S1 Fig

Distributions of the number of chromosome gains minus the number of chromosome losses (G-L) with and without *Melampodium repens*. G-L distributions reconstructed using maximum likelihood in CHROMEVOL (ML-CE, grey) and in BAYESTRAITS (ML-BT, shades of red) on phylogenetic trees obtained from analyses of (a) nuclear sequence data using BEAST (ITS-B), (b) nuclear sequence data using MRBAYES (ITS-MB), (c) plastid sequence data using BEAST (matK-B) and (d) plastid sequence data using MRBAYES (matK-MB) before (dark grey and orange) and after (light grey and red) pruning *Melampodium repens*, the sole species with $n = 14$, and restricting minimum and maximum chromosome number to 9 and 12, respectively.