Table S2: Genes showing unequal allelic expression levels (B73 allele ≠ Mo17 allele) in the hybrids. All genes for which the null hypothesis was dismissed (m_1) and those which remain after applying a false discovery rate (FDR) of 5% depicted. In addition, the resulting genes are classified according to the distribution of alleles. Due to the mapping bias towards B73 only those genes showing a higher expression of the Mo17 allele are considered. The number of genes expected to overlap between the reciprocal hybrids B73xMo17 and Mo17xB73 as well as the observed overlap are shown.

Genotype	**Criteria**	**m_1**	**FDR 5%**						
			Total	**Overlap**	**B73 > Mo17**	**Overlap**	**B73 < Mo17**	**Overlap**[a]	
								expected	**observed**
B73xMo17	**$(b/m)_{BM} \neq 1$**	10,463	8,306	6,530	6,826	5,501	1,480	75	1,020*
Mo17xB73	**$(b/m)_{MB} \neq 1$**	10,463	8,259		6,710		1,549		

[a] Expected values were calculated as (# non-additive genes in B73x Mo17 * # non-additive genes in Mo17xB73) / # all expressed genes; # of all expressed genes is the sum of classes 1-9 from Table 1; expected and observed overlap values were compared using a Chi^2 test for independence; significant differences between expected and observed overlap values are indicated by * ($p \leq 0.01$); Y: yes, N: no