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Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes

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Comparison of the GBS tags aligned to the assembled sequences of B73 and Mo17 genomes.

The green blocks indicate pericentromere regions in B73 genome. The blue lines indicate aligned GBS tags to the two genomes.



The distribution of insertion ages of high-confidence full-length LTR retrotransposons in B73, Mo17 and PH207 genomes.

X axis represents insertion ages of LTR retrotransposons in the genome and Y axis represents the number of LTRs.



The chromosomal distribution of insertion ages of high-confidence full-length LTR retrotransposons in B73 and Mo17 genomes.

The insertion date of each LTR retrotransposon was averaged in 1 Mb bin window. The black blocks indicate pericentromere regions in B73 genome.



Whole-genome comparison between B73 and Mo17.

Blue lines represented the one-to-one aligned regions between each pair of pseudomolecules.



Length distribution of PAV sequences between B73 and Mo17 genomes.



B73 specifically present genes (compared with Mo17 genome)

Supplementary Figure 6

Coverage distribution of B73-, Mo17- and PH207-specific genes in 19 wild relatives, 23 landraces and 60 modern inbred lines.

For each gene, the coverage of CDS region was shown.



Histogram of indel numbers between B73 and Mo17 of the whole genome and coding regions.



Subgenome organization among B73, Mo17 and sorghum.

(a), B73 and Sorghum; (b). Mo17 and Sorghum. The red circle represents subgenome 1 and green circle represents subgenome 2.



Graphic representation of the alignment and polarity of homologous genes among B73, Mo17 and PH207 genomes.

Green blocks represent the homologs of germin-like plant defense related genes. Blue and red blocks indicate flank genes in each genome.