| KASP name and primers | Sequence |
|----------------------|----------|
| 1. *TaBradi2g14790*  |          |
| *TaBradi2g14790_KASP1_F* | gaaggtgaccaagtcatgcctCCTTGTCCTCCGTCCCTG |
| *TaBradi2g14790_KASP1_V* | gaaggtcggagtcaacggattGACAGCTCCTCCCGAG |
| *TaBradi2g14790_KASP1_generic* | TCGGTAATGTCTTCACTGTAAAA |

| 2. *TaELF3-B1* |          |
|----------------|----------|
| *TaELF3-B1_Kasp_F* | gaaggtgaccaagtcatgcctCCCTTGACGTCCCTG |
| *TaELF3-B1_Kasp_V* | gaaggtcggagtcaacggattCCCTTGACGTCCCG |
| *TaELF3-B1_Kasp2_generic* | CGACCCAACACTCAG |

| 3. *TaELF3-D1* |          |
|----------------|----------|
| *TaELF3-D1_Kasp1_F* | gaaggtgaccaagtcatgcgtGGGACATGACGGGAACA |
| *TaELF3-D1_Kasp1_V* | gaaggtcggagtcaacggattGGGACATGACGGGAAC |
| *TaELF3-D1_Kasp1_generic* | GGAAACCAGGCTCAG |
| *TaELF3-D1_Kasp2_F* | gaaggtgaccaagtcatgcctGCCTAGATCTGTT |
| *TaELF3-D1_Kasp2_V* | gaaggtcggagtcaacggattGCCTAGATCTGTC |
| *TaELF3-D1_Kasp2_generic* | GTAGACGACCCTTTCAG |

| 4. *TaMOT1-D1* |          |
|----------------|----------|
| *TaMOT1-D1_KASP1_F* | gaaggtgaccaagtcatgcgtGACATATAATGTAAGGATCAATCAT |
| *TaMOT1-D1_KASP1_V* | gaaggtcggagtcaacggattGACATATAATGTAAGGATGATCAT |
| *TaMOT1-D1_KASP1_generic* | AATATATAAGTAAACCCTCAGTAAAA |

Table S1. The KASP primer combinations used to score the same SNPs in the genes *TaBradi2g14790, TaELF3-B1* and *TaELF3-D1*. The molecular concentrations of the FAM (F) and VIC (V) labelled primers were 0.16mM while the generic primers were 0.4mM. The lower case in the sequence is the FAM or VIC sequence.
| B. distachyon | Match with T. aestivum | Match with T. aestivum | Gene or marker name or EST accession number |
|--------------|-----------------------|-----------------------|---------------------------------------------|
| Chromosome 2 | Gene number           | Group1                 | T. aestivum Group3 |
| Bradi2g28010 | yes                   | no                    | serine/threonine-protein kinase TOR-like (BF485305) |
| Bradi2g25820 | yes                   | no                    | Barley Flowering Locus T3 (*HvFT3) |
| Bradi2g19670 | yes                   | no                    | chloroplast unusual positioning1(CHUP1) chloroplastic-like |
| Bradi2g15630 | yes                   | no                    | Glucose-1-phosphate adenylyltransferase large subunit, chloroplastic/amyloplastic-like |
| Bradi2g14940 | yes                   | no                    | uncharacterised |
| Bradi2g14930 | yes                   | yes                   | probable indole-3-acetic-acid-amino synthetase GH3.5-like |
| Bradi2g14790 | yes                   | no                    | RNA polymerase sigma factor rpoD-like |
| Bradi2g14780 | no                    | partial 3B            | *Bj544902 |
| Bradi2g14770 | Yes (1DS)             | yes                   | *Xedo393 (*Sh09g030620) |
| Bradi2g14760 | no                    | no                    | *Xag24L |
| Bradi2g14750 | no                    | partial 3B            | *MODIFIER OF TRANScription I (MOT1) |
| Bradi2g14740 | yes                   | yes                   | Adenylate kinase 1 (*XADK1) |
| Bradi2g14730 | yes                   | yes                   | AtELF3/Eam8/Mat-a (early maturity)/XBarc62 |
| Bradi2g14660 | yes                   | no                    | UDP-glucose 4-epimerase GEPI48-like (LOC100838089), mRNA |
| Bradi2g14440 | yes                   | 3A and 3B             | Nucleoside diphosphate kinase 3 (*Ndk3) *Sh09g030810 |
| Bradi2g14400 | yes                   | no                    | uncharacterised |
| Bradi2g14380 | yes                   | no                    | Histone deacetylase HDT2-like |
| Bradi2g14370 | yes                   | no                    | rho GDP-dissociation inhibitor 1-like |
| Bradi2g14340 | yes                   | no                    | uncharacterised |
| Bradi2g14310 | yes                   | yes                   | probable inactive leucine-rich repeat receptor-like protein kinase (At1g66830-like) |
| Bradi2g14290 | yes                   | no                    | Adaptor protein complex 3 subunit delta (AP-3)-like |
| Bradi2g14250 | yes                   | no                    | |
| Bradi2g14210 | yes                   | no                    | |
| Bradi2g14190 | yes                   | no                    | |
| Bradi2g14130 | yes                   | no                    | |
| Bradi2g14120 | yes                   | partial               | |
| Bradi2g14110 | yes                   | yes                   | |
| Bradi2g14090 | partial               | no                    | |
| Bradi2g14080 | no                    | no                    | |
| Bradi2g14070 | no                    | yes                   | |
| Bradi2g13870 | no                    | no                    | |
| Bradi2g13860 | no                    | no                    | |
| Bradi2g13850 | no                    | no                    | |
| Bradi2g13840 | no                    | no                    | |
| Bradi2g13820 | no                    | no                    | |
| Bradi2g13810 | no                    | no                    | |
| Bradi2g13800 | no                    | no                    | |
| Bradi2g13790 | yes                   | no                    | |
| Bradi2g13750 | yes                   | no                    | |

*Valarik et al., 2006; Song et al., 2005; Faricelli et al., 2010; Higgins et al., 2010; and Zakhrabekova et al., 2012; Faure et al., 2012; Faure et al., 2007.

Table S2 The 40 syntenous B. distachyon genes used to define the 1DL deletion.
Wheat orthologues were assigned to chromosome arms by homology to chromosome arm sorted survey sequence as described in Materials and Methods. Of the forty genes, eleven
genes, TaBradi2g14730, TaBradi2g14460, Bradi2g14440, Bradi2g14400, Bradi2g14380, Bradi2g14370, Bradi2g14340, Bradi2g14310, Bradi2g14290 and Bradi2g14210, and TaBradi2g14190 were all shown to be part of the segment that has several genes deleted from Spark, and Cadenza and they are shown in red colour (Table S2). Twelve of the forty genes had no matches with wheat group one chromosomes and these are shown in blue (Table 1). Out of the twelve genes that do not match group 1 wheat chromosomes, five matched the wheat group three chromosomes and these are Bradi2g14070, Bradi2g13870, Bradi2g13820, Bradi2g13810, and Bradi2g13800 (Table S2).

The gene Bradi2g14770 matched group 3 genes but the match on group 1 was on 1DS. The genes Bradi2g14740, Bradi2g14120 and Bradi2g14110, matched homologues on both group 1 and group3 wheat chromosomes (Table S2) and these were not used to define the deletion because amplification from group 3 would not be distinguishable from group1 in the absence of polymorphism that can be used to differentiate the locations. The genes Bradi2g14780, Bradi2g14750, and Bradi2g14440 (Table S2), matched genes on both group1 and group3 chromosomes but none of the three had sequence match with the group 3 D genome chromosome of “Chinese Spring” and hence Bradi2g14440 was used to define the deletion. The gene Bradi2g14730 matched both group1 and group 3 but when the genes were aligned, the group 1 genes were sufficiently different from the group 3 genes hence primers were designed to be specific to 1DL and this gene was also found to be among the deleted genes (Fig. 2). Eleven genes outside the 1DL deletion matched group 1 chromosomes only and all these were used to define the deletion (bold black Table S2).
Fig. S1  Chromosomal location of the 1DL heading date QTL for and Spark X Rialto (A), Avalon X Cadenza (B) doubled haploid (DH) population vernalized at 7-10°C for 8 weeks and grown in short days (SD) 10 hrs light, long days (LD) 16 hrs light and very long days (LLD) 20 hrs light. The Avalon X cadenza (B) shows TaELF3-D1 coinciding with the peak of the QTL (B).
Fig. S2 Position of the Xbarc62 simple sequence repeat (SSR) 194 bases from the stop codon in the 3’ untranslated region (UTR) of TaELF3 gene. The letters in capital are part of the fourth exon of the TaELF3 gene and the octagon written stop marks the position of the stop.
codon (TGA). The sequence labelled Xbarc62 is the expressed sequence tag (EST) accession BV211449 used to design the XBarc 62 SSR marker (Song et al., 2005). The PCR primers are underlined and labelled primer 1, Primer 2 (designed to be specific to 1DL) while primer 3 and 4 were designed by Song et al., (2005) and amplify from both 1DL and 1AL (Fig. 1). The difference between primer 2 and 3 is that primer 3 is shown by the single underline while primer 2 includes the whole of primer 3 and four additional bases (gaag) shown by double underlining which make primer 2 1DL specific (fig1). The D homeologue is 11bp longer than the A and B homeologues in the region between the two black downward arrows (Fig. 1). The start and end of the ‘ATCT’ SSR that is scored by the XBac62 marker is shown by the upward arrows and also by the dotted underline and the black horizontal bar flanked by the two upward facing arrows.
Fig. S3.1 The 1D genes that match the *B. distachyon* chromosome 2 genes that were used to define the proximal end of the 1DL deletion. Non genome specific primers are shown as ngs.

Key: tau = *A. tauschii*, Cha = Charger, Sav = Savannah, Bad = Badger, Cad = Cadenza, Ria = Rialto, Ava = Avalon.
Fig. S3.2 The wheat chromosome 1DL genes that match the *B. distachyon* chromosome 2 genes that were used to show that the 1DL deletion includes *TaBradi2g14740* (H), *TaBradi2g14460* (I), *TaBradi2g14730* (J), *TaBradi2g14190* (K) and *TaBradi2g14130* (L). Key: Spa = Spark, Ria = Rialto. The genes *TaBradi2g13790* and *TaBradi2g13750* define the 1DL deletion on the distal end of the deletion. The gene *TaBradi2g14130* (L) amplifies on the 5' end for both Spark and Rialto and about 1Kb of this gene was sequenced from both varieties but the rest of the gene is not amplified from Spark suggesting that the distal deletion breakpoint maybe within this gene.
Fig. S4 Chromosomal location of the 1BL heading QTL for Avalon X Cadenza (A), and 1DL heading date QTL for Savannah X Rialto (B) doubled haploid (DH) population grown in the field. Both QTLs show that *TaELF3-B1* and *TaELF3-D1* coincide with the peak of the QTLs. The QTLs seem to respond to environmental cues given that they are not significant in some years.
Figure S5. The genotypes of the outliers in the *Eps-D1* region. P1_78 has no recombination as well as P2_23 and P3_65 suggesting that there may be another gene(s) in the background responsible for the phenotype of the outliers.
Figure S6 Mutations at the TaELF3-D1 (A), TaELF3-B1 (B), TaELF3-A1 (C) TaMOT1-D1 (D), TaFTSH4-D1 (E), and TaFTSH4-B1 (F) genes. The black rectangles with numbers at the top are the exons (4 for TaELF3 genes (A, B and C), 28 for TaMOT1-D1 (D) and 7 for TaFTSH4 genes (E and F)). The unshaded solid rectangles are the miniature inverted
transposable elements (MITE) in intron 2 and the 3’UTR of TaELF3-D1 gene 305 and 308 bases long respectively (A). The dotted rectangles for TaELF3-D1, TaELF3-B1 and TaELF3-A1 are the XBarc62 ATCT repeats and each arrow in the dotted box represents a single ATCT repeat of which the third one for TaELF3-B1 is ATTT and the second and fourth for TaELF3-A1 are ATCA and ACCT respectively. The XBarc62 ATCT SSR has 8 repeats for the D copy and 5 each for the A and B copies of TaELF3. Key: Rialto (Ria), Spark (Spa), Avalon (Ava), Cadenza (Cad), Charger (Cha), Badger (Bad) and Savannah (Sav)
Fig. S7 The partial alignment of ELF3 genes from *Hordeum vulgare* (Hv), *Triticum aestivum* (Ta), *Brachypodium distachyon* (Bd), *Sorghum bicolor* (Sb), Si and *Oryza sativa* (Os). The alignment shows the change in the conserved serine (S) to glycine (G). This mutation distinguishes Avalon (mutant) from Cadenza (wild type).