

KASP name and primers	Sequence
<b>1. <i>TaBradi2g14790</i></b>	
<i>TaBradi2g14790_KASP1_F</i>	gaaggtgaccaagttcatgctCCTTGTCTCCGTCCCTG
<i>TaBradi2g14790_KASP1_V</i>	gaaggtcggagtcaacggattGACAGCTCCTCCCGAG
<i>TaBradi2g14790_KASP1_generic</i>	TCGGTAATGTCTTCAGTGTTTTA
<b>2. <i>TaELF3-B1</i></b>	
<i>TaELF3-B1_Kasp_F</i>	gaaggtgaccaagttcatgctCCCTTGCAGCTCGCT
<i>TaELF3-B1 Kasp_V</i>	gaaggtcggagtcaacggattCCCTTGCAGCTCGCC
<i>TaELF3-B1 Kasp2_generic</i>	CGACCCAACACTCACG
<b>3. <i>TaELF3-D1</i></b>	
<i>TaELF3-B1_Kasp1_F</i>	gaaggtgaccaagttcatgctTGGAGACATGACGGGAACA
<i>TaELF3-D1_Kasp1_V</i>	gaaggtcggagtcaacggattTGGAGACATGACGGGAACG
<i>TaELF3-D1_Kasp1_generic</i>	GGAAACCAGGCTTCACG
<i>TaELF3-D1_Kasp2_F</i>	gaaggtgaccaagttcatgctGCCTCAGAATCAGTGGCTT
<i>TaELF3-D1_Kasp2_V</i>	gaaggtcggagtcaacggattGCCTCAGAATCAGTGGCTC
<i>TaELF3-D1_Kasp2_generic</i>	GTAGACGAACCCTTCCGA
<b>4. <i>TaMOT1-D1</i></b>	
<i>TaMOT1-D1_KASP1_F</i>	gaaggtgaccaagttcatgctGGCACATATAATGTAAGGATCAATCAT
<i>TaMOT1-D1_KASP1_V</i>	gaaggtcggagtcaacggattGGCACATATAATGTAAGGATGAATCAT
<i>TaMOT1-D1_KASP1_generic</i>	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.

<i>B. distachyon</i> Chromosome 2 Gene number	Match with <i>T. aestivum</i> Group1	Match with <i>T. aestivum</i> Group3	Gene or marker name or EST accession number
<b>Bradi2g28010</b>	yes	no	serine/threonine-protein kinase TOR-like (BF485305)
<b>Bradi2g25820</b>	yes	no	peptide methionine sulfoxide reductase B3, chloroplastic-like
<b>Bradi2g19670</b>	yes	no	<i>Barley Flowering Locus T3</i> ( <sup>ψ</sup> HvFT3)
<b>Bradi2g15630</b>	yes	no	chloroplast unusual positioning1(CHUP1) chloroplastic-like
<b>Bradi2g14970</b>	yes	no	Glucose-1-phosphate adenylyltransferase large subunit, chloroplastic/amyloplastic-like
<b>Bradi2g14940</b>	yes	no	uncharacterised
<b>Bradi2g14830</b>	yes	no	probable indole-3-acetic acid-amino synthetase GH3.5-like
<b>Bradi2g14790</b>	yes	no	<i>RNA polymerase sigma factor rpoD-like</i>
Bradi2g14780	no	partial 3B	
Bradi2g14770	Yes ( <b>1DS</b> )	yes	
Bradi2g14760	no	no	
Bradi2g14750	no	partial 3B	
<b>Bradi2g14740</b>	yes	yes	
<b>Bradi2g14730</b>	yes	yes	CTP synthase-like
<b>Bradi2g14460</b>	yes	no	<sup>a</sup> BJ544902
<b>Bradi2g14440</b>	yes	3A and 3B	<sup>μ</sup> Xcdo393 ( <sup>μ</sup> Sb09g030620)
<b>Bradi2g14400</b>	yes	no	vacuolar <b>ATP</b> synthetase subunit <b>C</b> ( <sup>*</sup> vatpC) ( <sup>a</sup> XAL503851)
<b>Bradi2g14380</b>	yes	no	<sup>*</sup> XCA608558
<b>Bradi2g14370</b>	yes	no	<sup>*</sup> Xwg241
<b>Bradi2g14340</b>	yes	no	<sup>β</sup> <b>MODIFIER OF TRANSCRIPTION 1 (MOT1)</b>
<b>Bradi2g14310</b>	yes	yes	<i>Adenylate kinase 1</i> ( <sup>*</sup> XADK1)
<b>Bradi2g14290</b>	yes	no	<i>AtELF3/Eam8/Mat-a</i> (early maturity)/ <sup>a</sup> XBarc62
<b>Bradi2g14290 3'UTR</b>	yes	no	<sup>a</sup> XBarc62
<b>Bradi2g14250</b>	yes	no	UDP-glucose 4-epimerase GEPI48-like (LOC100838089), mRNA
<b>Bradi2g14210</b>	yes	no	Nucleoside diphosphate kinase <b>3</b> ( <sup>*</sup> Ndk3) <sup>μ</sup> Sb09g030810
<b>Bradi2g14190</b>	yes	no	uncharacterised
<b>Bradi2g14130</b>	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	
<b>Bradi2g13790</b>	yes	no	probable inactive leucine-rich repeat receptor-like protein kinase (At1g66830-like)
<b>Bradi2g13750</b>	yes	no	<i>Adaptor protein complex 3 subunit delta (AP-3)-like</i>

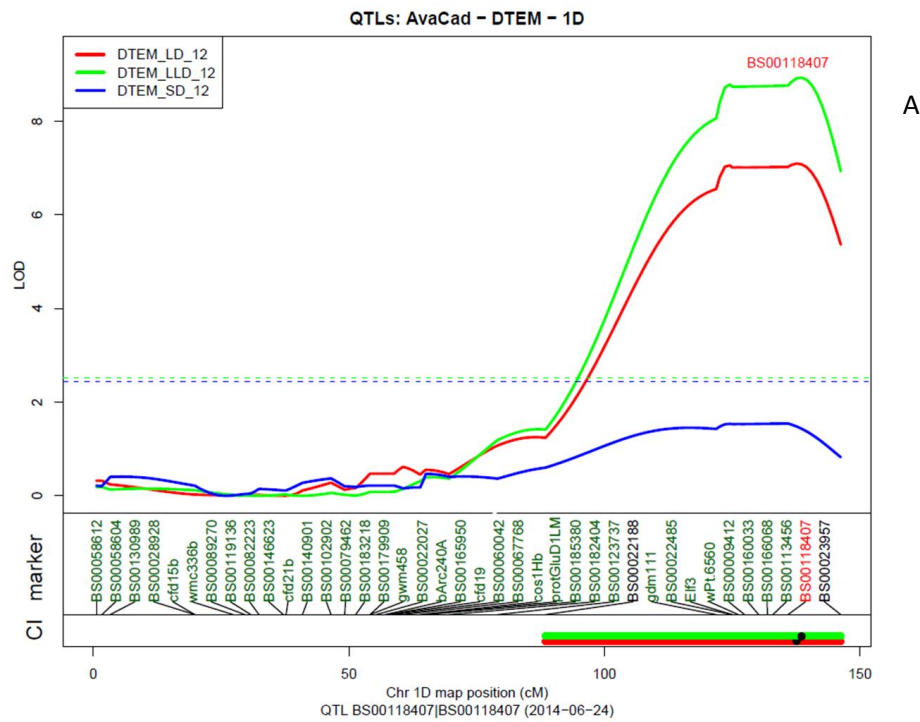
\*Valarik *et al.*, 2006; <sup>a</sup>Song *et al.*, 2005; <sup>β</sup>Faricelli *et al.*, 2010; <sup>γ</sup>Higgins *et al.*, 2010; and <sup>μ</sup>Zakhrabekova *et al.*, 2012; <sup>δ</sup>Faure *et al.*, 2012; <sup>ψ</sup>Faure *et al.*, 2007.

Table S2 The 40 syntenous *B. distachyon* genes used to define the 1DL deletion.

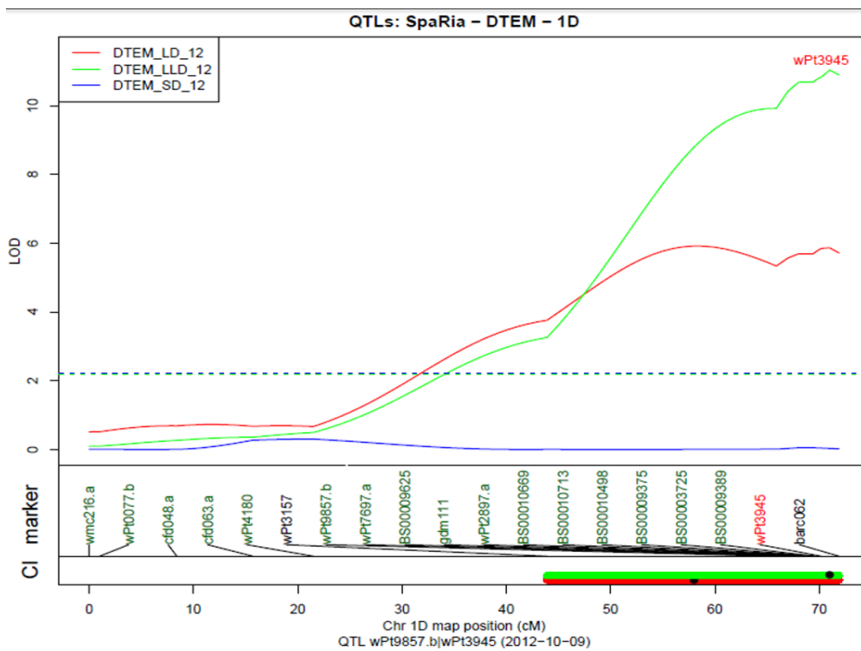
Wheat orthologues were assigned to chromosome arms by homology to chromosome arm sorted survey sequence as described in Materials and Methods. Of the forty genes, eleven

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).



A



B

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).

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1BL_TaELF3 CCGGGTGGTCCCGCACACGGCGCGCACCGCGTCGGAGTCGGCGGCGCGCATCTTCCGGTC 60
1AL_TaELF3 CCGGGTGGTCCCGCACACAGCGCGCACCGCGTCAGAGTCGGCGGCGCGCATCTTCCGGTC 60
TuELF3 CCGGGTGGTCCCGCACACAGCGCGCACCGCGTCAGAGTCGGCGGCGCGCATCTTCCGGTC 60
AtELF3 CCGGGTGGTACCGCACACGGCGCGCACCGCGTCGGAGTCGGCAGCGCGCATCTTCCGGTC 60
1DL_TaELF3 CCGGGTGGTACCGCACACGGCGCGCACCGCGTCGGAGTCGGCAGCGCGCATCTTCCGGTC 60
XBarc62 -----
                                Stop!
1BL_TaELF3 GATCCAGATGGAGAGGCAGCAGAACGGCCCGTGAaccgagcgaccgcatgcggtgcttggc 120
1AL_TaELF3 GATCCAGATGGAGAGGCAGCAGAACGGCCCGTGAaccgagcgaccgcatgagtggttggc 120
TuELF3 GATCCAGATGGAGAGGCAGCAGAACGGCCCGTGAaccgagcgaccgcatgcggtggttggc 120
AtELF3 GATCCAGATGGAGAGGCAGCAGAACGGCCCGTGAaccgagcgaccgcatgcggtggttggc 120
1DL_TaELF3 GATCCAGATGGAGAGGCAGCAGAACGGCCCGTGAaccgagcgaccgcatgcggtggttggc 120
XBarc62 -----

1BL_TaELF3 cggcacaagaagaaa---aggaaggaagaagacttagccaattagcgcttgggagtatgttg 177
1AL_TaELF3 cggcacaagaagaaaaggaaggaagaagacttagccaattagcgcttgggagtatgttg 180
TuELF3 cggcacaagaagaaaaggaaggaagaagacttagccaattagcgcttgggagtatgttg 180
AtELF3 cggcacaagaagaaaaggaaggaagaagacttagccaattagcgcttgggagtatgttg 180
1DL_TaELF3 cggcacaagaagaaaaggaaggaagaagacttagccaattagcgcttgggagtatgttg 180
XBarc62 -----caattagagcttgggagtatgttg 24
                                Primer 1 *****
1BL_TaELF3 ttatTTTTgagcaggca-----atagcattcctatatat--ttgtccct 219
1AL_TaELF3 ttatTTTTgagcaggcaggcag----caagcaaatagcattcctatatat--ttgtccct 234
TuELF3 ttatTTTTgagcaggcaggcag----caagcaaatagcattcctatatat--ttgtccct 234
AtELF3 ttatTTTTgagcaggcaggcaggcagcaagcaaatagcattcctatatatatttgtccct 240
1DL_TaELF3 ttatTTTTgagcaggcaggcaggcagcaagcaaatagcattcctatatatatatttgtccct 240
XBarc62 ttatTTTTgagcaggcaggcaggcagcaagcaaatagcattcctatatatatatttgtccct 84
*****

1BL_TaELF3 cggcgtcggtaaaagcgaatttttggcgactgtaaatatgcaaagcaaagcaggacttg- 278
1AL_TaELF3 cgggtgtcggtaaaagcgaatttttggcgactgtaaatatgcaaagcaaagcaggactt-- 294
TuELF3 cgggtgtcggtaaaagcgaatttttggcgactgtaaatatgcaaagcaaagcaggactt-- 294
AtELF3 ctgctcgtcggtaaaagcgaatttttggcgactgtaaatatgcaaagcaaagcaggacttg 300
1DL_TaELF3 ctgctcgtcggtaaaagcgaatttttggcgactgtaaatatgcaaagcaaagcaggacttg 300
XBarc62 ctgctcgtcggtaaaagcgaatttttggcgactgtaaatatgcaaagcaaagcaggacttg 144
* * *****

1BL_TaELF3 -----tatctatctatct 291
1AL_TaELF3 -----gccagaacagaatgagtgctggttggcacaagcaggacttgtatctatcaatct 346
TuELF3 -----gccagaacagaatgagtgctggttggcacaagcaggacttgtatctatcaatct 346
AtELF3 atgaaggccagaacagaatgagtgctggttggcacaagcaggacttgtatctatctatct 360
1DL_TaELF3 atgaaggccagaacagaatgagtgctggttggcacaagcaggacttgtatctatctatct 360
XBarc62 atgaaggccagaacagaatgagtgctggttggcacaagcaggacttgtatctatctatct 204
Primer2 Primer3 XBarc62 SSR start
                                ↓ ↓ ↑
1BL_TaELF3 atttattctat-----ctatgcccaaatgaaaactgtaactggttagt 332
1AL_TaELF3 acctatctat-----ttatgccagaatgaaaactgtaactggttagt 387
TuELF3 atctatctat-----ttatgccagaatgaaaactgtaactggttagt 387
AtELF3 atctatctatctatccatctatctatctatctatctatctatctatctatctatctatct 420
1DL_TaELF3 atctatctatctatctatctatct-----actatgccagaatgaaaactgtaactggttagt 412
XBarc62 atctatctatctatctatctatct-----actatgccagaatgaaaactgcaactggttagt 256
*****
                                XBarc62 SSR end
1BL_TaELF3 ttttaggtgtatgt---ctcaggcaaaaagaagtgaaacctgggagtgatgtctc-tgct 387
1AL_TaELF3 gtttaggtgtatgtatgtctcaggcaaaaagaagtgaaacctgggagtgatggctc-tgct 446
TuELF3 gtttaggtgtatgtatgtctcaggcaaaaagaagtgaaacctgggagtgatggctc-tgct 446
AtELF3 gtttaggtgtatgtatgtctcaggcaaaaagaagtgaaacctgggagtgatggctc-tgct 479
1DL_TaELF3 gtttaggtgtatgtatgtctcaggcaaaaagaagtgaaacctgggagtgatggctc-tgct 471
XBarc62 gtttaggtgtatgtatgtctcaggcaaaaagaagtgaaacctgggagtgatggctcgtgct 316
*****

1BL_TaELF3 gtattgtctatgtatgtgcagctatattgccctgctgatatcttat----- 432
1AL_TaELF3 atattatctatgtatgtgcagctatatgtgacctgctgatatcttat----- 491
TuELF3 atattatctatgtatgtgcagctatatgtgacctgctgatatcttat----- 491
AtELF3 gtattatctatgtatgtccagctatattgccctgctgatatcttatgggcctctttgattc 539
1DL_TaELF3 gtattatctatgtatgtccagctatattgccctgctgatatcttatgggcctctttgattc 531
XBarc62 gtattatctatgtatgtccagctatattgccct----- 348
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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.

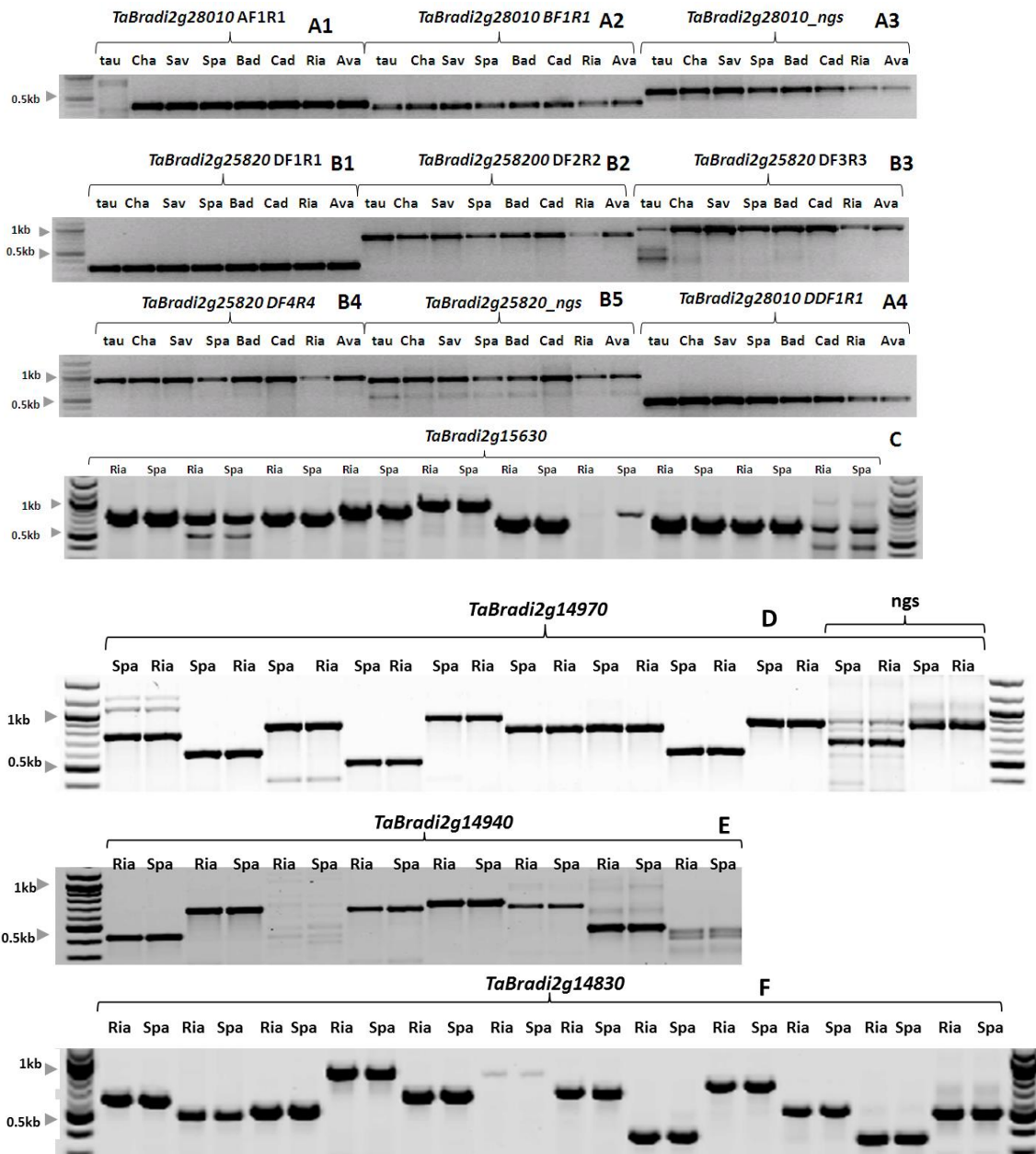


Fig. S3.1 The 1D genes that match the *B. distachyon* chromosome 2 genes that were used to define the proximal end of the 1DL deletion. Non genome specific primers are shown as ngs. Key: tau = *A. tauschii*, Cha = Charger, Sav = Savannah, Bad = Badger, Cad = Cadenza, Ria= Rialto, Ava = Avalon.

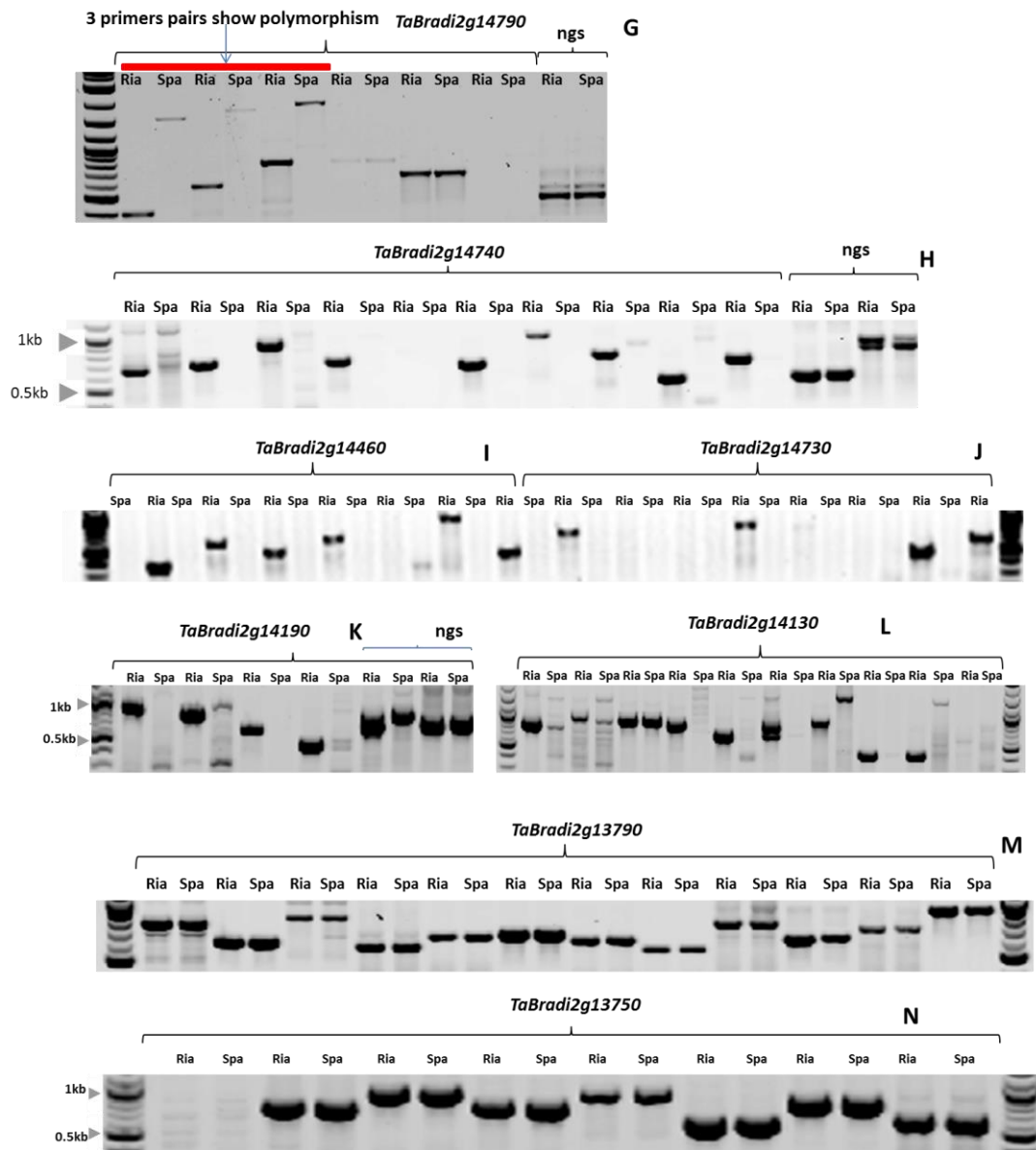
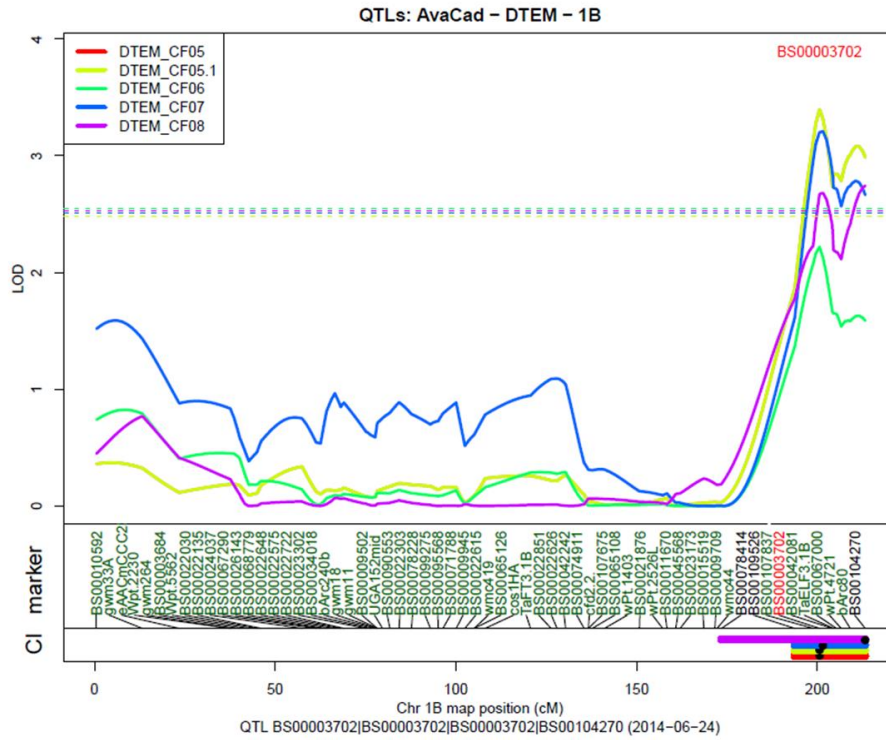
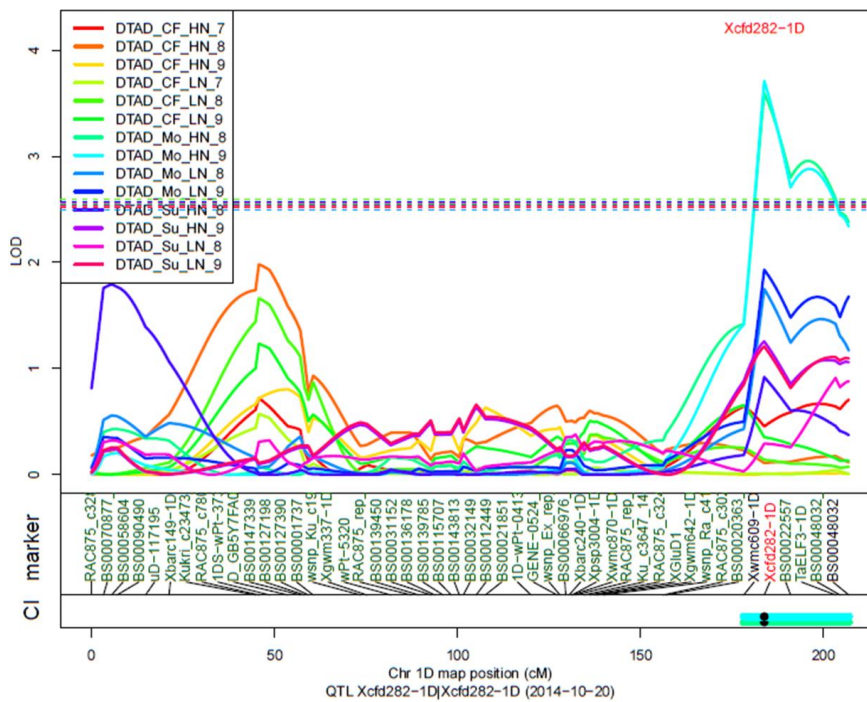


Fig. S3.2 The wheat chromosome 1DL genes that match the *B. distachyon* chromosome 2 genes that were used to show that the 1DL deletion includes *TaBradi2g14740* (H), *TaBradi2g14460* (I), *TaBradi2g14730* (J), *TaBradi2g14190* (K) and *TaBradi2g14130* (L). Key: Spa = Spark, Ria = Rialto. The genes *TaBradi2g13790*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

Recombinant class	Part of 1DL				1DL deletion			Number of recombinants and flowering time
	TaBradi2g19670	Xcfd63	Xgdm111	TaBradi2g14790	TaBradi2g14740	XBarc62	TaBradi2g14190	
Outliers								
P1_78	b	b	b	b	b	b	b	early
P2_23/P3_65	a	a	a	a	a	a	a	late
P2_92	a	a	b					late
P2_39/83	a	a	b	b	b	b	b	early
P2_64	a	a	a/b	b	b	b	b	early
P1_10/92/P3_60/88	b	b	a/b	b	b	b	b	early
P1_2/32/46/88	b	b	a	a	a	a	a	late
P3_17/26/P4_72/86	b	b	a	a	a	a	a	late
P3_48/60	a	a	b	b	b	b	b	early
P3_2	a	a	a/b	b	a	a	a	late
P3_35/P4_95	a	a	b	b	a	a	a	late
P4_21	b	b	a/b	b	b	b	b	early
P4_85	b	a/b	b	b	b	b	b	early

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.

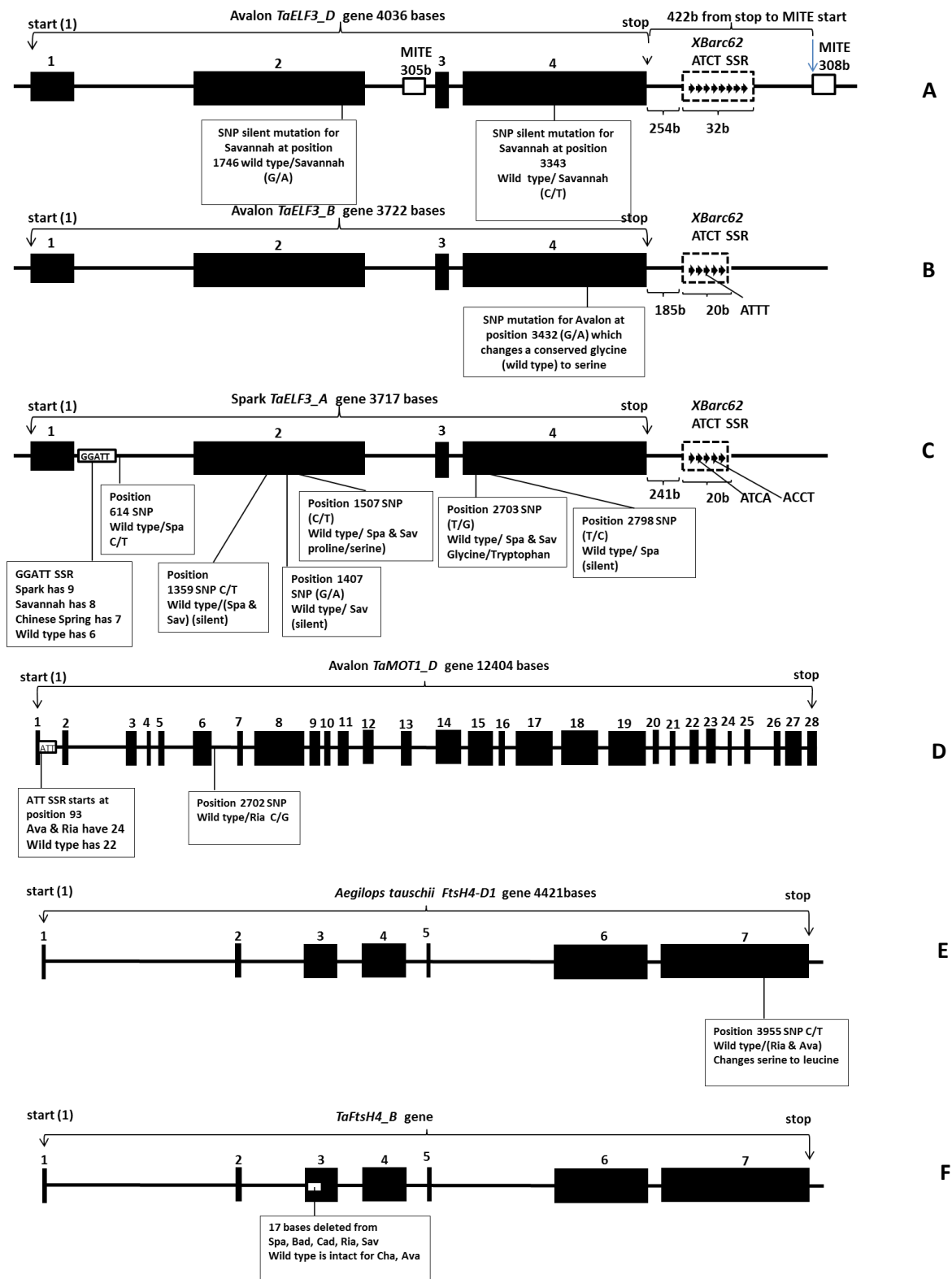


Figure S6 Mutations at the *TaELF3-D1* (A), *TaELF3-B1* (B), *TaELF3-A1* (C) *TaMOT1-D1* (D), *TaFTSH4-D1* (E), and *TaFTSH4-B1* (F) genes. The black rectangles with numbers at the top are the exons (4 for *TaELF3* genes (A, B and C), 28 for *TaMOT1-D1* (D) and 7 for *TaFTSH4* genes (E and F)). The unshaded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

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Hv_BAJ96537      SELQWS SAASS PFDRQQGQGEARGHAAAAPAAPLPTSS SAGNGNGNAAQQPQVSSGSQEN 724
Hv_BAJ94845      SELQWS SAASS PFDRQQGQGEARGHAAAAPAAPLPTSS SAGNGNGNAAQQPQVSSGSQEN 724
Hv_AEW48248      SELQGS SAASS PFDRQQGQGEARGHAAAAPAAPPTSS SAGNGNGNAAQQPQVSSGSQEN 724
Hv_AEZ53982      SELQGS SAASGPFDRQQGQGEARGHAAAAPAAPLPTSS SAGNGNGNAAQQPQVSSGSQEN 724
TaELF3_B_serine  SELQGS SAASS PFDRQQGQGEARGPAAAAPAAPLPTSS ---AGNGNAAQQPQVSSSSQEN 730
TaELF3_B_glycine CELQGS SAASS PFDRQQGQGEARGPAAAAPAAPLPTSS ---AGNGNAAQQPQVSSSSQEN 730
TaELF3_ABL11477 SELQGS SAASS PFDRQQGQGEARGPAAAAPAAPLPTSS ---AGNGNAAQQPQVSSSSQEN 730
Bd_XP_003567779 SELQAS SAASS PFDRQQG--EARGPAAPP---PIPTSS ---AGNG---QPQPSTGSKEN 699
Si_XP_004960992 SELQGS -SASSTFDRQQG--EGRG-----PAQPFPS SS---VGN---GQPQSSGSREN 714
Sb_XP_002440379 SELQGS -SASSPFDRQQG--EGRG-----PAPFPASS ---VGNRQAQAQAQSSGSREN 710
Os_AB683966      SEAQAS -SASSPFDRFQCSGSG-----PVSAFPTVS ---AQNN---QPQPSYSSRDN 726
.* * * :**..*** * .. . *: * * * * * :*:*

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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).