizes themselves appeared unreliable, in part because this parameter is inherently challenging to estimate and perhaps due to low signal for these estimates in the data (Supplementary Table 5, ref. 3).

H. Bayes Factor analysis



Supplementary Figure 2.
Comparison of likelihoods of five models on the yeast data set

Supplementary Table 5. Estimates of ancestral population sizes for species tree.

The estimates for ancestral θ and species divergence times for the analysis involving a joint model, and prior on θ of (1,200), were as follows:

1) joint model without a molecular clock

node	popsize(mean±sd)	divtime(mean±sd)
(1,2,3,4,5,6,7,8)	0.515(0.483,0.547)	0.581(0.600,0.562)
(1,2,3,4,5,6,7)	0.115(0.101,0.129)	0.327(0.319,0.335)
(1,2,3,4,5,6)	0.143(0.119,0.167)	0.235(0.224,0.246)
(1,2,3,4,5)	0.006(0.004,0.008)	0.110(0.108,0.112)
(1,2,3,4)	0.005(0.004,0.006)	0.088(0.086,0.090)
(1,2,3)	0.003(0.002,0.004)	0.063(0.062,0.064)
(1,2)	0.005(0.004,0.006)	0.038(0.037,0.039)

2) joint model with a molecular clock

node	popsize(mean±sd)	divtime(mean±sd)
(1,2,3,4,5,6,7,8)	0.459(0.432,0.487)	0.354(0.346,0.362)
(1,2,3,4,5,6,7)	0.120(0.106,0.134)	0.212(0.207,0.217)
(1,2,3,4,5,6)	0.126(0.106,0.146)	0.170(0.165,0.175)
(1,2,3,4,5)	0.015(0.013,0.017)	0.063(0.062,0.064)
(4,5)	0.024(0.017,0.031)	0.053(0.052,0.054)
(1,2,3)	0.002(0.001,0.003)	0.049(0.048,0.050)
(1,2)	0.003(0.002,0.004)	0.029(0.028,0.030)

(1= *S. cerevisiae*, 2 = *S. paradoxus*, 3 = *S. mikatae*, 4 = *S. Kudriavzevii*, 5 = *S. bayanus*, 6 = *S. castellii*, 7 = *S. kluyveri*, 8 = *C. albicans*)

For both parameters the units are in substitutions per site. Clearly the estimates of θ are unreliable, as they increase to unrealistically high values in progressively ancestral species. The trend in θ here is similar to estimates from other methods (3, 9, 10) and presumably results because ancestral θ is very difficult to estimate and because there is relatively little information for this parameter in the sequence data.

II. Simulations of 4- and 8-taxon species trees

For the analysis 1 in which the proportion of gene trees matching the species tree was low, for the four species data set (Fig. 3B), our species tree topology for species A-D was:

```
((A , B ) : 0.0057 #.008, C) : 0.0062 #.005, D) :.014 #.006;
```

The numbers after the colons are the divergence times before present in units of substitutions per site. The numbers after the pound signs (#) are the ancestral effective population sizes in units of substitutions per site (θ). There are no branch lengths in the terminal branches leading to the tips because we are focusing attention on the two internal branches.

For analysis 1 and the eight species data set for species A-H (Fig. 3C), our species tree topology was:

```
((((A, B) : 0.005 #.008, C) : 0.0076 #.009, D) :.008 #.005, ((E,F):.003 #.001, (G,H):0.0068#0.014):0.007#0.001):0.018#0.011;
```

For analysis 2, in which the proportion of gene trees matching the species tree was high (Fig. 3A) the four- and 8-species trees were:

4 species: (((A , B) : 0.0057 #.005, C) : 0.0102 #.005, D) :.024 #.006;

8 species: ((((A, B) : 0.003 #.005, C) : 0.0086 #.004, D) :.014 #.002,((E,F):.003 #.001,(G,H):0.0048#0.004):0.012#0.001):0.018#0.021;

For each of these trees, from 20 to 120 gene trees were simulated. These simulated gene trees were then assumed to represent the joint posterior distribution from the species tree, and were used to estimate the species tree using joint models and (1,200) and (1,1000) for the hyperpriors on θ .

III. Simulation comparison of concatenation and joint models

True species tree:

(H , (G , (F , (E , (D , (C , (A, B):0.038095 #0.005427) :0.063516
#0.008777) :0.069509 #0.039239) :0.073728 #0.047876):0.080717
#0.099646) :0.128138 #0.107017) :0.572334 #0.147364;

IV. References

1. Liu, L. & Pearl, D. K. (2006) *Mathematical Biosciences Institute Technical Report* (Ohio State University, Columbus, OH), pp. 50.
2. Liu, L. & Pearl, D. K. (2006) *Systematic Biology* submitted.
3. Rannala, B. & Yang, Z. (2003) *Genetics* **164**, 1645-56.
4. Liu, L. & Pearl, D. K. (2006) *Mathematical Biosciences Institute Technical Report #53* <http://mbi.osu.edu/publications/pub2006.html> (Ohio State University, Columbus), pp. 24.
5. Felsenstein, J. (1981) *Journal of Molecular Evolution* **17**, 368-76.
6. Swofford, D. L., Olsen, G. J., Waddell, P. J. & Hillis, D. M. (1996) in *Molecular Systematics*, eds. Hillis, D. M., Moritz, C. & Mable, B. K. (Sinauer, Sunderland, MA).
7. Huelsenbeck, J. P. & Ronquist, F. (2001) *Bioinformatics* **17**, 754-755.
8. Yang, Z. & Rannala, B. (1997) *Molecular Biology and Evolution* **14**, 717-724.
9. Takahata, N. (1986) *Genetical Research* **48**, 187-190.
10. Yang, Z. (2002) *Genetics* **162**, 1811-1823.