**New Phytologist Supporting Information**

Article title **Sequence based mapping identifies a candidate transcription repressor underlying awn suppression at the *B1* locus in wheat**

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The following supporting information is available for this article:

**Fig. S1.** Expression of *TraesCS5A02G542800* and *TraesCS4D01G476700LC* in different tissues. Expression is quantified in transcripts per million (TPM), representing raw reads scaled by gene length and total reads sequenced (Source: https://wheat.pw.usda.gov/WheatExp/).

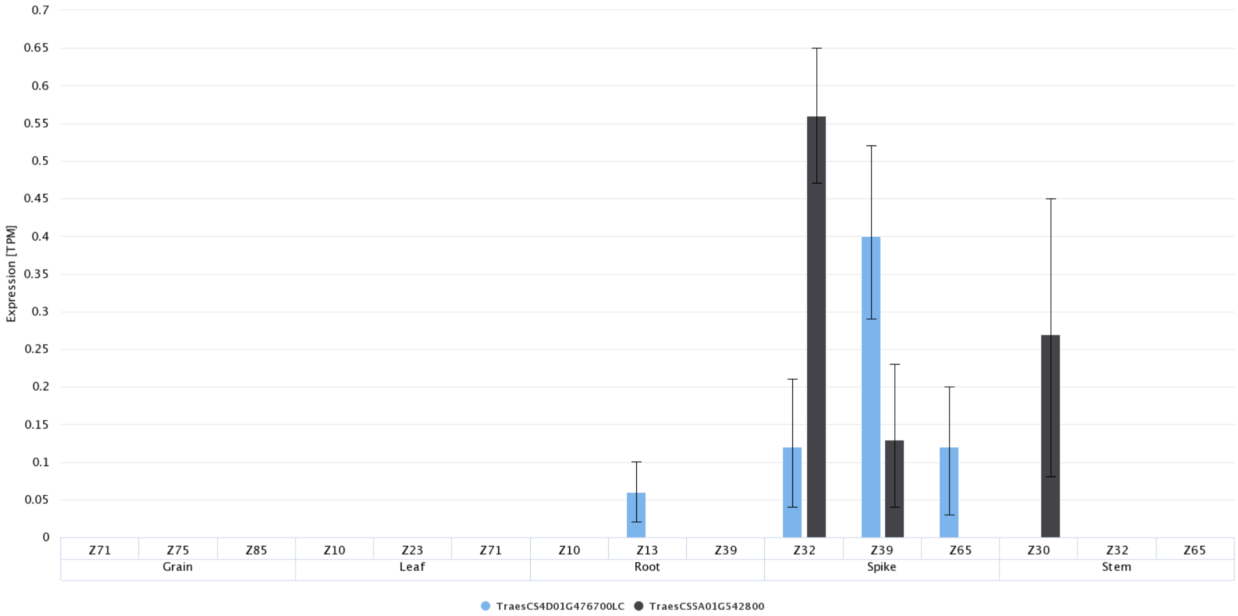
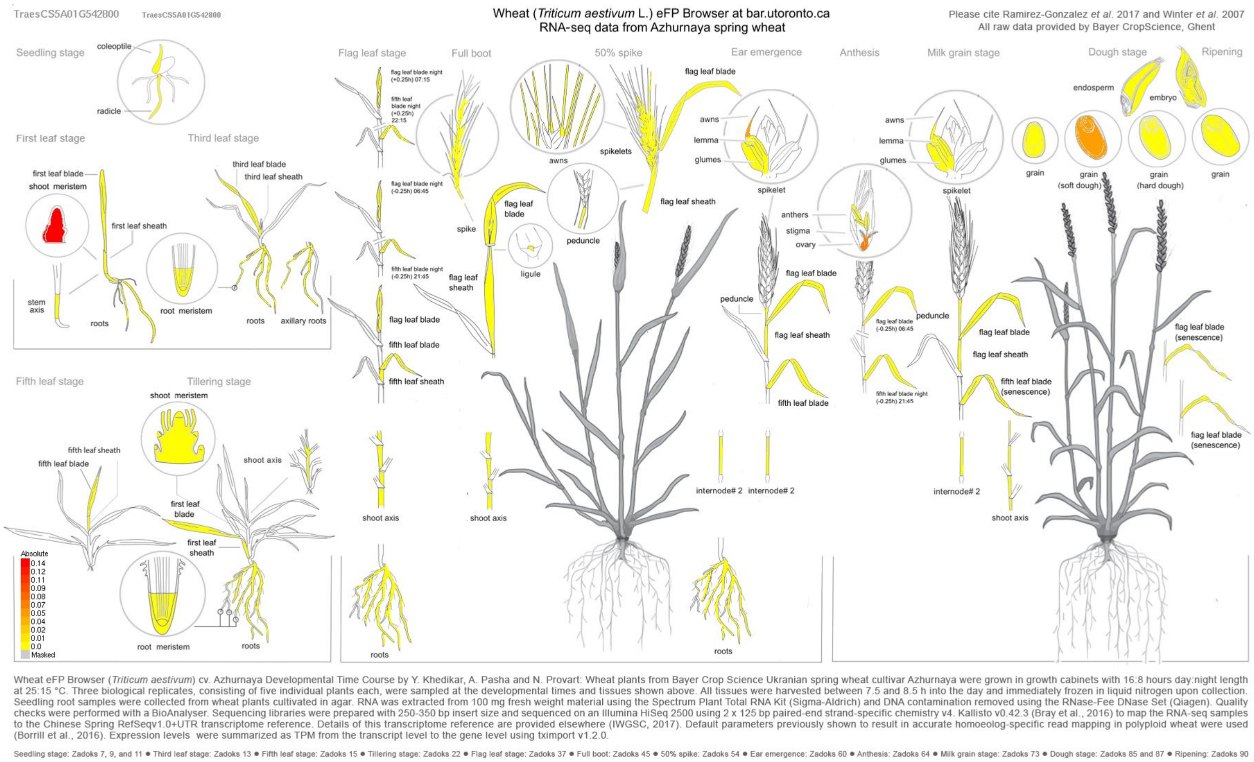


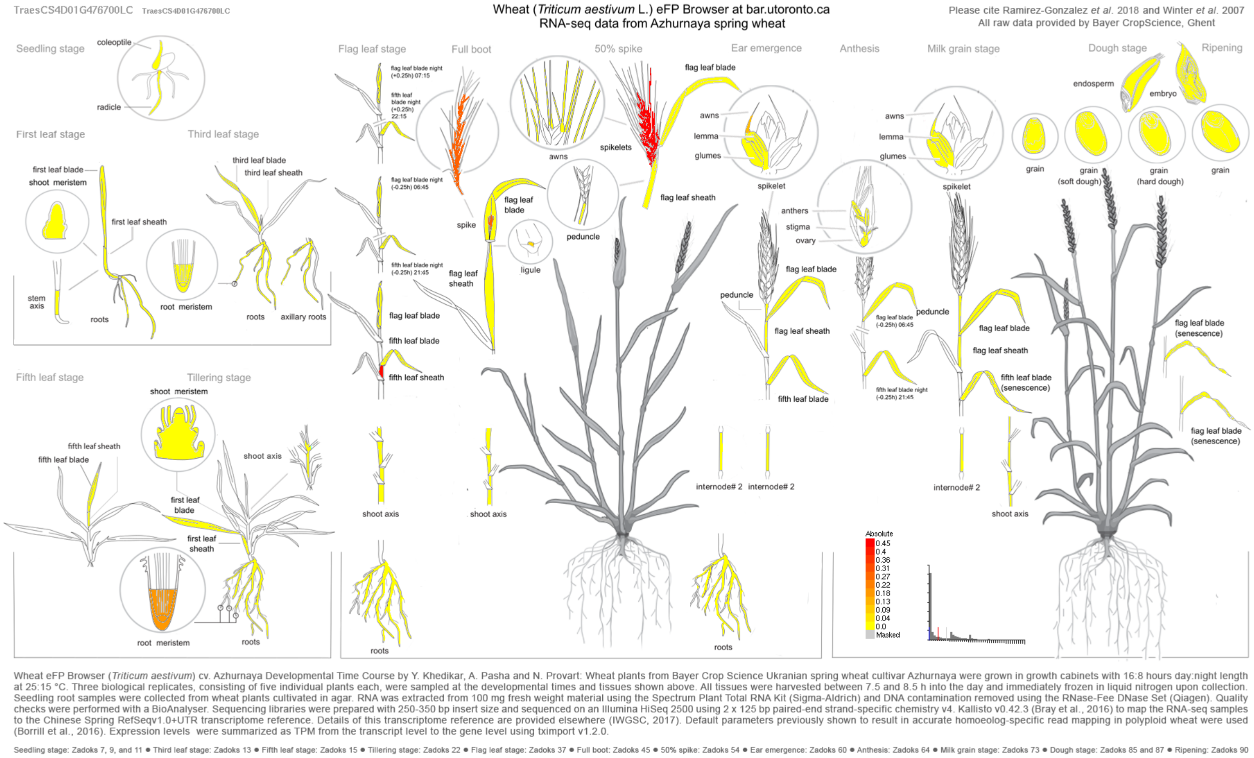
**Fig. S2.** Expression patterns of *TraesCS5A02G542800*. Wheat eFP browser output displaying regions with no or low expression of *B1*candidate gene *TraesCS5A02G542800* (yellow), and regions with higher expression (orange to red) in the awned spring wheat *Azhurnaya*. The *TraesCS5A02G542800* zinc finger protein is primarily expressed within the developing spike, as well as expressed in the awns, developing grain, and ovary. Source: (<u>http://bar.utoronto.ca/efp_wheat/cgi-bin/efpWeb.cgi</u>) (Ramirez-Gonazales *et al.*, 2018, Winter *et al.*, 2007).



Wheat eFP Browser (*Triticum aestivum*) cv. Azhurnaya Developmental Time Course by Y. Khedikar, A. Pasha and N. Provart: Wheat plants from Bayer Crop Science Ukranian spring wheat cultivar Azhurnaya were grown in growth cabinets with 16:8 hours day:night length at 25:15 °C. Three biological replicates, consisting of five individual plants each, were sampled at the developmental times and tissues shown above. All tissues were harvested between 7.5 and 8.5 h into the day and immediately frozen in liquid nitrogen upon collection. Seedling root samples were collected from wheat plants cultivated in agar. RNA was extracted from 100 mg fresh weight material using the Spectrum Plant Total RNA Kit (Sigma-Aldrich) and DNA contamination removed using the RNase-Fee DNase Set (Qiagen). Quality checks were performed with a BioAnalyser. Sequencing libraries were prepared with 250-350 bp insert size and sequenced on an Illumina HiSeq 2500 using 2 x 125 bp paired-end strand-specific chemistry v4. Kallisto v0.42.3 (Bray et al., 2016) to map the RNA-seq samples to the Chinese Spring RefSeqv1.0+UTR transcriptome reference. Details of this transcriptome reference are provided elsewhere (IWGSC, 2017). Default parameters previously shown to result in accurate homoeolog-specific read mapping in polyploid wheat were used (Borrill et al., 2016). Expression levels were summarized as TPM from the transcript level to the gene level using tximport v1.2.0.

Seedling stage: Zadoks 7, 9, and 11 ● Third leaf stage: Zadoks 13 ● Fifth leaf stage: Zadoks 15 ● Tillering stage: Zadoks 22 ● Flag leaf stage: Zadoks 37 ● Full boot: Zadoks 45 ● 50% spike: Zadoks 54 ● Ear emergence: Zadoks 60 ● Anthesis: Zadoks 64 ● Milk grain stage: Zadoks 73 ● Dough stage: Zadoks 85 and 87 ● Ripening: Zadoks 90

**Fig. S3.** Expression patterns of *TraesCS4D01G476700LC*. Wheat eFP browser output displaying regions with no or low expression of *TraesCS4D01G476700LC* (yellow), and regions with higher expression (orange to red) in the awned spring wheat *Azhurnaya*. *TraesCS4D01G476700LC* is primarily expressed in the spike after the development of awn tissue. Source: (http://bar.utoronto.ca/efp_wheat/cgi-bin/efpWeb.cgi) (Ramirez-Gonazales *et al.*, 2018, Winter *et al.*, 2007).


TraesCS4D01G476700LC TraesCS4D01G476700LC

Wheat (*Triticum aestivum* L.) eFP Browser at bar.utoronto.ca
RNA-seq data from Azhurnaya spring wheat

Please cite Ramirez-Gonzalez *et al*. 2018 and Winter *et al*. 2007
All raw data provided by Bayer CropScience, Ghent

Wheat eFP Browser (*Triticum aestivum*) cv. Azhurnaya Developmental Time Course by Y. Khedikar, A. Pasha and N. Provart: Wheat plants from Bayer Crop Science Ukranian spring wheat cultivar Azhurnaya were grown in growth cabinets with 16:8 hours day:night length at 25:15 °C. Three biological replicates, consisting of five individual plants each, were sampled at the developmental times and tissues shown above. All tissues were harvested between 7.5 and 8.5 h into the day and immediately frozen in liquid nitrogen upon collection. Seedling root samples were collected from wheat plants cultivated in agar. RNA was extracted from 100 mg fresh weight material using the Spectrum Plant Total RNA Kit (Sigma-Aldrich) and DNA contamination removed using the RNase-Fee DNase Set (Qiagen). Quality checks were performed with a BioAnalyser. Sequencing libraries were prepared with 250-350 bp insert size and sequenced on an Illumina HiSeq 2500 using 2 x 125 bp paired-end strand-specific chemistry v4. Kallisto v0.42.3 (Bray et al., 2016) to map the RNA-seq samples to the Chinese Spring RefSeqv1.0+UTR transcriptome reference. Details of this transcriptome reference are provided elsewhere (IWGSC, 2017). Default parameters previously shown to result in accurate homoeolog-specific read mapping in polyploid wheat were used (Borrill et al., 2016). Expression levels were summarized as TPM from the transcript level to the gene level using tximport v1.2.0.

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**Fig. S4.** Expression patterns of *TraesCS5A01G542700*. Wheat eFP browser output displaying regions with no or low expression of predicted gene *TraesCS5A01G542700* (yellow), and regions with higher expression (orange to red) in the awned spring wheat *Azhurnaya*. *TraesCS5A01G542700* is annotated as universal stress protein family with protein kinase domain and expressed in most tissues, with higher expression in the spike and in grain tissues after the development of awns. Source: (http://bar.utoronto.ca/efp_wheat/cgi-bin/efpWeb.cgi) (Ramirez-Gonazales *et al.*, 2018, Winter *et al.*, 2007).

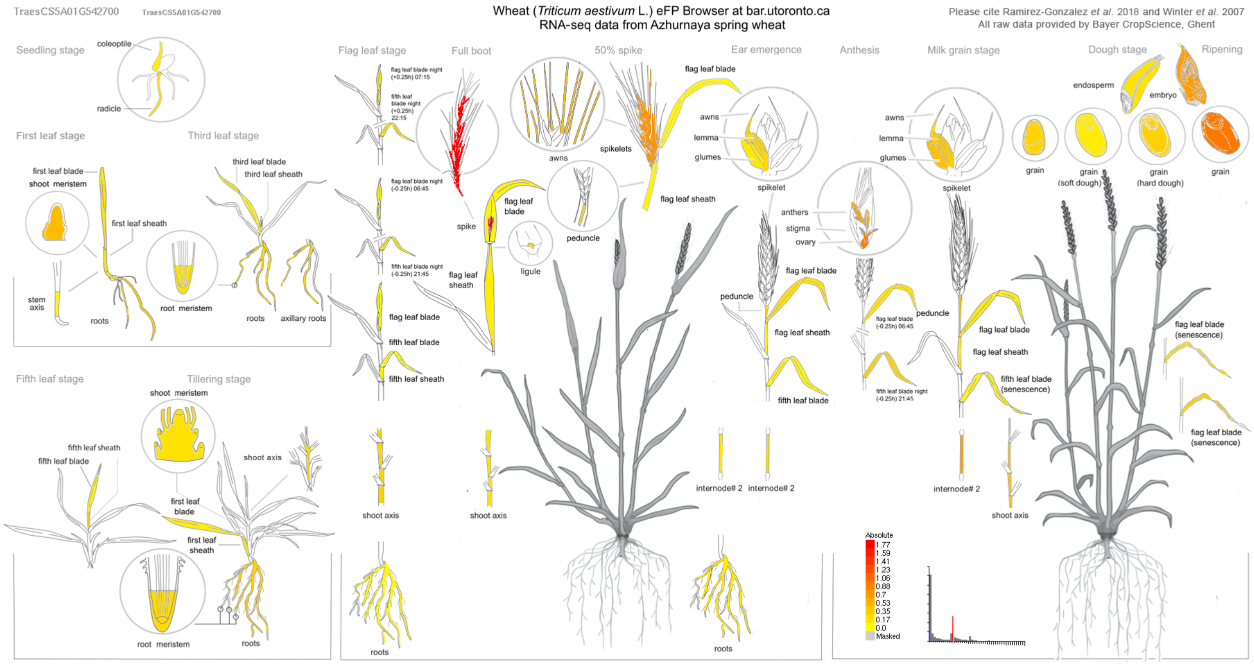

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**Fig. S5.** Expression of *TraesCS5A02G542700* in apical meristems of awned and awnless wheat. (a) Expression of *TraesCS5A02G542700* in apical meristems of awned (blue) and awnless (red) wheat plants at different developmental stages where 1 = younger meristems and 4 = older meristems. Number of biological replicates (n) is given per group, with three technical replications per biological replicate. (b) Representative spikes at each developmental stage.

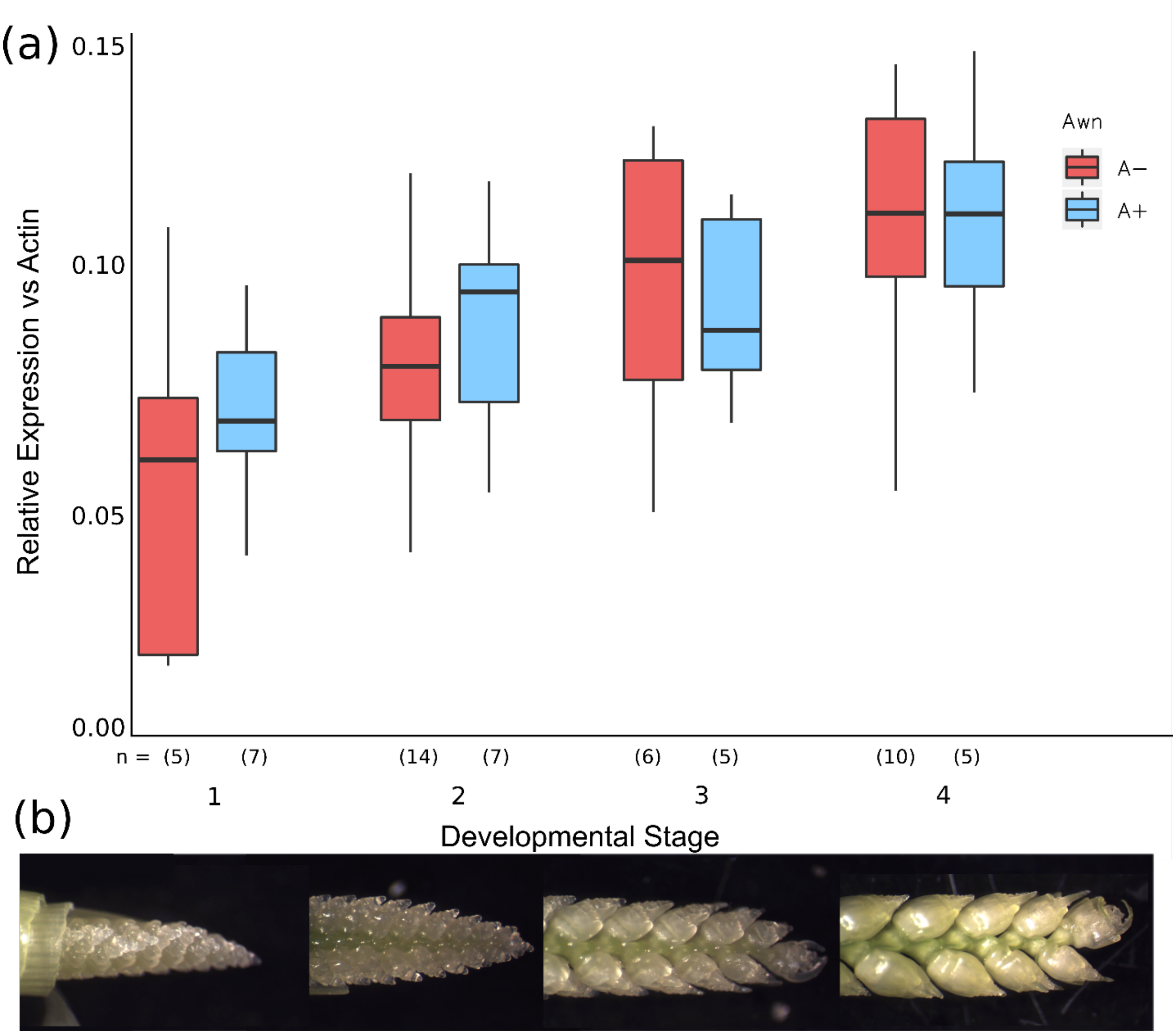

**Table S1.** Positions and descriptions of KASP markers (NA where information non-applicable).

| Name | SNP Position | Type | Source | SNP | Gene Id | Annotated Functional Domains |
|---|---|---|---|---|---|---|
| 5A814 | 696993814 | Intergenic | GBS | G/C | NA | NA |
| 5A78871 | 697887148 | Intron variant | Exome capture | G/A | TraesCS5A02G540400 | Formyl transferase |
| 5A208800 | 698208800 | Intron variant | Exome capture | A/C | TraesCS5A02G541400 | SNF2 family domain, Helicase conserved domain |
| BW8226_227 | 698508163 | Missense exon 2 | Illuminia SNP array (Mackay et. al 2014) | T/G | TraesCS5A02G542600 | Sugar -and other - Transporter |
| 5A13057 | 698513057 | Intron variant | Exome Capture | T/G | TraesCS5A02G542700 | Universal stress protein family, protein kinase |
| 5A15019 | 698515019 | Intron variant | Exome Capture | A/G | TraesCS5A02G542700 | Universal stress protein family, protein kinase |
| 5A16541 | 698516541 | Missense exon 9 | Sequence Alignment | A/G | TraesCS5A02G542700 | Universal stress protein family, protein kinase |
| 5A28417 | 698528417 | Upstream | GBS | T/C | TraesCS5A02G542800 | C2H2 Zinc Finger |
| 5A29396 | 698529396 | Downstream | Sequence alignment | G/A | TraesCS5A02G542800 | C2H2 Zinc Finger |
| 5A32641 | 698532641 | Intergenic | Sequence alignment | Del | NA | NA |
| 5A91913 | 698591913 | Intergenic | Sequence alignment | C/T | NA | NA |
| 5A10592 | 698610592 | Intergenic | Sequence alignment | A/G | NA | NA |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 5A13482 | 698613482 | Intergenic | Sequence alignment | AA/CT | NA | NA |
| 5A14919 | 698614919 | Intergenic | Sequence alignment | Del | NA | NA |
| 5A30334 | 698630334 | Synonymous variant | Exome capture | C/T | TraesCS5A02G542900 | F-box-like, Armadillo -beta-catenin-like repeat |
| 5A48195 | 702748195 | Upstream | Exome capture | T/G | TraesCS5A02G548800 | Helicase domain, P-loop_NTPase superfamily, EBV_NA3 super family |
| 5A70348 | 705570348 | Missense | Exome capture | C/G | TraesCS5A02G552800 | Domain of unknown function -DUF 4220 -, DUF594 |

**Table S2:** Sequences of KASP markers.

| Name | Allele | Sequence |
|---|---|---|
| 5A814 | A1 | GAAGGTGACCAAGTTCATGCTAAATTCCTGCTAGACACTCGTGAG |
|  | A2 | GAAGGTCGGAGTCAACGGATTAAATTCCTGCTAGACACTCGTGAC |
|  | C | GTTTGCGCGAATCCTGCAGCGAA |
| 5A78871 | A1 | GAAGGTGACCAAGTTCATGCTGTGCCGCCTCCATTTCCCAC |
|  | A2 | GAAGGTCGGAGTCAACGGATTCGTGCCGCCTCCATTTCCCAT |
|  | C | CCGTCGAACAGGTGTCGGAGC |
| 5A208800 | A1 | GAAGGTGACCAAGTTCATGCTCCTTCCCCGCTGCCCGA |
|  | A2 | GAAGGTCGGAGTCAACGGATTCCTTCCCCGCTGCCCGC |
|  | C | GTGCTCAAGGAGAAGCTAAGAGGTA |
| 5A13057 | A1 | GAAGGTGACCAAGTTCATGCTGGTCGATCCATCCATTCATTCATGA |
|  | A2 | GAAGGTCGGAGTCAACGGATTGTCGATCCATCCATTCATTCATGC |
|  | C | CCGTTTCATGTTCTAGACTGAATCTGAAT |
| 5A15019 | A1 | GAAGGTGACCAAGTTCATGCTATGAACATCTTCATTGAAACTATATTTACACA |
|  | A2 | GAAGGTCGGAGTCAACGGATTGAACATCTTCATTGAAACTATATTTACACG |
|  | C | GAACCCTGCAATTAACCAAAACAAAAGCTA |

| | | |
|---|---|---|
| 5A28417 | A1 | GAAGGTGACCAAGTTCATGCTTGCGGCCGCTCAG |
| | A2 | GAAGGTCGGAGTCAACGGATTGCATGCTTGCGGCCGCTCAA |
| | C | GACAGTAATAATGCTGCAGTAGATGTGTA |
| 5A29396 | A1 | GAAGGTGACCAAGTTCATGCTGCCTAGAGACAAAAATAAAGTTATTATTATTC |
| | A2 | GAAGGTCGGAGTCAACGGATTGGCCTAGAGACAAAAATAAAGTTATTATTATTT |
| | C | ACCATTGCAATTATAGCACCAAGATATAAA |
| 5A32641 | A1 | GAAGGTGACCAAGTTCATGCTAGCTACGGGCCCACTTRGACA |
| | A2 | GAAGGTCGGAGTCAACGGATTCTACGGGCCCACTTRGACG |
| | C | CCTGCGGGGCTCCCAGCAA |
| 5A91913 | A1 | GAAGGTGACCAAGTTCATGCTCACATGCAACACACCACTTGTCA |
| | A2 | GAAGGTCGGAGTCAACGGATTCACATGCAACACACCACTTGTCG |
| | C | TTCACACTCCTACTTCCCCAGGTT |
| 5A613482 | A1 | GAAGGTGACCAAGTTCATGCTTTCCAGCAAAGTTGGAAGTACAATTTA |
| | A2 | GAAGGTCGGAGTCAACGGATTCCAGCAAAGTTGGAAGTACAATTTC |
| | C | TAGTAAAGCGCGTCCAACCCTTCTA |
| 5A614989 | A1 | GAAGGTGACCAAGTTCATGCTGATTAAGATATTCAATTTTGGATTTGATTCATA |

| | | |
|---|---|---|
| | A2 | GAAGGTCGGAGTCAACGGATTAAGATATTCAATTTTGGATTTGATTCATG |
| | C | GATCAAAATTGAAAGCGTTGATCTGGTCAA |
| 5A610592 | A1 | GAAGGTGACCAAGTTCATGCTATACACGGCTTTCCACAATTAGTTGT |
| | A2 | GAAGGTCGGAGTCAACGGATTACACGGCTTTCCACAATTAGTTGC |
| | C | CCCTAACTAACATATAGCCATGTGCAAT |
| 5A30334 | A1 | GAAGGTGACCAAGTTCATGCTCTTCGAGTGGCAAGCGCAAC |
| | A2 | GAAGGTCGGAGTCAACGGATTCTCTTCGAGTGGCAAGCGCAAT |
| | C | CCATGTGGGTTGGTCTCAGGGAT |
| 5A48195 | A1 | GAAGGTGACCAAGTTCATGCTGGTTTCTTCAGAAAATGGAGGTCGA |
| | A2 | GAAGGTCGGAGTCAACGGATTGTTTCTTCAGAAAATGGAGGTCGC |
| | C | CTTCATTGATGACCTCCCCATCTTTATAT |
| 5A70348 | A1 | GAAGGTGACCAAGTTCATGCTGCGGTCTTGCAGGATGCTGAC |
| | A2 | GAAGGTCGGAGTCAACGGATTGCGGTCTTGCAGGATGCTGAG |
| | C | GGGGTAGCCATACTTCCTCTATAGAT |
| BW8226_227 | A1 | CGTCCATGGAGTCGTTCCTCAAT |
| | A2 | GTCCATGGAGTCGTTCCTCAAG |
| | C | GTGGTACACGTCCGGGAAGAAT |

**Table S3**. Haplotypes and awn status of sequenced lines. Observed haplotypes and geographic origin of accessions selected for sequencing of B1 and the surrounding region.

| Name | Haplotype | Origin | Awns |
|---|---|---|---|
| SS_MPV-57 | Hap8 | Virginia | - |
| LA-95135 | Hap1 | Louisiana | + |
| AR05055-1-1 | Hap3 | Arkansas | + |
| Echinoides | Hap3 | Afghanistan | + |
| Ideal | Hap3 | Denmark | + |
| Sandu 22 | Hap6 | Romania | + |
| Tadzyksaja 13 | Hap8 | Tajikstan | - |
| Winter Bearded | Hap8 | UK | - |
| IWA 8613594 | Hap8 | Iran | - |
| IWA 8606785 | Hap3 | Iran | + |

**Table S4.** Sequences of RT-qPCR markers. Sequences for qPCR primers used for quantifying gene expression.

| Name | Sequence |
|---|---|
| Actin-SYBR-F1<br>(Li *et al.*, 2013) | ATGGAAGCTGCTGGAATCCAT |
| Actin-SYBR-R1<br>(Li *et al.*, 2013) | CCTTGCTCATACGGTCAGCAATAC |
| B1_24_F | GGAGATGGAAGAGGGGCTCGAT |
| B1_8_R | TTGAAGCTGCGTGAGCAGTAGG |
| 2700_exon9_F | CGGAACTGGGTCTAATGGGACT |
| 2700_exon9_R | CTTGATTGAAATGCTTGGTACTGGAGG |

**Table S5.** SNPs significantly associated with awn suppression. Genome position and LOD scores of markers significantly associated with presence or absence of awns in association mapping panel of 640 soft red winter wheat lines. Most significant marker in the region is noted in bold font.

| SNP | maf | FDR Adjusted P-values |
|---|---|---|
| S5A_681455268 | 0.163964 | 0.000321 |
| S5A_684942630 | 0.320721 | 3.43E-07 |
| S5A_685141655 | 0.368468 | 7.79E-06 |
| S5A_690417237 | 0.083784 | 1.56E-09 |
| S5A_693326887 | 0.227027 | 0.000183 |
| S5A_695581531 | 0.451351 | 2.75E-08 |
| S5A_696479493 | 0.477477 | 0.000153 |
| S5A_696993814 | 0.446847 | 1.11E-08 |
| S5A_697552811 | 0.266667 | 1.56E-09 |
| S5A_697590026 | 0.252252 | 7.37E-08 |
| S5A_698003176 | 0.283784 | 3.21E-06 |
| S5A_698127281 | 0.285586 | 6.38E-07 |
| S5A_698225912 | 0.263964 | 1.05E-07 |
| S5A_698320453 | 0.257658 | 2.35E-08 |
| **S5A_698528417** | **0.404505** | **7.19E-57** |
| S5A_699803948 | 0.308108 | 2.32E-16 |
| S5A_700181210 | 0.252252 | 2.63E-09 |
| S5A_700435349 | 0.097297 | 6.16E-14 |
| S5A_702633797 | 0.223423 | 4.09E-05 |

| | | |
|---|---|---|
| S5A_702908675 | 0.227027 | 0.001581 |
| S5A_703364169 | 0.222523 | 0.001969 |
| S5A_704142049 | 0.233333 | 0.003892 |
| S5A_705293051 | 0.100901 | 3.16E-09 |
| S5A_705351694 | 0.102703 | 1.11E-08 |
| S5A_705365208 | 0.097297 | 1.56E-09 |
| S5A_706065949 | 0.276577 | 8.60E-06 |
| S5A_706487909 | 0.407207 | 1.70E-08 |
| S5A_706574241 | 0.384685 | 1.33E-08 |
| S5A_706673002 | 0.338739 | 2.87E-07 |
| S5A_706705101 | 0.285586 | 1.94E-06 |

**Table S6.** QTL results for yield components in LxM population. Location of significant QTL and estimated effects for thousand kernel weight (TKW), estimated test weight, spikelets per spike (SPS), kernel width (K Width), kernel length (K Length), kernel area (K Area) from data collected in the field in 2018 or in the greenhouse (GH) in 2017. Data was collected in the field in Raleigh in 2018 for most traits, and in Raleigh and Kinston, North Carolina in 2018 for spikelets per spike.

| **Trait** | **Exp.** | **Chr** | **LOD** | **Peak Marker** | **cM** | **Mean** | **Effect** | **SE** |
|---|---|---|---|---|---|---|---|---|
| TKW (g) | Field | 4D | 33.76 | RhtD1 | 13 | 27.68 | -2.56 | 0.19 |
| TKW (g) | Field | 3D | 7.4 | S3D_476608044 | 219 | 27.68 | 1.09 | 0.21 |
| TKW (g) | Field | 5A | 6.51 | Awns | 269 | 27.68 | 0.88 | 0.17 |
| TKW (g) | Field | 7A | 4.22 | S7A_71631668 | 82 | 27.68 | 0.79 | 0.19 |
| TKW (g) | GH | 4D | 23.24 | RhtD1 | 12 | 28.78 | -3.53 | 0.33 |
| TKW (g) | GH | 2D | 8.1 | PpdD1 | 60 | 28.78 | 1.99 | 0.32 |
| TKW (g) | GH | 5A | 4.06 | S5A_698528417 | 269 | 28.78 | 1.47 | 0.31 |
| Test Weight (g) | Field | 4D | 33.66 | RhtD1 | 12 | 7.91 | -0.42 | 0.03 |
| Test Weight (g) | Field | 7A | 6.58 | S7A_672150738 | 187 | 7.91 | 0.18 | 0.03 |

|  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|
| Test Weight (g) | Field | 5A | 5.56 | S5A_698528417 | 269 | 7.91 | 0.15 | 0.03 |
| SPS | Field | 7A | 16.89 | S7A_673996636 | 186 | 20.4 | -0.51 | 0.05 |
| SPS | Field | 2D | 9.11 | PpdD1 | 59 | 20.4 | 0.41 | 0.06 |
| SPS | Field | 5A | 8.44 | S5A_698528417 | 269 | 20.4 | -0.37 | 0.05 |
| SPS | Field | 4D | 6.99 | RhtD1 | 14 | 20.4 | 0.35 | 0.06 |
| SPS | Field | 2B | 5.47 | S2B_600741549 | 108 | 20.4 | 0.24 | 0.05 |
| SPS | Field | 4B | 4.31 | S4B_34025485 | 54 | 20.4 | 0.21 | 0.05 |
| SPS | GH | 2D | 25.12 | PpdD1 | 60 | 17.7 | 1.07 | 0.09 |
| SPS | GH | 4D | 10.6 | RhtD1 | 12 | 17.7 | -0.77 | 0.09 |
| SPS | GH | 2B | 9.08 | S2B_642534505 | 110 | 17.7 | 0.65 | 0.09 |
| SPS | GH | 5A | 5.27 | S5A_698528417 | 269 | 17.7 | -0.48 | 0.09 |
| SPS | GH | 5B | 5.1 | S5B_517797845 | 85 | 17.7 | -0.66 | 0.13 |
| K Width (mm) | Field | 4D | 35.13 | RhtD1 | 12 | 2.98 | -0.09 | 0.01 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| K Width (mm) | Field | 6A | 5.75 | S6A_115348315 | 69 | 2.98 | 0.04 | 0.01 |
| K Width (mm) | Field | 5A | 5.56 | S5A_73816555 | 58 | 2.98 | 0.03 | 0.01 |
| K Width (mm) | Field | 3D | 4.98 | S3D_496955493 | 229 | 2.98 | 0.03 | 0.01 |
| K Width (mm) | Field | 7A | 4.43 | S7A_71631668 | 81 | 2.98 | 0.03 | 0.01 |
| K Length (mm) | Field | 3D | 13.58 | S3D_298356803 | 206 | 6.28 | 0.1 | 0.01 |
| K Length (mm) | Field | 5A | 9.48 | Awns | 269 | 6.28 | 0.08 | 0.01 |
| K Length (mm) | Field | 1D | 7.7 | S1D_253081308 | 82 | 6.28 | -0.08 | 0.01 |
| K Length (mm) | Field | 3B | 5.67 | S3B_576228566 | 104 | 6.28 | -0.06 | 0.01 |
| K Length (mm) | Field | 6B | 5.01 | S6B_687553875 | 95 | 6.28 | 0.05 | 0.01 |
| K Length (mm) | Field | 1B | 4.72 | S1B_639043667 | 40 | 6.28 | 0.05 | 0.01 |
| K Area (mm$^2$) | Field | 4D | 20.41 | RhtD1 | 14 | 13.97 | -0.55 | 0.05 |
| K Area (mm$^2$) | Field | 3D | 8.73 | S3D_298356803 | 205 | 13.97 | 0.33 | 0.05 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| K Area (mm$^2$) | Field | 5A | 6.08 | S5A_73816555 | 58 | 13.97 | 0.28 | 0.05 |
| K Area (mm$^2$) | Field | 6A | 5.34 | S6A_115348315 | 68 | 13.97 | 0.27 | 0.05 |

**Table S7.** Geographic distribution of *B1* haplotypes. Number of lines having observed haplotypes in spring and winter wheat germplasm based on geographic region of origin for accessions. For each haplotype, left column represents number of awnless lines (A-) and the right column the number of accessions having awns (A+).

| Region | Growth habit | Hap1 | | Hap2 | | Hap3 | | Hap4 | | Hap5 | | Hap6 | | Hap7 | | Hap8 | | Total |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | A- | A+ | A- | A+ | A- | A+ | A- | A+ | A- | A+ | A- | A+ | A- | A+ | A- | A+ | |
| North America | Spring | 5 | 47 | - | - | - | - | - | - | - | - | - | 7 | - | - | 35 | - | 94 |
| | Winter | - | 15 | - | - | - | - | - | - | - | - | - | 1 | - | - | 11 | - | 27 |
| Central America | Spring | 1 | 61 | - | 1 | - | 2 | - | - | - | - | - | - | 1 | - | 20 | - | 86 |
| South America | Spring | 3 | 191 | - | 4 | - | 4 | - | 1 | - | - | - | - | 1 | - | 58 | 1 | 263 |
| | Winter | - | 5 | - | - | - | 1 | - | - | - | - | - | - | - | - | 29 | - | 35 |
| Western Europe | Spring | 5 | 81 | - | 1 | - | 2 | - | 1 | - | 1 | - | 3 | 3 | - | 119 | - | 216 |
| | Winter | - | 3 | - | - | - | 1 | - | - | - | - | - | 4 | - | - | 107 | - | 115 |
| Eastern Europe | Spring | 2 | 46 | - | - | - | 3 | - | 3 | - | - | - | 10 | 1 | - | 48 | - | 113 |
| | Winter | - | 42 | - | - | - | - | - | - | - | - | - | 31 | - | - | 72 | 2 | 147 |
| South Asia | Spring | 39 | 58 | 2 | 2 | - | 3 | - | - | - | - | - | - | - | - | 12 | - | 116 |
| East Asia | Spring | 2 | 43 | - | - | - | 2 | - | 1 | - | - | - | - | - | - | 13 | - | 61 |
| | Winter | - | 15 | - | - | - | - | - | - | - | - | - | - | - | - | 4 | - | 19 |
| Central Asia | Spring | 15 | 193 | - | 2 | - | 13 | - | - | - | 9 | - | 1 | 1 | - | 70 | - | 304 |
| | Winter | 1 | 45 | - | - | - | 8 | - | - | - | - | - | 5 | - | - | 28 | 1 | 88 |
| Caucuses | Spring | 4 | 52 | - | - | - | 1 | - | - | - | 2 | - | - | - | - | 20 | - | 79 |
| | Winter | 1 | 11 | - | - | - | - | - | - | - | - | - | - | - | - | 4 | - | 16 |
| Middle East | Spring | 6 | 156 | - | 3 | - | 2 | - | - | - | - | - | - | 1 | - | 38 | 4 | 210 |
| | Winter | - | - | - | - | - | - | - | - | - | - | - | 1 | - | - | 1 | - | 2 |
| North Africa | Spring | 5 | 104 | - | 1 | - | 1 | - | - | - | - | - | 2 | - | - | 30 | 10 | 153 |
| Sub-Saharan Africa | Spring | 8 | 149 | 1 | 3 | - | 1 | - | 1 | - | - | - | - | 1 | - | 79 | - | 243 |
| | Winter | - | 1 | - | - | - | - | - | - | - | - | - | - | - | - | 1 | - | 2 |
| Oceania | Spring | - | 6 | - | - | - | - | - | - | - | - | - | - | 2 | - | 38 | - | 46 |
| | Winter | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 4 | - | 4 |
| **Total** | | 97 | 1324 | 3 | 17 | - | 44 | - | 7 | - | 12 | - | 65 | 11 | - | 841 | 18 | 2439 |

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