

Cloning and Characterization of the Wheat Domestication Gene, *Q*

by

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B.S., North Dakota State University, 1999
M.S., North Dakota State University, 2001

AN ABSTRACT OF A DISSERTATION

submitted in partial fulfillment of the requirements for the degree

DOCTOR OF PHILOSOPHY

Department of Plant Pathology
College of Agriculture

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ABSTRACT

The *Q* gene is largely responsible for the widespread cultivation of durum and common wheat because it confers the square spike phenotype and the free-threshing character. It also pleiotropically influences many other domestication related traits such as glume shape, glume tenacity, rachis fragility, spike length, plant height, and spike emergence time. The objectives of this research were to confirm or reject the hypothesis that a candidate *AP2*-like gene is *Q*, confirm the dosage and pleiotropic effects attributed to *Q*, and begin defining the differences between the *Q* and *q* alleles. The identity of the *Q* gene was verified by analysis of knockout mutants and found to have a high degree of similarity to members of the *AP2* family of transcription factors. Southern analysis of multiple *Triticum* taxa containing either *Q* or *q* indicated that the *Q* locus is not composed of duplicated *q* alleles. Ectopic expression analysis allowed the observation of both silencing and over-expression effects of *Q*. Rachis fragility, glume shape, and glume tenacity mimicked the *q* phenotype in transgenic plants exhibiting transcriptional silencing of the transgene and the endogenous *Q* gene. Variation in spike compactness and plant height were directly associated with the level of transgene expression due to the dosage effects of *Q*. Comparisons of *Q* and *q* indicated structural differences as well as variation in the level of transcription. One amino acid difference and several base changes within the promoter were identified as possible critical differences between *Q* and *q*. Very little genetic variability was found within the sequenced *Q* alleles suggesting it arose only once and that *q* is the more primitive allele.

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INTRODUCTION

Wheat as well as the other cereals, rice, maize and sorghum, constitute a majority of the calories consumed by humans. Wheat is considered a major staple crop second only to rice. In 2004, more than 600 million metric tons of wheat were produced according to FAOSTAT data, 2005 (<http://www.faostat.fao.org>), making it an economically significant crop.

Most wheat cultivated today can be classified into two types, durum (or macaroni wheat) and bread wheat. Durum wheat is a tetraploid consisting of the two genomes, A and B. It is a very hard wheat with an amber color. It is coarsely ground into semolina which is used to make pasta. Bread wheat, which consists of the A, B, and D genomes, is softer than durum wheat and can be very light in color to a deep reddish-brown color. It is ground into flour and used primarily in bread but also in cakes, cookies, crackers, and noodles. The wheat gluten (protein) which gives bread wheat flour its unique elasticity property also makes it useful in the preparation of adhesives, coatings, polymers, and resins.

Wheat and the other cereals were domesticated 5,000 to 10,000 years ago. They each lost the ability for natural seed dispersion, tightly encased seeds, and staggered germination which resulted in easier human cultivation. The progenitors of most of the major cereals have been identified, but the exact times and locations of domestication are still points of contention. The current consensus is that wheat domestication occurred in the Middle East, rice in Asia, maize in Mesoamerica, and sorghum in Africa. Through domestication each species, accumulated traits for uniform germination, shatter resistance, and less tightly enclosed seeds. The genes controlling these traits are being identified to further delineate the lineage of the domesticated cereals, to decipher the mechanisms, genetic interactions, and biochemical pathways involved in

domestication, and to understand why cereals are more productive for different purposes or more productive under different environments.

LITERATURE REVIEW

CEREAL ORIGIN AND DOMESTICATION

Wild, undomesticated cereals have several characteristics which make them undesirable for cultivation or domestication (<http://www.answers.com/topic/wheat> and <http://www.museums.org.za/bio/plants/poaceae/triticum.htm>). They do not germinate uniformly, the inflorescence shatters, and the seed is protected within an encasement. Seed dormancy is an advantage in the wild because staggered germination throughout the growing year ensures a better chance of some individuals completing their life cycle. Staggered germination across years ensures that difficult environmental conditions such as drought do not eliminate the species. Under cultivation, staggered germination is not advantageous because one would prefer every seed to produce a plant so as to not waste available land.

The inflorescence of wild cereals is very brittle, which leads to the shattering of the encased seed upon maturity. This mechanism is essential for natural seed dispersal, but it likely made harvest difficult for early farmers trying to cultivate wheat, rice, or sorghum. The inflorescence would have had very few seeds remaining on the rachis to collect, and this probably resulted in the farmers spending additional time and effort to locate more plants still having seeds attached.

The seed of wild cereals is also encased, which helps protect the seed from harsh environmental conditions and herbivores. In addition, it aids in soil burial. Early farmers had to remove this encasement by mechanical means. In wheat, pounding removed the encasement but also broke the seed making it more difficult to store for long periods and almost useless for planting. Naked wheat would have been much easier to prepare. It only needed to be threshed and winnowed to allow the glumes, lemmas, and paleae to be blown away (Appendix A).

Besides choosing individuals that had a nonfragile rachis, germinated uniformly, and had naked grains, early farmers also selected for increased yield and larger seed. This also helped reduce the time required to harvest a given amount of seed. Less planting meant less distance to travel during harvest. Less time spent threshing left more time for other activities.

Sorghum

All cultivated sorghums and the closest wild relatives are classified as *Sorghum bicolor* which is subdivided into subspecies and then races (Harlan and DeWet 1972). The four wild races most closely related to cultivated sorghum are in the subspecies *arundinaceum*. Race *arundinaceum* is characterized by its growth in tropical forest zones with higher levels of rainfall and is found primarily in West Africa. It was not a likely progenitor of domesticated sorghum. Race *virgatum* is a smaller sorghum found primarily in the Nile flood plain. Race *aethiopicum* is not found in any natural stands and may in fact be a secondary hybridization between a wild and cultivated sorghum. Race *verticilliflorum* is abundant in the eastern half of Africa. It stands four meters high, produces numerous panicles and seeds, and forms fully fertile hybrids with cultivated sorghums (Harlan 1989). Cultivated sorghum is placed in subspecies *bicolor* and is divided into races primarily by where it is cultivated (Harlan and DeWet 1972). Race *bicolor* is found nearly everywhere sorghum is grown and is characterized by very loose, open panicles similar to wild sorghum. Race *guinea* is found primarily in West Africa but is also in India. It is grown in areas of greater rainfall. Race *caudatum* is found mostly from Lake Chad to the Ethiopian border (Figure 1). Race *kafir* is grown in southern Africa. Race *durra* is found at the edge of the Sahara and in India.

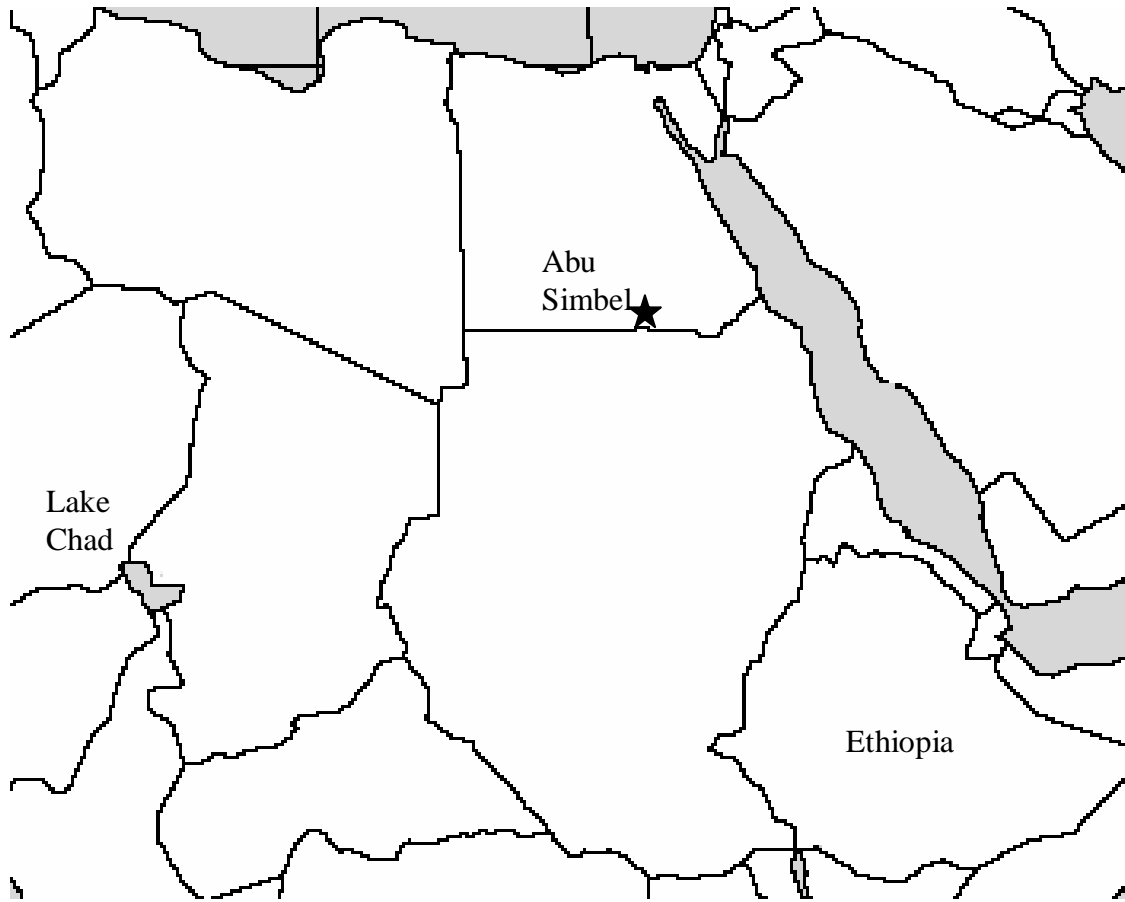


Figure 1. Location of an archeological site within Africa.

The lack of archeological data makes it difficult to determine when and where sorghum was domesticated. Impressions of sorghum grains were found on the Arabian peninsula dating 2500 bc¹ and remains in India and Yemen by 2000 bc (Harlan 1989). These serve as a guide to the latest possible time which sorghum was domesticated since it's generally believed to be domesticated somewhere in the African savannah. The lack of archeological evidence is partially due to poor preservation of organic materials in the savannah which is now a rainless desert. One site on the southern edge of Egypt (100 km west of Abu Simbel) produced hundreds of carbonized seeds of sorghums and millets dating 8,000 years before present (bp) (Wendorf *et al.* 1992). Morphologically, these seeds resembled wild sorghums. Using infrared spectroscopy, the lipids from the sorghum grains were found to be more closely related to the cultivated species today than the wild species. This suggests that sorghum domestication may have already begun in this area of Africa.

Rice

There are two cultivated rice species, *Oryza sativa* L. and *O. glaberrima* Steud. The former is primarily grown in Asia and the latter in Africa. *O. rufipogon* Griff. is considered to be the ancestor of *O. sativa* and is the only wild species, that when crossed with cultivated rice produces fertile hybrids (Oka 1974). Asian rice is believed to have evolved from rice grown from the southern foothills of the Himalayas, through Upper Burma, northern Thailand, and Laos to north Vietnam and south and southwest China (Chang 1976). Its location and time of domestication remains uncertain. Asian cultivated rice is also further classified into at least two groups, with indica and japonica commonly used for research purposes. Two hypotheses exist

¹ Lower case letters in reference to archeological dating indicate either ¹⁴C dating or author did not specify whether the dates were calibrated or not. Upper case letters refer to dates that have been calibrated to increase accuracy.

about the origin of the indica and japonica groups. In one scenario, they diverged before the domestication of rice which would indicate that rice was domesticated at least twice (Kato *et al.* 1928). In the second scenario, the two groups diverged after the domestication of rice (Ting 1957).

Archeological records placed the oldest domesticated rice in the Yangtze River basin in China (Chen 1999) during the late Neolithic period (Figure 2). Specifically the Bashidang site in Hunan province produced rice dating 7,700 to 8,400 years bp (Pei 1998). Microscopic and phytolith analysis indicated this rice was of a domesticated form (Zhang and Pei 1997). Large quantities of rice husks and straw were found as pottery tempers in Pentoushan (Hunan province) dating approximately 8,000 to 8,900 years BP suggesting at least rice cultivation, if not domestication, had occurred (Chen and Hedges 1994). From Hemudu (Zhejiang providence) cooked rice was found in a pot dating around 7,000 years BP (Liu and Yao 1993). The Xianrendong site (Jiangxi providence) produced phytoliths of domesticated rice (Zhao *et al.* 1995) at the same time or earlier than Hemudu (MacNeish *et al.* 1998). This suggested that rice was domesticated only once and then spread, or there is a gap in the archeological record. Rice was later found in Jiahu (Henan providence) in the Huaihe river basin that is 7,800 to 8,800 years old (Higham 1998). It is unknown if the rice was wild or domesticated, but if it is domesticated, it suggests that rice domestication occurred at the same time in multiple sites.

Work by Maruyama, Glaszmann and Vitte supports the multiple domestication origins hypothesis. Maruyama (1973) used the genetic distance determined by isozyme pattern differences between indica and japonica to estimate 300,000 to 2 million years had elapsed since divergence. Vitte *et al.* (2004) compared the transpositional history of 110 LTR retrotransposons



Figure 2. Provinces of major archeological findings of domesticated rice.

between an indica and a japonica cultivar. The amount of diversity between these two cultivars should be proportional to the divergence time. Vitte *et al.* (2004) estimated indica and japonica diverged more than 200,000 years ago, therefore they diverged long before domestication occurred. Glaszmann (1987) screened 1688 Asian cultivars from different countries for 15 isozymes. He placed 95% of the 1688 cultivars into 6 different groups, indica, japonica, aus, ashinas, rayada, and Indian aromatic. This suggests the possibility of 6 different origins. Khush (1997) suggested that the indica group was domesticated in the foothills of the Himalayas in India and the japonica group in southern China.

Maize

Maize and teosinte are very different morphologically when comparing the female inflorescence or ear. Teosinte ears typically produce only 5-12 seeds enveloped within a hard, stony casing. The mature ear disarticulates such that each encased seed becomes a dispersal unit. Maize has a much larger ear and produces as many as 500 or more seeds which are fully exposed. At maturity, the ear does not disarticulate and the entire ear falls to the ground as an ineffective dispersal unit. In appearance, teosinte seems to be more similar to rice than maize and was initially classified as a closer relative of rice. Yet some forms of teosinte, particularly the Mexican annual form, produce fully fertile progeny when crossed with maize (Collins 1919). This provides some of the first evidence that teosinte was the progenitor of maize. Further cytological evidence was provided by Emerson, Beadle, and Longley. Emerson and Beadle (1932) observed similar crossing over frequencies between maize hybrids and maize by teosinte hybrids. The chromosome sizes, centromere positions, knob sizes, and knob positions in Mexican annual teosintes were the same as in maize (Longley 1941).

Molecular evidence provided by Doebley and Matsuoka further supported the hypothesis that teosinte was the progenitor of maize. Doebley *et al.* (1984) examined the isozyme variation between various maize and teosinte populations. They found distinctive isozyme allele frequencies for most teosinte and maize populations. One Mexican annual teosinte, *Zea mays* ssp. *mexicana*, was similar to maize but still slightly different. A different Mexican annual teosinte, *Z. mays* ssp. *parviglumis* or Balsas teosinte, has identical isozyme allele frequencies when compared to maize suggesting this subspecies is the progenitor of maize. Later research by Matsuoka *et al.* (2002) studying the microsatellite diversity further confirmed the isozyme results. Matsuoka *et al.* (2002) also used the microsatellite study to develop a phylogenetic tree. From this tree they observed that maize most likely arose from a single domestication event in Mexico and probably descended from the populations of Balsas teosinte grown where the states of Guerrero, Michoacan, and Mexico meet (Central Balsas Valley, Figure 3). Maize and Balsas teosinte diverged about 9000 years ago according to the molecular dating which is compatible with the archeological evidence.

The earliest evidence of domesticated maize comes from archeological sites near Tehuacán, Oaxaca and San Andrés (Figure 3). The San Marcos Cave in the Tehuacán Valley produced one of the earliest cobs from Mexico which was dated with accelerator mass spectrometry to 5,500 years BP (Long *et al.* 1989). Analysis of the cobs indicated that they had already undergone substantial genetic modification to produce better grain accessibility and productivity (Benz and Long 2000). When the site in Oaxaca, Guilá Naquitz Cave, was excavated in 1966, several cobs were found, which were considered to be either maize-teosinte hybrids or primitive maize with a large teosinte influence (Flannery 1986). These cobs were dated by accelerator mass spectrometry in 1999 resulting in an estimate of 6,200 years BP

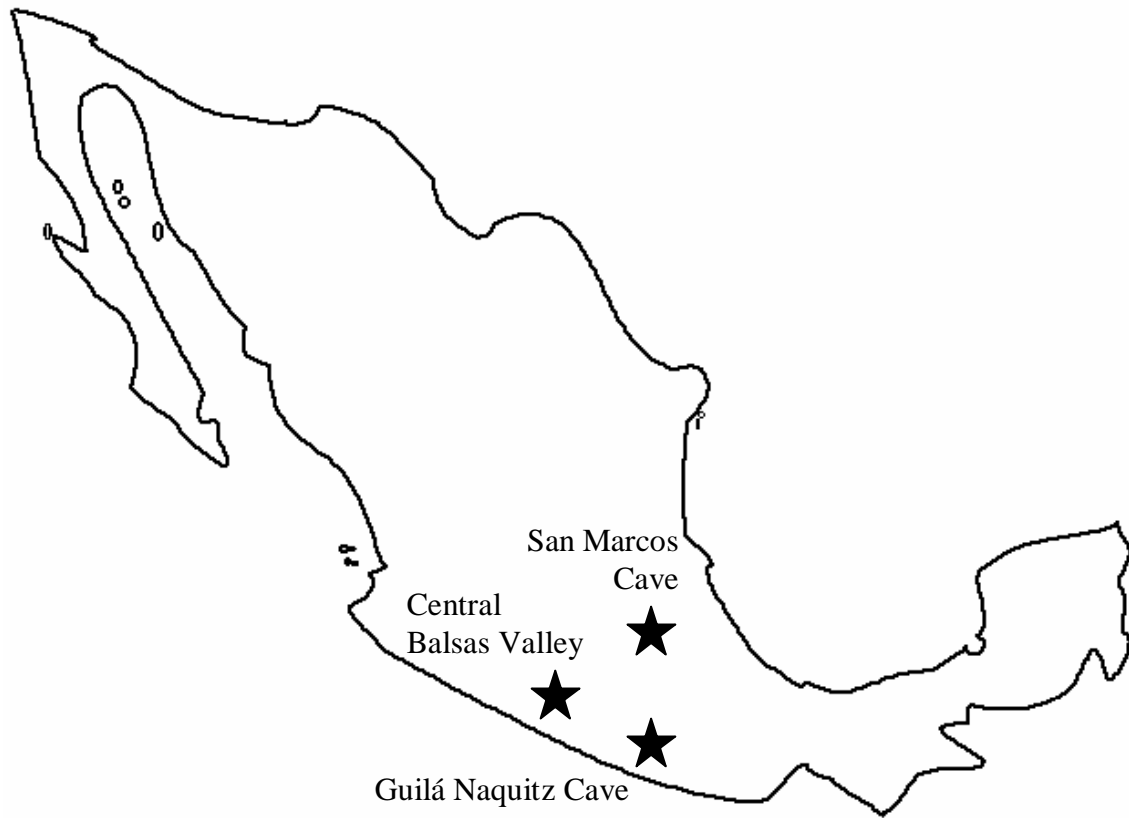


Figure 3. Major archeological sites for maize domestication.

(Piperno and Flannery 2001) making them even older than those from San Marcos Cave. Phytoliths from earlier layers in the Guilá Naquitz Cave were collected in hopes of finding evidence of domesticated maize even earlier, but no maize or teosinte phytoliths were identified (Piperno and Flannery 2001). This suggests that neither the Oaxaca region nor Tehuacán was the site of domestication. The site near San Andrés produced both small and large pollen grains from the genus *Zea* (Pope *et al.* 2001). The smaller grains dated to about 7,100 years BP and the larger beginning 100 years later. The smaller grains were characteristic of modern day teosinte whereas the larger grains were more similar to maize (Whitehead and Langham 1965). This provides the earliest evidence of domesticated maize cultivation in an area where teosinte was not native. More archeological sites are needed to shed light on where maize was domesticated.

Wheat

Wheat consists of two genera, *Triticum* and *Aegilops* (van Slageren 1994), and can be grouped into three groups based on ploidy level, diploid, tetraploid and hexaploid, with wild species existing for the diploid and tetraploid groups. There are a multitude of wild wheat species. The ones implicated in domestication include the diploids, *T. monococcum* ssp. *aegilopoides* (wild einkorn), and *T. urartu*, and the tetraploid, *T. turgidum* ssp. *dicoccoides* (wild emmer). The cultivated diploid is *T. monococcum* ssp. *monococcum* also called einkorn. Cultivated tetraploids are divided into two species, *T. timopheevii* and *T. turgidum*. Only the subspecies *timopheevii* within *T. timopheevii* is cultivated. Seven subspecies within *T. turgidum* are cultivated, ssp. *dicoccum* (emmer), ssp. *paleocolchicum* (Georgian), ssp. *durum* (macaroni), ssp. *turgidum* (rivet or cone), ssp. *polonicum* (Polish), ssp. *turanicum* (Khorassan), and ssp. *carthlicum* (Persian). The cultivated hexaploids are *T. zhukovskiyii* and *T. aestivum*. There are five subspecies within *T. aestivum* that are cultivated, ssp. *spelta* (dinkel or large spelt), ssp.

macha, ssp. *aestivum* (common or bread), ssp. *compactum* (club), and ssp. *sphaerococcum* (shot).

The progenitors of wheat were initially identified by performing cross hybridizations and evaluating hybrid fertility and later chromosome pairing. Einkorn wheat, (*T. monococcum*) was considered to be the donor of the A genome in cultivated tetraploid and hexaploid wheat (Kihara 1924; Lilienfeld and Kihara 1934; Sax 1922), but it was later discovered that *T. monococcum* was a mixture of two species, *T. monococcum* and *T. urartu*. *T. urartu* is more closely related to the A genome of both tetraploid and hexaploid wheats (Dvorak *et al.* 1988; Konarev *et al.* 1979; Nishikawa 1984). The contributor of the B genome is not clear, but *Ae. speltoides* is considered the most closely related. The D genome of bread wheat was contributed by goat grass, *Aegilops tauschii* (Kihara 1944; McFadden and Sears 1946).

Wild einkorn is currently found in the central and eastern portion of the Fertile Crescent. Kernels of wild einkorn have been frequently found in the central portion of Fertile Crescent 12,500 years BP (Salamini *et al.* 2002). Later, plumper kernels were found mixed with the *T. monococcum* ssp. *aegilopoides* about 10,500 years BP possibly indicating the beginnings of domestication (Gopher *et al.* 2002; Zohary and Hopf 2000). At 9,500 years BP domesticated einkorn occurs frequently in the western Fertile Crescent particularly southeastern Turkey (Figure 4). The archeological site Cafer Hoyuk produced both wild and cultivated kernels dating 8,200 to 9,600 years bp (de Moulins 1993; van Zeist 1968). Cayönü produced wild and cultivated kernels dating 9,000 years BP (van Zeist and de Roller 1991/2). Nevali Cori produced cultivated kernels dating 9,200 bc (Pasternak 1998). These three sites contain some of the oldest dated domesticated wheat suggesting domestication occurred in southeastern Turkey. AFLP

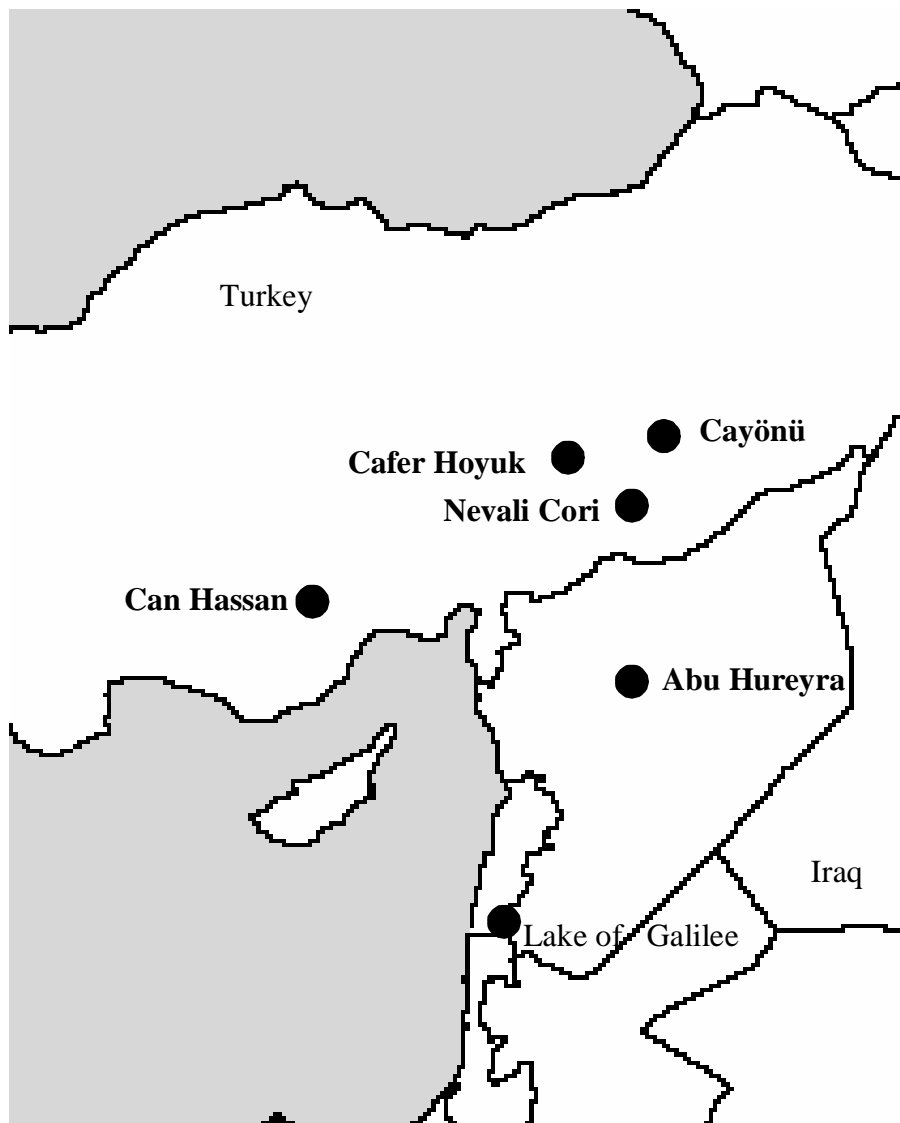


Figure 4. Major archeological locations important in wheat domestication.

fingerprinting data revealed wild einkorn lines collected in the Karacadag mountains are the most closely related to cultivated einkorn lines as compared to lines from other areas of the Fertile Crescent and outside the Fertile Crescent (Heun *et al.* 1997). This data supports the domestication of wheat near the Karacadag Mountains before 10,000 years BP.

Within the last 500,000 years, *T. urartu* (Dvorak *et al.* 1988; Konarev *et al.* 1979; Nishikawa 1984) hybridized with the B-genome donor to form wild emmer. Seeds from wild emmer were found in Ohalo II near the lake of Galilee dating 19,300 years bp (Kislev 1992). Today wild emmer (*T. turgidum* ssp. *dicoccoides*) is native to the western Fertile Crescent and into southeastern Turkey. *T. turgidum* ssp. *dicoccum* is considered domesticated emmer, because it has a nonbrittle rachis but produces nonfree-threshing seed. *T. turgidum* ssp. *parvicoccum*, which is presumed extinct, (Kislev 1980), had small free-threshing seeds, and a more compact spike. The remains of domesticated emmer have been found at several sites. Cayönü produced remains dating from 10,600 years BP and forward (van Zeist and de Roller 1991/2). Abu Hureyra 1 produced remains of wild emmer dated earlier than 10,400 years BP (Hillman 2000) followed by remains of emmer dated 10,400 years BP and onward at Abu Hureyra 2 (de Moulins 2000). This places emmer domestication before 10,400 years BP. This date should be taken with caution because it is difficult to determine the fragility of the rachis from archeological remnants (Kislev 1989). Free-threshing emmer was found at Abu Hureyra 2 (de Moulins 2000), Aswad (10,800 years BP) (Kislev 1980; Kislev 1992) and Can Hassan at 8,600 to 8,900 years bp (Hillman 1996; van Zeist and Bakker-Heeres 1985). This puts domestication of free-threshing emmer before 8,600 years bp (when calibrated should be greater than 9,000 years BP).

The Karacadag mountain region has been suggested as the location of emmer domestication (Özkan *et al.* 2002). AFLP fingerprinting indicated that hulled and free-threshing

emmers clustered into separate clades suggesting a single origin of each (Özkan *et al.* 2002). These domesticated emmers were most closely related to wild emmer populations collected in southeastern Turkey (Özkan *et al.* 2002). The rapid emergence of the two domesticated emmers can explain the appearance of free-threshing forms found about the same time as the hulled forms.

The hybridization of *T. turgidum* with *Ae. tauschii* (Kihara 1944; McFadden and Sears 1946) to form *T. aestivum* occurred about 8,000 to 9,000 years BP based on archeological findings. DNA sequence analysis of the *Acc-1* (plastid acetyl-CoA carboxylase) and *Pgk-1* (plastid 3-phosphoglycerate kinase) genes confirm that this hybridization occurred recently because the gene sequences of *Ae. tauschii* and the D-genome of *T. aestivum* are indistinguishable (Huang *et al.* 2002). It is suspected that a domesticated emmer was involved because *Ae. tauschii* distribution does not overlap with wild emmer (Nesbitt and Samuel 1996). Kislev (1980) extracted the A and B genomes out of modern bread wheat. The spike morphology of the extracted tetraploid was similar to *ssp. parvicoccum*, a free-threshing tetraploid, rather than to *ssp. dicoccum*, a hulled tetraploid suggesting that *ssp. parvicoccum* may be the tetraploid progenitor of bread wheat.

T. aestivum exists today as two forms, free-threshing and hulled. *T. aestivum* *ssp. aestivum*, *ssp. compactum*, and *ssp. sphaerococcum* are free-threshing with differences in spike morphology and seed shape. *Spp. compactum* and *sphaerococcum* are differentiated from *ssp. aestivum* by single genes, *C* and *S*, respectively. The hulled, nonfree-threshing group of hexaploids includes the *ssp. spelta*, *ssp. vavolovii*, and *ssp. macha*. This group tends to have a somewhat fragile rachis and tough glumes. *Ssp. spelta* disarticulates below the junction of the

rachilla and rachis (barrel disarticulation) while ssp. *vavilovii* and ssp. *macha* disarticulate above the junction of the rachilla and rachis (wedge disarticulation, Appendix A).

The hulled form has been identified at archeological sites in Europe dating 2,700 to 4,500 years bp (Körber-Grohne 1989). Earlier remains have been found about 7,000 years bp in Transcaucasia (Lisitsina 1984), north of the Black Sea (Janushevich 1984), and northern Iraq (Bakhteyev and Yanushevich 1980) but the identification criteria are poorly documented (Nesbitt and Samuel 1996). Hulled *T. aestivum* has not been found in archeological sites in the Near East. Free-threshing *T. aestivum* has been found at Can Hassan III dating to 8,500 years BP (Hillman 1978) and at Cafer Hoyuk dating to 8,000 to 9,000 years BP (de Moulins 1993; Salamini *et al.* 2002). Archeological findings thus far indicate the cultivation of free-threshing hexaploid wheat before cultivation of hulled hexaploid wheats.

DOMESTICATION GENES

Most QTL studies have been used to identify quality traits of interest or sources of resistance with the goal of transferring the traits into breeding lines. Relatively few QTL studies have been employed to identify QTLs playing a major role in domestication within a single crop. Many of these identified domestication QTLs represent single genes, likely regulatory in nature, but exhibit quantitative inheritance due to pleiotropic effects. These domestication genes were prominent factors in the spread of agriculture worldwide.

Sorghum

QTL analysis in sorghum compares several selected traits such as shattering, seed size, and short-day flowering to QTLs underlying the same traits in rice and maize (Paterson *et al.* 1995). Paterson *et al.* (1995) observed one QTL for shattering in sorghum compared to three in rice and ten in maize, but the single QTL from sorghum corresponded to QTLs found in syntenic

regions in both rice and maize. For seed mass, five of seven QTLs in sorghum corresponded to five of eight QTLs in rice, and four of seven corresponded to four of eight in maize. One QTL was primarily responsible for variation in flowering in sorghum which was syntenic to one QTL in rice and possibly a duplicated one in maize.

Maize

Mangelsdorf and Reeves (1939) identified at least four factors which they believed largely contributed to the difference between teosinte and maize ear morphology. The factors were believed to consist of a large block of genes and concluded that it was impossible for maize to have evolved from teosinte in a few thousand years. Beadle (1972) also wanted to understand the differences in ear morphology and developed an F₂ population of 50,000 individuals by crossing a primitive maize with teosinte. He observed about 1 in 500 individuals that were identical to the maize parent as well as 1 in 500 to the teosinte parent. These ratios indicated only five major genes were responsible for the difference in ear morphology and that under human selection it was possible for maize to have evolved from teosinte.

Doebley and Stec (1993) used QTL mapping in two F₂ populations and found five or six QTLs largely responsible for the difference in ear morphology located on 1S, 1L, 2S, 3L, 4S, and 5S. The QTL on 1S was due to the *teosinte branched1* gene (*tb1*; Doebley *et al.* 1997), which controls the plant architecture by negatively regulating organ growth as a class II TCP transcription regulator. Differences upstream of this gene cause the difference in the level of transcription between maize and teosinte. The QTL on 4S is due to the *teosinte glume architecture1* gene (*tgal*; Dorweiler *et al.* 1993). The maize allele of *tgal* in a teosinte background freed the kernel from its encasing (Dorweiler and Doebley 1997). The teosinte allele in a maize background influences several inflorescence traits and is therefore believed to

be a regulatory gene (Dorweiler and Doebley 1997). It causes longer, deeper inflorescence internodes, longer, thicker glumes angled more upwards to close over the cupule, and the deposition of silica into the epidermal cells of the fruitcase. It has been cloned and identified as a squamosa-promoter binding protein (Wang *et al.* 2005). A single amino acid differentiates between the maize and teosinte alleles. The QTL on 2S was near the maize *floricaula/leafy* gene, *zfl2*, and may be a regulatory gene. Increased expression of *zfl2* was associated with an increase in the number of spikelet pairs around the maize ear, a major difference between maize and teosinte (Bomblies *et al.* 2003). It was also involved in the vegetative to floral transition, and may help establish the pattern of expression of the ABC floral genes (Bomblies *et al.* 2003). The remaining three QTLs had more general effects and thus far have not been associated with particular genes.

Rice

Xiong *et al.* (1999) developed an F₂ population with 172 individuals from the wild rice accession P16 and the indica cultivar 'Aijiao Nante'. They scored 19 different traits distinctly different between the wild and cultivated parents including traits related to growth habit, gigantism, panicle structure, spikelet structure, photoperiod sensitivity and anthocyanin pigmentation. Seven traits segregated qualitatively and the remaining 12 traits resolved 44 putative QTLs with peaks explaining 20% to almost 60% of the variation. This can be interpreted one of two ways. First, a large number of genes are responsible for the domestication of rice with each QTL representing a different gene playing a significant role in domestication. Second, many of the traits identified were not necessarily major players in the initial domestication event(s) but were selected later through breeding programs. This effect could be minimized by using different F₂ populations and identifying QTLs common to both populations.

Careful selection of parents for these F₂ populations would be critical because each domestication event may have been dependent on the selection of different genes. One gene for shattering, *Sh3*, has been identified on chromosome 4L (Sobrizal *et al.* 1999) and may have been a key player in domestication (Eiguchi and Sano 1990).

Wheat

Peng *et al.* (2003) developed a segregating F₂ population using *T. turgidum* ssp. *dicoccoides* with typical wild traits and cultivated *T. turgidum* ssp. *durum* cultivar ‘Langdon’. They measured 11 characteristics important to domestication including rachis brittleness, height, heading date, spike number per plant, spike weight per plant, single spike weight, kernel number per plant, kernel number per spike, kernel number per spikelet, 100-grain weight, grain yield per plant, and spikelet number per spike. Seven major QTLs were identified, one on chromosome 1BS, 1BL, 3AS, and two on 2AL and 5AL. Possible candidate genes are the *Q*, *vrn1*, and *vrn2* genes on 5AL and the *Br* gene on 3A.

Three major genes identified as playing important roles in wheat domestication are the *tenacious glumes* (*tg*), *brittle rachis* (*br*), and *Q* genes. *Tg* is partially dominant and is located on chromosome 2D (Kerber and Rowland 1974). Hybridization between a free-threshing tetraploid homozygous for *Q* with *Ae. tauschii* produced a synthetic nonfree-threshing hexaploid (Villareal *et al.* 1996). Therefore, *Tg* inhibits the expression of *Q*. The genes controlling brittle rachis are on group 3 chromosomes in *Ae. bicornis*, *Ae. sharonensis*, *Ae. longissima*, *Ae. uniaristata*, and Tibetan weedrace (Chen *et al.* 1998; Miller *et al.* 1995; Riley *et al.* 1966; Urbano *et al.* 1988). *Br*₁ on chromosome 3DS is a dominant gene that is solely responsible for the brittle rachis found in the Tibetan weedrace. *Br*₂ and *Br*₃ are also dominant genes (Cao *et al.* 1997; Chen *et al.* 1998)

found on chromosomes 3A and 3B, respectively (Watanabe and Ikebata 2000). *Q* is discussed below.

HISTORY OF *Q*

The first genes described in wheat were named by single letters. Different researchers had different letters for the same trait making it difficult to follow the nomenclature. Some of the genes involved in spike morphology were *C*, *S*, *q* and *k*. The *C* factor of *T. aestivum* ssp. *compactum* described by Nilsson-Ehle (1911) was found to be responsible for the compact spike. This factor was not the same as the mutation for a compactoid spike (MacKey 1954). This was shown by crossing both ssp. *compactum* and a compactoid mutant with ssp. *spelta* and a speltoid mutant. The results indicated that the compactoid mutant compensated for the speltoid character in the speltoid mutant and in ssp. *spelta* but that ssp. *compactum* had a different gene responsible for compact spikes. The *K* factor described by Watkins (1927; 1928; 1940) was responsible for keeled glumes, which was later associated with the speltoid spike type (MacKey 1954). Therefore *K* became known as the speltoid suppressing or compactoid promoting factor with *k* as the spelt factor. Philiptschenko (1934) labeled the spelt factor *S* which is no longer used. *S* is now used to designate the gene responsible for the spherical seed of *T. aestivum* ssp. *sphaerococcum*.

The *q* factor was initially considered a collection of unidentified factors responsible for governing square spike morphology (Philiptschenko 1934). Early linkage studies placed both *k* and *q* approximately 30 crossover units from the bearded gene, *B₁*. Under the assumption that *k* and *q* were not the same, Philiptschenko (1934) placed *q* and *k* on either side of *B₁*. MacKey (1954) determined that *q* and *k* were actually the same and combined the two factors with the designation *Q*.

Winge (1924) placed the speltoid mutation or q on chromosome C which is equivalent to 5A (Sears 1954). Winge (1924) also proposed a counterbalancing theory in which Q could not be counterbalanced by a single gene on any genome. He suggested that there must instead be multiple factors regulating internode length, glume shape, and rachis brittleness, and that there is no difference at the q locus between speltoid mutants and *T. aestivum* ssp. *spelta*, only a difference in the other genes that interact with q . This hypothesis was supported by the analysis of the progeny derived from crosses of a compactoid mutant with the speltoid mutant and ssp. *spelta* (MacKey 1954). This hypothesis received further support through the analysis of chromosome 5A substitution lines. Chinese Spring is a free-threshing wheat with a square spike and considered to have Q . Hope is a free-threshing hexaploid wheat considered to possess Q , but it does not have a square spike. Sears (1956) substituted the Hope 5A chromosomes for the Chinese Spring 5A chromosomes in the Chinese Spring background. He observed a square spike indicating that it was the genetic background in combination with Q that lent a square spike.

Sears and others (Huskins 1946; Muramatsu 1963; Sears 1952; Sears 1954) also developed various aneuploids with varying numbers of chromosome 5A and therefore varying numbers of Q . One copy resulted in a speltoid spike, two in a square or normal spike, three in a subcompactoid spike, and four in a compactoid spike (Huskins 1946; Muramatsu 1963; Sears 1952; Sears 1954). This suggested that spike morphology was dependant on the dosage of Q . Sears continued in this fashion by substituting various numbers of *T. aestivum* ssp. *spelta* 5A chromosomes (q) into Chinese Spring and found that one to four copies of q still produced speltoid spikes. Muramatsu (1963) carried the experiment further and developed lines with five and six copies of q . He found that five copies produced a square spike and six produced a subcompactoid spike. The work of both Sears and Muramatsu indicate that Q is dosage

dependent and that *q* is not a deficiency because five copies of *q* (derived from the ssp. *spelta* 5A chromosome) resulted in the equivalent of the square spikes observed with two copies of *Q*.

WHEAT GENOTYPES

With the combining of the *k* and *q* factors into *Q*, the tetraploid wheats were considered to possess the *q* allele with the exception of *T. turgidum* ssp. *carthlicum* which is free-threshing, has round glumes, and is considered to have the *Q* allele. Ssp. *polonicum* is also free-threshing but has keeled glumes. Muramatsu (1978) substituted the ssp. *polonicum* 5A chromosome into Chinese Spring. Square spikes were observed so ssp. *polonicum*, though it had keeled glumes, possessed the *Q* allele. Muramatsu (1979; 1985) repeated this process for two types of *T. turgidum* ssp. *dicoccum*. Farrum was of ssp. *dicoccum* type with keeled glumes and a partially brittle rachis, whereas iguliforme had broad, compact spikes, round glumes and a partially brittle rachis. The farrum substitution produced speltoid spikes and therefore possessed *q* (Muramatsu 1985), whereas the liguliforme substitution produced square spikes and therefore possessed *Q* (Muramatsu 1979).

The free-threshing hexaploids, spp. *aestivum*, *compactum*, and *sphaerococcum*, are presumed to all have *Q*. The nonfree-threshing hexaploids, spp. *spelta*, *vavolovii*, and *macha*, are all presumed to have *q*. Since ssp. *spelta* is nonfree-threshing and has speltoid spikes it was assumed all speltas possessed *q*. Sears made substitutions with two different *T. aestivum* ssp. *speltas*, one of European descent and one of Iranian decent. The European spelt substitution produced plants with speltoid spikes whereas the Iranian spelt produced plants with square spikes. Therefore, it was concluded the European spelt has *q* while Iranian spelt possesses the *Q* allele (Luo *et al.* 2000). The genotypes of these various species are summarized in Table 1.

Table 1. List of species, and their ploidy level, genomic constitution, genotype, and Genbank number of *Q* sequence.

	Ploidy	Genomic Constitution	chrom. 5A Q/q Allele	Genbank Number
<i>T. urartu</i>	2X	AA	<i>qq</i>	AY702958
<i>T. monococcum</i>	2X	A ^M A ^M	<i>qq</i>	AY170867
<i>T. turgidum</i> ssp. <i>dicoccoides</i>	4X	AABB	<i>qq</i>	AY702957
<i>T. turgidum</i> ssp. <i>dicoccum</i>	4X	AABB	<i>qq</i> QQ	AY714343 -
<i>T. turgidum</i> ssp. <i>durum</i>	4X	AABB	QQ	AY702955
<i>T. turgidum</i> ssp. <i>polonicum</i>	4X	AABB	QQ	AY714339
<i>T. turgidum</i> ssp. <i>carthlicum</i>	4X	AABB	QQ	AY702959
<i>T. aestivum</i> ssp. <i>aestivum</i>	6X	AABBDD	QQ	AY702956
<i>T. aestivum</i> ssp. <i>spelta</i> (Iranian)	6X	AABBDD	QQ	AY714340
<i>T. aestivum</i> ssp. <i>spelta</i> (European)	6X	AABBDD	<i>qq</i>	AY714341
<i>T. aestivum</i> ssp. <i>macha</i>	6X	AABBDD	<i>qq</i>	AY714342
<i>T. aestivum</i> ssp. <i>compactum</i>	6X	AABBDD	QQ	-
<i>T. aestivum</i> ssp. <i>sphaerococcum</i>	6X	AABBDD	QQ	-

***Q*, THE SUPER GENE**

The action of the *Q* locus is very complex. *Q* influences multiple characters depending on the genetic background. *Q* can exist in a genetic background where keeled glumes and speltoid spikes are observed, but it can also exist in a free-threshing condition with round glumes and square spikes. Besides the spike squareness and glume shape, *Q* influences heading date, plant height, spike length, spikelet size, seed fertility, glume tenacity, rachis fragility, and threshability (Jantasuriyarat *et al.* 2004; Kato *et al.* 1999; Kato *et al.* 2003; Leighty and Boshnakian 1921; MacKey 1966; Muramatsu 1963; Muramatsu 1979; Muramatsu 1985; Singh

et al. 1957; Singh 1969; Tsunewaki and Jenkins 1961). In Chinese Spring *Q* is recessive while glume and rachis traits are incompletely dominant (Muramatsu 1963).

***Q* EMERGENCE**

It is common belief that the tetraploid progenitor of hexaploid wheat was *T. turgidum* ssp. *dicoccum* which contains the *q* allele. It has been debated as to whether *Q* arose only once or more than once, in tetraploid wheat or hexaploid wheat, and if *q* is the more primitive allele. *Q* and *q* are dosage dependent, therefore it is possible that *Q* arose from *q* by duplication. Evidence for duplication is the dosage response obtained by Muramatsu (1963) and Sears (1952; 1954) mentioned previously as well as data from others (Kuckuck 1959; Swaminathan 1963; Faris and Gill 2002). Kuckuck (1959) crossed two ssp. *speltas* resulting in some progeny with ssp. *aestivum* type spikes. Unequal crossing over was proposed to explain the ssp. *aestivum* type spikes. Swaminathan (1963) proposed that the *Q* locus represented a tandem series of *q* alleles, and speltoid or compactoid spikes resulted due to unequal crossing over. Faris and Gill (2002) performed high resolution mapping of the *Q* locus and found several loci near *Q* that were duplicated on other parts of chromosome 5A. This data taken together suggests *Q* may have arose from *q* through duplication. The other possibility is that *Q* arose from *q* or vice versa through mutation (Muramatsu 1963).

MAPPING *Q*

From previous research, *Q* was known to reside on the long arm of chromosome 5A and was distal to the bearding gene, *B*₁. Multiple researchers employed deletion mapping to further delineate the physical location (Endo and Gill 1996; Endo and Mukai 1988; Miller and Reader 1982; Ogihara *et al.* 1994; Tsujimoto and Noda 1989; Tsujimoto and Noda 1990). Endo and Gill (1996) placed *Q* within a submicroscopic region between the break points of 5AL-7 and 5AL-23

(Figure 5). Faris and Gill (2002) undertook the high resolution mapping of *Q* and employed several types of markers including restriction fragment length polymorphisms (RFLPs), amplified fragment length polymorphisms (AFLPs), and markers developed from RNA differential display. RNA differential display led to the identification of numerous genes differentially expressed between the two deletion lines, 5AL-7 and 5AL-23, suggesting the presence of a regulatory gene. The AFLP marker, *XksuP23* was 1.3 cM proximal to *Q* and the AFLP marker, *XksuP16* was 0.7 cM distal to *Q*.

Faris *et al.* (2003) performed chromosome walking at the *Q* locus using a BAC library constructed from *T. monococcum*. The first BAC was identified using the marker *XksuP16*. Low copy sequences were selected after sequencing the entire BAC. These low copy sequences were mapped to orientate the BAC and then used to identify the next BAC for sequencing. Four BACs were sequenced extending the contig so the last marker cosegregated with *Q*. The fast neutron-induced deletion line, fndel-143, was characterized as having the last two markers on the contig cosegregating with *Q* but missing the *Q* gene. Therefore, the contig spanned the *q* allele and narrowed the region for *q* to approximately 100 kb. An AP2-like gene (*TMAP2*) was the only major gene found within the 100 kb (Figure 6).

APETELA2

The *APETELA2* (*AP2*) gene in *Arabidopsis* is the founding member of the AP2-like members of the AP2/EREBP transcription factors (reviewed in Riechmann and Meyerowitz 1998). These factors are categorized based on the presence of AP2 DNA binding domains. The AP2-like groups of factors contain two AP2 domains, typically have multiple introns, and are key regulators in developmental processes. The *AP2* gene in *Arabidopsis* regulates multiple processes of flower development including specification of organ and meristem identity

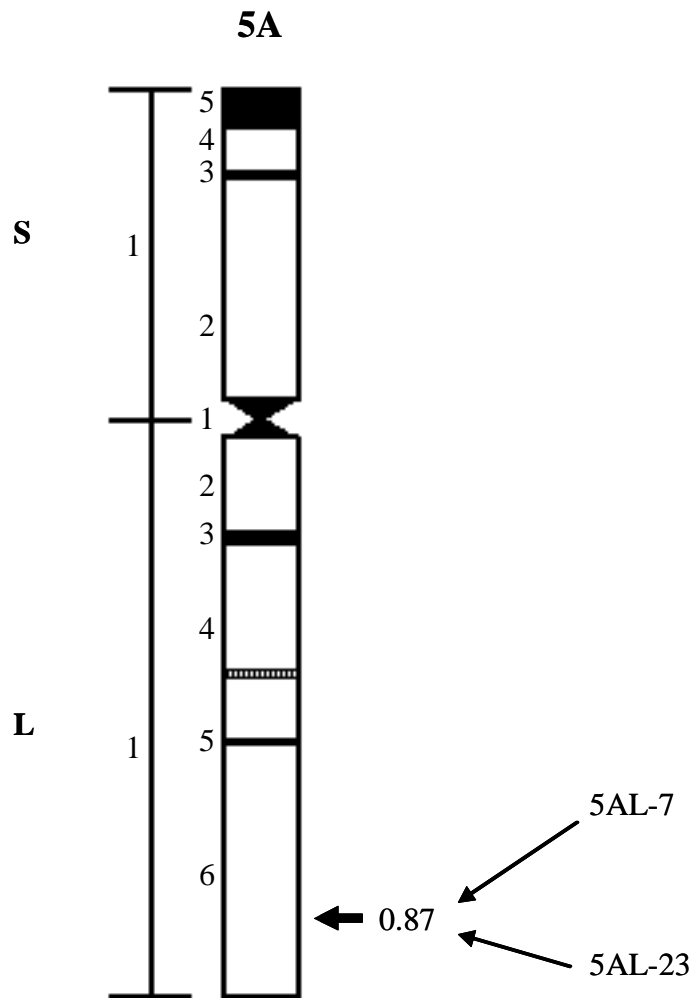


Figure 5. Chinese Spring deletion lines. The region between the breakpoints of Chinese Spring wheat deletion lines 5AL-7 and 5AL-23 is a submicroscopic deletion. Deletion 5AL-7 has speltoid spikes while 5AL-23 has square spikes indicating Q is located within the submicroscopic region.

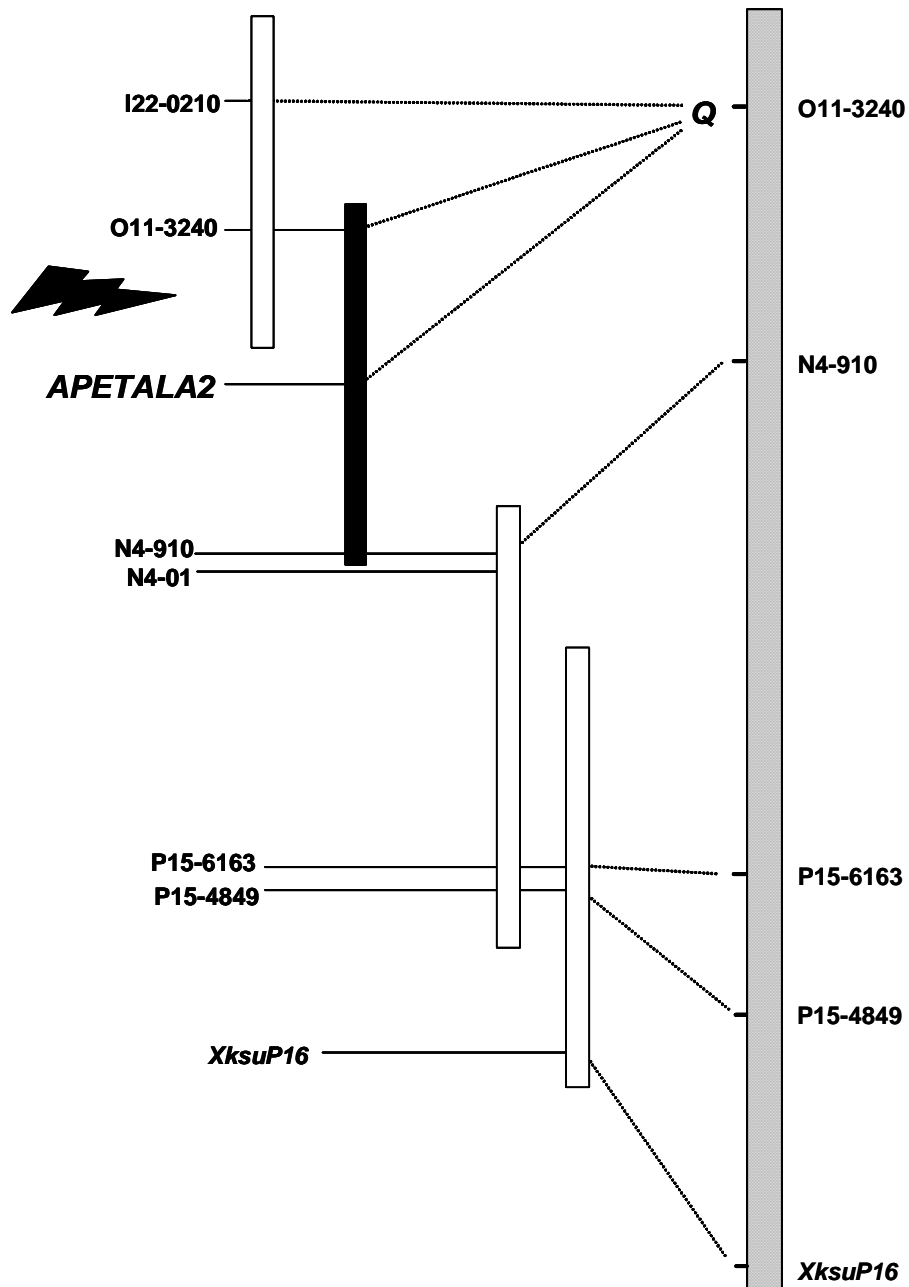


Figure 6. Chromosome walking and candidate gene identification. BACs are represented by the white rectangles on the left. The genetic linkage map is represented on the right. Lightning bolt indicates the breakpoint of fndel-143.

and ovule and seed development (Bowman *et al.* 1989; Drews *et al.* 1991; Jofuku *et al.* 1994; Komaki *et al.* 1988; Kunst *et al.* 1989). *AP2* is translationally inhibited by a microRNA, miRNA172 (Chen 2004). Recently, *AP2* was identified as an important factor in governing seed mass and yield (Jofuku *et al.* 2005). *AP2* knockouts had increased seed mass of more than 100% but seeds lost developmental uniformity. It was hypothesized that *AP2* negatively effects gibberellin activity to regulate metabolism in both sink and source tissues, therefore affecting cell size and cell number during growth.

OBJECTIVES

VALIDATE THAT THE *AP2*-LIKE GENE IS *Q*

The gene sequence will be obtained from Chinese Spring which possesses the *Q* allele. It will then be sequenced from unique EMS mutants with speltoid spikes. Differences within the coding region, splice sites, or promoter will validate that the *AP2*-like gene is *Q*. Validation opens the door to many other areas of research beginning with the identification of the mechanism and genetic interactions of *Q* to determine where *Q* fits in the biochemical pathways.

CONFIRM DOSAGE AND PLEIOTROPIC EFFECTS OF *Q*

The *Q* gene will be inserted into the hexaploid cultivar 'Bobwhite'. The dosage effects should be observable as speltoid spikes due to silencing, and subcompactoid/compactoid spikes due to the equivalent of three or more doses of *Q*. Other differences in plant and spike morphology would confirm pleiotropic effects attributed to *Q*.

DEFINE STRUCTURAL AND EXPRESSION DIFFERENCES BETWEEN *Q* AND *q*

The *Q* locus of numerous species and accessions within species will be sequenced to identify conserved differences between the *Q* and *q* alleles. Expression of the *Q* locus will be determined in a line homozygous for *Q* and in a second line homozygous for *q*. These two series of comparisons should shed light on whether the observed dosage effect is due to reduced transcript level or altered function of the protein. Phylogenetic analysis of the sequence information should shed further light on wheat evolution.

Enhanced knowledge of *Q* along with other domestication related genes is important because this knowledge helps us understand the diversity which exists within the cereals to increase productivity under different environmental conditions. Crop inflorescences can be transformed for either crop improvement or food improvement. These domestication genes can

be used as a domestication cassette for other wild species with specific end uses or ability to withstand abiotic or biotic stresses.

MATERIALS AND METHODS

PLANT MATERIALS

Genomic sequence of the *Q* gene was obtained from *T. aestivum* ssp. *aestivum* cv ‘Chinese Spring’ (CS), *T. turgidum* ssp. *durum* cv ‘Langdon’ (LDN), CS / *T. turgidum* ssp. *dicoccoides* 5A disomic chromosome substitution line (CS-*Dic5A*), *T. turgidum* ssp. *carthlicum* (TTC), *T. turgidum* ssp. *dicoccum* (TTD), *T. turgidum* ssp. *polonicum*(TTP), *T. aestivum* ssp. *spelta* (TAS), *T. aestivum* ssp. *macha* and *T. urartu* (TU) as found on Table 1. The CS fast neutron-induced speltoid deletion mutant fndel-143 described by Faris *et al.* (2003), was used as a negative control in various experiments. The *T. aestivum* ssp. *aestivum* cv. ‘Bobwhite’ was used for transformation experiments.

SOUTHERN ANALYSIS

Leaf tissue from each species for DNA extraction was collected and frozen. All DNA extractions, digestions, Southern transfers, and hybridizations were done according to Faris *et al.* (2000).

GENERATION OF MUTANTS

Mutants were generated by Dr. Bikram Gill’s lab by treating CS seeds with 0.4% EMS in phosphate buffer for 24 h according to Williams *et al.* (1992). After washing in tap water, the seeds were planted into root-trainers and grown in a greenhouse. M₁ individuals were grown and M₂ seed collected. M₂ seed was planted and screened. Multiple lines were selected by Dr. Bikram Gill showing some degree of speltoid or nonfree-threshing spikes. Ten seeds from selected M₂ families were then planted and homozygous individuals with speltoid spikes were identified. Homozygous deletion mutants were eliminated by Southern analysis.

SEQUENCING AND SEQUENCE ANALYSIS

The genomic sequence for the *AP2*-like gene was obtained from CS, CS-*Dic* 5A, TTC, TTD, TAS, TM, TU, and the EMS mutants (mq36, mq125, and mq194) using PCR and the *T. monococcum AP2*-like gene sequence for primer construction. The *AP2*-like gene was PCR-amplified as three separate overlapping fragments using primers AP5P.11-3: 5'-GCCCTCGCAGCCCGCGGCCACCGCGCTCCCA or AP2startF: 5'-ATGGTGCTGGATCTCAATGTGGAGTCGCCGGCGGA with AP2.8R: 5'-CGCGGCCAAATCGGGGCAAAGGAATTCAAACGA for fragment 1, WAP2.2F: 5'-CACTGGATAATTTCTTCAGGTGGTTTCGACACTGC with AP2.15R: 5'-ACATGGAACCTTAATTTTCAGGAACGAACTTGTCG for fragment 2, and AP2.16F: 5'-CTGCTTGGTGCGCTGCTCCACCAGCTTACTGAAA with AP45.1R: 5'-CAGAAGGCCCAACGGTTAACGCAACAATGGC for fragment 3. PCR conditions for fragment 1 were 250 ng *Dra*I-digested genomic DNA, 0.4 μ M of forward and reverse primer, 200 μ M dNTPs, 1X Herculase reaction buffer, 8% DMSO, and 2.5 U Herculase Hotstart DNA Polymerase (Stratagene, La Jolla, CA) in a 50 μ L volume. Cycling conditions for fragment 1 amplification were: 98°C - 3 min, 10 cycles of 98°C - 40 s, 71°C - 30 s, 72°C - 2 min, 30 cycles of 98°C - 40 s, 71°C - 30 s, 72°C - 2 min with extension time increasing 10 s each cycle. One unit of Biolase DNA Polymerase (Bioline USA Inc., Randolph, MA) was added and allowed to finish cycling at 72°C for 10 min. Fragment 2 and 3 were amplified using 1 μ L Advantage cDNA Polymerase Mix (Clontech, Palo Alto, CA), 300 ng of DNA, 200 μ M dNTPs, 1X buffer and 0.4 μ M of forward and reverse primers in a 50 μ L reaction. Cycling conditions for fragment 2 were: 94°C - 4 min, 35 cycles of 94°C - 40 s, 66°C - 30 s, 72°C - 3 min, and a 10 min final elongation step. Cycling conditions for fragment 3 were nearly identical to fragment 2 except

the annealing temperature was 68°C and the extension time was shortened from 3 min to 2 min. The 5' region extending from position -140 to -1,121 from the transcription start site was PCR amplified with primers AP5P.16F: 5' - GGATCACGTGGGTGGTTCTTTGTCCATGCC and AP5P.12R: 5' - GTCGGGGAGGCCAAGGGGCATCAGAGG. Cycling conditions were: 94°C - 4 min, 35 cycles of 94°C - 40 s, 66°C - 30 s, 72°C - 2 min, and a 10 min final extension step.

Products from five independent PCR reactions for each segment of the gene from each genotype were electrophoresed through an agarose gel and gel-purified using the QIAquick Gel Extraction Kit (Qiagen, Chatsworth, CA). Fragments were cloned using the TA Cloning Kit (Invitrogen, Carlsbad, CA) and sequenced by the Kansas State University DNA Sequencing Facility or the Iowa State University DNA Sequencing Facility. The sequences were reassembled to obtain the full length gene sequences. All sequence alignments were done using ClustalW. The genomic *AP2*-like sequence from CS was tested for similarity to sequences in the NCBI EST database (<http://www.ncbi.nlm.nih.gov/blast>) and the Grain Genes wEST database (<http://wheat.pw.usda.gov/wEST/blast>) using the BLASTn algorithm (Altschul *et al.* 1997) to determine partial coding sequence of the *AP2*-like gene.

TRANSFORMATION

Dr. Justin Faris had previously identified a BAC clone from chromosome 5A in the Langdon library containing the *Q* gene. From this clone a 5 kb *DraI* fragment containing *Q* and its native promoter (1134 bases upstream of predicted translation start site) was cloned and sequenced. It was then ligated into the pSMART vector (Lucigen Corporation, Middleton, WI). Dr. Harold Trick proceeded with the tissue culture and particle bombardment of immature embryos according to Chen *et al.* (1998) and Altpeter *et al.* (1996). *T. aestivum* cv 'Bobwhite' (BW), chosen because of its transformability, was cobombarded with the transgenic construct

and the pAHC20 vector (contains the *bar* gene as a selectable marker driven by the maize ubiquitin promoter) using microprojectile bombardment. Dr. John Fellers screened the transgenic plants for presence of the *bar* gene by applying Liberty and using PCR amplification.

Positive individuals were grown to maturity and the spike type recorded. Six T₁ seeds were planted from a speltoid spike and six from compactoid spikes. DNA was extracted from young leaves. Confirmation of transgene integration was determined by digesting the DNA with *EcoRI*, Southern blotting, and hybridizing with a portion of the *AP2*-like gene. One plant containing speltoid spikes (tq32), one containing subcompactoid spikes (tq30), and one containing compactoid spikes (tq39) were selected for further analysis and immature spike tissue was collected for RNA extraction.

RNA ANALYSIS

Tissue for RNA extractions was collected, immediately frozen and stored at -80C. RNA was isolated from immature spikes of CS, fndel-143, CS-*Dic* 5A, mq36, mq125, mq194, tq32, BW, tq30, tq39, and stem and leaves of CS using the Qiagen RNeasy Plant Mini Kit (Qiagen, Chatsworth, CA) and on-column DNA digestion.

Reverse transcriptase-PCR (RT-PCR) was used to amplify the region encompassing the point mutations observed in the genomic sequence of the three EMS induced mutants, mq36, mq125, and mq194. RT-PCR was done using the BD TITANIUM One-Step RT-PCR Kit (Clontech, Palo Alto, CA) in combination with primers (AP45.6F: 5'-ATGGGGCAGCAGGCCCGGCGCCTGCGCCGATGGC and AP2.13R: 5'-CTCTTGGGATCGTGCGCGGTGGGTTGCGACATC) flanking the regions containing single base mutations following the suggested protocol. RNA from immature spikes of CS and fndel-143 were also included as positive and negative controls, respectively. The RT-PCR products

were electrophoresed through a 1% agarose gel, purified, cloned and sequenced using previously mentioned methods.

The primers, AP2startF: 5'- ATGGTGCTGGATCTCAATGTGGAGTCGCCGGCGGA and AP2.17R2: 5' – TCAGTTGTCCGGCGGGCGGGGGAAGTAGAAC were used to amplify the complete cDNA from start to stop codon using Stratagene Herculase Hotstart DNA Polymerase. The reaction consisted of 1 μ L undiluted cDNA (made with the TaqMan RT Reagents as described later under relative quantitative PCR) 0.4 μ M of forward and reverse primer, 200 μ M dNTPs, 1X Herculase reaction buffer, 4% DMSO, and 2.5 U Herculase Hotstart DNA Polymerase (Stratagene, La Jolla, CA) in a 50 μ L volume. Cycling conditions were: 98°C - 4 min, 10 cycles of 98°C - 40 s, 65°C - 30 s, 68°C - 3 min, 30 cycles of 98°C - 40 s, 65°C - 30 s, 68°C - 3 min with extension time increasing 10 s each cycle, and a 10 min final extension at 68°C. For cloning and sequencing one unit of Biolase DNA Polymerase (Bioline USA Inc., Randolph, MA) was added before the final elongation step.

UTR IDENTIFICATION

The length of the 3' untranslated region (UTR) was determined by searching the public databases for 3' ESTs of the AP2-like gene containing a poly (A+) tail. One clone was identified. The 5'UTR from CS was obtained using the BD SMART RACE cDNA Amplification Kit (Clontech, Palo Alto, CA) and following the suggested protocol for low copy transcripts. The BD Advantage2 PCR Kit (Clontech, Palo Alto, CA) and the gene specific primer APrace2 (5'-GGGCGGCGACGCGGGGAAGAGCTGCCTCGTG) were used to attempt to amplify the 5' UTR. After failing to amplify, the BD Advantage-GC 2 PCR Kit (Clontech, Palo Alto, CA) was used to successfully amplify the 5' UTR. The amplicon was cloned and sequenced.

NORTHERN ANALYSIS

The mRNA was isolated from CS and fndel-143 with the Qiagen Oligotex mRNA Mini Kit (Qiagen, Chatsworth, CA) and quantified using the Invitrogen DNA Dipstick (Invitrogen, Carlsbad, CA). One microgram of mRNA per lane was electrophoresed through a MOPS/formaldehyde gel (1% agarose, 1X MOPS Buffer, and 6.7% formaldehyde) at 4 volts/cm. The gel was washed in 10 volumes of water for 20 minutes three times, then stained 10 minutes with ethidium bromide, destained 20 minutes, and photographed. The RNA was neutrally transferred to a positively charged membrane, Hybond-XL (Amersham Bioscience, Piscataway, NJ) using capillary transfer with 10X SSC. After 20-24 hours the transfer was complete. The membrane was rinsed in 2X SSC, 0.1% SDS and photographed on a short wave UV box which also cross-linked the RNA. Membranes were prehybridized in hybridization buffer (5X SSC, 1X Denhardt's Solutions, 20 mM sodium phosphate pH 6.8, 1.4% SDS, 5% dextran sulphate, 50% formamide and 5 mg denatured salmon sperm DNA) for 2 hours. Probe was labeled using the random hexamer method with [³²P]dCTP (Feinberg and Vogelstein 1983). Labeling was terminated by adding 0.5 ml hybridization buffer. The probe was denatured by boiling for 5 minutes and added to the membranes. After 18-22 hours, membranes were washed twice with 2X SSC, 0.1% SDS for 10 minutes at room temperature followed by two additional washes with 1X SSC, 0.1% SDS at 65°C. Hybridization with a 314 bp fragment of the *GA3PDH* gene PCR amplified using the GAPDHF1 primer (5' GAGGGTCTGATGACAACCTGTTTCATGC) and the GAPDHR2 primer (5' TGGCATCAAAGATGCTCGACCTGCTGTCA) allowed normalization between lanes. The membranes were hybridized with probes representing the 5' and 3' region of the *AP2*-like gene.

VIRTUAL NORTHERNS

The cDNA was generated using the BD SMART PCR cDNA Synthesis Kit (Clontech, Palo Alto, CA) as suggested by the manufacturer. The starting material was 1 µg of total RNA. The long distance PCR amplification step was done using 1 µL of diluted cDNA with the BD Advantage-PCR Kit and 1 µL of the diluted cDNA with the BD Advantage-GC 2 PCR Kit (Clontech, Palo Alto, CA). The optimum number of cycles was determined as suggested. The amplified cDNA was used to make Southern blots. Membranes were hybridized with a 200 bp probe located at the 5' end of the *AP2*-like gene PCR amplified using the AP2startF primer and the AP2race2 primer (5' GGGCGGCGACGCGGGGAAGAGCTGCCTCGTG). Hybridization with a 314 bp fragment of the *GA3PDH* gene allowed normalization between lanes.

RELATIVE QUANTITATIVE PCR (RQ-PCR)

The cDNA was prepared using TaqMan RT Reagents and MultiScribe Reverse Transcriptase (Applied Biosystems, Foster City, CA). The reactions consisted of 200 ng of cDNA per 10 µL reaction volume with 1X TaqMan RT Buffer, 5.5 mM Magnesium Chloride, 500 µM per dNTP, 2.5µM oligo dT(16) primer, 0.4 U/µL RNase Inhibitor, and 1.25 U/µL Reverse Transcriptase incubated at 25°C for 10 min, 48°C for 30 min and 95°C for 5 min. The cDNA was diluted 1:5 before RQ-PCR was performed in a 7500 Real Time PCR System (Applied Biosystems, Foster City, CA). The TaqMan system used to detect the *18S* ribosomal gene was described by Podkowinski *et al.* (2003). The *Q* TaqMan System consisted of the *Q*-Left primer, (5'-CCCTGAATCGTCAACCACAATG), the *Q*-Right primer, (5'-CCGTGCCATGTTGATGCA), and the *Q*-Probe (5'-FAM-CTTCGTCCCAGTGGCCTG-NFQ). The reactions were done in quadruplicate using TaqMan Universal PCR Master Mix (Applied Biosystems, Foster City, CA). Each experiment was repeated twice. The 20 µL reaction

contained 1X TaqMan Universal PCR Master Mix, 0.2 μ M each primer, 0.1 μ M of probe, and 5 μ L diluted cDNA and were cycled for 50°C for 2 min, 95°C for 10 min, and 40 cycles of 95°C for 15 s and 60°C for 1 min.

Templates to determine the amplification efficiency of *18S* and *Q* consisted of five 4-fold dilutions of CS cDNA. Raw C_T values were averaged for each dilution. The log of RNA concentration versus the C_T value was plotted and linear regression was used to draw the best fit line. Amplification efficiencies were calculated based on slope where efficiency = $100\% * \tan^{-1}(\text{slope}^{-1}) / 45$. Efficiency similarity is assumed if the slope of the line from the difference between the target gene and the endogenous control gene is between -0.1 and 0.1.

Sample C_T values were averaged omitting outlying C_T values for each gene. Sample averages were linearized using the $2^{(-\Delta\Delta C_T)}$ method (Livak and Schmittgen 2001).

Relative quantity of target gene in relation to calibrator sample = $2^{-[C_{T(se)} - C_{T(st)}] - [C_{T(ce)} - C_{T(ct)}]}$

where $C_{T(se)}$ = averaged C_T value of the sample's endogenous gene

$C_{T(st)}$ = averaged C_T value of the sample's target gene

$C_{T(ce)}$ = averaged C_T value of the calibrator's endogenous gene

$C_{T(ct)}$ = averaged C_T value of the calibrator's target gene

Q MICROSATELLITE GENOTYPING

DNA from all lines in Appendix B was obtained. PCR primers, Qsnp2A.F: GCACTAGCTAATTCAGTGGTTAGATTTGCTCA and Qsnp.R: ATTCAGTGGTAGCAACAGTTTCAGTAAGCTGG were used to amplify the microsatellite within intron 9 of the *Q* gene using 0.5 Units Biolase DNA Polymerase, 1X Biolase NH_4 -based

buffer, 2.2 mM MgCl₂, 100 ng of DNA, 200 μM dNTP, and 0.4 μM of forward and reverse primers in a 10 μL reaction. Cycling conditions were: 94°C - 3 min, 35 cycles of 94°C - 40 s, 65°C - 30 s, 72°C - 1 min, and a 7 min final elongation step. PCR products were electrophoresed through a 42 cm polyacrylamide gel [1X TBE, 8% Long Ranger (BioWhittaker Molecular Applications, Rockland, ME FMC Biozym), and 7 M urea] for 8-9 hours at 70 Watts. The DNA was visualized by staining with 30 ml of 1X SYBR Green II solution for 25 minutes. The gel was scanned on an Amersham Biosciences Typhoon 9410 variable mode imager.

PHYLOGENETIC ANALYSIS

Phylogenetic trees were constructed from CLUSTALW alignments of the complete genomic DNA sequences of *Q/q* using the neighbor-joining method and multiple distance-based methods available in the MacVector v7.2 software. Confidence values for nodes were calculated using 1,000 bootstraps.

RESULTS

STRUCTURE OF *Q* AND VALIDATION

The wheat *AP2*-like (*WAP2*) genomic sequence was obtained by assembling the sequences of three cloned, overlapping fragments. This sequence extended 141 bases upstream of the predicted start codon and 359 bases downstream of the predicted stop codon. It was 3,229 bases from start to stop codon with an average GC content of 54%. Most of the coding regions were identified by subjecting the genomic sequence to BLASTn searches against the EST database. No ESTs were identified that spanned the 5' end of the gene therefore gene prediction programs were used to initially identify these exons. This was later confirmed by amplifying the cDNA from start to stop codon. The *WAP2* gene consisted of 10 exons and 9 introns (Figure 7). The deduced protein sequence was 447 amino acids with two AP2 DNA binding domains. The length of the 5' and 3' untranslated regions (UTRs) was determined to ensure the genomic sequence contained the entire coding region. One EST with high similarity to *WAP2* was identified which contained a poly A tail (Figure 8). The 3' UTR was 255 bases long and was contained within the obtained genomic sequence. Since there were no ESTs spanning the 5' region of *WAP2*, 5' RACE was used. One clone was 99% identical to the genomic sequence with the mismatches likely due to PCR errors. Several more clones from *CS-Dic5A* were identical to the genomic sequence (Figure 9). The 5' UTR was 128 bases long and completely contained within the available genomic sequence.

The M₂ generation of the EMS treated seed had been previously screened. Seventeen putative mutants were identified as being only partially free-threshing or having speltoid spikes. Ten seeds from each of the 17 M₂ plants were sown. Six families had plants with speltoid or

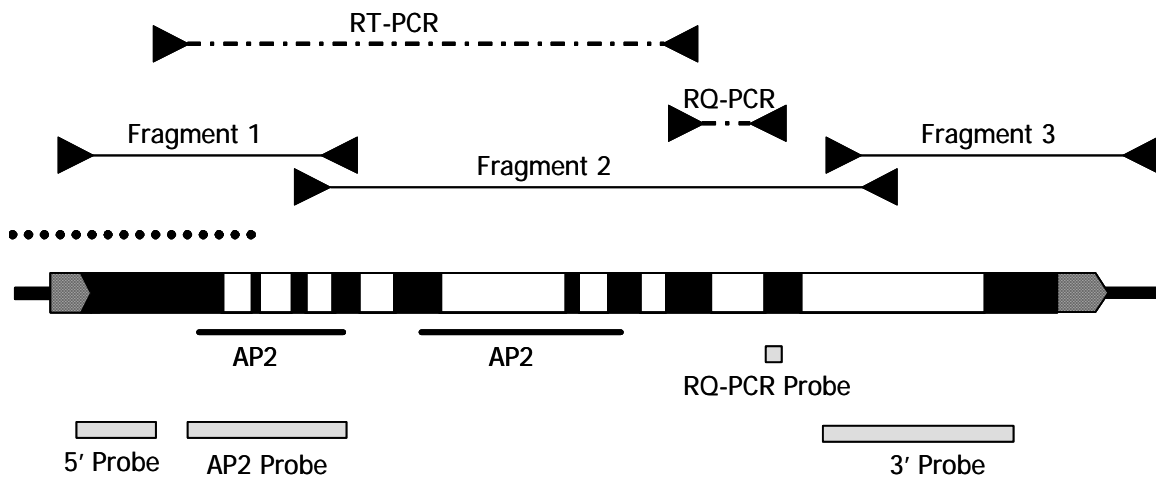


Figure 7. The structure of the *WAP2 (Q)* gene. Checkered boxes indicate UTRs. Black boxes indicate exons. White boxes indicate introns. The large black dotted line indicates a GC rich region. Solid black lines indicate the AP2 DNA binding domains. Solid lines with inverted arrows indicated the PCR fragments amplified for genomic sequencing. The dotted lines with the inverted arrows indicate region of amplification for either reverse transcription-PCR or relative quantitative-PCR. Probes are indicated by grey boxes.

		3249
Chinese Spring EST BE217023	TTCTACTTCCCCCGCCCGCCGGACAACTGAAGCTGGCCGTTGTGACCAGA TTCTACTTCCCCCGCCCGCCGGACAACTGAAGCTGGCCGTTGTGACCAGA	
		3299
Chinese Spring EST BE217023	CGGCGGTGGGTGCGCGCGGTTCGAGGTGTTTCGCTCCTCGTCGTCGGTAACG CGGCGGTGGGTGCGCGCGGTTCGAGGTGTTTCGCTCCTCGTCGTCGGTAACG	
		3349
Chinese Spring EST BE217023	CTTGTTGTGAAACTATAATCGGAGAGAGATGACATTGCCAGGCCATGTGT CTTGTTGTGAAACTATAATCGGAGAGAGATGACATTGCCAGGCCATGTGT	
		3399
Chinese Spring EST BE217023	GGTGACACTACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACG GGTGACACTACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACG	
		3449
Chinese Spring EST BE217023	CGGATCATGGCTGTTTCATTAGATTCTCATGTATCCAATGTTCAAGTTTCC CGGATCATGGCTGTTTCATTAGATTCTCATGTATCCAATGTTCAAGTTTCC	
		3499
Chinese Spring EST BE217023	CAAACGGTTGAAAAAACTTTGAAATTTGTGATGGCAAATTCATGCATGGG CAAACGGTTGAAAAAACTTTGAAATTTGGATGGC <u>AAAAAAAAAAAAAAAA</u>	

Figure 8. 3' UTR identification of the *WAP2 (Q)* gene. Alignment indicates a 3' UTR length of 255 bp. Shading indicates the stop codon. Underlined letters indicate the polyA tail. Bases are numbered from the translation start site. The source of EST BE217023 was a library generated from the leaf of a nine day old seedling of *Triticum aestivum*.

			-132
CS	-----		GCCCTCGCAG
5' RACE	<u>CTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGTACGCG</u>		
			-82
CS	CCCGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCACTCATCGGTC		
5' RACE	<u>GGGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCACTCATCGGTC</u>		
			-32
CS	CAGGTCGGTCGCTCGGAGCCGAGCGGCGGGCGGGCGAGGAGTGC GTT		
5' RACE	CAGGTCGGTCGCTCGGAGCCGAGCGGCGGGCGGGCGAGGAGTGC GTT		
			19
CS	TTATTTCGGTCCCGGCGGGCCTCGGATCGGAG	ATGGTGCTGGATCTCAATG	
5' RACE	TTATTTCGGTCCCGGCGGGCCTCGGATCGGAG	ATGGTGCTGGATCTCAATG	

Figure 9. 5' UTR identification of the *WAP2 (Q)* gene. Alignment of the genomic sequence from CS and the 5' RACE product indicates a 5' UTR of 128 bases. The underlined letters are the 5' RACE primer. Shaded letters represent the beginning of the predicted coding region.

partially speltoid spikes. These individuals were screened by Southern analysis which indicated that three of the families with partially speltoid spikes were hemizygous deletions for the region encompassing *WAP2*. One very speltoid individual, presumably homozygous, was selected from each of the three remaining families.

The *WAP2* gene was amplified, cloned, and sequenced from three individuals with putative point mutations, mq36, mq125, and mq194 (Figure 10, Appendix C). Mutant mq194 had a base change within exon 5. This changed the predicted protein sequence from a cysteine to a tyrosine at position 221. The mutants mq36 and mq125 did not have any base changes within the coding sequence that changed the deduced protein sequence. They did however have base changes within the splice sites. Mutant mq36 had a base change of G to A in the acceptor site of intron 7. Mutant mq125 also had a base change of G to A but in the donor site of intron 2. Analysis with Genscan (<http://genes.mit.edu/GENSCAN.html>), FGENESH (<http://www.softberry.com/berry.phtml?topic=index&group=programs&subgroup=gfind>) and GeneMark.hmm (<http://opal.biology.gatech.edu/GeneMark/>) predicted altered splice sites. In *Arabidopsis* the change to the 5' intron site produced a splicing block due to accumulation of lariat-exon intermediates (Bradley *et al.* 1995; Liu and Filipowicz 1996; Orozco *et al.* 1993). The splicing behavior due to the specific change in the 3' splice site had not been determined in *Arabidopsis* but other changes resulted in unspliced transcripts, activation of cryptic splice sites, and exon skipping (McNellis *et al.* 1994). Splicing behavior was validated by RT-PCR, which indicated intron transcription (Figure 11). The amplicon in mq194 remained the same size as in wild type CS, but the amplicons in both mq36 and mq125 were larger than in CS. The amplicons were sequenced for further confirmation that the introns in question



Figure 10. Spike morphology of the EMS mutants. Chinese Spring (CS) has a square spike. The EMS mutants, the fast neutron deletion line (fndel-143), and the CS-*T. dicoccoides* 5A chromosomal substitution line (CS-*Dic* 5A) have speltoid spikes.

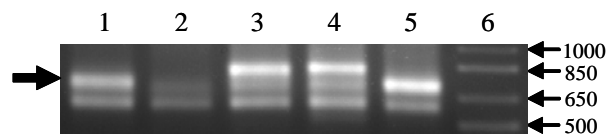


Figure 11. Reverse transcription-PCR of EMS mutants. Lane 1: CS, Lane 2: fndel-143, Lane 3: mq36, Lane 4: mq125, Lane 5: mq194, and Lane 6: Marker. The arrow on the left indicates the wild type transcript in CS. Mutants, mq36 and mq125, have transcripts longer than wild type Chinese Spring indicating that the base substitutions removed the splice sites.

CS	MVLDLNVEPADSGTSSSSVLNSADAGGGGFRFGLLGSPDDDDCSGEPAPVGPFGFVTRQL
mq194	MVLDLNVEPADSGTSSSSVLNSADAGGGGFRFGLLGSPDDDDCSGEPAPVGPFGFVTRQL
mq36	MVLDLNVEPADSGTSSSSVLNSADAGGGGFRFGLLGSPDDDDCSGEPAPVGPFGFVTRQL
mq125	MVLDLNVEPADSGTSSSSVLNSADAGGGGFRFGLLGSPDDDDCSGEPAPVGPFGFVTRQL
CS	FPASPPGHAGAPGVTMGQQAPAPAPMAPVWQPRRAEELLVAQRMAPAKKTRRGPRSRSSQ
mq194	FPASPPGHAGAPGVTMGQQAPAPAPMAPVWQPRRAEELLVAQRMAPAKKTRRGPRSRSSQ
mq36	FPASPPGHAGAPGVTMGQQAPAPAPMAPVWQPRRAEELLVAQRMAPAKKTRRGPRSRSSQ
mq125	FPASPPGHAGAPGVTMGQQAPAPAPMAPVWQPRRAEELLVAQRMAPAKKTRRGPRSRSSQ
CS	YRGVTFYRRTGRWESH IWDCGKQVYLGGFDTAHAARAYDRAAIKFRGLEADINFNLSDY
mq194	YRGVTFYRRTGRWESH IWDCGKQVYLGGFDTAHAARAYDRAAIKFRGLEADINFNLSDY
mq36	YRGVTFYRRTGRWESH IWDCGKQVYLGGFDTAHAARAYDRAAIKFRGLEADINFNLSDY
mq125	YRGVTFYRRTGRWESH IWDCGKQVYLDLQKIPARAPISSVSNFDYLSMGS-----
CS	EEDLKQMRNWTKEEFVHILRRQSTGFARGSSKYRGVTLHKCGRWEARMGQLLGKKYIYLG
mq194	EEDLKQMRNWTKEEFVHILRRQSTGFARGSSKYRGVTLHKYGRWEARMGQLLGKKYIYLG
mq36	EEDLKQMRNWTKEEFVHILRRQSTGFARGSSKYRGVTLHKCGRWEARMGQLLGKKYIYLG
mq125	-----
CS	LFDSEVEAARAYDRAAIRFNGREAVTNFESSYNGDAPPDAENE-----
mq194	LFDSEVEAARAYDRAAIRFNGREAVTNFESSYNGDAPPDAENE-----
mq36	LFDSEVEAARAYDRAAIRFNGREAVTNFESSYNGDAPPDAENEGTTTIGLTCRISPITP
mq125	-----
CS	-----AIVDADALDLDRMSQPTAHDPKRDNI IAGLQLTFDSPESSTTMISSQ
mq194	-----AIVDADALDLDRMSQPTAHDPKRDNI IAGLQLTFDSPESSTTMISSQ
mq36	KSYLIDIVVVFLTIVDADALDLDRMSQPTAHDPKRDNI IAGLQLTFDSPESSTTMISSQ
mq125	-----
CS	PMSSSSSQWPVHQHGTAVAPQQHQRLYPSACHGFYPNVQVQVQERPMEARPPEQPSSFPG
mq194	PMSSSSSQWPVHQHGTAVAPQQHQRLYPSACHGFYPNVQVQVQERPMEARPPEQPSSFPG
mq36	PMSSSSSQWPVHQHGTAVAPQQHQRLYPSACHGFYPNVQVQVQERPMEARPPEQPSSFPG
mq125	-----
CS	WGWAQAMPPGSSHSPLLYAAAASSGFSTAAAGANLAPPPYPDHHRFYFPRPPDN
mq194	WGWAQAMPPGSSHSPLLYAAAASSGFSTAAAGANLAPPPYPDHHRFYFPRPPDN
mq36	WGWAQAMPPGSSHSPLLYAAAASSGFSTAAAGANLAPPPYPDHHRFYFPRPPDN
mq125	-----

Figure 12. Alignment of predicted protein products of the EMS mutants. The amino acid difference in mq194 at position 221 is denoted with an arrow.

were transcribed. The cDNA sequence for mq36 contained intron 7 inserted in frame, which led to a longer predicted protein sequence (Figure 12). The cDNA sequence for mq125 encountered a stop codon within the transcribed intron 2, which led to a truncated protein sequence (Figure 12). Sequence analysis of the three independent mutants confirmed *WAP2* is *Q*.

Q ALLELE COMPARISON

Previous research (Kuckuck 1959; Swaminathan 1963) suggested that *Q* evolved as a duplication of *q* due to unequal crossing over. DNA from various *Triticum* taxa representing various ploidy levels, subspecies, and accessions (Table 1) was isolated, Southern blotted and hybridized with a probe for the *Q* gene (Figure 13). The result was a single band appearing for each of the *Q* homeoalleles (easily distinguished using the group 5 nullisomic-tetrasomic stocks). Similar hybridization intensities of the 5A locus across ploidy levels was also observed. The absence of extra bands or differences in hybridization intensities indicated that the *Q* locus is not duplicated within the genome and is not a series of repeats of the *q* allele but that *Q* is a different allele. Sequence analysis of the 142 kb BAC harboring the *Q* allele from LDN indicated a single open reading frame (ORF) corresponding in size and structure to the *q* ORF from TM (Simons *et al.* 2005).

Alignments with the sequences of CS, LDN, and TM indicated multiple differences between the *Q* and *q* alleles, making it difficult to identify which nucleotide difference was responsible for the functional variation. The remaining species used for the Southern hybridization experiment described above were sequenced. Subsequent alignments including these sequences indicated six conserved differences between the *Q* and *q* alleles (Figure 14).

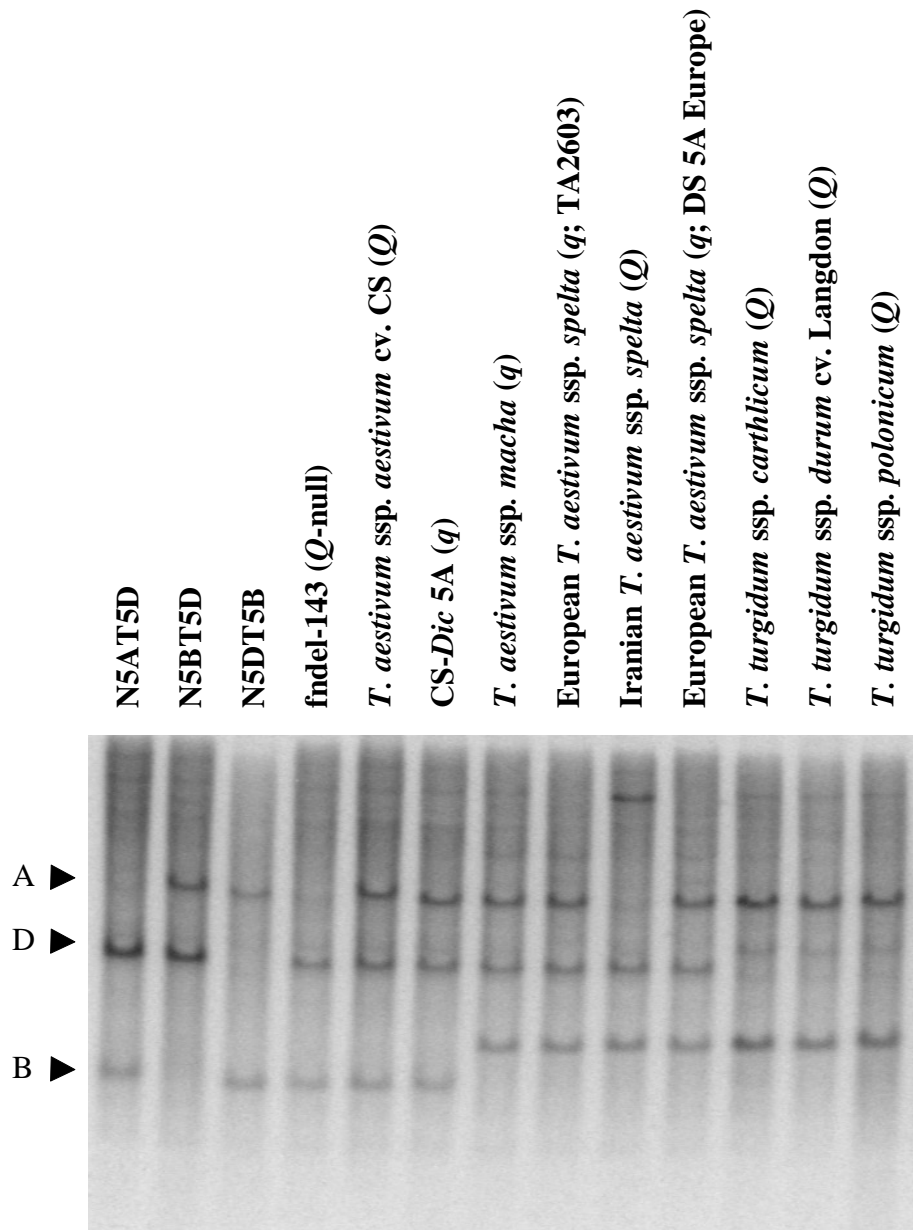


Figure 13. Southern analysis of various wheat species hybridized with a fragment of *Q* (AP2 probe).



Figure 14. Locations of six conserved nucleotide differences between *Q*- and *q*-genotypes within the genomic sequence of the gene. Arrows represent single nucleotide polymorphisms between *Q* and *q*. Green = intron; Red = exon; Blue = 3' UTR. The polymorphism indicated in red represents the amino acid difference between *Q* and *q* alleles at position 329 of the predicted protein. The green bar represents a variable microsatellite within intron 9.

One difference was found in the 3' UTR where *Q* contained a C instead of an A in *q*. Another difference was in the number of repeats in a microsatellite located in intron 9. *Q*-genotypes consistently had seven CTC repeats while *q*-genotypes varied with five, eight, and nine repeats. Three differences were found within noncoding sequences including two in intron 2 (*Q*:T, *q*:C and *Q*:G, *q*:A) and one in intron 9 (*Q*:A, *q*:G). Finally, one conserved difference was identified in the coding sequence where the *Q* allele encoded an isoleucine at amino acid position 329 whereas *q* possessed a valine.

NORTHERN ANALYSIS

A probe for the *glyceraldehyde-3-phospho-dehydrogenase* gene (*GA3PDH*) was generated and used as a control for normalization because the ribosomal RNA was not visible after selection for mRNA. Probes containing both the 3' and 5' region of the *Q* gene were also generated. A northern blot with 1 µg mRNA from CS (*QQ*), CS-*Dic* 5A (*qq*), and fndel-143 (null) immature spikes was obtained. The *GA3PDH* hybridization produced bands of similar intensity but no signals were detected when various fragments of the *Q* gene were hybridized as probes (Figure 15). The level of transcription of *Q* was not high enough to be detected with a traditional northern using 1 µg mRNA.

VIRTUAL NORTHERN

The optimum number of amplification cycles was determined to be 15 cycles because a light smear was produced with no distinct bands. Hybridization with the *GA3PDH* probe indicated consistent amplification (Figure 16) but hybridization with *Q* did not work (Figure 16) when using the Advantage 2 PCR Kit for amplification. The second attempt used the Advantage GC 2 Kit for amplification of the cDNA. The *GA3PDH* hybridization worked (Figure 16) as did the hybridization with *Q* (Figure 16). The intensity of the band differed between CS and CS-*Dic*

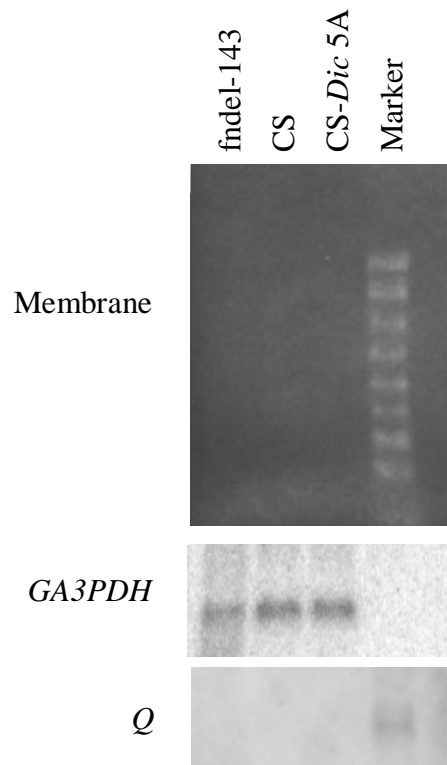


Figure 15. Northern analysis with *GA3PDH* and *Q*. One microgram of mRNA was not visible on the membrane. Hybridization with *GA3PDH* was used for normalization. Hybridization with a 5' region of *Q* showed only nonspecific binding within the ladder.

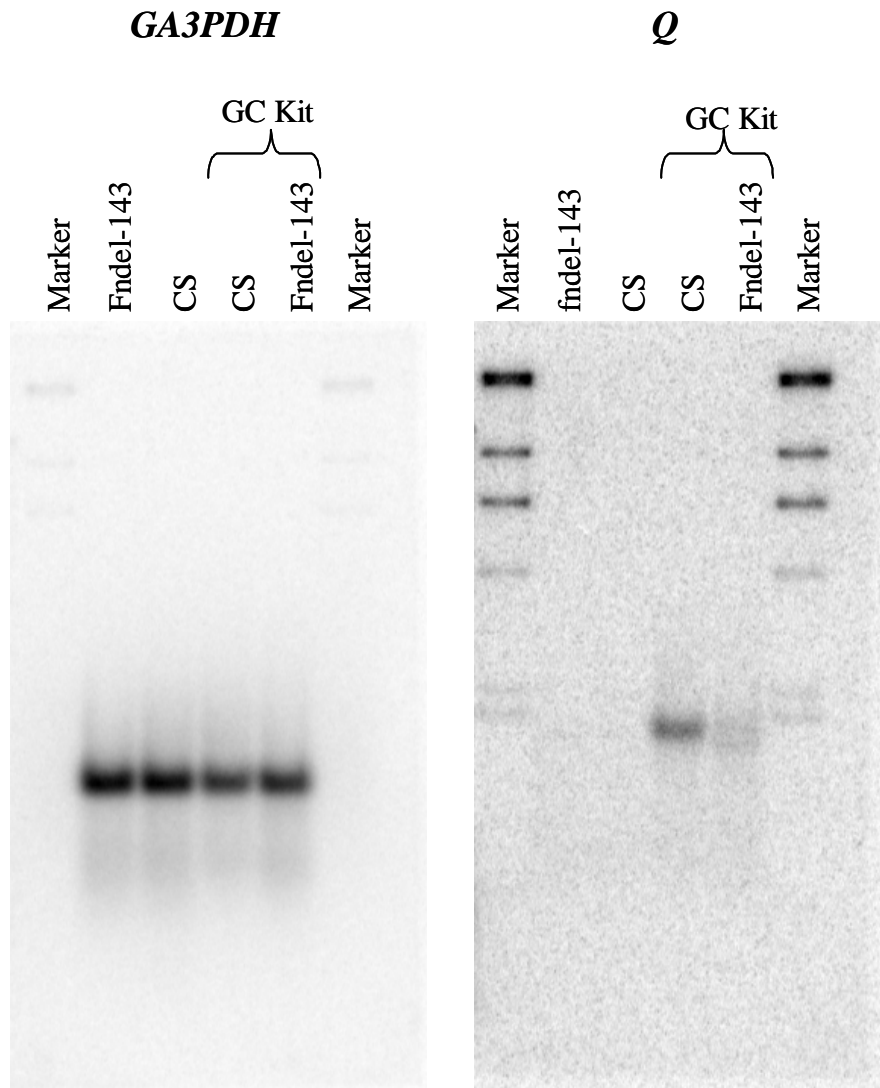


Figure 16. Virtual northern analysis with *GA3PDH* and *Q*. Hybridization with *GA3PDH* indicated a difference in amplification efficiency between using and not using the amplification kit for GC rich regions. Hybridization with *Q* indicated the kit for amplifying GC rich regions would amplify the *Q* cDNA but the other kit would not.

5A making it difficult to determine if a difference existed between them (Figure 17). The cDNAs of *Q* and *q* were similar in size.

cDNA SEQUENCING

The cDNA from the *Q* gene was amplified from both CS and CS-*Dic* 5A, cloned and sequenced (Appendix D). Some of the clones were missing the 5' end of the cDNA possibly due to the long primer length or RNA degradation. The primers were not specific to 5A and some clones were not identical to the 5A *Q* cDNA. These sequences were placed into two groups. The first group was identified as being the 5B homeoallele by alignment with the Langdon 5B BAC . The second group may be the 5D homeoallele. The putative D genome cDNA is very similar to the A genome with a few indels and base substitutions (Appendix E). However, the B genome cDNA indicates that the B genome is spliced differently than the A genome (Appendix E). Assuming the cDNAs extend further upstream than the sequence obtained and that translation would begin with the same start codon, the protein encoded by both the B and D genome transcripts are truncated (Appendix F).

RQ-PCR

The TaqMan system, primers and probe, were designed by ABI for the *Q* gene based on a putative single nucleotide difference between the homeoalleles. Amplification was tested for both *18S* (ribosome) and *Q* using a 2-fold serial dilution of cDNA made using random hexamers. The efficiencies based on slope were 94.3% for *18S* (Figure 18) and 94.8% for *Q* (Figure 18). For the amplification efficiencies to be deemed similar, the slope of the difference of the C_T value needed to be less than 0.1. These two efficiencies were deemed similar (Figure 18) fulfilling the assumption necessary to use the $2^{-\Delta\Delta C_T}$ method of linearizing the data. The

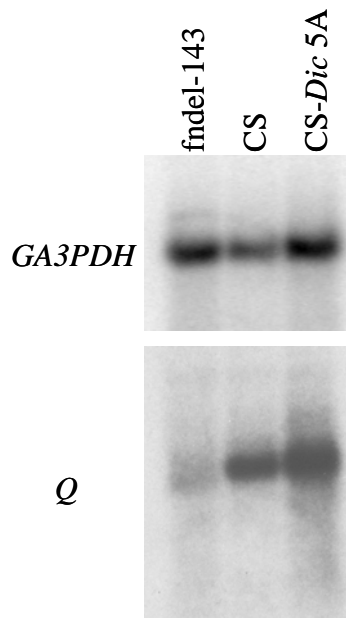


Figure 17. Virtual northern of CS and CS-*Dic 5A* hybridized with *GA3PDH* and *Q*. Uneven amplification occurred between samples as indicated with *GA3PDH*. Hybridization with *Q* suggested a difference in expression between CS and CS-*Dic 5A*.

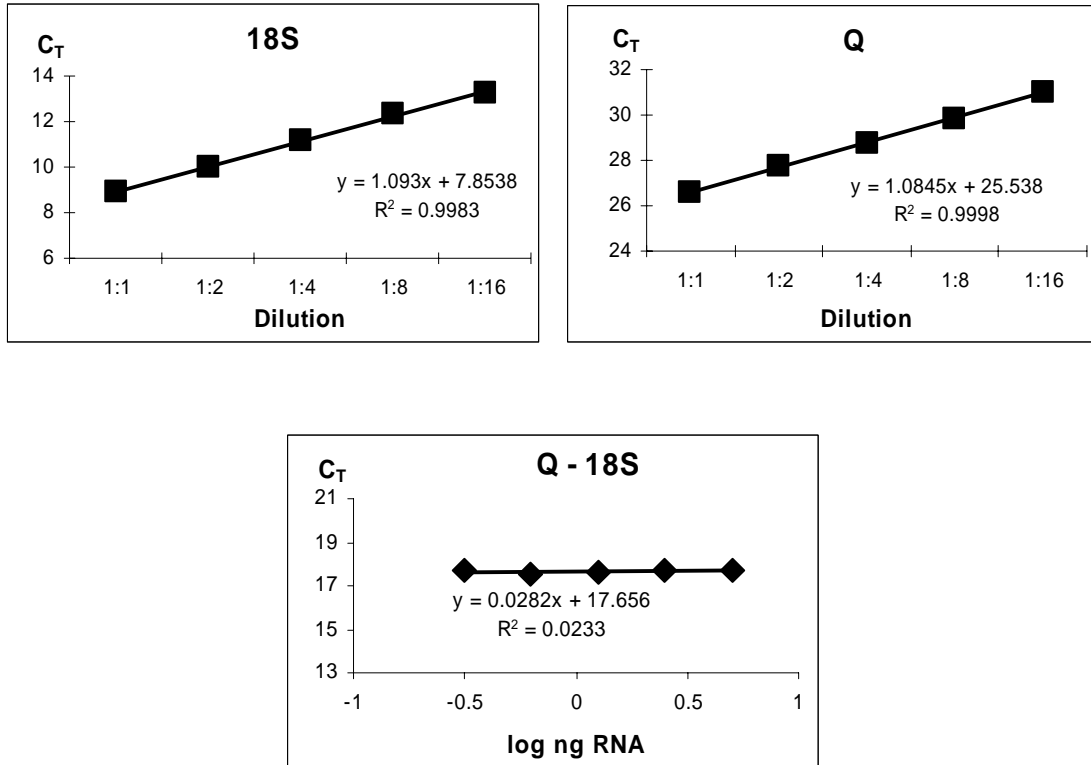


Figure 18. Amplification efficiencies and similarity of efficiency. *18S* amplified at 94.3% efficiency based on a slope of 1.093. *Q* amplified at 94.8% efficiency based on a slope of 1.0845. The difference between the slope of *Q* and *18S* was less than 0.1 and were therefore presumed to be similar.

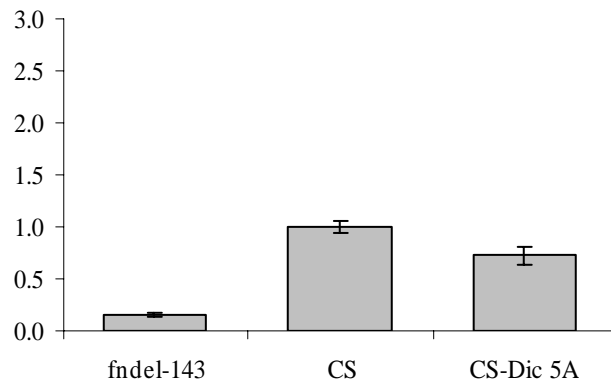


Figure 19. Relative transcription levels of Q in CS and q in CS-*Dic* 5A in immature spikes. Q was transcribed at higher levels than q . Transcription level in fndel-143 (null for Q) is shown to indicate the specificity of the Taqman system. Bars represent standard error. The same pattern was observed in each experimental replication.

deletion line, fndel-143, was used to determine the specificity of the *Q* TaqMan system. Small amounts of background were present, very likely resulting from the other homeoalleles or possibly other artifacts. A significant difference in transcript abundance was observed between CS (*QQ*) and CS-*Dic* 5A (*qq*; Figure 19) suggesting that differences in spike morphology were due to varying levels of gene expression. The observed differences in the amount of *Q* transcript in each of the four transgenic plants that varied for transgene copy number and spike morphology (see below) lent further support to this notion.

REGULATORY REGION

The sequence of more than 1000 bases upstream from the start codon was available from the previously sequenced TM and LDN BACs. Many differences existed between these two sequences (TM and LDN). To eliminate some of these differences as potentially critical regulatory elements, the region from -140 to -1,121 was amplified, cloned and sequenced from six additional species, three containing the *Q* allele and three containing the *q* allele. Various attempts with differing primers, polymerases, additives, and digestions to amplify the sequence between -10 and -140 failed but this region was nearly identical between TM and LDN. The sequence of this segment was reconfirmed by PCR amplification directly from the BACs followed by sequencing. ClustalW alignments of these sequences were used to generate a consensus of the promoter regions of *Q* and *q*. A total of five conserved differences were identified (Figure 20), but searches of plant promoter databases PlantCARE (<http://intra.psb.ugent.be:8080/PlantCARE/index.html>), PlantProm (<http://www.softberry.com>), and PLACE (<http://www.dna.affrc.go.jp/PLACE/>) indicated that only two of these differences are likely to be associated with putative regulatory elements. The *Q* promoter region contained a G-box, an ABRE element, and a GCN4 motif due to the 2 base pair difference at position -380

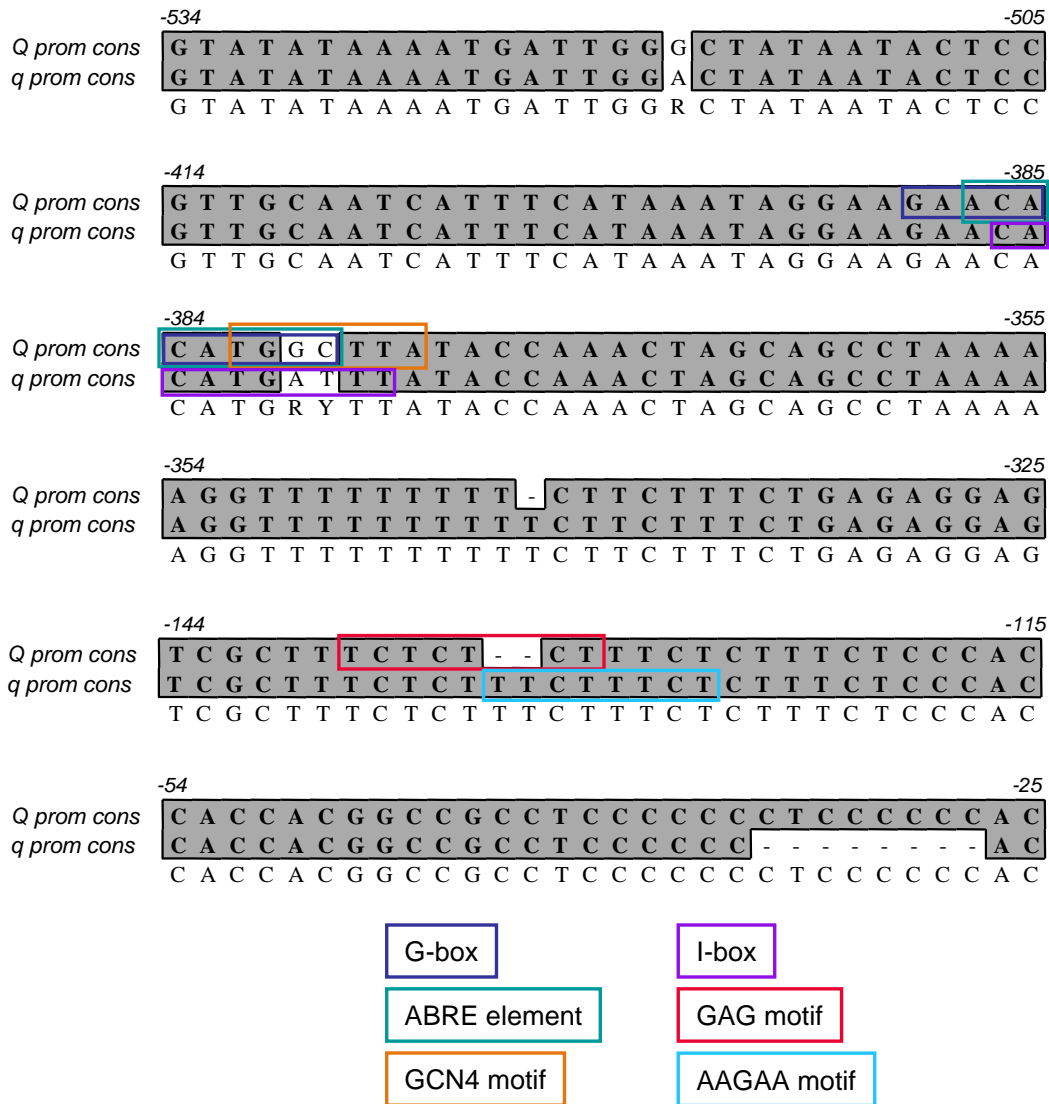


Figure 20. Genomic alignment of consensus promoter regions of *Q*- and *q*-genotypes. The compared sequence corresponds to position -1 to $-1,121$ from the transcription start site. The sequences from position -140 to $-1,121$ are based on *T. aestivum* ssp. *aestivum* cv. Chinese Spring, *T. turgidum* ssp. *carthlicum*, *T. turgidum* ssp. *durum* cv. Langdon and *T. aestivum* ssp. *spelta* (Iranian; DS 5A Iran) for the *Q* consensus, and on *T. turgidum* ssp. *dicoccoides* (CS-DIC 5A), *T. turgidum* ssp. *dicoccum*, *T. monococcum*, and *T. aestivum* ssp. *spelta* (European; DS 5A Europe and TA2603) for the *q* consensus. The sequence corresponding to position -1 to -139 is based on *T. turgidum* ssp. *durum* cv. Langdon for *Q* and on *T. monococcum* for *q*. Only regions of the alignment harboring conserved differences between the *Q* and *q* consensus promoter sequences are shown. Putative regulatory sequences are shown in colored boxes.

from transcription start and a GAG motif from the 2 base pair deletion at position -133. The *q* promoter region has an I-box associated with position -380 and an AAGAA motif with position -133. The G-box, I-box, and GAG motifs are involved in light responsiveness, the ABRE element with abscisic acid responsiveness, and the GCN4 motif relates to endosperm expression (PlantCARE: <http://intra.psb.ugent.be:8080/PlantCARE/>). The AAGAA motif is involved in cryptic splicing (Fairbrother *et al.* 2002).

ECTOPIC EXPRESSION OF *Q*

Seventeen putative transformants were obtained. The T₀ generation was screened for individuals with either speltoid or compactoid spikes. One speltoid T₀ plant was identified, and six T₁ progeny derived from this plant were grown for further analysis. In addition to having speltoid spikes (Figure 21A), the T₀ and all six T₁ plants were taller than Bobwhite (Figure 21E), had keeled tenacious glumes that adhered strongly to the seed, and had fragile rachises. The disarticulation pattern was such that the rachis broke above the junction of the rachis and rachilla leaving a portion of the rachis at the base of the spikelet. This tendency mimics the disarticulation pattern of the shatter-prone wild wheats that lack the *Q* allele. Southern analysis showed each T₁ individual harbored an abundance of transgene copies in addition to the endogenous gene (Figure 22).

Two partially sterile T₀ plants with compactoid spikes were identified. Three T₁ plants derived from one compactoid T₀ and two T₁'s from a second compactoid T₀ showed a range of phenotypes. One plant was of normal height and had square spikes, two plants were slightly shorter than Bobwhite (Figure 21E) and had subcompactoid spikes (Figure 21C), and two were very short (Figure 21E) with compactoid spikes (Figure 21D). All plants had tough rachises and

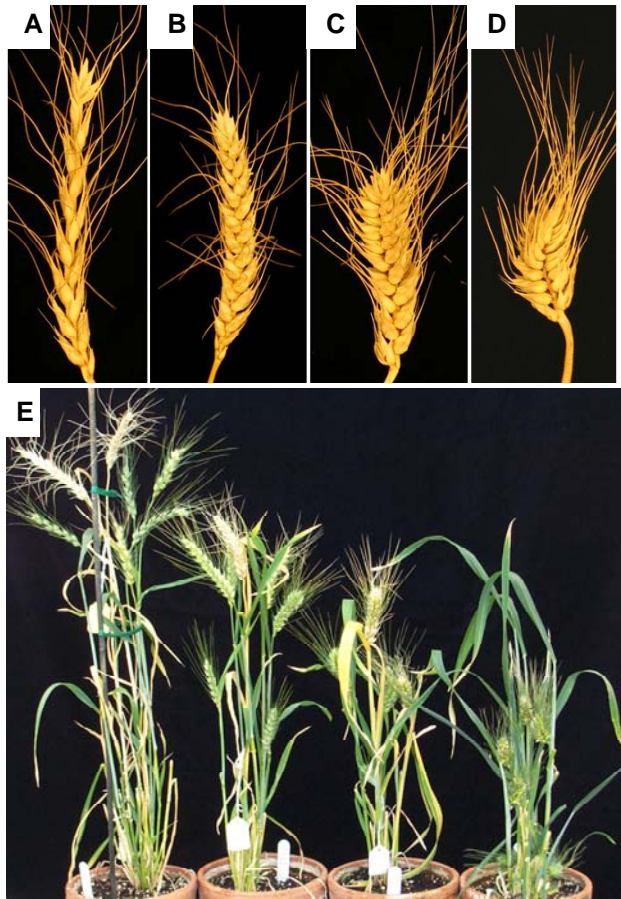


Figure 21. Morphology of T₁ transgenic plants. A) T₁ transgenic speltoid spike (tq32). B) Untransformed Bobwhite square spike. C) T₁ transgenic subcompactoid spike (tq30). D) T₁ transgenic compactoid spike (tq39). E) T₁ transgenic individuals show that plant height and spike length are associated with the level of *Q* transcription. Left to right: tq32, Bobwhite, tq30, and tq39.

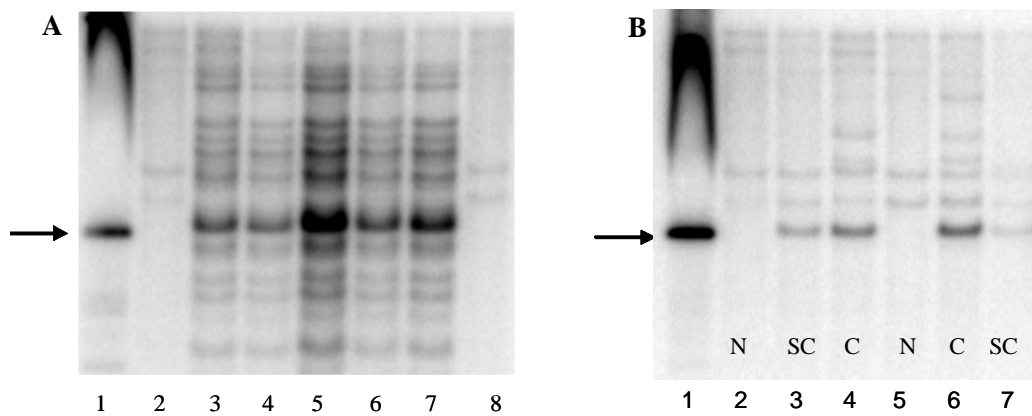


Figure 22. Southern analysis of T₁ progeny showing the integration of multiple copies of *Q*. The *Eco*RI-digested DNA was hybridized with a probe from the 3' region of *Q*. The arrow indicates 3.0 kb fragment of plasmid construct. A) T₁ progeny derived from the speltoid T₀ spike, lane 1: plasmid construct, lane 2: untransformed Bobwhite, lanes 3-8: T₁ progeny, all of which had speltoid spikes. B) T₁ progeny derived from compactoid T₀ spikes, lane 1: plasmid construct, lane 2: untransformed Bobwhite, lanes 3-7: T₁ progeny segregating for spike type (N=normal; SC=subcompactoid; C=compactoid).

round, soft glumes that loosely held the seed, and were free-threshing. Compactoid spikes were mostly sterile. Southern analysis indicated the T₁ plants segregated for copy number and were either lacking the transgene (square spike) or possessed multiple copies of the transgene in addition to the endogenous gene (subcompactoid and compactoid spikes; Figure 22).

One plant of each spike type, compactoid – tq39, subcompactoid – tq30, wild type Bobwhite – normal, and speltoid – tq32, was selected for expression analysis. The expression level of *Q* in each of the lines was determined by RQ-PCR and recorded (Figure 23). The expression pattern followed a stepwise pattern suggesting the presence of an equivalent to one dose in the speltoid individual, two doses in the normal individual, three doses in the subcompactoid individual, and four doses in the compactoid individual. The pleiotropic effects of *Q* were also observable. Plants with speltoid spikes flowered one week earlier, had longer spikes, more keeled glumes, tougher glumes, nonfree-threshing seeds and a semi-fragile rachis compared to plants with compactoid spikes.

PHYLOGENETIC ANALYSIS

Phylogenetic analysis of the twelve *Triticum* genotypes indicated that all *Q*-genotypes were highly similar, while *q*-genotypes were more divergent (Figure 24). The genomic sequence of the *Q* homeoallele from *T. turgidum* ssp. *durum* cv. Langdon chromosome 5B was used to root the tree. Alignment between these homeoalleles is found in Appendix G. In this tree all *Q*-genotypes cluster suggesting that *Q* arose only once.

GENOTYPING

The length of the microsatellite in intron 9 was conserved among all initially sequenced lines containing the *Q* allele. Primers were designed to amplify this microsatellite and PCR products were run on polyacrylamide gels followed by staining with SYBR Green II. A

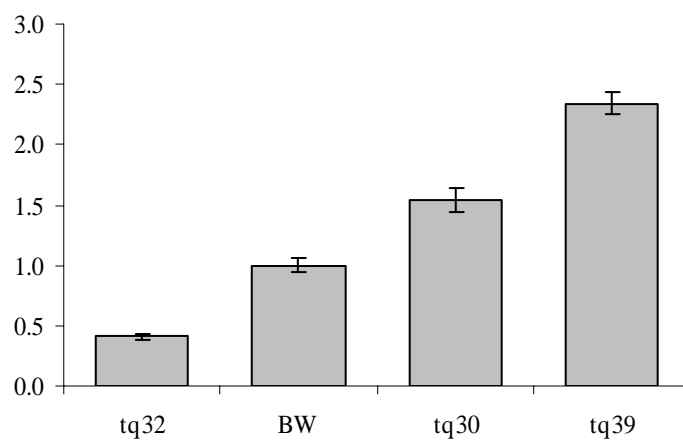


Figure 23. Relative expression levels of tq32 (speltoid transgenic), untransformed Bobwhite, tq30 (subcompactoid transgenic) and tq39 (compactoid transgenic). Bars represent standard error. The same pattern was observed in each experimental replication.

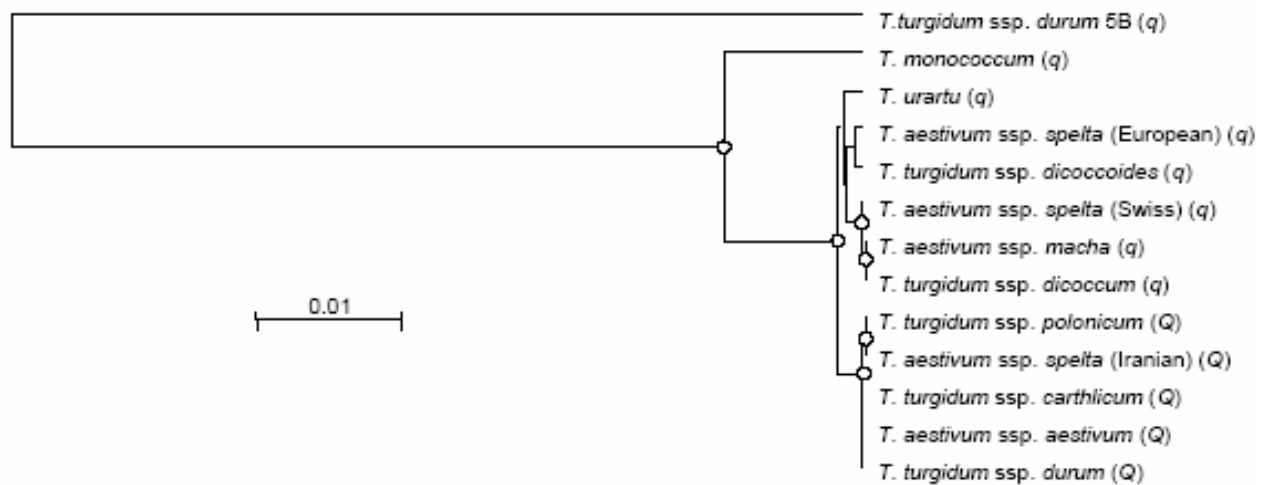


Figure 24. Phylogenetic tree of 12 *Triticum* taxa (Table 1). Tree is based on full-length genomic DNA sequences (start to stop codon) of the *Q/q* gene calculated by the neighbor-joining method and rooted by the *q* homeoallele from *T. turgidum* ssp. *durum* chromosome 5B as an outgroup. Open circles indicate nodes supported by bootstrap values >70%.

Table 2. Summary of microsatellite amplification results within various *Triticum* species.

<i>Triticum</i> species	Number Screened	Number Successfully Amplified	Number of Individuals - Repeat Length
<i>T. urartu</i>	11	4	1 - 4 1 - 5 2 - 7
<i>T. monococcum</i>	16	16	4 - 4 3 - 5 9 - 6
<i>T. turgidum</i> ssp. <i>dicoccoides</i>	64	64	3 - 4 14 - 7 35 - 8 12 - 9
<i>T. turgidum</i> ssp. <i>dicoccum</i>	40	40	1 - 7 11 - 8 29 - 9
<i>T. turgidum</i> ssp. <i>durum</i>	9	9	9 - 7
<i>T. turgidum</i> ssp. <i>polonicum</i>	28	28	27 - 7 1 - 8
<i>T. turgidum</i> ssp. <i>carthlicum</i>	28	28	28 - 7
<i>T. aestivum</i> ssp. <i>aestivum</i>	45	45	45 - 7
<i>T. aestivum</i> ssp. <i>spelta</i>	61	61	12 - 7 7 - 8 43 - 9
<i>T. aestivum</i> ssp. <i>macha</i>	1	1	1 - 9
<i>T. aestivum</i> ssp. <i>compactum</i>	1	1	1 - 7
<i>T. aestivum</i> ssp. <i>sphaerococcum</i>	1	1	1 - 7

summary of the results are found in Table 2. The accessions genotyped are listed in Appendix B along with the number of repeats. The number of repeats associated with *Q* was seven and was conserved in all *T. aestivum* ssp. *aestivum*, *T. turgidum* ssp. *durum*, *T. turgidum* ssp. *carthlicum*, and nearly all the *T. turgidum* ssp. *polonicum* accessions. Ssp. *polonicum* contained one accession which was a winter type with a longer microsatellite of eight repeats. The accessions tested of *T. monococcum*, *T. urartu*, and *T. turgidum* ssp. *dicoccum* did not contain seven repeats but for the known exception of *liguliforme*. *T. aestivum* ssp. *spelta* also contained a variety of different repeat lengths including seven, eight and nine repeats. *T. turgidum* ssp. *dicoccoides* contained four different microsatellite lengths including the seven repeats associated with *Q*. It is common belief that all *T. turgidum* ssp. *dicoccoides* do not possess *Q*.

Sequence data from several lines in addition to the 12 already sequenced (Appendix F) indicate each line will need to be crossed to CS to determine the allele present at the *Q* locus. The second spelt of Iranian descent and the fourth ssp. *dicoccum* do not contain the conserved *Q* and *q* allele differences, respectively, at position 576 and 617. A third ssp. *dicoccoides* does not contain the conserved *q* allele difference at position 3531. A fourth ssp. *dicoccoides* does not contain the conserved *q* allele differences at positions 2123, 2189, or the microsatellite but may possess the *Q* allele.

DISCUSSION

STRUCTURE AND VALIDATION

Q, using the EMS mutants, was shown to be a member of the AP2 class of transcription factors which are characterized by plant-specific DNA binding motifs referred to as AP2 domains. They have been implicated in a wide range of plant development roles. In *Arabidopsis*, *AP2* is a floral homeotic gene involved in the establishment of floral meristem identity (Bowman *et al.* 1993; Irish and Sussex 1990), floral organ identity (Bowman *et al.* 1989; Jofuku *et al.* 1994; Komaki *et al.* 1988; Kunst *et al.* 1989) and temporal and spatial regulation of floral homeotic gene expression (Drews *et al.* 1991). *AP2* is not only expressed in floral tissue but also in vegetative tissue. Recently, *AP2* was identified as playing a significant role in governing seed mass and yield (Jofuku *et al.* 2005).

A putative orthologue of *AP2* designated *PhAp2A*, has been identified in petunia. *PhAp2A* is expressed in both floral and vegetative tissues. *AP2* and *PhAp2A* share a 64% amino acid sequence homology, a conserved putative nuclear localization signal and a conserved serine-rich putative transcription activation domain. Mutants containing a transposon within the first exon of *PhAp2A* displayed the same phenotype as wild type plants. Complementation indicated *PhAp2A* will compensate for the loss of *AP2* in *Arabidopsis* while a second *AP2*-like gene from petunia, *PhAp2B*, will not (Maes *et al.* 2001). *PhAp2A* is a true orthologue of *AP2* but its function must vary in petunia. The lack of a mutant phenotype suggests either functional duplication or that regulation of class C floral genes does not occur in petunia.

The homology between *Q* and *AP2* is limited to the two AP2 binding domains suggesting the two are not orthologues. Other *Arabidopsis* genes belonging to the AP2 group of transcription factors have been identified (Okamuro *et al.* 1997) but *Q* shows homology only

within the AP2 binding domains. Putative orthologues of *Q* have been identified in maize, rice, and barley (Faris *et al.* 2003). The barley orthologous amino acid sequence is 91% similar to *Q*, the maize sequence is 75% similar to *Q*, and the rice sequence is 73% similar to *Q*. In maize, *indeterminant spikelet1 (ids1)* is expressed in both vegetative and floral tissues. One known function is to determine the number of floral meristems produced (Chuck *et al.* 1998). Its hypothesized that *ids1* suppresses indeterminate growth by repressing determinacy factors. *Ids1* does not complement *AP2* in *Arabidopsis* and is therefore probably not an orthologue of *AP2*.

Functions have not yet been assigned to the orthologues in rice and barley, and *Q* is so far the only *AP2*-like gene implicated in domestication. Based on the research already done with *AP2*-like genes, it's logical to expect that many of these genes are going to be expressed in both vegetative and floral tissues as is the case with *AP2*, *PhAp2A*, *PhAp2B*, *ids1*, and *Q*. More than likely they will be regulatory in nature and therefore more highly expressed in differentiating tissues. Functional duplication may make it difficult to identify the mutant phenotypes particularly in polyploids. These same duplications allow the orthologues to evolve losing some functions while gaining others.

Q ALLELE SEQUENCE DIFFERENCES

Previous research suggested that *Q* might have arisen through duplication of *q*. Evidence for this was presented by Kuckuck (1959) who reported observing occasional square spike phenotypes in progeny derived from two speltoid parents. Also, Muramatsu (1963) suggested that approximately five doses of *q* conferred the same phenotype as two doses of *Q*. However, data collected from Southern analysis and sequencing of a large BAC spanning *Q* (Simons *et al.* 2005) indicates that *Q* is not a duplication of *q*, but most likely arose through a gain-of-function mutation.

It is clear from previous research with the *T. aestivum* ssp. *spelta* 5A chromosome aneuploids (Muramatsu 1963) that both *Q* and *q* alleles are functional, but they confer different phenotypes. The *Q* and *q* alleles differ both in structure and in the level of transcription. An obvious and consistent difference in the level of transcription between *Q* and *q* alleles was associated with phenotypic differences from dosage effects observed in transgenic plants, which agreed with conclusions derived by Muramatsu (1963).

The amino acid change from isoleucine to valine does not suggest a significant biochemical alteration because the two are very similar amino acids. Further examination found that the isoleucine in the *Q* defines a putative fork-head associated (FHA) domain interacting motif. FHA domain interacting motifs have been implicated in protein-protein interactions, protein transport, signal transduction, protein degradation, DNA damage repair, and transcription (Durocher and Jackson 2002). It is possible this could be a gain of function mutation which resulted in *Q* from *q*. This mutation allowed the formation of *Q* homodimers in yeast cells, whereas the valine in the *q* protein substantially limits the ability to form homodimers (Simons *et al.* 2005). This finding is being investigated further to determine if homodimer formation is a mechanism for self-regulation of transcription.

Microsatellites have been implicated as regulatory elements recognized by transcription factors (Kashi *et al.* 1997). These microsatellites can be within introns, 5' UTR, 3' UTR, or the promoter region (Albanese *et al.* 2001; Contente *et al.* 2002; Frisch *et al.* 2001; Rothenburg *et al.* 2001). The repeat, CTC, as found in intron 9 of *Q*, has been implicated in regulation of the *PAX7* gene in humans as determined by a significant increase of activity in a luciferase assay (Sygailo *et al.* 2002). The CTC repeat, when present, was found to be preferentially located within 1 kb upstream of the transcription start site or within the first intron. Genes with this

repeat tended to be involved in developmental processes or transcription regulation (Iglesias *et al.* 2004). Iglesias *et al.* (2004) proposed that these repeats can take on a double stranded B-DNA conformation leaving the chromatin in an open state, thereby allowing access to other transcription factors or acting as a transcription factor itself. The CTC repeat is found within intron 9 of the *Q* gene. This conserved difference is not likely to be the critical difference between *Q* and *q* since it is so far from the transcription start site, but should not be completely disregarded since other microsatellites farther from the transcription start site have been implicated in gene transcription, splicing and silencing (Li *et al.* 2004).

Q or *q* may contain a translation inhibition element in the 3' UTR. The 3' UTR of *Xenopus* FGF receptor contains a translational inhibitory element. This was determined by injecting a synthetic transcript missing the 3' UTR into cells where translation was known to be inhibited followed by western analysis. The result was no protein from translation of the synthetic transcript with the 3' UTR and protein from the transcript missing the 3' UTR (Robbie *et al.* 1995). A second instance is the *CaMKII α* gene which contains a *cis*-acting signal for localization and translation in the 3' UTR. This signal causes the mRNA to be localized to the dendrites (Mayford *et al.* 1996). The 3' UTR differences affect the transcript by changing localization or translation. In light of the fact that there exists the single amino acid difference and the difference in transcription level between *Q* and *q*, this conserved difference would not appear to be responsible for the functional difference between *Q* and *q*.

The conserved differences within introns 2 and 8 are not likely responsible for the morphological difference between *Q* and *q*. Sequence analysis of cDNA from both alleles indicated no difference in splicing behavior between *Q* and *q*, and most regulatory elements are found within the first 1 kb upstream of the transcription start site or within the first intron. This

reasoning eliminates the difference within intron 8. It is possible that the differences within intron 2 are significant but the other conserved differences are better candidates.

Additional sequencing of genotypes possessing either *Q* or *q* should positively eliminate some of these possibilities. The sequence data of an additional two ssp. *spelta*, three ssp. *dicoccoides*, and one ssp. *dicoccum* accessions suggest that not all identified differences are truly conserved, however the allele at the *Q* locus needs to be functionally validated. The sequencing data suggests that some ssp. *dicoccoides* contain *Q* and that the differences at position 576, 617, and 3531 are not conserved. Implications of ssp. *dicoccoides* containing *Q* are discussed below.

***Q* Expression**

Q is expressed at low levels and undetectable via conventional northern analysis as expected with a regulatory gene. It was interesting that the *Q* cDNA would not amplify with a regular amplification kit but needed additives for GC rich regions. This indicates that the amplification step in the virtual northern did not representatively amplify all transcripts. One may be able to assume the misrepresentation would be the same when comparing the same tissue and cell types but not when comparing different tissues and cell types. The virtual northern was useful in determining that the transcripts of *Q* and *q* were similar in size and that there were differences in transcript levels that needed to be further characterized using other methods.

It is interesting to note that *AP2* in *Arabidopsis* is regulated at the level of translation by a microRNA, which binds to an AASSGF box (CHEN 2004). The AASSGF box is conserved among the various *AP2*-like genes mentioned previously, and between *Q*- and *q*-genotypes. The lack of variation would suggest that a microRNA is not responsible for governing regulation between *Q* and *q*. However, the possibility of a variable microRNA existing within or near the *Q* gene cannot be completely ruled out because most microRNAs are encoded within or very near

genes though seldom near the gene they regulate (Wang *et al.* 2004). The *Q* locus may contain one of these microRNAs which regulate a host of other genes, though the likelihood with respect to the other differences observed is small.

Ectopic expression analysis of transgenic plants allowed observation of both dosage and pleiotropic effects of *Q*. The increased transcription of *Q* observed was most obviously associated with spike compactness and reduced plant height. This observation agreed precisely with findings reported a half century ago using cytogenetic stocks (Huskins 1946; Muramatsu 1963; Sears 1952; Sears 1954). Variation in other important morphological characters such as spike length, rachis fragility, glume shape, and glume tenacity observed in the transgenic plants agree with previous experiments that located QTLs for these traits to the *Q* locus on chromosome 5A (Jantasuriyarat *et al.* 2004; Kato *et al.* 1999; Kato *et al.* 2003) and confirmed the pleiotropic effects of *Q* without the addition of other genes present on chromosome 5A.

Promoter Region

Only two different *cis*-acting regulatory elements are associated with the conserved deletion at position -133. The AAGAA motif when found within exons, has been implicated in alternative splicing in humans (Fairbrother *et al.* 2002) and selection of alternative poly(A) sites when found in the 3' UTR (Düvel and Braus 1999). The GAG motif is involved with light responsiveness and six other GAG motifs were identified within the sequenced promoter region.

A better candidate to explain the difference in transcript levels is the two base substitution at position -380 associated with four different motifs. There are more than thirty I-boxes, twenty G-boxes, and five ABRE elements identified, but only a single GCN4 motif found in the *Q* promoter region. GCN4 is the primary regulator of amino acid synthesis in response to amino acid starvation (Hinnebusch and Fink 1983). The other possibility is that none of these

specific motifs are involved or the difference is due to a regulatory element further upstream. It may be that the Q homodimer may be responsible for the increased level of transcription. The homodimer may recognize a region identical in both alleles, or a region containing one of the conserved differences. This recognition by a Q protein homodimer complex may lead to upregulation.

WHEAT DOMESTICATION AND EVOLUTION

It is well known that the A-genome donor of tetraploid and hexaploid wheats is *T. urartu* (Dvorak *et al.* 1993), and the D-genome donor of hexaploid wheat is *Ae. tauschii* (Kihara 1944; McFadden and Sears 1946). However, it is not known which AB tetraploid (*qq* or *QQ* genotype) was involved in the hybridization with *Ae. tauschii* (D genome) that gave rise to hexaploid wheat. With regards to *Q*, it has been a matter of speculation whether it first arose in the tetraploid progenitor of hexaploid wheat, or if it arose independently in hexaploids and tetraploids.

Results indicate that the mutation that gave rise to the *Q* allele occurred only once. However, one cannot conclude whether it first arose in a tetraploid or a hexaploid. It is possible that the *Q* allele arose first in a tetraploid similar to present day *T. turgidum* spp. *durum* or the extinct tetraploid *T. turgidum* ssp. *parvicoccum*, which then hybridized with *Ae. tauschii* in some farmer's field to give rise to the first hexaploid. Alternatively, the *Q* allele may have occurred first in a hexaploid and the present day *Q*-bearing tetraploids are a result of secondary hybridizations with *Q*-bearing hexaploids.

The archaeological record indicates remnants of free-threshing tetraploid and hexaploid wheats appear about the same time and about a thousand years earlier than spelt wheats. This suggests that neither Iranian spelt or European spelt are progenitors of free-threshing hexaploid

wheat (reviewed in Feldman 2001; Nesbitt and Samuel 1996). It could also mean that there is a gap in the archeological record and that Iranian spelt may be a direct descendent from the first hexaploid.

Iranian spelt contains *Q* and may be the link between the hexaploid progenitor and modern free-threshing bread wheat. It clusters with the other *Q* containing species but does not exhibit the associated square free-threshing spikes. It is known that other background factors effect the expression of *Q*. It has been hypothesized that one of the major factors influencing the lack of phenotype is the *Tg* gene. Research by Dvorak *et al.* (1998) suggests *T. aestivum* ssp. *aestivum* is more closely related to Iranian spelt than to European spelt. The genetic distance between ssp. *aestivum* and Iranian spelt was one tenth that of European spelt and ssp. *aestivum*. The other possibly is that Iranian spelt is a recent hybridization event between a free-threshing tetraploid and *Ae. tauschii*, or between a hulled *T. turgidum* and a free-threshing *T. aestivum*. The sequence data supports either possibility for Iranian spelt. Research (Bertsch 1943; Bertsch 1950; MacKey 1966; Ohtsuka 1998; Yan *et al.* 2003) suggests European spelt is derived from the hybridization of *T. aestivum* ssp. *compactum* and *T. turgidum* ssp. *dicoccum*. The generated phylogentic tree supports this hypothesis with regard to some European spelts clustering with ssp. *dicoccum*. Others are more similar to ssp. *dicoccoides* suggesting multiple hybridization events.

The genotyping results confirmed some expectations but also raised questions. All species suspected of containing *Q* had seven repeats in the microsatellite with one exception. One particular line of ssp. *polonicum* contained an additional repeat. This line was also a winter type which is not common in ssp. *polonicum*. This suggests that this line may have outcrossed to another species or possibly that an emmer plant had a mutation within the gene for elongated

panicles. Overall, diversity in the number of repeats decreased with polyploidization and cultivation as expected. The ssp. *spelta* contained various numbers of repeats, of which about a quarter were associated with *Q*.

The only line of ssp. *dicoccum* which contained the seven repeats was liguliforme as expected based on Muramatsu's research (1979). The definition of ssp. *dicoccum* is a tetraploid with a nonbrittle rachis but is nonfree-threshing. The fact that it has a nonbrittle rachis and is not free-threshing suggests a second mutation within liguliforme which doesn't allow it to be free-threshing but does allow the more compactoid spikes.

The biggest surprise was ssp. *dicoccoides* lines containing seven repeats. The major characters determining if a line is ssp. *dicoccoides* are its being a tetraploid with a brittle rachis and nonfree-threshing seed. It remains to be determined if these lines contain *Q* or if the microsatellite length and amino acid difference do not differentiate the *Q* and *q* alleles. Ssp. *dicoccoides* may have obtained *Q* through out-crossing and one reason why the effects of *Q* are not observed, may be the presence of modifying genes similar to the effect of the *Tg* gene in the ssp. *spelta* background. Since the major difference between ssp. *dicoccoides* and ssp. *dicoccum* is its fragile rachis, perhaps the gene controlling rachis brittleness (*br*) effects the expression of *Q*. The presence of *Q* in ssp. *dicoccoides* will renew the debate on wheat evolution, domestication, and the genes involved in these processes.

CONCLUSIONS

The objectives of this research were to confirm or reject the candidate *AP2*-like gene as *Q*, confirm the dosage and pleiotropic effects attributed to *Q*, and begin identifying the differences between the *Q* and *q* alleles. Knockout analysis indicated that the candidate *AP2*-like gene is *Q* and therefore belongs to the AP2 transcription factor group. *Q* pleiotropically affects numerous characteristics as shown with ectopic expression and is therefore regulatory in nature. RQ-PCR confirmed that dosage of expressed *Q* transcripts was associated with the observed differences in morphology.

The *Q* allele does not consist of duplicated *q* alleles as determined by Southern analysis which left mutation as an explanation for the difference between the *Q* and *q* alleles. Numerous conserved differences between *Q* and *q* were identified. Those most likely to play a critical role differentiating *Q* and *q* are the conserved amino acid difference and differences within the promoter region. The difference in transcription levels is a critical difference but the mechanism underlying the functional variation between *Q* and *q* alleles remains to be determined.

The sequence and microsatellite findings open the debate as to the role of the speltis in wheat evolution. It also calls into question the role of *ssp. dicoccum* and *ssp. dicoccoides*. The sequence suggests *Q* arose only once since there is very little sequence differences within the tetraploid and hexaploid sequences. There is however greater sequence diversity within the *q* allele. Whether *Q* arose in the tetraploid or hexaploid cannot be determined from this data.

FUTURE RESEARCH AREAS

Research on *Q* can continue in many different directions. It can be pursued to shed more light on wheat evolution. Some of the *T. turgidum ssp. dicoccoides* lines had the microsatellite associated with *Q* as well as the same coding sequences. Determining that these lines have the *Q*

allele may indicate that *ssp. dicoccum* did not necessarily play a role in formation of hexaploid wheat and suggests the presence of a repressor of *Q* within the *ssp. dicoccoides* background. In this same regard it would be of interest to determine if the *Q* locus is differentially expressed between Iranian and European spelts since Iranian spelt carries the *Q* allele and European spelt, the *q* allele. Both spelts have the same spike morphology but it is unknown whether this similarity is due to transcriptional or translational inhibition of *Q*.

Further research can focus on the functionality between alleles. Some of the remaining conserved differences may be eliminated by sequencing more accessions of *ssp. spelta*, *ssp. dicoccum*, and *ssp. dicoccoides* including the promoter region. The amino acid difference between *Q* and *q* is important in homodimer formation. The importance of the homodimer remains undetermined. Yeast-two-hybrids can determine what the homodimer binds to. They can also be used to identify the critical elements within the promoter and if the homodimer is responsible for self upregulation. Microarray analysis could identify a large number of genes that are up or down regulated by the *Q* locus. This data coupled with the yeast-two-hybrid data should help identify the pathway(s) *Q* functions within. The relationship between the homeoalleles could also be determined since the presence of the 5D homeoallele appears to affect rachis length.

Studies of *Q* may also lead to the identification of other genes important in domestication. Determining if *Tg* directly represses *Q* may allow the identification of *Tg* through the yeast-two-hybrid studies. Identifying these and other genes may make it possible to rapidly domesticate other plants with specific end uses or ability to withstand abiotic or biotic stresses.

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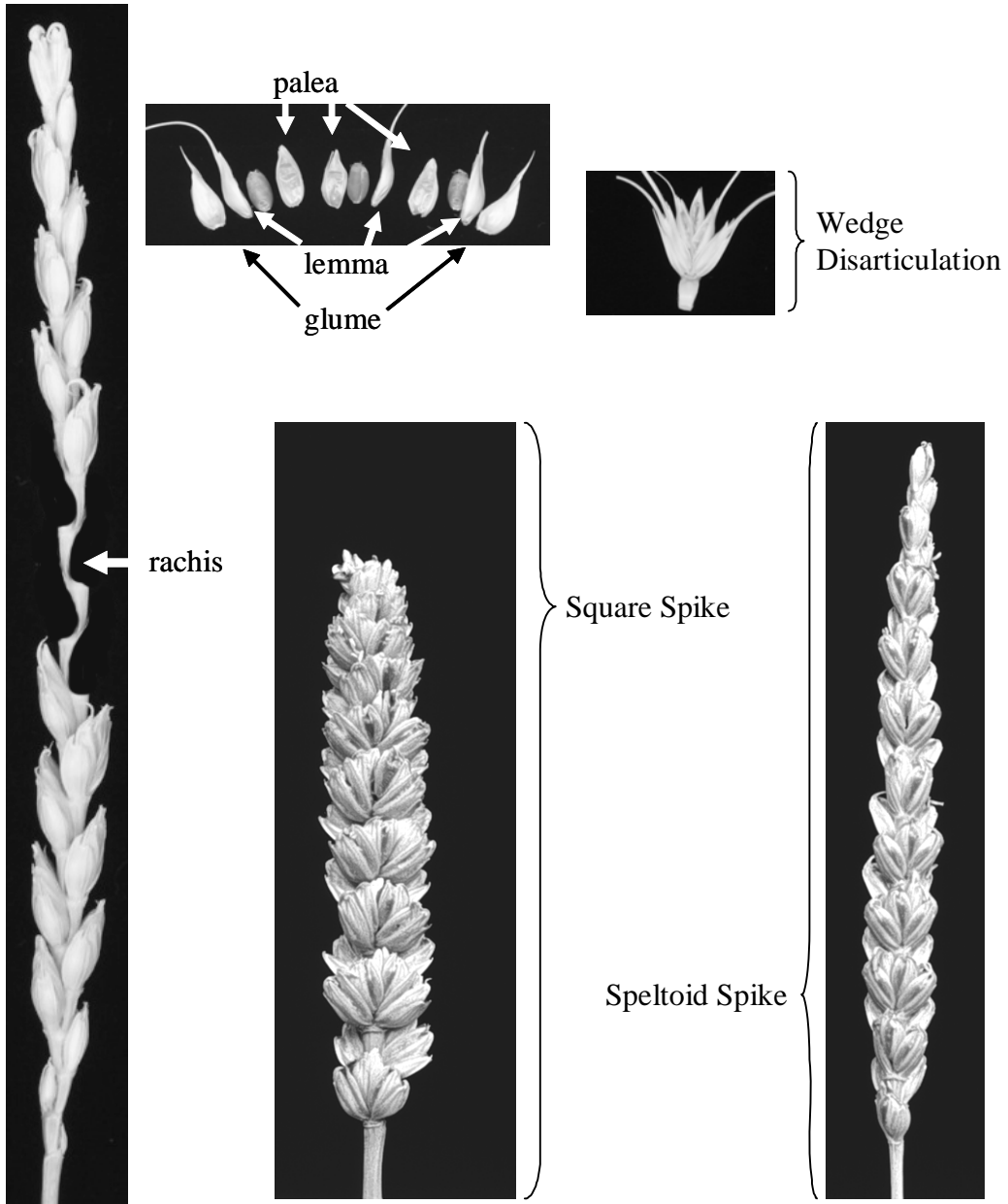
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APPENDIX A. Wheat Inflorescence Morphology.*

* Wheat typically develops multiple spikes per plant. Wheat spikes have a main stem called a rachis. Off the rachis small groups of flowers or florets develop and are collectively called a spikelet. Each spikelet is bracketed by glumes. Each spikelet can further be broken down into individual florets. Each floret is capable of producing one seed. This seed is surrounded by the lemma and palea. Hulled wheats are those in which the lemma and palea tightly enclose the seed. In naked or free-threshing wheats the lemma and palea loosely hold the seed. Naked wheats also tend to have softer glumes; these tend to be rounder in cross-section than the hulled wheats which are stiffer and more keeled. Hulled wheats tend to have a fragile rachis and disarticulate either above or below the junction of the rachilla and rachis called wedge or barrel disarticulation, respectively.



APPENDIX B. List of all *Triticum* accessions genotyped by the microsatellite and size of the amplicon.*

* NSGC – National Small Grains Collection in Aberdeen, ID.

WGRC – Wheat Genetics Resource Center in Manhattan, KS

S. Xu – Dr. Steven Xu, NCSL, USDA-ARS, Fargo, ND

Frohberg – Dr. Richard Frohberg, Retired Wheat Breeder, NDSU, Fargo, ND

Kianian – Dr. Shahryar Kianian, Wheat Germplasm Enhancement, NDSU, Fargo, ND

T. urartu

Accession/Line	Cultivar	Repeat Length	Maintained by	Genbank Number
TA704		4		AY702958
PI 427328		5	NSGC	
PI 428180		9	NSGC	
PI 428187		-	NSGC	
PI 428213		-	NSGC	
PI 428260		-	NSGC	
PI 428280		-	NSGC	
PI 428316		-	NSGC	
PI 428338		-	NSGC	
PI 487265		9	NSGC	
PI 487269		-	NSGC	
PI 538748		-	NSGC	

T. monococcum

Accession/Line	Cultivar	Repeat Length	Maintained by	Genbank Number
DV92		6		AY170867
PI 94740		6	NSGC	
PI 94743		6	NSGC	
PI 167526		5	NSGC	
PI 191381		4	NSGC	
PI 272560		5	NSGC	
PI 277130		6	NSGC	
PI 307984		6	NSGC	
PI 326317		6	NSGC	
PI 343181		5	NSGC	
PI 355519		4	NSGC	
PI 377648		6	NSGC	
PI 428151		6	NSGC	
PI 428152		4	NSGC	
PI 429154		4	NSGC	
PI 591871		6	NSGC	

T. turgidum* ssp. *dicoccoides

Accession/Line	Cultivar	Repeat Length	Maintained by	Genbank Number
TA3446	CS-DIC 5A*	8	WGRC	AY702957
15-1		9	S. Xu	
15-17		9	S. Xu	
15-18		9	S. Xu	
15-19		9	S. Xu	
15-2		9	S. Xu	
15-26		9	S. Xu	
15-37		9	S. Xu	
15-43		9	S. Xu	
15-52		9	S. Xu	
15-55		9	S. Xu	
16-1		4	S. Xu	
16-29		8	S. Xu	
18-1		8	S. Xu	
18-10		8	S. Xu	
18-15		8	S. Xu	
18-20		8	S. Xu	
A-33		8	S. Xu	
A-35		8	S. Xu	
A-52		7	S. Xu	
A-56		7	S. Xu	
A-61		7	S. Xu	
A-82		7	S. Xu	
B-13		8	S. Xu	
B-16		8	S. Xu	
B-19		8	S. Xu	
B-31		8	S. Xu	
B-32		8	S. Xu	
B-35		8	S. Xu	
B-37		8	S. Xu	
B-6		8	S. Xu	
B-8		8	S. Xu	
C-13		8	S. Xu	
C-19		8	S. Xu	

C-21		8	S. Xu	
C-27		8	S. Xu	
C-36		8	S. Xu	
C-52		8	S. Xu	
C-7		7	S. Xu	
I-15		8	S. Xu	
I-17		8	S. Xu	
I-18		8	S. Xu	
I-20		7	S. Xu	
I-29		8	S. Xu	
I-39		8	S. Xu	
I-4		7	S. Xu	
I-40		7	S. Xu	
I-45		7	S. Xu	
I-50		4	S. Xu	
L-1		4	S. Xu	
L-10		8	S. Xu	
L-25		7	S. Xu	
L-28		8	S. Xu	
L-29		8	S. Xu	
L-33		8	S. Xu	
L-34		8	S. Xu	
L-40		8	S. Xu	
L-43		7	S. Xu	
L-56		7	S. Xu	
L-61		7	S. Xu	
PI 343446		-	S. Xu	
PI 466995		7	S. Xu	
PI 272852		8	S. Xu	
PI 252328		9	S. Xu	
PI 355459		9	S. Xu	

* Disomic chromosome substitution line where a pair of 5A chromosomes from *T. turgidum* ssp. *dicoccoides* (TA106) was substituted for the native pair of 5A chromosomes in Chinese Spring

T. turgidum* ssp. *dicoccum

Accession/Line	Cultivar	Repeat Length	Maintained by	Genbank Number
Cltr 14621		9	NSGC	AY714343
Cltr 3686		8	NSGC	
Cltr 4013		8	NSGC	
PI 2789		8, 9	NSGC	
PI 41024		9	NSGC	
PI 56234		9	NSGC	
PI 57394		9	NSGC	
PI 74108		8	NSGC	
PI 168673		9	NSGC	
PI 79899		8	NSGC	
PI 94680		9	NSGC	
PI 94683		9	NSGC	
PI 191781		9	NSGC	
PI 221400		9	NSGC	
PI 40919		9	NSGC	
PI 94664		9	NSGC	
PI 94656		9	NSGC	
PI 94654		9	NSGC	
PI 94649		9	NSGC	
PI 94648		8	NSGC	
PI 94641		8	NSGC	
Cltr 14824		9	NSGC	
PI 11650		8	NSGC	
PI 168674		9	NSGC	
PI 191252		8	NSGC	
Cltr 14086		9	NSGC	
Cltr 14751		9	NSGC	
Cltr 12213		9	NSGC	
PI 168678		9	NSGC	
Cltr 7962		9	NSGC	
Cltr 14750		9	NSGC	
Cltr 14454		9	NSGC	
Cltr 7686		9	NSGC	
Cltr 7687		9	NSGC	
Cltr 74106		9	NSGC	

Cltr 14098		9	NSGC	
Cltr 14133		8	NSGC	
Cltr 7779		8	NSGC	
Cltr 168676		9	NSGC	
TA 10435	Liguliforme	7	WGRC	

T. turgidum ssp. durum

Accession/Line	Cultivar	Repeat Length	Maintained by	Genbank Number
	Landgon-16	7		AY702955
	Monroe	7		
	Ben	7		
	Munich	7		
	Maier	7		
	Renville	7		
	Lebsock	7		
	Rugby	7		
	Pierce	7		

T. turgidum ssp. polonicum

Accession/Line	Cultivar	Repeat Length	Maintained by	Genbank Number
PI 384265		7	NSGC	
PI 223171		7	NSGC	
PI 245663		7	NSGC	
PI 254214		7	NSGC	
PI 266846		7	NSGC	
PI 286547		7	NSGC	
PI 306548		7	NSGC	
PI 299447		7	NSGC	
Cltr 17442		7	NSGC	
PI 167622		7	NSGC	
PI 185309		7	NSGC	
PI 190951		7	NSGC	
PI 191852		7	NSGC	
PI 208911		7	NSGC	
Cltr 14803		7	NSGC	
PI 533593		7	NSGC	

PI	608017		7	NSGC	
PI	42209		7	NSGC	
PI	56261		7	NSGC	
PI	352487		7	NSGC	
PI	352488		7	NSGC	
PI	352489		7	NSGC	
PI	361757		8	NSGC	
PI	366117		7	NSGC	
PI	629119		7	NSGC	
PI	582015		7	NSGC	
Cltr	225334		7	NSGC	
Cltr	191826		7	NSGC	AY714339

T. turgidum ssp. carthlicum

Accession/Line	Cultivar	Repeat Length	Maintained by	Genbank Number
TA2801		7	WGRC	AY702959
Cltr 7665		7	NSGC	
PI 61102		7	NSGC	
PI 70738		7	NSGC	
PI 94748		7	NSGC	
PI 94752		7	NSGC	
PI 168672		7	NSGC	
PI 182471		7	NSGC	
PI 190949		7	NSGC	
PI 272521		7	NSGC	
PI 283887		7	NSGC	
PI 585017		7	NSGC	
PI 532505		7	NSGC	
PI 232510		7	NSGC	
PI 532515		7	NSGC	
PI 283889		7	NSGC	
PI 286070		7	NSGC	
PI 349040		7	NSGC	
PI 352279		7	NSGC	
PI 387696		7	NSGC	
PI 470730		7	NSGC	
PI 470733		7	NSGC	

PI	499972		7	NSGC	
PI	532482		7	NSGC	
PI	532488		7	NSGC	
PI	532495		7	NSGC	
PI	532499		7	NSGC	
PI	532504		7	NSGC	

T. aestivum* ssp. *aestivum

Accession/Line	Cultivar	Repeat Length	Maintained by	Genbank Number
	Chinese Spring	7		AY702956
	Hanna	7		
	Briggs	7		
	Oaklee	7		
	Dapps	7		
	Cheyenne	7		
	Kundson	7		
	Opata85	7		
	Kulm	7		
	Jagger	7		
	Tam105	7		
	Golden Ball	7		
	Grandin	7		
	Sumai3	7		
	Bobwhite	7		
	Erik	7		
	Hope	7		
	Timstein	7		
	Atlas66	7		
	Steele-ND	7		
	BR-34	7		
Cltr	10003	Thatcher	7	NSGC
Cltr	4966	Java	7	NSGC
		Chris	7	Froberg
PI	116066	Gehun	7	NSGC
Cltr	4762	Gypsum	7	NSGC
Cltr	12345	Red Egyptian	7	NSGC
PI	512282	Andrews	7	NSGC

Citr 15090	Hard Red Calcutta	7	NSGC	
	Olaf	7		
Citr 10045	Utac	7	NSGC	
Citr 6282	Canadian Red	7	NSGC	
Citr 6047	Ruby	7	NSGC	
	Selkirk	7	Kianian	
	Alsen	7		

T. aestivum ssp. spelta

Source Number	Cultivar	Repeat Length	Maintained by	Genbank Number
P78-81-1*	European Spelt	8		AY714341
407a**	Iranian Spelt	7		AY714340
TA2603		9	WGRC	AY702960
PI 191392		9	NSGC	
PI 191617		9	NSGC	
PI 221404		8	NSGC	
PI 221419		8	NSGC	
PI 171073		9	NSGC	
PI 225271		7	NSGC	
PI 225295		7	NSGC	
PI 266848		7	NSGC	
PI 272573		8	NSGC	
PI 286060		9	NSGC	
PI 290513		9	NSGC	
PI 290514		8	NSGC	
PI 294576		9	NSGC	
PI 295062		9	NSGC	
PI 295068		9	NSGC	
PI 297861		7	NSGC	
PI 306550		9	NSGC	
PI 338366		9	NSGC	
PI 338367		9	NSGC	
PI 346853		7, 9	NSGC	
PI 347874		8	NSGC	
PI 348002		9	NSGC	
PI 348032		9	NSGC	
PI 348189		9	NSGC	

PI 348288		9	NSGC	
PI 348301		9	NSGC	
PI 348372		9	NSGC	
PI 348483		9	NSGC	
PI 348682		9	NSGC	
PI 355564		8	NSGC	
PI 355619		9	NSGC	
PI 355625		9	NSGC	
PI 355626		9	NSGC	
PI 355642		9	NSGC	
PI 355651		9	NSGC	
PI 355653		9	NSGC	
PI 355681		9	NSGC	
PI 355687		9	NSGC	
PI 355701		9	NSGC	
PI 361768		9	NSGC	
PI 362062		9	NSGC	
PI 367199		7	NSGC	
PI 367200		7	NSGC	
PI 378469		9	NSGC	
PI 378480		9	NSGC	
PI 386129		9	NSGC	
PI 469028		9	NSGC	
PI 520066		7	NSGC	
PI 572914		7	NSGC	
PI 572915		7	NSGC	
PI 585008		9	NSGC	
PI 591890		9	NSGC	
PI 591892		7	NSGC	
PI 591902		9	NSGC	
PI 591904		9	NSGC	
PI 615233		9	NSGC	
PI 615298		9	NSGC	
PI 631161		9	NSGC	

* Sears accession number. Seed provided by J. Dvorak, University of California-Davis.

** H. Kuckuck accession number. Seed provided by J. Dvorak, University of California-Davis.

T. aestivum ssp. macha

Accession/Line	Cultivar	Repeat Length	Maintained by	Genbank Number
PI 361862		9	WGRC	AY714342

T. aestivum ssp. compactum

Accession/Line	Cultivar	Repeat Length	Maintained by	Genbank Number
TA 2601		7	WGRC	

T. aestivum ssp. sphaerococcum

Accession/Line	Cultivar	Repeat Length	Maintained by	Genbank Number
TA 2605		7	WGRC	

APPENDIX C. Genomic sequence of the three EMS mutants, mq194, mq36, and mq125.*

* Coding sequence are shaded gray in Chinese Spring (CS) and critical base changes boxed.

50

CS ATGGTGCTGGATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAG
mq194 ATGGTGCTGGATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAG
mq36 ATGGTGCTGGATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAG
mq125 ATGGTGCTGGATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAG

100

CS CTCCTCCGTGCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCCG
mq194 CTCCTCCGTGCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCCG
mq36 CTCCTCCGTGCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCCG
mq125 CTCCTCCGTGCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCCG

150

CS GCCTGCTCGGGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCG
mq194 GCCTGCTCGGGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCG
mq36 GCCTGCTCGGGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCG
mq125 GCCTGCTCGGGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCG

200

CS GTCGGGCCCGGGTTCGTACAGAGGCAGCTCTTCCCCGCGTCGCCGCCCGG
mq194 GTCGGGCCCGGGTTCGTACAGAGGCAGCTCTTCCCCGCGTCGCCGCCCGG
mq36 GTCGGGCCCGGGTTCGTACAGAGGCAGCTCTTCCCCGCGTCGCCGCCCGG
mq125 GTCGGGCCCGGGTTCGTACAGAGGCAGCTCTTCCCCGCGTCGCCGCCCGG

250

CS GCACGCGGGCGCGCCCGGGGTGACGATGGGGCAGCAGGCCCGGGCGCCTG
mq194 GCACGCGGGCGCGCCCGGGGTGACGATGGGGCAGCAGGCCCGGGCGCCTG
mq36 GCACGCGGGCGCGCCCGGGGTGACGATGGGGCAGCAGGCCCGGGCGCCTG
mq125 GCACGCGGGCGCGCCCGGGGTGACGATGGGGCAGCAGGCCCGGGCGCCTG

300

CS CGCCGATGGCGCCCGTGTGGCAGCCGCGGCGCGCCGAGGAGCTCCTCGTG
mq194 CGCCGATGGCGCCCGTGTGGCAGCCGCGGCGCGCCGAGGAGCTCCTCGTG
mq36 CGCCGATGGCGCCCGTGTGGCAGCCGCGGCGCGCCGAGGAGCTCCTCGTG
mq125 CGCCGATGGCGCCCGTGTGGCAGCCGCGGCGCGCCGAGGAGCTCCTCGTG

350

CS GCGCAGCGGATGGCGCCCGCGAAGAAGACGCGGCGGGGCCCGAGGTCCGG
mq194 GCGCAGCGGATGGCGCCCGCGAAGAAGACGCGGCGGGGCCCGAGGTCCGG
mq36 GCGCAGCGGATGGCGCCCGCGAAGAAGACGCGGCGGGGCCCGAGGTCCGG
mq125 GCGCAGCGGATGGCGCCCGCGAAGAAGACGCGGCGGGGCCCGAGGTCCGG

400

CS CAGCTCGCAGTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGG
mq194 CAGCTCGCAGTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGG
mq36 CAGCTCGCAGTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGG
mq125 CAGCTCGCAGTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGG

450

CS AGTCGCACATCTGGTFCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATG
mq194 AGTCGCACATCTGGTFCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATG
mq36 AGTCGCACATCTGGTFCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATG
mq125 AGTCGCACATCTGGTFCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATG

500

CS ACTATAGTTATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCT
mq194 ACTATAGTTATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCT
mq36 ACTATAGTTATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCT
mq125 ACTATAGTTATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCT

550

CS GATTCCACCAGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACA
mq194 GATTCCACCAGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACA
mq36 GATTCCACCAGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACA
mq125 GATTCCACCAGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACA

600

CS AATCCCAGCTCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTA
mq194 AATCCCAGCTCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTA
mq36 AATCCCAGCTCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTA
mq125 AATCCCAGCTCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTA

650

CS GCTGTATGGGCTCGTGATTAACACTGGATAAATTTCTTCAGGTGGTTTCGA
mq194 GCTGTATGGGCTCGTGATTAACACTGGATAAATTTCTTCAGGTGGTTTCGA
mq36 GCTGTATGGGCTCGTGATTAACACTGGATAAATTTCTTCAGGTGGTTTCGA
mq125 GCTGTATGGGCTCGTGATTAACACTGGATAAATTTCTTCAGGTGGTTTCGA

700

CS CACTGCGCACGCGGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTT
mq194 CACTGCGCACGCGGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTT
mq36 CACTGCGCACGCGGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTT
mq125 CACTGCGCACGCGGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTT

750

CS TGAATTCCTTTTGGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGAC
mq194 TGAATTCCTTTTGGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGAC
mq36 TGAATTCCTTTTGGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGAC
mq125 TGAATTCCTTTTGGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGAC

800

CS GGTGTGGCGTGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGG
mq194 GGTGTGGCGTGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGG
mq36 GGTGTGGCGTGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGG
mq125 GGTGTGGCGTGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGG

850

CS GCTGGAGGCCGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGA
mq194 GCTGGAGGCCGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGA
mq36 GCTGGAGGCCGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGA
mq125 GCTGGAGGCCGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGA

900

CS AGCAGGTAATCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTG
mq194 AGCAGGTAATCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTG
mq36 AGCAGGTAATCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTG
mq125 AGCAGGTAATCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTG

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950
CS      CGCCGGATACATATGTATCGGTGGTTTGTCCGATGGTTGATATCTGGTGG
mq194  CGCCGGATACATATGTATCGGTGGTTTGTCCGATGGTTGATATCTGGTGG
mq36   CGCCGGATACATATGTATCGGTGGTTTGTCCGATGGTTGATATCTGGTGG
mq125  CGCCGGATACATATGTATCGGTGGTTTGTCCGATGGTTGATATCTGGTGG
*****

1000
CS      GTGGTGGTGGTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTC
mq194  GTGGTGGTGGTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTC
mq36   GTGGTGGTGGTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTC
mq125  GTGGTGGTGGTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTC
*****

1050
CS      GTGCACATCCTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAA
mq194  GTGCACATCCTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAA
mq36   GTGCACATCCTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAA
mq125  GTGCACATCCTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAA
*****

1100
CS      GTACCGCGGCGTCACGCTCCACAAGTTCGGCCGCTGGGAGGCAAGGATGG
mq194  GTACCGCGGCGTCACGCTCCACAAGTTCGGCCGCTGGGAGGCAAGGATGG
mq36   GTACCGCGGCGTCACGCTCCACAAGTTCGGCCGCTGGGAGGCAAGGATGG
mq125  GTACCGCGGCGTCACGCTCCACAAGTTCGGCCGCTGGGAGGCAAGGATGG
*****

1150
CS      GCCAGCTGCTCGGCAAGAAATAAGCAGGCACACACACAGCTCACGCACTA
mq194  GCCAGCTGCTCGGCAAGAAATAAGCAGGCACACACACAGCTCACGCACTA
mq36   GCCAGCTGCTCGGCAAGAAATAAGCAGGCACACACACAGCTCACGCACTA
mq125  GCCAGCTGCTCGGCAAGAAATAAGCAGGCACACACACAGCTCACGCACTA
*****

1200
CS      AAATTAATTCACTTCGCCACATTATCATAGTAGTAGTTTCTTTTATCAA
mq194  AAATTAATTCACTTCGCCACATTATCATAGTAGTAGTTTCTTTTATCAA
mq36   AAATTAATTCACTTCGCCACATTATCATAGTAGTAGTTTCTTTTATCAA
mq125  AAATTAATTCACTTCGCCACATTATCATAGTAGTAGTTTCTTTTATCAA
*****

1250
CS      ATGCCATTGACAAGATTCAGTTGAAATGAAATTTACAGACTGCTCATGA
mq194  ATGCCATTGACAAGATTCAGTTGAAATGAAATTTACAGACTGCTCATGA
mq36   ATGCCATTGACAAGATTCAGTTGAAATGAAATTTACAGACTGCTCATGA
mq125  ATGCCATTGACAAGATTCAGTTGAAATGAAATTTACAGACTGCTCATGA
*****

1300
CS      ACTTGACACTAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTG
mq194  ACTTGACACTAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTG
mq36   ACTTGACACTAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTG
mq125  ACTTGACACTAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTG
*****

1350
CS      GACGTTTAATTAGCCTGTCGCAGGTAATCATCTTAGATTACCCCTTTTGA
mq194  GACGTTTAATTAGCCTGTCGCAGGTAATCATCTTAGATTACCCCTTTTGA
mq36   GACGTTTAATTAGCCTGTCGCAGGTAATCATCTTAGATTACCCCTTTTGA
mq125  GACGTTTAATTAGCCTGTCGCAGGTAATCATCTTAGATTACCCCTTTTGA
*****

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1400
CS AACATAATCTTAGCTGGTTTAGGGTAGGGTCATCAAGTTAATCCATGTTG
mq194 AACATAATCTTAGCTGGTTTAGGGTAGGGTCATCAAGTTAATCCATGTTG
mq36 AACATAATCTTAGCTGGTTTAGGGTAGGGTCATCAAGTTAATCCATGTTG
mq125 AACATAATCTTAGCTGGTTTAGGGTAGGGTCATCAAGTTAATCCATGTTG

1450
CS TTAGTTGTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCC
mq194 TTAGTTGTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCC
mq36 TTAGTTGTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCC
mq125 TTAGTTGTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCC

1500
CS CGACACGACACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCC
mq194 CGACACGACACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCC
mq36 CGACACGACACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCC
mq125 CGACACGACACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCC

1550
CS ACATAAGTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCC
mq194 ACATAAGTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCC
mq36 ACATAAGTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCC
mq125 ACATAAGTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCC

1600
CS GTGCACATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTTCACACCC
mq194 GTGCACATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTTCACACCC
mq36 GTGCACATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTTCACACCC
mq125 GTGCACATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTTCACACCC

1650
CS CTATCTCCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTA
mq194 CTATCTCCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTA
mq36 CTATCTCCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTA
mq125 CTATCTCCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTA

1700
CS TCATCACACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTG
mq194 TCATCACACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTG
mq36 TCATCACACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTG
mq125 TCATCACACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTG

1750
CS AAGCTGCAAGGTACTTTGATTTGCGCTGATCATTAACATTTGGGCTCACA
mq194 AAGCTGCAAGGTACTTTGATTTGCGCTGATCATTAACATTTGGGCTCACA
mq36 AAGCTGCAAGGTACTTTGATTTGCGCTGATCATTAACATTTGGGCTCACA
mq125 AAGCTGCAAGGTACTTTGATTTGCGCTGATCATTAACATTTGGGCTCACA

1800
CS AAACCTTCCTTAATCTTTGCTCACTCACTCTAGTGTTCATGTTGGATTTGGT
mq194 AAACCTTCCTTAATCTTTGCTCACTCACTCTAGTGTTCATGTTGGATTTGGT
mq36 AAACCTTCCTTAATCTTTGCTCACTCACTCTAGTGTTCATGTTGGATTTGGT
mq125 AAACCTTCCTTAATCTTTGCTCACTCACTCTAGTGTTCATGTTGGATTTGGT

1850
CS AGGGCGTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGAC
mq194 AGGGCGTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGAC
mq36 AGGGCGTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGAC
mq125 AGGGCGTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGAC

1900
CS TAACTTTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAA
mq194 TAACTTTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAA
mq36 TAACTTTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAA
mq125 TAACTTTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAA

1950
CS ATGAGGGTACTACTACAATCGGTCTCACCTGTCGAATTTCTCCAATCACA
mq194 ATGAGGGTACTACTACAATCGGTCTCACCTGTCGAATTTCTCCAATCACA
mq36 ATGAGGGTACTACTACAATCGGTCTCACCTGTCGAATTTCTCCAATCACA
mq125 ATGAGGGTACTACTACAATCGGTCTCACCTGTCGAATTTCTCCAATCACA

2000
CS CCCAAGTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGA
mq194 CCCAAGTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGA
mq36 CCCAAGTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGA
mq125 CCCAAGTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGA

2050
CS TGCTGATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACG
mq194 TGCTGATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACG
mq36 TGCTGATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACG
mq125 TGCTGATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACG

2100
CS ATCCCAAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCC
mq194 ATCCCAAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCC
mq36 ATCCCAAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCC
mq125 ATCCCAAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCC

2150
CS CCTGAATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTA
mq194 CCTGAATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTA
mq36 CCTGAATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTA
mq125 CCTGAATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTA

2200
CS TGTTTAGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTT
mq194 TGTTTAGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTT
mq36 TGTTTAGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTT
mq125 TGTTTAGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTT

2250
CS GCTGTTGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGT
mq194 GCTGTTGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGT
mq36 GCTGTTGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGT
mq125 GCTGTTGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGT

2300
CS ATGGCATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCG
mq194 ATGGCATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCG
mq36 ATGGCATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCG
mq125 ATGGCATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCG

2350
CS CTGTAGCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGG
mq194 CTGTAGCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGG
mq36 CTGTAGCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGG
mq125 CTGTAGCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGG

2400
CS CACGGCAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTC
mq194 CACGGCAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTC
mq36 CACGGCAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTC
mq125 CACGGCAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTC

2450
CS ATGGCTTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCA
mq194 ATGGCTTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCA
mq36 ATGGCTTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCA
mq125 ATGGCTTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCA

2500
CS CCTCCTCCTCCTCCTCCTCCTCTGCTTGGTGGCGCTGCTCCACCAGCTTAC
mq194 CCTCCTCCTCCTCCTCCTCCTCTGCTTGGTGGCGCTGCTCCACCAGCTTAC
mq36 CCTCCTCCTCCTCCTCCTCCTCTGCTTGGTGGCGCTGCTCCACCAGCTTAC
mq125 CCTCCTCCTCCTCCTCCTCCTCTGCTTGGTGGCGCTGCTCCACCAGCTTAC

2550
CS TGAAACTGTTGCTACCCTGAATAATGTTTCTGAAGAAACTGCTAATAAC
mq194 TGAAACTGTTGCTACCCTGAATAATGTTTCTGAAGAAACTGCTAATAAC
mq36 TGAAACTGTTGCTACCCTGAATAATGTTTCTGAAGAAACTGCTAATAAC
mq125 TGAAACTGTTGCTACCCTGAATAATGTTTCTGAAGAAACTGCTAATAAC

2600
CS ATTTTCAGTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTTC
mq194 ATTTTCAGTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTTC
mq36 ATTTTCAGTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTTC
mq125 ATTTTCAGTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTTC

2650
CS TTTCCCTAAAACTAATCACGCCTGCTCTCCTAAAAACATCTACAGGTGCAAG
mq194 TTTCCCTAAAACTAATCACGCCTGCTCTCCTAAAAACATCTACAGGTGCAAG
mq36 TTTCCCTAAAACTAATCACGCCTGCTCTCCTAAAAACATCTACAGGTGCAAG
mq125 TTTCCCTAAAACTAATCACGCCTGCTCTCCTAAAAACATCTACAGGTGCAAG

2700
CS AATTTTGGGTGTAGTGATGTGTCTGTTGACTGAGCATCTCGTCTCATGGA
mq194 AATTTTGGGTGTAGTGATGTGTCTGTTGACTGAGCATCTCGTCTCATGGA
mq36 AATTTTGGGTGTAGTGATGTGTCTGTTGACTGAGCATCTCGTCTCATGGA
mq125 AATTTTGGGTGTAGTGATGTGTCTGTTGACTGAGCATCTCGTCTCATGGA

2750

CS CAGACAGAGCATGCTGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGC
mq194 CAGACAGAGCATGCTGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGC
mq36 CAGACAGAGCATGCTGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGC
mq125 CAGACAGAGCATGCTGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGC

2800

CS ACTACTGTTTGCCCTGTGAGCTCGCACCACCTTTCGAAAAAACTGCAGG
mq194 ACTACTGTTTGCCCTGTGAGCTCGCACCACCTTTCGAAAAAACTGCAGT
mq36 ACTACTGTTTGCCCTGTGAGCTCGCACCACCTTTCGAAAAAACTGCAGT
mq125 ACTACTGTTTGCCCTGTGAGCTCGCACCACCTTTCGAAAAAACTGCAGT

2850

CS GCGCCCTCCGGTTCTTGACAGTTCCATCCGTCCCCCATGGCACAGCTTTAG
mq194 GCGCCCTCCGGTTCTTGACAGTTCCATCCGTCCCCCATGGCACAGCTTTAG
mq36 GCGCCCTCCGGTTCTTGACAGTTCCATCCGTCCCCCATGGCACAGCTTTAG
mq125 GCGCCCTCCGGTTCTTGACAGTTCCATCCGTCCCCCATGGCACAGCTTTAG

2900

CS ATGCAGCAGCAGCTTGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCT
mq194 ATGCAGCAGCAGCTTGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCT
mq36 ATGCAGCAGCAGCTTGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCT
mq125 ATGCAGCAGCAGCTTGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCT

2950

CS TTATTCTTGGTAGCCACTGTGCATTCACATGAAAGCAAAGCTTTGGTGCA
mq194 TTATTCTTGGTAGCCACTGTGCATTCACATGAAAGCAAAGCTTTGGTGCA
mq36 TTATTCTTGGTAGCCACTGTGCATTCACATGAAAGCAAAGCTTTGGTGCA
mq125 TTATTCTTGGTAGCCACTGTGCATTCACATGAAAGCAAAGCTTTGGTGCA

3000

CS TGCACGGCCATGACTTGACGCTCTATCTCACTGCTGGTGCTGGTGCAAGT
mq194 TGCACGGCCATGACTTGACGCTCTATCTCACTGCTGGTGCTGGTGCAAGT
mq36 TGCACGGCCATGACTTGACGCTCTATCTCACTGCTGGTGCTGGTGCAAGT
mq125 TGCACGGCCATGACTTGACGCTCTATCTCACTGCTGGTGCTGGTGCAAGT

3050

CS GCAGGTGCAGGAGAGGCCCATGGAGGCAAGGCCCTGAGCAGCCGTCGT
mq194 GCAGGTGCAGGAGAGGCCCATGGAGGCAAGGCCCTGAGCAGCCGTCGT
mq36 GCAGGTGCAGGAGAGGCCCATGGAGGCAAGGCCCTGAGCAGCCGTCGT
mq125 GCAGGTGCAGGAGAGGCCCATGGAGGCAAGGCCCTGAGCAGCCGTCGT

3100

CS CCTTCCCCGGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCC
mq194 CCTTCCCCGGTTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCC
mq36 CCTTCCCCGGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCC
mq125 CCTTCCCCGGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCC

3150

CS CACTCGCCGTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGC
mq194 CACTCGCCGTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGC
mq36 CACTCGCCGTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGC
mq125 CACTCGCCGTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGC

3200
CS CGCCGGCGCGAACCTCGCCCCGCCGCCCGTACCCGGACCACCACCGGT
mq194 CGCCGGCGCGAACCTCGCCCCGCCGCCCGTACCCGGACCACCACCGGT
mq36 CGCCGGCGCGAACCTCGCCCCGCCGCCCGTACCCGGACCACCACCGGT
mq125 CGCCGGGGCGAACCTCGCCCCGCCGCCCGTACCCGGACCACCACCGGT

3250
CS TCTACTTCCCCCGCCCGCCGACAACCTGAAGCTGGCCGTTGTGACCAGAC
mq194 TCTACTTCCCCCGCCCGCCGACAACCTGAAGCTGGCCGTTGTGACCAGAC
mq36 TCTACTTCCCCCGCCCGCCGACAACCTGAAGCTGGCCGTTGTGACCAGAC
mq125 TCTACTTCCCCCGCCCGCCGACAACCTGAAGCTGGCCGTTGTGACCAGAC

3300
CS GGCGGTGGGTGCGCGCGGTGCGAGGTGTTTCGCTCCTCGTCGTCGGTAACGC
mq194 GGCGGTGGGTGCGCGCGGTGCGAGGTGTTTCGCTCCTCGTCGTCGGTAACGC
mq36 GGCGGTGGGTGCGCGCGGTGCGAGGTGTTTCGCTCCTCGTCGTCGGTAACGC
mq125 GGCGGTGGGTGCGCGCGGTGCGAGGTGTTTCGCTCCTCGTCGTCGGTAACGC

3350
CS TTGTTGTGAAACTATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTG
mq194 TTGTTGTGAAACTATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTG
mq36 TTGTTGTGAAACTATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTG
mq125 TTGTTGTGAAACTATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTG

3400
CS GTGACACTACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGC
mq194 GTGACACTACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGC
mq36 GTGACACTACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGC
mq125 GTGACACTACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGC

3450
CS GGATCATGGCTGTTTCATTAGATTCTCATGTATCCAATGTTCAAGTTTCCC
mq194 GGATCATGGCTGTTTCATTAGATTCTCATGTATCCAATGTTCAAGTTTCCC
mq36 GGATCATGGCTGTTTCATTAGATTCTCATGTATCCAATGTTCAAGTTTCCC
mq125 GGATCATGGCTGTTTCATTAGATTCTCATGTATCCAATGTTCAAGTTTCCC

3500
CS AAACGGTTGAAAAAATTTGAAATTTGTGATGGCAAATTCATGCATGGGT
mq194 AAACGGTTGAAAAAATTTGAAATTTGTGATGGCAAATTCATGCATGGGT
mq36 AAACGGTTGAAAAAATTTGAAATTTGTGATGGCAAATTCATGCATGGGT
mq125 AAACGGTTGAAAAAATTTGAAATTTGTGATGGCAAATTCATGCATGGGT

3550
CS CGCACGGTGCGCCCTTGACACAAGCGCGGGGAAGCACTCTGTTGTTTTACA
mq194 CGCACGGTGCGCCCTTGACACAAGCGCGGGGAAGCACTCTGTTGTTTTACA
mq36 CGCACGGTGCGCCCTTGACACAAGCGCGGGGAAGCACTCTGTTGTTTTACA
mq125 CGCACGGTGCGCCCTTGACACAAGCGCGGGGAAGCACTCTGTTGTTTTACA

3588
CS GCAGTCCGCCATTGTTGCGTTAACCGTTGGGCCTTCTG
mq194 GCAGTCCGCCATTGTTGCGTTAACCGTTGGGCCTTCTG
mq36 GCAGTCCGCCATTGTTGCGTTAACCGTTGGGCCTTCTG
mq125 GCAGTCCGCCATTGTTGCGTTAACCGTTGGGCCTTCTG

APPENDIX D. Alignment of *Q* cDNA from Chinese Spring with partial B- and putative D-genome *q* cDNAs.*

* The sequences of the putative B- and D-genome sequences were obtained while cloning the full length A-genome *Q* cDNA with primers nonspecific to the A-genome. The partial B-genome cDNA sequence aligns nearly identical to the genomic B-genome sequence obtained from the tetraploid Langdon.

```

D genome          ATGTGGAGTCGNNGGCGGACTCCGGNACGTCCAGCTCGTCCGTG
A genome  ATGGTGCTGGATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGTG
B genome          ATGTGGAGTCGCCGGCGGACTCCGGCACGTCCAGCTCGTCCGTG
                  *****  *****  ** *****  *****

D genome  CTCAACTCCGCGGACGCCGGCGGGCGGGCTTCAGGTTCCGGCTGCTCGGGAGCCCC
A genome  CTCAACTCCGCGGACGCCGGTGGCGGGCGGC---TTCCGGTTCGGCCTGCTCGGGAGCCCT
B genome  CTCAACTCCGCGGACGCCGGCGGC-----TTCCGGTTCGGCCTGCTCGGGAGCCCC
                  *****  *****  *****

D genome  GATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTCCGGTCCGGTTCGTGACGAGGCAG
A genome  GATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTCCGGTCCGGTTCGTGACGAGGCAG
B genome  GATGACGACGACTGGTCCGGCGAGCCGGCGCCGGTCCGGTTCGTGACGAGGCAG
                  *****  *****  *****

D genome  CTCTTCCCCGCGTCGCCGCCCGGTACGCGGGCGCGCCCGGGATGATGACGGGGCAGCTG
A genome  CTCTTCCCCGCGTCGCCGCCCGGGCACGCGGGCGCGCCCGGGTACGATGGGGCAGCAG
B genome  CTCTTCCCCGCGTCGCCGCC-----CGCGCCCGGGATGATGATGGGGCAGCAG
                  *****  *****  *****

D genome  GCACCGGCGCC--GCCGATGGCCCCCGTGTGGCAGCCCGCGGCGCGCCGAGGAGCTCGTG
A genome  GCCCCGGCGCCTGCGCCGATGGCGCCCGTGTGGCAGCCCGCGGCGCGCCGAGGAGCTCCTC
B genome  GCCCCGGGCGCC--GCCGATGGCCCCCGTGTGGCAGCCCGCGGCGCGCCGAGGAGCTGGTC
                  ** *****  *****  *****

D genome  ATGGCGCAGCGGGTGGCGCCCCGGAAGAAGACCGGGCGGGGGCCGAGGTTCGCGGAGCTCG
A genome  GTGGCGCAGCGGATGGCGCCCCGGAAGAAGACCGGGCGGGGGCCGAGGTTCGCGCAGCTCG
B genome  GCGGCGCAGCGGGTGGCGCCCCGGAAGAAGACCGGGCGGGGGCCGAGGTTCGCGGAGCTCG
                  *****  *****  *****

D genome  CAGTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACATCTGGGAC
A genome  CAGTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACATCTGGGAT
B genome  CAGTACAGTG-----
                  *****  *

D genome  TGCGGGAAGCAGGTCTACTTAGGTGGTT-CGACACTGCGCACGCGGCCGCAAGGGCCTAC
A genome  TGCGGGAAGCAGGTCTACTTAGGTGGTTTTCGACACTGCGCACGCGGCCGCAAGGGCCTAC
B genome  -----

D genome  GATCGCGCGGCGATCAAGTTCGGGGGCTGGAGGCCGACATCAACTTCAATCTGAGCGAT
A genome  GATCGCGCGGCGATCAAGTTCGGGGGCTGGAGGCCGACATCAACTTCAATCTGAGCGAC
B genome  -----

D genome  TATGAGGAGGATTTGAAGCAG-----
A genome  TACGAGGAGGATTTGAAGCAG-----
B genome  -GTAGTCAGTGCCCGGATAAATATATGGGTGGTTTGTCCGATGGTTGATATCCTGTGGGT
                  ▲

D genome  -----ATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATCCTC
A genome  -----ATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATCCTC
B genome  GGTGGTGGTGCTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATCCTC
                  *****

```

D genome CGCCGCCAGAGCACGGGGTTCGCCAGGGGGAGCTCCAAGTACCGCGGGCCACGCTCCAC
A genome CGCCGCCAGAGCACGGGGTTCGCCAGGGGGAGCTCCAAGTACCGCGGGGTACGCTCCAC
B genome CGCCGCCAGAGCACGGGGTTCGCCAGGGGGAGCTCCAAGTACCGCGGGGTACGCTCCAC

D genome AAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGCTCGGCAAGAAGTACATATATCTT
A genome AAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGCTCGGCAAGAAGTACATATATCTG
B genome AAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGCTCGGCAAGAAGTACATATATCTT

D genome GGCCTCTTTGACAGCGAAGTTGAAGCTGCAAGGGCGTACGACAGGGCGGCGATTTCGCTTC
A genome GGCCTCTTTGACAGCGAAGTTGAAGCTGCAAGGGCGTACGACAGGGCGGCGATTTCGCTTC
B genome GGCCTCTTTGACAGCGAAGTTGAAGCTGCAAGGGCGTACGACAGGGCGGCGATTTCGCTTC

D genome AATGGGAGGGAAGCTGTGACTAACTTTGAGAGCAGCTCCTACAATGGGGATGCTCCACCC
A genome AATGGGAGGGAAGCTGTGACTAACTTTGAGAGCAGCTCCTACAATGGGGATGCTCCACCC
B genome AATGGGAGGGAAGCTGTGACTAACTTTGAGAGCAGCTCCTACAATGGGGATGCTCCACCC

D genome GACGCCGAAAATGAGGCAATTGTTGATGCTGATGCTCTTGACTTGTATCTACGGATGTCTG
A genome GACGCCGAAAATGAGGCAATTGTTGATGCTGATGCTCTTGACTTGGATCTGCGGATGTCTG
B genome GACGCCGAAAATGAGGCAATTGTTGATGCTGATGCTCTTGACTTGGATCTTTCGGATGTCTG

D genome CAACCTACCGCGCACGATCCCAAGCGGGACAACATCATCGCCGGCCTTCAGTTAACTTTT
A genome CAACCTACCGCGCACGATCCCAAGCGGGACAACATCATCGCCGGCCTTCAGTTAACTTTT
B genome CAACCTACCGCGCACGATCCCAAGCGGGACAACATCATCGCCGGCCTTCAGTTAACTTTT

D genome GATTCCCCTGAATCGTCAACCACAATGCTCTTTCTCAGCCAATGAGCTCATCTTCTTCC
A genome GATTCCCCTGAATCGTCAACCACAATGATCTCTTTCTCAGCCAATGAGCTCATCTTCTTCC
B genome GATTCCCCTGAATCGTCAACCACAATGCTCTTTCTCAGCCAATGAGCTCATCTTCTTCC

D genome CAGTGGCCTGTGCATCAACATGGCACGGCAGTAGCACCTCAGCAGCACCAGCGTTTGTAC
A genome CAGTGGCCTGTGCATCAACATGGCACGGCAGTAGCACCTCAGCAGCACCAGCGTTTGTAC
B genome CAGTGGCCTGTGCATCAACATGGCACGGCAGTAGCACCTCAGCAGCACCAGCGTTTGTAC

D genome CCATCTGCTTGTGCATGGCTTCTACCCGAACGTACAGGTGCAGGTGCAGGTGCAGGAGAGG
A genome CCATCTGCTTGTGCATGGCTTCTACCCGAACGTACAGGTGCAGGTGCAGG-----AGAGG
B genome CCATCTGCTTGTGCATGGCTTCTACCCGAACGTACAGGTGCAGGTGCAGG-----AGAGG

D genome CCCATGGAGCCAAGGCCCCCTGAGCCGCCGTCTGCTCCTCCCCAGCTGGGGGTGGCAAGCG
A genome CCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCTGCTCCTCCCCGGCTGGGGGTGGCAAGCG
B genome CCGATGGAGGCAAGGCCCCCTGAGCCGCCGTCTGCTCCTCCCCGGCTGGGGGTGGCAAGCG
** *****

D genome CAAGCCATGCCGCGGGCTCCTCCCACTCGCCGTTGCTTTACGCTGCAGCATCGTCAGGA
A genome CAAGCCATGCCGCGGGCTCCTCCCACTCGCCGTTGCTTTACGCTGCAGCATCATCAGGA
B genome CAAGCCACGCCGCGGGCTCCTCCCACTCGCCGTTGCTTTACGCTGCAGCATCATCAGGA

D genome TTCTCTACCGCCGCCG---GCGCGCACCCCGCCCCGCCGCCGCCGCGTTCGTACCCGGAT
A genome TTTTCTACCGCCGCCGCCGGCGCGAACCTCGCCCCGCCGCCGCCG-----TACCCGGAC
B genome TTCTCTACCGCCGCCG---GCGCGCACCCCGCCCCGCCGCCGCCG---TCGTACCCGGAT
** *****
***** ** *****

D genome CACCACCGGTATCTACTTCCCCCGCCCCGCCGGACAACCTG-
A genome CACCACCGGT-TCTACTTCCCCCGCCCCGCCGGACAACCTGA
B genome CACCACCGGT-TCTACTTCCCCCGCCCCGCC-----
***** *****

APPENDIX E. Alignment of putative B- and D-genome q protein sequences to the sequence of Q.*

* Assumption: translation start site is identical in all three genomes.

D-genome -----VESXADSGTSSSSSVLNSADAGGGGGFRFGLLGSPDDDDCSGEPAPVGSFVTRQ
B-genome -----VESPADSGTSSSSSVLNSADAGG---FRFGLLGSPDDDDWSGEPAPAASGFVTRQ
A-genome MVLDLNVESPADSGTSSSSSVLNSADAGGGG-FRFGLLGSPDDDDCSGEPAPVGPVTRQ
 *** *****

D-genome LFPASPPGHAGAPGMMTGQLAPAP-PMAPVWQPRRAEELVMAQRVAPAKKTRRGPRSRSS
B-genome LFPASPP---APGMMMGQQAPAP-PMAPVWQPRRAEELVAAQRVAPAKKTRRGPRSRSS
A-genome LFPASPPGHAGAPGVTMGQQAPAPAPMAPVWQPRRAEELLVAQRMAPAKKTRRGPRSRSS
 ***** ***: ** ***** *****: ***:*****

D-genome QYRGVTFYRRTGRWESHIWDCGKQVYLGGSTLRTRPQGPTIARRSSSGWRPTSTSI---
B-genome QYSGSQCAG-----
A-genome QYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAAARAYDRAAIKFRGLEADINFNLSD
 ** *

D-genome -----
B-genome -----
A-genome YEEDLKQMRNWTKEEFVHILRRQSTGFARGSSKYRGVTLHKCGRWEARMGQLLGKKYIYL

D-genome -----
B-genome -----
A-genome GLFDSEVEAARAYDRAAIRFNGREAVTNFESSYNGDAPPDAENEAIVDADALDLDRMS

D-genome -----
B-genome -----
A-genome QPTAHDPKRDNI IAGLQLTFDSPESTTMISSQPMSSSSSQWPVHQHGTAVAPQHQRLY

D-genome -----
B-genome -----
A-genome PSACHGFYPNVQVQVQERPMEARPPEQPSSFPGWGWQAQAMPPGSSHSPLLYAAASSGFS

D-genome -----
B-genome -----
A-genome TAAAGANLAPPPYPDHHRFYFPRPPDN

APPENDIX F. DNA alignment of all sequenced *Q/q* alleles.* §

* Alignment is number based on the translation start codon in *T. aestivum* ssp. *aestivum* 'Chinese Spring'. Conserved differences identified from the initial 12 sequences are identified with arrows.

§ List of abbreviations:

urartu (q):	<i>T. urartu</i> TA 704
monococcum (q):	<i>T. monococcum</i> DV 92
dicoccoides 1 (q):	<i>T. turgidum</i> ssp. <i>dicoccoides</i> PI 355459
dicoccoides 2 (q):	<i>T. turgidum</i> ssp. <i>dicoccoides</i> PI 466995
dicoccoides 3 (q):	<i>T. turgidum</i> ssp. <i>dicoccoides</i> 16-1
dicoccoides 4 (q):	Chinese Spring - <i>T. turgidum</i> ssp. <i>dicoccoides</i> (TA3446) 5A Substitution Line
dicoccum 1 (q):	<i>T. turgidum</i> ssp. <i>dicoccum</i> CItr 14621
dicoccum 2 (q):	<i>T. turgidum</i> ssp. <i>dicoccum</i> CItr 14454
dicoccum 3 (q):	<i>T. turgidum</i> ssp. <i>dicoccum</i> PI 74108
dicoccum 4 (Q):	<i>T. turgidum</i> ssp. <i>dicoccum</i> ‘Liguliforme’ TA 10435
polonicum 1 (Q):	<i>T. turgidum</i> ssp. <i>polonicum</i> CItr 191826
polonicum 2 (Q):	<i>T. turgidum</i> ssp. <i>polonicum</i> CItr 225334
carthlicum (Q):	<i>T. turgidum</i> ssp. <i>carthlicum</i> TA2801
durum (Q):	<i>T. turgidum</i> ssp. <i>durum</i> ‘Landgon’
aestivum (Q):	<i>T. aestivum</i> ssp. <i>aestivum</i> ‘Chinese Spring’
compactum (Q):	<i>T. aestivum</i> ssp. <i>compactum</i> TA 2601
sphaerococcum (Q):	<i>T. aestivum</i> ssp. <i>sphaerococcum</i> TA 2605
macha (q):	<i>T. aestivum</i> ssp. <i>macha</i> PI 361862
spelta 1 (Eur; q):	<i>T. aestivum</i> ssp. <i>spelta</i> type European P78-81-1
spelta 2 (Eur; q):	<i>T. aestivum</i> ssp. <i>spelta</i> type European TA 2603
spelta 3 (Eur; q):	<i>T. aestivum</i> ssp. <i>spelta</i> type European PI 378469
spelta 4 (Iran; Q):	<i>T. aestivum</i> ssp. <i>spelta</i> type Iranian 407 a
spelta 5 (Iran; Q):	<i>T. aestivum</i> ssp. <i>spelta</i> type Iranian PI367199

polonicum 1 (Q) -----
 aestivum (Q) GCCCTCGCAGCCCGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCA
 carthlicum (Q) -----
 polonicum 2 (Q) -----
 dicoccum 4 (Q) GCCCTCGCAGCCCGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCA
 durum (Q) GCCCTCGCAGCCCGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCA
 compactum (Q) GCCCTCGCAGCCCGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCA
 sphaerococcum (Q) GCCCTCGCAGCCCGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCA
 spelta 4 (Iran; Q) -----
 spelta 5 (Iran; Q) GCCCTCGCAGCCCGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCA
 dicoccoides 2 (q) GCCCTCGCAGCCCGCGGCCACCGCGCTCCCATGCCATAGACGCGAGCCCA
 dicoccoides 3 (q) GCCCTCGCAGCCCGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCA
 dicoccoides 1 (q) GCCCTCGCAGCCCGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCA
 dicoccum 3 (q) GCCCTCGCAGCCNGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCA
 spelta 1 (Eur; q) -----
 dicoccoides 4 (q) GCCCTCGCAGCCCGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCA
 spelta 2 (Eur; q) -----
 macha (q) -----
 dicoccum 1 (q) -----
 dicoccum 2 (q) -----
 spelta 3 (Eur; q) GCCCTCGCAGCCCGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCA
 urartu (q) -----
 monococcum (q) GCCCTCGCAGCCCGCGGCCACCGCGCTCCCATGCCATAGACGCGACCCCA

polonicum 1 (Q) -----
 aestivum (Q) CTCATCGGTCCAGGTCCGGTTCGCTCGGAGCCGAGCGGCGGGCGGGCGGA
 carthlicum (Q) -----
 polonicum 2 (Q) -----
 dicoccum 4 (Q) CTCATCGGTCCAGGTCCGGTTCGCTCGGAGCCGAGCGGCGGGCGGGCGGA
 durum (Q) CTCATCGGTCCAGGTCCGGTTCGCTCGGAGCCGAGCGGCGGGCGGGCGGA
 compactum (Q) CTCATCGGTCCAGGTCCGGTTCGCTCGGAGCCGAGCGGCGGGCGGGCGGA
 sphaerococcum (Q) CTCATCGGTCCAGGTCCGGTTCGCTCGGAGCCGAGCGGCGGGCGGGCGGA
 spelta 4 (Iran; Q) -----
 spelta 5 (Iran; Q) CTCATCGGTCCAGGTCCGGTTCGCTCGGAGCCGAGCGGCGGGCGGGCGGA
 dicoccoides 2 (q) CTCATCGGTCCAGGTCCGGTTCGCTCGGAGCCGAGCGGCGGGCGGGCGGA
 dicoccoides 3 (q) CTCATCGGTCCAGGTCCGGTTCGCTCGGAGCCGAGCGGCGGGCGGGCGGA
 dicoccoides 1 (q) CTCATCGGTCCAGGTCCGGTTCGCTCGGAGCCGAGCGGCGGGCGGGCGGA
 dicoccum 3 (q) CTCATCGGTCCAGGTCCGGTTCGCTCGGAGCCGAGCGGCGGGCGGGCGGA
 spelta 1 (Eur; q) -----
 dicoccoides 4 (q) CTCATCGGTCCAGGTCCGGTTCGCTCGGAGCCGAGCGGCGGGCGGGCGGA
 spelta 2 (Eur; q) -----
 macha (q) -----
 dicoccum 1 (q) -----
 dicoccum 2 (q) -----
 spelta 3 (Eur; q) CTCATCGGTCCAGGTCCGGTTCGCTCGGAGCCGAGCGGCGGGCGGGCGGA
 urartu (q) -----
 monococcum (q) CTCATCGGTCCAGGTCCGGTTCGCTCGGAGCCGAGCGGCGGGCGGGTCA

polonicum 1 (Q) -----ATGGTGCTG
 aestivum (Q) GGAGTGCCTTTTATTTCGGTCCCAGCGGGCCTCGGATCGGAGATGGTGCTG
 carthlicum (Q) -----ATGGTGCTG
 polonicum 2 (Q) -----ATGGTGCTG
 dicoccum 4 (Q) GGAGTGCCTTTTATTTCGGTCCCAGCGGGCCTCGGATCGGAGATGGTGCTG
 durum (Q) GGAGTGCCTTTTATTTCGGTCCCAGCGGGCCTCGGATCGGAGATGGTGCTG
 compactum (Q) GGAGTGCCTTTTATTTCGGTCCCAGCGGGCCTCGGATCGGAGATGGTGCTG
 sphaerococcum (Q) GGAGTGCCTTTTATTTCGGTCCCAGCGGGCCTCGGATCGGAGATGGTGCTG
 spelta 4 (Iran; Q) -----ATGGTGCTG
 spelta 5 (Iran; Q) GGAGTGCCTTTTATTTCGGTCCCAGCGGGCCTCGGATCGGAGATGGTGCTG
 dicoccoides 2 (q) GGAGTGCCTTTTATTTCGGTCCCAGCGGGCCTCGGATCGGAGATGGTGCTG
 dicoccoides 3 (q) GGAGTGCCTTTTATTTCGGTCCCAGCGGGCCTCGGATCGGAGATGGTGCTG
 dicoccoides 1 (q) GGAGTGCCTTTTATTTCGGTCCCAGCGGGCCTCGGATCGGAGATGGTGCTG
 dicoccum 3 (q) GGAGTGCCTTTTATTTCGGTCCCAGCGGGCCTCGGATCGGAGATGGTGCTG
 spelta 1 (Eur; q) -----ATGGTGCTG
 dicoccoides 4 (q) GGAGTGCCTTTTATTTCGGTCCCAGCGGGCCTCGGATCGGAGATGGTGCTG
 spelta 2 (Eur; q) -----ATGGTGCTG
 macha (q) -----ATGGTGCTG
 dicoccum 1 (q) -----ATGGTGCTG
 dicoccum 2 (q) -----ATGGTGCTG
 spelta 3 (Eur; q) GGAGTGCCTTTTATTTCGGTCCCAGCGGGCCTCGGATCGGAGATGGTGCTG
 urartu (q) -----ATGGTGCTG
 monococcum (q) --AGCGAGTTCAGGAGCGCCAGCGGGCCTCGGATCGGAGATGGTGCTG

polonicum 1 (Q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 aestivum (Q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 carthlicum (Q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 polonicum 2 (Q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 dicoccum 4 (Q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 durum (Q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 compactum (Q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 sphaerococcum (Q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 spelta 4 (Iran; Q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 spelta 5 (Iran; Q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 dicoccoides 2 (q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 dicoccoides 3 (q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 dicoccoides 1 (q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 dicoccum 3 (q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 spelta 1 (Eur; q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 dicoccoides 4 (q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 spelta 2 (Eur; q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 macha (q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 dicoccum 1 (q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 dicoccum 2 (q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 spelta 3 (Eur; q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 urartu (q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT
 monococcum (q) GATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCGT

polonicum 1 (Q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 aestivum (Q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 carthlicum (Q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 polonicum 2 (Q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 dicoccum 4 (Q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 durum (Q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 compactum (Q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 sphaerococcum (Q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 spelta 4 (Iran; Q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 spelta 5 (Iran; Q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 dicoccoides 2 (q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 dicoccoides 3 (q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 dicoccoides 1 (q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 dicoccum 3 (q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 spelta 1 (Eur; q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 dicoccoides 4 (q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 spelta 2 (Eur; q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 macha (q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 dicoccum 1 (q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 dicoccum 2 (q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 spelta 3 (Eur; q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 urartu (q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG
 monococcum (q) GCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCG

polonicum 1 (Q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 aestivum (Q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 carthlicum (Q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 polonicum 2 (Q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 dicoccum 4 (Q) GGAGCCCTGATGATGACGAATGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 durum (Q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 compactum (Q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 sphaerococcum (Q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 spelta 4 (Iran; Q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 spelta 5 (Iran; Q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 dicoccoides 2 (q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 dicoccoides 3 (q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 dicoccoides 1 (q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 dicoccum 3 (q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 spelta 1 (Eur; q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 dicoccoides 4 (q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 spelta 2 (Eur; q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 macha (q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 dicoccum 1 (q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 dicoccum 2 (q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 spelta 3 (Eur; q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 urartu (q) GAAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 monococcum (q) GGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCC
 * *****

polonicum 1 (Q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 aestivum (Q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 carthlicum (Q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 polonicum 2 (Q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 dicoccum 4 (Q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 durum (Q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 compactum (Q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 sphaerococcum (Q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 spelta 4 (Iran; Q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 spelta 5 (Iran; Q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 dicoccoides 2 (q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 dicoccoides 3 (q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 dicoccoides 1 (q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 dicoccum 3 (q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 spelta 1 (Eur; q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 dicoccoides 4 (q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 spelta 2 (Eur; q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 macha (q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 dicoccum 1 (q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 dicoccum 2 (q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 spelta 3 (Eur; q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 urartu (q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG
 monococcum (q) GGGTTCGTCACGAGGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGG

polonicum 1 (Q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 aestivum (Q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 carthlicum (Q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 polonicum 2 (Q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 dicoccum 4 (Q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 durum (Q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 compactum (Q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 sphaerococcum (Q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 spelta 4 (Iran; Q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 spelta 5 (Iran; Q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 dicoccoides 2 (q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 dicoccoides 3 (q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 dicoccoides 1 (q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 dicoccum 3 (q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 spelta 1 (Eur; q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 dicoccoides 4 (q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 spelta 2 (Eur; q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 macha (q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 dicoccum 1 (q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 dicoccum 2 (q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 spelta 3 (Eur; q) CGCGCCCGGGGTGACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 urartu (q) CGCGCCTGGGGTACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG
 monococcum (q) CGCGCCTGGGGTACGATGGGGCAGCAGGCCCCGCGCCTGCGCCGATGG

polonicum 1 (Q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 aestivum (Q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 carthlicum (Q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 polonicum 2 (Q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 dicoccum 4 (Q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 durum (Q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 compactum (Q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 sphaerococcum (Q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 spelta 4 (Iran; Q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 spelta 5 (Iran; Q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 dicoccoides 2 (q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 dicoccoides 3 (q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 dicoccoides 1 (q) CGCCCGTGTGGCAGCCGCGGACGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 dicoccum 3 (q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 spelta 1 (Eur; q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 dicoccoides 4 (q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 spelta 2 (Eur; q) CGCCCGTGTGGCAGCCGCGGACGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 macha (q) CGCCCGTGTGGCAGCCGCGGACGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 dicoccum 1 (q) CGCCCGTGTGGCAGCCGCGGACGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 dicoccum 2 (q) CGCCCGTGTGGCAGCCGCGGACGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 spelta 3 (Eur; q) CGCCCGTGTGGCAGCCGCGGACGCGCCGAGGAGCTCCTCGTGGCGCAGCGG
 urartu (q) CGCCCGTGTGGCAGCCGCGGGCGCGCCGAGGAGCTCGTGGCGCAGCGG
 monococcum (q) CGCCCGTGTGGCAGCCGCGGGCGCGGAGGAGCTCGTGGCGCAGCGG

polonicum 1 (Q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 aestivum (Q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 carthlicum (Q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 polonicum 2 (Q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 dicoccum 4 (Q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 durum (Q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 compactum (Q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 sphaerococcum (Q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 spelta 4 (Iran; Q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 spelta 5 (Iran; Q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 dicoccoides 2 (q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 dicoccoides 3 (q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 dicoccoides 1 (q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 dicoccum 3 (q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 spelta 1 (Eur; q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 dicoccoides 4 (q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 spelta 2 (Eur; q) ATGGCGCCCGCGGAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 macha (q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 dicoccum 1 (q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 dicoccum 2 (q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 spelta 3 (Eur; q) ATGGCGCCCGCGGAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 urartu (q) ATGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA
 monococcum (q) GTGGCGCCCGCGAAGAAGACGCGGGCGGGGCCCGAGGTTCGCGCAGCTCGCA

polonicum 1 (Q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 aestivum (Q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 carthlicum (Q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 polonicum 2 (Q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 dicoccum 4 (Q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 durum (Q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 compactum (Q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 sphaerococcum (Q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 spelta 4 (Iran; Q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 spelta 5 (Iran; Q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 dicoccoides 2 (q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 dicoccoides 3 (q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 dicoccoides 1 (q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 dicoccum 3 (q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 spelta 1 (Eur; q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 dicoccoides 4 (q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 spelta 2 (Eur; q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 macha (q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 dicoccum 1 (q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 dicoccum 2 (q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 spelta 3 (Eur; q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 urartu (q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA
 monococcum (q) GTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGGAGTCGCACA

polonicum 1 (Q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 aestivum (Q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 carthlicum (Q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 polonicum 2 (Q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 dicoccum 4 (Q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 durum (Q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 compactum (Q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 sphaerococcum (Q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 spelta 4 (Iran; Q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 spelta 5 (Iran; Q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 dicoccoides 2 (q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 dicoccoides 3 (q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 dicoccoides 1 (q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 dicoccum 3 (q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 spelta 1 (Eur; q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 dicoccoides 4 (q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 spelta 2 (Eur; q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 macha (q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 dicoccum 1 (q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 dicoccum 2 (q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 spelta 3 (Eur; q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 urartu (q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 monococcum (q) TCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATGACTATAGTT
 ***** ** * ** *****

polonicum 1 (Q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 aestivum (Q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 carthlicum (Q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 polonicum 2 (Q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 dicoccum 4 (Q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 durum (Q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 compactum (Q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 sphaerococcum (Q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 spelta 4 (Iran; Q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 spelta 5 (Iran; Q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 dicoccoides 2 (q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 dicoccoides 3 (q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 dicoccoides 1 (q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 dicoccum 3 (q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 spelta 1 (Eur; q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 dicoccoides 4 (q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 spelta 2 (Eur; q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 macha (q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 dicoccum 1 (q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 dicoccum 2 (q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 spelta 3 (Eur; q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 urartu (q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC
 monococcum (q) ATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCTGATTCCACC

polonicum 1 (Q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 aestivum (Q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 carthlicum (Q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 polonicum 2 (Q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 dicoccum 4 (Q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 durum (Q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 compactum (Q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 sphaerococcum (Q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 spelta 4 (Iran; Q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 spelta 5 (Iran; Q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 dicoccoides 2 (q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 dicoccoides 3 (q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 dicoccoides 1 (q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 dicoccum 3 (q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 spelta 1 (Eur; q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 dicoccoides 4 (q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 spelta 2 (Eur; q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 macha (q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 dicoccum 1 (q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 dicoccum 2 (q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 spelta 3 (Eur; q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 urartu (q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
 monococcum (q) AGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACAAATCCCAGC
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polonicum 1 (Q) TCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 aestivum (Q) TCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 carthlicum (Q) TCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 polonicum 2 (Q) TCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 dicoccum 4 (Q) TCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 durum (Q) TCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 compactum (Q) TCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 sphaerococcum (Q) TCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 spelta 4 (Iran; Q) TCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 spelta 5 (Iran; Q) TCGAGCTCCGATCTCCCCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 dicoccoides 2 (q) TCGAGCTCCGATCTCCCCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 dicoccoides 3 (q) TCGAGCTCCGATCTCCCCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 dicoccoides 1 (q) TCGAGCTCCGATCTCCCCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 dicoccum 3 (q) TCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 spelta 1 (Eur; q) TCGAGCTCCGATCTCCCCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 dicoccoides 4 (q) TCGAGCTCCGATCTCCCCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 spelta 2 (Eur; q) TCGAGCTCCGATCTCCCCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 macha (q) TCGAGCTCCGATCTCCCCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 dicoccum 1 (q) TCGAGCTCCGATCTCCCCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 dicoccum 2 (q) TCGAGCTCCGATCTCCCCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 spelta 3 (Eur; q) TCGAGCTCCGATCTCCCCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 urartu (q) TCGAGCTCCGATCTCCCCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 monococcum (q) TCAAGCTCCGATCTCCCCGGTGTCTAATTTTCGATTATCTTAGCTGTATGG
 ** *****



polonicum 1 (Q) GCTCGTGATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 aestivum (Q) GCTCGTGATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 carthlicum (Q) GCTCGTGATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 polonicum 2 (Q) GCTCGTGATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 dicoccum 4 (Q) GCTCGTGATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 durum (Q) GCTCGTGATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 compactum (Q) GCTCGTGATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 sphaerococcum (Q) GCTCGTGATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 spelta 4 (Iran; Q) GCTCGTGATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 spelta 5 (Iran; Q) GCTCGTAATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 dicoccoides 2 (q) GCTCGTAATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 dicoccoides 3 (q) GCTCGTAATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 dicoccoides 1 (q) GCTCGTAATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 dicoccum 3 (q) GCTCGTGATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 spelta 1 (Eur; q) GCTCGTAATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 dicoccoides 4 (q) GCTCGTAATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 spelta 2 (Eur; q) GCTCGTAATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 macha (q) GCTCGTAATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 dicoccum 1 (q) GCTCGTAATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 dicoccum 2 (q) GCTCGTAATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 spelta 3 (Eur; q) GCTCGTAATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 urartu (q) GCTCGTAATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA
 monococcum (q) GCTCGTAATTAACACTGGATAATTTCTTCAGGTGGTTTTCGACACTGCGCA

polonicum 1 (Q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 aestivum (Q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 carthlicum (Q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 polonicum 2 (Q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 dicoccum 4 (Q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 durum (Q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 compactum (Q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 sphaerococcum (Q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 spelta 4 (Iran; Q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 spelta 5 (Iran; Q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 dicoccoides 2 (q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 dicoccoides 3 (q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 dicoccoides 1 (q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 dicoccum 3 (q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 spelta 1 (Eur; q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 dicoccoides 4 (q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 spelta 2 (Eur; q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 macha (q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 dicoccum 1 (q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 dicoccum 2 (q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 spelta 3 (Eur; q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 urartu (q) CGCGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTTTGAATTCCT
 monococcum (q) CGCGCCGCAAGGTGAACTAATTAATTAATCAGGCCTCGTTTGAATTCCT

polonicum 1 (Q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 aestivum (Q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 carthlicum (Q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 polonicum 2 (Q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 dicoccum 4 (Q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 durum (Q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 compactum (Q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 sphaerococcum (Q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 spelta 4 (Iran; Q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 spelta 5 (Iran; Q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 dicoccoides 2 (q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 dicoccoides 3 (q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 dicoccoides 1 (q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 dicoccum 3 (q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 spelta 1 (Eur; q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 dicoccoides 4 (q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 spelta 2 (Eur; q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 macha (q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 dicoccum 1 (q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 dicoccum 2 (q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 spelta 3 (Eur; q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 urartu (q) TTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGACGGTGTGGCG
 monococcum (q) TTTGCCCCGATTTGGCCGCGAACTGTGTACTGAGATGAGACGGTGTGGCG

polonicum 1 (Q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 aestivum (Q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 carthlicum (Q) TGGCGCAGGGGCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 polonicum 2 (Q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 dicoccum 4 (Q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 durum (Q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 compactum (Q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 sphaerococcum (Q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 spelta 4 (Iran; Q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 spelta 5 (Iran; Q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 dicoccoides 2 (q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 dicoccoides 3 (q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 dicoccoides 1 (q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 dicoccum 3 (q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 spelta 1 (Eur; q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 dicoccoides 4 (q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 spelta 2 (Eur; q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 macha (q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 dicoccum 1 (q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 dicoccum 2 (q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 spelta 3 (Eur; q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 urartu (q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC
 monococcum (q) TGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGCTGGAGGC

polonicum 1 (Q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 aestivum (Q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 carthlicum (Q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 polonicum 2 (Q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 dicoccum 4 (Q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 durum (Q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 compactum (Q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 sphaerococcum (Q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 spelta 4 (Iran; Q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 spelta 5 (Iran; Q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 dicoccoides 2 (q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 dicoccoides 3 (q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 dicoccoides 1 (q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 dicoccum 3 (q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 spelta 1 (Eur; q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 dicoccoides 4 (q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 spelta 2 (Eur; q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 macha (q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 dicoccum 1 (q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 dicoccum 2 (q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 spelta 3 (Eur; q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 urartu (q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA
 monococcum (q) CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGGTAA

polonicum 1 (Q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 aestivum (Q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 carthlicum (Q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 polonicum 2 (Q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 dicoccum 4 (Q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 durum (Q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 compactum (Q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 sphaerococcum (Q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 spelta 4 (Iran; Q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 spelta 5 (Iran; Q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 dicoccoides 2 (q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 dicoccoides 3 (q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 dicoccoides 1 (q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 dicoccum 3 (q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 spelta 1 (Eur; q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 dicoccoides 4 (q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 spelta 2 (Eur; q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 macha (q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 dicoccum 1 (q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 dicoccum 2 (q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 spelta 3 (Eur; q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 urartu (q) TCTTATCCAAGCCTAGTTGATTGCTGTACTACCAAGTAGTGCGCCGGATA
 monococcum (q) TCTTAGCCAAGCTTAGTTGATTGCTGTACTACCAGGTAGTGCGCCGGATA

polonicum 1 (Q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 aestivum (Q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 carthlicum (Q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 polonicum 2 (Q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 dicoccum 4 (Q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 durum (Q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 compactum (Q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 sphaerococcum (Q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 spelta 4 (Iran; Q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 spelta 5 (Iran; Q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 dicoccoides 2 (q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 dicoccoides 3 (q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 dicoccoides 1 (q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 dicoccum 3 (q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 spelta 1 (Eur; q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 dicoccoides 4 (q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 spelta 2 (Eur; q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 macha (q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 dicoccum 1 (q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 dicoccum 2 (q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 spelta 3 (Eur; q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 urartu (q) CATATGTATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 monococcum (q) ---ACATATCGGTGGTTTTGTCCGATGGTTGATATCTGGTGGGTGGTGGTG
 * *****

polonicum 1 (Q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 aestivum (Q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 carthlicum (Q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 polonicum 2 (Q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 dicoccum 4 (Q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 durum (Q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 compactum (Q) GTGTTTTTTTGCCAGATGAGGAACTGGACNAAGGAGGAGTTCGTGCACATC
 sphaerococcum (Q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 spelta 4 (Iran; Q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 spelta 5 (Iran; Q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 dicoccoides 2 (q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 dicoccoides 3 (q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 dicoccoides 1 (q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 dicoccum 3 (q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 spelta 1 (Eur; q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 dicoccoides 4 (q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 spelta 2 (Eur; q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 macha (q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 dicoccum 1 (q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 dicoccum 2 (q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 spelta 3 (Eur; q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 urartu (q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC
 monococcum (q) GTGTTTTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATC

polonicum 1 (Q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 aestivum (Q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 carthlicum (Q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 polonicum 2 (Q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 dicoccum 4 (Q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 durum (Q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 compactum (Q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 sphaerococcum (Q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 spelta 4 (Iran; Q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 spelta 5 (Iran; Q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 dicoccoides 2 (q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 dicoccoides 3 (q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 dicoccoides 1 (q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 dicoccum 3 (q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 spelta 1 (Eur; q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 dicoccoides 4 (q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 spelta 2 (Eur; q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 macha (q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 dicoccum 1 (q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 dicoccum 2 (q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 spelta 3 (Eur; q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 urartu (q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG
 monococcum (q) CTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGAGCTCCAAGTACCGCGG

polonicum 1 (Q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 aestivum (Q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 carthlicum (Q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 polonicum 2 (Q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 dicoccum 4 (Q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 durum (Q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 compactum (Q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 sphaerococcum (Q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 spelta 4 (Iran; Q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 spelta 5 (Iran; Q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 dicoccoides 2 (q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 dicoccoides 3 (q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 dicoccoides 1 (q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 dicoccum 3 (q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 spelta 1 (Eur; q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 dicoccoides 4 (q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 spelta 2 (Eur; q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 macha (q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 dicoccum 1 (q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 dicoccum 2 (q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 spelta 3 (Eur; q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 urartu (q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC
 monococcum (q) CGTCACGCTCCACAAGTGC GGCCGCTGGGAGGCAAGGATGGGCCAGCTGC

polonicum 1 (Q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 aestivum (Q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 carthlicum (Q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 polonicum 2 (Q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 dicoccum 4 (Q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 durum (Q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 compactum (Q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 sphaerococcum (Q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 spelta 4 (Iran; Q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 spelta 5 (Iran; Q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 dicoccoides 2 (q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 dicoccoides 3 (q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 dicoccoides 1 (q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 dicoccum 3 (q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 spelta 1 (Eur; q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 dicoccoides 4 (q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 spelta 2 (Eur; q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 macha (q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 dicoccum 1 (q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 dicoccum 2 (q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 spelta 3 (Eur; q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 urartu (q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT
 monococcum (q) TCGGCAAGAAGTAAGCAGGCACACACACAGCTCACGCACTAAAATTAATT

polonicum 1 (Q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 aestivum (Q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 carthlicum (Q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 polonicum 2 (Q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 dicoccum 4 (Q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 durum (Q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 compactum (Q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 sphaerococcum (Q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 spelta 4 (Iran; Q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 spelta 5 (Iran; Q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 dicoccoides 2 (q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 dicoccoides 3 (q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 dicoccoides 1 (q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 dicoccum 3 (q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 spelta 1 (Eur; q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 dicoccoides 4 (q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 spelta 2 (Eur; q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 macha (q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 dicoccum 1 (q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 dicoccum 2 (q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 spelta 3 (Eur; q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 urartu (q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG
 monococcum (q) CACTTCGCCCACATTATCATAGTAGTAGTTTCTTTTATCAAATGCCATTG

polonicum 1 (Q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 aestivum (Q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 carthlicum (Q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 polonicum 2 (Q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 dicoccum 4 (Q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 durum (Q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 compactum (Q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 sphaerococcum (Q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 spelta 4 (Iran; Q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 spelta 5 (Iran; Q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 dicoccoides 2 (q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 dicoccoides 3 (q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 dicoccoides 1 (q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 dicoccum 3 (q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 spelta 1 (Eur; q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 dicoccoides 4 (q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 spelta 2 (Eur; q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 macha (q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 dicoccum 1 (q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 dicoccum 2 (q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 spelta 3 (Eur; q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 urartu (q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC
 monococcum (q) ACAAGATTCAGTTGAAATGAAATTTTACAGACTGCTCATGAACCTTGACAC

polonicum 1 (Q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 aestivum (Q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 carthlicum (Q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 polonicum 2 (Q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 dicoccum 4 (Q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 durum (Q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 compactum (Q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 sphaerococcum (Q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 spelta 4 (Iran; Q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 spelta 5 (Iran; Q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 dicoccoides 2 (q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 dicoccoides 3 (q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 dicoccoides 1 (q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 dicoccum 3 (q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 spelta 1 (Eur; q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 dicoccoides 4 (q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 spelta 2 (Eur; q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 macha (q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 dicoccum 1 (q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 dicoccum 2 (q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 spelta 3 (Eur; q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 urartu (q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA
 monococcum (q) TAATTAGTAGTAGATGTGACAGGGCAGCTGTTTCATGCTGTGGACGTTTTAA

polonicum 1 (Q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 aestivum (Q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 carthlicum (Q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 polonicum 2 (Q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 dicoccum 4 (Q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 durum (Q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 compactum (Q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 sphaerococcum (Q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 spelta 4 (Iran; Q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 spelta 5 (Iran; Q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 dicoccoides 2 (q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 dicoccoides 3 (q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 dicoccoides 1 (q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 dicoccum 3 (q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 spelta 1 (Eur; q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 dicoccoides 4 (q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 spelta 2 (Eur; q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 macha (q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 dicoccum 1 (q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 dicoccum 2 (q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 spelta 3 (Eur; q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 urartu (q) TTAGCCTGTTCGCAGGTAATCATC---TTAGATTACCCCTTTTGAAACATA
 monococcum (q) TTAGCCTGTTCGCAGGTAATCATCATCTTAGATTATCCCTTTTGAACATA

polonicum 1 (Q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 aestivum (Q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 carthlicum (Q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 polonicum 2 (Q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 dicoccum 4 (Q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 durum (Q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 compactum (Q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 sphaerococcum (Q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 spelta 4 (Iran; Q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 spelta 5 (Iran; Q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 dicoccoides 2 (q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 dicoccoides 3 (q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 dicoccoides 1 (q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 dicoccum 3 (q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 spelta 1 (Eur; q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 dicoccoides 4 (q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 spelta 2 (Eur; q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 macha (q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 dicoccum 1 (q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 dicoccum 2 (q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 spelta 3 (Eur; q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 urartu (q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT
 monococcum (q) ATCTTAGCTGGTTTtagggtagggTCATCAAGTTAATCCATGTTGTTAGTT

polonicum 1 (Q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 aestivum (Q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 carthlicum (Q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 polonicum 2 (Q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 dicoccum 4 (Q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 durum (Q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 compactum (Q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 sphaerococcum (Q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 spelta 4 (Iran; Q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 spelta 5 (Iran; Q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 dicoccoides 2 (q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 dicoccoides 3 (q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 dicoccoides 1 (q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 dicoccum 3 (q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 spelta 1 (Eur; q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 dicoccoides 4 (q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 spelta 2 (Eur; q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 macha (q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 dicoccum 1 (q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 dicoccum 2 (q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 spelta 3 (Eur; q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 urartu (q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
 monococcum (q) GTTGGCGCGTCCTGTGTTGGTGCTGGTGAGACGTCCACTTCCCCCGACAC
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polonicum 1 (Q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
  aestivum (Q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
  carthlicum (Q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
polonicum 2 (Q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
  dicocccum 4 (Q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
    durum (Q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
    compactum (Q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
  sphaerococccum (Q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
spelta 4 (Iran; Q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
spelta 5 (Iran; Q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
  dicoccoides 2 (q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
  dicoccoides 3 (q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
  dicoccoides 1 (q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
    dicocccum 3 (q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
  spelta 1 (Eur; q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
  dicoccoides 4 (q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
  spelta 2 (Eur; q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
    macha (q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
    dicocccum 1 (q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
    dicocccum 2 (q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
  spelta 3 (Eur; q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
    urartu (q) GACTACTCGATTGCAGACATCTATTTGGAGCAACTGTTAGGCTCCACATAA
  monococccum (q) GACTACTCGATTGCAGACATCTATTTGGAGCAA-----TCCACATAA
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polonicum 1 (Q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
  aestivum (Q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
  carthlicum (Q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
polonicum 2 (Q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
  dicocccum 4 (Q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
    durum (Q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
    compactum (Q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
  sphaerococccum (Q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
spelta 4 (Iran; Q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
spelta 5 (Iran; Q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
  dicoccoides 2 (q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
  dicoccoides 3 (q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
  dicoccoides 1 (q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
    dicocccum 3 (q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
  spelta 1 (Eur; q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
  dicoccoides 4 (q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
  spelta 2 (Eur; q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
    macha (q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
    dicocccum 1 (q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
    dicocccum 2 (q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
  spelta 3 (Eur; q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
    urartu (q) GTATATGATCGAGTCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
  monococccum (q) GTATATGATCGAGCCGTCCAGACAAAATTAGTCTAATCCAATCCGTGCAC
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polonicum 1 (Q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
  aestivum (Q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
  carthlicum (Q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
polonicum 2 (Q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
  dicoccum 4 (Q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
    durum (Q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
  compactum (Q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
sphaerococcum (Q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
spelta 4 (Iran; Q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
spelta 5 (Iran; Q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
  dicoccoides 2 (q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
  dicoccoides 3 (q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
  dicoccoides 1 (q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
    dicoccum 3 (q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
  spelta 1 (Eur; q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
  dicoccoides 4 (q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
  spelta 2 (Eur; q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
    macha (q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
      dicoccum 1 (q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
      dicoccum 2 (q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
  spelta 3 (Eur; q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
    urartu (q) ATTATGGTCCAGACCCAGAATTGTCACCCTACACCTTCACACCCCTATCT
  monococcum (q) ATTATGGTCCAGACCCAGAATCGTCACCCTAC-----CT
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polonicum 1 (Q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
  aestivum (Q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
  carthlicum (Q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
polonicum 2 (Q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
  dicoccum 4 (Q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
    durum (Q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
  compactum (Q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
sphaerococcum (Q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
spelta 4 (Iran; Q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
spelta 5 (Iran; Q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
  dicoccoides 2 (q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
  dicoccoides 3 (q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
  dicoccoides 1 (q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
    dicoccum 3 (q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
  spelta 1 (Eur; q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
  dicoccoides 4 (q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
  spelta 2 (Eur; q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
    macha (q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
      dicoccum 1 (q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
      dicoccum 2 (q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
  spelta 3 (Eur; q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
    urartu (q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATACCCACATTATCATCA
  monococcum (q) CCGTTGAGCTGTGGTCTCATCTCATATACCTGATATCCACATTATCATCA
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polonicum 1 (Q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 aestivum (Q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 carthlicum (Q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 polonicum 2 (Q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 dicoccum 4 (Q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 durum (Q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 compactum (Q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 sphaerococcum (Q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 spelta 4 (Iran; Q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 spelta 5 (Iran; Q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 dicoccoides 2 (q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 dicoccoides 3 (q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 dicoccoides 1 (q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 dicoccum 3 (q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 spelta 1 (Eur; q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 dicoccoides 4 (q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 spelta 2 (Eur; q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 macha (q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 dicoccum 1 (q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 dicoccum 2 (q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 spelta 3 (Eur; q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 urartu (q) CACGCGCAGGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCTG
 monococcum (q) CACGCGCAGGTACATATATCTGGGCCTGTTTGACAGCGAAGTTGAAGCTG

polonicum 1 (Q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 aestivum (Q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 carthlicum (Q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 polonicum 2 (Q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 dicoccum 4 (Q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 durum (Q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 compactum (Q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 sphaerococcum (Q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATT-GGGCTCACAAAA-CT
 spelta 4 (Iran; Q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 spelta 5 (Iran; Q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 dicoccoides 2 (q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 dicoccoides 3 (q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 dicoccoides 1 (q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 dicoccum 3 (q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 spelta 1 (Eur; q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 dicoccoides 4 (q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 spelta 2 (Eur; q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 macha (q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 dicoccum 1 (q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 dicoccum 2 (q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 spelta 3 (Eur; q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 urartu (q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAA-CT
 monococcum (q) CAAGGTACTTTGATTTGCGCTGATCATTAAACATTTGGGCTCACAAAACT

polonicum 1 (Q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 aestivum (Q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 carthlicum (Q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 polonicum 2 (Q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 dicoccum 4 (Q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 durum (Q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 compactum (Q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 sphaerococcum (Q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 spelta 4 (Iran; Q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 spelta 5 (Iran; Q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 dicoccoides 2 (q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 dicoccoides 3 (q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 dicoccoides 1 (q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 dicoccum 3 (q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 spelta 1 (Eur; q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 dicoccoides 4 (q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 spelta 2 (Eur; q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 macha (q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 dicoccum 1 (q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 dicoccum 2 (q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 spelta 3 (Eur; q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 urartu (q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC
 monococcum (q) TCCTTAATCTTTGCTCACTCACTCTAGTGTGTCATGTTGGATTTGGTAGGGC

polonicum 1 (Q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 aestivum (Q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 carthlicum (Q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 polonicum 2 (Q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 dicoccum 4 (Q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 durum (Q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 compactum (Q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 sphaerococcum (Q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 spelta 4 (Iran; Q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 spelta 5 (Iran; Q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 dicoccoides 2 (q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 dicoccoides 3 (q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 dicoccoides 1 (q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 dicoccum 3 (q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 spelta 1 (Eur; q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 dicoccoides 4 (q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 spelta 2 (Eur; q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 macha (q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 dicoccum 1 (q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 dicoccum 2 (q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 spelta 3 (Eur; q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 urartu (q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
 monococcum (q) GTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT

polonicum 1 (Q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 aestivum (Q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 carthlicum (Q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 polonicum 2 (Q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 dicoccum 4 (Q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 durum (Q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 compactum (Q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 sphaerococcum (Q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 spelta 4 (Iran; Q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 spelta 5 (Iran; Q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 dicoccoides 2 (q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 dicoccoides 3 (q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 dicoccoides 1 (q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCTGAAAATGAG
 dicoccum 3 (q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 spelta 1 (Eur; q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 dicoccoides 4 (q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 spelta 2 (Eur; q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCTGAAAATGAG
 macha (q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCTGAAAATGAG
 dicoccum 1 (q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCTGAAAATGAG
 dicoccum 2 (q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCTGAAAATGAG
 spelta 3 (Eur; q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCTGAAAATGAG
 urartu (q) TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCTGAAAATGAG
 monococcum (q) TCGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAG
 * *****

polonicum 1 (Q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 aestivum (Q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 carthlicum (Q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 polonicum 2 (Q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 dicoccum 4 (Q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 durum (Q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 compactum (Q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 sphaerococcum (Q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 spelta 4 (Iran; Q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 spelta 5 (Iran; Q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 dicoccoides 2 (q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 dicoccoides 3 (q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 dicoccoides 1 (q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 dicoccum 3 (q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 spelta 1 (Eur; q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 dicoccoides 4 (q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 spelta 2 (Eur; q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 macha (q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 dicoccum 1 (q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 dicoccum 2 (q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 spelta 3 (Eur; q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 urartu (q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 monococcum (q) GGTACTACTACAATCGGTCTCACCTGTGCAATTTCTCCAATCACACCCAA
 ***** **** ***** ***** ***** ***** ***** ***** *****

polonicum 1 (Q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 aestivum (Q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 carthlicum (Q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 polonicum 2 (Q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 dicoccum 4 (Q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 durum (Q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 compactum (Q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 sphaerococcum (Q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 spelta 4 (Iran; Q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 spelta 5 (Iran; Q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 dicoccoides 2 (q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 dicoccoides 3 (q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 dicoccoides 1 (q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 dicoccum 3 (q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 spelta 1 (Eur; q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 dicoccoides 4 (q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 spelta 2 (Eur; q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 macha (q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 dicoccum 1 (q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 dicoccum 2 (q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 spelta 3 (Eur; q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 urartu (q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG
 monococcum (q) GTCTTATCTCATCGATATCGTTGTTGTTTTCTTAGCAATTGTTGATGCTG

polonicum 1 (Q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 aestivum (Q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 carthlicum (Q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 polonicum 2 (Q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 dicoccum 4 (Q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 durum (Q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 compactum (Q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 sphaerococcum (Q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 spelta 4 (Iran; Q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 spelta 5 (Iran; Q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 dicoccoides 2 (q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 dicoccoides 3 (q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 dicoccoides 1 (q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 dicoccum 3 (q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 spelta 1 (Eur; q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 dicoccoides 4 (q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 spelta 2 (Eur; q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 macha (q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 dicoccum 1 (q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 dicoccum 2 (q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 spelta 3 (Eur; q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 urartu (q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC
 monococcum (q) ATGCTCTTGACTTGGATCTGCGGATGTCGCAACCCACCGCGCACGATCCC

polonicum 1 (Q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 aestivum (Q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 carthlicum (Q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 polonicum 2 (Q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 dicoccum 4 (Q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 durum (Q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 compactum (Q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 sphaerococcum (Q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 spelta 4 (Iran; Q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 spelta 5 (Iran; Q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 dicoccoides 2 (q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 dicoccoides 3 (q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 dicoccoides 1 (q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 dicoccum 3 (q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 spelta 1 (Eur; q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 dicoccoides 4 (q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 spelta 2 (Eur; q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 macha (q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 dicoccum 1 (q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 dicoccum 2 (q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 spelta 3 (Eur; q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 urartu (q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA
 monococcum (q) AAGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGA



polonicum 1 (Q) ATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 aestivum (Q) ATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 carthlicum (Q) ATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 polonicum 2 (Q) ATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 dicoccum 4 (Q) ATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 durum (Q) ATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 compactum (Q) ATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 sphaerococcum (Q) ATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 spelta 4 (Iran; Q) ATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 spelta 5 (Iran; Q) ATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 dicoccoides 2 (q) ATCGTCAACCACAATGATCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 dicoccoides 3 (q) ATCGTCAACCACAATGGTCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 dicoccoides 1 (q) ATCGTCAACCACAATGGTCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 dicoccum 3 (q) ATCGTCAACCACAATGGTCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 spelta 1 (Eur; q) ATCGTCAACCACAATGGTCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 dicoccoides 4 (q) ATCGTCAACCACAATGGTCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 spelta 2 (Eur; q) ATCGTCAACCACAATGGTCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 macha (q) ATCGTCAACCACAATGGTCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 dicoccum 1 (q) ATCGTCAACCACAATGGTCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 dicoccum 2 (q) ATCGTCAACCACAATGGTCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 spelta 3 (Eur; q) ATCGTCAACCACAATGGTCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 urartu (q) ATCGTCAACCACAATGGTCTCTTCTCAGGTAAAGAAACAAAATTATGTTT
 monococcum (q) ATCGTCAACCACAATGGTCTCTTCTCAGGTAAAGAAACAAAATTATGTTT



polonicum 1 (Q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTTGCTGT
 aestivum (Q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTTGCTGT
 carthlicum (Q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTTGCTGT
 polonicum 2 (Q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTTGCTGT
 dicoccum 4 (Q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTTGCTGT
 durum (Q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTTGCTGT
 compactum (Q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTTGCTGT
 sphaerococcum (Q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTTGCTGT
 spelta 4 (Iran; Q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTTGCTGT
 spelta 5 (Iran; Q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTTGCTGT
 dicoccoides 2 (q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCAAATAGAAAATTTGCTGT
 dicoccoides 3 (q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCGAATAGAAAATTTGCTGT
 dicoccoides 1 (q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCGAATAGAAAATTTGCTGT
 dicoccum 3 (q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCGAATAGAAAATTTGCTGT
 spelta 1 (Eur; q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCGAATAGAAAATTTGCTGT
 dicoccoides 4 (q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCGAATAGAAAATTTGCTGT
 spelta 2 (Eur; q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCGAATAGAAAATTTGCTGT
 macha (q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCGAATAGAAAATTTGCTGT
 dicoccum 1 (q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCGAATAGAAAATTTGCTGT
 dicoccum 2 (q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCGAATAGAAAATTTGCTGT
 spelta 3 (Eur; q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCGAATAGAAAATTTGCTGT
 urartu (q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCGAATAGAAAATTTGCTGT
 monococcum (q) AGCACTAGCTAATTCAGTGGTTAGATTTGCTCGAATAGAAAATTTGCTGT

polonicum 1 (Q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 aestivum (Q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 carthlicum (Q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 polonicum 2 (Q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 dicoccum 4 (Q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 durum (Q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 compactum (Q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 sphaerococcum (Q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 spelta 4 (Iran; Q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 spelta 5 (Iran; Q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 dicoccoides 2 (q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 dicoccoides 3 (q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 dicoccoides 1 (q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 dicoccum 3 (q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 spelta 1 (Eur; q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 dicoccoides 4 (q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 spelta 2 (Eur; q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 macha (q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 dicoccum 1 (q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 dicoccum 2 (q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 spelta 3 (Eur; q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 urartu (q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC
 monococcum (q) TGGCCCAGTTGTGTCGGTGGATGAGATATTATTGATCCAGGTCGTATGGC

polonicum 1 (Q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 aestivum (Q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 carthlicum (Q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 polonicum 2 (Q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 dicoccum 4 (Q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 durum (Q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 compactum (Q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 sphaerococcum (Q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 spelta 4 (Iran; Q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 spelta 5 (Iran; Q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 dicoccoides 2 (q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 dicoccoides 3 (q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 dicoccoides 1 (q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 dicoccum 3 (q) ATTTACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 spelta 1 (Eur; q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 dicoccoides 4 (q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 spelta 2 (Eur; q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 macha (q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 dicoccum 1 (q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 dicoccum 2 (q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 spelta 3 (Eur; q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 urartu (q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 monococcum (q) ATATACTCTGTCCTAAACTTACGATATTTGTGCCTTTTGATATCGCTGTA
 ** *****

polonicum 1 (Q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 aestivum (Q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 carthlicum (Q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 polonicum 2 (Q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 dicoccum 4 (Q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 durum (Q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 compactum (Q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 sphaerococcum (Q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 spelta 4 (Iran; Q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 spelta 5 (Iran; Q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 dicoccoides 2 (q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 dicoccoides 3 (q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 dicoccoides 1 (q) GCCAATGAGCTCGTCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 dicoccum 3 (q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 spelta 1 (Eur; q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 dicoccoides 4 (q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 spelta 2 (Eur; q) GCCAATGAGCTCGTCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 macha (q) GCCAATGAGCTCGTCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 dicoccum 1 (q) GCCAATGAGCTCGTCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 dicoccum 2 (q) GCCAATGAGCTCGTCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 spelta 3 (Eur; q) GCCAATGAGCTCGTCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 urartu (q) GCCAATGAGCTCGTCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG
 monococcum (q) GCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGG

polonicum 1 (Q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 aestivum (Q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 carthlicum (Q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 polonicum 2 (Q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 dicoccum 4 (Q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 durum (Q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 compactum (Q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 sphaerococcum (Q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 spelta 4 (Iran; Q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 spelta 5 (Iran; Q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 dicoccoides 2 (q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 dicoccoides 3 (q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 dicoccoides 1 (q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 dicoccum 3 (q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 spelta 1 (Eur; q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 dicoccoides 4 (q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 spelta 2 (Eur; q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 macha (q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 dicoccum 1 (q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 dicoccum 2 (q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 spelta 3 (Eur; q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 urartu (q) CAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC
 monococcum (q) CAGTAGCTCCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTTCATGGC

polonicum 1 (Q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 aestivum (Q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 carthlicum (Q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 polonicum 2 (Q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 dicoccum 4 (Q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 durum (Q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 compactum (Q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 sphaerococcum (Q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 spelta 4 (Iran; Q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 spelta 5 (Iran; Q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 dicoccoides 2 (q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 dicoccoides 3 (q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 dicoccoides 1 (q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 dicoccum 3 (q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCACC
 spelta 1 (Eur; q) TTCTACCCGAACGTACAGGTATCATCATCACTACAAGAACGACCACCTCC
 dicoccoides 4 (q) TTCTACCCGAACGTACAGGTATCATCATCACTACAAGAACGACCACCTCC
 spelta 2 (Eur; q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 macha (q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 dicoccum 1 (q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 dicoccum 2 (q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 spelta 3 (Eur; q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 urartu (q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC
 monococcum (q) TTCTACCCGAACGTACAGGTATCATCATCACTACGAGAACGACCACCTCC



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polonicum 1 (Q)	TCCTCCTCCTCCTCCTC-----TGCTTGGTGCGCTGCTCCACCAGCTTA
aestivum (Q)	TCCTCCTCCTCCTCCTC-----TGCTTGGTGCGCTGCTCCACCAGCTTA
carthlicum (Q)	TCCTCCTCCTCCTCCTC-----TGCTTGGTGCGCTGCTCCACCAGCTTA
polonicum 2 (Q)	TCCTCCTCCTCCTCCTC-----TGCTTGGTGCGCTGCTCCACCAGCTTA
dicoccum 4 (Q)	TCCTCCTCCTCCTCCTC-----TGCTTGGTGCGCTGCTCCACCAGCTTA
durum (Q)	TCCTCCTCCTCCTCCTC-----TGCTTGGTGCGCTGCTCCACCAGCTTA
compactum (Q)	TCCTCCTCCTCCTCCTC-----TGCTTGGTGCGCTGCTCCACCAGCTTA
sphaerococcum (Q)	TCCTCCTCCTCCTCCTC-----TGCTTGGTGCGCTGCTCCACCAGCTTA
spelta 4 (Iran; Q)	TCCTCCTCCTCCTCCTC-----TGCTTGGTGCGCTGCTCCACCAGCTTA
spelta 5 (Iran; Q)	TCCTCCTCCTCCTCCTC-----TGCTTGGTGCGCTGCTCCACCAGCTTA
dicoccoides 2 (q)	TCCTCCTCCTCCTCCTC-----TGCTTGGTGCGCTGCTCCACCAGCTTA
dicoccoides 3 (q)	TCCTCCTC-----TGCTTGGTGCGCTGCTCCACCAGCTTA
dicoccoides 1 (q)	TCCTCCTCCTCCTCCTCCTC---TGCTTGGTGCGCTGCTCCACCAGCTTA
dicoccum 3 (q)	TCCTCCTCCTCCTCCTCCTC---TGCTTGGTGCGCTGCTCCACCAGCTTA
spelta 1 (Eur; q)	TCCTCCTCCTCCTCCTCCTC---TGCTTGGTGCGCTGCTCCACCAGCTTA
dicoccoides 4 (q)	TCCTCCTCCTCCTCCTCCTC---TGCTTGGTGCGCTGCTCCACCAGCTTA
spelta 2 (Eur; q)	TCCTCCTCCTCCTCCTCCTCCTCTGCTTGGTGCGCTGCTCCACCAGCTTA
macha (q)	TCCTCCTCCTCCTCCTCCTCCTCTGCTTGGTGCGCTGCTCCACCAGCTTA
dicoccum 1 (q)	TCCTCCTCCTCCTCCTCCTCCTCTGCTTGGTGCGCTGCTCCACCAGCTTA
dicoccum 2 (q)	TCCTCCTCCTCCTCCTCCTCCTCTGCTTGGTGCGCTGCTCCACCAGCTTA
spelta 3 (Eur; q)	TCCTCCTCCTCCTCCTCCTCCTCTGCTTGGTGCGCTGCTCCACCAGCTTA
urartu (q)	TCCTCCTCCTCCTCCTCCTCCTCTGCTTGGTGCGCTGCTCCACCAGCTTA
monococcum (q)	TCCTCCTCCTC-----TGCTTGGTGCGCTGCTCCACCAGCTTA

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polonicum 1 (Q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
aestivum (Q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
carthlicum (Q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
polonicum 2 (Q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
dicoccum 4 (Q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
durum (Q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
compactum (Q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
sphaerococcum (Q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
spelta 4 (Iran; Q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
spelta 5 (Iran; Q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
dicoccoides 2 (q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
dicoccoides 3 (q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
dicoccoides 1 (q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
dicoccum 3 (q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
spelta 1 (Eur; q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
dicoccoides 4 (q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
spelta 2 (Eur; q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
macha (q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
dicoccum 1 (q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
dicoccum 2 (q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
spelta 3 (Eur; q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
urartu (q)	CTGAAACTGTTGCTACCACTGAATAATGTTTCTGAAGAAACTGCTAATAA
monococcum (q)	CTGAAACTGTTGCTACCACTGAACAATGTTTCTGAAGAAACTGCTAATAA

polonicum 1 (Q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 aestivum (Q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 carthlicum (Q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 polonicum 2 (Q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 dicoccum 4 (Q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 durum (Q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 compactum (Q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 sphaerococcum (Q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 spelta 4 (Iran; Q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 spelta 5 (Iran; Q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 dicoccoides 2 (q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 dicoccoides 3 (q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 dicoccoides 1 (q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 dicoccum 3 (q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 spelta 1 (Eur; q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 dicoccoides 4 (q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 spelta 2 (Eur; q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 macha (q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 dicoccum 1 (q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 dicoccum 2 (q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 spelta 3 (Eur; q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 urartu (q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT
 monococcum (q) CATTTCAGTTTTTCGACAAGTTCGTTCCCTGAAATTAAGGTTTCCATGCTT

polonicum 1 (Q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 aestivum (Q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 carthlicum (Q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 polonicum 2 (Q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 dicoccum 4 (Q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 durum (Q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 compactum (Q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 sphaerococcum (Q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 spelta 4 (Iran; Q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 spelta 5 (Iran; Q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 dicoccoides 2 (q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 dicoccoides 3 (q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 dicoccoides 1 (q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 dicoccum 3 (q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 spelta 1 (Eur; q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 dicoccoides 4 (q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 spelta 2 (Eur; q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 macha (q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 dicoccum 1 (q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 dicoccum 2 (q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 spelta 3 (Eur; q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 urartu (q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCAA
 monococcum (q) CTTTCCTAAAATAATCACGCCTGCTCTCCTAAAACATCTACAGGTGCTA

polonicum 1 (Q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 aestivum (Q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 carthlicum (Q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 polonicum 2 (Q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 dicoccum 4 (Q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 durum (Q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 compactum (Q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 sphaerococcum (Q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 spelta 4 (Iran; Q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 spelta 5 (Iran; Q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 dicoccoides 2 (q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 dicoccoides 3 (q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 dicoccoides 1 (q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 dicoccum 3 (q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 spelta 1 (Eur; q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 dicoccoides 4 (q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 spelta 2 (Eur; q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 macha (q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 dicoccum 1 (q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 dicoccum 2 (q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 spelta 3 (Eur; q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 urartu (q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC
 monococcum (q) TGTGTGGTAGTACCAGAGTACTTACTAGATGTGGGCACTACTGTTTGCCC

polonicum 1 (Q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 aestivum (Q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGGCGCCCTCCGGTTC
 carthlicum (Q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 polonicum 2 (Q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 dicoccum 4 (Q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 durum (Q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 compactum (Q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 sphaerococcum (Q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 spelta 4 (Iran; Q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 spelta 5 (Iran; Q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 dicoccoides 2 (q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 dicoccoides 3 (q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 dicoccoides 1 (q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 dicoccum 3 (q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 spelta 1 (Eur; q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 dicoccoides 4 (q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 spelta 2 (Eur; q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 macha (q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 dicoccum 1 (q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 dicoccum 2 (q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 spelta 3 (Eur; q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 urartu (q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC
 monococcum (q) TGTGAGCTCGCACCACCTTTTCGAAAAAACTGCAGTGCGCCCTCCGGTTC

polonicum 1 (Q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 aestivum (Q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 carthlicum (Q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 polonicum 2 (Q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 dicoccum 4 (Q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 durum (Q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 compactum (Q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 sphaerococcum (Q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 spelta 4 (Iran; Q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 spelta 5 (Iran; Q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 dicoccoides 2 (q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 dicoccoides 3 (q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCACCT
 dicoccoides 1 (q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 dicoccum 3 (q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 spelta 1 (Eur; q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 dicoccoides 4 (q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 spelta 2 (Eur; q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 macha (q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 dicoccum 1 (q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 dicoccum 2 (q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 spelta 3 (Eur; q) TTGCAGTTCCATCCGTCCCCCATGGCACAGCTTTAGATGCAGCAGCAGCT
 urartu (q) TTGCAGTTCCATCCGTCCCCCATGACACAGCTTTAGATGCAGCAGCAGCT
 monococcum (q) TTGCAGTTCCATCCGTCCCCCATGACACAGCTTTAGATGCAGCAGCAGCT
 ***** **

polonicum 1 (Q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 aestivum (Q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 carthlicum (Q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 polonicum 2 (Q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 dicoccum 4 (Q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 durum (Q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 compactum (Q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 sphaerococcum (Q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 spelta 4 (Iran; Q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 spelta 5 (Iran; Q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 dicoccoides 2 (q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 dicoccoides 3 (q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 dicoccoides 1 (q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 dicoccum 3 (q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 spelta 1 (Eur; q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 dicoccoides 4 (q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 spelta 2 (Eur; q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 macha (q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 dicoccum 1 (q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 dicoccum 2 (q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 spelta 3 (Eur; q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 urartu (q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 monococcum (q) TGCTTAGTTGTAGTACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGC
 ***** **

polonicum 1 (Q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 aestivum (Q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 carthlicum (Q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 polonicum 2 (Q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 dicoccum 4 (Q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 durum (Q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 compactum (Q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 sphaerococcum (Q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 spelta 4 (Iran; Q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 spelta 5 (Iran; Q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 dicoccoides 2 (q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 dicoccoides 3 (q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 dicoccoides 1 (q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 dicoccum 3 (q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 spelta 1 (Eur; q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 dicoccoides 4 (q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 spelta 2 (Eur; q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 macha (q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 dicoccum 1 (q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 dicoccum 2 (q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 spelta 3 (Eur; q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 urartu (q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC
 monococcum (q) CACTGTGCATTACATGAAAGCAAAGCTTTGGTGCATGCACGGCCATGAC

polonicum 1 (Q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 aestivum (Q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 carthlicum (Q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 polonicum 2 (Q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 dicoccum 4 (Q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 durum (Q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 compactum (Q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 sphaerococcum (Q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 spelta 4 (Iran; Q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 spelta 5 (Iran; Q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 dicoccoides 2 (q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 dicoccoides 3 (q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 dicoccoides 1 (q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 dicoccum 3 (q) TTGACGCTCTATCTCACTGCCGGTGCTGGTGCTGGTGCAGGTGCAGGTGC
 spelta 1 (Eur; q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 dicoccoides 4 (q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 spelta 2 (Eur; q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 macha (q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 dicoccum 1 (q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 dicoccum 2 (q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 spelta 3 (Eur; q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 urartu (q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 monococcum (q) TTGACGCTCTATCTCACTGC-----TGGTGCTGGTGCAGGTGCAGGTGC
 ***** ** ***** *****

polonicum 1 (Q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 aestivum (Q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 carthlicum (Q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 polonicum 2 (Q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 dicoccum 4 (Q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 durum (Q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 compactum (Q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 sphaerococcum (Q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 spelta 4 (Iran; Q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 spelta 5 (Iran; Q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 dicoccoides 2 (q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 dicoccoides 3 (q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 dicoccoides 1 (q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 dicoccum 3 (q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 spelta 1 (Eur; q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 dicoccoides 4 (q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 spelta 2 (Eur; q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 macha (q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 dicoccum 1 (q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 dicoccum 2 (q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAACAGCCGTCGTCCTTCCCC
 spelta 3 (Eur; q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 urartu (q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC
 monococcum (q) AGGAGAGGCCCATGGAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCC

polonicum 1 (Q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 aestivum (Q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 carthlicum (Q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 polonicum 2 (Q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 dicoccum 4 (Q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 durum (Q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 compactum (Q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 sphaerococcum (Q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 spelta 4 (Iran; Q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 spelta 5 (Iran; Q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 dicoccoides 2 (q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 dicoccoides 3 (q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 dicoccoides 1 (q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 dicoccum 3 (q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 spelta 1 (Eur; q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 dicoccoides 4 (q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 spelta 2 (Eur; q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 macha (q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 dicoccum 1 (q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 dicoccum 2 (q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 spelta 3 (Eur; q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 urartu (q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC
 monococcum (q) GGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCC

polonicum 1 (Q) GTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGCCGCCGGCG
 aestivum (Q) GTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGCCGCCGGCG
 carthlicum (Q) GTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGCCGCCGGCG
 polonicum 2 (Q) GTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGCCGCCGGG
 dicoccum 4 (Q) GTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGCCGCCGGCG
 durum (Q) GTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGCCGCCGGCG
 compactum (Q) GTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGCCGCCGGCG
 sphaerococcum (Q) GTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGCCGCCGGCG
 spelta 4 (Iran; Q) GTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGCCGCCGGCG
 spelta 5 (Iran; Q) GTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGCCGCCGGCG
 dicoccoides 2 (q) GTTGCTTTACGCTGCAGCATCATCAGGATTCTCTACCGCCGCCGCCGGCG
 dicoccoides 3 (q) GTTGCTTTACGCTGCAGCATCATCAGGATTCTCTACCGCCGCCGCCGGCG
 dicoccoides 1 (q) GTTGCTTTACGCTGCAGCATCATCAGGATTCTCTACCGCCGCCGCCGGCG
 dicoccum 3 (q) GTTGCTTTACGCTGCAGCATCATCAGGATTCTCTACCGCCGCCGCCGGCG
 spelta 1 (Eur; q) GCCGC-----CGGCAGCATCATCAGGATTCTCTACCGCCGCCGCCGGCG
 dicoccoides 4 (q) GTTGCTTTACGCTGCAGCATCATCAGGATTCTCTACCGCCGCCGCCGGCG
 spelta 2 (Eur; q) GTTGCTTTACGCTGCAGCATCATCAGGATTCTCTACCGCCGCCGCCGGCG
 macha (q) GTTGCTTTACGCTGCAGCATCATCAGGATTCTCTACCGCCGCCGCCGGCG
 dicoccum 1 (q) GTTGCTTTACGCTGCAGCATCATCAGGATTCTCTACCGCCGCCGCCGGCG
 dicoccum 2 (q) GTTGCTTTACGCTGCAGCATCATCAGGATTTTCTACCGCCGCCGCCGGCG
 spelta 3 (Eur; q) GTTGCTTTACGCTGCAGCATCATCAGGATTCTCTACCGCCGCCGCCGGCG
 urartu (q) GTTGCTTTACGCTGCAGCATCATCAGGATTCTCTACCGCCGCCGCCGGCG
 monococcum (q) GTTGCTTTACGCTGCAGCATCATCAGGATTCTCTACCGCCGCCGCCGGCG
 * * * ***** ***** ***** *

polonicum 1 (Q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 aestivum (Q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 carthlicum (Q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 polonicum 2 (Q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 dicoccum 4 (Q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 durum (Q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 compactum (Q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 sphaerococcum (Q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 spelta 4 (Iran; Q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 spelta 5 (Iran; Q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 dicoccoides 2 (q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 dicoccoides 3 (q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 dicoccoides 1 (q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 dicoccum 3 (q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 spelta 1 (Eur; q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 dicoccoides 4 (q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 spelta 2 (Eur; q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 macha (q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 dicoccum 1 (q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 dicoccum 2 (q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 spelta 3 (Eur; q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 urartu (q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC
 monococcum (q) CGAACCTCGCCCCGCCGCCGCCGTACCCGGACCACCACCGTTTCTACTTC

polonicum 1 (Q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 aestivum (Q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 carthlicum (Q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 polonicum 2 (Q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 dicoccum 4 (Q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 durum (Q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 compactum (Q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 sphaerococcum (Q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 spelta 4 (Iran; Q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 spelta 5 (Iran; Q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 dicoccoides 2 (q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 dicoccoides 3 (q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 dicoccoides 1 (q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 dicoccum 3 (q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 spelta 1 (Eur; q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 dicoccoides 4 (q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 spelta 2 (Eur; q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 macha (q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 dicoccum 1 (q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 dicoccum 2 (q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 spelta 3 (Eur; q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 urartu (q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG
 monococcum (q) CCCC GCCCGCCG GACA AACTGAAGCTGGCCGTTGTGACCAGACGGCGGTGG

polonicum 1 (Q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 aestivum (Q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 carthlicum (Q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 polonicum 2 (Q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 dicoccum 4 (Q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 durum (Q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 compactum (Q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 sphaerococcum (Q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 spelta 4 (Iran; Q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 spelta 5 (Iran; Q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 dicoccoides 2 (q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 dicoccoides 3 (q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 dicoccoides 1 (q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 dicoccum 3 (q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 spelta 1 (Eur; q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 dicoccoides 4 (q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 spelta 2 (Eur; q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 macha (q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 dicoccum 1 (q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 dicoccum 2 (q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 spelta 3 (Eur; q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 urartu (q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG
 monococcum (q) GTGCGCGCGGTGCGAGGTGTTGCTCCTCGTCGTCGGTAACGCTTGTTGTG

polonicum 1 (Q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 aestivum (Q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 carthlicum (Q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 polonicum 2 (Q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 dicoccum 4 (Q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 durum (Q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 compactum (Q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 sphaerococcum (Q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 spelta 4 (Iran; Q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 spelta 5 (Iran; Q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 dicoccoides 2 (q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 dicoccoides 3 (q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 dicoccoides 1 (q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 dicoccum 3 (q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 spelta 1 (Eur; q) AAAC TATAATCGGAGAGGGATGACATTGCCAGGCCATGTGTGGTGACACT
 dicoccoides 4 (q) AAAC TATAATCGGAGAGGGATGACATTGCCAGGCCATGTGTGGTGACACT
 spelta 2 (Eur; q) AAAC TATAATCGGAGAGGGATGACATTGCCAGGCCATGTGTGGTGACACT
 macha (q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 dicoccum 1 (q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 dicoccum 2 (q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 spelta 3 (Eur; q) AAAC TATAATCGGAGAGGGATGACATTGCCAGGCCATGTGTGGTGACACT
 urartu (q) AAAC TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 monococcum (q) AAAT TATAATCGGAGAGAGATGACATTGCCAGGCCATGTGTGGTGACACT
 *** *****

polonicum 1 (Q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 aestivum (Q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 carthlicum (Q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 polonicum 2 (Q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 dicoccum 4 (Q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 durum (Q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 compactum (Q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 sphaerococcum (Q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 spelta 4 (Iran; Q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 spelta 5 (Iran; Q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 dicoccoides 2 (q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 dicoccoides 3 (q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 dicoccoides 1 (q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 dicoccum 3 (q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 spelta 1 (Eur; q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 dicoccoides 4 (q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 spelta 2 (Eur; q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 macha (q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 dicoccum 1 (q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 dicoccum 2 (q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 spelta 3 (Eur; q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 urartu (q) ACTGGCTGGTCTCTCGCCGCCTCGCCATGATCGGGATCACGCGGATCATG
 monococcum (q) ACTGGCTGGTCTCTC CGCCGCCTCGCCATGATCGGGATCACGCGGATCATG

polonicum 1 (Q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 aestivum (Q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 carthlicum (Q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 polonicum 2 (Q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 dicoccum 4 (Q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 durum (Q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 compactum (Q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 sphaerococcum (Q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 spelta 4 (Iran; Q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 spelta 5 (Iran; Q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 dicoccoides 2 (q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 dicoccoides 3 (q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 dicoccoides 1 (q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 dicoccum 3 (q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 spelta 1 (Eur; q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 dicoccoides 4 (q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 spelta 2 (Eur; q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 macha (q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 dicoccum 1 (q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 dicoccum 2 (q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 spelta 3 (Eur; q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 urartu (q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT
 monococcum (q) GCTGTTCAATTAGATTCTCATGTATCCAATGTTCAAGTTTCCCAAACGGTT

polonicum 1 (Q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 aestivum (Q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 carthlicum (Q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 polonicum 2 (Q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 dicoccum 4 (Q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 durum (Q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 compactum (Q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 sphaerococcum (Q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 spelta 4 (Iran; Q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 spelta 5 (Iran; Q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 dicoccoides 2 (q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 dicoccoides 3 (q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 dicoccoides 1 (q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 dicoccum 3 (q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 spelta 1 (Eur; q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 dicoccoides 4 (q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 spelta 2 (Eur; q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 macha (q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 dicoccum 1 (q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 dicoccum 2 (q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 spelta 3 (Eur; q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 urartu (q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACGGT
 monococcum (q) GAAAAAAGTTTGAATTTGTGATGGCAAATTCATGCATGGGTCGCACAGT



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polonicum 1 (Q) GCGCCCTTGCACAAGCGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 aestivum (Q) GCGCCCTTGCACAAGCGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 carthlicum (Q) GCGCCCTTGCACAAGCGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 polonicum 2 (Q) GCGCCCTTGCACAAGCGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 dicoccum 4 (Q) GCGCCCTTGCACAAGCGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 durum (Q) GCGCCCTTGCACAAGCGCGGGGAAGCACTCTGTKGTTTTACAGCAGTCCG
 compactum (Q) GCGCCCTTGCACAAGCGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 sphaerococcum (Q) GCGCCCTTGCACAAGCGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 spelta 4 (Iran; Q) GCGCCCTTGCACAAGCGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 spelta 5 (Iran; Q) GCGCCCTTGCACAAGCGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 dicoccoides 2 (q) GCGCCCTTGCACAAGAGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 dicoccoides 3 (q) GCGCCCTTGCACAAGAGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 dicoccoides 1 (q) GCGCCCTTGCACAAGAGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 dicoccum 3 (q) GCGCCCTTGCACAAGAGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 spelta 1 (Eur; q) GCGCCCTTGCACAAGAGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 dicoccoides 4 (q) GCGCCCTTGCACAAGAGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 spelta 2 (Eur; q) GCGCCCTTGCACAAGAGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 macha (q) GCGCCCTTGCACAAGAGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 dicoccum 1 (q) GCGCCCTTGCACAAGAGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 dicoccum 2 (q) GCGCCCTTGCACAAGAGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 spelta 3 (Eur; q) GCGCCCTTGCACAAGAGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG
 urartu (q) GCGCCCTTGCACAAGAGCGGGGAAGCACTCTGTTGTTTTGCAGCAGTCCG
 monococcum (q) GCGCCCTTGCACAAGAGCGGGGAAGCACTCTGTTGTTTTACAGCAGTCCG

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polonicum 1 (Q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 aestivum (Q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 carthlicum (Q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 polonicum 2 (Q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 dicoccum 4 (Q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 durum (Q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 compactum (Q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 sphaerococcum (Q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 spelta 4 (Iran; Q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 spelta 5 (Iran; Q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 dicoccoides 2 (q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 dicoccoides 3 (q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 dicoccoides 1 (q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 dicoccum 3 (q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 spelta 1 (Eur; q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 dicoccoides 4 (q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 spelta 2 (Eur; q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 macha (q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 dicoccum 1 (q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 dicoccum 2 (q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 spelta 3 (Eur; q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 urartu (q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG
 monococcum (q) CCATTGTTGCGTTAACCGTTGGGCCTTCTG

APPENDIX G. Genomic alignment of *Q* homeoalleles from *T. turgidum* ssp. *durum* cv. Langdon chromosomes 5A (*Q*-5A) and 5B (*q*-5B).*

* The alignment extends from start to stop codon for *Q*-5A. Exons for the *Q*-5A gene are highlighted in grey. The apparent two base pair deletion in exon 2 of *q*-5B that may cause a frameshift are highlighted in red. The putative stop codon is highlighted in yellow.

Aligned Length = 3410 Gaps = 42 Identities = 2879 (86%)

Q-5A	1	ATGGTGCTGGATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAG	50
Q-5B	1	ATGGTGCTGGATCTCAATGTGCGAGTCGCCGGCGGACTCCGGCACGTCCAG	50

Q-5A	51	CTCCTCCGTGCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCCG	100
Q-5B	51	CTCGTCCGTGCTTAACTCCGCGGACGCCGG-----CGGCTTCCGGTTCCG	94
		*** *****	
Q-5A	101	GCCTGCTCGGGAGCCCTGATGATGACGACTGCTCCGGCGAGCCGGCGCCG	150
Q-5B	95	GCCTGCTCGGGAGCCCCGATGACGACGACTGGTCCGGCGAGCCGGCGCCG	144

Q-5A	151	GTCGGGCCCGGGTTTCGTACAGAGGCAGCTCTTCCCCGCGTCGCCGCCCGG	200
Q-5B	145	GCCGCGTCCGGGTTTCGTGACGAGGCAGCTTTTCCCCGCGTCGCCGCCCG-	193
		* * * *****	
Q-5A	201	GCACGCGGGCGCGCCCGGGGTGACGATGGGGCAGCAGGCCCGGCGCCTG	250
Q-5B	194	-----CGCCCGGGATGATGATGGGGCAGCAGGCCCGGCGGCC--	230

Q-5A	251	CGCCGATGGCGCCCGTGTGGCAGCCGCGGCGCGCCGAGGAGCTCCTCGTG	300
Q-5B	231	-GCCGATGGCCCCCGTGTGGCAGCCGCGCCGCGCCGAGGAGCTGGTCCGCG	279

Q-5A	301	GCGCAGCGGATGGCGCCCGGAAGAAGACGCGGCGGGGCCCGAGGTCCGG	350
Q-5B	280	GCGCAGCGGGTGGCGCCCGGAAGAAGACGCGGCGGGGCCCGAGGTCCGG	329

Q-5A	351	CAGCTCGCAGTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGG	400
Q-5B	330	GAGCTCGCAGTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGTGGG	379

Q-5A	401	AGTCGCACATCTGGTCAGCCCTCCTCTCGTCTCCCTACTCCTCCTCCATG	450
Q-5B	380	AGTCGCACATCTGGTCAGCCC--TCTCATCTCCCTACTCATCCTCCATG	426

Q-5A	451	ACTATAGTTATTACCCAAATCACTAATCAATCGCTGGCCTTTGTCCGTCT	500
Q-5B	427	ACTAT---TACTTACCAAATCATTAAATCAATCGCTCGCCTTTGTCCGTCT	473

Q-5A	501	GATTCCACCAGGGATTGCGGGAAGCAGGTCTACTTGGGTGAGCTCAAACA	550
Q-5B	474	AATTCCACCAGGGACTGCGGGAAGCAG-CTACTTAGGTGAGCTCAA-CA	520

Q-5A	551	AATCCCAGCTCGAGCTCCGATCTCCTCGGTGTCTAATTTTCGATTATCTTA	600
Q-5B	521	AATCCCCTGCTCAAGCTCCGATCTCCCCGGCGTCTAATTTTCGATTATCTTG	570
		** *** *****	
Q-5A	601	GCTGTATGGGCTCGTGATTAACACTGGATAATTTCTTCAGGTGGTTTCGA	650
Q-5B	571	GCCATATGTGCTCGTAATTAACACTGGTAAATTTCTTCAGGTGGGTTTCGA	620
		** *****	
Q-5A	651	CACTGCGCACGCGGCCGCAAGGTGAACTAATTAATTAACCAGGCCTCGTT	700
Q-5B	621	CACTGCGCACGCGGCCGCAAGGTGAATTAATTAATTAATCAGGCCTCGTT	670


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Q-5A 701 TGAATTCCTTTTGCCCCGATTTGGCCACGAACTGTGTACTGAGATGAGAC 750
Q-5B 671 TGAATCCATTTTACCCCGATTTGACCATGAACTGTGTACTGAGACGA--C 718
***** * ***** ***** ***** ***** ***** *****
Q-5A 751 GGTGTGGCGTGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGG 800
Q-5B 719 GGTGTGGCGTGGCGCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGG 768
*****
Q-5A 801 GCTGGAGGCCGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGA 850
Q-5B 769 GCTGGAGGCCGACATCAACTTCAATCTGAGCGACTATGAGGAGGATTTGA 818
*****
Q-5A 851 AGCAGGTAATCTTATC-----CAAGCCTAGTTGATTGCTG 885
Q-5B 819 AGCAGGTAATCATCTAAGCTACTATAAGCTATAATCTGGGTAGAAGATTG 868
***** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
Q-5A 886 TACTACCAAGTAGTGCGCCGATAACATA-TGTATCGGTGGTTTGTCCGAT 934
Q-5B 869 TACTACCAGGTAGTCAGTGCGCCGATAATATATGGGTGGTTTGTCCGAT 918
***** ***** * * * * * * * * * * * * * * * * * * * * * *
Q-5A 935 GGTTGATATCTGGTGGGTGGTGGTGGTGGTGGTTTTTTGCCAGATGAGGAACTG 984
Q-5B 919 GGTTGATATCTGTGGGTGGTGGTGGTGGTGGTTTTTTGCCAGATGAGGAACTG 968
***** *****
Q-5A 985 GACCAAGGAGGAGTTCGTGCACATCCTCCGCCGCCAGAGCACGGGGTTTCG 1034
Q-5B 969 GACCAAGGAGGAGTTCGTGCACATCCTCCGCCGCCAGAGCACGGGGTTTCG 1018
*****
Q-5A 1035 CCAGGGGGAGCTCCAAGTACCGCGGCGTCACGCTCCACAAGTGCGGCCGC 1084
Q-5B 1019 CCAGGGGGAGCTCCAAGTACCGCGGCGTCACGCTCCACAAGTGCGGCCGC 1068
*****
Q-5A 1085 TGGGAGGCAAGGATGGGCCAGCTGCTCGGCAAGAAGTAAGCAGGCACACA 1134
Q-5B 1069 TGGGAGGCAAGGATGGGCCAGCTGCTCGGCAAGAAGTAAGCAGGCACACA 1118
*****
Q-5A 1135 CACAGCTCACGCACTAAAATTAATTCACTTCGCCACATTATCATAGTAG 1184
Q-5B 1119 C-----ACTAAAATTAATAAATTTTCATCCACATTATCATACTAG 1157
* ***** * * * * * * * * * * * * * * * * * * * * * *
Q-5A 1185 TAGTTTCTTTTATCAAATGCCATTGACA-----AGATTTCAGTTGAAATGA 1229
Q-5B 1158 ---TTTCTCTAATCAGATGCCATATACAGTACAAGATTACGTTGAAAAGA 1204
***** * ***** ***** ***** ***** ***** *****
Q-5A 1230 AATTTTCACAGACTGCTCATGAACTTGACACTAATTAGTAGTAGATGTGAC 1279
Q-5B 1205 AATT-CACAAGCTGTTTCATGAACTTGACCCTAATTAGTACTAGATGTGAC 1253
***** ***** ***** ***** ***** ***** *****

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Q-5A 1280 AGGGCAGCTGTTTCATGCTGTGGACGTTTAATTAGCCTGTCGCAGGTAATC 1329
 Q-5B 1254 AAGGCAGCTGTTTCGTGCTGTGGACGTTTAATTAGCCTGTCGTAGGTAATC 1303
 * *****

 Q-5A 1330 ATCTTAGATTACCCCTTTTGAACATAATCTTAGCTGGTTTAGGGTAGGG 1379
 Q-5B 1304 ATCTTAGATTATCCCTTTTGAACATAATCTTAGCTGGTTTAGGGTAGGG 1353
 * *****

 Q-5A 1380 TCATCAAGTTAATCCATGTTGTTAGTTGTTGGCGCGTCCTGTGTTGGTGC 1429
 Q-5B 1354 TCATCAAGTTAATCCATGTTGTTAGTTCTTGGCGTGTCTGTGTTGGTGC 1403
 * *****

 Q-5A 1430 TGGTGAGACGTCCACTTCCCCGACACGACACTCGATTGCAGACATCTAT 1479
 Q-5B 1404 TGGTGAGACGTCCACTTCCCCGACAC----TCTGATTGCAGACATCTAT 1449
 * *****

 Q-5A 1480 TTGGAGCAACTGTTAGGCTCCACATAAGTATATGATCGAGTCGTCCAGAC 1529
 Q-5B 1450 TTGGAGCAACTGTTAAAGGTTCCACA--TATATGATCGACTTGTCCAAAC 1497
 * ***** ** * ***** * ***** **

 Q-5A 1530 AAAATTAGTCTAATCCAATCCGTGCACATTATGGTCCAGACCCAGAATTG 1579
 Q-5B 1498 AAAATTAATCTAATCCAATCCGTGCACATTATGGTCCAGACCCGGAATTG 1547
 * *****

 Q-5A 1580 TCACCCTACACCTTACACCCCCTATCTCCGTTGAGCTGTGGTCTCATCTC 1629
 Q-5B 1548 TCACCCTACACAC-----CCCCTATCTCCGTTGAGCTGTG-----ATCTC 1587
 * *****

 Q-5A 1630 ATATACCTGATACCCACATTATCATCACACGCGCAGGTACATATATCTGG 1679
 Q-5B 1588 ATATACCTGATATCCACATTATCATCGCACG--CAGGTACATATATCTTG 1635
 * *****

 Q-5A 1680 GCCTCTTTGACAGCGAAGTTGAAGCTGCAAGGTACTTTGATTTGCGCTGA 1729
 Q-5B 1636 GCCTCTTTGACAGCGAAGTTGAAGCTGCAAGGTACTGTGATTATCCCTGA 1685
 * ***** * *****

 Q-5A 1730 TCATTAACATTTGGG---CTCACAAAACCTCCTTAATCTTTGCTCACTCA 1776
 Q-5B 1686 T-ATCCACATTAAGGAAGCTCACAAAACCTCCTTAATTTCCGCTCACTCG 1734
 * ** ***** ** ***** * *****

 Q-5A 1777 CTCTAGTGTGCATGTTGGATTTGGTAGGGCGTACGACAGGGCGGCGATTCC 1826
 Q-5B 1735 CTCTAGTGTGCATGTTGGATTTGGTAGGGCGTACGACAGGGCGGCGATTCC 1784
 * *****

 Q-5A 1827 CTTCAATGGGAGGGAAGCTGTGACTAACTTTGAGAGCAGCTCCTACAATG 1876
 Q-5B 1785 CTTCAATGGGAGGGAAGCTGTGACTAACTTTGAGAGCAGCTCCTACAATG 1834
 * *****

 Q-5A 1877 GGGATGCTCCACCCGACGCCGAAAATGAGGGTACTAC--TACAATCGGTC 1924
 Q-5B 1835 GGGATGCTCCACCCGACGCCGAAAATGAGGGTACTACAACAATCAGTC 1884
 * ***** **

Q-5A 1925 TCACCTGTCTGAATTTCTCCAATCACACCCAAGTCTTATCTCATCGATATC 1974
 Q-5B 1885 TCACCTGTCTGATTTTCTCCAATCACACCCAAGTCTTATCTCATTGATATC 1934

Q-5A 1975 GTTGTGTTTTCTTAGCAATTGTTGATGCTGATGCTCTTGACTTGGATCT 2024
 Q-5B 1935 TTCGTTGTTTTCTTAGCAATTGTTGATGCTGATGCTCTTGACTTGGATCT 1984
 * *****

Q-5A 2025 GCGGATGTCGCAACCCACCGCGCACGATCCCAAGAGGGACAACATCATCG 2074
 Q-5B 1985 TCGGATGTCGCAACCTACCGCGCACGATCCCAAGCGGGACAACATCGTCG 2034

Q-5A 2075 CCGGCCTTCAGTTAACTTTTGATTCCCCTGAATCGTCAACCACAATGATC 2124
 Q-5B 2035 CCGGCCTTCAGTTAACTTTTGATTCCCCTGAATCGTCAACCACAATGCTC 2084

Q-5A 2125 TCTTCTCAGGTAAAGAAACAAAATTA---TGTTTAGCACTAGCTAATTC 2170
 Q-5B 2085 TCTTCTCAGGTAAAGAAATTAATTAATCATGTTTAGCACTAGCTAGCTC 2134

Q-5A 2171 AGTGGTTAGATTTGCTCAAATAGAAAAT-TTGCTGTTGGCCAGTTGTGT 2219
 Q-5B 2135 AGTGGTTAGATC-GCTGGAATAGAAAAAATTCCTGTTGGCCAGTTGTGT 2183

Q-5A 2220 CGGTGGATGAGATATTATTGATCCAGGTCGTATGGCATATACTCTGTCCT 2269
 Q-5B 2184 CGGTGGATGAGATATTATTGATCCAGGTCGTATGGCATATACTCC-TCCT 2232

Q-5A 2270 AAACCTACGATATTTGTGCCTTTT-GATATCGCTGTAGCCAATGAGCTCA 2318
 Q-5B 2233 AAACCTACGATATTTGTGCCTTTTGTGATATCGCTGTAGCCAATGAGCTCA 2282

Q-5A 2319 TCTTCGTCCCAGTGGCCTGTGCATCAACATGGCACGGCAGTAGCACCTCA 2368
 Q-5B 2283 TCTTCTTCCCAGTGGCCTGTGCATCAACATGGCACGGCAGTACCACCTCA 2332

Q-5A 2369 GCAGCACCAGCGTTTGTACCCATCTGCTTGTGCATGGCTTCTACCCGAACG 2418
 Q-5B 2333 GCAGCACCAGCGTTTGTACCCATCTGCTTGTGCATGGCTTCTACCCGAACG 2382

Q-5A 2419 TACAGGTATCATCATCACTACGAGAACGACCACCTCCTCCTCCTCCTCCT 2468
 Q-5B 2383 TACAGGTATCATCACTACGAGAACGACC-CCTCCTCCTCCTAGTCCTCAT 2431

Q-5A 2469 CCTCTGCTTGGTGCCTGCTCCACCAGCTTACTGAAACTGTTGCTACCAC 2518
 Q-5B 2432 CCTCTGCTTGGCGCGCTGCTCCACCAGCTTACTGAAACTGTTGCTACTGC 2481

Q-5A 2519 TGAATAATGTTTCTGAAGAAACTGCTAATAACATTTTTCAGTTTTTCGACAA 2568
 Q-5B 2482 TGAATAATGTTTTCAGACGAAACTGTTGATGACATTT-CAGTTTTTCGACAA 2530

Q-5A 2569 GTTCGTTCTGAAATTAAGGTTTCCATGCTTCTTTCCTA---AAACTAAT 2615
 Q-5B 2531 GTTCATTCTGAAATTAAGGTTTCCATGTTTCTTTCCTGGTGAAACTAAT 2580

Q-5A 2616 CACGCCTGCTCTCCTAAAA-CATCTACAGGTGCAAGAATTTTGGGTGTAG 2664
 Q-5B 2581 CATGCCTGCTCTCCTAAAAACGTGTACAAGTGCTGGAATTCTGGGTGTAG 2630
 ** *****

Q-5A 2665 TGATGTGTCTGTTGACTGAGCATCTCGTCTCATGGACAGACAGAGCATGC 2714
 Q-5B 2631 TGATGTGTCTATTGACTGAGCTGCTTGTCTTTTTTGAACGAAACGCAAGC 2680

Q-5A 2715 TGTGTGGTAGTACC-----AGAGTACTTACTAGATGTGGGCAC- 2752
 Q-5B 2681 TTTTCGTTGGCATCTCGTCTCATGGACAGAGCATGCTGTGTAGTACCAGA 2730
 * * * * * * * * * *

Q-5A 2753 -TACT--GTTTGCCCTGTGAGCTCGCACACCTTTC-GAAAAAACTGCA 2798
 Q-5B 2731 GTACTTGGTTTTCTCCTGTGAGCTTGCACCTCCTTTCAGAAAAAACTGCA 2780

Q-5A 2799 GTGCGCCCTCCGGTTCTTGCAGTTCCATCCGTCCCCCATGGCACAGCTTT 2848
 Q-5B 2781 GTGCGTCCCTCCGGTTCTTACAGTTGCATCCGTCCATGACACAGCTTT 2830

Q-5A 2849 AGATGCA----- 2855
 Q-5B 2831 AGATGTACTCCCTCCGTTCTGAATTACTTGTCTTAAATTTGTCTAGATAC 2880
 ***** *

Q-5A 2856 ----- 2855
 Q-5B 2881 GGATGTATCTAGACTCATTTTAGTGCTAGACATATCTGTATCTAGACAAA 2930

Q-5A 2856 -----GCAGCAGCTTGCTTAGTTGTAGT- 2878
 Q-5B 2931 TCGAAGACAAGTAATTTGGAACGGAGGGAGTAGCTTGCTTAGGTGTAGTG 2980
 * * * * *

Q-5A 2879 --ACCCTGATCACATGGCGCAGCTTTATTCTTGGTAGCCACTGTGCATTC 2926
 Q-5B 2981 GTACCCTGATCACATGGTGCAGCTTTATTCTTGGTAGACACTGTGCATTC 3030

Q-5A 2927 ACATGAAAGCAAAGCTTTGGTGC----ATGCACGGCCATGACTTGACGCT 2972
 Q-5B 3031 ACATGAAAGCAA-GCTTTGGTGTGCTGCATGCACGGCCATAAATTGACGCT 3079

Q-5A 2973 CTATCTCACTGCTGGTGCTGGTGCAGGTGCAGGTGCAGGAGAGGCCCATG 3022
 Q-5B 3080 CTCTCTCTC-----AGGTGCAGGTGCAGGAGAGGCCGATG 3114
 ** *****

Q-5A 3023 GAGGCAAGGCCCCCTGAGCAGCCGTCGTCCTTCCCCGGCTGGGGGTGGCA 3072
 Q-5B 3115 GAGGCAAGGCCCCCTGAGCCGCCGTCGTCGCTTCCCCGGCTGGGGGTGGCA 3164

Q-5A 3073 AGCGCAAGCCATGCCGCCGGGCTCCTCCCCTCGCCGTTGCTTTACGCTG 3122
Q-5B 3165 AGCGCAAGCCACGCCGCCGGGCTCCTCCCCTCGCCGTTGCTTTACGCTG 3214

Q-5A 3123 CAGCATCATCAGGATTTTCTACCGCCGCCGCCGGCGCGAACCTCGCCCCG 3172
Q-5B 3215 CAGCATCATCAGGATTCTCTACCGCCGC---CGGCGCGCACCCCGCCCCG 3261

Q-5A 3173 CCGCCGCCGT---ACCCGGACCACCACCGTTCTACTTCCCCCGCCCGCC 3219
Q-5B 3262 CCGCCGCCGTTCGTACCCGGATCACCACCGTTYTACTTCCCCCGCCCGCC 3311

Q-5A 3220 GGACAACTGA 3229
Q-5B 3312 GGACAACTAG 3321
