

Appendix S8. BEAST Maximum Clade Credibility tree (yule model) using *Salvia* nrDNA and rooted with a monophyletic outgroup of *Lepechinia* and *Melissa*. Major clades that were well-supported based on AHE genomic data (see Fig. 2) were used as topological constraints in BEAST. This tree is same as shown in Fig. 4 but with species terminals and 95% nodal age intervals provided.

