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A High-Density Linkage Map for *Eucalyptus urophylla* and *E. grandis* based on 1,100 F1 Progenies Genotyped with 6,000 SNP Markers

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Next generation sequencing (NGS) technologies and high-throughput genotyping methods offer the possibility to produce dense linkage maps with highly reliable markers which can be anchored on the physical map of the genome. To this end, we developed a 6,000 SNP Infinium bead array (Illumina Inc.) for an inter-specific cross between *E. urophylla* x *E. grandis*. The SNP discovery was based on whole genome sequencing (100bp paired-end) with theoretical haploid genome coverage of 40X for the *E. urophylla* parent and 36X for the *E. grandis* parent. After read alignment on the *Eucalyptus grandis* BRASUZ1 reference genome sequence, variant calling procedure with GATK software resulted into 6,667,808 SNPs. Applying different selection criteria, three final independent sets of polymorphic SNPs were kept: 2,618 SNPs heterozygous in *E. urophylla*, 2,524 SNPs heterozygous in *E. grandis* and 858 double heterozygous SNPs. The array was used to genotype over 1,100 progenies, providing very high accuracy in marker order and genetic distances between loci. We expect an average of 200-250 markers in each of the 11 linkage group of the two parental maps. These high density linkage maps will provide a key tool: to overlay recombination and physical distances of the genome, to map quantitative trait loci (QTL) with high statistical power and to propose positional candidate genes.