**Suppl. Table 1** PCR primers used and PCR fragment size

|  |  |  |
| --- | --- | --- |
| **Primer name** | **Primer sequence (5’-3’)** | **PCR fragment size** |
| StY\_34\_F | GCCGCGAGCATTTTGAGTAC | 537 bp |
| StY\_34\_R | AGGCCTGGAGTACCCTCAAA |
| StY\_107\_F | GAACGGGCGTAATCTGGTCA | 515 bp |
| StY\_107\_R | CAAGGTAAGTTGATCGCGCG |
| CL90\_F | AAAGCTCTCGGGAAACTGGG | 348 bp |
| CL90\_R | TCGTTCTCATCCGCGTTGAT |

**Suppl. Table 2** Probes used in this study

|  |  |  |  |
| --- | --- | --- | --- |
| **Probe name** | **GenBank accession no.** | **Reference** | **Probe labelling** |
| Oligo-pTa71 | Wheat rDNA 25S-18S intergenic region (X07841.1) | Tang et al., 2014 | 5’-labeled oligo |
| St2-80 | not available | Wang et al., 2017 | nick-translation |
| StY\_34 | MW025811 | This study | nick-translation |
| StY\_107 | MW025810 | This study | nick-translation |
| StY\_90 | MW025812 | This study | nick-translation |
| StY\_93 | MW025813 | This study | directly synthesis |



**Suppl Fig 1** Graph representation of repeat clusters read similarities *in silico*.

(a-b) St enriched repeat clusters, (c-d) Y enriched repeats. Individual reads from *(Pse. stipifolia)* StSt and *(R. ciliaris)* StY plants are represented by blue and green nodes, respectively. Nodes are placed according to sequence similarity, where similar sequences are close together and connected with edges (gray lines). Circular or globular structure of graphs is typical for repeats with tandem arrangement in the genome.

merge

**Suppl Fig 2** The repeat cluster distribution in *Triticum aestivum* (c.v. Chinese spring, CS)

(a-c) Localization of pTa71 (green) and StY\_34 (red); (d-f) pTa71 (green) and StY\_107 (red); (g-i) pTa71 (green) and StY\_90 (red); (j-l) pTa71 (green) and StY\_93 (red). Chromosomes with secondary constriction were marked with white arrowheads. Scale bar equals 10 μm.