



**Supplementary Table S1.** Characterization of morphological features in plants of wheat species, varieties and alloplasmic lines derived from interspecific crossing *T. dicoccum* Schuebl. var. Araratum (Host.) × *T. aestivum* (Mironovskaya 808). Selection on economically valuable signs was starting with F<sub>3</sub>BC<sub>2</sub>.

| Species, Allolines                                                     | Height   | Stem Characters                                    | Gglume Characters                                                                                                               | Kernel Characters                    | Threshing | Grain Formation |
|------------------------------------------------------------------------|----------|----------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|--------------------------------------|-----------|-----------------|
| <i>T. dicoccum</i> Schuebl. var. araratum (Host.) from IBBP collection | ≤ 140 cm | Brown, medium thickness, under the spike is hollow | Brown, with pubescence; Keel beak short, acute; Sholder shape: narrow, square                                                   | Dark red, harder texture             | difficult | 65%             |
| <i>T. aestivum</i> (M808) from IBBP collection                         | ≤ 130 cm | White, medium thickness, under the spike is hollow | White, without pubescence; Sholder shape: square, slightly slanted in the lower part and raised in the upper part of the spike. | Dark red, vitreous, smooth endosperm | easy      | 57%             |
| D-a-05                                                                 | ≤ 100 cm | White, medium thickness, under the spike is hollow | White, without pubescence; Keel beak: acuminate; Sholder shape: narrow, square                                                  | Dark red, vitreous, smooth endosperm | easy      | 81%             |
| D-b-05                                                                 | ≤ 100 cm | White, medium thickness, under the spike is hollow | White, without pubescence; Keel beak: acuminate; Sholder shape: narrow, square                                                  | Dark red, vitreous, smooth endosperm | easy      | 78%             |
| D-d-05                                                                 | ≤ 110 cm | White, medium thickness, under the spike is hollow | White, foundation of spikes without pubescence or with pubescence; Keel beak: small, obtuse; Sholder shape: narrow, square      | Dark red, vitreous, smooth endosperm | easy      | 57%             |
| D-d-05b                                                                | ≤ 110 cm | White, thick, under the spike is hollow            | White, without pubescence; Keel beak: acute, long (1 sm); Sholder shape: elevated                                               | Dark red, vitreous, smooth endosperm | easy      | 70%             |
| D-f-05                                                                 | ≤ 130 cm | White, thick, under the spike is hollow            | White, with pubescence (or unevenly brown, with pubescence), Keel beak: acuminate; Sholder shape: wide, square                  | Dark red, vitreous, smooth endosperm | easy      | 47%             |
| D-n-05                                                                 | ≤ 130 cm | White, medium thickness, under the spike is hollow | White, with low pubescence; Keel beak: small, obtuse; Sholder shape: wide, square                                               | Dark red, vitreous, smooth endosperm | easy      | 58%             |
| D-40-05                                                                | ≤ 117 cm | White, medium thickness, under the spike is hollow | White, without pubescence; Keel beak: small, obtuse; Sholder shape: wide, square                                                | Dark red, vitreous, smooth endosperm | easy      | 56%             |
| D-41-05                                                                | ≤ 123 cm | White, medium thickness, under the spike is hollow | White, without pubescence; Keel beak: small, obtuse; Sholder shape: wide, square                                                | Dark red, vitreous, smooth endosperm | easy      | 59%             |
| D-42-05                                                                | ≤ 120 cm | White, medium thickness, under the spike is hollow | White, without pubescence; Keel beak: small, obtuse; Sholder shape: wide, square                                                | Dark red, vitreous, smooth endosperm | easy      | 57%             |



**Supplementary Table S2.** Length of PCR fragments detected using microsatellite markers at alloplasmic lines and their parents. ((-) -No PCR fragment).

| Marker/Chromosome   | T. dicoccum | Mironovskaya 808 | D-a-05   | D-b-05   | D-d-05   | D-d-05-b | D-f-05   | D-n-05   | D-40-05  | D-41-05  | D-42-05  |
|---------------------|-------------|------------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| Xgwm437<br>7D       | -           | 101              | 101      | 101      | 101      | 101      | 101      | 115      | 101      | -        | 101      |
| Xgwm357<br>1A       | 127         | 121              | 121      | 121      | 119      | 119      | 127      | 123      | 121      | 121      | 121      |
| Xgwm3<br>3D         | 78          | 78               | 78       | 78       | 78       | 78       | 78       | 78       | 78       | 78       | 78       |
| Xgwm155<br>3A       | 139         | 147              | 147      | 147      | 141, 147 | 141, 147 | 139      | 143      | 147      | 141      | 147      |
| Xtaglgap<br>1B      | 573         | 569, 573         | 569, 573 | 569, 573 | 569, 573 | 569, 573 | 573      | 569, 573 | 569, 573 | -        | 569, 573 |
| Xgwm389<br>3B       | 147         | 137              | 137      | 137      | 137      | 137      | 137      | 135      | 137      | 137      | 137      |
| Xgwm261<br>2D       | 154         | 182              | 182      | 182      | 182      | 182      | 182      | 182      | 182      | 182      | 182      |
| Xgwm513<br>4B       | 145         | -                | 139, 145 | 139, 145 | 139, 145 | 139, 145 | 139, 147 | 139, 145 | 137, 143 | 137, 143 | 137, 143 |
| Xgwm190<br>5D       | 209         | 217              | 217      | 217      | 217      | 217      | 217      | 217      | 209, 217 | 217      | 217      |
| Xgwm18<br>1B        | 217         | 193              | 193      | 193      | 193      | 193      | 193      | 193      | 193      | 193      | 193      |
| Xgwm95<br>2A        | 121         | 121              | 123      | 123      | 123      | 123      | 123      | 125      | 121      | 121      | -        |
| Xgwm160<br>4A       | 194         | 184              | 184      | 184      | 184      | 184      | 184      | 180, 190 | 180, 186 | 184      | 184      |
| Xgwm186<br>5A       | 134         | 136              | 136      | 136      | 136      | 136      | 136      | 136      | 136      | 136      | 136      |
| Xgwm334<br>6A       | 122         | 124              | 124      | 124      | 124      | 124      | 124      | 126      | 124      | -        | 124      |
| Xgpw2255<br>1D      | 232         | 222              | 222      | 220      | 220      | 224      | 216      | 220      | -        | 212      | 224      |
| Xgwm130<br>7A       | 122         | 124              | 124      | 124      | 124      | 128      | 124      | 126      | 124      | 128      | 124      |
| Xgwm192<br>4A,4B,4D | 196         | 148, 212         | 148, 212 | 148, 212 | 148, 212 | 148, 210 | 148, 196 | 148, 206 | -        | 148, 212 | 148, 212 |

[illegible]

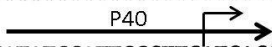


|          |                                                              |     |
|----------|--------------------------------------------------------------|-----|
| DN05     | GTATTAAGGTTCTTCTCTCCAGCGTTTAGTATTCAAGTTCTTCTCTCCAGCCCCCGG    | 60  |
| AP013106 | GTATTAAGGTTCTTCTCTCCAGCGTTTAGTATTCAAGTTCTTCTCTCCAGCCCCCGG    | 60  |
| X56186   | GTATTAAGGTTCTTCTCTCCAGCGTTTAGTATTCAAGTTCTTCTCTCCAGCCCCCGG    | 60  |
| GU985444 | GTATTAAGGTTCTTCTCTCCAGCGTTTAGTATTCAAGTTCTTCTCTCCAGCCCCCGG    | 60  |
| *****    |                                                              |     |
| DN05     | CCCCCTTTGATAAGGAAAGTTTGCATTCTCAAATAAAAAATGACAAATATGGTTCGAT   | 120 |
| AP013106 | CCCCCTTTGATAAGGAAAGTTTGCATTCTCAAATAAAAAATGACAAATATGGTTCGAT   | 120 |
| X56186   | CCCCCTTTGATAAGGAAAGTTTGCATTCTCAAATAAAAAATGACAAATATGGTTCGAT   | 120 |
| GU985444 | CCCCCTTTGATAAGGAAAGTTTGCATTCTCAAATAAAAAATGACAAATATGGTTCGAT   | 120 |
| *****    |                                                              |     |
| DN05     | GGCTCTTCTCCACTAGCAGGTTTACTGCTTTCTATTTGCACTTTTGTATTAAGTTTCCTT | 180 |
| AP013106 | GGCTCTTCTCCACTAGCAGGTTTACTGCTTTCTATTTGCACTTTTGTATTAAGTTTCCTT | 180 |
| X56186   | GGCTCTTCTCCACTAGCAGGTTTACTGCTTTCTATTTGCACTTTTGTATTAAGTTTCCTT | 180 |
| GU985444 | GGCTCTTCTCCACTAGCAGGTTTACTGCTTTCTATTTGCACTTTTGTATTAAGTTTCCTT | 180 |
| *****    |                                                              |     |
| DN05     | ATATATACGATTTTTTATTATTTTCTATTTGTCTATTTTCTTTTTAGTGCCTTTTATTT  | 240 |
| AP013106 | ATATATACGATTTTTTATTATTTTCTATTTGTCTATTTTCTTTTTAGTGCCTTTTATTT  | 240 |
| X56186   | ATATATACGATTTTTTATTATTTTCTATTTGTCTATTTTCTTTTTAGTGCCTTTTATTT  | 240 |
| GU985444 | ATATATACGATTTTTTATTATTTTCTATTTGTCTATTTTCTTTTTAGTGCCTTTTATTT  | 240 |
| *****    |                                                              |     |
| DN05     | CGATTATTCTTCTCCCAATTTGCAATCTTTTCGGAGCCTCCTTCATTATTACTCTTCCTC | 300 |
| AP013106 | CGATTATTCTTCTCCCAATTTGCAATCTTTTCGGAGCCTCCTTCATTATTACTCTTCCTC | 300 |
| X56186   | CGATTATTCTTCTCCCAATTTGCAATCTTTTCGGAGCCTCCTTCATTATTACTCTTCCTC | 300 |
| GU985444 | ATATTATTCTTCTCCCAATTTTACATCTTTTCGGAGCCTCCTTCATTATTACTCTTCCTC | 300 |
| *****    |                                                              |     |
| DN05     | CAGAGATTGAGGATCCCCAAGCTCTAGCTCATTTAGCAGGGCTAAACTTCTATCTGAGCC | 360 |
| AP013106 | CAGAGATTGAGGATCCCCAAGCTCTAGCTCATTTAGCAGGGCTAAACTTCTATCTGAGCC | 360 |
| X56186   | CAGAGATTGAGGATCCCCAAGCTCTAGCTCATTTAGCAGGGCTAAACTTCTATCTGAGCC | 360 |
| GU985444 | CAGAGATTGAGGATCCCCAAGCTCTAGCTCATTTAGCAGGGCTAAACTTCTATCTGAGCC | 360 |
| *****    |                                                              |     |
| DN05     | TTTACGAGCAGGATC                                              | 375 |
| AP013106 | TTTACGAGCAGGATC                                              | 375 |
| X56186   | TTTACGAGCAGGATC                                              | 375 |
| GU985444 | TTTACGAGCAGGATC                                              | 375 |
| *****    |                                                              |     |

**Supplementary Figure S1.** Alignment of the *orf256* sequences of mtDNA, including those from D-N-05 alloplasmic line (sequenced in this work), *T. timopheevii* (AP013106), *T. timopheevii* x *T. aestivum* CMS line (X56186) and *T. aestivum* (GU985444).

|          |                                                            |     |
|----------|------------------------------------------------------------|-----|
|          | rps19f                                                     |     |
| AP013106 | TGCTCCGTACTCATTTACAATGGAAAACTCCTGTTGTTGTAAGATCACTGAAGGAAAG | 60  |
| X56186   | TGCTCCGTACTCATTTACAATGGAAAACTCCTGTTGTTGTAAGATCACTGAAGGAAAG | 60  |
| GU985444 | TGCTCCGTACTCATTTACAATGGAAAACTCCTGTTGTTGTAAGATCACTGAAGG---- | 56  |
| *****    |                                                            |     |
|          | rps19r                                                     |     |
| AP013106 | GTTGGTCATAAATTTGGAGAGTTTGCTTTTACACGGAGACGAAGACCCTAT        | 111 |
| X56186   | GTTGGTCATAAATTTGGAGAGTTTGCTTTTACACGGAGACGAAGACCCTAT        | 111 |
| GU985444 | -----TCATAAATTTGGAGAGTTTGCTTTTACACGGAGACGAAGACCCTAT        | 102 |
| *****    |                                                            |     |

**Supplementary Figure S2.** Alignment of the *rps-19-p* sequences of mtDNA. The samples corresponding to Acc. No are presented in the legend to Suppl.Fig.1. The primers used for PCR are indicated by arrows. No sequences were obtained in this work because of a short length of the PCR fragment.

|          |                                                                                    |     |
|----------|------------------------------------------------------------------------------------|-----|
| DQ195069 | TGTTTTAGATTTATACGACTTTTTTTCTCTGAGAAAGATTTATATGACTCTGACTGCTT                        | 60  |
| Tdic     | TGTTTTAGATTTATACGACTTTTTTTCTCTGAGAAAGATTTATATGACTCTGACTGCTT                        | 60  |
| DF05     | TGTTTTAGATTTATACGACTTTTTTTCTCTGAGAAAGATTTATATGACTCTGACTGCTT                        | 60  |
| D4105    | TGTTTTAGATTTATACGACTTTTTTTCTCTGAGAAAGATTTATATGACTCTGACTGCTT                        | 60  |
|          | *****                                                                              |     |
|          |  |     |
| DQ195069 | ATGTTTTTTGTTTCAACGTGGTTTCACCTTGTGATATGGATTGCCTTGATGACCAGGAAG                       | 120 |
| Tdic     | ATGTTTTTTGTTTCAACGTGGTTTCACCTTGTGATATGGATTGCCTTGATGAACAGGAAG                       | 120 |
| DF05     | ATGTTTTTTGTTTCAACGTGGTTTCACCTTGTGATATGGATTGCCTTGATGAACAGGAAG                       | 120 |
| D4105    | ATGTTTTTTGTTTCAACGTGGTTTCACCTTGTGATATGGATTGCCTTGATGAACAGGAAG                       | 120 |
|          | *****                                                                              |     |
| DQ195069 | AAGAAAGTGCAGGAGAAGCACTGGTCCTGATTCGGTTGCTGAAACCATCAAGAAGTGG                         | 180 |
| Tdic     | AAGAAAGTGCAGGAGAAGCACTGGTCCTGATTCGGTTGCTGAAACCATCAAGAAGTGG                         | 180 |
| DF05     | AAGAAAGTGCAGGAGAAGCACTGGTCCTGATTCGGTTGCTGAAACCATCAAGAAGTGG                         | 180 |
| D4105    | AAGAAAGTGCAGGAGAAGCACTGGTCCTGATTCGGTTGCTGAAACCATCAAGAAGTGG                         | 180 |
|          | *****                                                                              |     |

**Supplementary Figure S3.** Alignment of a part of the *Dreb-B1* sequences, isolated from *T. dicoccum* and alloplasmic lines D-41-05 and D-f-05. The corresponding sequence of *T. aestivum* was downloaded from NCBI database under the Acc. No DQ195069. The position of P40 primer used for AS-PCR is indicated. The characteristic SNP is localized at the 3'-end of the primer (see text). The start ATG-codon of translation is depicted by the vertical line with arrow.