

---

**Table S3.** Polymorphisms detected by W22 3'-anchored 454-sequence-reads

---

Consensus tags with 2 to 75 reads (n = 1263)	
Total polymorphic W22 alleles	56.6%
B73 MAGI Matches <sup>1</sup>	92.4%
Consensus tags with 7 to 75 reads (n=107)	
Total polymorphic W22 alleles	52
# confirmed	47 (43.9%) <sup>‡</sup>
Total polymorphisms	146*
# confirmed	137 (93.8%) <sup>‡</sup>
Consensus tags with 5 to 75 reads (n=211)	
Total polymorphisms	257*
# confirmed	231 (89.9%) <sup>‡</sup>
Homopolymer-type polymorphisms	60*
# confirmed	53 (88.8%) <sup>‡</sup>

---

<sup>1</sup> Contiguous BLASTN alignment of >50 bp or > 90% of query length.

\* Percent of matches having one or more SNP or indel polymorphism within the best aligned segment.

<sup>‡</sup> Allele sequences supported by identity to independent EST sequences.