

Table S1: Genes whose allelic expression levels in the hybrids significantly differ from the expected allelic expression ratio of the parents.

Tissue	Hybrid	Genes with unexpected allelic expression ratio					
		Total			Nonadditively expressed genes		
		(FDR <5%)	Overlap		(FDR <5%)	Overlap	
	Expected ^c	Observed	Expected ^c	Observed	Expected ^c	Observed	
Meristematic zone	B73xMo17 ^a	150	1	47*	58	0	27*
	Mo17xB73 ^b	99			40		
Elongation zone	B73xMo17 ^a	106	1	41*	29	0	12*
	Mo17xB73 ^b	112			26		
Stele	B73xMo17 ^a	228	3	92*	33	0	19*
	Mo17xB73 ^b	185			36		
Cortex	B73xMo17 ^a	126	1	47*	28	0	14*
	Mo17xB73 ^b	87			27		
In all tissues	B73xMo17 ^a	498	7	160*	57	0	15*
	Mo17xB73 ^b	401			56		

Expected allelic expression levels in the hybrids are calculated from the allelic expression ratio of their parents:

$$^a \frac{b_{B73}/m_{Mo17}}{b_{B73xMo17}/m_{B73xMo17}}$$

$$^b \frac{b_{B73}/m_{Mo17}}{b_{Mo17xB73}/m_{Mo17xB73}}$$

The number of genes is shown for which the depicted criteria are fulfilled under controlling the false discovery rate (FDR) at 5%.

^c Expected values were calculated as [(# of genes with unexpected allelic ratio in B73xMo17) x (# of genes with unexpected allelic ratio in Mo17xB73)] / (total # of genes with B73-Mo17 SNP position). The numbers of expected and observed overlapping genes were compared using a χ^2 -test. Significant differences between expected and observed values are indicated by *: $p \leq 0.01$.

Table S2: Classification of the gene expression level in the two reciprocal hybrids B73xMo17 and Mo17xB73 relative to the level of their parental inbred lines according to nine gene expression classes.

Class	Expression pattern ^a	Tissue	Nonadditively expressed genes ^b (Total # of differentially expressed genes)							
			B73xMo17		Mo17xB73		Overlap			
			Expected ^c	Observed	Expected ^c	Observed	Expected ^c	Observed		
1	LP<H<HP	MZ	432	(1,427)	412	(1,249)	9	(85)	343*	(1,017*)
		EZ	300	(989)	336	(1,141)	5	(57)	244*	(798*)
		S	294	(1,314)	293	(1,239)	4	(74)	239*	(1,025*)
		C	205	(930)	214	(850)	2	(37)	159*	(649*)
2	LP=H<HP	MZ	81	(2,409)	11	(1,238)	0	(143)	4*	(784*)
		EZ	1	(828)	8	(1,004)	0	(42)	0	(416*)
		S	16	(1,320)	12	(1,041)	0	(62)	3*	(634*)
		C	4	(799)	14	(690)	0	(26)	1*	(314*)
3	LP<H=HP	MZ	201	(1,316)	262	(1,765)	3	(111)	105*	(751*)
		EZ	339	(1,912)	277	(1,617)	5	(155)	190*	(1,128*)
		S	217	(1,745)	271	(1,896)	3	(150)	148*	(1,271*)
		C	232	(1,734)	336	(2,041)	4	(166)	158*	(1,212*)
4	LP=HP=H	MZ	0	(11,161)	0	(11,936)	0	(6,374)	0	(10,901*)
		EZ	0	(11,650)	0	(11,640)	0	(6,799)	0	(11,557*)
		S	0	(13,288)	0	(13,320)	0	(8,045)	0	(13,193*)
		C	0	(13,779)	0	(13,747)	0	(8,903)	0	(13,666*)
5	LP<HP<H	MZ	1	(1)	1	(1)	0	(0)	0	(0)
		EZ	0	(0)	0	(0)	0	(0)	0	(0)
		S	2	(2)	2	(2)	0	(0)	1*	(1*)
		C	1	(1)	0	(0)	0	(0)	0	(0)
6	LP=HP<H	MZ	26	(26)	3	(3)	0	(0)	1*	(1*)
		EZ	3	(3)	2	(2)	0	(0)	1*	(1*)
		S	1	(1)	5	(5)	0	(0)	0	(0)
		C	2	(2)	4	(4)	0	(0)	0	(0)
7	H<LP<HP	MZ	3	(3)	2	(2)	0	(0)	1*	(1*)
		EZ	0	(0)	0	(0)	0	(0)	0	(0)
		S	0	(0)	0	(0)	0	(0)	0	(0)
		C	1	(1)	0	(0)	0	(0)	0	(0)
8	H<LP=HP	MZ	109	(120)	3	(16)	0	(0)	3*	(3*)
		EZ	1	(2)	1	(7)	0	(0)	1*	(1*)
		S	12	(16)	4	(9)	0	(0)	4*	(4*)
		C	4	(5)	2	(2)	0	(0)	1*	(1*)
9	ambiguous	MZ	100	(4,436)	12	(4,689)	0	(995)	0	(2,884*)
		EZ	5	(4,562)	8	(4,535)	0	(1,037)	1*	(3,831*)
		S	6	(4,315)	9	(4,489)	0	(880)	1*	(3,635*)
		C	10	(4,025)	17	(3,942)	0	(746)	1*	(3,260*)
Total			1,056		824		35		439*	

^a The classification of gene expression levels in the hybrids (H) into nine classes is based on three pairwise *t*-tests: Tests 1 and 2 estimate if the expression level of the considered gene in the hybrid is significantly different from that of the lower parent (LP) and/or higher parent (HP) (LP≠H; HP≠H) by controlling the false discovery rate (FDR) at 5%. Test 3 compares the expression level of the two parents (LP≠HP).

^b In each expression class, the number of nonadditively expressed genes have been estimated by comparing the gene expression levels in the hybrids with the mid-parent values.

^c The number of genes expected to overlap between the two reciprocal hybrids in each class were calculated as [(# of nonadditive genes in B73xMo17) x (# of nonadditive genes in Mo17xB73)]/(# of all expressed genes in the tissue under investigation). The numbers of expected and observed overlapping genes were compared using a χ^2 -test. Significant differences are indicated by *: $p \leq 0.01$.

Table S3: Functional categorization of nonsyntenic nonadditively expressed genes. The 'X' indicates overrepresented categories in the considered gene set in comparison to the GO terms in all expressed genes in the corresponding tissue. For genes of the meristematic zone and stele no GO terms were significantly enriched.

	GO term	Description	Nonsyntenic nonadditively expressed genes			
			Cortex		Elongation zone	
			B73xMo17	Mo17xB73	B73xMo17	Mo17xB73
Molecular process	GO:0004497	Monoxygenase activity		X		
	GO:0070001	Aspartic-type peptidase activity				X
	GO:0004190	└ Aspartic-type endopeptidase activity				X
	GO:0005506	Iron ion binding	X			
	GO:0046906	Tetrapyrrole binding	X			
	GO:0020037	└ Heme binding	X			
Biological process	GO:0016265	Death	X	X		
	GO:0008219	Cell death	X	X		
	GO:0012501	└ Programmed cell death	X	X		
	GO:0006915	└ Apoptosis	X	X		