Supplementary Material to:

Assessing the expected response to genomic selection of individuals and families in *Eucalyptus* breeding with a model including dominance

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Table S1. Incomplete diallel mating design amongst the ten parents (P1-P10) either as males (♂) or females (♀) and the corresponding families with the numbers of phenotyped /genotyped individuals.

♂ \ ♀	P1	P2	P3	P4	P5	P6	P7	P8	P9
P1		18/18		23/23		20/14	29/28	21/14	
P2	7/7			8/8	12/11	6/6		5/3	8/8
P3		23/20		22/15	17/13	19/14	25/24	13/10	21/20
P4		16/15				5/5	27/26	24/17	26/26
P5	26/25	19/12				17/16	15/14	18/16	27/25
P6		15/15		21/21	7/7		4/3	6/6	5/5
P7		25/25			9/9	20/16		16/15	8/7
P8		18/18				18/18	6/6		25/16
P9	29/28	15/15				20/19	17/17		
P10		23/22	17/16		15/11				

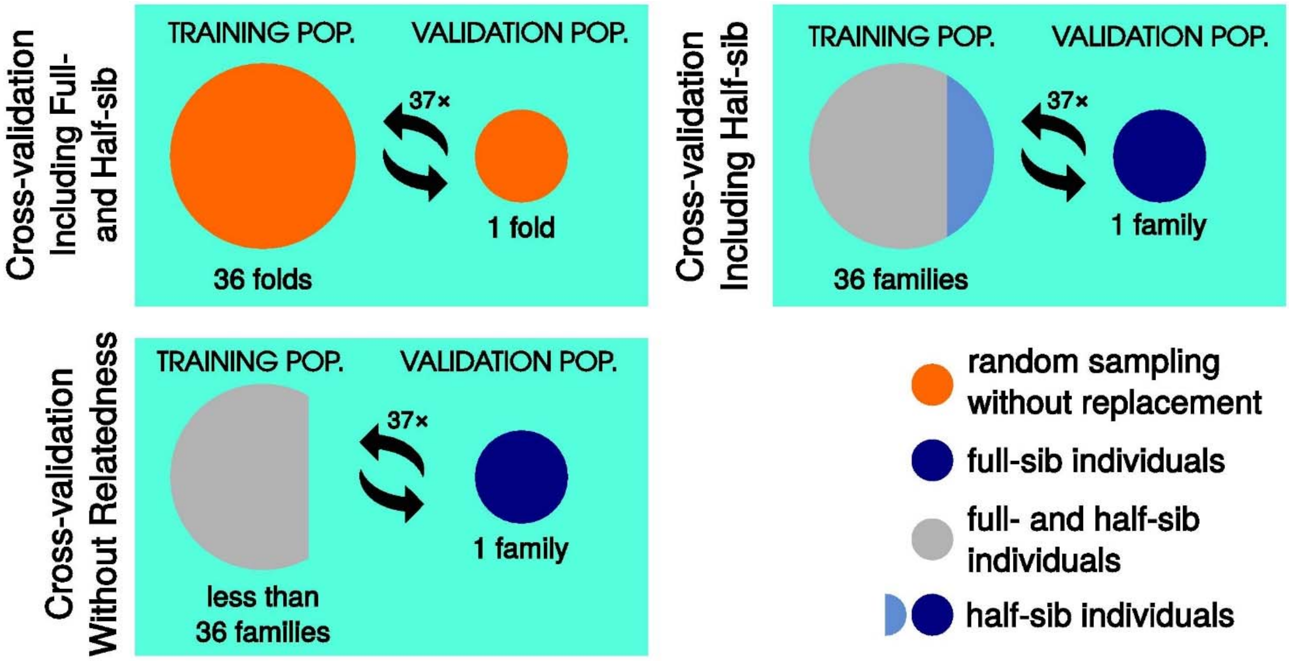

Figure S1. The three cross validation schemes controlling for relatedness between training and validation sets used to estimate the predictive abilities.

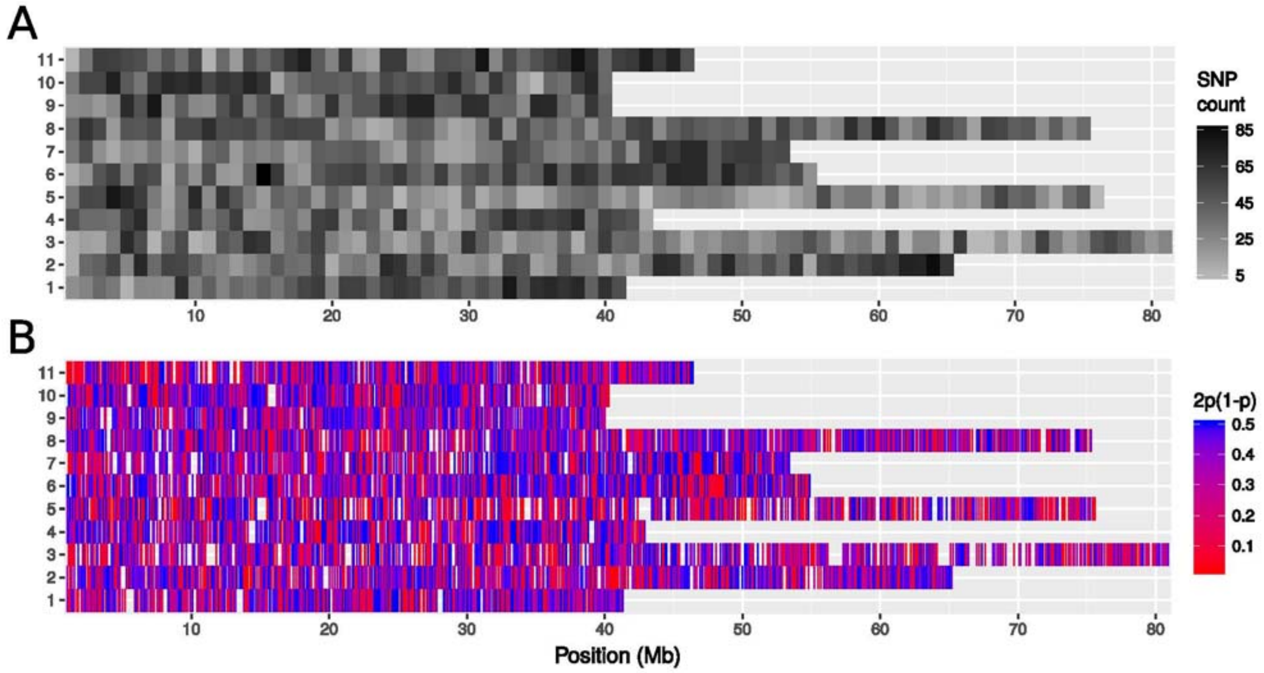

Figure S2. Distribution of the 24,806 polymorphic SNPs across the eleven *Eucalyptus* chromosomes. (A) SNP density per 1 Mb interval; (B) Expected heterozygosity of the genotyped SNPs for 100kb interval