

Table S1 Primer sequences, annealing temperatures, and expected PCR product sizes of candidate genes from locus at 7B. The primers were designed in this study to analyze the expression of candidate genes for maturity time in spring wheat panel.

| Gene ID | Primer name | Primer sequence (5'→3') | T _m (°C) | Amplicon length (bp) |
|---------------------------|-------------|---------------------------|---------------------|----------------------|
| <i>TraesCS7B02G391800</i> | 7B_391800_F | CGCAGCTAACTGACCTTGAG | 62 | 120 |
| | 7B_391800_R | GGATTCTGTTGTCCGTGACT | 62 | |
| <i>TraesCS7B02G396600</i> | 7B_396600_F | CCGGAGGTTTGCCTATAGAATTA | 62 | 101 |
| | 7B_396600_R | GTCTCCAAGTGAGATCGGAATC | 62 | |
| <i>TraesCS7B02G411800</i> | 7B_411800_F | GAACATTGAGACAGGCAAGAAC | 62 | 119 |
| | 7B_411800_R | CACCACCGCAAGACAATCTA | 62 | |
| <i>TraesCS7B02G401600</i> | 7B_401600_F | AGAAACATGGGTGGGCTATC | 62 | 82 |
| | 7B_401600_R | AAGGCCTTATGGCCCTTATC | 62 | |
| <i>TraesCS7B02G400600</i> | 7B_400600_F | GCGTCGGGAGCTTAGAGAT | 63 | 139 |
| | 7B_400600_R | TCCGGCACCGTCAAGTAT | 63 | |
| <i>TraesCS7B02G412200</i> | 7B_412200_F | CTGCCACTGAGGTTGAGCTT | 64 | 123 |
| | 7B_412200_R | CCACCCATCTGAAGGAGGTTT | 64 | |
| <i>TraesCS7B02G399700</i> | 7B_399700_F | CTTGCCAGGGAGGTGTATAG | 61 | 135 |
| | 7B_399700_R | ATCACCTCGTCCTCTGCC | 63 | |
| <i>TraesCS7B02G404300</i> | 7B_404300_F | GTCGTCTTCATCCGTTCCAGAG | 62 | 78 |
| | 7B_404300_R | TTTGCCGTTGTGTATCCAG | 63 | |
| <i>TraesCS7B02G395600</i> | 7B_395600_F | TGTTTCGCGTATGTCCGATAG | 62 | 109 |
| | 7B_395600_R | TTTCCTAGTTGTGCTAAGTAATGTG | 61 | |
| <i>TraesCS7B02G400500</i> | 7B_400500_F | TCTGCACAGCCGTAAGTA | 60 | 135 |
| | 7B_400500_R | GAGAAATCATTGTGATGGAAATC | 58 | |
| <i>TraesCS7B02G398700</i> | 7B_398700_F | AGACCTGAGCACCGTCTT | 63 | 91 |
| | 7B_398700_R | TAGAAGCGCAGATGACTCCA | 63 | |
| <i>TraesCS7B02G413400</i> | 7B_413400_F | GGGAGTAGTGCTCAACCTG | 61 | 135 |
| | 7B_413400_R | CGGTAGTGGTCTCCGTAT | 62 | |

Table S2 Primer sequences and expected PCR product sizes of reference genes to be tested used in the experiment aimed to analyzing expression of candidate genes for maturity time in spring wheat panel. The primer sequences are from articles dedicated to selecting reference genes with stable expression in wheat (see column “Reference”).

| Gene name | | Forward Primer (5' → 3') | Reverse Primer(5' → 3') | Amplicon | Reference |
|----------------------------|-----------|---------------------------|--------------------------|----------|-----------------------|
| Elongation factor 1-alpha | ELF1a_F | CAGATTGGCAACGGCTACG | CGGACAGCAAAACGACCAAG | 227 | Crismani et al., 2006 |
| 60S Ribosomal protein L18a | 60S_Rib | CAAGGAGTACCGTGACAC | GCGGGAACCTTGATCTTCG | 179 | Paolacci et al., 2009 |
| Ta.14126.1.S1_at | SAR | GAGTCTGCCACCCATTCGTAA | GACATGCCATAGGTTTCAGCGAC | 155 | Long et al., 2010 |
| Ta.7894.3.A1_at | MetAP1 | AGCAAGTTGTGACCCGAGGA | GGCGTCAGCAAATAGCAAGTG | 115 | Long et al., 2010 |
| Ta2291 | TaADP-RF | GCTCTCCAACAACATTGCCAAC | GCTTCTGCCTGTCACATACGC | 165 | Paolacci et al., 2009 |
| Ta2776 | RNaseLing | CGATTTCAGAGCAGCGTATTGTTG | AGTTGGTCGGGTCTCTTCTAAATG | 242 | Paolacci et al., 2009 |
| Ta54227 | CDCP | CAAATACGCCATCAGGGAGAACATC | CGCTGCCGAAACCACGAGAC | 227 | Paolacci et al., 2009 |

Table S3 Summary statistics for the maturity time detected during the phenotyping of 92 spring wheat varieties cultivated in the two experimental fields of ICG SB RAS in the Novosibirsk Region from 2005 to 2014 and 2018, spanning eleven years.

| | year 2005 | year 2006 | year 2007 | year 2008 | year 2009 | year 2010 | year 2011 | year 2012 | year 2013 | year 2014 | BLUE s | 2018 Field 1 | 2018 Field 2 |
|----------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|-----------|-----------------|-----------------|
| Min | 64 | 66 | 65 | 64 | 70 | 60 | 68 | 63 | 65 | 63 | 67.9 | 76 | 74 |
| max | 86 | 88 | 90 | 89 | 91 | 91 | 96 | 81 | 91 | 85 | 83 | 105 | 111 |
| range | 22 | 22 | 25 | 25 | 21 | 31 | 28 | 18 | 26 | 22 | 15.1 | 29 | 37 |
| sum | 6392 | 6606 | 6838 | 6360 | 7433 | 7178 | 7151 | 6290 | 6785 | 6378 | 6894.2 | 7780 | 8137 |
| median | 72 | 76 | 78 | 71.5 | 86 | 83 | 81 | 71 | 77 | 72 | 76.8 | 90 | 89 |
| mean | 72.64 | 75.07 | 77.7 | 72.27 | 84.47 | 81.57 | 81.26 | 71.48 | 77.1 | 72.48 | 76.6 | 90.74 | 88.45 |
| SE.mean | 0.42 | 0.52 | 0.45 | 0.5 | 0.48 | 0.51 | 0.49 | 0.36 | 0.41 | 0.42 | 0.32 | 0.76 | 0.78 |
| CI.mean | 0.84 | 1.04 | 0.89 | 1 | 0.95 | 1.02 | 0.97 | 0.71 | 0.82 | 0.84 | 0.64 | 1.52 | 1.56 |
| var | 15.64 | 24.16 | 17.59 | 22.41 | 20.07 | 23.28 | 21.02 | 11.29 | 14.85 | 15.63 | 9.46 | 50.01 | 57.13 |
| std.dev | 3.95 | 4.91 | 4.19 | 4.73 | 4.48 | 4.83 | 4.59 | 3.36 | 3.85 | 3.95 | 3.08 | 7.08 | 7.56 |
| coef.var | 0.05 | 0.07 | 0.05 | 0.07 | 0.05 | 0.06 | 0.06 | 0.05 | 0.05 | 0.05 | 0.04 | 0.078 | 0.085 |

SE.mean - standard error on the mean, CI.mean - confidence interval of the mean, var – variance, std.dev - standard deviation, coef.var - variation coefficient

Table S4 Analysis of variance (ANOVA) on the data for the phenotyping of the maturity time of 92 spring wheat varieties cultivated in the two experimental fields of ICG SB RAS in the Novosibirsk Region from 2005 to 2014 and 2018.

| | Df | Sum Sq | Mean | Sq F | value Pr(>F) |
|-----------|-----|--------|--------|---------|--------------|
| Cultivar | 89 | 8417 | 94.6 | 9.568 | <2e-16 *** |
| Year | 9 | 17161 | 1906.7 | 192.893 | <2e-16 *** |
| Residuals | 801 | 7918 | 9.9 | | |

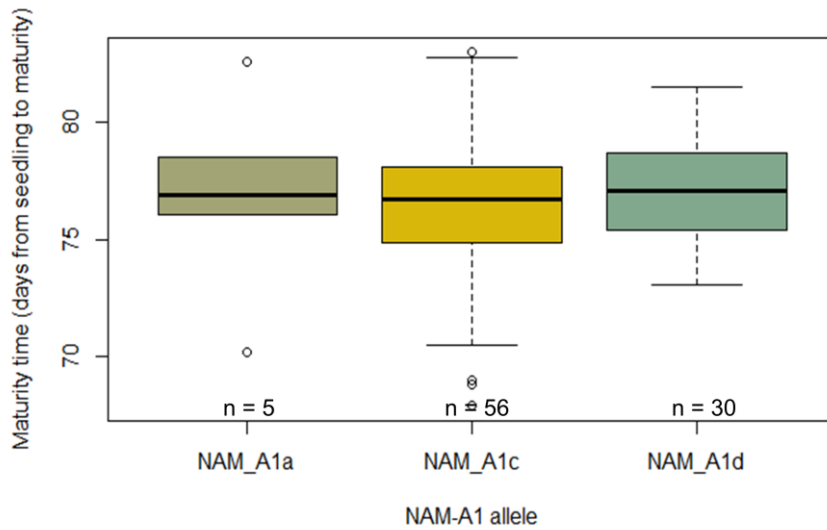


Fig. S1 Boxplots of the maturity time variation for genotypes showing different alleles of *NAM-A1* gene. “n” denotes the number of samples in each group.

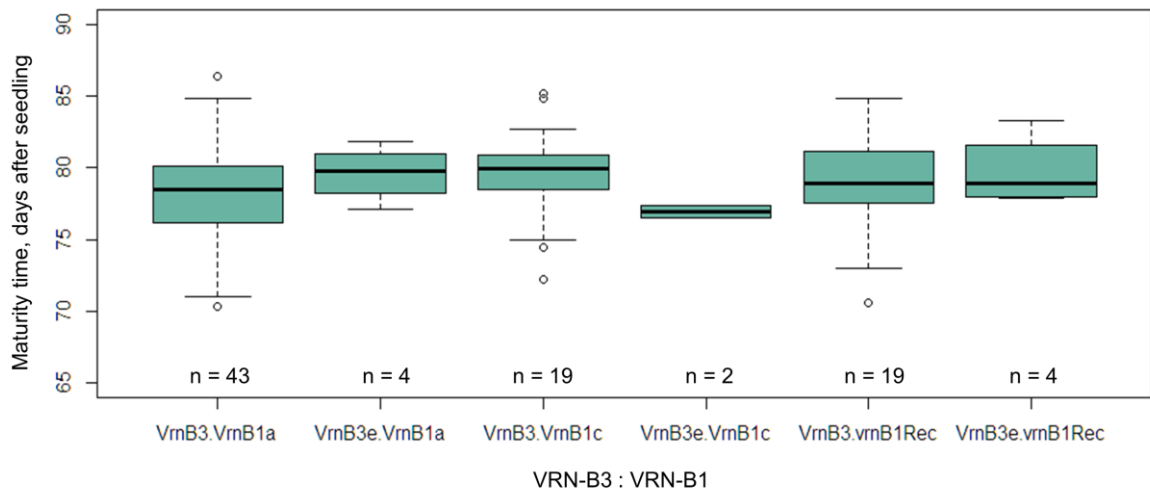


Fig. S2 Boxplots of the maturity time variation for genotypes showing different allele combinations of *Vrn-B1* and *Vrn-B3*. “n” denotes the number of samples in each group.

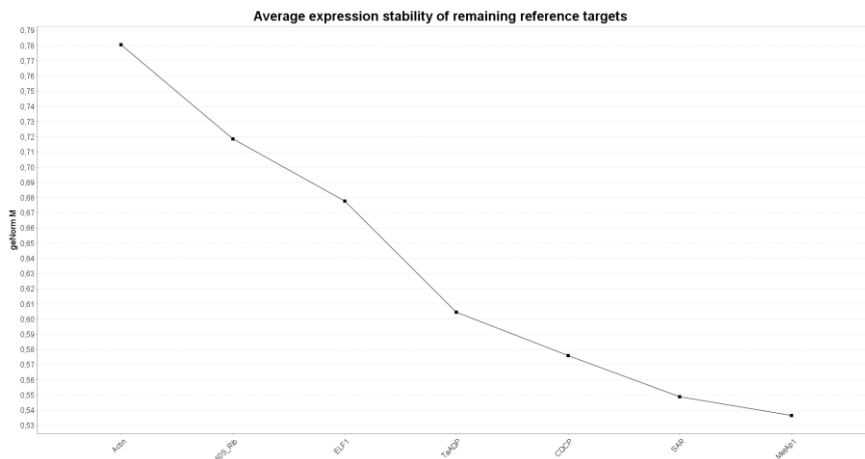


Fig. S3. Expression stability of reference genes, evaluated with geNorm algorithm.

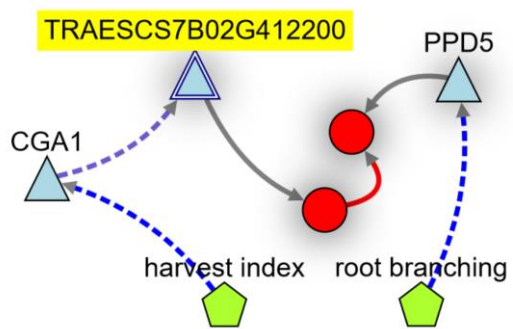


Fig. S4. Gene networks of *TraesCS7B02G412200* (KnetMiner).

Table S5. Annotation of candidate genes based on the functional annotation by IWGSC RefSeq v1.0 and expression with the use of the developmental time course data of the common wheat cultivar Azhurnaya (Ramírez-González et al. 2018).

| Gene ID | Peak of the expression | Blast-Hit-Accession | Human-Readable-Description | Pfam-IDs-(Description) | Interpro-IDs-(Description) |
|---------------------------|------------------------------------------------------------------------------|--------------------------------|---------------------------------------------------------|----------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <i>TraesCS7B02G391800</i> | in the flag leaf at the flowering stage | tr A0A0K9Q033 A0A0K9Q033_ZOSMR | Basic-leucine zipper (BZIP) transcription factor family | PF00170: bZIP transcription factor | IPR004827: Basic-leucine zipper domain |
| <i>TraesCS7B02G396600</i> | in flag leaf and flag leaf sheath from heading to the maturity | tr B9SUC9 B9SUC9_RICCO | Receptor-kinase, putative | PF13855: Leucine rich repeat; PF00560: Leucine Rich Repeat; PF07714: Protein tyrosine kinase | IPR000719: Protein kinase domain; IPR001245: Serine-threonine/tyrosine-protein kinase, catalytic domain; IPR001611: Leucine-rich repeat; IPR008271: Serine/threonine-protein kinase, active site; IPR011009: Protein kinase-like domain; IPR017441: Protein kinase, ATP binding site; IPR032675: Leucine-rich repeat domain, L domain-like |
| <i>TraesCS7B02G411800</i> | in flag leaf and flag leaf sheath from heading to the maturity | tr A0A1D6C995 A0A1D6C995_WHEAT | Patatin | PF01734: Patatin-like phospholipase | IPR002641: Patatin-like phospholipase domain; IPR016035: Acyl transferase/acyl hydrolase/lysophospholipase |
| <i>TraesCS7B02G401600</i> | in flag leaf during the anthesis and then in embryo proper in ripening stage | tr C1MYP8 C1MYP8_MICPC | Mitochondrial carrier family | PF00153: Mitochondrial carrier protein | IPR002067: Mitochondrial carrier protein; IPR018108: Mitochondrial substrate/solute carrier; IPR023395: Mitochondrial carrier domain |
| <i>TraesCS7B02G400600</i> | in flag leaf from heading to the maturity | tr C7E143 C7E143_ALLCE | CONSTANS-like protein | PF00643: B-box zinc finger; PF06203: CCT motif | IPR000315: B-box-type zinc finger; IPR010402: CCT domain; IPR011011: Zinc finger, FYVE/PHD-type |
| <i>TraesCS7B02G412200</i> | in flag leaf since the flag leaf stage | tr A0A0F7GYK8 A0A0F7GYK8_9ASPA | Photosystem II reaction center PsbP family protein | PF01789: PsbP | IPR002683: PsbP family; IPR016123: Mog1/PsbP, alpha/beta/alpha sandwich |
| <i>TraesCS7B02G399700</i> | in flag leaf since heading to milk grain stage | AT5G38350.1 | Disease resistance protein (NBS-LRR class) family | PF00931: NB-ARC domain | IPR002182: NB-ARC; IPR003593: AAA+ ATPase domain; IPR011991: Winged helix-turn-helix DNA-binding domain; IPR027417: P-loop containing nucleoside triphosphate hydrolase; IPR032675: Leucine-rich repeat domain, L domain-like |
| <i>TraesCS7B02G404300</i> | in flag leaf since full boot to milk grain stage | tr A0A164TMY6 A0A164TMY6_DAUCA | UDP-glycosyltransferase | PF00201: UDP-glucuronosyl and UDP-glucosyl transferase | IPR002213: UDP-glucuronosyl/UDP-glucosyltransferase |
| <i>TraesCS7B02G395600</i> | in flag leaf in full boot stage and then in milk grain stage | tr S4YYQ6 S4YYQ6_HORVV | NAD(P)H-quinone oxidoreductase subunit I, chloroplastic | PF00037: 4Fe-4S binding domain | IPR017896: 4Fe-4S ferredoxin-type, iron-sulphur binding domain; IPR017900: 4Fe-4S ferredoxin, iron-sulphur binding, conserved site |
| <i>TraesCS7B02G400500</i> | in flag leaf in milk grain ripening and heading stage | tr A0A1D6D8L7 A0A1D6D8L7_WHEAT | Protein DETOXIFICATION | PF01554: MatE | IPR002528: Multi antimicrobial extrusion protein |
| <i>TraesCS7B02G398700</i> | in flag leaf in ripening | AT5G02220.1 | cyclin-dependent kinase inhibitor | | |
| <i>TraesCS7B02G413400</i> | in flag leaf in heading stage | tr A0A0K9P8I3 A0A0K9P8I3_ZOSMR | Chaperone protein dnaJ | PF00226: DnaJ domain | IPR001623: DnaJ domain |