

## Description of Additional Supplementary Files

### Supplementary Data 1:

RFL groups inferred with CD-Hit. CD-Hit was used to group putatively orthologous sequences across accessions. A threshold of 96% sequence identity was chosen as it was found to be the best compromise between distinguishing paralogous sequences within each accession whilst grouping putatively orthologous sequences across accessions.

### Supplementary Data 2:

Genotyping of the transgenic wheat plants. Transgene insertion in the genome was confirmed by PCR. Real-time PCR was carried out in 384-well reaction plates to estimate the number of transgenes integrated per plant. Two replicates were performed for each sample and a calibrator sample (known 1 copy of Bar control). An expression value of  $\sim 1$  indicates single insertion of the transgene whereas a value higher than 1 indicates multiple insertions.