

Electronic supplementary material: Supplementary Figure 1

Title: Genetic dissection of growth, wood basic density and gene expression in interspecific backcrosses of *Eucalyptus grandis* and *E. urophylla*

Journal name: BMC Genetics

Authors: Anand R.K. Kullan, Maria M van Dyk, Charles A. Hefer, Nicoletta Jones, Arnulf Kanzler, Alexander A. Myburg*

Affiliation and e-mail address of corresponding author:

Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, 0002, South Africa

zander.myburg@fabi.up.ac.za

Supplementary Figure 1. Framework linkage maps of the *E. grandis* (gr), *E. urophylla* (ur) and F₁ hybrid parent of the *E. grandis* (grh) and *E. urophylla* (urh) backcross families showing the location of putative QTLs associated with DBH (white vertical bars) and wood basic density (black vertical bars). The backcross and F₁ hybrid parental maps are connected by dotted lines using the physical position of the DArT marker fragments in the draft (V1.0) *E. grandis* genome sequence (<http://www.phytozome.net/>). Map positions in centiMorgan (cM Kosambi) and megabase-pair (Mbp) are shown for the genetic and physical maps, respectively. The F₁ hybrid maps constructed for the two backcross families are connected through shared testcross markers that segregated in both backcrosses. Positions (solid bars, 95% CI; lines, 90% CI) of QTLs detected using composite interval mapping (CIM) are projected onto the genetic maps.





















