**Table S4: Location and annotation of SNPs and INDELs found in the sequenced chromosome-loss strains.** Listed are SNPs that deviate in the chromosome loss strains from the respective corresponding ancestral strain Zt09, IPO323 or Za17. Also listed are the SNPs that differ between the ancestral strains Zt09 and IPO323 and the reference genome. Polymorphisms in coding regions are indicated in **bold**.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Strain** | **Species** | **SNP (total)** | **SNP (coding)** | **Coordinates** | **Mutation** | **Gene annotation** |
| Zt09∆14 | *Z. tritici* | 0 | 0 |  |  |  |
| Zt09∆15 | *Z. tritici* | 0 | 0 |  |  |  |
| Zt09∆20 | *Z. tritici* | 2 | 0 | chr 10: 1,547,664  chr 15: 639,408 | A -> G  TTA ->TTATA |  |
| Zt09∆21 | *Z. tritici* | 0 | 0 |  |  |  |
| IPO323∆14 | *Z. tritici* | 1 | **1** | **chr 1: 4,492,118** | **G -> C (non-syn)** | **hypoth. protein** |
| IPO323∆15 | *Z. tritici* | 2 | 0 | chr 6: 746,848  chr 10: 517,128 | G -> C  17 bp del |  |
| IPO323∆18 | *Z. tritici* | 3 | **2** | **chr 3: 3,145,507**  **chr 10: 735,717**  chr 19: 395,097 | **C -> T (non-syn)**  **9 bp del (in frame)**  G -> A | **zinc-finger**  **histidine-kinase** |
| IPO323∆19 | *Z. tritici* | 1 | 0 | chr 9: 1,937,298 | A -> G |  |
| Za17∆24 | *Z. ardabiliae* | 0 | 0 |  |  |  |
| Za17∆49 | *Z. ardabiliae* | 0 | 0 |  |  |  |
| Za17∆51 | *Z. ardabiliae* | 0 | 0 |  |  |  |
|  |  |  |  |  |  |  |
| Zt09 | *Z. tritici* | 17 | 5 | chr 1: 125  **chr 1: 4,373,965**  chr 2: 1,137,727  chr 3: 831,118  chr 3: 2,780,000  **chr 4: 807,372**  chr 5: 690, 228  **chr 5: 1,102,332**  chr 5: 1,814,335  chr 5: 1,814, 365  chr 7: 2,644,548  chr 9: 2,142,382  chr 10: 1,630,016  **chr 11: 223,110**  chr 12: 415,459  chr 12: 935,185  **chr 12: 979,588** | C -> A  **CA -> AC (non-syn)**  G -> A  A -> G  A -> T  **AG -> AAGGG**  T -> C  **C -> T (syn)**  GT -> GTT  T -> C  A -> G  T -> A  G -> T  **404 bp deletion (in frame)**  C -> T  TG -> T  **A -> G (syn)** | **hypoth. protein**  **pred. protein**  **hypoth. protein**  **white collar-11)**  **hypoth. protein** |
| IPO323 | *Z. tritici* | 22 | 3 | **chr 1: 4,373,965**  chr 2: 400,119  chr 2: 1,137,727  chr 2: 1,459,200  chr 3: 831,118  **chr 3: 2,633,702**  chr 4: 999,781  chr 5: 690, 228  chr 5: 1,814,335  chr 5: 1,814, 365  chr 7: 2,644,548  chr 9: 2,142,382  chr 10: 1,321,821  chr 10: 1,630,016  chr 11: 1,063,938  chr 12: 415,459  **chr 12: 596,261**  chr 12: 605,733  chr 15: 586,233  chr 16: 245,451  chr 19: 263,608  chr 20: 449,279 | **CA -> AC (non-syn)**  C -> T  G -> A  T -> C  A -> G  **AGGCGG -> AGG (in frame)**  G -> C  T -> C  GT -> GTT  T -> C  A -> G  T -> A  A -> C  G -> T  A -> C  C -> T  **G -> A (syn)**  GCTCC -> GC  G -> C  A -> C  A -> C  A -> T | **hypoth. protein**  **RNAi gene Qde2**  **hypoth. protein** |

1) Notably, one difference between Zt09 and the reference was a 404 bp deletion (resulting in a truncated, in frame transcript) in the gene of a known regulator of the circadian clock, white collar-1 (Crosthwaite *et al.*, 1997). Zt09 shows phenotypic differences compared to IPO323 and further studies will be conducted to elucidate a possible effect of this deletion in these two strains.