

Supplementary material 1

Sequence of contig BC000036325 in bread wheat and annotated SNP from the cereals database (<http://www.cerealsdb.uk.net/cerealgenomics/CerealsDB>). The start-codon and Stop-codon of the identified gene are indicated in green and in red, respectively. The SNP position in the sequence was coded 'W', designating either nucleotides 'A' or 'T', and is highlighted in yellow. Two forward allele-specific primers and one common reverse primer are shown in Bold and highlighted in blue. Amplicon size is indicated. Sequences of primers and Universal probes are shown beneath. Specific 'tags' or 'tails' are in Italics. More details about allele-specific primers and Universal probes are available in our previous paper (Jatayev et al., 2017).

KATU-W62 - BC000036325

Contig sequence

ACGCCTAACCCCTAACCCCTAGCTACGATCCCCTTCTGCAACCCGGTCGTGTCTCAGGGCGCAT
CGCCGAAGGCCAAGCCCTCCCTCCCTAGCAGCGCCGGACCCATCGATCCCGGCGGGACGCG
CCGTCCGCGCCCCAGGCTCAAGCTCCATCGCGCGCTCGACGGCGAGGGATCGATCCGATGGA
CATCGTGGGCAAGTCCAAGGAGGACGTCTCCCTCCCCAAATCAACAATGACCAAGATTATTA
AGGAGATGCTACCGCCTGATGTTTCGAGTAGCAAGAGATACACAAGATCTTCTTGTGAATGC
TGTGTAGAGTTCATCAATCTTCTTTCTTCGGAATCCAATGACGTGTGCAGCCGGGACGACAA
GAAGACTATTGCTCCTGAACATGTTATTAGGGCTCTGCAGGATCTTGGCTTCAAGGAGTACG
TTGAAGAAGTTTATGCAGCCTACGAACAGCACAAGCTTGAAACTCTGGACTCTCCAAAAGCA
ACCAAGTTCACTGGTATAGAGATGACTGAAGAAGAAGCTGTTGCGGAACAGCAGAGAATGTT
TGCTGAAGCCCGAGCAAGGATGAACAATGAAGCTGCCAAACCAAAGGAGCCTGCATTAGAAC
CACAGAATCAACCCCAACAGCCCCCACAACCTCAACTGCAGCTGCATCCTCAAGCACAGCAG
CCTCCACAACCCCAATCGCAACTGCATCATCCTCAATCACAGCAGCCCCTGCATCCTCAACT
GCAACCGTATACTCAGGCTCCACCACAGCAACCCCTGCATCCTCAACTGCAACCGTATACTC
AGGCTCCACCACAGCAACCCCTACAACCTCCACTGCAGCTGTATCCTCAGGCTCAACCTGAG
CAACCCCTGCAGCCTCAATCCTCAGGATCAACCACAGGAACCTGTGTAATCTCAACTGCAGC
TCCATCTACAACCGGCACCCTGCTGCTGCAACCGCCGCCCCAGCAATCCCCGCAATCTCAA
CTGCAGCTCCATCAGCAACCCCAAGCCGACGCTAGTGCCGCGCGGCCGCAACCTCAACCCCA
GCCACCTGAACTGCAGCAGCCCCAGCCGCTAACACAACCTGCAAGCGGAACATGGCGTGGACT
GGACAGT **TAG**TGGTTCGGAACATGTAGCGTCACTATAAGTTAAGACTCTGCCTCCTTTAAAA
TTGTGCGTTAGGTTTGCCTGCATCTTGTACAATGTAAATTGA **GTGTGATTTACGCCACCGTG**
TCTGTAATAATCTGAAGCTCTCTAGTAAGTGATGTACTTACTGTACTGGATATTGTGTTTAT
GACTGCTGT **WGTCTCATGGTATTGTGCGTGT**CGTGTTCAGAAGCTACTCCATTACCAGTGTA
TCAATTGCCTAACTTA

W = A/T

KATU-W62-SNP-F1: ACACGCACAATACCATGAGACT T_m=53C 45%GC

Rev. Comp. **ASTCTCATGGTATTGTGCGTGT**

KATU-W62-SNP-F2: ACACGCACAATACCATGAGACA T_m=53C 45%GC

Rev. Comp. **TGTCTCATGGTATTGTGCGTGT**

KATU-W62-SNP-R: GTGTGATTTACGCCACCGTG T_m=53.8C 55%GC

PCR product size = 113 bp.

Ordered and used allele-specific primers:

KATU-W62-SNP-F1: *GAAGGTGACCAAGTTCATGCTACACGCACAATACCATGAGACT*

KATU-W62-SNP-F2: *GAAGGTCGGAGTCAACGGATTACACGCACAATACCATGAGACA*

KATU-W62-SNP-R: *GTGTGATTCAGCCACCGTG*

Universal probe 1:

5' -FAM-AGCGATGCGTTCGAGCATCGC (T*-BHQ1) GAAGGTGACCAAGTTCATGCT-3'

Universal probe 2:

5' -VIC-AGGACGCTGAGATGCGTCC (T*-BHQ1) GAAGGTCGGAGTCAACGGATT-3'

Supplementary material 2

A fragment of the BLASTN comparison of three *TaDr1* gene sequences. Accession AF464903 was annotated in the NCBI database as the *TaDr1A* gene in bread wheat and accession BT009234 from NCBI database was identified as the *TaDr1B* gene by Stephenson et al. (2007). Accession BC000036325 was identified in the current study from Cereals DB (Supplementary material 1). Primers for qPCR analysis highlighted in pink and in green were designed and used for *TaDr1A* and *TaDr1A*, respectively, by Stephenson et al. (2007). Primers highlighted in blue for qPCR analysis for total expression of both genes, *TaDr1A* and *TaDr1B* (= *TaDr1*) were developed in the current study based on the sequence of BC000036325. The stop-codon of *TaDr1* is shown in red and the annotated SNP is shown in yellow. Mismatches are indicated in Bold and those in the designed primers are underlined.

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AF464903      CCCAGCCGCTAACACAACCTGCAAGCGGAACATGGCCTGGACTGGGACAGTTAGTGGTTTCG
BT009234      CCCAGCCGCTAACACAACCTGCAAGCGGAACATGGCCTGAACTGG-ACAGTTAGTGGTTTCG
BC000036325   CCCAGCCGCTAACACAACCTGCAAGCGGAACATGGCGTGGACTGG-ACAGTTAGTGGTTTCG
*****      *****      *****      *****      *****
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AF464903      GAACATGTAGCGTCACTATAAGTTAAGACTCTGCCTCCTTTAAAATTGTGCGTTAGGTTT
BT009234      GAACATGTAGCGTCACTATAAGTTAAGACTCTGCCTCCTTTAAAATTGTGCGTTAGGTTT
BC000036325   GAACATGTAGCGTCACTATAAGTTAAGACTCTGCCTCCTTTAAAATTGTGCGTTAGGTTT
*****      *****      *****      *****      *****
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AF464903      GCCTGCATCTTGTACAATGTAAATCGTGTGTGATTTTCAGCCAACCGTGTC--TAATAATCT
BT009234      GCCTGCATCTTGTACAATGTAAATCGTGTGTGATTTTCAGCCACCGTGTCCTAATAATCT
BC000036325   GCCTGCATCTTGTACAATGTAAATTGAETGTGATTTTCAGCCACCGTCTCTGTAATAATCT
*****      *****      *****      *****      *****
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AF464903      GAAGCTCTCTAGTAAGCGATGTACTTACTGCGCTGGGTACTGTGTTTATGACTGCTGTAG
BT009234      GAAGCTCTCTAGTAAGCGATGTACTTACTGCGCTGGATACTGTGTTTATGACTGTTGTAG
BC000036325   GAAGCTCTCTAGTAAGTATGTACTTACTGTACTGGATATTGTGTTTATGACTGCTGTW
*****      *****      *****      *****      *****
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AF464903      TCTCATGGTATTGTGTGTGACGTGTCAGAAGCTACTCCATTACCAGTGAATCAATTGCC
BT009234      TCTCATGCTATTGTGTGTGACGTGTCAGAGCTACTCCATTACCAGTGAATCAATTGCC
BC000036325   TCTCATGGTATTGTGCGTGTGTCGTGTCAGAAGCTACTCCATTACCAGTGAATCAATTGCC
*****      *****      *****      *****      *****
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AF464903      TAACTTAATGTTTCAACCGTGATGAT-----
BT009234      TGACTTAACTGTTCAACCGTGATGATAGTAATTGATTTTCAGTGTGCTAA
BC000036325   TAACTTA-----
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Sequence of Reference genes used for qPCR

ATP-dependent 26S proteasome

Ta22845-F: GCTGGCTCGTTCAACTGATG

Ta22845-R: GGACCAAGCGTTCTGATTACTC

Size of amplicon: 202 bp (Paolacci et al., 2009)

Actin

Ta54825-F: TGACCGTATGAGCAAGGAG

Ta54825-R: CCAGACAACCTCGCAACTTAG

Size of amplicon: 215 bp (Paolacci et al., 2009)