Electronic Supplementary Material for Pontin, D.R. & Cruickshank, R.H. Molecular phylogenetics of the genus *Physalia* (Cnidaria: Siphonophora) in New Zealand coastal waters reveals cryptic diversity.
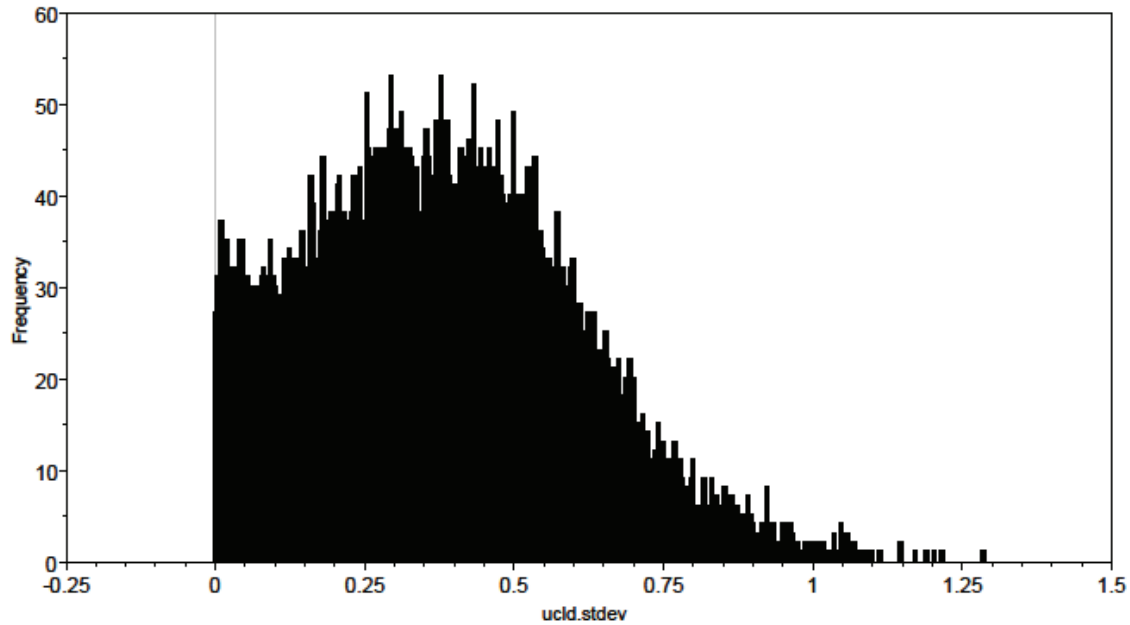

Figure S1: Posterior frequency distribution of the values of the ucld.stdev parameter for 18,000 sampled trees (after removal of the first 10% as burnin) from a Bayesian phylogenetic analysis of sequences of 566bp of the mitochondrial Cytochrome Oxidase (COI) gene from 64 specimens of *Physalia* assuming a GTR+I+Γ substitution model and an uncorrelated lognormal molecular clock constructed using BEAST v1.6.1 and Tracer v1.5. Sequences represent those included in table 1 of the main text, plus three sequences from Ortman et al (2010).
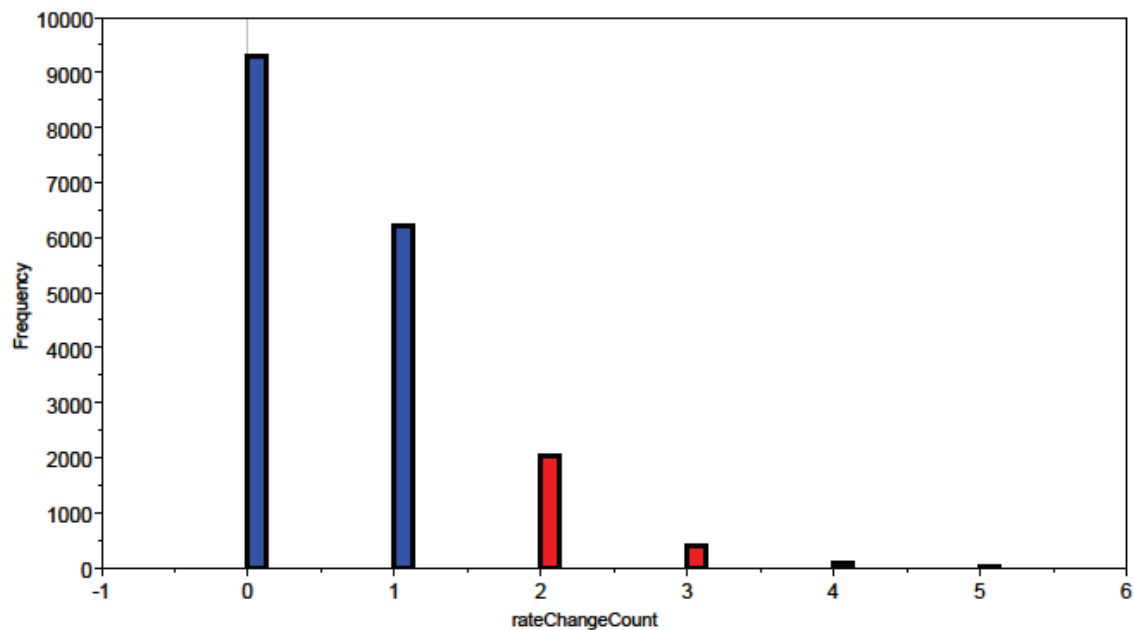

Figure S2: Posterior frequency distribution of the values of the K parameter (rateChangeCount = the number of discrete rate changes) for 18,000 sampled trees (after removal of the first 10% as burnin) from a Bayesian analysis of sequences of 566bp of the mitochondrial Cytochrome Oxidase (COI) gene from 64 specimens of *Physalia* assuming a GTR+I+Γ substitution model and random local molecular clocks constructed using BEAST v1.6.1 and Tracer v1.5. Sequences represent those included in table 1 of the main text, plus three sequences from Ortman et al (2010). Bars in blue represent values of K within the 95% highest posterior density (HPD) interval, those in red represent values outside this interval.
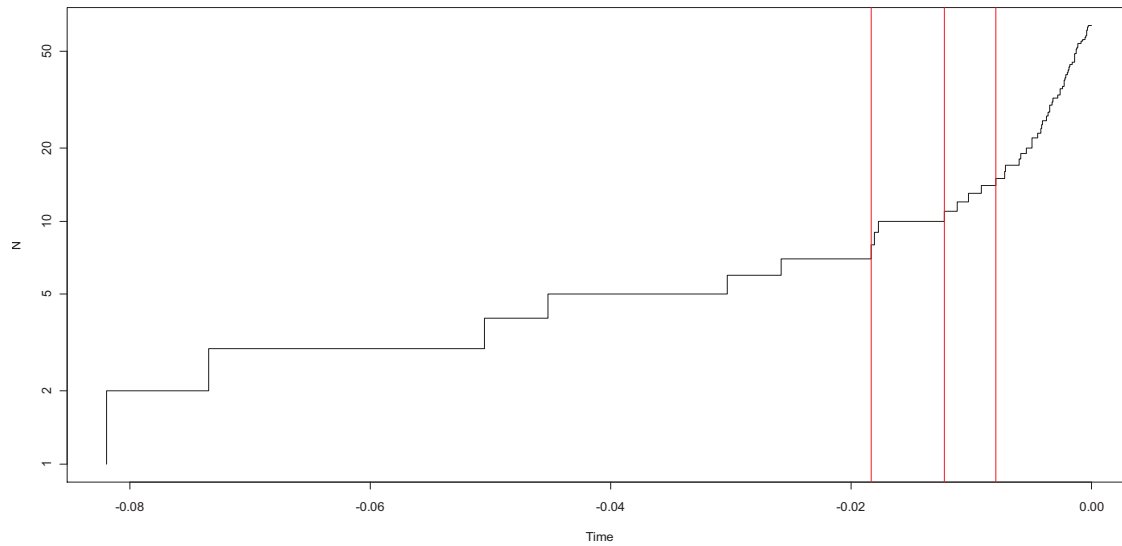
Figure S3: Lineage-through-time plot for a maximum clade credibility (MCC) tree constructed from 18,000 sampled trees (after removal of the first 10% as burnin) from a Bayesian analysis of sequences of 566bp of the mitochondrial Cytochrome Oxidase (COI) gene from 64 specimens of *Physalia* assuming a GTR+I+Γ substitution model and a strict molecular clock constructed using BEAST v1.6.1 and TreeAnnotator v1.6.1. Sequences represent those included in table 1 of the main text, plus three sequences from Ortman et al (2010). Vertical red lines indicate the thresholds for species delimitation predicted by a multiple threshold general mixed Yule-coalescent (GMYC) analysis as implemented in the R package "splits". The middle line corresponds to the threshold for species delimitation predicted by the single threshold analysis.
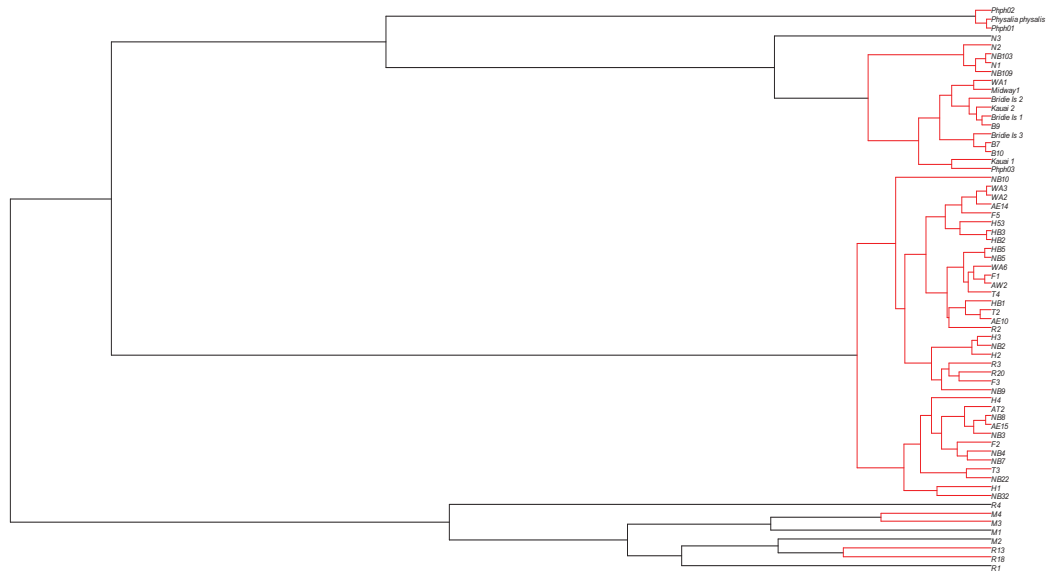

Figure S4: Maximum clade credibility tree constructed from 18,000 sampled trees (after removal of the first 10% as burnin) from a Bayesian analysis of sequences of 566bp of the mitochondrial Cytochrome Oxidase (COI) gene from 64 specimens of *Physalia* assuming a GTR+I+Γ substitution model and a strict molecular clock constructed using BEAST v1.6.1 and TreeAnnotator v1.6.1. Sequences represent those included in table 1 of the main text, plus three sequences from Ortman et al (2010). Branches in red are inferred as fitting a coalescent branching model and therefore connect tips that are inferred as belonging to the same species. This figure is horizontally aligned with Fig.S3 (above) so that the effects of different thresholds on species delimitation can be assessed.