

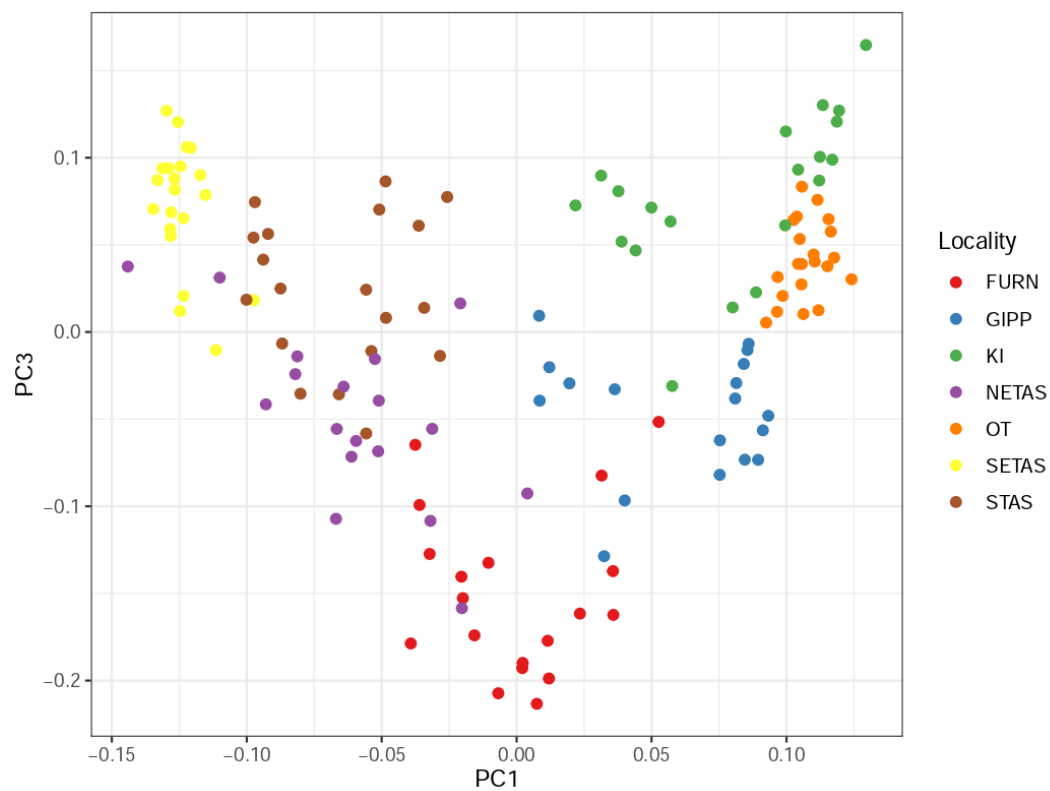
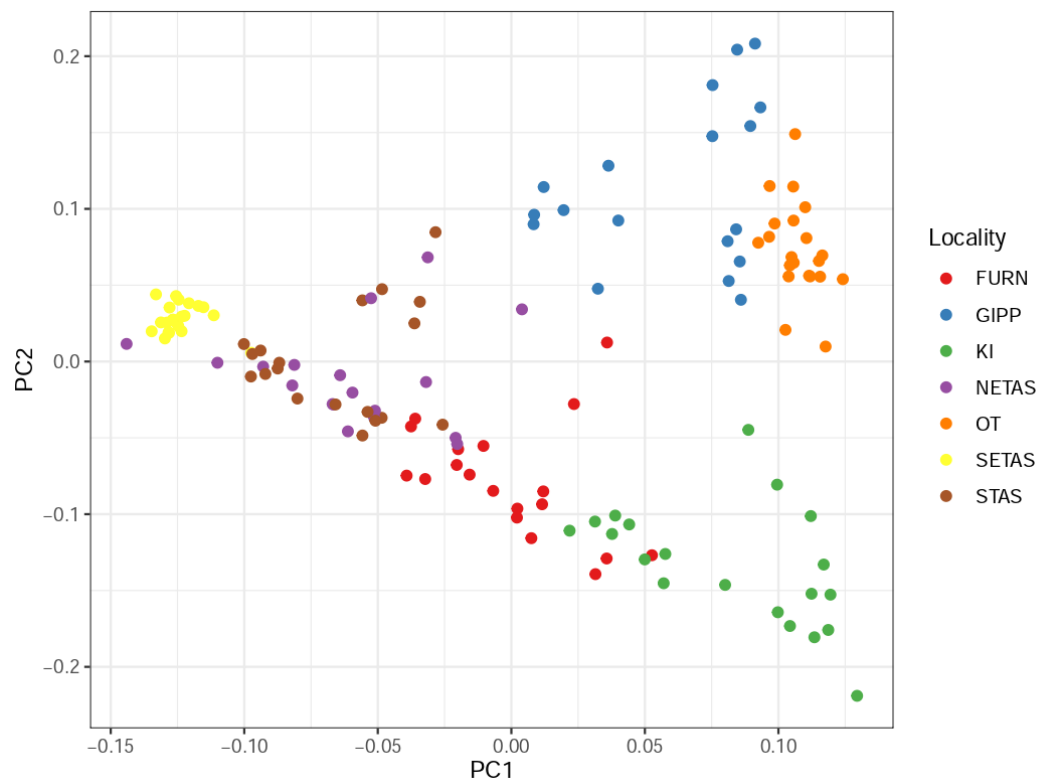
Supplementary information (Online Resources 2, 4, 6 & 9) for the following paper submitted to Tree Genetics and Genomes:

Patterns of genomic diversity and linkage disequilibrium across the disjunct range of the Australian forest tree *Eucalyptus globulus*

**Jakob B. Butler\***, Jules S. Freeman, Brad M. Potts, René E. Vaillancourt, Hossein V. Kahrood, Peter K. Ades, Philippe Rigault and Josquin F. G. Tibbits

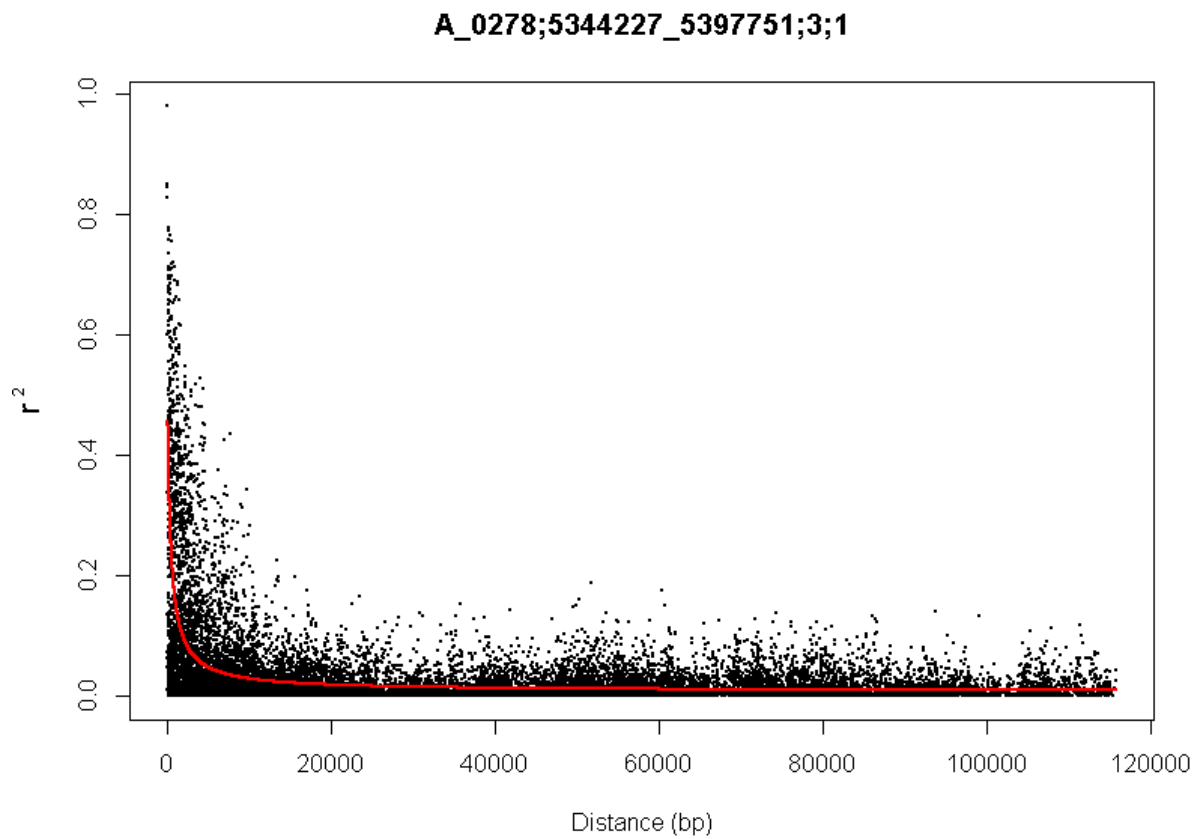
\*Author for correspondence: Jakob B. Butler, Private Bag 55, Hobart 7001, Australia. Ph. +61 439323751 Email: [Jakob.Butler@utas.edu.au](mailto:Jakob.Butler@utas.edu.au)

Online Resource 2: Principal component analysis of individuals using an unlinked subset of SNPs. Samples are colored by locality. Variance explained by each axis was 8.6%, 4.2% and 3.4% for PC1, PC2 and PC3 respectively.



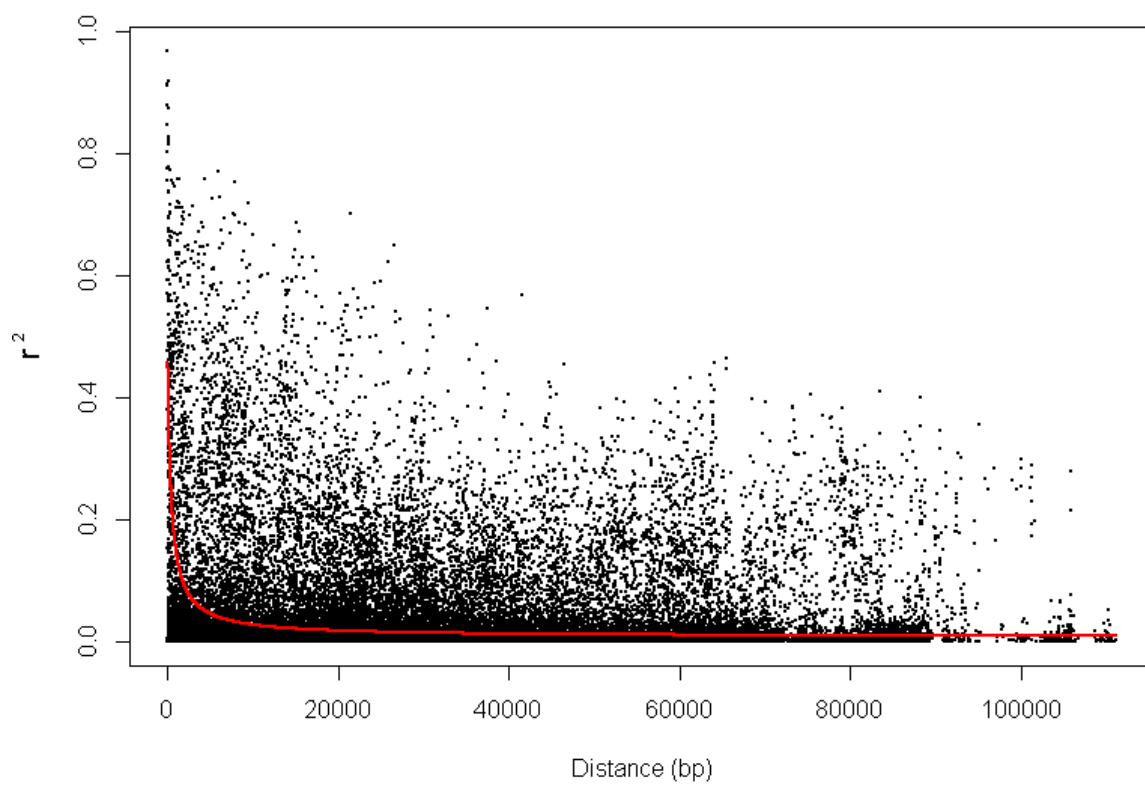
Online Resource 4: Examples of contig LD decay distributions. a) typical contig; b) atypical contig; c) contig in region of high LD decay distance. Red line indicates the decay curve for that contig.

4a)

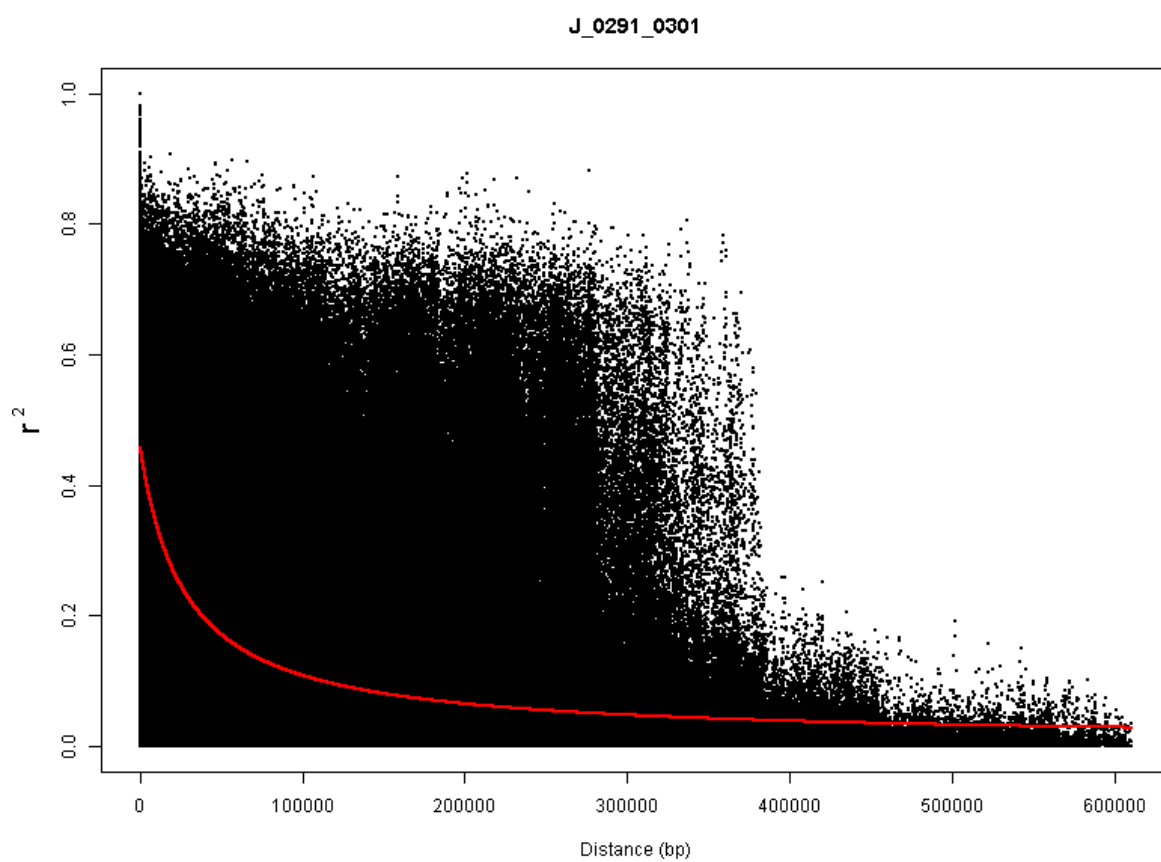


4b)

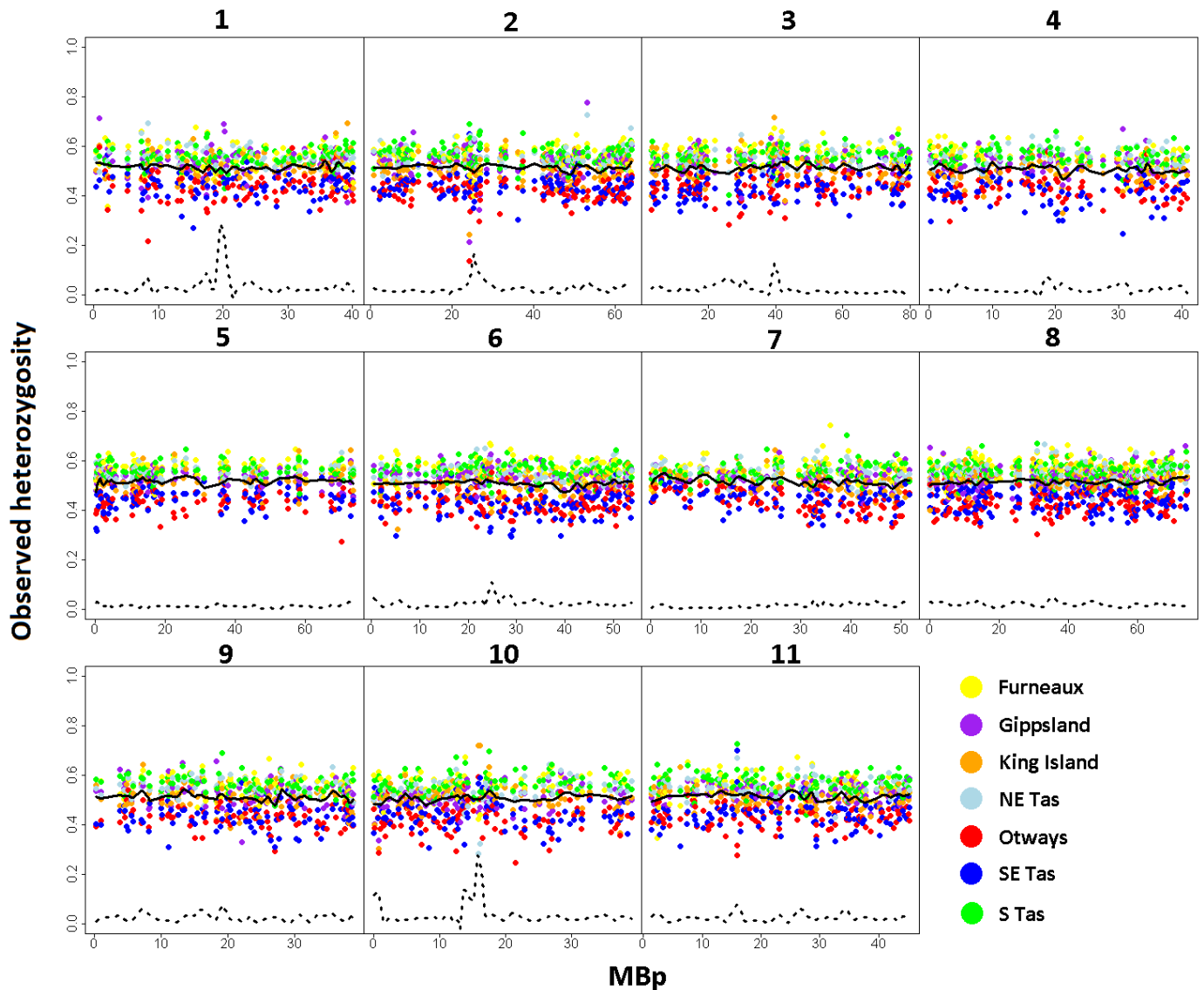
**I\_1048;25682769\_25837187;06;1**



4c)



Online Resource 6: Observed heterozygosity across *Eucalyptus globulus* chromosomes. Each point represents a contig position based on synteny with the *E. grandis* reference genome for each race. The solid curve shows the average observed heterozygosity across all races, drawn using locally weighted scatterplot smoothing (LOESS) polynomial regression with a smoothing parameter of 0.1. The dotted curve shows peaks of high LD decay distance along the chromosome, averaged across all races (see Figure 7). Contigs are coloured by race.



Online Resource 9: *Eucalyptus* species-differentiating markers compared to patterns of genome-wide  $F_{ST}$  in *E. globulus*. Markers and positions were identified by Hudson et al. (2015).

