Table S5 SNP markers segregation in the IBM linkage mapping population (B73 x Mo17) showing correspondence between direction of QTL effects (Chintamanani *et al.* 2010) and GWAS SNP allele effects.

Chr[1]	SNP physical position (bp)	Genotype[2]		Allele increasing HR	Parental QTL additive effect increasing HR[3]
		B73	Mo17		
5	183737260	A	G	G	na[4]
7	148173418	G	G	A	na[4]
9	121167503	G	G	G	Mo17
10	21693685	A	G	G	Mo17
10	21722883	C	T	T	Mo17
10	21823409	A	C	C	Mo17

[1]chr: chromosome; [2]genotypes are homozygtes; [3]additive effect of the QTL: for lesion (LES), the ratings are in terms of a 1–10 scale, while for mutant-to-wild type height ratio (HTR), ratings are in terms of a ratio with ‘‘1’’ meaning a 1:1 ratio. A positive number means the allele for decreased score (lower lesion level), increased ratio, or decreased anthesis differential derived from B73; [4]QTL not detected in IBM population.