

Table S5. Alignment of RNA seq reads to genome and genes

Genotype	Total Reads ^a	No. Non-uniquely mapped ^b	No. Uniquely Mapped Reads		Total genes ^e
			To Genome ^c	To Genes ^d	
<i>mop1/mop1</i>	4,474,243	950,295 (21%)	2,775,266 (62%)	2,156,241 (78%)	24,743 (76%)
<i>Mop1/mop1</i>	5,982,599	1,350,921 (23%)	4,113,045 (69%)	3,248,869 (79%)	

^a The number of reads after trimming low quality bases at the 3' end and removing the reads shorter than 32 bp ; ^b The number of reads (percentage) that aligned to more than 1 genomic locations on B73 reference genome allowing a maximum of 2 mismatches including insertion/deletions; ^c The number of reads (percentage of total reads) that aligned to a unique location of the B73 reference genome; ^d The number of uniquely mapped reads (percentage of uniquely mapped to genome) that can be projected onto gene models; ^e The union of genes (percentage of all 32,540 all genes) captured from two genotypes.