

Electronic supplementary material: Figure S4

Article title:

High-density genetic linkage maps with over 2000 sequence-anchored DArT markers for genetic dissection in *Eucalyptus grandis* x *E. urophylla* hybrids

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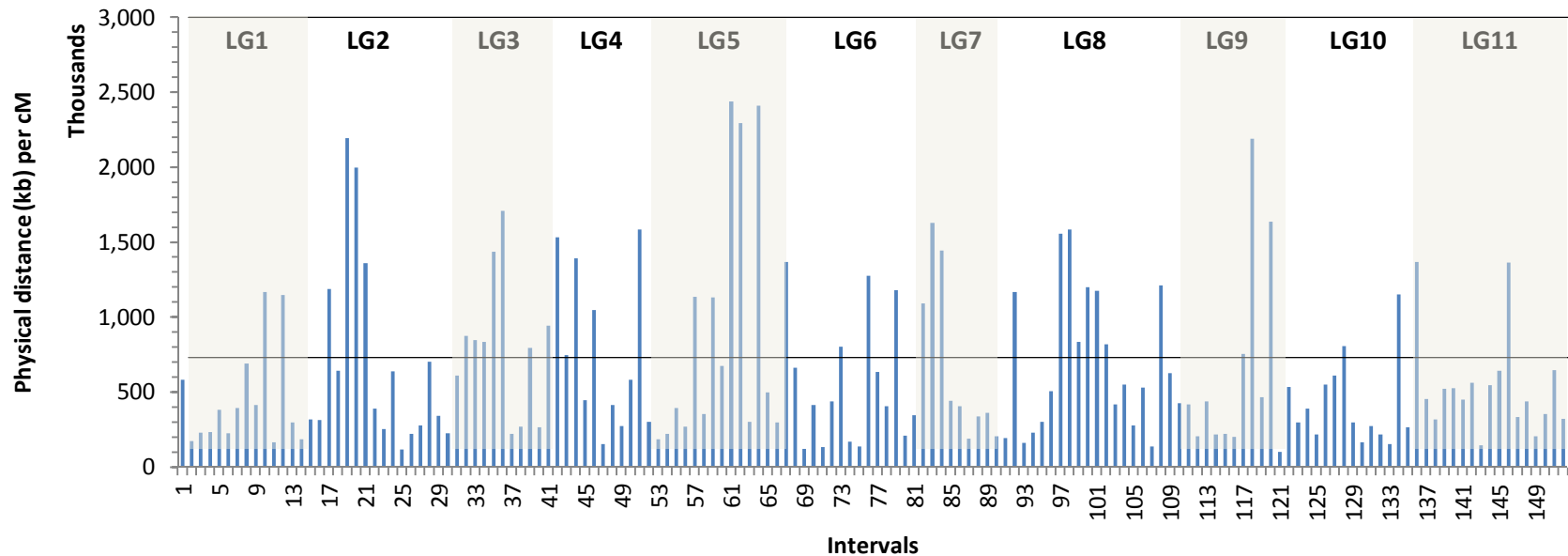
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Supplemental Figure S4. Comparison of physical and genetic distance in the *E. grandis* genome. The y-axis represents the physical distance in kb. The 153 randomly selected genetic map intervals (of approx 1 cM each) are shown with their respective linkage group (shaded areas) on the x-axis. Bars represent the physical distance (kb) per cM in each interval. The physical and genetic distances are based on the alignment of DArT fragment sequences in the consensus map to genomic scaffolds in the DOE-JGI *E. grandis* V1.0 genome assembly ([www. phytozome.net](http://www.phytozome.net)). The mean physical distance per cM of genetic distance was 633 kb (horizontal line).