





Figure 1. Phylogeny of *Bombus* estimated from Bayesian analysis of combined sequence data from five gene fragments (16S, opsin, ArgK, EF-1 α , and PEPCK). Subgeneric clades are individually colour-coded and labelled with the subgeneric name. Values above branches are Bayesian posterior probabilities; values below branches are parsimony bootstrap values. Alternative resolution from parsimony analysis shown as dotted lines. Outgroup branches (in grey), represented by dashed lines, have been shortened for visual purposes. NW, New World clade; SF, short-faced clade; LF, long-faced clade.