

Table S4: Genomic presence/absence variation (PAV) could explain between 2.5% and 15% of SPE_B expression patterns. All SPE_M genes were detected in the B73 genome and thus cannot be explained by PAV (data not shown). The Mo17 genome assembly is not completely sequenced yet. However, among 1470 SPE_M genes, only 7 (0.5%) were not detected with at least 90% coverage in the Mo17 genome. Among 1051 genes displaying SPE_B, 261 (25%) were not detected in the Mo17 genome sequence. Up to 155 SPE_B genes (15%) could be putative genomic PAVs in Mo17 because of their very low expression, but for only for 26 (2.5%) genes no RNA sequencing reads were detected in Mo17 making them very likely candidates for genomic PAV.

	SPE_B
Total	1051
BLAST match in Mo17 genome at >90% sequence identity and >90% coverage	790
No BLAST match in Mo17 genome at >90% sequence identity and >90% coverage	261
Expression level of 261 putative PAVs in Mo17	# of putative PAVs
None or less than 0.1 FPKM	155
No RNA sequencing reads	26