KASP name and primers	Sequence
1. *TaBradi2g14790*	
*TaBradi2g14790*_KASP1_F	gaaggtgaccaagttcatgctCCTTGTCTCCGTCCCTG
*TaBradi2g14790*_KASP1_V	gaaggtcggagtcaacggattGACAGCTCCTCCCGAG
*TaBradi2g14790*_KASP1_generic	TCGGTAATGTCTTCAGTGTTTTA
2. *TaELF3-B1*	
*TaELF3-B1*_Kasp_F	gaaggtgaccaagttcatgctCCCTTGCAGCTCGCT
TaELF3-B1 Kasp_V	gaaggtcggagtcaacggattCCCTTGCAGCTCGCC
TaELF3-B1 Kasp2_generic	CGACCCAACACTCACG
3. *TaELF3-D1*	
*TaELF3-B1*_ Kasp1_F	gaaggtgaccaagttcatgctTGGAGACATGACGGGAACA
*TaELF3-D1*_Kasp1_V	gaaggtcggagtcaacggattTGGAGACATGACGGGAACG
*TaELF3-D1*_Kasp1_generic	GGAAACCAGGCTTCACG
*TaELF3-D1*_ Kasp2_F	gaaggtgaccaagttcatgctGCCTCAGAATCAGTGGCTT
*TaELF3-D1*_Kasp2_V	gaaggtcggagtcaacggattGCCTCAGAATCAGTGGCTC
*TaELF3-D1*_Kasp2_generic	GTAGACGAACCCTTCCGA
4. *TaMOT1-D1*	
*TaMOT1-D1*_KASP1_F	gaaggtgaccaagttcatgctGGCACATATAATGTAAGGATCAATCAT
*TaMOT1-D1_KASP1*_V	gaaggtcggagtcaacggattGGCACATATAATGTAAGGATGAATCAT
*TaMOT1-D1*_KASP1_generic	AATATATAAGTTAACCATCTCATGAAAGTAAG

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 Chromosome 2 Gene number	Match with *T. aestivum* Group1	Match with *T. aestivum* Group3	Gene or marker name or EST accession number
Bradi2g28010	yes	no	serine/threonine-protein kinase TOR-like (BF485305)
Bradi2g25820	yes	no	peptide methionine sulfoxide reductase B3, chloroplastic-like
Bradi2g19670	yes	no	*Barley **F**lowering Locus **T3*** (ᵠ*HvFT3*)
Bradi2g15630	yes	no	chloroplast unusual positioning1(CHUP1) chloroplastic-like
Bradi2g14970	yes	no	Glucose-1-phosphate adenylyltransferase large subunit, chloroplastic/amyloplastic-like
Bradi2g14940	yes	no	uncharacterised
Bradi2g14830	yes	no	probable indole-3-acetic acid-amino synthetase GH3.5-like
Bradi2g14790	yes	no	*RNA polymerase sigma factor rpoD-like*
Bradi2g14780	no	partial 3B	
Bradi2g14770	Yes (**1DS**)	yes	
Bradi2g14760	no	no	
Bradi2g14750	no	partial 3B	
Bradi2g14740	yes	yes	
Bradi2g14730	yes	yes	CTP synthase-like
Bradi2g14460	yes	no	ᵅ*BJ544902*
Bradi2g14440	yes	3A and 3B	**Xcdo393* (ᵘ*Sb09g030620*)
Bradi2g14400	yes	no	**v**acuolar **ATP** synthetase subunit **C** (**vatpC*) (ᵅ*XAL503851*)
Bradi2g14380	yes	no	**XCA608558*
Bradi2g14370	yes	no	**Xwg241*
Bradi2g14340	yes	no	ᵝ***M**ODIFIER **O**F **T**RANSCRIPTION **1** (MOT1)*
Bradi2g14310	yes	yes	***Ad**enylate **k**inase **1** (*XADK1)*
Bradi2g14290	yes	no	*AtELF3/Eam8/Mat-a* (early maturity)/ ᵅ*XBarc62*
Bradi2g14290 3'UTR	yes	no	ᵅ*XBarc62*
Bradi2g14250	yes	no	UDP-glucose 4-epimerase GEPI48-like (LOC100838089), mRNA
Bradi2g14210	yes	no	**N**ucleoside **d**iphosphate **k**inase **3** *(*Ndk3*)* ᵘ*Sb09g030810*
Bradi2g14190	yes	no	uncharacterised
Bradi2g14130	yes	no	uncharacterised
Bradi2g14120	yes	partial	Histone deacetylase HDT2-like
Bradi2g14110	yes	yes	rho GDP-dissociation inhibitor 1-like
Bradi2g14090	partial	no	uncharacterised
Bradi2g14080	no	no	
Bradi2g14070	no	yes	
Bradi2g13870	no	yes	
Bradi2g13860	no	no	
Bradi2g13850	no	no	
Bradi2g13840	no	no	
Bradi2g13820	no	yes	
Bradi2g13810	no	yes	
Bradi2g13800	no	yes	
Bradi2g13790	yes	no	probable inactive leucine-rich repeat receptor-like protein kinase (At1g66830-like)
Bradi2g13750	yes	no	*Adaptor protein complex 3 subunit delta (AP-3)-like*

*Valarik *et al*., 2006; ᵅSong *et al*., 2005; ᵝFaricelli *et al*., 2010; ᵞHiggins *et al*., 2010; and ᵘZakhrabekova *et al*., 2012; ᵟFaure *et al*., 2012; ᵠFaure *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).

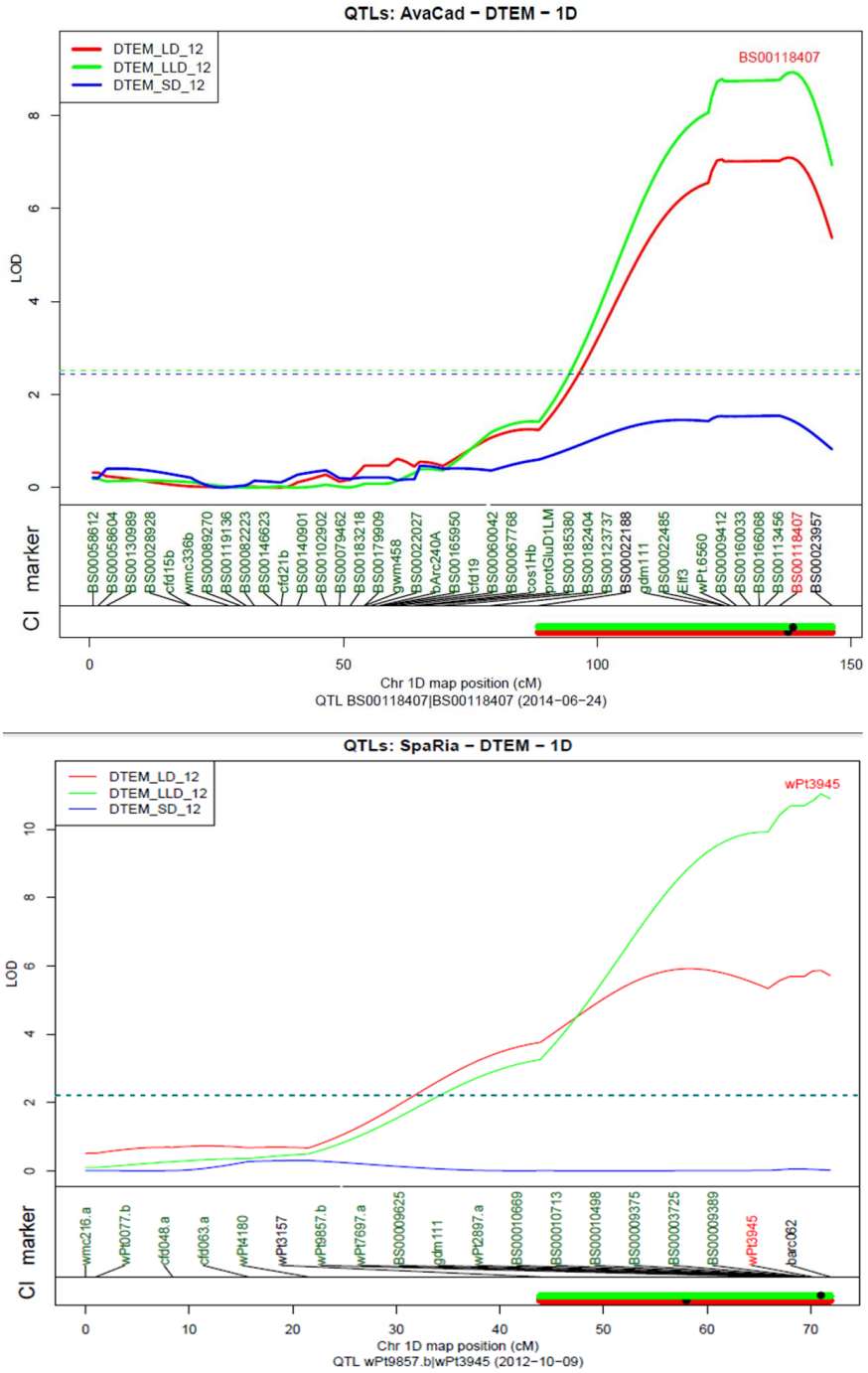


Fig. S1 Chromosomal location of the 1DL heading date QTL for and Spark X Rialto (A), Avalon X Cadenza (B) doubled haploid (DH) population vernalized at 7-10°C for 8 weeks and grown in short days (SD) 10 hrs light, long days (LD) 16 hrs light and very long days (LLD) 20 hrs light. The Avalon X cadenza (B) shows *TaELF3-D1* coinciding with the peak of the QTL (B).

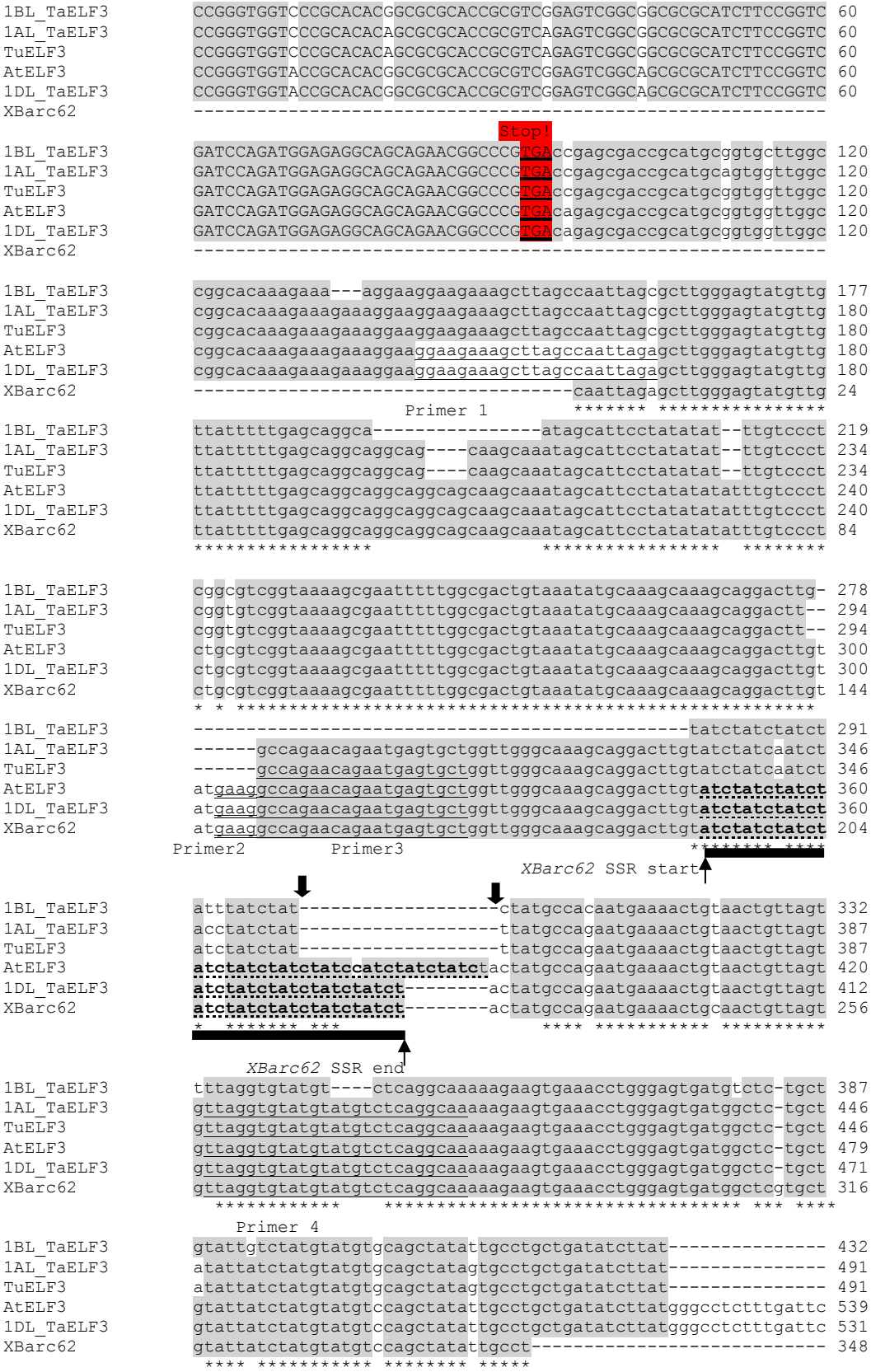


Fig. S2 Position of the *Xbarc62* simple sequence repeat (SSR) 194 bases from the stop codon in the 3' untranslated region (UTR) of *TaELF3* gene. The letters in capital are part of the fourth exon of the *TaELF3* gene and the octagon written stop marks the position of the stop

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.

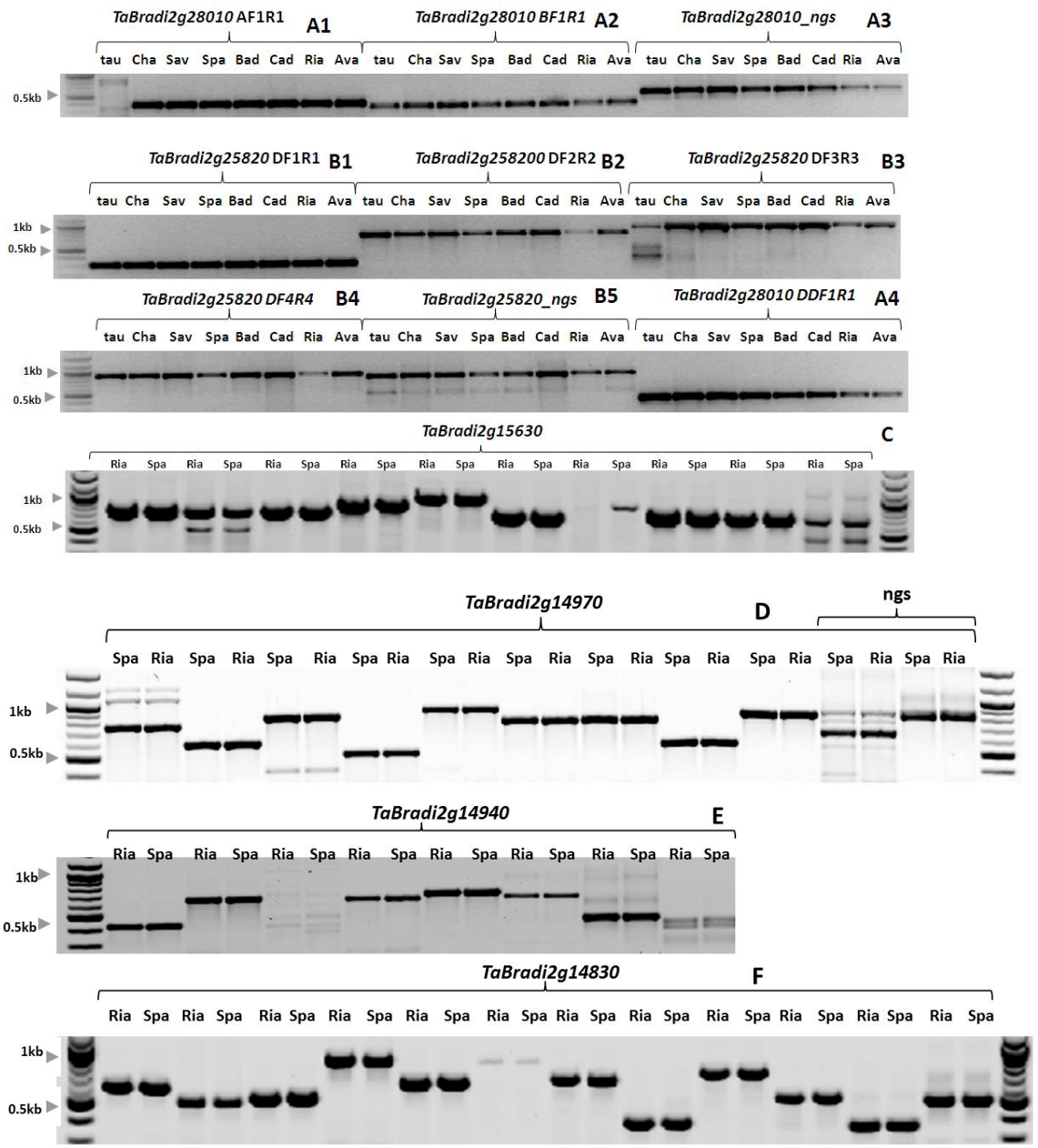


Fig. S3.1 The 1D genes that match the *B. distachyon* chromosome 2 genes that were used to define the proximal end of the 1DL deletion. Non genome specific primers are shown as ngs. Key: tau = *A. tauschii*, Cha = Charger, Sav = Savannah, Bad = Badger, Cad = Cadenza, Ria= Rialto, Ava = Avalon.

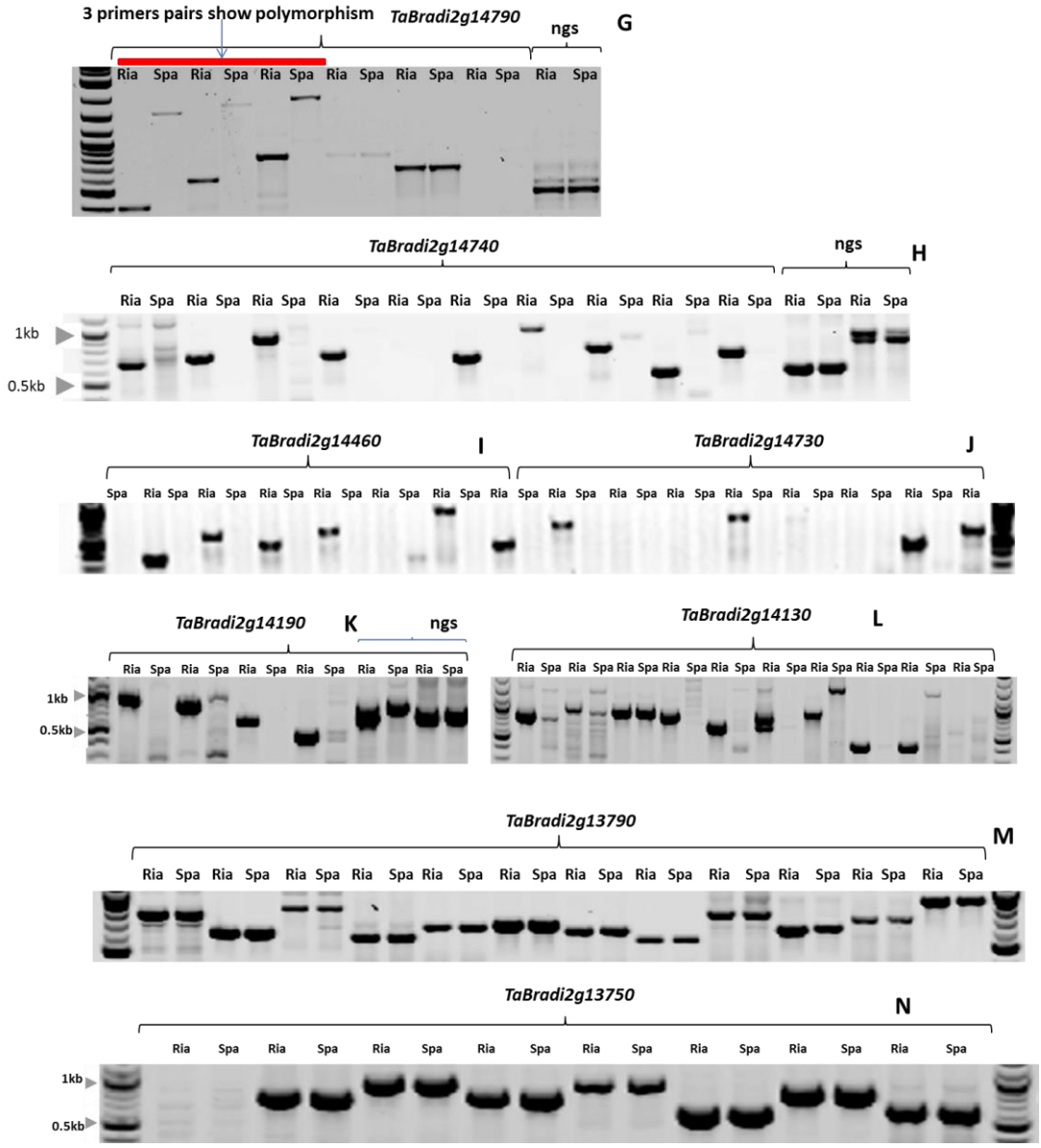
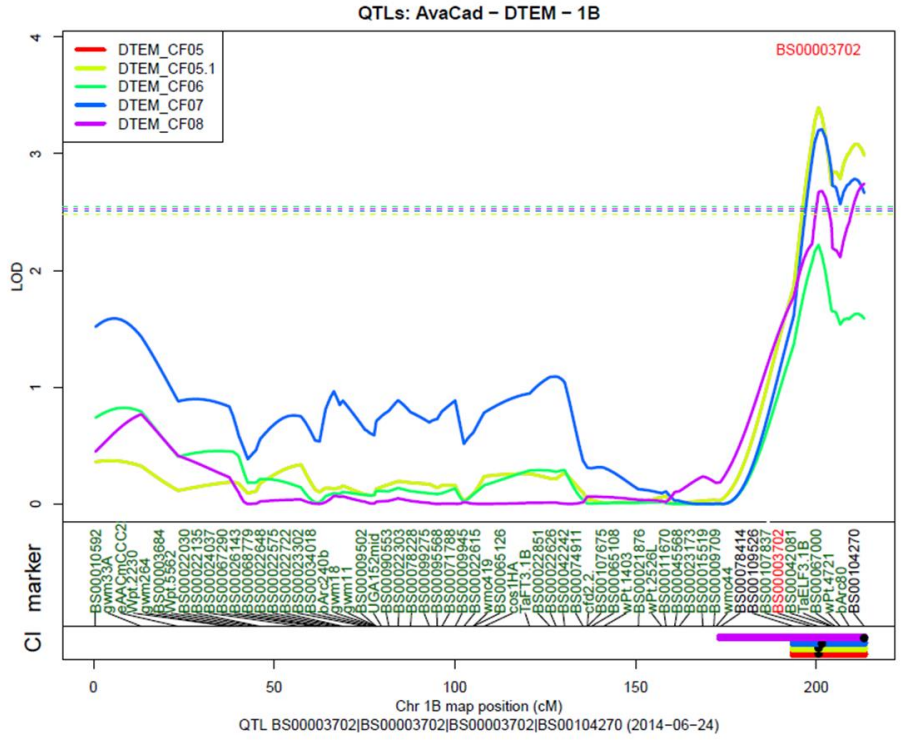
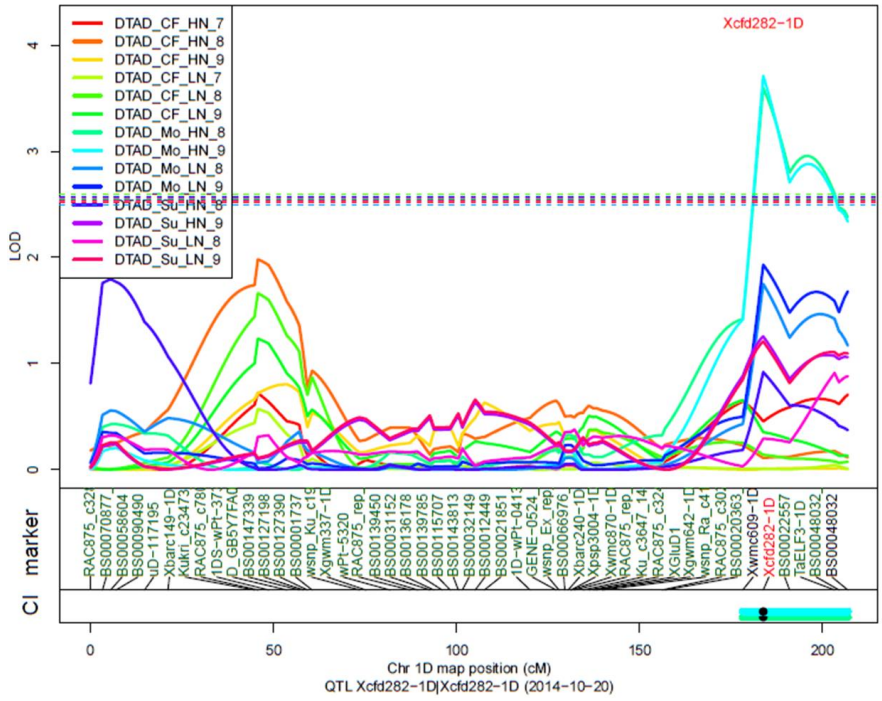


Fig. S3.2 The wheat chromosome 1DL genes that match the *B. distachyon* chromosome 2 genes that were used to show that the 1DL deletion includes *TaBradi2g14740* (H), *TaBradi2g14460* (I), *TaBradi2g14730* (J), *TaBradi2g14190* (K) and *TaBradi2g14130* (L). Key: Spa = Spark, Ria = Rialto. The genes *TaBradi2g13790* 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.



A



B

Fig. S4 Chromosomal location of the 1BL heading QTL for and 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.

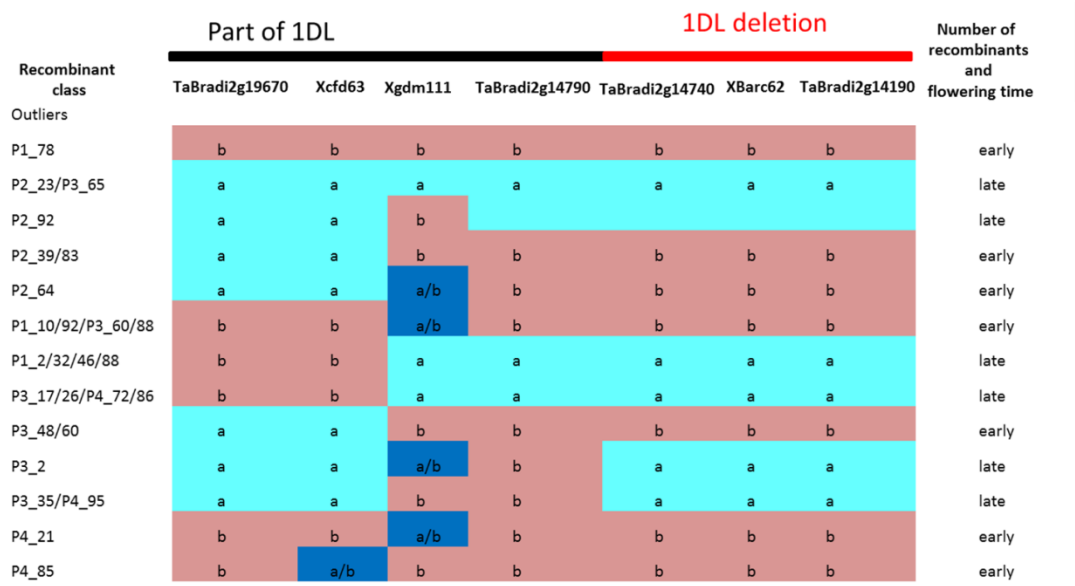


Figure S5. The genotypes of the outliers in the *Eps-D1* region. P1_78 has no recombination as well as P2_23 and P3_65 suggesting that there may be another gene(s) in the background responsible for the phenotype of the outliers.

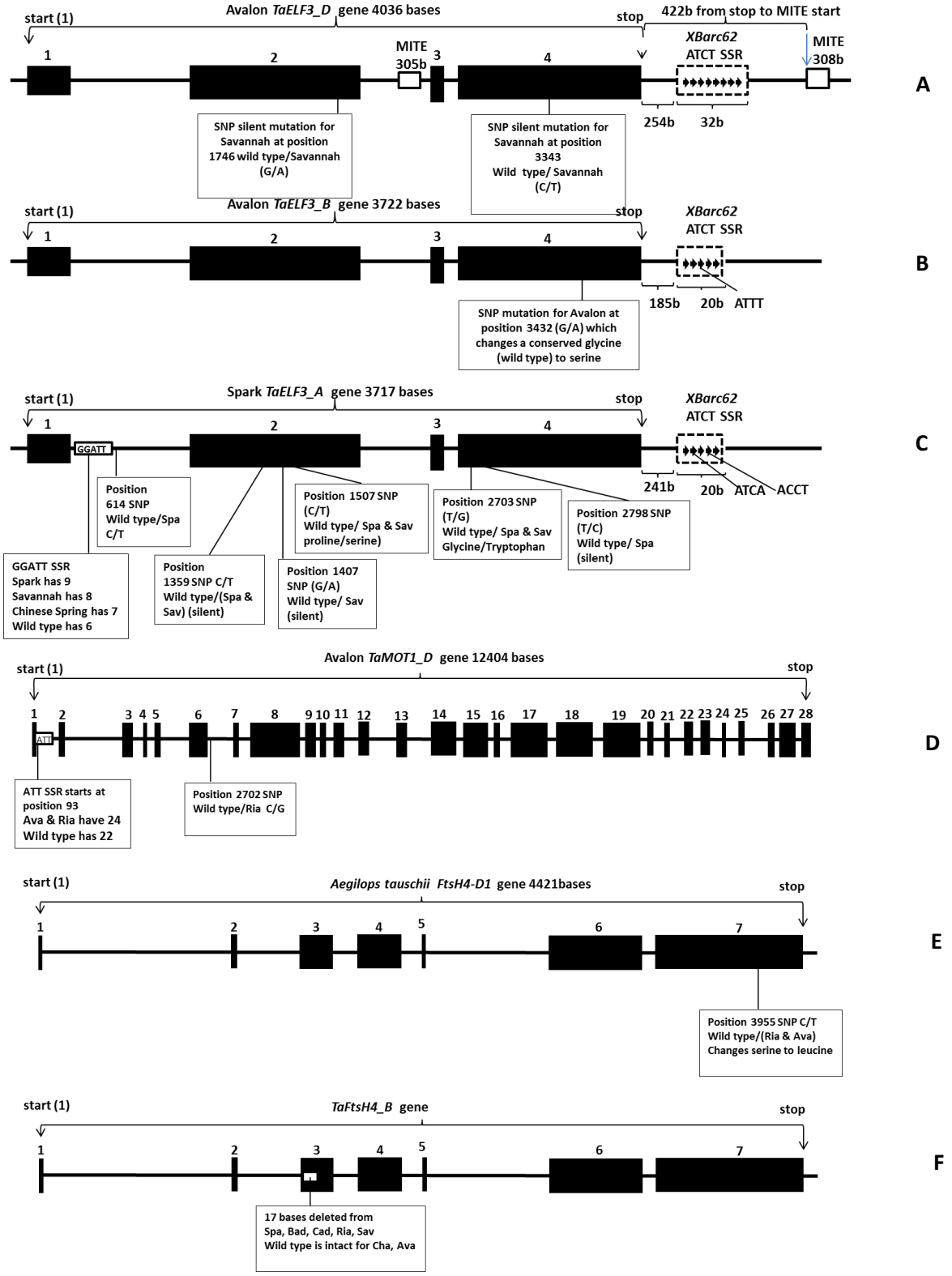


Figure S6 Mutations at the *TaELF3-D1* (A), *TaELF3-B1* (B), *TaELF3-A1* (C) *TaMOT1-D1* (D), *TaFTSH4-D1* (E), and *TaFTSH4-B1* (F) genes. The black rectangles with numbers at the top are the exons (4 for *TaELF3* genes (A, B and C), 28 for *TaMOT1-D1* (D) and 7 for *TaFTSH4* genes (E and F)). The unshaded 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)

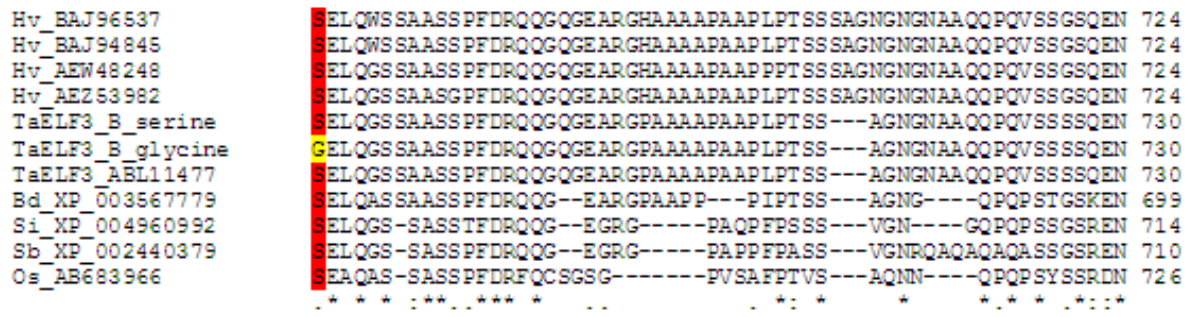


Fig. S7 The partial alignment of *ELF3* genes from *Hordeum vulgare* (*Hv*), *Triticum aestivum* (*Ta*), *Brachypodium distachyon* (*Bd*), *Sorghum bicolor* (*Sb*), Si and *Oryza sativa* (*Os*). The alignment shows the change in the conserved serine (S) to glycine (G). This mutation distinguishes Avalon (mutant) from Cadenza (wild type).