

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

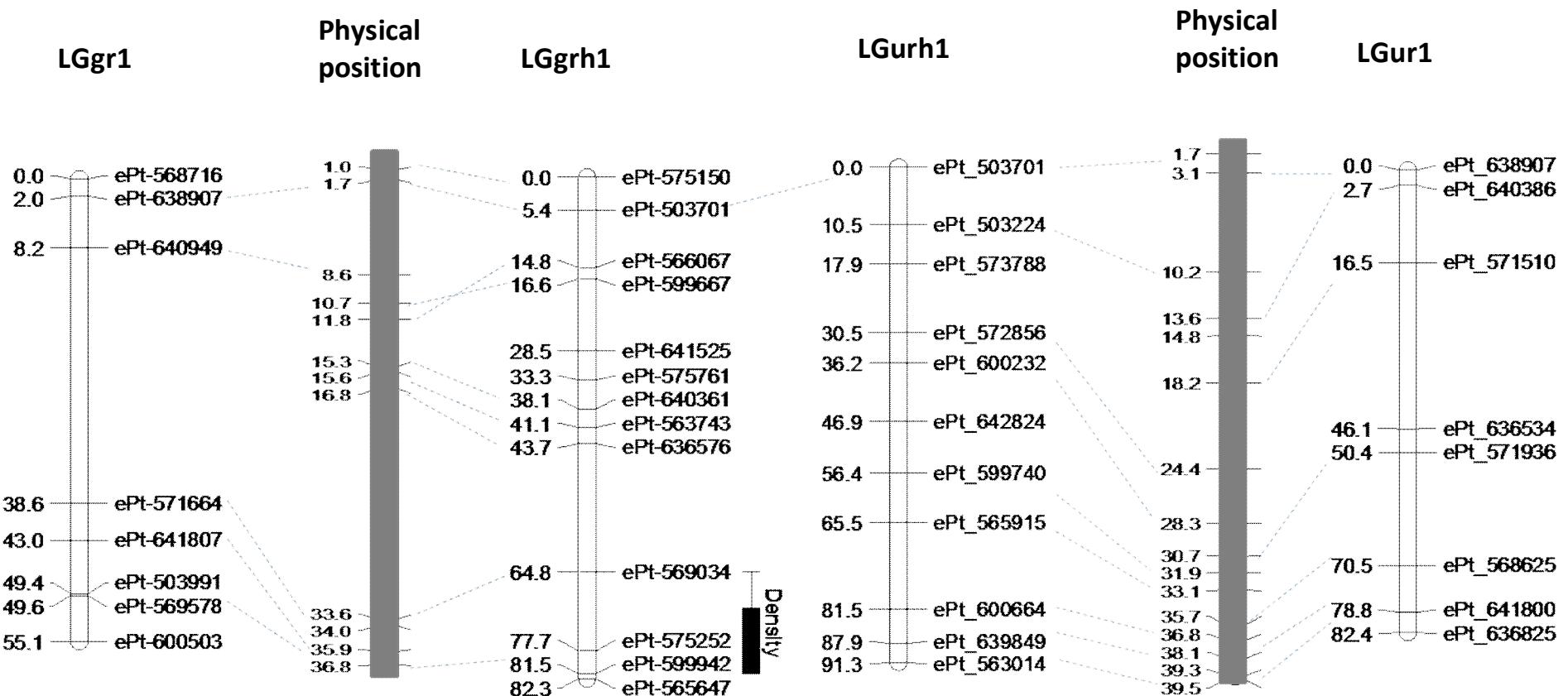
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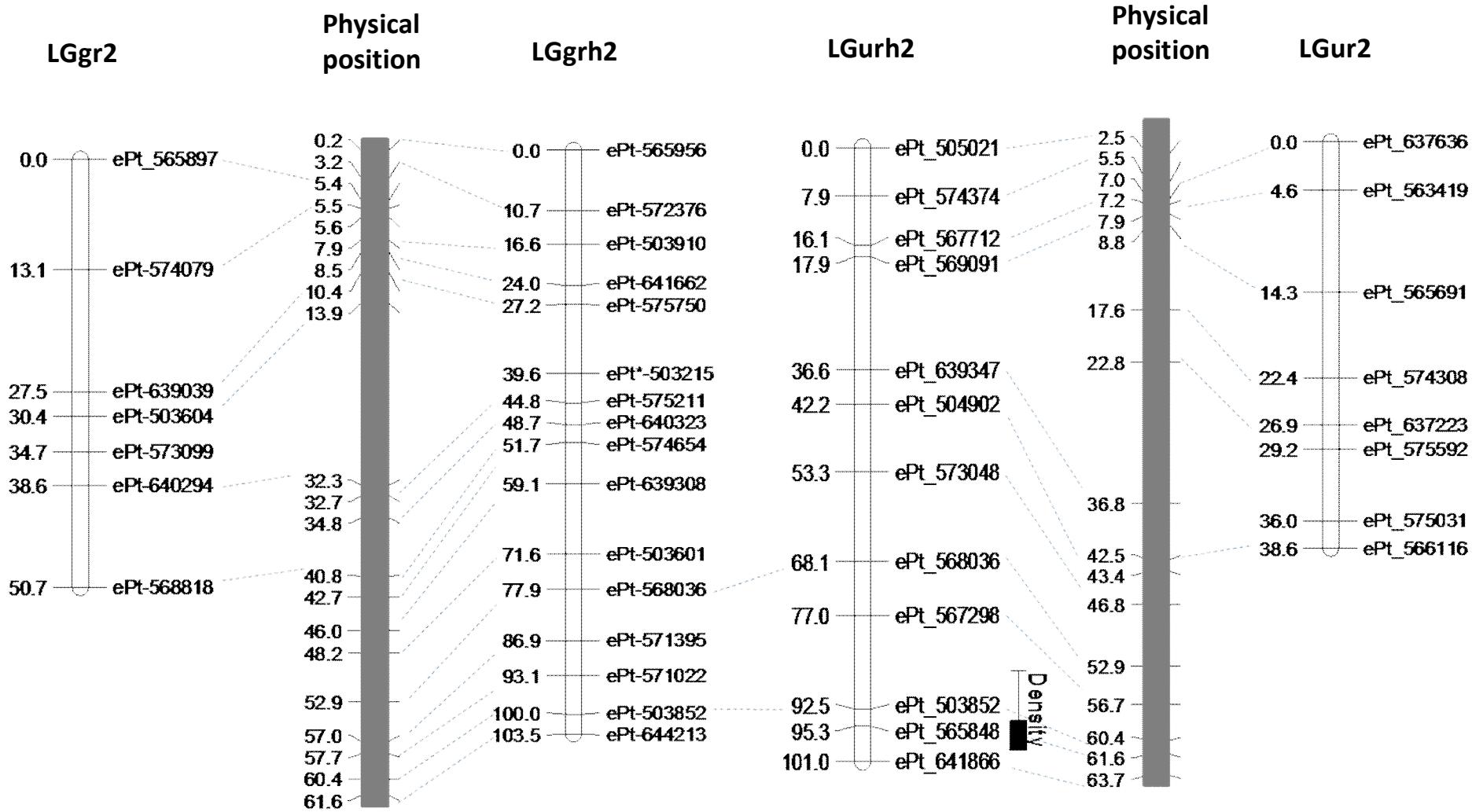
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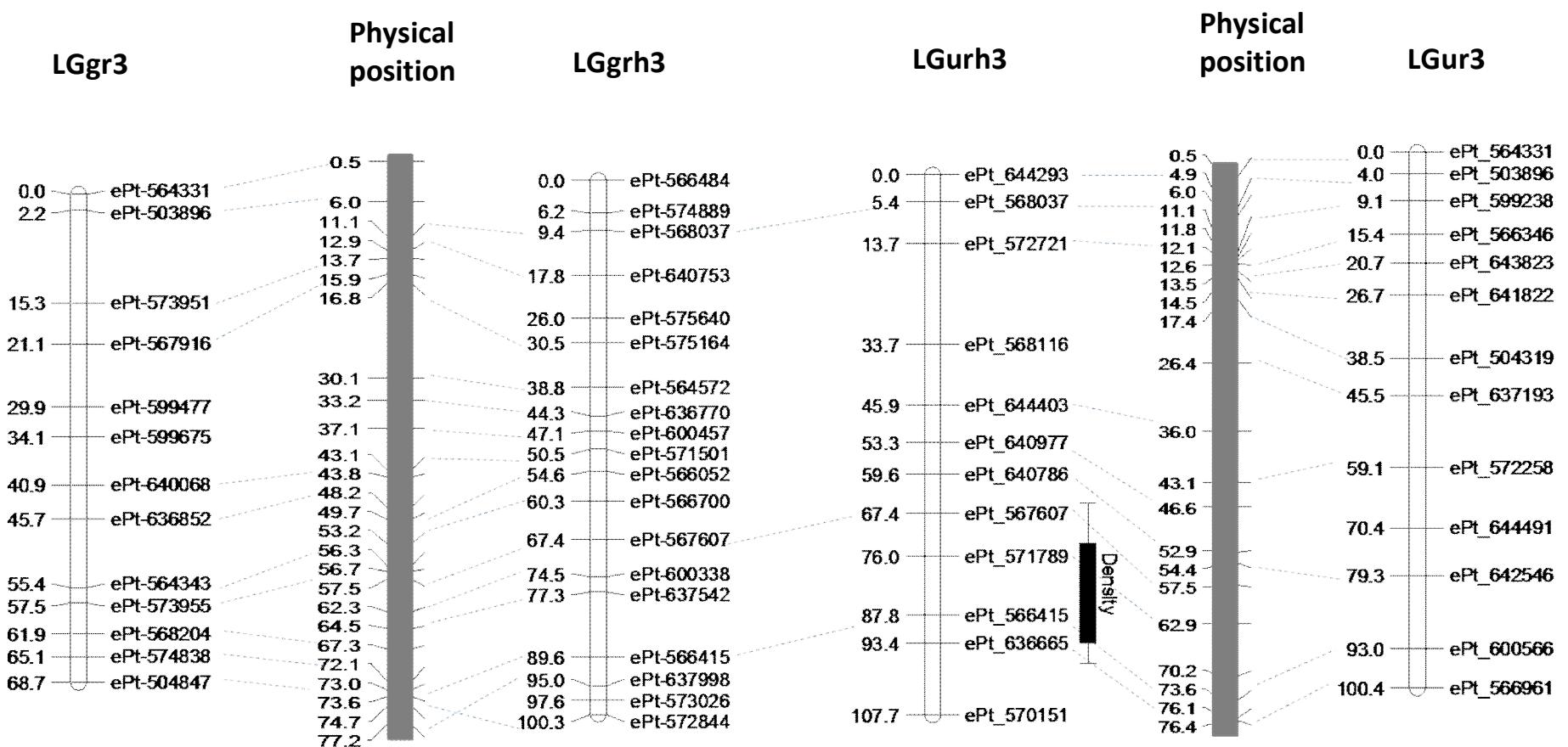
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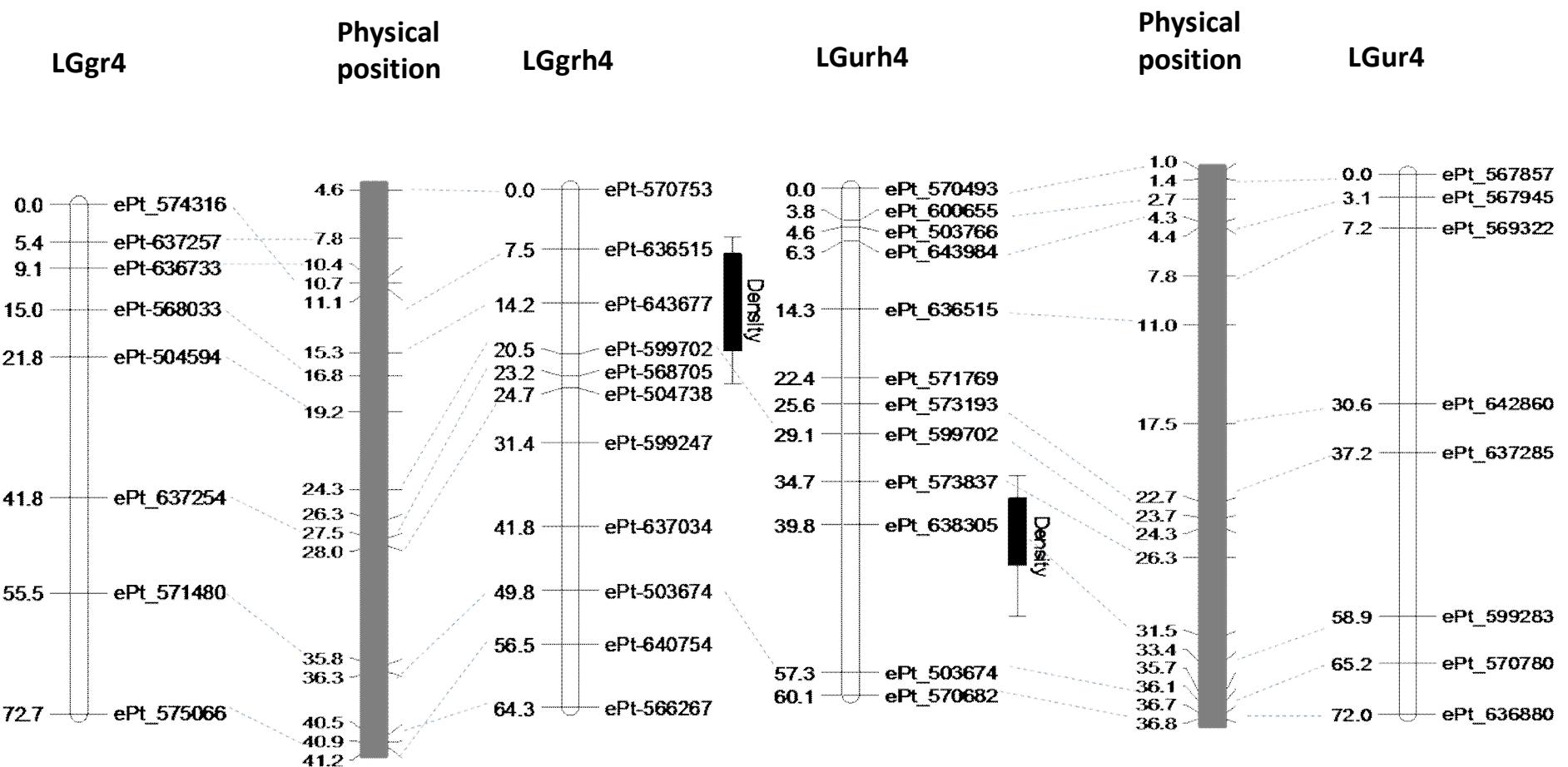
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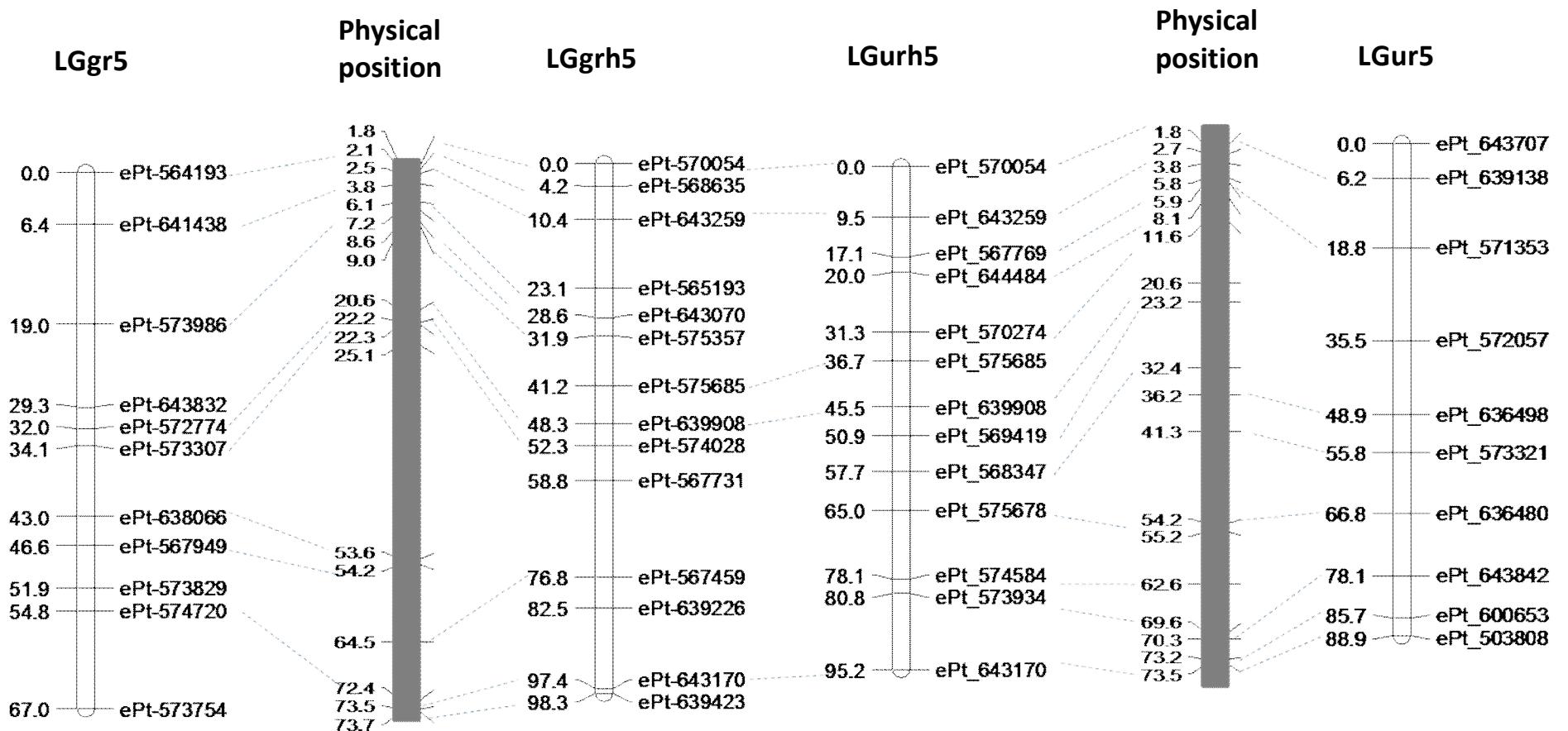
Supplementary Figure 1. Framework linkage maps of the *E. grandis* (gr), *E. urophylla* (ur) and F₁ hybrid parent of the *E. grandis* (grh) and *E. urophylla* (urh) backcross families showing the location of putative QTLs associated with DBH (white vertical bars) and wood basic density (black vertical 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.

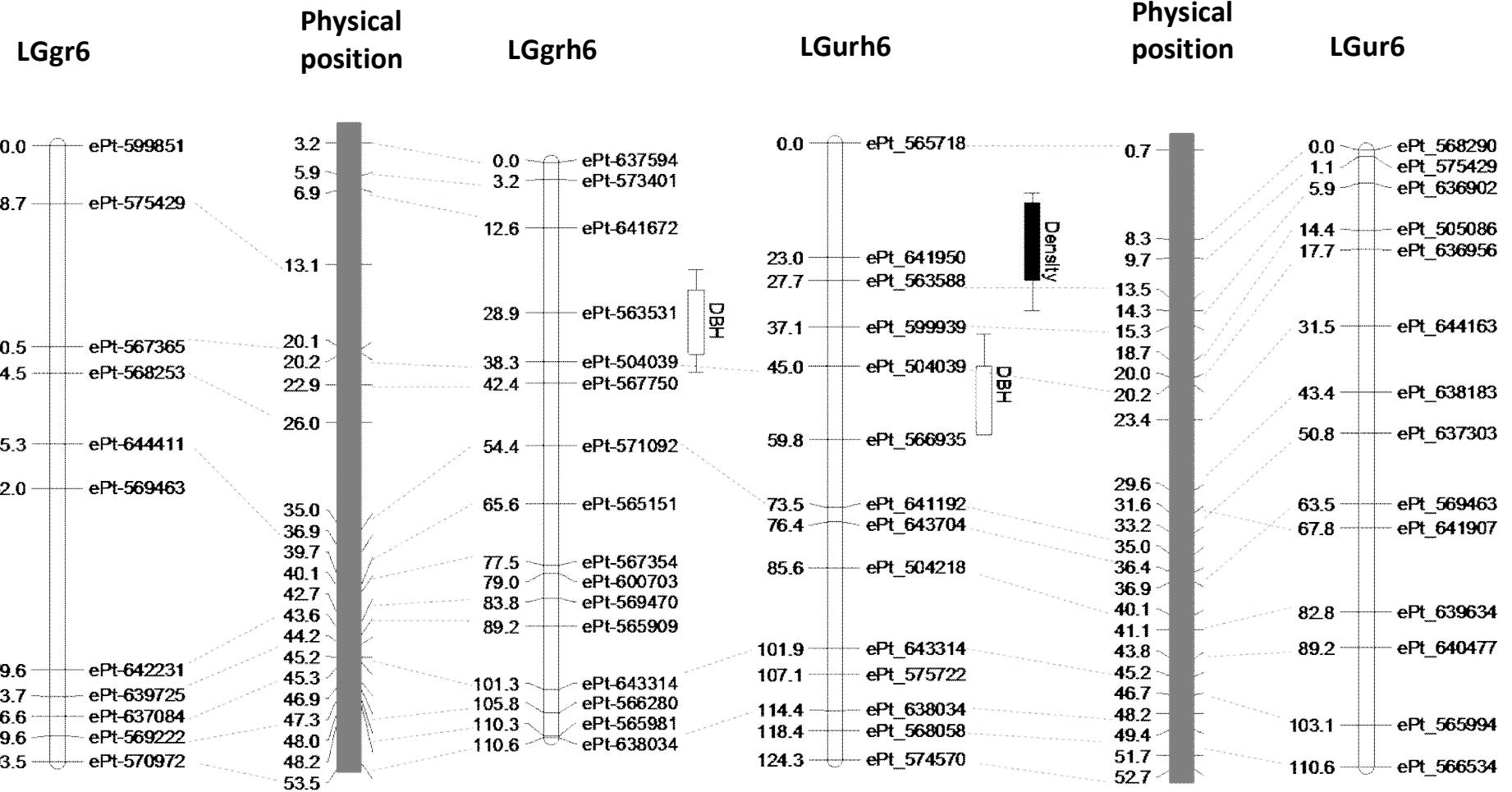






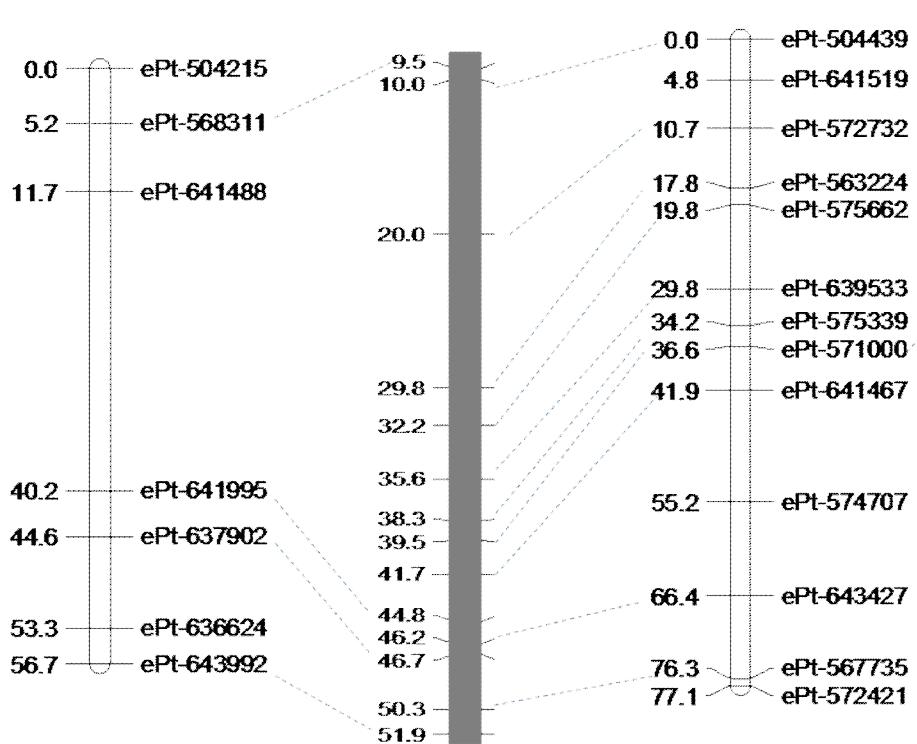






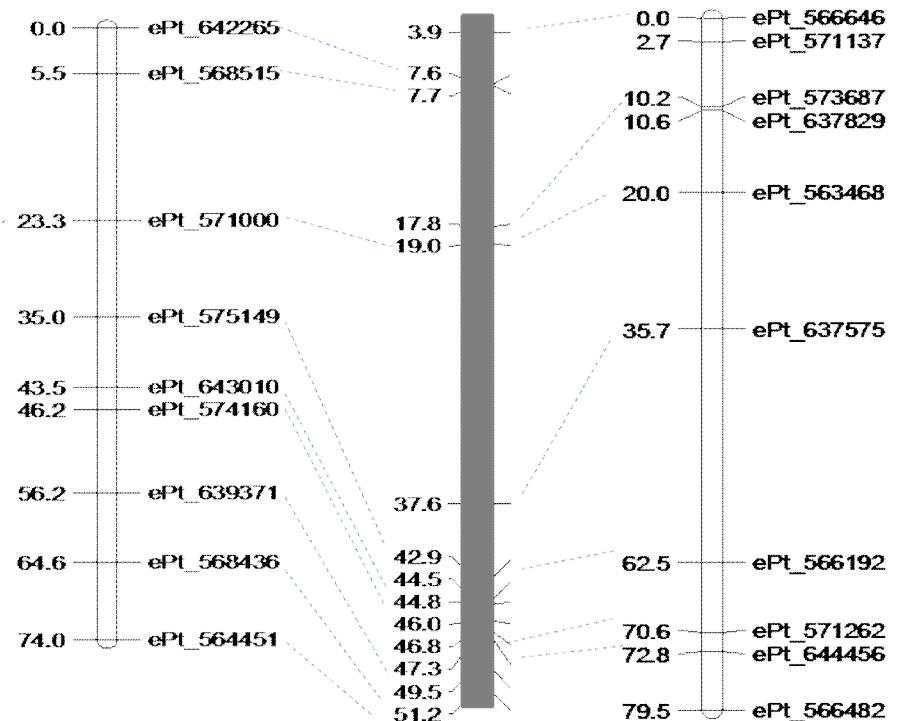
LGgr7

Physical
position



LGurh7

Physical
position



LGur7

