

Description of Additional Supplementary Files

File name: Supplementary Data 1

Description: Matrix of shared kmer state rates between all pairs of accessions

File name: Supplementary Data 2

Description: Loci for minimal SNP panel plus observed genotypes for 150 non-redundant accessions

File name: Supplementary Data 3

Description: Details of 183 selected metabolites

File name: Supplementary Data 4

Description: Scaffold from the Tsesey genome assembly by Cannarozzi *et al.* (2014) containing the A genome copy of the tef *TT2* orthologue (Et_4A_032842). The gene model is highlighted with background colours in the sequence. The LTR insertion is shown in the green text.

File name: Supplementary Data 5

Description: Scaffold from the Tsesey genome assembly Cannarozzi *et al.* (2014) containing the B genome copy of the tef *TT2* orthologue (Et_4B_039404). The gene model is highlighted with background colours in the sequence. The LTR insertion is shown in the green text.

File name: Supplementary Data 6

Description: Details of accessions used in the study

File name: Supplementary Data 7

Description: Original field trial design; Updated field trial design based on definition of redundant accession groups

File name: Supplementary Data 8

Description: Raw field and grain phenotypic data. The main trait columns are highlighted in blue