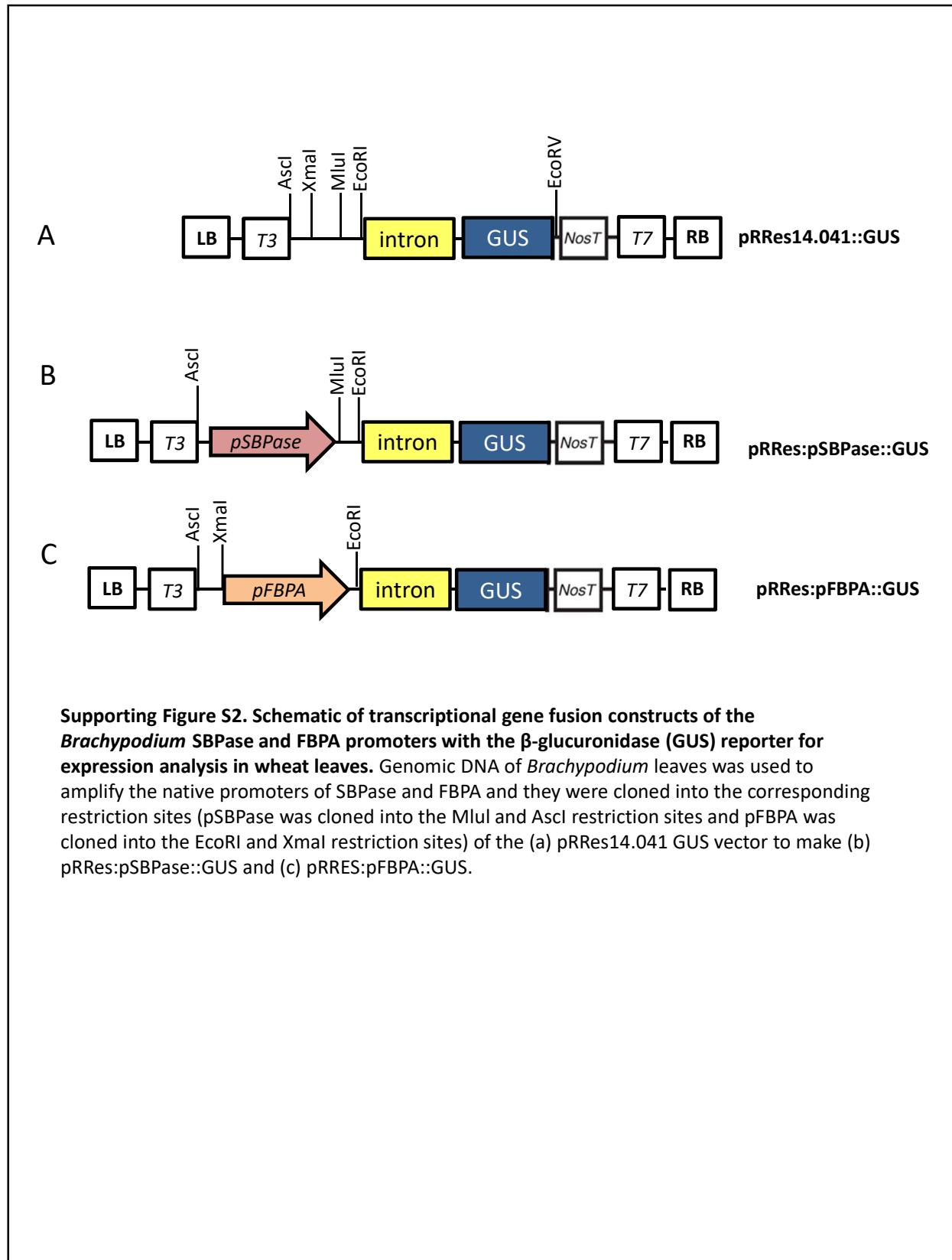
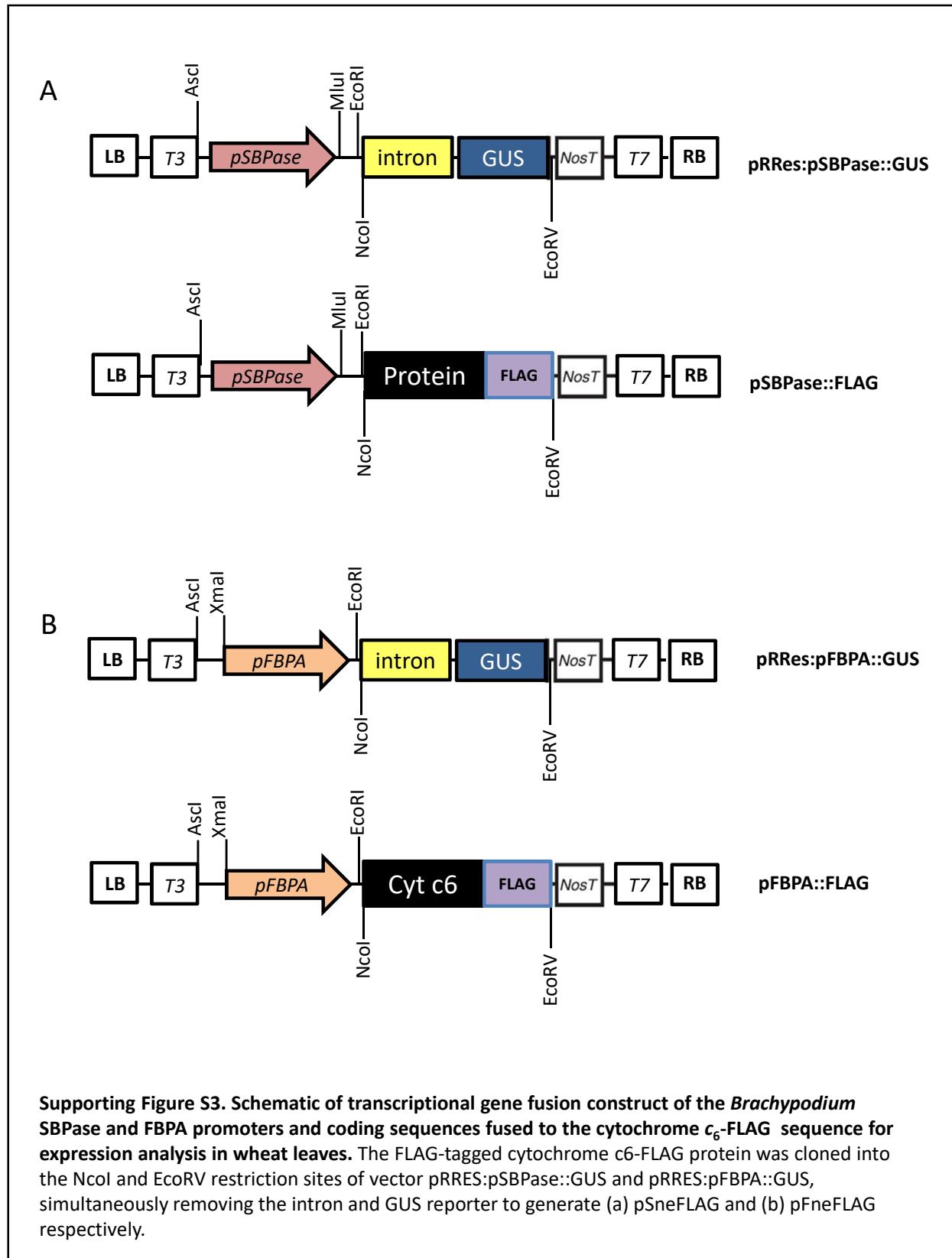


Supporting Figure S1. Schematic of transcriptional gene fusion constructs of the *Brachypodium* SBPase and FBPA promoters with the β -glucuronidase (GUS) reporter for expression analysis into *Nicotinia benthamiana* leaves. Genomic DNA of *Brachypodium* leaves was used to amplify the native promoters of SBPase and FBPA. They were cloned into the pENTR vector (Invitrogen). The resulting product was transferred into the (a) pGWB3 vector by LR recombination to make (b) pGW:pSBPase::GUS and (c) pGW:pFBPA::GUS.



Supporting Figure S2. Schematic of transcriptional gene fusion constructs of the *Brachypodium* SBPase and FBPA promoters with the β -glucuronidase (GUS) reporter for expression analysis in wheat leaves. Genomic DNA of *Brachypodium* leaves was used to amplify the native promoters of SBPase and FBPA and they were cloned into the corresponding restriction sites (pSBPase was cloned into the MluI and Ascl restriction sites and pFBPA was cloned into the EcoRI and XbaI restriction sites) of the (a) pRRes14.041 GUS vector to make (b) pRRes:pSBPase::GUS and (c) pRRes:pFBPA::GUS.



1 TCGACGTCCA TATGGCCCAG GACGGCGGCT TCGCTCCTAG TATTACCTCT GTTCACATAT
 61 GAATTCTATG AATAGTAAGT TCTCCGTGTT GCGGTTGGTG ACAAGAATT AGAATAGTAA
 121 TATTTTACGT GTGGTGTAA TGACTGTCGC TGATTTCTT AGACCATGAA ATCTTCTTG
 181 GCCATGAAAA TGTGAAATCT TTCTTGACCA TGATTAGAGG TAAACTAGTA CTGTGTAGAA
 241 CACTTGCCT TGGGAATTTC CAGATCCGTT AGCTTAGGG AAATATGTTT TTTCCACCAA
 301 CGGGATTGTC TGCGAAGCTC TTTGTTTGA TTCGTCTGTC ACTTGTAACT **CAAT**AAGGTT
 361 GAGTTCTTT CAGTTCTAG GACCGGTTT TTCTAAAAGC TGATCTCAC TAGCTTCTTA
 421 GAGAAGCCGC ATCTTAGATT TAGCTAGGTT TCCAAAATAA TTTGGTAGCC **CAAT**CAAATT
 481 TAGATGGTGA CTTCTTCAGG AAGCTGGGG AGTG **CAGCTT** TTGGAGAAG CCGATCCAGG
 541 AAACCGAAAA GAACTGGCCC TACGACGTCT ATTGATTTC TCCGTAGTT TTTACTTTT
 601 AGAAACGTAG GTCTAGTTGA GCTATTGAAT AGATGGGCCT CTCATTTGA TTTGATTG
 661 GGATTTGTCG AACCGAGTCA ACCTGTGGTG ATTTATAACC TCTCTAAATT TCCGATTCTC
 Gap Box **E Box**
 721 **AAAATGAAAA** ACCTCTCTAA ATTCCTAAA AAACCACAT AAATAAGG**CA** AATGAGTGA
 AE Box
 781 AACAGGCTGA GAACTCTCGC TCCATATCCC GCCATATT TTCTCTTACA GCTCGTTGA
 E Box AE Box **Box 1**
 841 CACCAAT**CAT** CTGGTTAG AATTCTGAAA TTCAT**TTCA** AAAATCAACT TATTGATTG
 901 GCGCAAGATT GGCCACGGAA ATT**CAAT**CTC AAAAATTCA TAAAGTCACA CTATAAAGTC
 AE Box **SP1**
 961 **CAAT**TCCAAA AATGGACGGT TAAATGGACG GCTAAGAAAT ATCCACTCCA TT**CCACCTG**
 Pi Box
 1021 TACGAAAGCA CAGTGGT**GAT** CAACAAGACA ACAAAAGCTGG ATCAAATCCC TTGTCACGAA
 1081 CTACTGCGGG CGGTGCCACG AAAAGCCAAC TTGCAAAGTA AGGTCCGGAT GAAACCTCCT
 1141 AACTCCTAAG GCTAAGGGGC TGTAAAAC TAATGTGGAT GCACCGTCTG ATGTAGATGA
 ACGT Box
 1201 ACTCCGAGGA ACA**GACCTG** TGTCAATTATT TCCGGACTCC AAGGGCGATT TTGTGGTGGC
 ACGT Box
 1261 TACCTATAAG AAGTTGCGG CGTGTCTT**GA** CGTT**CA**TGTT CCGGAAGCTT CTGCACTACA
 1321 CTTCGGACTC CTCGCACAAA TGGTGGGATG TAACAGGATG GTCATCGGTG GGTTGCACAA
 1381 CCAGGAAATG ATTGGTACCG CGAGCCAGCA CGAGCGATGA GGTACGGTGG AGCTGCGATC
 1441 TACGGAAACT CAAGTTTCAG GCAGACGAGT CCGTGGACAT TCGTGGACAT ATCCTTCAA
 CAAT Box
 1501 CATGCGCACC GCGAGTCAAA CATGGTGGCA CACGAACCTG CTCCGATGGC AAA**GCAT**TCT
 E Box
 1561 CCCTCCGCTA CTTGGATCGA AACCC**CACTT** GGTAACATTA TACCTCTGCT CTTGGAAGAT
 1621 GTAACGGCTA TTGAAGCCTG GTAAAATGGT ATTTGTGTCA AAAACAAAGA CAACAAAGCT
 F Box Gap Box
 1681 CGATCTCTAC ACCTTAGGAA TTCAGTT**GAT** **AAAAA** TAGCA GGACACTTCA CTGAATT
 1741 TTGACGAGTA CACTTCACTG AATTAAATCC GATGTGTTAC GACTTACAAG TCGCGACTAA
 Pi Box G Box/ ACGT Box
 1801 TTAATCTGCC CCTCCCTGTC AAGCGCGCAC ATACGTACGG ACCCGATT**GA** TCACGT**CGCA**
 1861 GGAGGGCCAC ACAACCCACG GACGGTCGTC GCGCGCCCCG GGACGCTCCC GGCGCGCTCT
 G Box/ACGT Box
 1921 ATCTTCTCCC GCG**CCACGTC** **GGCGCCCGGC** TTATCTGGTC CAGTCGT**GC** TCCGCCGTGT
 *
 1981 GTGATCCCAA ATCCCCCATC CGAGCTTAGC TGCAGCCGCA GGTAGGTGCG TCACCAACGCA
 2041 ACGTAAAATC GTATGACAAC TAAATAACAC ACTCCCCCT CCAAAGAAAA GCTTAAGCTC
 2101 AGTCCGCCTC GGTCACCTCG TCGGCGTCTA CCAGAGATTA CGGCAGCAGC TCGCATCGCA
 2161 GC**ATG**

Supporting Figure S4. Sequence of and regulatory motifs in the 2 Kb upstream region of the *Brachypodium* SBPase gene . The different coloured boxed sequences represent the promoter motifs (see Figure 1).

1 TCATTGGACG TGTTGATGTG CTGCGAGAAG CTATGCCAT TGCTGAGGCA GAAGCTTGTG
 61 GCTTTTTAT CTAGTAGCAG TCCTGGAGCA GCTGAAGAAG CTTGTGGTAA ACAGATTAAT
 121 GAGGTTTCTA AAGCAGCAGA GTTGA**AGAGA** GT**TTGCTCAA** ACTAGATGTC ACAACCTCT
 181 ATGTCCAGAA TGAACACAG CCAGCACTAG TTTCCCAGCA ATTTGTACTT TTGTATGTTC
 241 CTGGAAAGGA AAGAATAAGC AGAGGAATCG CAAGGCTTTA CGAGTATCAC AATTACAAAG
 301 GAGTGGAGAT TGATGAACAC ATCTTTGAA CAAGCAAGAG AAAGGAACCTT GGCCCCTGCT
 361 TGCCTCTGG AGCTACAAAC CTGGACCTCA CCAGCCACGG **TCCACCCGGT** ATGTATGGAG
AE Box
 421 **AAACACTCCC** ATCAGAGGCT GCCCTGACAG TCAGATTAAA TCAGAAGTTA ACTTCATTG
 481 TGTCAACCA AATACATAAT GCCAGAGTAA ATGGAGATCA CGCATGATGC TTGATTTCA
 541 ATTCTGCTG GTTGAACAA CTGAACCTTAT GGTACCTCG ATTGATATGC AGCCCAACAC
G Box
 601 **ATGGTATCTT** TTGTTGTTA CGGAGGATAG AATGCATTAA ACTGAAGGAT AGACTGTGCT
E Box
 661 TCCTGTGCTT CATTACAAGT TAGCTT**CAGA** TGTGATGAAT TTATGTGCTG GCAGCAAAGG
E Box
 721 AAATAATTGT CTGTGCAAAC CTATCTCTG CCTGAACCTGA TGAAAGAAAT GATA**CAGCTG**
Gap Box
 781 CACAGTAGAT GCATTAACG **ATGGTATCA** GAGTTAAGGT CTGGTG**CATA TGAAGC** TTGT
 841 GATACTGGAT GTTTTCACT TTTTGTTCA GGCATGCTCA TACTCTTAC AGAAAAAGGC
E Box
 901 ACATACACCA CAGCAGGGAG TCTTGGATGT ATTTCTCCCG AGTTATAGGA GAT**CATCTGA**
E Box
 961 TTTAAGTAGG CCAACCTGT GTACTTGTGA ACAATTGTA ACTAT**CAGCT** TTTGTTATTC
 1021 AATAGTAGTA AAATCCCTT CATGGTACTC TGTGTCCTT TTCATTGAGG GCAGTAGGTT
 1081 CCATATACCA ACTTGCTCTG TGATGTTAAT GTTTTGGTG ATTAGTGACA AGGGTGCCTA
Box 1
 1141 ATTTCTTTC TGATGTTAAT AT**TTTGAAAG** ATCTTCACTC TGAAAAAAA ATGCATGTT
 1201 ATATCCATGT TTCTCTAAAA ATAATCCATA GCCAGTGTGT GATACTTTCT ACTAGTTCCC
 1261 ACTAAATGCA TTGTGAAATT AAATTCTATA AAATTTGTA ATTTCTAATA TTTAGTAAGG
AE Box
 1321 GT**AGAAACAG** AGATTTTTT CTTAATTATA AATCATCATG TATCAGGAGT CGCAAAGGTC
 1381 CAGGAATGAT ATGCAAGATT GCTACATGGT TGGTATCCTC TTAATGTCAT CCTTGGCAGG
 1441 GAGTTGTGGT GGATATGCC TCTGCTGCCA GGCACGGGG CACAAGAAGA ATGGTGTCTG
SP1
 1501 CCACACA**AGC** **CACCC** TGAC CCTACAAACA ACTCACAGCT **GGAATGGTTA** TCACCAA**ACC**
CAAT Box
 1561 **AATG**ACAGAA AAAACTGTGT ATT**CCACCGTA** ATTGATGGTT ACTGGAAAA TTCATGGATG
 1621 TAATACATCA GGGCATCTCA ACCGTCGAAA GATGCTCATG GGCACACTC CTCGGCGAAA
AE Box
 1681 TGCGCCCACA GAAACCOAGA ATTGTTCATC AGCCAAGACC ATCCTTAAGG TCAAGAATGT
AE Box
 1741 CCAGATAATA TTTATGGACG GTGCAGCGCA AACGATAAAA TTCCAGTATT GCAGATTTTA
E Box
 1801 **CATGGTACAC** AGAGAAGCTA AGGAAATCAT AGAGACAA**AGC** **ATGTGGCAGA** GCCAGGACAA
CAAT Box
 1861 AAACAGAAGG TGGCAAGAGG ATTGGAGCAA **CCAAATCACA** GCCATTCTATA TCCAGAAGGC

 1921 CAGCCTCCAC CTCACAACTC ATATCCTTG TACTCAGGTA CTCACCCCTTA AAT**CTGAGCA**
 1981 GGCGCTTCAC TTCTCACCCCC CCCTAAGGAA AGGCTGCAAT TGCAAGCTTG TGTCAAAGAA
 2041 GAGGGTAGCA CCTGATCCTC TTGCCTTTGG AGCCAGAAC **AATG**

Supporting Figure S5. Sequence of and regulatory motifs in the 2 Kb upstream region of the *Brachypodium* FBPA gene . The different coloured boxed sequences represent the promoter motifs (see Figure 1).