

Supplementary Figures

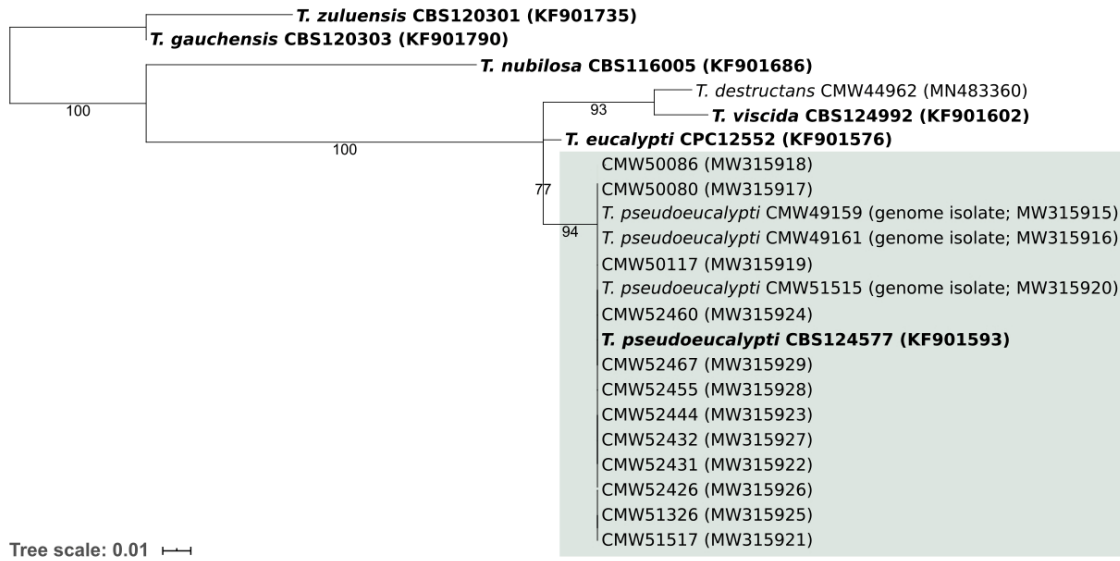


Figure S1 Maximum likelihood phylogeny of the Internal Transcribed Spacer (ITS) region, confirming the identity of 11 *Teratosphaeria pseudoecalypti* isolates sampled from Australia and Uruguay. Ex-type isolates are in bold; GenBank accession numbers are shown in brackets. The tree was rooted with *T. gauchensis* and *T. zuluensis*. Support values were calculated from 1000 bootstrap replicates.

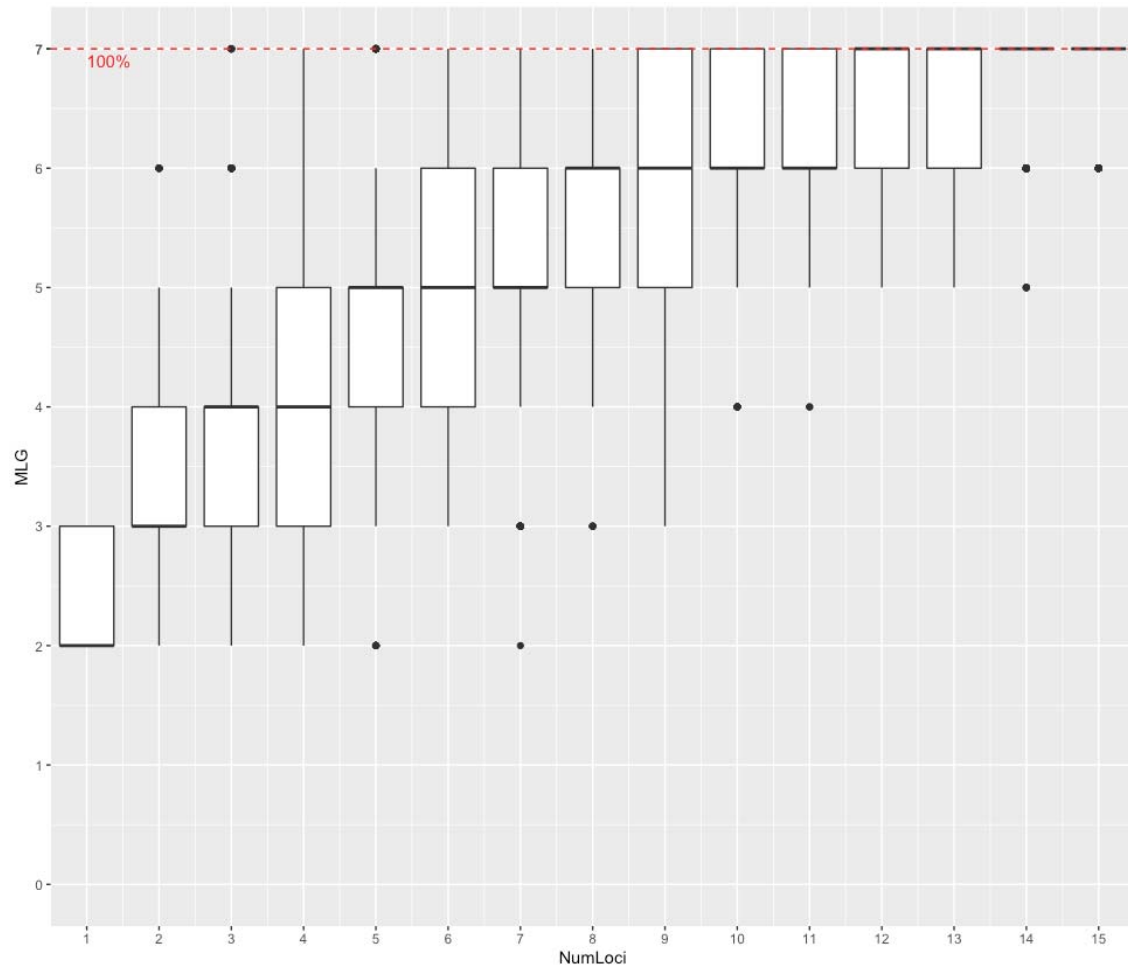


Figure S2 Genotype accumulation curve calculated from the 16 polymorphic *Teratosphaeria pseudoecalypti* loci in equilibrium. The curve depicts the number of multilocus genotypes (MLGs) observed when randomly sampling a certain number of loci 1000 times. Twelve loci were sufficient to identify 100% of MLGs present in the clone-corrected dataset.

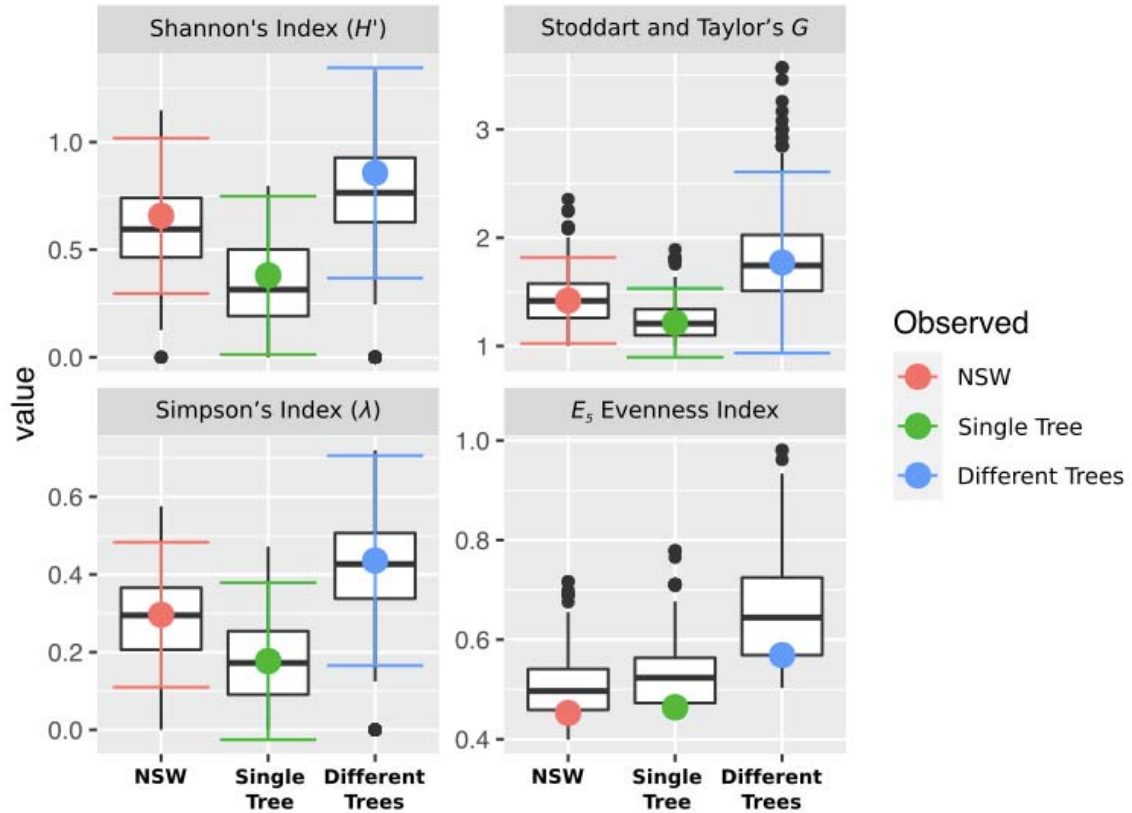


Figure S3 Comparison between the observed genotypic diversity and evenness indices at the different sampling levels in New South Wales (NSW), Australia. Sample size was standardised at $n=15$ using rarefaction. Boxplots represent the distribution of these indices for 1000 bootstrap permutations. Coloured lines show the 95% confidence interval of the bootstrap distribution.