A

IPO323
Zt05
Zt1E4
Zt1A5
Zt3D1
Zt3D7
Zt10
Zt289
Zt469

B

Non-syntenic   Syntenic TE

Number of TEs (log10)

Chromosomes/contigs

C

DXX-MITE   Zt09_13_00269

IPO323
chromosome 13
760kb   780kb   800kb   820kb

Zt289
contig 12
−360kb   −340kb   −320kb   −300kb

Zt05
contig 18
−450kb   −4250kb   −400kb   −375kb

Zt10
contig 12
840kb   860kb   880kb   900kb   920kb

Zt469
contig 16
800kb   850kb

Figure S4: Intraspecific variation in TE coverage per chromosome/contig

A) Circos plot of the TE content along chromosomes of nine *Z. tritici* isolates. The first track represents the karyotype of the reference isolate IPO323; the second track shows a heatmap of TE density per 100kb windows in IPO323. Track three to ten represent the density of TE copies per 100kb windows in other *Z. tritici* isolates. Chromosomal coordinates refer to the closest orthologous gene projected on the IPO323 genome. Darker colors correspond to a higher TE density. B) Synteny of genomic positions with TE insertions among nine *Z. tritici* isolates. The boxplots illustrate the distribution of "syntenic" (orange) and "non-syntenic" (blue) TEs per chromosome or contig among the nine *Z. tritici* isolates. Syntenic regions were identified by whole-genome alignment and in pairwise comparison with the reference strain IPO323 using SyRi software with 500pb windows. "Syntenic TE" insertions are overlapping by at least 50% of sequence length with a corresponding region. C) TE orders coverage contributions per core chromosome/contig of nine *Z.tritici* isolates. Example of a presence/absence polymorphism of the candidate effector Zt09_13_00269 identified (Haueisen *et al.* 2018) in a TE-rich region. TEs are shown in orange, genes in grey and the effector of interest is shown in blue boxes. Connecting lines in grey represent the orthologous genes in each genome.