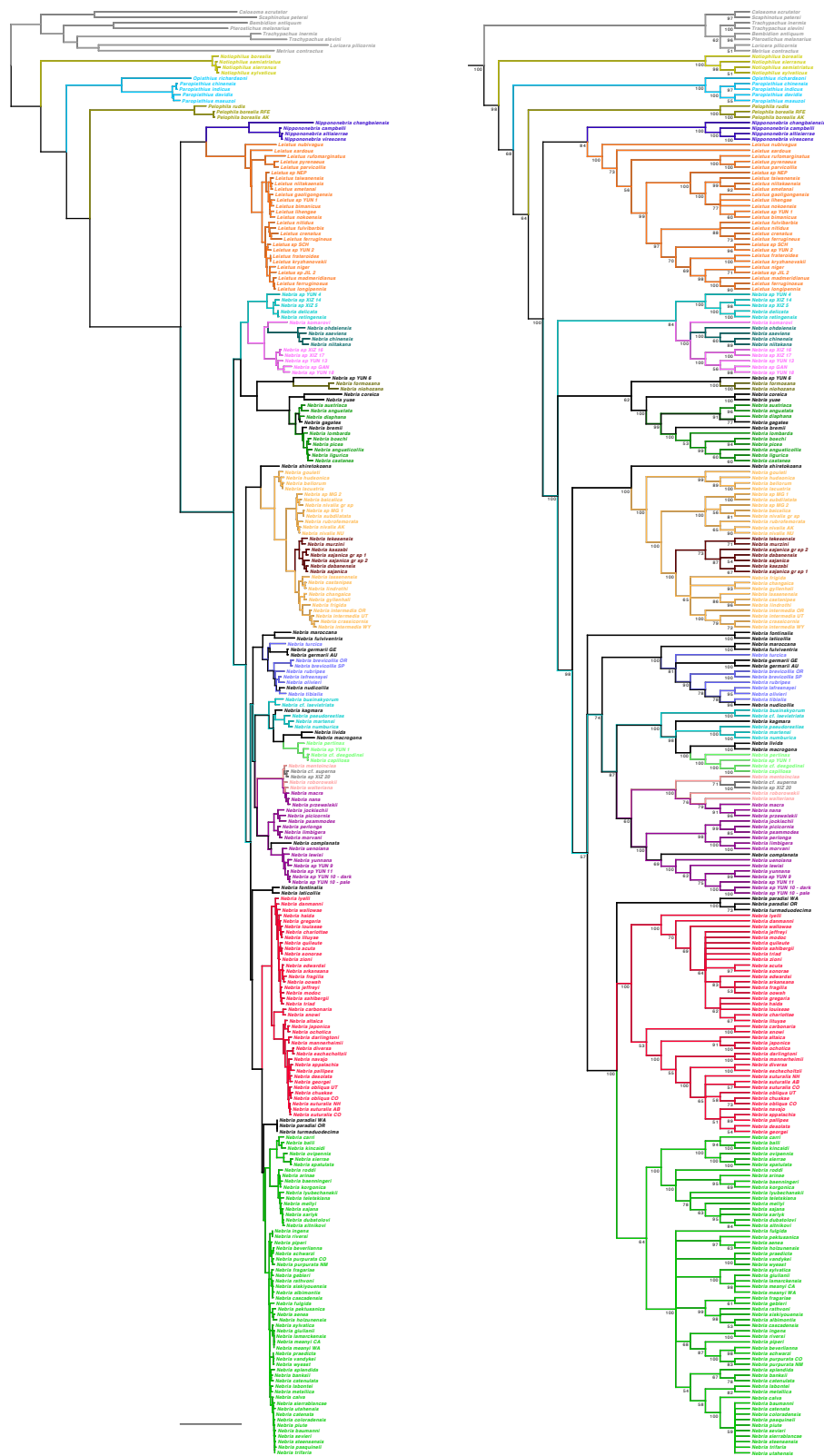
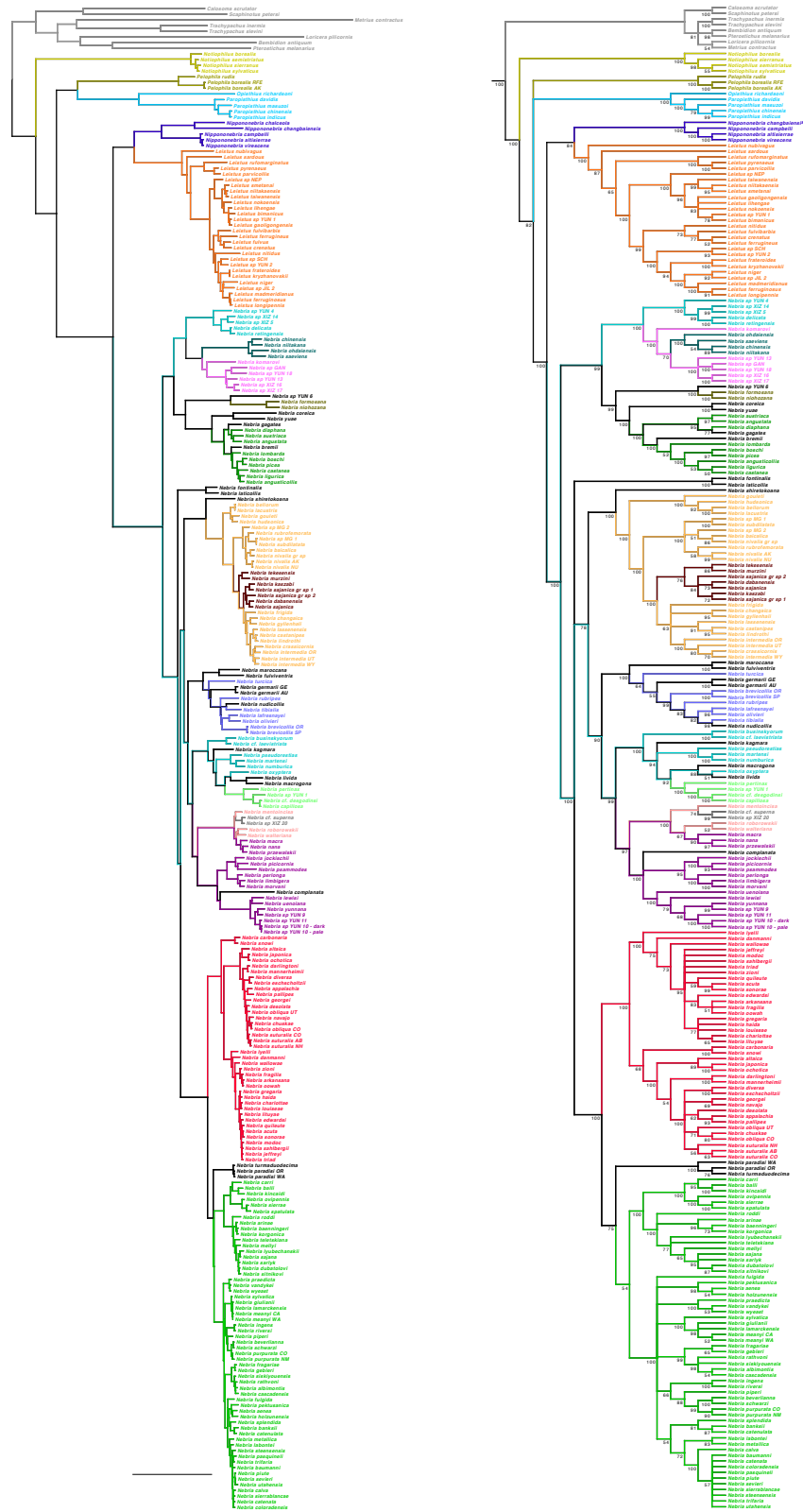


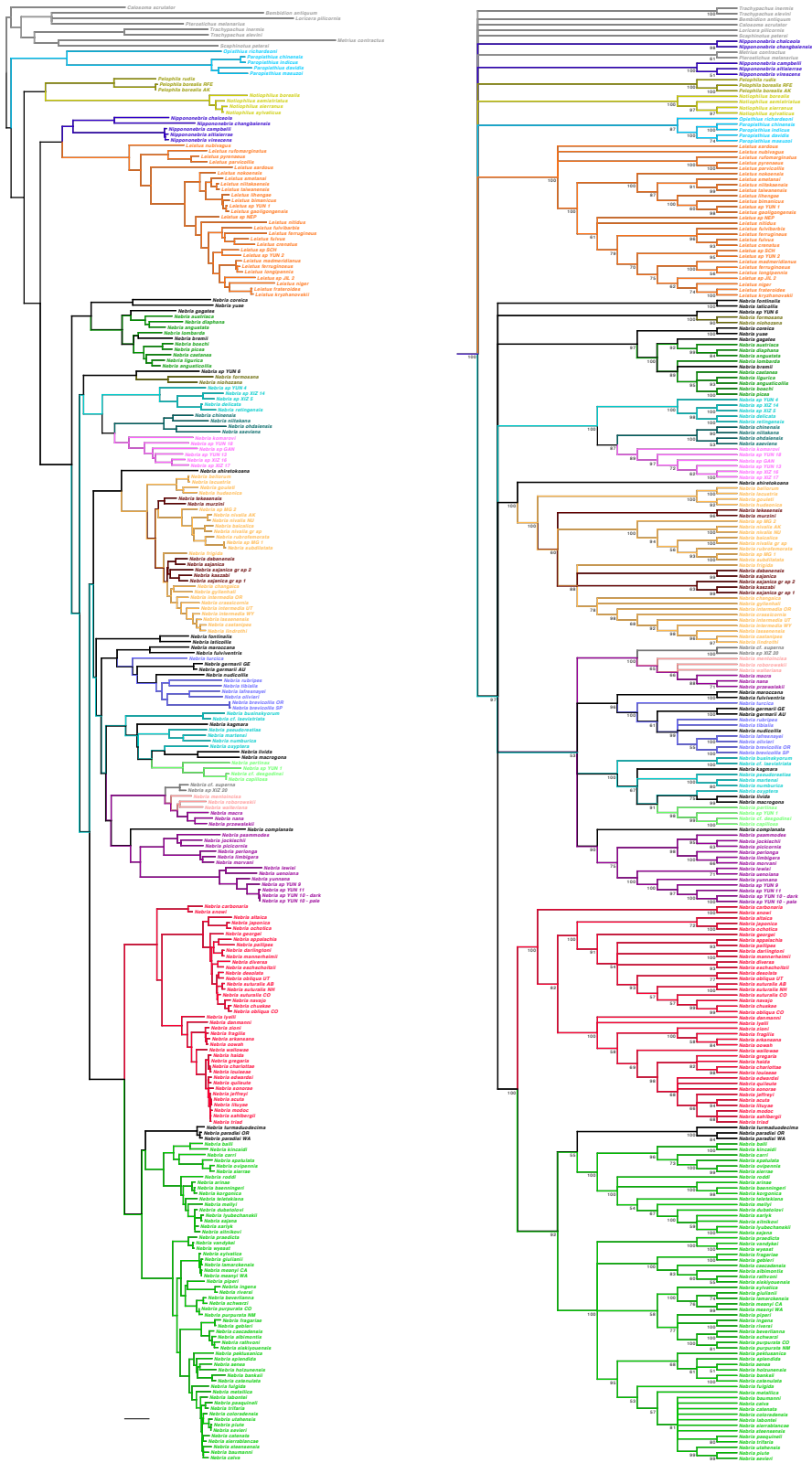
**Figure S1.** Majority rule consensus tree of 150,000 trees from Bayesian analysis of eight-gene concatenated matrix; numbers on branches indicate estimates of posterior probabilities, expressed as percentages.



**Figure S2.** Maximum likelihood trees for concatenated matrix of all nuclear genes. Left: maximum likelihood tree; scale bar = 0.1 units, as estimated by RAxML. Right: majority rule consensus tree of trees from bootstrap replicates; numbers on branches indicate percentage of bootstrap replicates with that clade.



**Figure S3.** Maximum likelihood trees for concatenated matrix of all nuclear protein-coding genes. Left: maximum likelihood tree; scale bar = 0.1 units, as estimated by RAxML. Right: majority rule consensus tree of trees from bootstrap replicates; numbers on branches indicate percentage of bootstrap replicates with that clade.



**Figure S4.** Maximum likelihood trees for concatenated matrix of all mitochondrial genes. Left: maximum likelihood tree; scale bar = 0.1 units, as estimated by RAxML. Right: majority rule consensus tree of trees from bootstrap replicates; numbers on branches indicate percentage of bootstrap replicates with that clade.



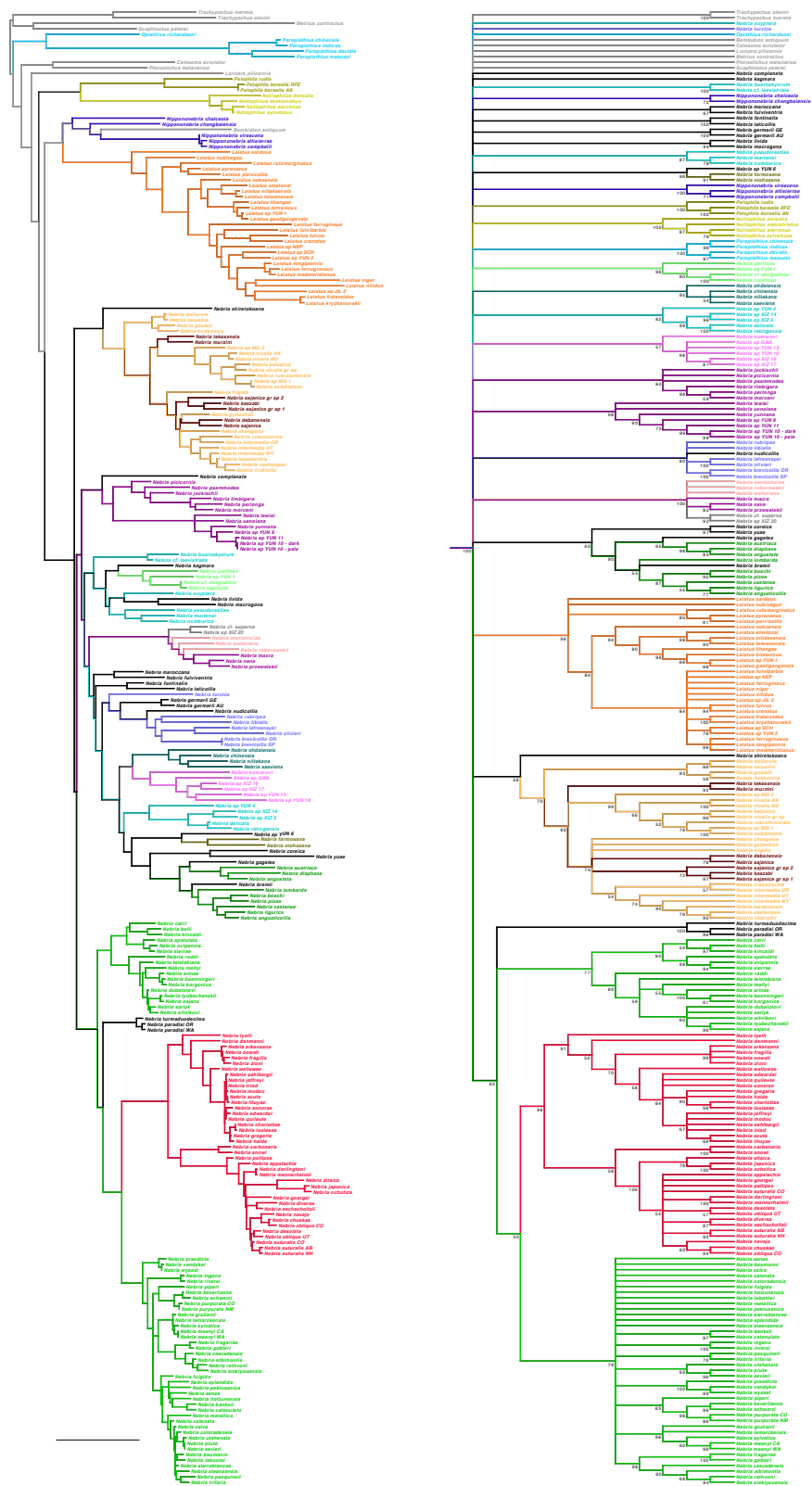
**Figure S5.** Maximum likelihood trees for 28S. Left: maximum likelihood tree; scale bar = 0.1 units, as estimated by RAxML. Right: majority rule consensus tree of trees from bootstrap replicates; numbers on branches indicate percentage of bootstrap replicates with that clade. Outgroups graphically omitted.



**Figure S6.** Maximum likelihood trees for 16S-ND1. Left: maximum likelihood tree; scale bar = 0.1 units, as estimated by RAxML. Right: majority rule consensus tree of trees from bootstrap replicates; numbers on branches indicate percentage of bootstrap replicates with that clade.



**Figure S7.** Maximum likelihood trees for the COI BC. Left: maximum likelihood tree; scale bar = 0.1 units, as estimated by RAxML. Right: majority rule consensus tree of trees from bootstrap replicates; numbers on branches indicate percentage of bootstrap replicates with that clade.



**Figure S8.** Maximum likelihood trees for the COI PJ. Left: maximum likelihood tree; scale bar = 0.1 units, as estimated by RAxML. Right: majority rule consensus tree of trees from bootstrap replicates; numbers on branches indicate percentage of bootstrap replicates with that clade.





**Figure S9.** Maximum likelihood trees for the CAD2. Left: maximum likelihood tree; scale bar = 0.1 units, as estimated by RAxML. Right: majority rule consensus tree of trees from bootstrap replicates; numbers on branches indicate percentage of bootstrap replicates with that clade.



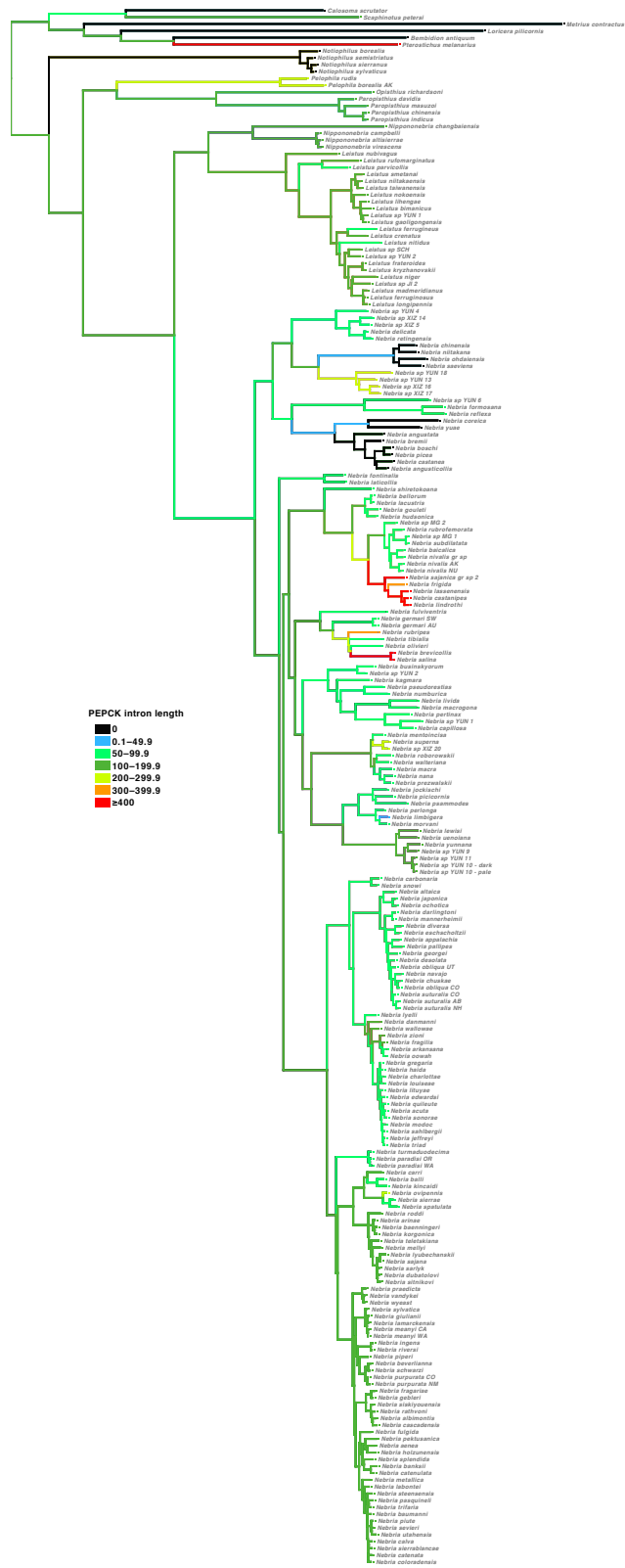
**Figure S10.** Maximum likelihood trees for the PEPCK. Left: maximum likelihood tree; scale bar = 0.1 units, as estimated by RAxML. Right: majority rule consensus tree of trees from bootstrap replicates; numbers on branches indicate percentage of bootstrap replicates with that clade.



**Figure S11.** Maximum likelihood trees for the *Topo*. Left: maximum likelihood tree; scale bar = 0.1 units, as estimated by RAxML. Right: majority rule consensus tree of trees from bootstrap replicates; numbers on branches indicate percentage of bootstrap replicates with that clade.



**Figure S12.** Maximum likelihood trees for the *wg*. Left: maximum likelihood tree; scale bar = 0.1 units, as estimated by RAxML. Right: majority rule consensus tree of trees from bootstrap replicates; numbers on branches indicate percentage of bootstrap replicates with that clade.



**Figure S13.** Maximum likelihood tree for concatenated matrix showing only those taxa for which PEPCK was sequenced, with branches colored according to the squared-change parsimony reconstruction of the length of the PEPCK intron.