

Table S1: Overview of lane distribution on flow cells, biological replication, mRNAseq output and mapping results. The total reads of each sequenced sample have been mapped onto the filtered gene set (FGS) of *Zea mays* L.. Only uniquely mapping reads have been further considered. Stacked PCR artifacts (overlapping reads with the same start and end point) have been removed. Using previously identified single nucleotide polymorphisms (SNPs) B73 and Mo17 alleles were distinguished.

Flow cell	Lane	Replicate	Genotype	Number of reads					
				Total	Uniquely mapped on genome ^a	Uniquely mapped on genome without stacks ^b	Uniquely mapped without stacks mapped on FGS ^c	Allele-specific ^d	
								B73	Mo17
1	1	1	B73	33,234,526	21,328,227	12,267,068	11,570,430	872,471	4,909
	2		Mo17	35,955,236	19,118,497	10,868,356	10,029,386	9,871	594,869
	3		B73xMo17	32,782,191	19,055,049	11,718,448	10,954,923	456,036	319,549
	4		Mo17xB73	36,445,647	22,259,222	12,204,641	11,388,051	547,118	418,242
	7	2	B73	32,098,456	20,899,929	10,770,070	10,080,543	813,952	3,492
	8		Mo17	31,288,481	17,517,471	9,795,846	9,011,261	7,850	570,795
	6		B73xMo17	34,756,464	20,539,186	11,049,208	10,203,856	463,443	343,477
	5		Mo17xB73	32,772,571	21,309,187	10,834,708	10,039,140	452,546	332,658
2	2	3	B73	32,232,074	21,809,433	9,450,478	9,028,832	783,690	1,740
	1		Mo17	34,882,886	20,767,234	10,881,671	10,284,321	6,687	683,788
	3		B73xMo17	36,204,588	23,202,047	10,798,241	9,844,378	506,718	386,066
	4		Mo17xB73	36,142,580	22,702,689	10,830,826	10,265,593	502,743	384,146
	8	4	B73	32,330,408	21,862,109	10,089,830	9,658,141	842,557	2,062
	7		Mo17	34,413,964	22,899,946	10,276,388	9,645,122	6,642	662,850
	5		B73xMo17	36,299,499	22,203,710	10,344,764	9,844,378	500,527	387,362
	6		Mo17xB73	36,698,267	21,671,494	10,392,346	9,851,114	500,350	384,599

^a mapped to the reference genome of B73 (Schnable *et al.*, 2009)

^b after removal of PCR artifacts (stacked reads)

^c mapped to the gene models of the filtered gene set (FGS) of *Zea mays* (Release 5b.60) allowing 2 mismatches

^d using 4 million single nucleotide polymorphisms (SNPs)