A rice centromeric sequence is conserved between wheat and rice, as well as between monocots and dicots

Qi LL, Friebe B, Gill BS

Wheat Genetic and Genomic Resources Center, Department of Plant Pathology, Kansas State University, Manhattan, KS 66506-5502, USA

ABSTRACT

The rice centromeric clone 6730.t11, located in the kinetochore region of the rice chromosome 8 centromere, was mapped to the centromeric regions of wheat group-7 chromosomes by Southern hybridization. PCR amplification with an RT-PCR (Reverse Transcription-PCR) primer of 6730.t11 was conducted on genomic DNA isolated from Triticeae species, including T. urartu, T. monococcum subsp. monococcum, T. monococcum subsp. aegilopoides, Ae. speltoides, Ae. tauschii, barley, rye, and H. villosa, the rice cultivars (O. sativa subsp. Japonica) 'Nipponbare' and (O. sativa subsp. Indica) 'IRBB7', maize, soybean, tomato, and Arabidopsis. A 211-bp sequence was amplified from Nipponbare, which showed 100% identity to the sequenced rice genomic DNA covered by the 6730.t11 RT-PCR primer. Of eight plasmid clones of PCR products sequenced from IRBB7, six had the same 211-bp sequence as found in Nipponbare. Two clones had a 202-bp sequence that shared 100 percent and 87 percent similarity in the first 38 and the last 72 nucleotides, respectively, with the 211-bp sequence amplified from Nipponbare. Surprisingly, the 202-bp sequence amplified from IRBB7 was found in all monocot and dicot species used in this study except Nipponbare. Sequence similarity ranged from 99% to 100% when compared to the 202-bp sequence in IRBB7. A PCR-amplified fragment from genomic DNA of Chinese Spring (CS) wheat using an RT-PCR primer of the clone 6730.t11 was mapped to the same region as clone 6730.t11 in wheat. The RT-PCR results from CS cDNA with primers of 6730.t11 indicated that the rice centromeric gene was expressed in wheat leaf tissue. Our data demonstrate strong selection pressure for the conservation of this DNA element in the kinetochore region of plants, although its functional role remains to be established.

INTRODUCTION

Most eukaryotic centromeres are generally at the megabase level and known to be devoid of genes. Sequencing and assembling such highly repetitive centromeres are a big challenge for genome sequencing projects. Although the genomes of several eukaryotes, including *Drosophila melanogaster*, human, mouse, *Arabidopsis thaliana*, and rice, have been sequenced, only three centromeres of rice chromosomes 3, 4, and 8 were sequenced and assembled^{3, 7, 8}. Previous studies

have identified expressed genes and transcripts in the flanking regions of some centromeres¹ and reported active genes and their normal transcription in a human neocentremere⁵. Discovery of active genes in the sequenced centromere was first reported in rice chromosome 8^3 . Recent research indicated that there are at least 16 active genes within a ~750 kb core domain associated with CENH3 of the centromere of chromosome 8. The ~1,881 kb CENH3 domain of the centromere of rice chromosome 3 also contains 19 transcribed genes⁸. The active genes found in the rice centromere provide a good opportunity to study syntenic relationships between the centromeres of wheat and rice.

MATERIALS AND METHODS

Plant materials: The following species were used: *Triticum urartu, T. monococcum subsp. aegilopoides, T. monococcum subsp. monococcum, Aegilops. speltoides, Ae. tauschii, Hordeum vulgare* cv. Betzes, *Secale cereale* cv. Imperal, *Haynaldia villosa, Oryza sativa* sp. *Japonica* cv. Nipponbare, *Oryza sativa* sp. *Indica* cv. IRBB7, *Zea mays* cv. B73, *Glycine max* cv. Jack, *Lycopersicon esculentum* cv. Pto.R, and *Arabidopsis thaliana Columbia*. Genetic stocks used in the study included 21 wheat nullisomic-tetrasomic (NT) lines, six ditelosomic (Dt) lines, and 19 deletion (del) lines of homoeologous group 7 chromosomes.

DNA extraction and PCR: Genomic DNA was extracted from leaves as reported in Qi et al.⁴. Sequences of the primer of 6730t11 were according to Nagaki et al.³. PCR reactions were performed in a final volume of 25 μ l containing 50 ng DNA, 1,5 mM MgCl₂, 0.3 mM dNTPs, 1X reaction buffer, 12.5 pmol forward and revised primers, and 1 unit *Taq* polymerase (BIOLINE, Boston).

RNA extraction and RT-PCR: Total RNA was extracted from the CS leaf tissue using TRIzol reagent (Invitrogen Corp., Carlsbad, MA). The first strand cDNA was synthesized using oligo $(dT)_{20}$ primer with SuperScriptTM III Reverse Transcriptase (Invitrogen, Corp., Carlsbad, MA). RT-PCR was conducted using the first strand cDNA as template with gene-specific primers.

RESULTS

A conserved, possible centromeric sequence in monocots and dicots

Three rice centromeric clones, 6729.t09, 6729.t10, and 6730.t11, located in the kinetochore region of the rice

chromosome 8 centromere, were assigned to the centromeric regions of homoeologous group-7 chromosomes (our unpublished data). The RT-PCR primers of these clones were used to amplify DNA fragments from genomic DNA of CS wheat. Two pairs of primers, 6729.t09 and 6729.t10, amplified multifragments, while primer 6730.t11 amplified a unique DNA fragment. When the PCR products from a set of wheat nulli-tetrasomic lines amplified by RT-PCR primer 6730.t11 were separated on a SSCP gel, three fragments could be distinguished from chromosomes 7A, 7B, and 7D. A 202-bp sequence was found in these chromosomes. The rice genomic DNA recovered by the 6730.t11 RT-PCR primer has a 211-bp sequence (http://www.tigr.org/tdb/e2k1/osa1/pseudomolecules/inf o.shtml), which shares 100 percent and 87 percent similarity in first 38 and last 72 nucleotides, respectively, with the 202-bp sequence amplified from CS-7A. Amplification from rice cultivar IRBB7 with the 6730.t11 RT-PCR primer gave two sequences, 202-bp and 211-bp. However, only the 211-bp sequence was recovered from rice cultivar Nipponbare, an original source for rice genomic sequencing. Further, PCR amplifications with the 6730.t11 RT-PCR primer were conducted in T. uratu, T. monococcum subsp. aegilopoides and monococcum, Ae. speltoides, Ae. tauschii, barley, rye, H. villosa, maize, soybean, tomato, and Arabidopsis.

CS-7A and A-genome species: The CS-7A and two accessions, TA709 and TA829, of *T. urartu* have a 202-bp sequence that is identical with the 202-bp sequence in rice IRBB7. Both *T. monococcum* subspecies also have a 202-bp sequence, that share a common SNP; subspecies aegilopoides has an additional SNP (Fig. 1).

CS-7B and *Ae. speltoides*: The amplified sequences from CS-7B and two accessions of *Ae. speltoides* are heterogeneous. Most clones sequence have a 204-bp sequence with an insertion of two nucleotides (AT) in position 94 and a SNP in position 38 compared with the rice 202-bp sequence. A 202-bp sequence, identical with that of rice IRBB7, is also present in CS-7B and *Ae. speltoides* accession TA2780 (Fig. 1).

CS-7D and *Ae. tauschii*: The 202-bp sequences among the CS-7D and two accessions, TA1691 and TA10132, of *Ae. tauschii* are identical and share a common SNP in position 157 with *Ae speltoides* accession TA1770, barley, rye, and soybean compared with the 202-bp sequence in rice IRBB7 (Fig. 1).

Barley: Sequence data from the barley cultivar Betzes are more complicated. Four sequence types were present in barley. Among eight clones sequenced, four have a 198-bp sequence that shows two deletions in positions 124 and 137 and eight independent SNPs compared with the 202-bp sequence in rice IRBB7. Four clones have the 202-bp sequence of these, two are identical with the 202-bp sequence of rice IRBB7, and another two share two conserved SNPs in positions 157 and 165 with several other species (Fig. 1).

Rye: Only the 202-bp sequence was amplified from rye cultivar Imperal, but they are heterogeneous. Of six 202-bp sequences, three are identical with the rice 202-bp

sequence, one has a SNP in position 157, and two have a SNP in position 165 (Fig. 1).

H. villosa: *H. villosa* is a distant relative of wheat and a cross-pollinating species. A 204-bp sequence found in *H. villosa* is identical with that in CS-7B. Of four 202-bp sequences, two are identical in sequence to rice IRBB7, and the other two have a SNP at position 165 (Fig. 1).

Maize: The sequences amplified from maize cultivar B-73 are divergent. Five of nine clones sequenced have a 184-bp sequence. Three maize clones have a 202-bp sequence identical to the rice 202-bp sequence and one clone has a 211-bp sequence identical with the rice 211-bp sequence.

Soybean: Three soybean clones have a 202-bp sequence identical with the rice 202-bp sequence. The other two 202-bp sequences in soybean have SNPs in positions 82 and 165 (Fig. 1).

Tomato and *Arabidopsis*: The amplified sequence from tomato cultivar Pto.R is unique and has 100 percent similarity to the rice 202-bp sequence. Three of four sequenced clones from *A. thaliana* accession Columbia (Col) have the rice 202-bp sequence. A 204-bp sequence found in Col is the same as the 204-bp sequence of CS-7B except for two additional SNPs in positions 97 and 159.

Mapping the 6730t11-CS fragment to the centromere regions of group-7 chromosomes

The DNA fragment amplified from CS gDNA, named 6730.t11-CS, was mapped to the centromeric regions of the group-7 chromosomes using a set of wheat NT and Dt lines and group-7 chromosome deletion lines by Southern hybridization. The location of this clone in wheat chromosomes is the same as that of rice clone 6730t11, which mapped to the long arm of chromosomes 7A and 7B but to the short arm of chromosome 7D. 6730t11-CS appears to be a single copy clone with three hybridization fragments after CS gDNA was digested with *Eco*RI.

Rice centromeric gene expression in wheat

Rice centromeric clone 6730t11 is an expressed gene, coding a putative cystathionine- β -synthase (CBS) domain containing protein. RT-PCR analysis was conducted in the wheat cultivar CS. The primer of 6730.t11 amplified a RT-PCR ~95-bp fragment from CS cDNA isolated from leaf tissue with a size similar to that in rice, indicating that the rice gene is expressed in wheat.

DISCUSSION

Centromeric DNA organization varies widely among species, especially centromeric repeat sequences. Species-specific centromeric DNA was found not only in human but also in mouse, rice, maize, and budding

IRBB7-2	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
CS_7A-2	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
TA709-1	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
TA829-1	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
CS 7B-1	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
TA2780-1	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
Barley-7	CTCCCTCAAACTACTAACCTTCAACATCCTCCAACCTACCTCCACCA	60
Buo-5	CTCCCTCALACTACTACCTTCALCOTCCACCTCCALCCTCACCACCACCACCACCACCACCACCACCACCACCACC	60
H w=3	CTCCCTCALACTACTACCTTCALCOTCCACCTCCALCCTCACCACCACCACCACCACCACCACCACCACCACCACC	60
D72 E	CECCCECA A A CER A COMECA A COMECCE A COMECCE A COMECA CONCERNATION I I COMECCE A COME	60
B/3-J	GIGCGIGARACIACIACIIGAAGAIGCIGCAAGGIACGIGIACAICACIGAIIGGIII	60
C01-1	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
Jack-5	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
pto-1	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
Jack-3	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
TA183-1	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
TA141-1	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
Barley-6	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
Rye-6	GTGCGTGAAACTACTAACCTTGAAGATGCTGCNAGGTACGTGTACATCACTGATTGGTTT	60
H.v8	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGCGTACATCACTGATTGGTTT	60
TA1770-4	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
CS 7D-2	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
TA1691-2	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
TA10132-2	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
Barley-9	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
Rye-2	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60
Jack-1	GTGCGTGAAACTACTAACCTTGAAGATGCTGCAAGGTACGTGTACATCACTGATTGGTTT	60

IRBB7-2	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
CS_7A-2	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
TA709-1	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
TA829-1	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
CS_7B-1	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
TA2780-1	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
Barley-7	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
Rye-5	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
H.v-3	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
в73-5	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
C01-1	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
Jack-5	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATGATGATGA	12
nto-1	CCAGAGATTATATGGACCAACTTGTATGTTATGTTTATGTTTATATGATG	12
Jack-3	CCAGAGATTATATGGACCAACCTATCTATGTATGTATATATA	12
TA193_1	CCACACACATTATATGCACCACCTCTATCTTATCTTTCTT	12
TA141-1	CCAGAGATTATATGGACCAACTTGTATGTTGTTTGTTTGT	12
Barlov-6		12
Burney 0		12
H v=8	CCAGAGATTATATGGACCAACTTGTATGTTGTTTGTTTGT	12
TA1770-4	CCAGAGATTATATGGACCAACTTGTACGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
CS 7D-2	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
TA1691-2	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
TA10132-2	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
Barley-9	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
Rye-2	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
Jack-1	CCAGAGATTATATGGACCAACTTGTATGTTAATGTTTCTTAAAGATAACTTAATTAGATG	12
IRBB7-2	GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG	18
IRBB7-2 CS_7A-2	GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG	18 18
IRBB7-2 CS_7A-2 TA709-1	GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCCCAGGCTGCCAGTAG GTGGTGATATTTTGGCAGGTACTTCTTGTTACTAAATACCCCAGGCTGCCAGTAG	18 18 18
IRBB7-2 CS_7A-2 TA709-1 TA829-1	GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCGCCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG	18 18 18
IRBB7-2 CS_7A-2 TA709-1 TA829-1 CS_7B-1	GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG	18 18 18 18
IRBB7-2 CS_7A-2 TA709-1 TA829-1 CS_7B-1 TA2780-1	GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGGCTGCCAGTAG GTGGTGATATTTTGGCACGGGTTACTTCTTGTTACTAAATACCGCAGGCGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCGTACTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCGTACTCTTGTTACTAAATACCGCAGGCTGCCAGTAG	18 18 18 18 18
IRBB7-2 CS_7A-2 TA709-1 TA829-1 CS_7B-1 TA2780-1 Barley-7	GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG	18 18 18 18 18 18 18
IRBB7-2 CS 7A-2 TA709-1 TA829-1 CS 7B-1 TA2780-1 Barley-7 Rye-5	GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG	18 18 18 18 18 18 18 18 18
IRBB7-2 CS_7A-2 TA709-1 TA829-1 CS_7B-1 TA2780-1 Barley-7 Rye-5 H.v-3	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG	18) 18) 18) 18) 18) 18) 18) 18) 18) 18)
IRBB7-2 CS_7A-2 TA709-1 TA829-1 CS_7B-1 TA2780-1 Barley-7 Rye-5 H.v-3 B73-5	GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG	18) 18) 18) 18) 18) 18) 18) 18) 18) 18)
IRBB7-2 CS 7A-2 TA709-1 CS 7B-1 TA2780-1 Barley-7 Rye-5 H.v-3 B73-5 C01-1	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG	18) 18) 18) 18) 18) 18) 18) 18) 18) 18)
IRBB7-2 CS 7A-2 TA709-1 TA829-1 CS 7B-1 TA2780-1 Barley-7 Rye-5 H.v-3 B73-5 C01-1 Jack-5	GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTCCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCCCCAGGCTGCCCAGTAG GTGGTGATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCCCCAGGCTGCCCAGTAG GTGGTGATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCCCCAGGCTGCCCAGTAG GTGGTGATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCCCCAGGCTGCCCAGTAG GTGGTGATTTTGGCAGGTACTCTTGTTACTAAATACCCCCAGGCTGCCCAGTAG	18) 18) 18) 18) 18) 18) 18) 18) 18) 18)
IRBB7-2 CS 7A-2 TA709-1 TA829-1 CS 7B-1 TA2780-1 Barley-7 Rye-5 H.v-3 B73-5 C01-1 Jack-5 pto-1	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCCCAGGCTCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCCCAGGCTCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCCCAGGCTCCCAGTAG	18) 18) 18) 18) 18) 18) 18) 18) 18) 18)
IRB87-2 CS 7A-2 TA709-1 TA829-1 CS 7B-1 TA2780-1 Barley-7 Rye-5 H.v-3 B73-5 C01-1 Jack-5 pto-1 Jack-3	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCCCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCCCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCCCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCCCAGGCTGCCCAGTAG	18) 18) 18) 18) 18) 18) 18) 18) 18) 18)
IRB87-2 CS 7A-2 TA709-1 TA829-1 CS 7B-1 TA2780-1 Barley-7 Rye-5 H.v-3 B73-5 C01-1 Jack-5 pto-1 Jack-3 TA183-1	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGGATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG	18 18 18 18 18 18 18 18 18 18 18 18 18 1
IRB87-2 CS 7A-2 TA709-1 TA829-1 CS 7B-1 TA2780-1 Barley-7 Rye-5 H.v-3 B73-5 C01-1 Jack-5 pto-1 Jack-3 TA183-1 TA141-1	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTGTTACTAAATACCGCAGGGCTGCCCAGTAG GTGGTGATTTTGGCATGCAGGTTACTTCTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATTTTGGCATGCAGGTTACTTCTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATTTTGGCATGCAGGTTACTTCTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATTTTGGCATGCAGGTTACTTCTGTTACTAAATACCGCAGGCTGCCAGTAG	18 18 18 18 18 18 18 18 18 18 18 18 18 1
IRBB7-2 CS TA-2 TA709-1 TA829-1 CS TB-1 TA2780-1 Barley-7 Rye-5 H.v-3 B73-5 C01-1 Jack-5 TA183-1 TA183-1 TA141-1 Barley-6	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATTTTGGCATGCAGGTACTTGTTGTTACTAAATACTGCAGGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTACTTGTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATTTTGGCATGCAGGTACTTGTTGTTACTAAATACTGCAGGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTACTTGTTGTTACTAAATACTGCCAGGCTGCCAGTAG	18 18 18 18 18 18 18 18 18 18 18 18 18 1
IRB87-2 CS 7A-2 TA709-1 TA829-1 CS 7B-1 TA2780-1 Barley-7 Rye-5 H.v-3 B73-5 C01-1 Jack-5 pto-1 Jack-3 TA183-1 TA141-1 Barley-6	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGGTGATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGGGATTTTGGCAGGTACCTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGGGATTTTGGCAGGTACCTGTTGTTACTAAATACCGCAGGCTGCCAGTAG	18 18 18 18 18 18 18 18 18 18 18 18 18 1
IRB87-2 CS TA-2 TA709-1 TA829-1 CS 7B-1 TA2780-1 Barley-7 Rye-5 H.v-3 B73-5 C01-1 Jack-5 pto-1 Jack-3 TA183-1 TA141-1 Barley-6 Rye-6 H.v-8	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCGCAGGCTCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCCCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCCCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACGCCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTACTCTTGTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTACTCTTGTTGTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTACTCTTGTTGTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATTTTGGCATGCAGGTACTCTGTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATTTGGCATGCAGGTACTCTTGTTGTACTAAATACTGCCAGGCTGCCAGTAG	18 18 18 18 18 18 18 18 18 18 18 18 18 1
IRB97-2 CS 7A-2 TA709-1 TA709-1 TA829-1 CS 7B-1 TA2780-1 Barley-7 Rye-5 H.v-3 B73-5 C01-1 Jack-5 pto-1 Jack-5 pto-1 Jack-3 TA183-1 TA183-1 TA141-1 Barley-6 Rye-6 H.v-8 TA1770-4	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCAGGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCAGGTGCAGTTACTTGTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCAGGTGCAGTTACTTGTGTTACTAAATACTGCCAGGGCCCCGCAGTAG GTGGTGATATTTGGCAGGTGCAGTTACTTGTGTTGTTACTAAATACTGCCAGGGTCCCAGTAG GTGGTGATATTTGGCAGGTGCAGTTACTTGTGTTACTAAATACTGCCAGGGTCCCGGTAG GTGGTGATATTTGGCAGGTGCCAGTTACTTGTGTTGTTACTAAATACCGCAGGGCCCCAGTAG GTGGTGATATTTGGCAGGTGCCAGTACTTCTTGTTACTAAATACCGCAGGGCCCCGAGTAG GTGGTGATATTTGGCAGGTACCTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATTTTGGCAGGTACCTCTTGTTACTAAATACTGCCAGGGTCCCGCAGTAG GTGGTGATATTTGGCAGGTACCTCTTGTTGTTACTAAATACTGCCAGGGTCCAGTAG GTGGTGATTTTGGCAGGTACCTCTTGTTGTTACTAAATACCCAGGGTCCCAGTAG GTGGTGATTTGGCAGGTACCTCTTGTTGTTACTAAATACTGCCAGGTCCAGTAG GTGGTGATTTGGCAGGTACCTCTGTTGTTACTAAATACCCCAGGGCCCCGCAGTAG GTGGGTGATTTGGCAGGTACCCTGTGTTGTTACTAAATACCCCAGGTCGCAGTAG GTGGTGATTTGGCAGGTACCCGCTGTTGTTGTTACTAAATACCCCAGGCTCCCAGTAG GTGGGTGATTGTGGCGAGTACCCTGTGTGTACTAAATACCCCAGGTCGCAGTAG GTGGTGATACCCAGGTACCCGCGCTGTTGTGTGTGTACTAAATACCCCAGGCGCCCAGTAG	18) 18) 18) 18) 18) 18) 18) 18) 18) 18)
$\begin{array}{c} {\rm IRB}7{-}2\\ {\rm CS}~7{\rm A}{-}2\\ {\rm TA}709{-}1\\ {\rm TA}829{-}1\\ {\rm CS}~7{\rm B}{-}1\\ {\rm TA}2780{-}1\\ {\rm Barley}{-}7\\ {\rm Rye}{-}5\\ {\rm H}{\cdot}{\rm V}{-}3\\ {\rm B}73{-}5\\ {\rm C0}1{-}1\\ {\rm Jack}{-}5\\ {\rm pto}{-}1\\ {\rm Jack}{-}5\\ {\rm pto}{-}1\\ {\rm Jack}{-}3\\ {\rm TA}183{-}1\\ {\rm TA}141{-}1\\ {\rm Barley}{-}6\\ {\rm Rye}{-}6\\ {\rm H}{\cdot}{\rm V}{-}8\\ {\rm TA}1770{-}4\\ {\rm CS}_{-}7D{-}2\\ \end{array}$	GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATATCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATTTTGGCATGCAGGTTACTTCTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATTTTGGCATGCAGGTTACTTCTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATTTGGCATGCAGGTTACTTCTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATTTGGCATGCAGGTTACTTCTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATTTGGCAGCTACGCAGGTTACTTCTGTTAG	180 180 180 180 180 180 180 180 180 180
$\begin{array}{c} IRBB7-2\\ CS: 7A-2\\ TA709-1\\ TA709-1\\ CS: 7B-1\\ RS29-1\\ CS: 7B-1\\ Barley-7\\ Rye-5\\ H:v-3\\ Barley-7\\ Barley-7\\ IA183-1\\ TA183-1\\ TA183-1\\ TA183-1\\ TA183-1\\ TA183-1\\ Rarley-6\\ Rye-6\\ Rye-6\\ Rye-6\\ Rye-7\\ TA183-1\\ TA$	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTTACTAAATACCGCAGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTTACTAAATACCGCAGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTAGTAAATACCGCAGGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTGTTAGTAAATACCGCAGGGTGCCAGTAG GTGGTGATTTGGCATGCAGGTTACTCTTGTTAGTAAATACCGCAGGGTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTTAGTAAATACCCCCAGGTGCCCCGCAGTAG GTGGTGATTTGGCATGCAGGTACTCTCTGTTAGTAAATACCCCCAGGTGCCCCGATAG GTGGTGATATTTGGCATGCAGGTACTCTCTGTTGTAGTAAATACCCCAGGGTGCCCCGCAGTAG GTGGTGATTTGGCATGCGAG	18) 18) 18) 18) 18) 18) 18) 18) 18) 18)
$\begin{array}{c} {\rm IRBB7-2}\\ {\rm CS}, 7h-2\\ {\rm TA}709-1\\ {\rm TA}29-1\\ {\rm CS}, 7h-2\\ {\rm R}29-1\\ {\rm CS}, 7B-1\\ {\rm TA}2780-1\\ {\rm Barley-7}\\ {\rm Rye-5}\\ {\rm C01-1}\\ {\rm C01-1}\\ {\rm C01-1}\\ {\rm Barley-6}\\ {\rm Fyc-6}\\ {\rm H}, {\rm V-8}\\ {\rm TA}1471-1\\ {\rm Barley-6}\\ {\rm H}, {\rm V-8}\\ {\rm TA}1770-4\\ {\rm TA}1691-2\\ {\rm TA}1691-2\\ {\rm TA}1691-2\\ {\rm TA}1691-2\\ {\rm TA}1691-2\\ {\rm C}\\ {\rm C}10012-2\\ {\rm C}\\ {\rm C}\\ {\rm C}10012-2\\ {\rm C}\\ {\rm C}\\$	GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATGCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATGCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATGCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATGCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTAGTAAATACCGCCAGGCTGCCCAGTAG GTGGTGATATTTGGCAGGTACCTTCTTGTTAGTAAATACCCCAGGCTGCCCAGTAG GTGGTGATATTTGGCAGGTGCAGGTACTTCTTGTTAGTAAATACCCCCAGGCTGCCCAGTAG GTGGTGATATTTGGCAGGTGCAGGTACTTCTTGTTAGTAAATACCCCCAGGTG	180 180 180 180 180 180 180 180 180 180
$\begin{array}{c} {\rm IRBS7-2}\\ {\rm CS} & {\rm 7A-2}\\ {\rm CS} & {\rm 7A-2}\\ {\rm TA}({\rm 70-1}\\ {\rm TA}({\rm 29-1}\\ {\rm TA}({\rm 270-1}\\ {\rm A}({\rm 280-1}\\ {\rm Barley-5}\\ {\rm Rye-5}\\ {\rm Rye-5}\\ {\rm Rye-5}\\ {\rm Rye-6}\\ {\rm Rye-6}\\ {\rm Rye-6}\\ {\rm Rye-6}\\ {\rm Rye-6}\\ {\rm Rye-6}\\ {\rm TA}({\rm 30-1}\\ {\rm TA}({\rm 30-1}\\ {\rm CS}({\rm 10-1}\\ {\rm TA}({\rm 30-1}\\ {\rm CS}({\rm 10-2}\\ {\rm TA}({\rm 30-1}\\ {\rm CS}({\rm 10-2}\\ {\rm TA}({\rm 10-1}\\ {\rm CS}({\rm 10-2}\\ {\rm C$	GTGGTGATATTTTGGCAGGTGCTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCAGGTGCTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCAGGTGCAGGTTACTTGTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCAGGTGCAGGTTACTTGTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCAGGTGCAGGTTACTTGTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCAGGTGCGCTGTGTGTACTAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCAGGTGCGGTGC	180 180 180 180 180 180 180 180 180 180
IRB87-2 CS 7A-2 CS 7A-2 CS 7A-1 TA229-1 CS 7B-1 TA2780-1 Barley-7 Rye-5 H.v-3 D1-1 Jack-3 TA183-1 TA181-1 Barley-6 H.v-8 TA141-1 Barley-6 H.v-8 TA1710-1 Jack-3 TA183-1 TA141-1 Barley-2 TA10132-2 TA10132-2 TA10132-2	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACTGCCAGGCTGCCCAGTAG GTGGTGATATTTGGCAGGTACGTCTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCAGCAGGTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCAGCAGGTACTTCTTGTTAGTAAATACCGCAGGGCCCAGTAG GTGGTGATATTTGGCAGCAGGTACTTCTTGTTAGTAAATACCGCAGGGCCCAGTAG GTGGTGATTTTGGCAGCAGGTACTTCTTGTTAGTAAATACCGCAGGGCCCAGTAG GTGGTGATATTTGGCAGCAGGTACTTCTTGTTAGTAAATACCGCAGGGCCCGCAGTAG GTGGGTGATTTTGGCAGCAGGTACTTCTTGTTAGTAAATACCGCAGGGCCCGCAGTAG GTGGGTGATTTTGGCAGCAGGTACTTCTTGTTAGTAAATACCGCAGGGCCGCAGTAG GTGGGTGATTTTGGCAGGTGCCGCTGCTGTTAGTAAATACCGCAGGGCCCGCAGTAG GTGGGTGATTTTGGCAGGTGCCGTTACTTGTTAGTAAATACCGCAGGGCCCGCAGTAG GTGGGTGATTTGTGGAGGTACTCTTGTTAGTAAATACCCCCAGGGCCGCCGCAGTAG GTGGGTGATTTTGGCAGGTGCG	180 188 188 180 180 180 180 180 180 180
$\begin{array}{c} {\rm IRBB7-2}\\ {\rm CS} & {\rm 7A-2}\\ {\rm CS} & {\rm 7A-2}\\ {\rm TA}({\rm 70}-{\rm 1})\\ {\rm TA}({\rm 270}-{\rm 1})\\ {\rm TA}({\rm 2$	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCCCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACCCCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTACTAAATACTCCAGGCTCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTGTACTAAATACTCCAGGCTCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTGTTGTACTAAATACTCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTGTTGTACTAAATACTCCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTGTTGTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTGTTGTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTGTGTTGTAAATAATCCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCAGGTACCTTGTTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCAGGTACCTTGTTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCAGGTGACTTCTTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGATTTGGCAGGTACCTGTTGTTGATAAATACCGCAGGCTGCCAGTAG GTGGTGATTTGGCAGGTACCTGTTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGAATTTGGCAGGTACCTGCTGTTGTTAGTAAATACCGCAGGCTGCCAGTAG GTGGTGAATTTGGCAGGTACCTGCTGTGTGTAGTAAATACCCCAGGGCGCCAGTAG GTGGTGAATTTGGCAGGTACCCGAGGTACCTTGTTGTAGTAAATACCCCAGGGCGCAGGTAG GTGGTGAATTTGGCAGGTACCCGCAGGTACCT	180 180 180 180 180 180 180 180 180 180
IRB87-2 (CS 7A-2 TA709-1 TA829-1 (S 7B-1 TA2780-1 Barley-7 Rye-5 B33-5 B33-5 B33-5 B33-5 B346k-5 Barley-6 Rye-6 Barley-6 Rye-6 Barley-1 TA1081-1 TA1081-2 TA1081-2 TA1082-2 Barley-9 Rye-2 Barley-9	GTGGTGATATTTTGGCATGCAGGTTACTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTACTAAATACCGCAGGTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTGTTACTAAATACCGCAGGGCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTGTACTAAATACCGCAGGGCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTGTACTAAATACCGCAGGGCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTATATAATGCCAGGGCCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTATAATAATCCCCAGGTGCCAGTAG GTGGTGATATTTGGCAGCAGGTACTCTCTGTTAGTAAATACCGCAGGGCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTGTATGATAATACCGCAGGGCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTATGATAATACCGCAGGGCCCCAGTAG GTGGTGATATTTGGCAGCAGGTTACTCTTGTTAGTAAATACCGCAGGGCCCCCGCAG GTGGTGATATTTGGCAGCAGGTTACTCTTGTTGTAGTAAATACCGCAGGGCCCCGCAGG GTGGTGATATTTGGCAGCAGGTTACTCTCTGTTAGTAAATACCGCAGGGCCCCGCAGG GTGGGTGATTTGGCAGCAGGTTACTCTCTGTTAGTAAATACCGCAGGGCCCCGCAGG GTGGGTGATTTGGCAGCAGGTGACCTCTGTTGTTAGTAAATACCGCAGGGCCCCGCAGGTG GTGGGTGATATTTGGCAGGTGACCTCTCTGTTAGTAAATACCGCAGGCCCCG	18: 18: 18: 18: 18: 18: 18: 18: 18: 18:
$\begin{array}{c} {\rm IRBB7-2}\\ {\rm CS} & {\rm 7A-2}\\ {\rm CS} & {\rm 7A-2}\\ {\rm TA}({\rm 70}-{\rm I})\\ {\rm TA}({\rm 29-1})\\ {\rm TA}({\rm 270}-{\rm I})\\ {\rm A}({\rm 28-1})\\ {\rm C}({\rm 28-1})\\ {\rm C$	Grogtgatatittegcatgcagetagetagetagetagetagetagetagetagetaget	18: 18: 18: 18: 18: 18: 18: 18: 18: 18:
$\begin{array}{c} {\rm IRBR7-2}\\ {\rm CS} & {\rm TA-2}\\ {\rm CS} & {\rm TA-2}\\ {\rm TA709-1}\\ {\rm TA829-1}\\ {\rm SS} & {\rm TB-1}\\ {\rm TA2780-1}\\ {\rm Barley-7}\\ {\rm Rye-5}\\ {\rm B3-5}\\ {\rm B3-5}\\ {\rm B3-5}\\ {\rm B3-5}\\ {\rm B3-5}\\ {\rm B3-5}\\ {\rm S3-1}\\ {\rm TA183-1}\\ {$	GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTTGTTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTGTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTGTACTAAATACCGCAGGTCCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTGTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTGTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTCTGTGTACTAAATACCGCAGGCTGCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCAGGCAGGTTACTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGGATATTTGGCATGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCAGGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCAGGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCAGGCAGGTTACTTCTTGTTACTAAATACCGCAGGCTGCCCAGTAG GTGGTGATATTTGGCAGGTACGCTGCTGTTGTATGATAATGCCAGGGCTGCCAGTAG GTGGTGATATTTGGCAGGTACGCTGCTGTTGTATGATAATGCCCAGGTCCCCAGTAG GTGGTGATATTTGGCAGGTACGCTGCTGTTGTATGATAATACCGCAGGGTCCCAGTAG GTGGTGATATTTGGCAGGTACGCTGCTGTTGTATGATAATACCGCAGGGTCCCAGTAG GTGGTGATATTTGGCAGGTACGCTGCTGTTGTATGATAATACCGCAGGGCCCCAGTAG GTGGTGATATTTGGCAGGTACGCTGCTGTTGTATGATAATACCGCAGGGCCCCAGTAG GTGGTGATATTTGGCAGGTACGCTGCTGTTGTATGATAATACCGCAGGGCCCCAGTAG GTGGTGATATTTGGCAGGTAGCTGCTGCTGTTAGTAAATACCGCAGGGCCCCAGTAG GTGGTGATATTTGGCAGGTAGCTGCTGCTGTTAGTAAATACCGCAGGGCCCCAGTAG GTGGGTGATATTTGGCAGGAGGTGCCTGCTGTTAGTAAATACCGCAGGCGCCCAGTAG GTGGGGATATTTGGCAGGTGCGCTGCTGCTGTTAGTAAATACCGCAGGCGCCAGTAG GTGGGGATATTTGGCAGGTGCGCTGCTGTTAGTAAATACCGCAGGCGCCAGTAG GTGGGGATATTTGGCAGGAGGTGCCTGCTGTTAGGTAAATACCGCAGGCGCCAGTAG GTGGGATATTTGGCAGGTAGCGTGCTGC	18: 18: 18: 18: 18: 18: 18: 18: 18: 18:
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Fig. 1. Multiple alignments of the 202-bp sequences from different species. SNPs were marked with bold and red color. IRBB7, rice; TA709 and TA829, *T. urartu*; TA141, *T. monococcum*; TA183, *T. monococcum aegilopoides*; TA1770 and TA2780, *Ae. speltoides*; TA1691 and TA10132, *Ae. tauschii*; H.v, *H. villosa*; B73, maize; Jack, soybean; Pto R, tomato; Col, Arabidopsis.

and fission yeasts. Even in Oryza species, centromerespecific satellite repeats are divergent². In spite of the extensive studies of centromeric heterochromatin, knowledge of the conservation of the genes in the centromeric region is still limited because only a few genes are found in the centromere. In this study, a conserved sequence of 202-bp was amplified from monocot and dicot species using the RT-PCR primer 6730.t11, an expressed centromeric gene of Cen8. This 202-bp sequence is present in the *indica* subspecies and absent in *japonica* subspecies, which has a 211-bp sequence divergent from the 202-bp sequence. The data support the hypothesis of independent domestications of indica and japonica from pre-differentiated pools of a wild ancestor⁶. The 202-bp sequence present in monocots and dicots is an ancestral sequence. Two conserved SNPs were found in position 157 and 165 (Fig. 1). The SNP in position 157 may have occurred before monocot / dicot divergence, because both monocot and dicot species share this SNP. However, the SNP in position 165 is only present in the Triticeae species. Our data demonstrate strong selection pressure for the conservation of this DNA element in the kinetochore region, although its functional role remains to be established.

REFERENCES

- Copenhaver, G.P., Nickel, K., Kuromori, T., Benito, M., Kaul, S., et al. 1999 Genetic definition and sequence analysis of Arabidopsis centromeres. Science 286: 2468-2474.
- Lee, H.R., Zhang, W., Langdon T., Jin, W., Yan, H., et al. 2005 Chromatin immunoprecipitation clone reveals rapid evolutionary patterns of centromeric DNA in Oryza species. Proc Natl Acad Sci 102:11793-11798.
- Nagaki, K., Cheng, Z., Ouyang, S., Talbert, P.B., Kim M., et al. 2004 Sequencing of a rice centromere uncovers active genes. Nature Genet 36: 138-145.
- Qi, L.L., Echalier B., Friebe B., Gill B.S. 2003 Molecular characterization of a set of wheat deletion stocks for using in chromosome bin mapping of ESTs. Funct Integr Genomics 3: 39-55
- Saffery, R., Sumer, H., Hassan, S., Wong, L.H., Craig, J.M., et al. 2003 Transcription within a functional human centromere. Mol Cell 12: 509-516.
- Sweeney, M., McCouch, S., 2007 The complex history of the domestication of rice. Ann Bot 100: 951-957.
- Zhang, Y., Huang, Y., Zhang, L., Li, Y., Lu, T., et al. 2004 Structural features of the rice chromosome 4 centromere. Nucleic Acids Res 32: 2023-2030.
- 8. Yan, H., Jiang, J. 2007 Rice as a model for centromere and heterochromatin research. Chromosome Res 15: 77-84.

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