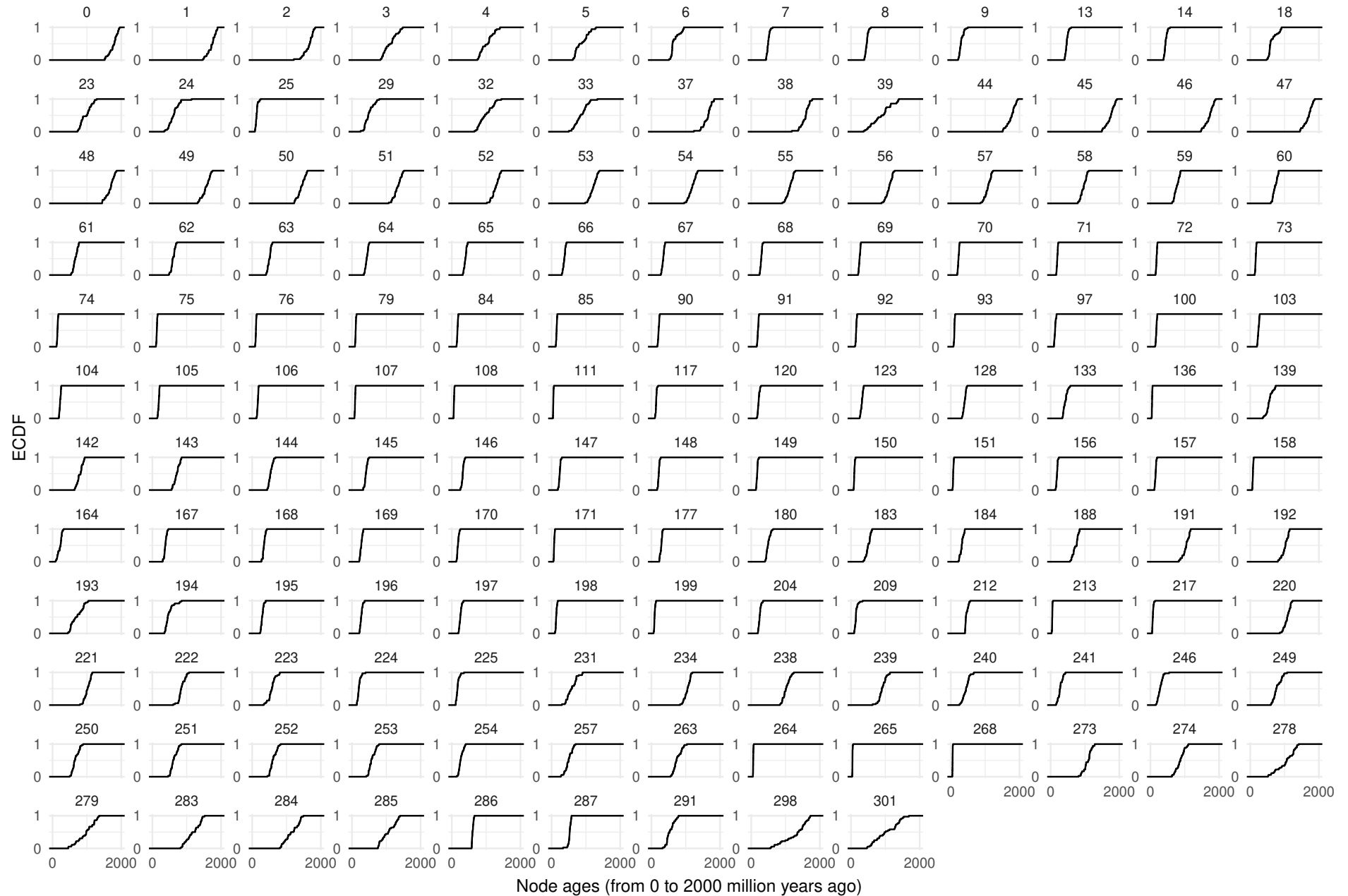

A timetree of Fungi dated with fossils and horizontal gene transfers

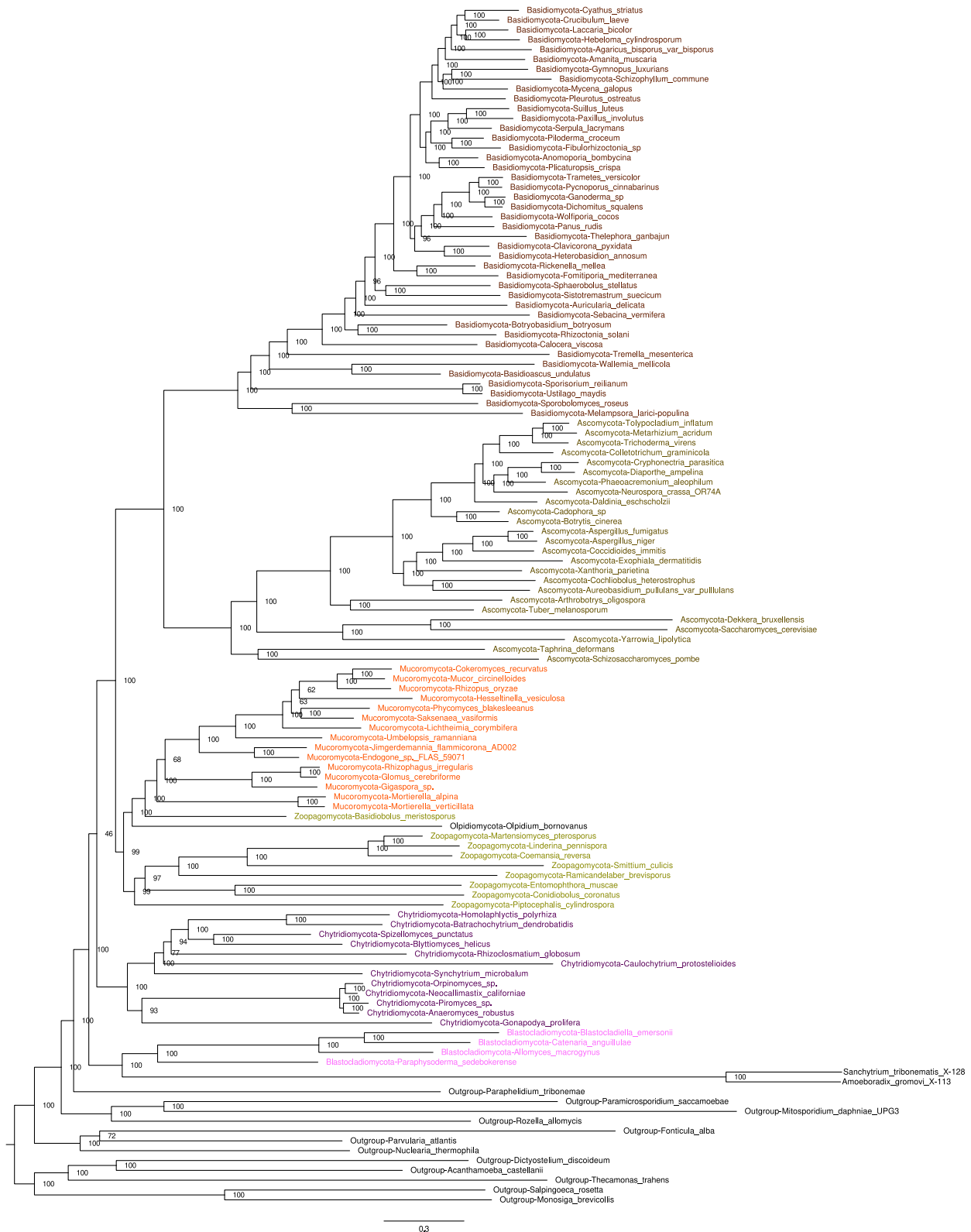
In the format provided by the
authors and unedited

Supplementary Figure 2



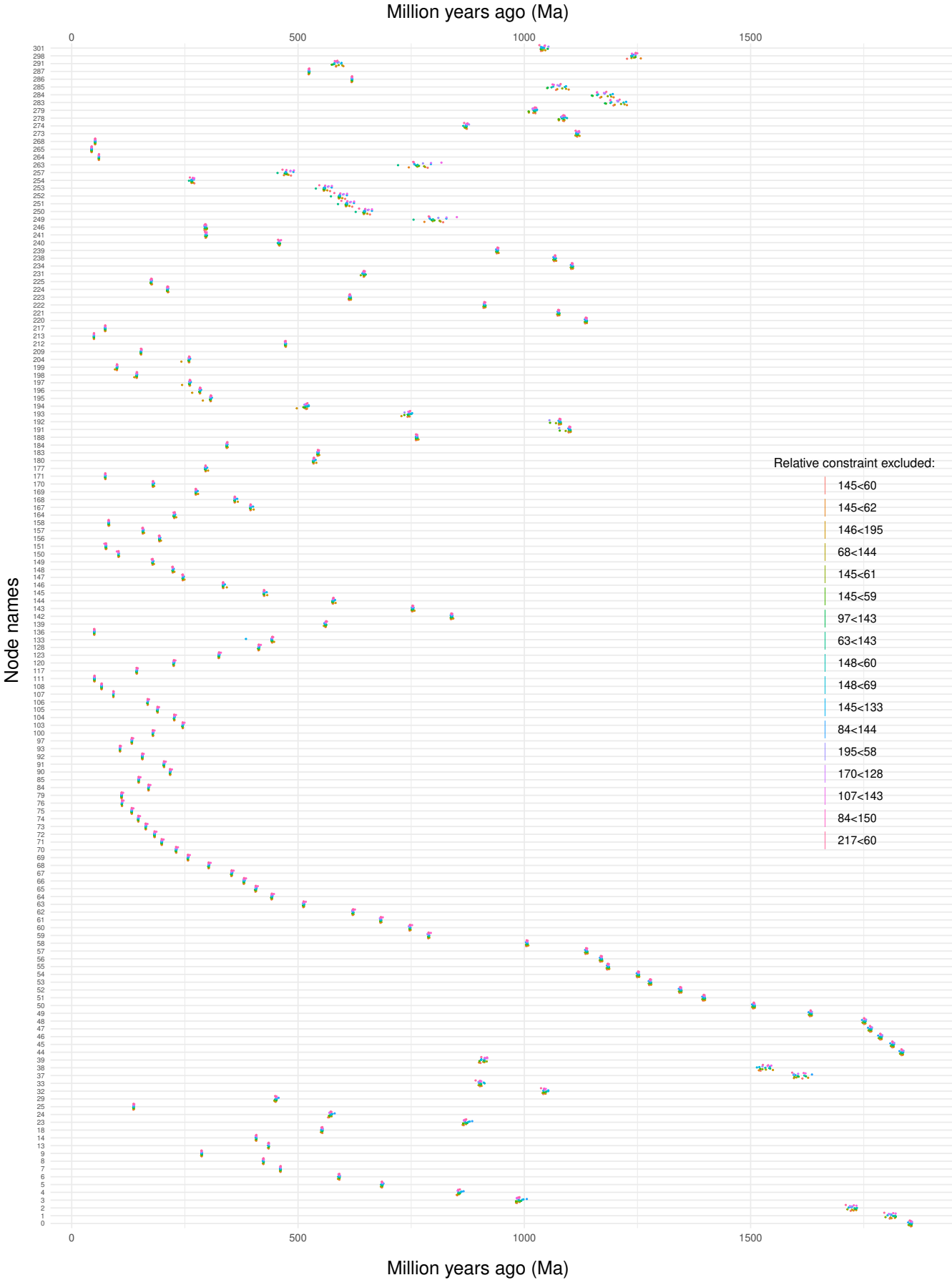
Supplementary Figure 2. Empirical cumulative distribution function (ECDF) showing the fraction of aggregated chronogram data supporting every node being younger than a certain age. By aggregated chronogram data, we refer to the $n=4$ chronogram sets sampled ('Default', 'PSE-constraint A', 'PSE-constraint A+calib', 'PSE-constraints B+C'), the set chronogram conditions used to build the conservative age ranges shown in Fig. 2. There is a subplot for every node, with node identifiers indicated above every subplot. ECDFs values go from 0 (zero support from chronogram data) to 1 (full support from chronogram data). Node ages cover the age range of our timescale (from 0 to 2,000 million years ago). See Supplementary Data for a correspondence between node identifiers and the phylogeny. See Supplementary Data to obtain a higher resolution of node age cumulative probability distributions, as well as information on the fraction of chronograms supporting a given node being older than some other node in the phylogeny. This information is available for the aggregated chronogram set as well as for the four independent dating conditions explored.

Supplementary Figure 3



Supplementary Figure 3. Phylogenetic tree of the original dataset of 122 taxa, reconstructed with a dataset of 97,487 amino acid sites, using the software IQ-TREE and the C60+LG+G4 model. Ultrafast bootstrap support values are shown in nodes. The root of the tree was set in the split of the tree separating Holomycota (fungi+some other taxa) from the rest of the tree.

Supplementary Figure 4



Supplementary Figure 4. Mean node ages retrieved for each internal node by re-running the relaxed molecular clock analysis with the 'Default' set of timing information, but excluding each time one of the 17 HGT-derived relative constraints. See Supplementary Data for the mapping of the internal node names in the phylogeny.