Table S3 Biallelic SNPs significant after Bonferroni correction from gene-centric association scans.

QTL	chr	base	$\%V_T$	P	$\%V_G$	MiAC	MaAC
CA1	*X*	14495288	10.3	7.9E-06	15.2	4	5
CB1	*2L*	12715263	9.1	2.7E-05	13.5	3	4
CB1	*2L*	12718169	9.5	1.9E-05	13.9	3	4
CB1	*2L*	12730194	9.5	2.0E-05	13.9	3	3
CB1	*2L*	12730331	9.1	2.9E-05	13.3	3	3
CB1	*2L*	12730336	9.1	2.9E-05	13.3	3	3
CB1	*2L*	12730358	9.1	2.9E-05	13.4	3	3
CB1	*2L*	12737838	9.0	3.2E-05	13.2	2	4
CB1	*2L*	12738050	9.0	3.1E-05	13.3	2	4
CB1	*2L*	12738104	9.0	3.3E-05	13.2	2	4
GB1	*3L*	3326126	4.3	2.6E-5	6.8	4	11

Note: QTL corresponds to QTL in Supplementary Table 2, chr=chromosome, base=base position in chromosome, $\%V_T$=percent of total variation explained by SNP, P=p-value, $\%V_G$=percent of genetic variation explained by SNP, MiAC= Minor Allele Count = Number of founder chromosomes having minor allele represented in panel at this position, MaAC=Major Allele Count.