Map-based cloning of susceptibility factors for *Bymovirus* in barley (*H. vulgare* L.)

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1. Introduction

Crop diseases caused by pathogens like fungi, bacteria, viruses, insects and even nematodes threaten global food security. Despite all efforts of crop protection, crop diseases cause an annual estimated average yield loss of 13.1% (Oerke 2007). It has been shown that a significant proportion of infectious crop diseases are caused by plant-associated viruses. As an example, approximately 3% or 93.6 million tones of the globally attainable production of six major crops (Oerke 2006) is lost due to the action of plant viruses. Infections by plant viruses may depend on environmental factors like weather or farming systems (Kang et al. 2005). But as soon as infections with plant viruses occur, no curative treatments are available to recover the crop or even to stop virus multiplication. In many cases plant protection to viruses is dependent of the control of the virus vector (fungi, insects) which most often is environmentally questionable. Thus, improving natural resistance to plant viruses is of major importance in plant breeding and provides often the most efficient way of crop protection.

1.1 Genetics of resistance to plant viruses

Resistance to plant viral diseases can either be classified into host or non-host resistance (Fraser 1990). If a plant never gets infected by a given virus it is most likely a non-host for the virus, hence the species carries genetic factors that control so-called non-host resistance to these viruses (Mysore and Ryu 2004). This is the predominant category of resistance to viruses since most plant species are never infected by most of the plant viruses. If a few genotypes show heritable resistance to a particular virus whereas other genotypes are susceptible, it is designated as host resistance. In order to prevent viral infection, plants evolved several mechanisms of resistance to virus diseases, comprising dominant *R*-gene mediated resistance (Cournoyer and Dinesh-Kumar 2011; Dangl 1995), recessive resistance conferred by the mutated susceptibility factors (Whitham and Wang 2004), systemic acquired resistance (SAR) (Loebenstein 2009), as well as small RNAs guided antiviral immunity (Baulcombe 2004; Burgyan and Havelda 2011; Ding and Voinnet 2007; Llave 2010). The identified viral resistance genes conferred by dominant *R*-genes mostly belong to nucleotide-binding leucine-rich repeat (NB-LRR) gene family, and the type of resistance frequently results in localized programmed cell death known as hypersensitive response (HR-PCD) therefore blocking the spread of virulent components (Cournoyer and Dinesh-Kumar 2011; Soosaar et al. 2005). Recessive resistance is conferred by loss of cellular components, which are essential for the establishment of virus infection (Whitham and Wang 2004). The infection of a plant virus could suppress the secondary infection of the same or other viruses, and the type of resistance is designated as systemic acquired resistance (Loebenstein 2009). The antiviral immunity by virus-derived small interfering RNAs (viRNAs) generally results in specific silencing of viruses (Ding and Voinnet 2007). Since the mechanisms of dominant *R*-gene regulated resistance, SAR and small RNAs guided resistance are irrelevant to this work, the recessive resistance mediated by mutated susceptibility factors is exclusively given in details.

Plant RNA viruses represent the largest group of plant viruses (Martelli 1992) and carry a reduced genome (relatively to the host plants) encoding a limited set of functional genes, for instance, 4 - 10 functional proteins in *Bymo*- and *Potyvirus* - too few for independently completing the viruses infectious lifecycle including (i) entering into host cells, (ii) release of viral nucleic acid, (iii) translation of viral proteins, (iv) replication of the viral genome, (v) assembly of ribonucleoprotein / virions and (vi) transport of viral components in the plant (local, systemic and plant-to-plant movement) (Figure 1-1) (Carrington et al. 1996). During evolution viruses recruited host factors to fulfill functions that were previously provided by viral proteins and that allowed reducing virus genome size (Whitham and Wang 2004). The dependence on host factors, however, opened the possibility in plant to adapt and develop mechanisms of tolerance or resistance. The absence of single or multiple host factors could interfere with viral infection or multiplication processes, resulting in mono- or polygenic recessive resistance. It was suggested that recessive resistances to plant viruses are more common in contrast to diseases caused by fungi, bacteria or insects. About half of the 200 known resistance genes to plant viruses are recessively inherited (Diaz-Pendon et al. 2004; Kang et al. 2005). The frequency of recessive resistance may depend on virus family or genus. Within the family *Potyviridae*, 40% of resistances to *Potyvirus* are reported to follow a recessive mode of inheritance (Provvidenti and Hampton 1992), while recessive resistance was observed in over 80% of the cases of resistance to *Bymovirus* (Kai et al. 2012; Ordon et al. 2005).

Apart from their regular function in plants host factors have become involved into the infectious steps of the virus lifecycle (Ahlquist et al. 2003; Kang et al. 2005; Whitham and Wang 2004). This includes viral replication, cell-to-cell movement, systemic movement and plant-to-plant movement (Kang et al. 2005). When positive-stand plant RNA virus particles enter host cells and release their nucleic acid, translation of viral proteins is initiated in competition to host mRNA translation by taking advantage of the host’s translation machinery, e.g. the eukaryotic translation initiation complex (Robaglia and Caranta 2006). It was confirmed by *in vivo* and *in vitro* studies, that EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (eIF4E) and its paralogous protein eIF(iso)4E may directly interplay with the cap structure of viral mRNAs or viral genome-linked protein (VPg) to catalyze the translation initiation of viral polyproteins (Leonard et al. 2000; Schaad et al. 2000; Wang et al. 2013; Wittmann et al. 1997). Incompatibility of interaction between virus and the eukaryotic translation initiation complex resulted in a lack of replication of multiple viruses in several plant species (Le Gall et al. 2011; Robaglia and Caranta 2006). eIF4G contributes to the stability of the translation complex by physically interacting with eIF4E and other components (PABP, eIF4A and eIF3) (Robaglia and Caranta 2006). Mutations of this protein were shown to confer resistance to *Rice yellow mottle virus* (Albar et al. 2006) and *Cucumber mosaic virus* (Yoshii et al. 2004). The synthesized viral proteins, e.g. RNA-dependent RNA polymerase (RdRp) contribute to generation of negative strand RNA genome as template, which is subsequently used for multiplication of progeny positive strand RNA genome generally on the membrane surface, therefore establishing viral replication successfully in a plant cell (Ahlquist et al. 2003).

Once viral multiplication has been established in a single plant cell, the viruses must move from the infected to neighboring cells (Cell-to-cell movement) (Figure 1-1). It was known that mutation of *eIF4E* and *eIF4G* in *A. thaliana* suppressed viral translocation locally through prohibiting the accumulation of the *Cucumovirus* 3a protein (Yoshii et al. 2004). When viral components enter into phloem, the systemic or long-distance movement of virus particles is initiated through the phloem transport system. The resistance or restriction to long-distance movement of plant viruses, e.g *Tobacco etch virus* is likely associated with dominant components (Mahajan et al. 1998; Whitham et al. 2000). Virus translocation from the infected to another individual could be prohibited by the control of the virus vector (e.g. fungi, insects), but chemical treatment is neither economical nor ecological in agriculture.

Overall, it can be realized that the identified host factors for establishing virus infection are weakly associated to the eukaryotic translation initiation complex (Castello et al. 2010; Robaglia and Caranta 2006; Schepetilnikov et al. 2011). In contrast to the advances in dicotelydenous species there is very limited knowledge about plant-virus interaction and antiviral responses in monocots. Only three susceptibility factors including *eIF4E*, *eIF(iso)4G* and a NAC-domain transcription factor were identified in barley or rice as being involved in the infection with *Barley yellow mosaic virus*, *Rice yellow mottle virus* or *Rice dwarf virus*, respectively (Albar et al. 2006; Stein et al. 2005; Yoshii et al. 2009). The identification of novel susceptibility factors in grass species could contribute to achieve a better understanding of plant-virus interaction, and bridge the gap of our knowledge in monocots. Selection and development of cultivars with the resistance alleles of susceptibility factors is a precise strategy to be effective against the infectious diseases in agriculture.

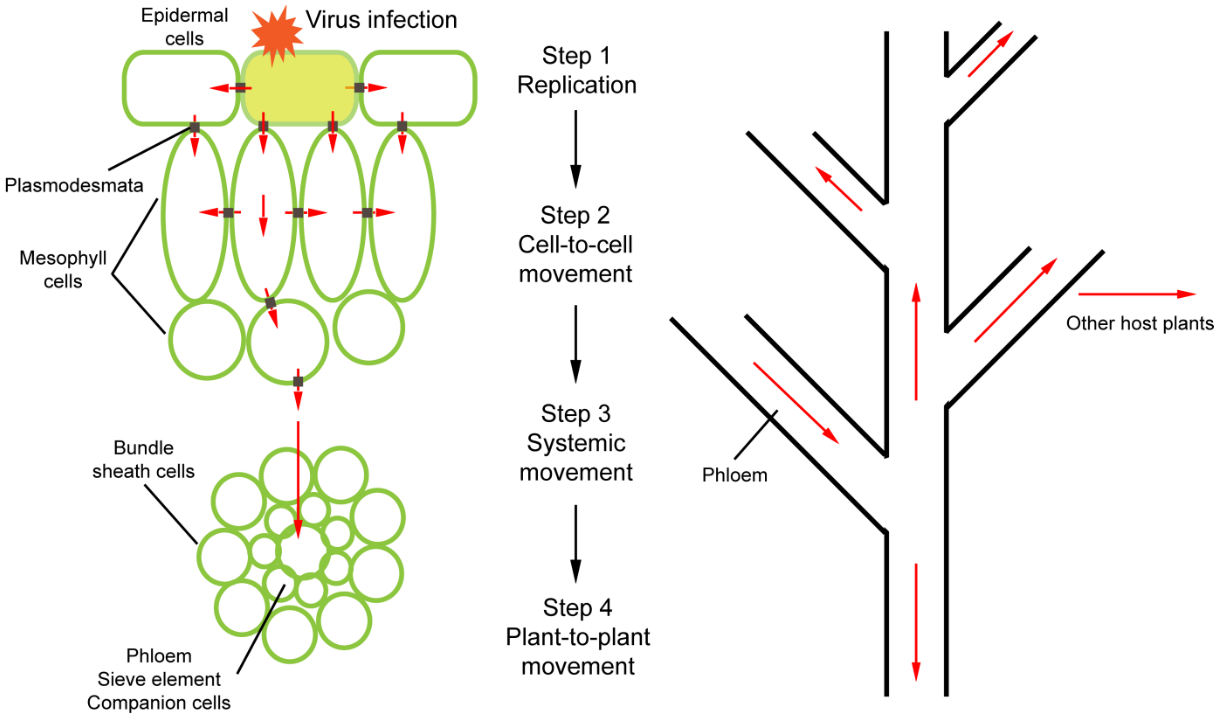


Figure 1-1 Steps of viral infection cycle. Red arrows indicate virus movement. The diagram was modified from Carrington et *al.* (1996) and Kang *et al.* (2005).

1.2 Soil-borne barley yellow mosaic virus disease

Cultivated barley (*Hordeum vulgare* L.) is one of the most important and most ancient cereal crops. It has been domesticated 10,000 years ago in the Fertile Crescent (Purugganan and Fuller 2009; Smith 1998). Based on global production barley currently ranges fourth among cereals after maize (*Zea mays*), rice (*Oryza sativa*) and wheat (*Triticum aestivum*) (USDA, 2011). 75% of global harvest of barley is used for animal feeding, 20% is used for malting, brewing and distilling industries, and only 5% is used for direct human consumption. However, it contributes most calories to the daily diets in large parts of Tibet and a few African countries (Ullrich 2010). Increased content of soluble fiber (i.e. β-glucans) in barley may provide a health benefit to human diet by contributing to reducing blood cholesterol levels (Baik and Ullrich 2008). Unfortunately, >80 different diseases caused by fungi, virus, insects, bacteria and nematodes threaten this important crop (Mathre 1997), and may reduce yield by up to 100% (Paulitz and Steffenson 2010). The yellow mosaic virus disease caused by *barley yellow mosaic virus* (BaYMV) and *barley mild mosaic virus* (BaMMV) is one of the most important infectious diseases, and may seriously damage winter barley production.

1.2.1 Barley yellow mosaic virus complex

Over the last few decades the soil-borne barley yellow mosaic virus disease was one of the most important threats to winter barley production in East Asia and Europe. When susceptible cultivars are grown in severely contaminated fields, >50% of yield losses could be observed (Adams and Hill 1992; Huth 1989b; Plumb et al. 1986). The yellow mosaic virus disease of barley was first described in Japan in the 1940s (Ikata and Kawai 1940). It was subsequently found in China during the 1950s (Kühne 2009; Ruan et al. 1984; Zhou and Cao 1985) and later in South Korea (Lee et al. 1996; Lee et al. 2006; Park et al. 2005). The outbreak of this disease caused nearly complete yield losses of barley in the mid-1970s in China (Chen 2005; Kühne 2009). In Europe, the first appearance of this disease was described in Germany in 1978 (Huth Winfried and Lesemann 1978) and was later on reported as well in other European countries (Kühne 2009). In accordance with the situation in East Asia (Kashiwazaki et al. 1989), it was rapidly widespread over large parts of the cultivation area, specifically in Germany (Huth 1984) and UK (Hill and Walpole 1989). Until 1994, >50%

of the winter barley cultivation area in Germany was considered to be contaminated by virulent isolates of BaMMV/BaYMV (Kühne 2009).

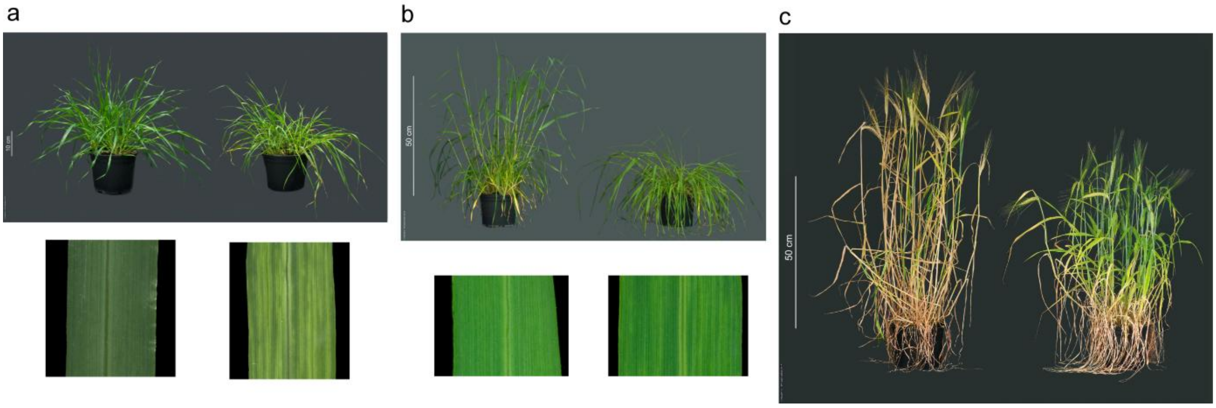


Figure 1-2 Symptoms of BaMMV infection in susceptible barley genotypes grown under greenhouse conditions. The seedlings at three-leaf stage (two weeks) were either mock-infected (inoculation with water only) or mechanically inoculated with BaMMV twice at the interval of 5-7 days. The mock inoculated and virus infected plants are shown as left and right plants in each of the a, b, c panels, respectively. (a) Yellow discoloration and necrotic patches of young leaves at the vegetative stage. (b) Stunted growth of infected plants at heading stage. The typical symptoms such as a mosaic of pale green and necrotic patches become less obvious. Old leaves and upper parts of young leaves are often free of any symptoms. (c) Delayed maturity of infected plants. The mock-inoculated plants have matured, while the infected plant is delayed in development and still remains green.

Natural infection by different strains of the *Bymovirus* complex occurs in autumn. The pathogenic symptoms of the disease will manifest in leaves that appear in winter or early spring. Before this stage, viral RNA and coat proteins are primarily detected in roots (Peerenboom et al. 1996). The typical symptoms of infected plants include a mosaic of pale green and yellow discolorations as well as necrotic patches (Figure 1-1, a). The yellow discoloration typically appears in newly emerging leaves, particularly in lower parts closely to the stem. The stunted growth and a reduced number of tillers are observed during the life cycle of susceptible barley plants (Figure 1-1, b and c). The severity of symptoms is influenced by the growth rate of barley plants, the environmental conditions, as well as reproduction and spread of virus within the plants. Leaf symptoms become less obvious along with increasing temperatures and plant growth. Old leaves and upper parts of young leaves are often completely free of symptoms. This phenomenon may be related to the major direction of phloem transports (Kang et al. 2005). Mechanical inoculation of BaMMV on a small area of leaves resulted in the accumulation of virus RNA and coat proteins in lower parts of the inoculation site, roots, and newly emerging leaves, but not in upper parts of the infected area and old leaves as was determined by using RT-PCR/ELISA (Schenk et al. 1995). However, the underlying mechanism of the *Bymovirus* movement in barley is still yet to be determined.

The barley yellow mosaic virus disease is transmitted by the soil-borne plasmodiophorid *Polymyxa graminis* (Adams et al. 1988; Chen et al. 1991) through the infection of the barley root system. Particles of BaMMV were observed inside zoospores and zoo-sporangial plasmodia of *P. graminis* by using electron microscopy, but this is still yet to be demonstrated for resting spores (Chen et al. 1991). The resting spores carrying viral particles remain in root debris after crop harvest, and may provide protection for virus particles under unfavourable environmental conditions allowing them to remain virulent for many years in soil even without a suitable host (Huth 1991). As a consequence of persistence in soil, viruses may become widespread because of short distance transport of the resting spores in debris and soil through cultivation as well as by longer distance transport through wind-promoted soil particles and even in soil associated water (Hill and Walpole 1989). Newly generated resting spores, e.g. on infected plants, accelerate the spread of virus particles. Thus, the existing yellow mosaic disease can widely distribute in the field. It was found that natural infection of barley yellow mosaic virus disease seems to be related with environmental conditions, e.g. temperature and growth cycle. Many spring barleys are susceptible under climate chamber condition, while these cultivars sown in spring are normally free of symptoms in the virus-contaminated field.

Barley yellow mosaic virus disease is caused by the infection with any of the different isolates of BaYMV and BaMMV. In Europe, BaMMV (Meyer and Dessens 1996; Peerenboom et al. 1996; Timpe and Kuhne 1994), BaYMV (Hariri et al. 2000; Shi et al. 1995) and BaYMV-2 (Kühne et al. 2003) are currently widespread, for example, >50% of the barley cultivation area was contaminated in Germany (Kühne 2009). Two new isolates BaMMV-SIL (Kanyuka et al. 2004) and BaMMV-Teik (Habekuß et al. 2008) were recently determined in France and Germany, respectively. They were virulent in cultivars carrying the naturally occurring resistance locus *rym5* which is predominant in European winter barleys. The situation is even more complicated in East Asian countries. For instance in Japan, four strains of BaYMV and two strains of BaMMV have been determined at nucleotide sequence level (Nishigawa et al. 2008; Nomura et al. 1996). In South Korea, two strains of BaMMV and BaYMV had been detected, and were different to German and Japanese strains at the serological and pathological levels (Lee et al. 1996; Lee et al. 2006; Park et al. 2005). In China, more than 10 strains / variants of both viruses were found (Chen et al. 1999; Chen et al. 1992; Zheng et al. 1999).

The complete nucleotide sequence of RNA1 and RNA2 of BaMMV and BaYMV was determined which revealed a similar genomic organization of both viruses (Davidson et al. 1991; Kashiwazaki et al. 1991; Kashiwazaki et al. 1990; Peerenboom et al. 1992). Coat proteins of BaMMV and BaYMV exhibit a relatively low level (35%) of amino acid sequence identity in comparison to 94% among different strains of BaMMV (Kashiwazaki 1996). Thus they are related but distinct members of the genus *Bymovirus* of the family *Potyviridae* (Adams et al. 2005). The RNAs encode two polyproteins, which are cleaved into 10 functional proteins. RNA1 encodes the coat protein, cytoplasmatic inclusion protein (C1), protease (NIa), genome-linked protein (VPg) as well as the RNA-dependent RNA polymerase (NIb). It is critically important but alone not sufficient for establishing a successful infection. RNA2 encodes for the P1 (Cysteine proteinase activity) and P2 (Unknown function) proteins which are dispensable for establishing a systemic infection (You and Shirako 2010). A single report indicated that the P2 protein of BaMMV may be involved as a factor in the transmission by the fungal vector since a 1000 bp deletion of BaMMV P2 resulted in loss of fungal transmission (Adams et al. 1988). Other studies showed that a spontaneous deletion at the 3'-terminal of the same protein P2 had no influence on the success of natural and artificial *Bymovirus* infection (Dessens and Meyer 1995; Dessens et al. 1995; Kühne et al. 2003; Ulrich Timpe and Kühne 1994). Thus, the presence of P2 protein is essential for virus infection, whereas the spontaneous variations at the 3'-terminal allow the establishment of virus infection.

Similarly to other plant and animal RNA viruses, BaYMV and BaMMV are not only virulent on a single species but may infect several of the closely related species belonging to the family *Poaceae*. The natural host is domesticated barley (*H. vulgare* L.). Infections could be established by artificial mechanical inoculation in wild barley (*H. spontaneum*), *H. bulbosum* (Dr. Habekuss, per. com.), *Triticosecale* (Kegler 1985), *S. cereale* (Ordon F. 1992) and *T. durum* L.(Proeseler 1993) as well as several species of the genus *Aegilops* (Proeseler 1988), *Eremopyrum* and *Lagurus* (Adams 2004).

1.2.2 Genetic resistances to the barley yellow mosaic virus disease

Transmission of *Bymovirus* occurs via the soil-borne plasmodiophorid *P*. *graminis* (Adams et al. 1988; Chen et al. 1991) which prohibits plant protection by pesticide treatment. Therefore the only sustainable measure of crop protection in barley may be achieved by improving natural resistance to *Bymovirus*. Systematic screening of germplasm collections led to the identification of genotypes that exhibited high levels of resistance (Chen et al. 1992; Chen et al. 1996; Huang et al. 1994; Ma et al. 1994; Ordon et al. 1993; Ruan et al. 1984; Zhou and Cao 1985). The inheritance of resistance to different *Bymovirus* strains was studied (Gotz and Friedt 1993; Ordon and Friedt 1993). So far, eighteen resistance genes, 15 providing recessive and 3 providing dominant resistance, were described (Kai et al. 2012; Ordon et al. 2005) in the primary (16, *H. vulgare/spontaneum*) and secondary (*Rym14* and *Rym16*, *H. Bulbosum*) gene pool of barley. Since the known resistance genes possibly derive from allelic mutations of the same underlying gene, for example, *rym4* and *rym5* from different mutations of *HvEIF4E* (Stein et al. 2005), these 18 genes are genetically situated to approximately 10 independent loci on 7 barley chromosomes (Figure 1-2).

Over the last two decades *rym4*/*rym5*-based resistance was the predominant source of resistance for most commercially registered barley varieties in Europe (Graner and Bauer 1993; Graner et al. 1999b). *rym4* and *rym5* represent two independent alleles of the eukaryotic translation initiation factor 4E (Kanyuka et al. 2005; Stein et al. 2005). The implementation of both resistance alleles to agriculture provided reliable protection for winter barley cultivars against the widely distributed European strains of *Bymovirus* complex (Ordon et al. 2005). Unfortunately, this resistance has been repeatedly overcome in parts of Europe and Japan. As early as at the end of 1980s, a new virulent pathotype referred as BaYMV-2 broke down the *rym4*-mediated resistance in Germany (Huth 1989a) and UK (Adams 1991), as well as in other European countries later on (Steyer et al. 1995). A single substitution (1307’, Lys > Arg) of virus genome-linked protein (VPg) of the viral polyprotein has been associated with the susceptibility in barley plants carrying *rym4* (Kühne et al. 2003). Recently two new strains of BaMMV virulent on *rym5*-carrying cultivars were identified in Germany (Habekuß et al. 2008) and France (Hariri et al. 2003; Kanyuka et al. 2004). Similar to the situation observed earlier in Japan, a new pathotype BaYMV-III (Japanese strain) broke down *rym5*-controlled resistance (Kashiwazaki et al. 1989). Thus there is a constant need for independent and also novel resources of resistance to ensure for sustainability of barley resistance breeding to the *Bymovirus* disease.

The identification and implementation of the known resistance genes that are resistant to the newly emerged virulent strains e.g. BaMMV-Sil and BaMMV-Teik is a precise strategy for barley protection against the *Bymovirus* disease. It was shown that by mechanical inoculation of BaMMV-Sil the genotypes carrying *rym1*, *rym4*, *rym8*, *rym9* and *rym11* were resistant, and plants with *rym7* and *rym10* showed partial resistance equally to delayed accumulation of virus particles (Kanyuka et al. 2004). For BaMMV-Teik in Germany, only *rym5*-based resistance was overcome (Habekuß et al. 2008) in tested genotypes carrying the resistance genes. Interestingly, several resistance genes could confer broad-spectrum resistance to all European strains of both viruses such as *rym1* and *rym11* (Habekuß et al. 2008; Kanyuka et al. 2004; Ordon et al. 2005). Genetic mapping of both genes pointed at the same position on the proximal long arm of chromosome 4H, relatively close to the genetic centromere (Figure 1-3). The third resistance gene allocated to this chromosome arm, *rym18*, was reported to be independent of *rym1* (Kai et al. 2012). In addition, several resistance genes including *rym2*, *rym12*, *rym13*, $Rym14^{Hb}$, *rym15*, and $Rym16^{Hb}$ have been approved to confer resistance against BaYMV, BaYMV-2, BaMMV and BaMMV-Teik (Habekuß et al. 2008), while the pathological response to BaMMV-Sil is yet to be tested. A straightforward approach in resistance breeding is to apply monogenic resistance genes such as *rym1* and *rym11*, which is expected to be effective or potentially effective against all virulent strains of *Bymovirus* complex.

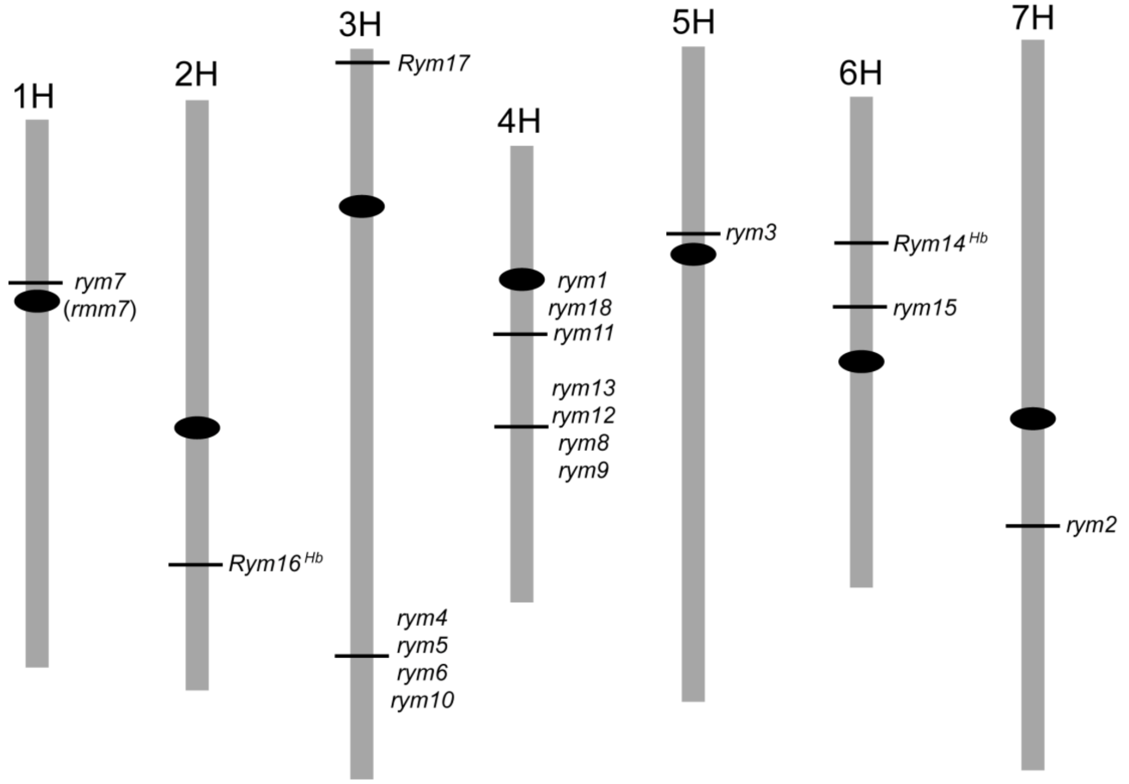


Figure 1-3 Genetic position of mapped loci conferring resistance / tolerance to BaYMV and BaMMV. The diagram was integrated and modified from Ordon *et al.* (2005) and Hiroomi *et al.* (2011).

1.3 Barley genomic resources for map-based cloning

Gene discovery by map-based cloning in barley was limited in the past due to the lack of genomic resources for marker saturation. Recently, significantly improved genomic resources became available for barley which should facilitate marker saturation as well as the procedure of chromosome walking. In the following an overview is provided for the improved genomic resources with relevance for the present thesis.

Over the last decades several genetic linkage / consensus maps have been developed for barley including different marker systems from hybridization-based restriction fragment length polymorphism (RFLP) markers to PCR-based simple sequence repeat (SSR) markers (Graner et al. 2010) plus microarray-based single nucleotide polymorphism (SNPs) markers (Close et al. 2009; Comadran et al. 2012). Several transcript-derived genetic maps were established on the basis of the improvement of barley genomics (Table 1-1). Varshney et al. (2007) integrated previously published microsatellites including 304 transcript-derived SSRs, and produced the consensus map spanning 1,068 cM yielding an average density of one SSR marker per 1.38 cM. Meanwhile, a consensus map was produced by exclusively transcript-derived markers consisting of 607 RFLPs, 190 SSRs and 258 SNPs, and covered total genetic length of 1118.3 cM with a global average marker interval of 0.9 cM (Stein et al. 2007). Later on, a high-density transcript-derived linkage map was developed based on a single segregating DH-population between parental genotypes 'Haruna Nijo' and 'H602' (Sato et al. 2009), and 2890 PCR-based sequence target site (STS) markers were generated. These user-friendly co-dominant genetic markers are the important resource for marker development. In order to further increase the marker density for genome-wide association study (GWAS), two commercial high-throughput hybridization-derived SNP assays were developed. By using 3,072 SNPs (BOPA), a consensus map containing 2,943 SNPs was produced (Close et al. 2009). The recently established iSelect SNP-assay integrating BOPA SNPs represents total 7,684 SNPs. >51.7% polymorphic markers (3,973 SNPs) were genetically distributed on the seven barley chromosomes (Comadran et al. 2012). The released commercial assays provide the possibility for rapid and efficient genome-wide identification of polymorphisms in barley. Therefore, the published maps provide a source of gene-based genetic markers for the new mapping projects in barley.

Table 1-1 Overview of recently established high-density genetic maps in barley

Reference	Marker type	Number of markers	Number of gene-based marker	Length of genetic map (cM)	Average marker distance (cM)	Comment
Rostoks *et al.* (2005)	SNP	1,237	1,237	1,211	0.98	Consensus map
Varshney *et al*. (2007)	SSR	775	304	1,068	1.38	Consensus map
Stein *et al.* (2007)	RFLP/SSR/SNP	1,032	1,032	1,118	0.9	Consensus map
Hearnden et al. (2008)	SNP, DArT	1,000	Unknown	1,100	1.1	Linkage map
Potokina *et al.* (2008)	TDM	1,596	1,596	Unknown	Unknown	Linkage map
Sato et al. (2009)	SNP/CAP/Indel	2,890	2,890	1,187	0.41	Linkage map
Close *et al.* (2009)	SNP	2,943	2,943	1,099	0.37	Consensus map
Aghnoum *et al.* (2010)	Multiple	6,990	Unknown	1,093	0.16	Consensus map
Comadran *et al.* (2012)	SNP	3,973	3,973	Unknown	Unknown	Linkage map
Poland *et al.* (2012)	SNP	>34,000	Unknown	Unknown	Unknown	Linkage map

Members of the grass family *Poaceae* have diverged from a common ancestor about 50 million years ago (Gaut 2002; Kellogg 2001). Comparative mapping of gene-based markers provided insights into conserved synteny of grass species genes (Keller and Feuillet 2000). By efficiently utilizing genomic resources available for grass species, map-based cloning of genes has become feasible in despite of the complexity of grass genomes (Feuillet et al. 2003; Yan et al. 2006). On the basis of increased marker density and eventually by whole genome sequencing of several grass species (Initiative 2010; Paterson et al. 2009) allowed in detailed comparison of inter-genomic synteny and to revisit the previously established grass genome synteny model (Moore et al. 1995) at much higher resolution (Initiative 2010). By combining flow sorting of chromosomes, next generation sequencing (NGS) and grass genome synteny information, the virtual gene order of barley chromosome 1H could be proposed in a model (Mayer et al. 2009). Mayer *et al.* (2011) unlocked the barley genome by the same approach and allocated 68% of the 32,000 barley genes to individual chromosomes or chromosome arms. This ordered and information-rich scaffold of the virtual barley genome, referred as barley genome zipper, provided an unprecedented resource for marker saturation especially in a targeted region in high-resolution mapping of candidate genes, e.g. *rym11* (Lüpken et al. 2013). Interestingly, the genome zipper integrates the full-length cDNAs datasets of barley, which was generated by sequencing clones of 12 cDNA libraries derived from the two-row malting barley cv. Haruna Nijo (Matsumoto et al. 2011). Out of total 22,651 representative FLcDNAs, 19,335 show the complete open reading frame (ORF). FLcDNA database represents longer and more accurate sequences of transcriptome in comparison to barley ESTs and Unigene clusters, therefore being a powerful tool for annotating candidate genes.

The virtual linear gene order model provided by the barley genome zipper was recently substantiated or even replaced by a whole genome sequence scaffold of barley. This genetic, physical and functional sequence assembly of the barley genome (IBSC 2012) describes the global barley gene-space. The physical map represented >95% barley genome (4.98 out of 5.1 Gb) containing a minimum tiling path (MTP) of 67,000 BAC clones. Of these, 4.56 Gb were anchored to individual chromosome arms and 3.9 Gb were anchored to a high-resolution genetic map. The genetic markers associated to the physical map or genomic sequence information integrated with the barley physical map open new possibilities to establish genome-assisted marker saturation in basically any target region of the barley genome. Thus marker development should no longer be recognized as limiting step for map-based cloning in barley. Relying on whole genome shotgun (WGS) sequence assembly, 26,159 high-confidence barley genes were reported (IBSC 2012) by sequencing and annotating the transcriptomes, and showed the sequence homolog to other grasses species (Initiative 2010). Once the genetic interval is determined by high-resolution mapping using a larger mapping population, the gene annotation information of the barley genome will facilitate the candidate gene identification.

1.4 The goals of the study

The principal aims of the present study are to characterize novel susceptibility factors for the barley yellow mosaic virus disease. The work included:

(a) Systematic utilization of barley genomic resources to rapidly and efficiently develop gene-based markers. Taking advantage of initial markers, this work intended to establish high-density mapping of *rym7* and produce flanking markers for recombinant selection to establish steps towards high-resolution mapping of the gene. In parallel, a large mapping population (DH and F_2) will be constructed, and segmental recombinant inbred lines (RILs) will be identified.

(b) Map-based cloning of *rym11* and functional analysis. This work attempted to construct a physical map and identify candidates for the resistance locus. If so, a set of genetic, mutagenic and transgenic approaches were subsequently applied to confirm the function of the identified candidate gene for *rym11*.

(c) Evaluation of geographic distribution and origin of *rym11*-based resistance. Re-sequencing of the candidate gene underlying *rym11*-based resistance in a large natural collection (>1,800 accession) of wild barleys, landraces and cultivated barleys will allow illustrating natural variations, geographic distribution and origin at *rym11* locus.

(d) Development of diagnostic markers for *rym11*.

2. Material and methods

2.1 Plant material

2.1.1 Mapping populations for *rym7*

A total of 53 double haploid (DH) genotypes were generated by Prof. Andreas Graner (IPK) from a cross between IPK GeneBank accession ‘HHOR3365’ (resistant, R) (http://gbis.ipk-gatersleben.de/gbis_i/, HOR 3365) and the cultivar (cv.) ‘Igri’ (susceptible, S), and were utilized for low-resolution mapping of *rym7*. A single DH line ‘DH93-04/34’ of this population carrying *rym7* was used in a cross with susceptible genotype ‘Igri’ to establish a larger DH population (>300 genotypes, DH and haploids are included) as well as a larger F_2 population (>12,000 gametes). A schematic overview of population development is provided in Figure 2-1. 246 DH or haploid individuals and 681 F_2 plants were initially used for screening segmental recombinant inbred lines (RILs). The parental genotypes and another susceptible cv. ‘Barke’ were used to analyze the gene *Hv-eIF(iso)4E*. Cultivar ‘Maris Otter’ was used as a positive control (susceptibility to *Bymovirus* infection) for the resistance test.

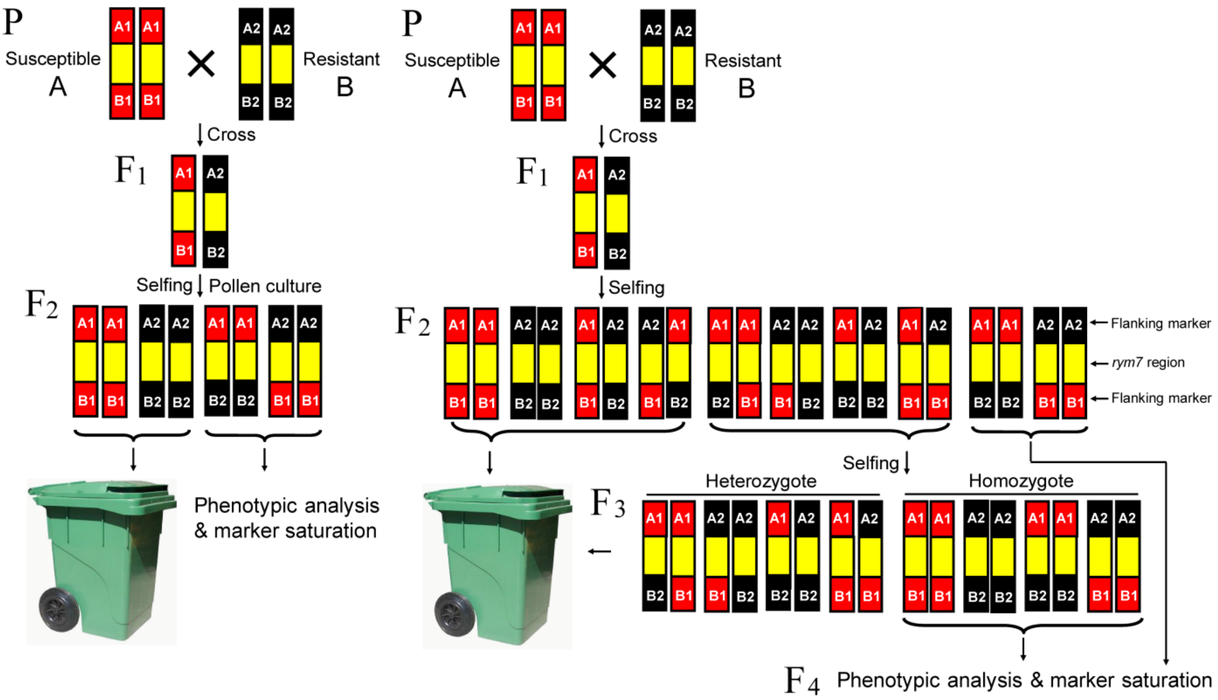


Figure 2-1 Schematic overview of population development for mapping of the *rym7* locus

2.1.2 Mapping population for *rym11*

According to high-resolution mapping of *rym11* (Lüpken et al. 2013), an F_2 population comprising a total of 5,012 individuals from the cross between susceptible cv. ‘Naturel’ and the *rym11*-carrying DH lines `W757/112´ and `W757/612’ was previously developed. In the present study only the most informative 18 RILs of the *rym11* containing 0.3 cM interval were used for physical and genetic delimitation of the resistance gene. DNA samples were kindly provided by Prof. Frank Ordon, JKI-Quedlinburg, Germany.

Table 2-1 Summary of natural genetic resources used for allele mining

Geographic region	Accessions	Hv	Hs	Countries	Number of countries
Europe	519	517	2	Albania, Armenia, Austria, Belarus, Belgium, Bulgaria, Croatia, Czech, Denmark, England, Finland, France, Georgia, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Moldova, Netherlands, Poland, Romania, Russia, Slovakia, Spain, Sweden, Switzerland, Ukraine, Yugoslavia (former)	31
East Asia	347	345	2	China, Japan, North Korea, South Korea	4
Near East	118	109	9	Afghanistan, India, Pakistan, Kazakhstan, Kyrgyzstan, Nepal, Tajikistan, Turkmenistan, Uzbekistan	9
West Asia	616	276	340	Cyprus, Iran, Iraq, Israel, Jordan, Lebanon, Oman, Syria, Turkey, Yemen	10
Africa	125	119	6	Algeria, Egypt, Ethiopia, Kenia, Libya, Morocco	6
North and South America	67	67	0	Argentina, Bolivia, Canada, Chile, Colombia, Mexico, Peru, Uruguay, USA	9
Australia	3	3	0	Australia	1
Unknown	21	15	6		
Total	1816	1451	365		70

2.1.3 Worldwide diversity collection for re-sequencing and allele mining

Re-sequencing of *HvPDIL5-1* was carried out in a large natural collection of 365 wild (*H. vulgare* ssp. *spontaneum*) and 1,451 domesticated barleys (*H. vulgare* ssp. *vulgare*) including 847 barley landraces, 559 cultivars and 5 *H.vulgare agriocrithon* (Table 2-1). In addition 197 old winter cultivars from Turkey and China were received from IPK Genebank (Gatersleben, Germany) and used. In summary, 1,816 non-redundant accessions were used in this study (Figure 2-1 and Table 2.1). Details of accession names, identified haplotypes, taxonomic designations, status of cultivation, growth habits, row types and collection sites are given (Appendix Table 1). The breeding line ‘Russia57’ (Accession name ‘HOR11192’, IPK Genebank) carrying the monogenic resistance locus *rym11* (Bauer et al. 1997) and a Chinese landrace ‘Mokusekko 3’ (Accession name ‘HOR11141’, IPK Genebank) carrying double resistance genes *rym1* and *rym5* are included in this collection. F_1 hybrids were produced by the crossing of the identified naturally occurring resistance alleles with the *rym11*-carrying parental lines `W757/112´ or `W757/612'.

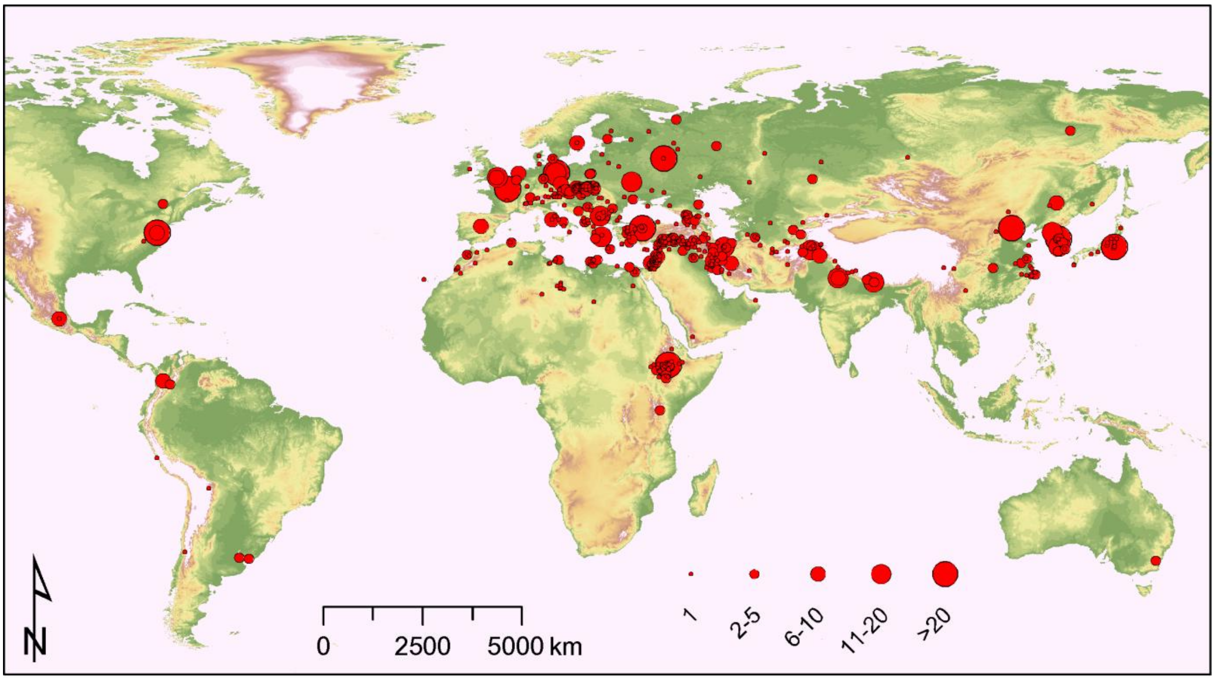


Figure 2-2 Geographic origin of the utilized barley genetic resources. The size of filled cycles briefly indicates the number of accessions, which were collected at each particular site. For accessions obtained from Genebank, where the precise collection site is unknown, the capital state of the source country was arbitrarily chosen as collected location.

2.2 DNA and RNA extraction, cDNA synthesis

Genomic DNA was extracted by using a previously described Cetyltrimethyl Ammonium Bromide (CTAB)-based DNA isolation approach (Doyle and Doyle 1987). Barley plants were cultivated under greenhouse (16h day/ 8h night, 20 °C) or climate chamber conditions (14h day / 10h night, 12°C) and young leaves at 3-leaf stage (ca. 2 weeks after sowing) or after BaMMV-inoculation (ca. 7 weeks post sowing) were sampled for DNA miniprep, which was previously described in details (Humbroich 2007). DNA quality and concentration were determined by measurement by using a NanoDrop spectrophotometer (Thermo Scientific, Wilmington, USA) and gel electrophoresis by using λDNA (Fermentas, Germany). The original DNA stocks were stored at -20°C, while a few aliquots were diluted to the working concentration [10-20 ng/µl] for PCR reaction.

RNA extraction was performed by using Trizol® solution with the recommended manual (Invitrogen, USA). The process of RNA extraction was performed in RNase-free conditions. That includes Diethylpyrocarbonate (DEPC) treated bottles and H_2O (pre-treated by 0.1% solution, incubated overnight at 37°C, and autoclaved at 121°C for 20 min), RNase-free tubes and tips (Biozym, Germany), and chemical solutions prepared with DEPC-treated H_2O. The working surface of fume hood was cleaned by using RNase AWAY solution (Molecular BioProducts, San Diego, CA). The young leaves at 3-leaf stage were harvested and frozen immediately in liquid nitrogen. RNA extraction was initiated by adding 1 ml Trizol® solution according to the provided protocol (Invitrogen, USA). The obtained RNA pellet was eluted to 20 µl DEPC-treated H_2O. 1 µl of the original RNA samples was used for determining concentration / quantity and quality by a NanoDrop spectrophotometer and gel electrophoresis. The stocks were stored at -80°C for use.

Prior to cDNA synthesis, digestion of genomic DNA in total RNA samples was performed in a reaction volume of 10 µl containing 1 µg total RNA, 1 µl DNase I [5 U/µl] (Fermentas, Germany), 1 µl 10 × reaction buffer (Fermentas, Germany), nuclease-free water. The reaction mix was incubated 30 min at 37°C, following by 10 min at 65°C via primarily adding 1 µl 50 mM EDTA solution for enzyme inactivation. The purified RNAs were directly used for reverse transcription by using the iScript cDNA synthesis kit (Bio-Rad, USA) with the supplier's instructions. The reaction was performed in a final volume of 20 µl including: 11 µl DNA-free RNA, 4 µl 5 × iScript reaction mix, 1 µl iScript reverse transcriptase and 4 µl nuclease-free water, with the suggested reaction procedure: 5 min at 25°C for initial denaturation, following by 30 min 42°C, and ultimately terminated by 5 min 85°C.

2.3 Polymerase chain reaction (PCR)

Standard PCR amplification in the thesis (e.g. marker saturation and re-sequencing) was performed in a final volume of 20 µl, containing 20 ng template-DNA, 0.1 µM forward and reverse primers, 0.5 U *Hot-star* polymerase (Qiagen, Düsseldorf, Germany), 1 × PCR reaction buffer (Qiagen, Düsseldorf, Germany), 1.5 mM $MgCl_2$, 0.1 mM dNTPs (Fermentas, Schwerte, Germany). Touch-down PCR amplification was performed: 10 min at 94°C for initial denaturation, followed by 6 cycles of 1 min at 94°C, 1 min annealing (64°C to 58°C, -1°C per cycle), 1 min 30 sec at 72°C, and plus 35 cycles including 1 min at 94°C, 1 min at 58°C, 1 min 30 sec at 72°C, and finally PCR step by 5 min at 72°C. Regarding to different primer sets and different experiments, the respective reaction volume and PCR cycling condition were changed with minor modifications. The PCR products were separated by gel electrophoresis. Details of the primer sets used in this study were given in Appendix Table 2.

PCR amplification in the analysis of gene expression was performed by using identical reaction mix / reagents, but few modifications of the cycling conditions including 10 min at 94°C for initial denaturation, followed by 27 to 35 cycles of 30 sec at 94°C, 30 sec annealing, 30 sec at 72°C, and finally PCR step by 5 min at 72°C. Quantitative reverse transcription (RT)-PCR was used for determining the transcriptional pattern of the candidate genes. The barley *Ubiquitin carrier* gene (NCBI accession ID: AK361071, *HvUBC*) was used as endogenous constitutively expressed control (Himmelbach et al. 2010).

2.4 Sanger sequencing and sequence analysis

Amplicon sequencing was performed in Plant Genome Resources Center, IPK, Gatersleben, Germany. PCR amplicons (e.g. amplified fragments of PCR markers and candidate genes) were primarily purified by using the NucleoFast 96 PCR Kit (Macherey-Nagel, Germany) according to the supplier’s instructions. 2 µl of purified DNA were subsequently resolved on a 1.5 % agarose gel to visually inspect for DNA quantity and determination of the required volume for cycle sequencing. Normalized amplicons (10 ng per 100 bp) were used for cycle-sequencing (BigDye®Terminator v3.1, Applied Biosystems, Darmstadt, Germany) by using ABI-3730xl technology.

Plasmid sequencing was performed in Eurofins MWG Operon, Ebersberg, Germany. The cultured *E.coli* solutions were sampled for the plasmid extraction by using the Plasmid Mini kit (Qiagen, Düsseldorf, Germany) with the recommended protocol. The pellet was eluted into 30 µl H_2O. 2 µl of plasmid solution were loaded on a 1.5 % agarose gel for determining concentration / quantity in comparison to λDNA (Fermentas, Germany). 15 µl of diluted plasmid solution [50-100 ng/µl] were delivered for plasmid sequencing in Eurofins (Ebersberg, Germany).

Sequence alignment and assembly were generated with the software Sequencher 4.7 (Gene Codes, Ann Arbor, MI USA). The trimmed sequences were quality controlled manually by visualization of chromatogram. The sequences that represent double peaks and/or heterozygosity are excluded in the subsequent analysis of marker development (Section 2.6.2) and haplotype analysis (Section 2.9.2).

2.5 Screening of BAC libraries, BAC sequencing, detecting overlap and identifying candidate genes

Physical mapping of the *rym11* locus took advantage of resources and data provided by generic efforts of building a whole genome physical map of barley (IBSC 2012). BAC contigs were identified either by sequence comparison of flanking markers to sequence resources integrated to the physical map or by PCR-based screening of cv. ‘Morex’ bacterial artificial chromosome (BAC) library HVVMRXALLeA as described previously (Schulte et al. 2011). Presence of previously un-observed overlaps was surveyed by re-assembly of all BACs belonging to the identified fingerprinted contigs (FPC) with software FPC (Soderlund et al. 2000) at Sulston cutoff e-10 as well as by sequencing minimum tilling path (MTP) of BACs of the respective contigs. MTP BACs were isolated from BAC libraries of cv. Morex (Schulte et al. 2011) and BAC sequencing was performed by Roche-454 GS FLX Titanium (Sequencing kit XLR70, Roche Applied Science, Germany) and 454-shotgun reads were assembled by using by the MIRA software version 3.2.1 essentially as described previously (IBSC 2012; Steuernagel et al. 2009).

Sequence overlaps between BACs were confirmed by PCR amplification and inspected by sequence comparison (BLASTN) (Altschul et al. 1990) and dot-plot analysis (dotter) (Sonnhammer and Durbin 1995). PCR amplification by using bridging primer pairs (Appendix Table 2) was carried out with minor changes compared to standard PCR (Section 2.3). The amount of template was reduced to 0.5-1 ng of BAC plasmid DNA and PCR was performed for 27 cycles only at annealing temperature (62°C). Template DNA of adjacent BAC clones overlapping to the terminal clones to be checked for contig overlaps were included in separate PCR reactions serving as negative controls. PCR amplicons generated from two putatively overlapping BAC clones were verified by Sanger sequencing and the overlap between BACs were visualized by sequence comparison (Altschul et al. 1990) and dot-plot analysis (Sonnhammer and Durbin 1995).

Repetitive elements of BAC clone sequences were masked by applying *K-mer* statistics (Schmutzer et al. 2013; Wicker et al. 2008). The repeat-masked BAC sequences were used to annotate coding sequences and identify candidate genes of *rym11*. Two strategies were applied: (i) Identification of potential mRNA by the software tool FGENESH (http://linux1.softberry.com/); (ii) Splicing of *K-mer* masked BAC sequences to fragments, which have 1500 bp each in length and share 500bp overlap to its adjacent fragment. Predicted mRNAs and spliced-fragments were compared to sequence databases by BLASTN (Altschul et al. 1990) (E-value < 1E-20, w=10) against barley high-confidence genes (IBSC 2012), barley full-length cDNAs (Matsumoto et al. 2011) and a barley EST unigene assembly (HarvEST_assembly35), as well as annotated gene sets of the sequenced grass species rice (CDs_V6_1) (Matsumoto et al. 2005), *Brachypodium* (CDs_V1.2) (Initiative 2010) and Sorghum (CDs_Sbi1_4) (Paterson et al. 2009). Putative open reading frames (ORF) of potential candidate genes were amplified and sequenced as described in section 2.3.

2.6 Marker development and genotyping

2.6.1 Primer design

Primer design was performed by using the online software batch primer 3 (Untergasser et al. 2007). The 454-shotgun reads from the genome zipper of barley (Mayer et al. 2011) were subjected to pick up primers. The standard parameters were applied plus a minor modification: Tm = 60°C (Arranged 59 to 61°C), product size = 300 bp (Arranged 150 to 500 bp) and GC content from 45% to 55%. Alternatively, repeat-masked BAC sequences were split into 1,500 bp fragments, and subjected for picking up primers. The respective PCR products ranged in length from 500 to 1000 bp. Primer sets for amplification of genes/gene fragments for the construction of transformation plasmid constructs of the gene *HvPDIL5-1* or for re-sequencing (and targeting induced local lesions in genomes - TILLING) of *HvPDIL5-1*, *β3-GT43*, *eIF4E* and *eIF(iso)4E* were selected manually. Details of oligonucleotide primers used in this study are given in Appendix Table 2.

2.6.2 Marker development

Sequence polymorphisms of either *rym7* or *rym11* were surveyed by PCR amplification (Section 2.3) and Sanger sequencing (Section 2.4) of the respective parental lines (*rym7*, section 2.1.1; *rym11*, section 2.1.2). The marker resources included expressed sequence target (EST) derived SSRs (GBM marker) (Varshney et al. 2007) and EST-derived SNPs (GBS marker) (Stein et al. 2007) as well as EST-derived STS (STS marker) (Sato et al. 2009) markers of chromosome 1H from three published transcript maps, STS markers developed from the 1H centromeric region of barley genome zipper (Zipper marker) (Mayer et al. 2011) and the primers produced from the sequenced BAC clones on 4HL as well as the newly developed 9k iSelect SNP-assay (Comadran et al. 2012). The target sequence of GBM / GBS / STS markers (Sato et al. 2009; Stein et al. 2007; Varshney et al. 2007) was compared (BLASTN, E-value < 1E-20, w=10) against the *Brachypodium distachyon* genome (Brachypodium database, CDs_V1.2) (Initiative 2010) to determine their location in the barley genome zipper (Mayer et al. 2011). The markers closely linked to the 1H centromere were the primary target to identify polymorphisms between the parental genotypes 'HHOR3365' and 'Igri'. The primers developed from the genome zipper of chromosome 1H (Mayer et al. 2011) was directly considered for *de novo* marker development.

The accumulated sequence dataset generated by Sanger approach was used for the development of cleaved amplified polymorphic sequence (CAPS) and derived-CAPS (dCAPS) markers by using the software SNP2CAPS (Thiel et al. 2004) and dCAPS finder (Neff et al. 2002), respectively, in order to detect single nucleotide polymorphisms. The insertion/deletion polymorphisms (InDel) were converted to size-polymorphism markers. PCR reactions of microsatellite markers (GBM marker) were performed (Section 2.3) with a few modifications: forward primers were used at 0.1 µM and combined with 1 µM forward primer carrying a 5' M13-universal primer tail (5'-CACGACGTTGTAAAACGAC-3') labeled with 5'-fluorescent dyes (Boutin-Ganache et al. 2001). Standard *Taq* Polymerase was replaced by 0.4 U Hot FIREPol®DNA polymerase (Solis BioDyne, Tartu, Estonia). Scoring of SSR markers was performed by using a capillary electrophoresis ABI-PRISM® 3100 genetic analyzer (Applied Biosystems, Darmstadt, Germany).

2.7 Screening for chemically induced mutants by TILLING

A 10,279 ethyl-methane-sulfonate (EMS) induced mutant population of cv. 'Barke' which is susceptible to the *Bymovirus* disease (Gottwald et al. 2009), was screened for induced mutations in the gene *HvPDIL5-1* by TILLING. To identify potential mutants, heteroduplex analysis of PCR amplicons was carried out by applying the mutation discovery dsDNA cleavage kit (DNF-480-3000, Advanced Analytical, Iowa, USA) and Gel - dsDNA reagent kit (DNF-910-3000T, Advanced Analytical, Iowa, USA) according to the supplier's instructions, and samples were subsequently loaded on *Advance*^{TM} *FS* system (Advanced Analytical, Iowa, USA) to score potential TILLING-mutants. For mutation verification PCR amplicons from positive M_2 plants were sequenced. All M_2 individuals with non-synonymous mutations were propagated. M_3 and M_4 progeny of TILLING mutants were subjected to artificial infection (Section 2.10) with BaMMV under greenhouse condition.

2.8 Plasmid vector construction and *agrobacterium*-mediated transformation

A 576 bp cDNA fragment containing the entire ORF of wild type *HvPDIL5-1* amplified from cv. 'Naturel' was cloned into the intermediate entry vector *pIPKTA38* (Douchkov et al. 2005) in a final reaction volume of 10 µl, containing 4 µl PCR amplicon, 1 µl *pIPKTA38* [150 ng/µl], 1 µl 10 x ligation buffer (Fermentas, Germany), 1 µl 50% PEG 4000 (Fermentas, Germany), 1 µl NaCl [500 mM], 0.5 µl *Swa*I restriction endonuclease [10 U/µl] (Fermentas, Germany), 0.5 µl T4 DNA ligase [5 U/µl] (Fermentas, Germany) as well as 1 µl nuclease-free water. The reaction mixture was incubated in a Thermocycler at 25°C for 1 h, following 10 min at 65°C for enzyme inactivation. Subsequently, the incubation was re-started at 25°C for 1 h by adding 5 µl mixed solution including 5 U *Swa*I restriction endonuclease (Fermentas, Germany), 1 x *Swa*I buffer (Fermentas, Germany), 50 mM NaCl. The transformation in *E. coli*, recombinant identification by restriction endonuclease-directed digestion and Sanger sequencing were consistent with the methods as described previously (Himmelbach et al. 2007). Recombinant vectors were combined with the binary destination plasmid *pIPKb002* (Himmelbach et al. 2007) for recombination by site-specific recombination of the Gateway® LR Clonase® II Enzyme mix (Life Technologies, Germany). The plasmid *pIPKb002* carries the selectable marker gene *Hygromycin Phosphotransferase* (*HPT*) under control of the maize *UBIQUITIN1* promoter and the candidate gene is controlled by a second maize *UBIQUITIN1* promoter (Himmelbach et al. 2007). The recombination reaction was initiated overnight at room temperature in a volume of 10 µl, containing 150 ng *pIPKb002*, 1 µl LR clonase Mix (Life Technologies, Germany) and 50 ng intermediate plasmid *pIPKTA38_cPDIL5-1_576*. The transformation in *E. coli* and identification of correct recombinants were essentially as previously described (Himmelbach et al. 2007).

Agrobacterium-mediated transformation in barley was performed essentially as described before (Hensel et al. 2009). Developing caryopses of the resistant genotype 'W757/612' were harvested 12-16 days post pollination and were surface sterilized. Immature embryos (IEs) of the resistant parent 'W757/612' were excised and pre-cultured on barley co-culture medium (BCCM) for five days (Pre-cultured immature embryos, PCIEs). For inoculation of IEs or PCIEs, the *Agrobacterium tumefaciens* strain AGL-1 harbouring the destination plasmid *IPKb002_cPDIL5-1_576* was used. Recombinant AGL-1 clones were grown and inoculated with the IEs or PCIEs. After co-culture IEs or PCIEs were transferred on barley callus induction medium (BCIM) supplemented with 50 mg/l hygromycin (Roche, Mannheim, Germany) to induce calli. After 2 rounds of 2 weeks each in the dark at 24°C, the calli were transferred to barley regeneration medium (BRM) supplemented with 25 mg/l hygromycin and transferred into light (16 hours per day). Plantlets with a leaf length of 2 to 3 cm were grown in glass tubes until root emerged. All regenerants were subsequently transferred into soil. Genomic DNA from young leaves was isolated for PCR amplification with the primers specific for the selectable marker gene *HPT*. All transgenic plants were propagated. T_1 segregating progenies were subjected for phenotyping and genotyping.

2.9 Computational data analysis

2.9.1 Linkage and syntenic analysis

Polymorphic markers were used for genotyping the DH population of *rym7*. A genetic map was constructed by JoinMap 4.0 (http://www.kyazma.nl/index.php/mc.JoinMap/) using the regression algorithm and applying the Kosambi function (Kasambi 1944). The resulting genetic map was further curated by help of the software Mapchart 2.0 (Voorrips 2002) for comparison of synteny. The entire barley gene sequences of the mapped markers were obtained by BLASTN analysis of marker sequences against a barley full-length cDNA database (Matsumoto et al. 2011). The targets were subsequently compared to *Brachypodium* CDs_V1.2 (Initiative 2010) for identification of putative orthologous genes. Collinearity between the mapped barley markers and the corresponding orthologs of rice and sorghum was determined by consulting the virtual linear gene order map of barley (genome zipper) (Mayer et al. 2011).

2.9.2 Haplotype analysis and Median Joining (MJ) network

For haplotype analysis 1,974 bp carrying full-length genomic sequences from the starting to the stop codon of *HvPDIL5-1* was applied to generate the primary file of sequence alignment. 456 bp full-length ORF of *HvPDIL5-1* were extracted in the accumulated file for sequence alignment. Allelic haplotypes were defined by using DNASP 5.10.1 (Librado and Rozas 2009) with gap-inclusion algorithm (Deletion included) according to sequence diversity. The haplotypes (singletons) that was only observed in single accession were further confirmed by independent PCR-amplification and Sanger sequencing. In order to produce the files applied for MJ-Network analysis, gap-inclusion and gap-exclusion algorithms were applied. The initial algorithm (gap-inclusion) was suited for clustering of sequence data served from wild and domesticated barleys, whereas the latter was applied for phylogenetic analysis including also more distantly related grass species. The rdf.file generated by the software DNA Alignment 1.3.1.1 was subjected to generate MJ-Networks, which were constructed by Network 4.6.1.1 (Bandelt et al. 1999). The networks were finally improved by Network publisher 1.3.0.0 (Fluxus Technology Ltd., Clare, and Suffolk, UK). According to the given geographically references (Appendix Table 1), the natural distribution of accessions on the topographic maps was performed essentially as described earlier (Comadran et al. 2012).

For sequences generated of the genes *eIF(iso)4E*, *eIF4E* and *β3-GT43* sequence assembly and polymorphism / haplotype survey was performed manually by Sequencher 4.7 (Gene Codes, Ann Arbor, MI USA). The MJ-network analysis was not performed for analysis of re-sequencing data of these genes.

2.9.3 Phylogenetic analysis

To identify barley protein disulfide isomerase (PDI) like proteins, cDNA sequences of the homologous genes of other plant species (d'Aloisio et al. 2010; Houston et al. 2005) were applied to perform local homology search (BLASTN and BLASTX) in barley full-length cDNAs and whole genome shotgun (WGS) sequence databases (IBSC 2012; Matsumoto et al. 2011). The output dataset was analyzed manually to obtain the homologous genes with highest nucleotide identity. Deduced protein sequences were analyzed by SignalP 4.0 (Petersen et al. 2011), THMMM 2.0 (Moller et al. 2001), TargetP 1.1 (Emanuelsson et al. 2007) and CDD (Marchler-Bauer et al. 2013), respectively, for the presence of signal peptides, transmembrane domains, motifs for sub-cellular localization, or other functional domains and active centers (Cys-x-x-Cys).

Homology search of *HvPDIL5-1* in plants and animals was performed by BLASTX and TBLASTX on NCBI and specific databases of *S. tuberosum* (Xu et al. 2011), *S. lycopersicum* (Sato et al. 2012) and *N. benthamiana* (Draft genome, v0.4.4) according to the protein similarity. Prediction of signal peptides, transmembrane domains, motifs for sub-cellular localization, or other functional domains and active centers was described above. Multiple sequence alignments of all identified homologous genes in monocots, dicots and mammals were performed by the online software tool ClustalW2 (Larkin et al. 2007). The homologous proteins of *HvPDIL5-1* from all evolutionary and organizational stages (e.g. unicellulate and multicellulate organisms, algae / primitive land plants / higher vascular plants etc.) were used for constructing the phylogenetic tree by the software MEGA version 5.05 with neighbor-joining method (Masatoshi Nei 2000), and its reliability was evaluated by Bootstrap analysis with 1,000 replicates.

2.9.4 Three dimensional (3D) modeling of protein structure

Three-dimensional model of *HvPDIL5-1* and the homologous proteins was carried out according to the protein similarity of human ERp18 (PDB code: 2k8vA) by using SWISS-modeling approach (Arnold et al. 2006; Rowe et al. 2009). The simulated structures were visualized with the software PyMol 0.97 in ‘pretty’ mode (DeLano and Lam 2005).

2.10 Artificial and natural infection with *Bymovirus* and testing for resistance

Artificial mechanical inoculation with the isolate BaMMV-ASL as well as testing for resistance / susceptibility was performed as previously described (Habekuß et al. 2008). After sowing, barley plants were cultivated in the greenhouse (16h day / 8h night, 12°C). At 3-leaves stage (~2 weeks after sowing), the plants were mechanically inoculated twice at an interval of 5-7 days by using leaf sap of BaMMV-infected plants of susceptible cv. 'Maris Otter', mixed in K_2HPO_4 buffer (1 : 10; 0.1 M; pH 9.1) containing silicon carbide (caborundum, mesh 400, 0.5 g/25 ml sap). Five weeks after the first inoculation, the number of infected plants with mosaic symptoms was scored, and double antibody sandwich - enzyme linked immunosorbent assay (DAS-ELISA) with BaMMV-specific antibodies was carried out in parallel according to the published protocols (Clark and Adams 1977). Presence of virus particles was estimated via extinction at 405 nm using a DynaTech MR 5000 microtiter-plate reader (DynaTech, Rückersdorf, Germany). Plants with absorbance > 0.1 were scored qualitatively as being susceptible.

Natural infection by strains of BaMMV and BaYMV was performed under field conditions. In autumn, thirty grains per accession were sown into the infested fields at JKI Quedlinburg, Germany. In spring of the following year, young leaves were harvested twice in February and April for ELISA test with BaMMV and BaYMV-specific antibodies. Details of ELISA-test procedure was given according to the catalogue of BIOREBA in 2009 (Reinach, Switzerland).

3. Results

3.1 Gene-based high-density mapping of *rym7*

3.1.1 Gene-based marker development

rym7 confers partial / complete resistance to different strains of BaMMV (Graner et al. 1999a; Habekuß et al. 2008; Kanyuka et al. 2004), and its implementation in modern cultivars may prevent yield losses of winter barley. Recently published barley genomic resources provided a straightforward tool for gene-based marker development at the *rym7* region of barley chromosome 1H (Graner et al. 1999a). The public information included transcript-derived genetic maps (Comadran et al. 2012; Sato et al. 2009; Stein et al. 2007; Varshney et al. 2007), a barley full-length cDNA database (Matsumoto et al. 2011) as well as whole genome or sorted chromosome shotgun sequences (IBSC 2012; Mayer et al. 2011). In the current study, these datasets were combined to develop gene-based markers surrounding the *rym7* locus (Table 3-1). Ninety-three GBM / GBS / STS markers of chromosome 1H were tested for polymorphism, and 4 GBM, 18 GBS as well as 23 STS markers detected a polymorphism between parental genotypes ‘HHOR3365’ and ‘Igri’ (Table 1). In order to further increase the pool of potential markers for mapping of *rym7*, 126 primer pairs were developed on the basis of Roche/454 sequence reads underlying gene-models of the virtual linear gene order model ‘genome zipper’ of barley in the tentative *rym7* region of chromosome 1H. One-hundred and one primers produced a specific product. Out of these, 66 amplicons (>300 bp) were sequenced for the determination of polymorphisms. However, a highly reduced frequency of marker polymorphisms was observed in this marker set (0.17) in comparison to the GBM / GBS / STS markers (0.27 / 0.67 / 0.45) (Table 1). Overall, four SSR- (GBM) and 52 SNP-based (GBS / STS / Zipper) markers provided the primary marker resource for genetic mapping of *rym7*.

During the period of marker development a new Illumina iSelect custom 9k bead assay became available comprising 7,864 SNP assays. This new assay for polymorphism was applied to survey between both parental genotypes ‘HHOR3365’ and ‘Igri’. 3,593 polymorphic loci were detected. 294 of the potential 546 SNP markers of the 9k chip that were previously assigned to be present on chromosome

1H were polymorphic, and 49 SNP-markers surrounding the centromere represented a novel pool of *rym7* candidate markers, in regard to the previously determined genetic position of *rym7*. These markers, however, were not further included in low-resolution mapping of the gene *rym7* with 53 DH population, but represent a high-value marker resource for future marker saturation of the *rym7* target interval.

Table 3-1 Summary of marker development for *rym7* by using the established genomic resources of barley

Collection[a]	Marker on 1H	Polymorphic markers	Frequency of polymorphic marker	SNPs	SNP frequency (bp)	Indels	Indel frequency (bp)
GBM-marker	15	4	0,27	nd	na	4	na
GBS-marker	27	18	0,67	30	1/407	1	1/12215
STS-marker	51	23	0,45	35	1/562	6	1/3283
Zipper-marker	66	11	0,17	22	1/1294	4	1/7120
iSelect-marker	546	294	0,54	294	na	nd	nd
Total	705	350					

na = not applicable, nd = not determined. [a] GBM-, GBS-, STS-, Zipper- and iSelect-markers were designated as Varshney *et al.* (2007), Stein *et al.* (2007), Sato *et al.* (2009), Mayer *et al.* (2011), Comadran *et al.* (2012), respectively.

3.1.2 High-density mapping of *rym7* and comparative analysis of conserved synteny to sequenced grass genomes

Gene-based marker mapping of *rym7* was performed by the analysis of 53 DH lines. Artificial inoculation by BaMMV revealed that 20 and 33 lines were resistant and susceptible, respectively, to virus infection under climate chamber conditions ($\chi^2_{1:1}$=3.19<3.84), therefore supporting that *rym7* controlled partial resistance is controlled by a single locus. In order to select markers for mapping, 56 previously identified polymorphic markers including GBM-, GBS- and STS-markers were used to identify their putative order and position on chromosome 1H according to the conserved synteny-based virtual linear gene order model (Mayer et al. 2011). Out of these, 23 polymorphic markers were selected to genotype the segregating population (Table 3-2 and Figure 3-1). A genetic map was constructed comprising a length of 104.7 cM containing the *rym7* locus (Figure 3-2). The resistance locus was assigned to a 9.9 cM interval flanked by markers k04311-1 and k04452 representing three and two recombinants, respectively. The results obtained by using this newly established mapping population (53 DH lines), confirm the previously determined genetic position of the gene *rym7* closely linked to the centromere of chromosome 1H (Graner et al. 1999a). Thus the gene *rym7* is likely situated in a genomic region characterized by highly suppressed recombination. Nine newly established markers co-segregated (1H-1079, k05001, 1H-1051, 1H-1006, eIF(iso)4E, k06232, Bmag347, GBM1029 and GBS821) with the gene *rym7* (Figure 3-2). Based on the respective interval of the virtual linear gene order map of chromosome 1H, the region characterized by these co-segregating markers comprises at least 200 putative genes. According to the same model, the entire 10 cM genetic interval between the closest flanking markers (k04311-1 and k04452) potentially contains more than six-hundred genes (Mayer et al. 2011).

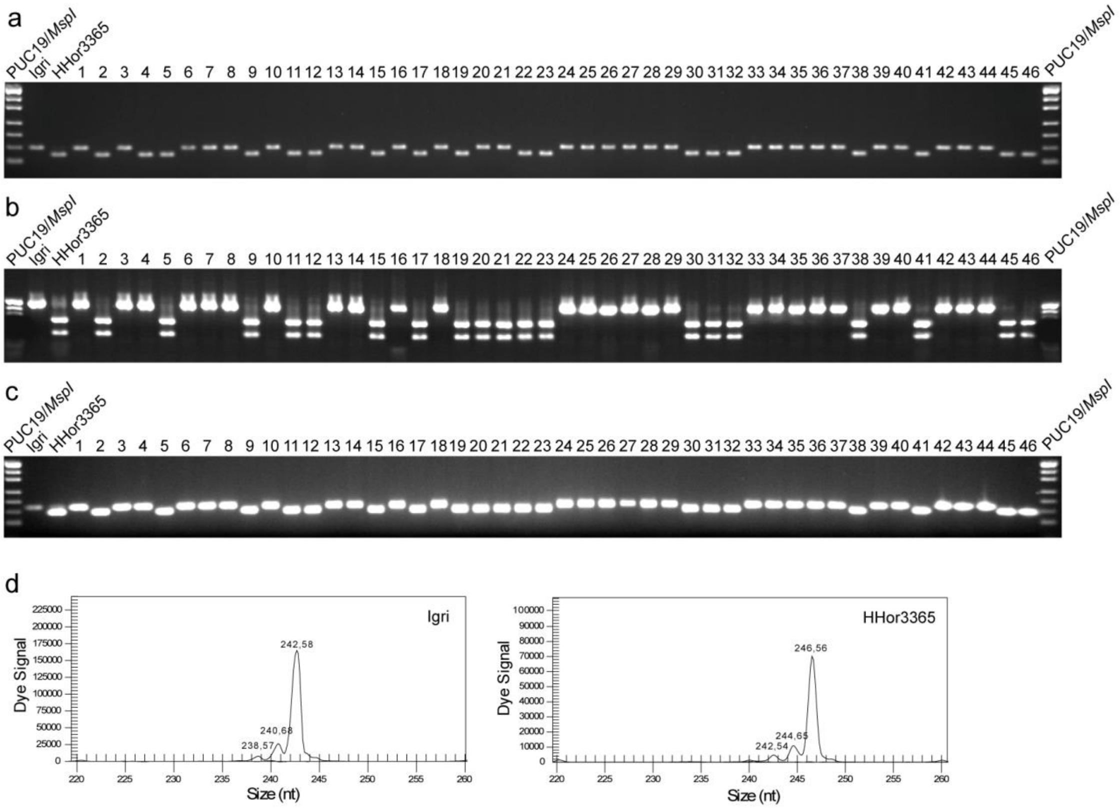


Figure 3-1 Examples of different gene-based marker types established for genetic mapping of the gene *rym7*. Two parents and 46 out of 53 DH lines are represented. (a) Genotyping with the dCAPS marker k04311-1. Amplicons were subsequently digested by *HinfI*. (b) Amplification of CAPS marker k08483 and subsequent digestion with *BbvI*. (c) Amplification of 1H-1006 (InDel) and gel separation revealed the size-polymorphism. (d) Amplicons of fluorescence-labeled microsatellite GBM1029 displays 4 bp size difference between Igri and HHOR3365.

Table 3-2 Genetic markers mapped at the *rym7* locus

Marker ID	Marker type	Igri (bp)	HHOR3365 (bp)	Zipper position[a]
k04311-1	dCAPS, *HinfI*	148	130, 18	1H-499
k06232	CAPS, *SphI*	229	177, 60	1H-952
k05001	CAPS, *BtgI*	533	406, 127	1H-1060
k08045	CAPS, *Tsp509I*	221,165,87,61,37,13	234,165,87,61,37	1H-1095
k04452	CAPS, *ApoI*	398, 119, 92	398, 211	1H-1122
k08546	CAPS, *DdeI*	705, 337, 247	705, 584	1H-1131
k02563	CAPS, *RsaI*	276, 66	341	1H-1181
k06493	CAPS, *StuI*	476	295, 181	1H-1166
k08483	CAPS, *BbvI*	438	286, 152	1H-1168
k09911-1	dCAPS, *BsrI*	173	147	1H-1552
GBS0821	CAPS, *FatI*	231,91,72,64,37,17	171,91,72,66,64,37,17	1H-938
GBS0765	CAPS, *SacI*	836, 168	1004	1H-1166
GBS0738	CAPS, *TseI*	419, 88, 23	308, 111, 88, 23	1H-1467
GBM1007	EST-SSR	227	219	No
GBM1029	EST-SSR	243	247	1H-943
GBM1032	EST-SSR	118	117	No
GBM1042	EST-SSR	312	309	1H-275
eIF(iso)4E	SNP	A	G	1H-1004
1H-1006	Indel	163	144	1H-1006
1H-1013	CAPS, *BtgZI*	465	239, 226	1H-1013
1H-1051	SNP	G	C	1H-1051
1H-1079	SNP	T	C	1H-1079
TC134653	CAPS, *PsiI*	288, 141	429	1H-1574
Bmac32	SSR	234	250	No
Bmag347	SSR	139	125	No
GMS21	SSR	173	175	No

[a]= refers to row number in chromosome 1H genome zipper of supplementary dataset 2 of Mayer et al. 2011.

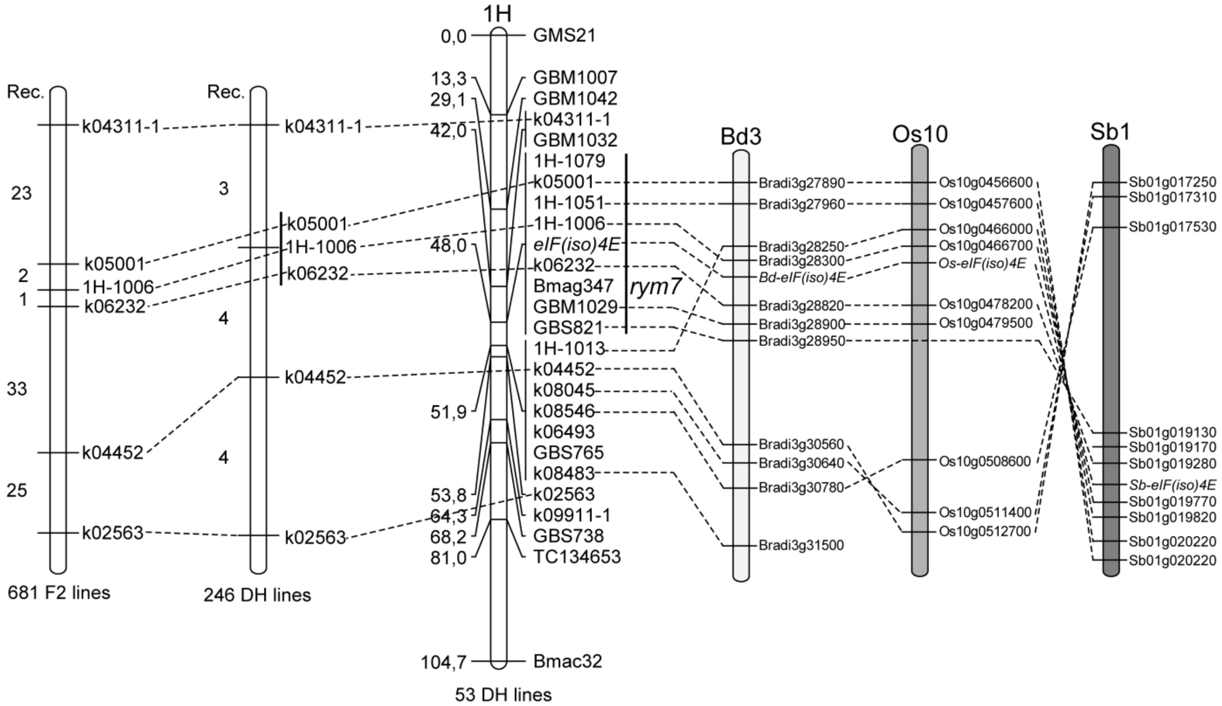


Figure 3-2 Genetic mapping of *rym7* in comparison to the syntenic regions in rice, *Brachypodium* and sorghum. The genetic map of *rym7* was constructed by gene-based markers on the basis of 53 DH lines. The screening of new RIL recombinants was performed in 246 DH lines and 681 F_2 lines. The numbers between markers indicate the number of recombinants. The genetic markers in three different populations and the putative orthologs from three different grass species are connected by dashed lines.

3.1.3 Screening for segmental RILs

In order to prepare for increased resolution genetic mapping of the gene *rym7* it is required to increase population size and survey for recombination events in the genetic neighbourhood of the gene. Two mapping populations consisting of >300 DH lines and >6,000 F_2 genotypes have been constructed. Initially, 246 DH lines and 681 F_2 individuals were genotyped by two flanking markers (k04311-1 and k02563) and four co-segregating markers (k04452, k05001, 1H-1006 and k06232) (Figure 3-2). Between markers k04311-1 and k02563, 11 recombinants (2 haploids included) from DH population and 100 recombinants from F_2 population were identified. The markers formerly co-segregated in 53 DH individuals but could be separated now in the enlarged population. Marker k04452 displayed 4 recombination events to the remaining cluster (k05001, 1H-1006 and k06232) in 246 DH lines. Two recombinants between k05001 and 1H-1006, and 1 recombinant between 1H-1006 and k06232 were obtained by the analysis of 681 F_2 plants. On the basis of homology search (Mayer et al. 2011) only 97 genes in *Brachypodium* were present in the collinear interval of k05001 and k06232. The phenotyping for *Bymovirus* resistance of the identified RIL families is pending and could not be finalized in frame of this thesis.

3.1.4 *Hv-eIF(iso)4E* - a potential candidate of *rym7*?

Recessive resistance to *Potyvirus* infection in different plant species was shown to be controlled by genes belonging to the eukaryotic translation initiation complex (Le Gall et al. 2011; Robaglia and Caranta 2006). In barley, allelic variants of the gene *Hv-eIF4E* conferred *rym4*/*rym5*-based immunity to BaMMV and BaYMV (Kanyuka et al. 2005; Stein et al. 2005). Non-synonymous mutations or knockout of its paralogous copy, *eIF(iso)4E*, in different species also confers resistance to different viruses of *Potyvirus* genus (Duprat et al. 2002; Jenner et al. 2010; Lellis et al. 2002; Ruffel et al. 2006; Wang et al. 2013). Interestingly, the barley gene of *Hv-eIF(iso)4E* was predicted by conserved synteny to other grasses to be located at the *rym7* region of chromosome 1H (Figure 3-2). Genetic mapping of the barley gene *Hv-eIF(iso)4E* revealed its linkage to the *rym7* locus (Figure 3-2). Thus, possibly, variants of the gene *Hv-eIF(iso)4E* could confer *rym7*-based resistance to BaMMV.

The candidate gene hypothesis for the gene *Hv-eIF(iso)4E* was followed up further. The entire open reading frame (ORF) was analyzed in both parents as well as in the susceptible cv. Barke. Sanger sequencing revealed a 3,216 bp genomic fragment and 633 bp comprising the entire ORF of *eIF(iso)4E* consisting of 5 exons and 4 introns (Appendix Table 2). A single base pair substitution within intron 1 (778', A>C) was subsequently suited for genetic mapping of the gene. However, no sequence diversity polymorphism was found in the coding sequence between the resistant and susceptible cultivars.

3.2 Map-based cloning and characterization of the gene *rym11*

3.2.1 Map-based cloning of *rym11*

The monogenic resistance locus *rym11* confers broad-spectrum resistance to all European isolates of BaYMV and BaMMV (Bauer et al. 1997; Habekuß et al. 2008; Kanyuka et al. 2004). Previously, low-resolution genetic mapping placed the gene to the long arm of chromosome 4H in close proximity to the centromere (Nissan-Azzouz et al. 2005). By the analysis of 5,102 F_2 segregants, Lüpken *et al.* (2013) assigned the recessive locus to a genetic interval of 0.074 cM between the markers C_1030750_B and C_1012894_B, and co-segregated with C_205243_B (Lüpken et al. 2013). By sequence comparison of flanking markers to sequence resources integrated to the physical map of the barley genome (IBSC 2012), the markers C_1030750_B and C_205243_B could be anchored to FPC contigs ctg551 and ctg1996, respectively (contigs at that time were identified from an intermediate FPC assembly of the genome-wide physical map assembled at Sulston cutoff stringency: e-50). The physical distance between the two flanking markers C_1030750_B and C_1012894_B was determined to be >2 Mbp plus at least 1 physical gap. Thus this step of physical mapping identified contigs bearing the closest flanking markers, but a single contig bridging the entire locus was not yet identified for the target region.

Taking advantage of a minimum tilling path derived for the two identified BAC contigs, thirty-six BAC clones from ctg551 and ctg1996 were sequenced by Roche/454-technology to 20-fold coverage and assembled. Interestingly, reassessment of the contig assembly for the original BAC clones plus two newly identified BACs (HVVMRXALLeA0320K22 and HVVMRXALLhA0172M09) by PCR-based screening of cv. Morex BAC libraries (Schulte et al. 2011) at lower assembly stringency (e-10) and sequence comparison of BAC clones revealed an overlap of around 18 kb between BAC clones HVVMRXALLhA0173N06 and HVVMRXALLhA0172k23 of the FPC contigs ctg551 and ctg1996. Thus a physical contig had been established between the flanking markers. New markers were developed on the basis of the newly available sequence information. By focusing on 18 RILs out of 5,102 F_2 individuals (Lüpken et al. 2013), the genetic interval was delimited to 0.0196 cM by the new flanking markers C5B4C and C2B18S2 (Figure 3-3, a). A single recombination event each was observed between the proximal (C5B4C) and the distal flanking markers (C2B18S2) and the gene *rym11*. A set of co-segregating markers derived from BAC sequences (dominant markers: C5B6D3, C5B6D4; co-dominant markers: C5B6coD1, C5b6coD2, C5B11S, C5B11C, C2B22C4, C2B23C18, C2B23C22, C2B22C7) was identified (Figure 3-3, b and Appendix Table 2). As intermediate result (Not shown in this thesis), 15 sequenced BAC clones were delimited within the genetic interval by the new flanking markers.

To construct the complete physical map and unravel the entire sequence of the *rym11* locus, the physical overlaps of the 15 sequenced BAC clones located between markers C5B4C and C2B18S2 were examined at sequence level by dot-plot analysis. In contrast to the expectation based on the FPC fingerprint data of the identified BAC contigs no sequence overlap could be detected between BAC clones HVVMRXALLeA0081K17 and HVVMRXALLeA0299M21, HVVMRXALLmA0317E07 and HVVMRXALLhA0197G10, HVVMRXALLhA0252M10 and HVVMRXALLhA0173N06, HVVMRXALLmA0209F07 and HVVMRXALLrA0058F23. The postulated gaps could be bridged by sequencing four additional BAC clones (HVVMRXALLmA0062A10, HVVMRXALLeA0028C08, HVVMRXALLeA0377C03 and HVVMRXALLmA0182L01) belonging to the same FPC contigs (Figure 3-3, b). In summary, nineteen BAC clones were sequenced for the interval of *rym11*. After completing BAC overlap analysis by bridging PCR-amplification and dot-plot validation, the physical interval of the gene *rym11* was finally represented by 12 non-redundant BACs (Figure 3-4) expanding over a physical distance of approximately 1.25 Mbp (Figure 3-3, b).

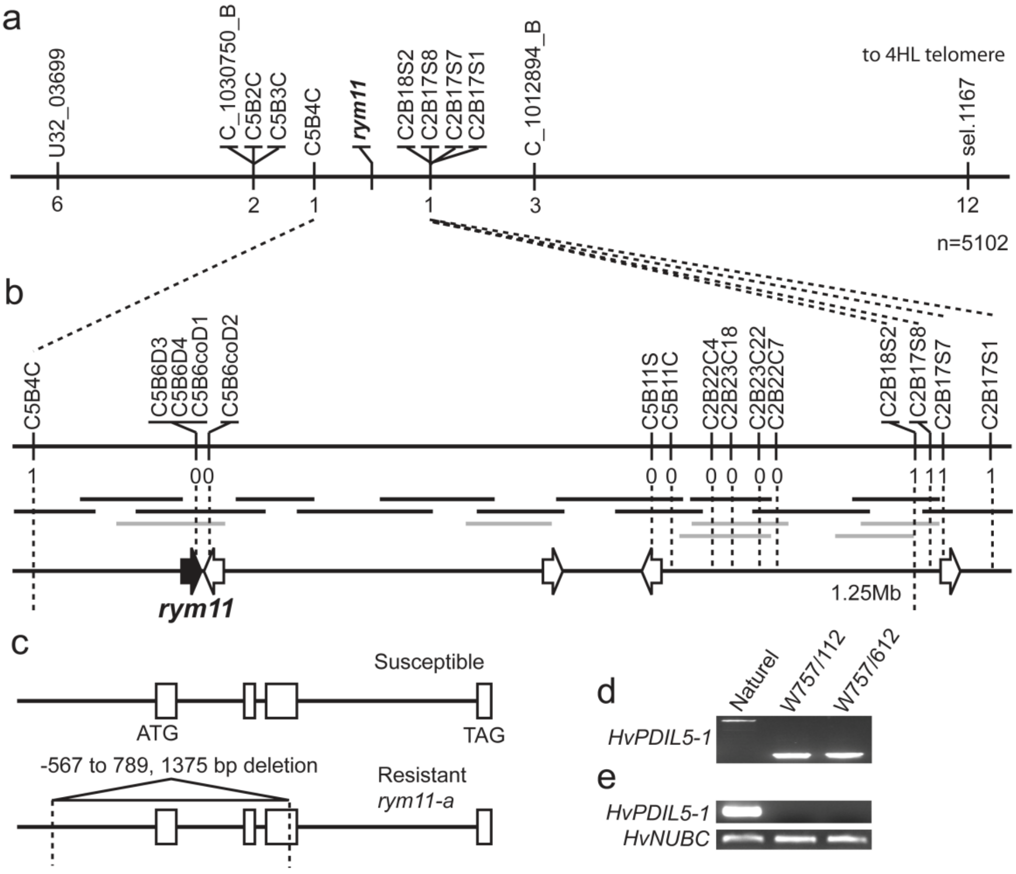


Figure 3-3 Map-based cloning of *rym11*. (a) High-resolution mapping of *rym11*. The number below each marker indicates the recombination events between *rym11* and the adjacent marker. (b) Schematic overview of the physical contig map at the *rym11* locus. (c) Sequence analysis of *HvPDIL5-1* in parental lines reveals 1,375 bp deletion in the 5'-region of the gene in resistant genotype. (d) PCR amplification of parental genomic DNAs represents a large deletion in 'W757/112' and 'W757/612'. (e) Due to the large deletion expression of the gene is completely knocked out and no transcript of *HvPDIL5-1* can be detected in resistant parents. The gene *HvNUBC* was included as positive endogenous transcriptional control.

Annotation of the non-repetitive sequences of this interval identified four open reading frames (ORF). This included two genes with sequence homology to *Elongation Factor 1-α* (*EF-1α*), one homolog to *β3-GlucuronylTransferase Like 43* (*β3-GT43*) and one gene with homology to *Protein Disulfide Isomerase Like 5-1* (*HvPDIL5-1*). *PDIL5-1* and *β3-GT43* were observed in the syntenic region of *Brachypodium* and rice (Figure 3-5). One of two *EF-1α* genes (On BAC clone HVVMRXALLmA0062A10) is present in barley and *Brachypodium*, but absent in rice. The second *EF-1α* on BAC clone HVVMRXALLhA0252M10 was exclusively found in barley. According to BAC sequences of cv. 'Morex', 5 SNPs were found in the coding sequences between the two *EF-1α* genes (988', T/G; 1029', C/T; 1308', A/C; 1341', A/G; 1344’, G/A), implying a gene duplication of *EF-1α* in barley. The high level of sequence identity between both genes complicated the aim of copy-specific amplification. Thus, both members were principally analyzed together in the following experiments. Re-sequencing of PCR products did not reveal any sequence polymorphism between the two parental genotypes of the mapping population (Lüpken et al. 2013). In addition, gene expression was determined by qRT-PCR, indicating similar transcriptional pattern in parental genotypes (Figure 3-6, a and c). For the two genes *β3-GT43* and *PDIL5-1* a 3-bp insertion and 1,375-bp deletion were detected in their respective coding sequences, respectively. Despite of the small in-frame insertion (3-bp, 1 Tryptophan insertion) just in front of the stop codon of gene *β3-GT43* in the resistant genotypes, this gene was ruled out as a candidate for *rym11*. The gene exhibited similar expression levels in resistant as well as susceptible genotypes (Figure 3-6, b and c). More importantly, re-sequencing of this gene in a breeding line ‘Russia57’ that is known to carry *rym11*-based *Bymovirus* resistance (Bauer *et al.*, 1997) did not reveal sequence variations in comparison to the susceptible genotype ‘Naturel’. Re-sequencing of this gene in 2 susceptible cultivars and 23 resistant accessions provided further evidence that *β3-GT43* was not the candidate gene for *rym11*. A single synonymous substitution (294’, G > A) was found in five accessions whereas twenty accessions carried the wild type allele of the susceptible genotype ‘Naturel’ (Details of re-sequencing *β3-GT43* are given in Table 3-6). Thus *HvPDIL5-1*, encoding for a *PROTEIN DISULFIDE ISOMERASE LIKE* protein, remained as the only candidate gene, since it carried a large 5’ deletion in the resistant genotype. A 1,375 bp deletion in promoter and first three exons in the resistant genotypes ‘W757/112’ and ‘W757/612’ (Referred as *rym11-a*, Figure 3-3, c and d) resulted in no detectable transcript levels of the gene *HvPDIL5-1* (Figure 3-3, e).

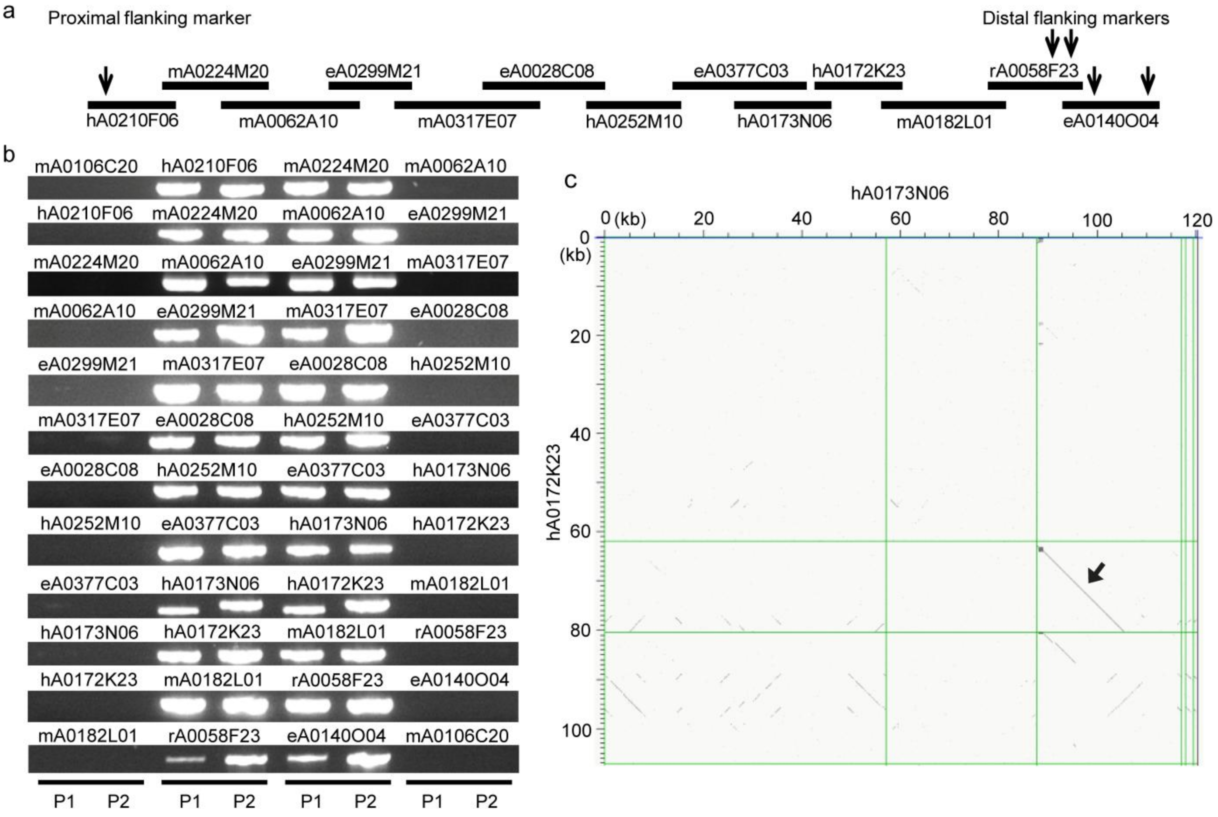


Figure 3-4 Physical map of *rym11*. (a) Schematic overview of the overlapping BACs. (b) Physical overlap of neighbor BACs was verified by PCR amplification with two pairs of primers independently (P1, P2). Different primer pairs were subjected to confirm the overlap between different neighbor BAC pairs. (c) Dot-plot analysis and visualization of an overlap detected between BACs HVVMRXALLhA0172K23 and HVVMRXALLhA0173N06. The overlap between these two BACs is presented as an example representative for other overlapping neighboring BACs. The black arrow indicates the shared fragment of two neighbor BACs.

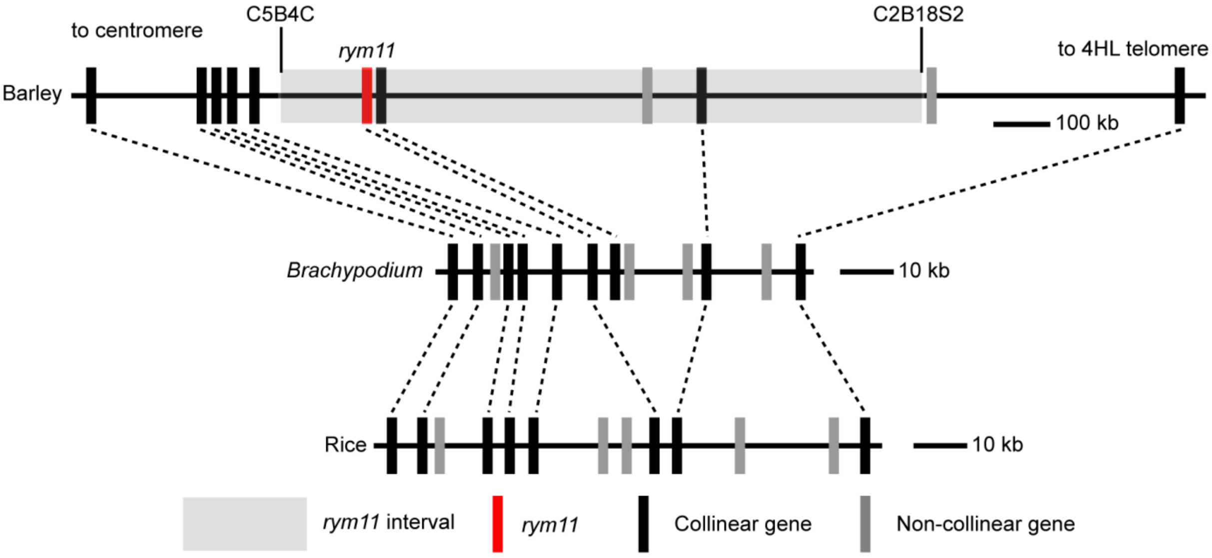


Figure 3-5 Conserved synteny of the *rym11* region between barley, *Brachypodium* and rice. The physical map was constructed on the basis of the published draft genome of cv. ‘Morex’ (IBSC, 2012). The homolog genes in *Brachypodium* and rice are referred as Mayer et al. (2011). The co-segregating region of *rym11* is highlighted in grey.

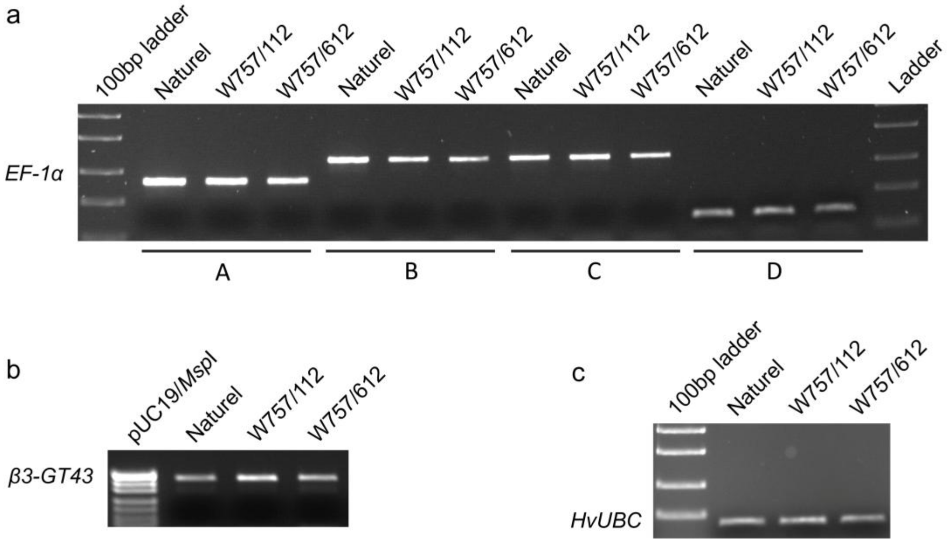


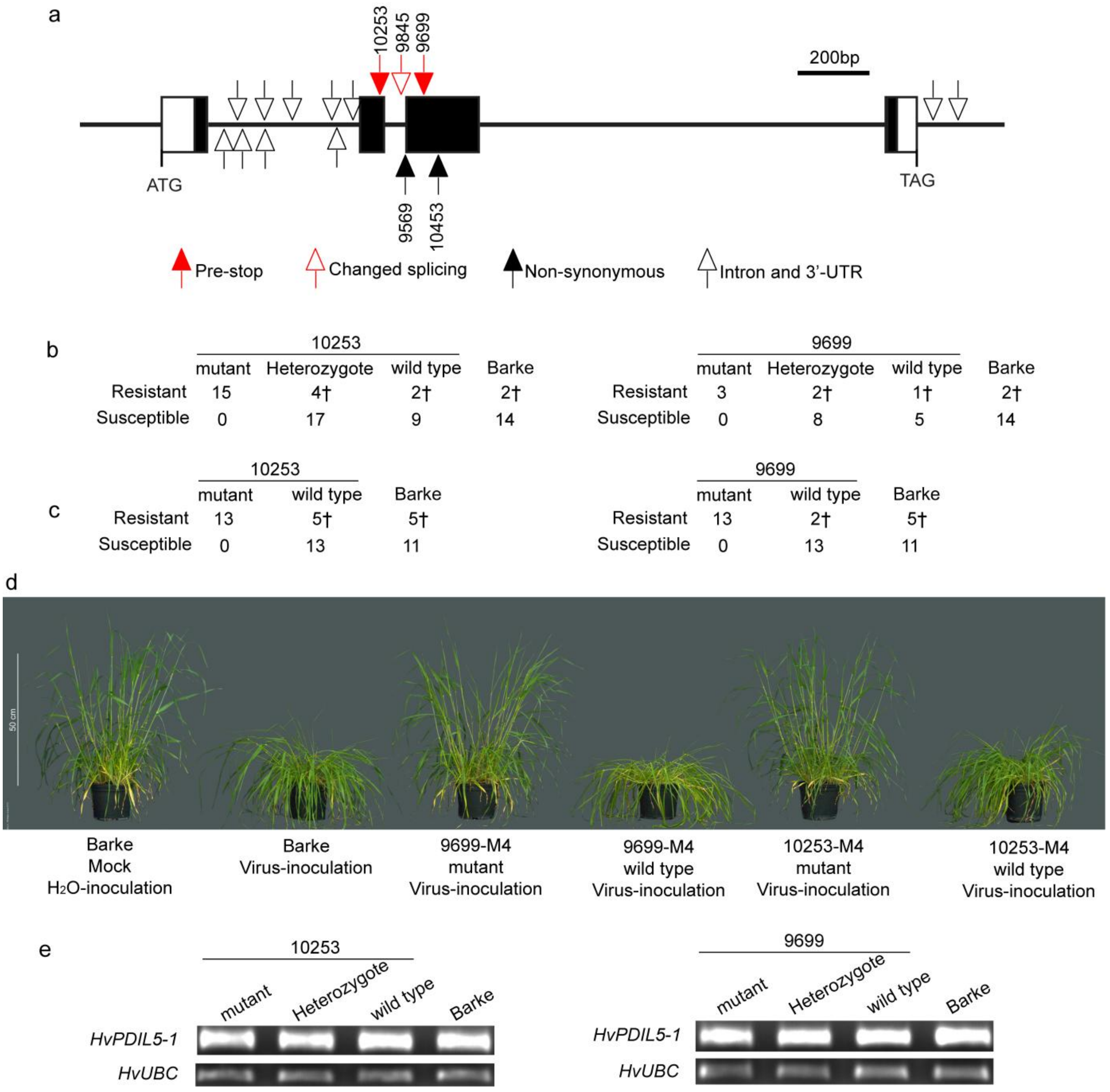
Figure 3-6 Expression analysis of *EF-1α* (a) and *β3-GT43* (b). The A, B, C and D indicate four independent primer pairs for *EF-1α*. (c) The *HvUBC* is the endogenous control.

3.2.2 Functional verification of *HvPDIL5-1*

The gene *HvPDIL5-1* was identified as the most likely candidate gene conferring *rym11*-based recessive *Bymovirus* resistance. Since the observed deletion in the 5’-end of the gene leads to complete knock-out of the gene in resistant genotypes the wild type version of the gene constitutes a susceptibility factor for *Bymovirus* infection in barley. Three independent approaches were applied to test this hypothesis: (i) TILLING for novel induced mutant alleles, (ii) transgene-induced complementation and (iii) analysis of allelism by producing and testing F_1 hybrids obtained from crossing a set of genotypes carrying independent natural alleles of the gene *rym11*. The results of these experiments are shown in the following.

3.2.2.1 EMS-derived mutagenesis of *HvPDIL5-1* induced resistance in susceptible cultivar

A large EMS-induced mutant population was previously established by utilizing the susceptible spring barley cv. ‘Barke’ (Gottwald et al. 2009) and DNA of the M_2 population (10,279 lines) was arranged in two-dimensional pools of eight individuals each. This allows screening for induced mutations in candidate genes by TILLING. The gene *HvPDIL5-1* was analyzed by screening the population with two pairs of primers to amplify separately exon 1-3 and exon 4. Sixteen independent mutations were detected (Figure 3-7, a). Among these, eleven mutations were situated in introns and 3'-untranslated region (UTR). These were excluded for any following experiments. The remaining five mutants were subjected for testing virus resistance. Progeny of the two lines 9569 and 9845 were lost during the propagation process possibly due to deleterious effects of the mutations in *HvPDIL5-1* but more likely due to too high mutational load or lethal mutations elsewhere in the genome. All M_3 progeny plants of 10453 were either wild type or heterozygous but no homozygous plant for the mutated locus was obtained. The two independent mutations in line 9699 (703' in the genomic sequence, G>A) and 10253 (568' in the genomic sequence, G>A) each lead to a premature stop codon (pre-stop) and these lines were subsequently used for further analysis.



b

	10253 mutant	10253 Heterozygote	10253 wild type	Barke
Resistant	15	4†	2†	2†
Susceptible	0	17	9	14

	9699 mutant	9699 Heterozygote	9699 wild type	Barke
Resistant	3	2†	1†	2†
Susceptible	0	8	5	14

c

	10253 mutant	10253 wild type	Barke
Resistant	13	5†	5†
Susceptible	0	13	11

	9699 mutant	9699 wild type	Barke
Resistant	13	2†	5†
Susceptible	0	13	11

Figure 3-7 TILLING for EMS-induced mutants of *HvPDIL5-1*. (a) Graphical representation of the position of the identified mutations in respect of the schematic gene structure. (b) BaMMV-inoculation of M_3 segregants. Two independent M_3 families were mechanically inoculated with BaMMV. Susceptible cultivar 'Barke' was used as the positive control for the efficiency of infectivity. † = resistant plants are unexpected here but can be explained by escapes of the artificial inoculation since also the positive infection control 'Barke' exhibited a few resistant cases. Purified PCR-amplificons were Sanger-sequenced for determination and verification of the expected genotype of each individual. (c) Resistance tests of homozygous M_4 mutants. (d) Phenotypes of BaMMV-inoculated homozygous M_4 mutants. Three plants are present in a single pot. (e) Semi-quantitative analysis of *HvPDIL5-1* in M_3 segregants of 10253 and 9699. The young leaves after 35 days post-inoculation were harvested. The *HvNUBC* is the endogenous control.

Resistance tests for two mutated lines were performed by artificial BaMMV-inoculation under climate chamber conditions. Firstly, the phenotyping and genotyping of M_3 segregating populations of heterozygous M_2 mutant were performed. The results showed that all M_3 plants homozygous for the mutation in *HvPDIL5-1* were resistant (Figure 3-7, b). Heterozygous or wild type individuals were found to be susceptible, however, in this group of plants between 10% and 20% of the plants showed resistant phenotypes. This may be explained by escapes of the artificial inoculation procedure since 12.5% (2 out of 14) of the susceptible control plants also showed a resistant phenotype. To confirm these results, M_4 progeny of the tested homozygous M_3 plants (mutant and wild type) was analyzed the same way. All homozygous mutants showed immunity to BaMMV-inoculation while wild type lines were susceptible (Figure 3-7, c). M_4 progeny plants of homozygous wild type M_3 showed stunted growth at heading stage, while homozygous mutant M_4 plants did not show a phenotypic deviation from wild type but mock-inoculated ‘Barke’ plants (Figure 3-7, d). Without BaMMV-inoculation all homozygous mutant and wild type M_4 developed comparably well until heading and maturation stages (Figure 3-8). Expression of the gene *HvPDIL5-1* could be detected in all homozygous mutant, heterozygote and wild type progeny of the TILLING mutants (Figure 3-7, e) thus the observed functional differences in respect to susceptibility to BaMMV can be assigned to the effect of the point mutations in the two TILLING lines leading to premature stop codon and most likely to formation of shorter probably mal-functional proteins and thus conferring resistance to the infection of BaMMV.

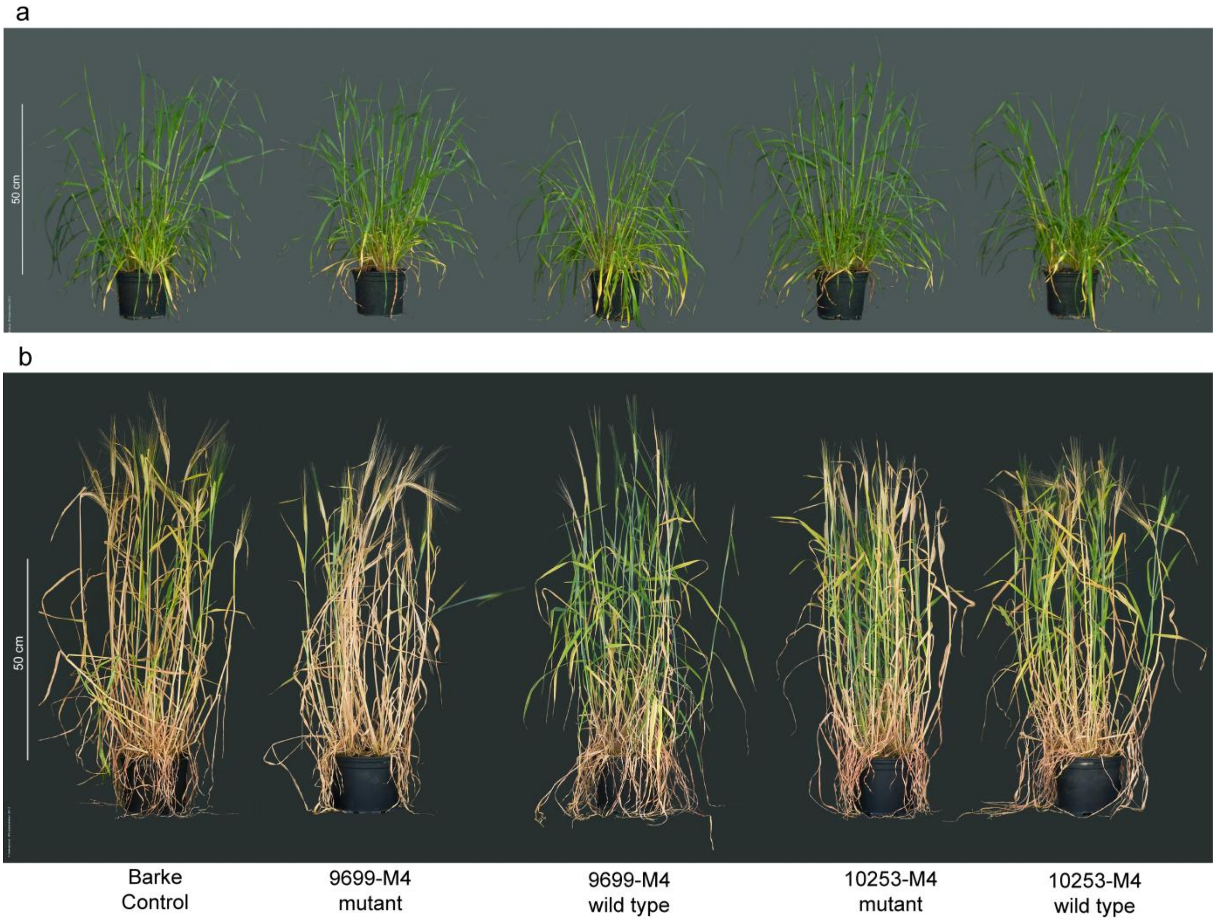


Figure 3-8 Phenotypes at heading (a) and maturation (b) stages of homozygous wild type and mutated M_4 mutants grown without artificial BaMMV-inoculation. The plants were grown under similar conditions as required for performing artificial BaMMV inoculations.

3.2.2.2 Complementation with wild type *HvPDIL5-1* induced susceptibility in resistant parent 'W757/612'

rym11 confers recessive resistance to *Bymovirus* and this effect is established due to putative loss-of-function of the underlying partially deleted *HvPDIL5-1* allele (*rym11-a*). Thus functional analysis of *rym11*-based resistance can not be induced by genetic complementation of a susceptible genotype through transformation and over-expression of a resistance allele. The endogenous wild type copy of the gene *HvPDIL5-1* will still serve as a functional susceptibility factor. Therefore, a 576 bp cDNA fragment containing the 456 bp full-length ORF of *HvPDIL5-1* from susceptible genotype 'Naturel' was used and transformed to induce susceptibility of the resistant genotype 'W757/612'. Two independent T_0 lines were obtained and propagated to T_1. T_1 families were analyzed for resistance. As the identified 1,375-bp deletion in

HvPDIL5-1 of W757/612 eliminates expression of the resistance conferring allele (*rym11-a*, Figure 3-3, e), presence / absence of the transgene could be determined by analyzing gene expression. RT-PCR amplification revealed 3:1 segregation (presence / absence) of the transgene by analyzing 70 and 58 individuals in two independent T_1 families E1 ($\chi^2 = 0.933 < 3.84$) and E2 ($\chi^2 = 1.86 < 3.84$), respectively, indicating the presence of a single transgene locus (Table 3-3). It was, however, not tested for the presence of multiple insertions of the transgene at the very same locus. T_1 progeny plants carrying the wild type *HvPDIL5-1* transgene were susceptible to BaMMV infection, whereas T_1 plants without the transgene were consistently resistant (Table 3-3). In family E1, 30 out of 70 inoculated plants were tested to be susceptible.19 plants were resistant although carrying the transferred susceptibility allele of *HvPDIL5-1*. In family E2, 45 transgenic plants were susceptible, while 3 transgenic plants were resistant. The resistant transgenic plants again can be explained by escapes of artificial inoculation with BaMMV since 10.7% susceptible control plants also showed resistant phenotype (Table 3-3). These results demonstrated that complementation with a wild type copy of *HvPDIL5-1* can induce susceptibility in a formerly resistant genotype.

Table 3-3 Transgene induced susceptibility of *rym11-a* mediated resistance

	E1 - T1 plants		E2 - T1 plants		Control		
	Transgenic (*HvPDIL5-1*)	*rym11*	Transgenic (*HvPDIL5-1*)	*rym11*	W757-612 (*rym11*)	Igri (*HvPDIL5-1*)	Maris Otter (*HvPDIL5-1*)
Resistance	19[a]	21	3[a]	10	19	4[a]	2[a]
Susceptibility	30	0	45	0	0	22	28

[a] can be explained by escapes of artificial inoculation with BaMMV.

3.2.2.3 Functional equivalence of *HvPDIL5-1* haplotypes confirms presence of multiple natural alleles of *rym11*

The third independent functional test was based on the analysis of allelism between naturally occurring alleles of *rym11*. The landrace 'HOR1363' (formerly called as 'PI1963') carrying *rym11* was the original resistance donor of the genotypes 'W757/112' and 'W757/612' (Nissan-Azzouz et al. 2005) used in the present study. A second Genebank accession 'Russia57' was also reported to carry monogenic resistance based on the *rym11* locus (Bauer et al. 1997). F_1 hybrids were formed in a previous study between both genotypes and resistance was observed in F_1 plants after artificial mechanical inoculation with BaMMV (Nissan-Azzouz et al. 2005) thus providing evidence that the resistance locus *rym11* was allelic in both accessions. In the present thesis the test of allelism was reproduced since the presence of independent alleles of the gene *HvPDIL5-1* could be demonstrated by re-sequencing of the gene. *HvPDIL5-1* in ‘HOR1363’ revealed a 1,375-bp deletion that was described in both resistant genotypes ‘W757/112’ and ‘W757/612’. Re-sequencing of *HvPDIL5-1* in ‘Russia57’ revealed a 17 bp deletion that resulted in a frame-shift of the reading frame of the *HvPDIL5-1* ORF. F_1 plants were obtained by a cross of resistant genotype ‘W757/612’ and ‘Russia57’. All F_1 individuals were resistant to BaMMV infection (Figure 3-9). Since allelism for *rym11*-based resistance in ‘W757/612’ and ‘Russia57’ thus could be confirmed and proven at gene sequence level, the allele of ‘W757/112’ (respectively ‘HOR1363’) was denominated *rym11-a* and the allele found in ‘Russia57’ was denominated *rym11-b*, respectively (Figure 3-9, a). By re-sequencing of *HvPDIL5-1* in a large natural collection of wild and domesticated barleys (detailed results provided in Chapter 3.4), two additional novel haplotypes encoding immature proteins were identified (and denominated as *rym11-c* and *rym11-d*, Figure 3-9, a). F_1 hybrids between *rym11-a* and either *rym11-c* or *rym11-d* were resistant to artificial BaMMV-inoculation (Figure 3-9, b). Therefore, loss-of-function of *HvPDIL5-1* in natural accessions of barley results in resistance to BaMMV.

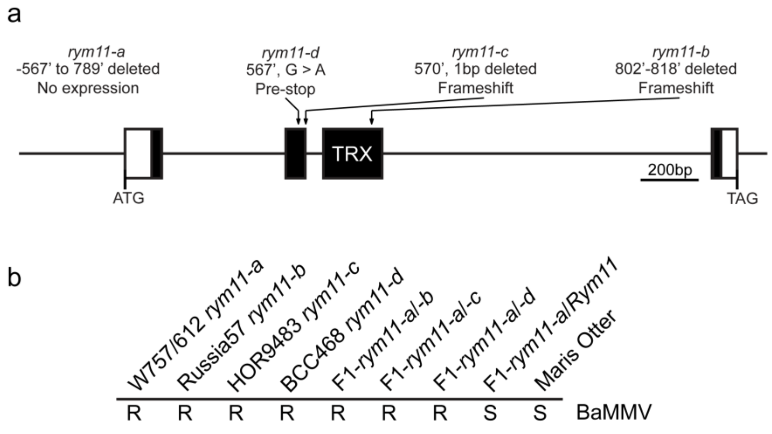


Figure 3-9 Multiple naturally occurring alleles of *rym11* conferring BaMMV resistance. F_1 hybrids were formed between genotypes carrying *rym11-a* and either of *rym11-b*, *-c* or *-d* (a) and tested for BaMMV resistance (b). Presence of resistance alleles in the tested F_1 hybrids was always confirmed by testing presence of diagnostic markers

3.3 Natural variation, geographical distribution and origin of *rym11*

3.3.1 Natural variation of *HvPDIL5-1*

Two independent naturally occurring alleles of *rym11* were observed from the genotypes ‘HOR1363’ and ‘Russia57’. This finding supported the possibility that screening a larger sample of diverse germplasm would allow uncovering additional alleles conferring resistance. Access to such a series of alleles would facilitate the functional analysis of *HvPDIL5-1* / *Bymovirus* interaction, and it would also provide flexibility to breeding of *Bymovirus* resistance cultivars. Natural variation of *HvPDIL5-1* was surveyed in a geographically referenced collection of 365 wild barleys (*H. vulgare ssp. spontaneum*) and 1,451 domesticated barleys (Appendix Table 1) by re-sequencing of the entire ORF of *HvPDIL5-1*. Results for 84 accessions were discarded because of low sequence quality, only partial availability of coding sequences or presence of heterozygosity. From 1,732 accessions high quality sequences could be obtained for 1,974 bp including the complete ORF from ATG to TAG. For calling exon-based sequence diversity only the 456 bp of assembled complete coding sequence (CDS) were then used, while intron-based sequence polymorphisms were not considered for further analysis.

Overall, 4 deletions and 26 SNPs defined 28 independent exon haplotypes (Table 3-4). The major haplotype I was present in 1,607 out of the 1,732 accessions (92.8%). Several accessions carrying haplotype I were tested to be susceptible to *Bymovirus* infection under field and climate chamber conditions (Table 3-5), indicating that susceptibility is predominant in accessions of natural collections of barley germplasm. Four haplotypes (II, VII, VIII and XXVIII) were identified to represent resistance alleles. As previously described, the originally identified *rym11-a* allele (Haplotype XXVIII) of ‘HOR1363’, isolated by map-based cloning in the present study, was only found in this single accession. Allele *rym11-b* (Haplotype II), identified in ‘Russia57’, was shared by 27 additional cultivars or landraces. Haplotype VII, containing a single base pair substitution (182’ in CDS, G > A, referred as *rym11-d*) and haplotye VIII containing a single base pair deletion (185’ in CDS, 1 bp deletion, referred as *rym11-c*) resulted in a premature stop codon and frameshift of *HvPDIL5-1*, respectively. The respective accessions are resistant to *Bymovirus* infection by artificial and natural inoculation (Table 3-5). Moreover, F_1 hybrids formed between genotypes carrying homozygous *rym11-a* (i.e. W757/612) and either of *rym11-c* or *-d* showed resistant infected by artificial BaMMV-inoculation (Figure 3-9), therefore confirming that both haplotypes (VII and VIII) are resistance conferring alleles of *rym11*. As a summary, four naturally occurring resistance alleles of *rym11* were identified by re-sequencing of *HvPDIL5-1* in a natural barley collection.

Table 3-4 The identified haplotypes of *HvPDIL5-1* in natural germplasm

Haplotypes	Mutation loci	Number of accessions	Frequency in total accessions	Descriptions
I	Wild type	1607	0,92783	Wild type
II	315'-331', 17bp deletion	28	0,01617	*rym11-b*, pre-stop
III	240', A > G	24	0,01386	Synonymous
IV	138', A > T	4	0,00231	Synonymous
V	60'-74', 15bp deletion	7	0,00404	Non-synonymous, 5 amino acids deletion
VI	411', C > T	1	0,00058	Synonymous
VII	182', G > A	4	0,00231	*rym11-d*, pre-stop
VIII	185', 1bp deletion	1	0,00058	*rym11-c*, pre-stop
IX	392', T > C	1	0,00058	Leu > Pro
X	56', C > A	2	0,00115	Ala > Asp
XI	172', T > C	9	0,00520	Cys > Arg
XII	288', A > G	3	0,00173	Synonymous
XIII	138', A > T; 374', C > G	9	0,00520	Synonymous (138'), Pro > Arg (374')
XIV	51', G > A	4	0,00231	Synonymous
XV	63', G > A	3	0,00173	Synonymous
XVI	66', A > C; 407', T > C	2	0,00115	Synonymous (66'), Leu > Ser (407')
XVII	26', C > A	3	0,00173	Ser > Tyr
XVIII	239', A > G	1	0,00058	Glu > Gly
XIX	213', T > A	5	0,00289	Synonymous
XX	277', G > A	5	0,00289	Gly > Ser
XXI	233', T > C; 407', T > C	1	0,00058	Val > Ser (233'), Leu > Ser (407')
XXII	382', G > C	1	0,00058	Val > Leu
XXIII	349', G > A	1	0,00058	Glu > Lys
XXIV	237', C > T	1	0,00058	Synonymous
XXV	9', G > A	2	0,00115	Synonymous
XXVI	407', T > C	1	0,00058	Leu > Ser
XXVII	70', G > T	1	0,00058	Ala > Ser
XXVIII	1'-299', 299bp deletion	1	0,00058	*rym11-a*, -567' to 789' deletion, complete silence

Natural variation of *HvPDIL5-1* in wild barleys, landraces and cultivars was visualized by median-joining network analysis constructed for the identified 28 haplotypes (Figure 3-10). Three haplotyes (I, III and IV) were shared between wild and domesticated barleys. Nine haplotypes (II, V, VI, VII, VIII, IX, X, XI and XXVIII) were exclusively found in domesticated barleys, while the remaining 16 haplotypes were only detected in wild barleys. The homologous genes of *HvPDIL5-1* in *B. distachyon*, *S. cereale*, *T. aestivum* and *H. bulbosum*, formed the outgroup for the analysis (Figure 3-11, a). These putative orthologs in grass species were most closely related to the major haplotype I in the *H. vulgare* lineage (Figure 3-11). The predominant haplotype I was found in accessions originating basically from all geographical origins (Figure 3-12 and Figure 3-13, a). The resistance haplotypes (II, *rym11-b*; VII, *rym11-d*; VIII, *rym11-c* and XXVIII, *rym11-a*) were derived directly by single mutation events (deletion or substitution) of haplotype I (Figure 3-10). Therefore, this major haplotype I is most closely related to or represents the ancestral haplotype of *HvPDIL5-1*, and alternative haplotypes were evolving in barley by natural variation and were maintained in the collection putatively by positive selection (Figure 3-10).

Table 3-5 Phenotypic analysis for *Bymovirus* resistance in natural barley accessions

No	Accessions	Haplotypes	BaMMV	BaYMV	BaYMV-2	*β3-GT-43*	Comments
1	W757/112	XXVIII, *rym11-a*	R	R	R[b]	1 AA insert	Resistant parent of mapping population
2	W757/612	XXVIII, *rym11-a*	R	R	R[b]	1 AA insert	Resistant parent of mapping population
3	Naturel[a]	I	R	R	S	wild type	Susceptible parent of mapping population
4	Morex	I	S	nd	nd	wild type	Cultivar
5	Barke	I	S	nd	nd	nd	Cultivar
6	Igri	I	S	S	S	nd	Cultivar
7	Golden promise	I	S	nd	nd	nd	Cultivar
8	HOR1363	XXVIII, *rym11-a*	R	R[b]	R[b]	1 AA insert	Natural collection
9	Russia57	II, *rym11-b*	R	R	R[c]	wild type	Breeding line
10	BCC453	II, *rym11-b*	R	nd	nd	nd	Natural collection
11	BCC461	II, *rym11-b*	R	nd	nd	nd	Natural collection
12	BCC463	II, *rym11-b*	R	nd	nd	nd	Natural collection
13	BCC471	II, *rym11-b*	R	R	nd	wild type	Natural collection
14	BCC484	II, *rym11-b*	R	R	nd	wild type	Natural collection
15	BCC649	II, *rym11-b*	R	R	nd	wild type	Natural collection
16	BCC682	II, *rym11-b*	R	R	nd	wild type	Natural collection
17	BCC697	II, *rym11-b*	R	R	nd	wild type	Natural collection
18	HOR2363	II, *rym11-b*	R	R	nd	wild type	Natural collection
19	HOR3299	II, *rym11-b*	R	R	nd	wild type	Natural collection
20	HOR9288	II, *rym11-b*	R	R	nd	wild type	Natural collection
21	HOR11024	II, *rym11-b*	R	R	nd	wild type	Natural collection
22	HOR11027	II, *rym11-b*	R	R	nd	wild type	Natural collection
23	HOR11099	II, *rym11-b*	R	R	nd	wild type	Natural collection
24	HOR11533	II, *rym11-b*	R	R	nd	wild type	Natural collection
25	HOR11594	II, *rym11-b*	R	R	nd	wild type	Natural collection
26	HOR11597	II, *rym11-b*	R	R	nd	wild type	Natural collection
27	HOR11598	II, *rym11-b*	R	R	nd	wild type	Natural collection
28	HOR11600	II, *rym11-b*	R	R	nd	wild type	Natural collection
29	HOR11650	II, *rym11-b*	R	nd	nd	nd	Natural collection
30	HOR11653	II, *rym11-b*	R	nd	nd	nd	Natural collection
31	HOR11655	II, *rym11-b*	R	nd	nd	nd	Natural collection
32	HOR11915	II, *rym11-b*	R	nd	nd	nd	Natural collection
33	HOR11922	II, *rym11-b*	R	nd	nd	nd	Natural collection
34	HOR12304	II, *rym11-b*	R	nd	nd	nd	Natural collection
35	HOR12732	II, *rym11-b*	R	R	nd	wild type	Natural collection
36	HOR13467	II, *rym11-b*	R	nd	nd	nd	Natural collection
37	HOR9483	VIII, *rym11-c*	R	R	nd	294‘, G > A	Natural collection
38	BCC468	VII, *rym11-d*	R	R	nd	294‘, G > A	Natural collection
39	BCC469	VII, *rym11-d*	R	R	nd	294‘, G > A	Natural collection
40	HOR11030	VII, *rym11-d*	R	R	nd	294‘, G > A	Natural collection
41	HOR11141	VII, *rym11-d*	R	R	nd	294‘, G > A	Natural collection

[a] The cultivar ‘Naturel’ carries *rym4* which is resistant to BaMMV and BaYMV, but susceptible to BaYMV-2 (Lüpken *et al.*, 2013).
[b] Referred as Nissan-Azzouz *et al.* (2005).
[c] Referred as Bauer et al. (1997).
BaMMV infection was performed under greenhouse and field condition, while BaYMV infection was exclusively carried out in the field. The substitution of single nucleotide in *β3-GT-43* leads to synonymous mutation (294’ in the entire coding region, G > A).
nd = not determined

Interestingly, one accession ‘HOR11141’ (also called ‘Mokusekko 3’) was included in the survey that was known to carry two resistance genes *rym1* on 4HL and *rym5* on 3HL (Konishi et al. 1997). Re-sequencing of *HvPDIL5-1* and *HvEIF4E* (functional gene underlying *rym4/5*-based resistance (Stein et al. 2005)) revealed that this accession represented resistance conferring mutations in both genes (*rym11-d* and *rym5*) representing a spontaneously occurring example of resistance gene pyramidization. *rym1* like *rym11* was assigned genetically to the same region of barley chromosome 4HL in close proximity to the centromere (Figure 2-3). F_1 hybrids were derived by crossing ‘W757/112’ (*rym11-a*, no *rym5*) with another Chinese landrace accession ‘BCC468’ (*rym11-d* and *rym5*) and progeny plants were resistant to artificial inoculation with of BaMMV. Since ‘BCC468’ and ‘HOR11141’ share the same allele for *rym11* it can be concluded that the former resistance loci *rym1* and *rym11* are in fact alleles of the same gene *HvPDIL5-1*, and not allelic to the third resistance gene *rym18* on 4HL (Kai et al. 2012).

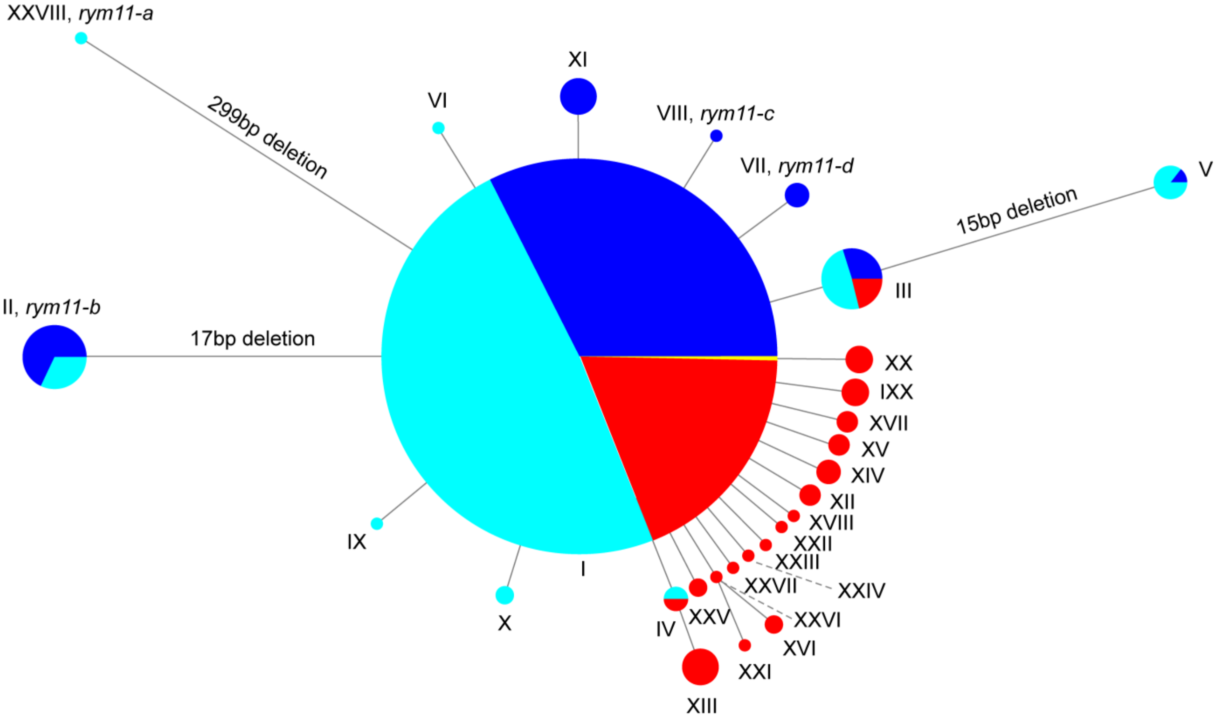


Figure 3-10 Median-joining network analysis of naturally occurring alleles of the gene *HvPDIL5-1*. Twenty-eight haplotypes were found in 1,732 accessions and four resistance conferring alleles (*rym11-a*, *-b*, *-c* and *-d*) were indicated. Circle size corresponds to the frequency of particular haplotype. Red = wild barley; light blue = landrace barley; dark blue = barley cultivar; yellow = *H. vulgare* ssp. *agriocrithon*. If not otherwise indicated (XXVIII, *rym11-a*; II, *rym11-b*; V) the distance between haplotypes represents one nucleotide substitution or deletion. Three haplotypes (I, III and IV) were shared among wild and domesticated barleys.

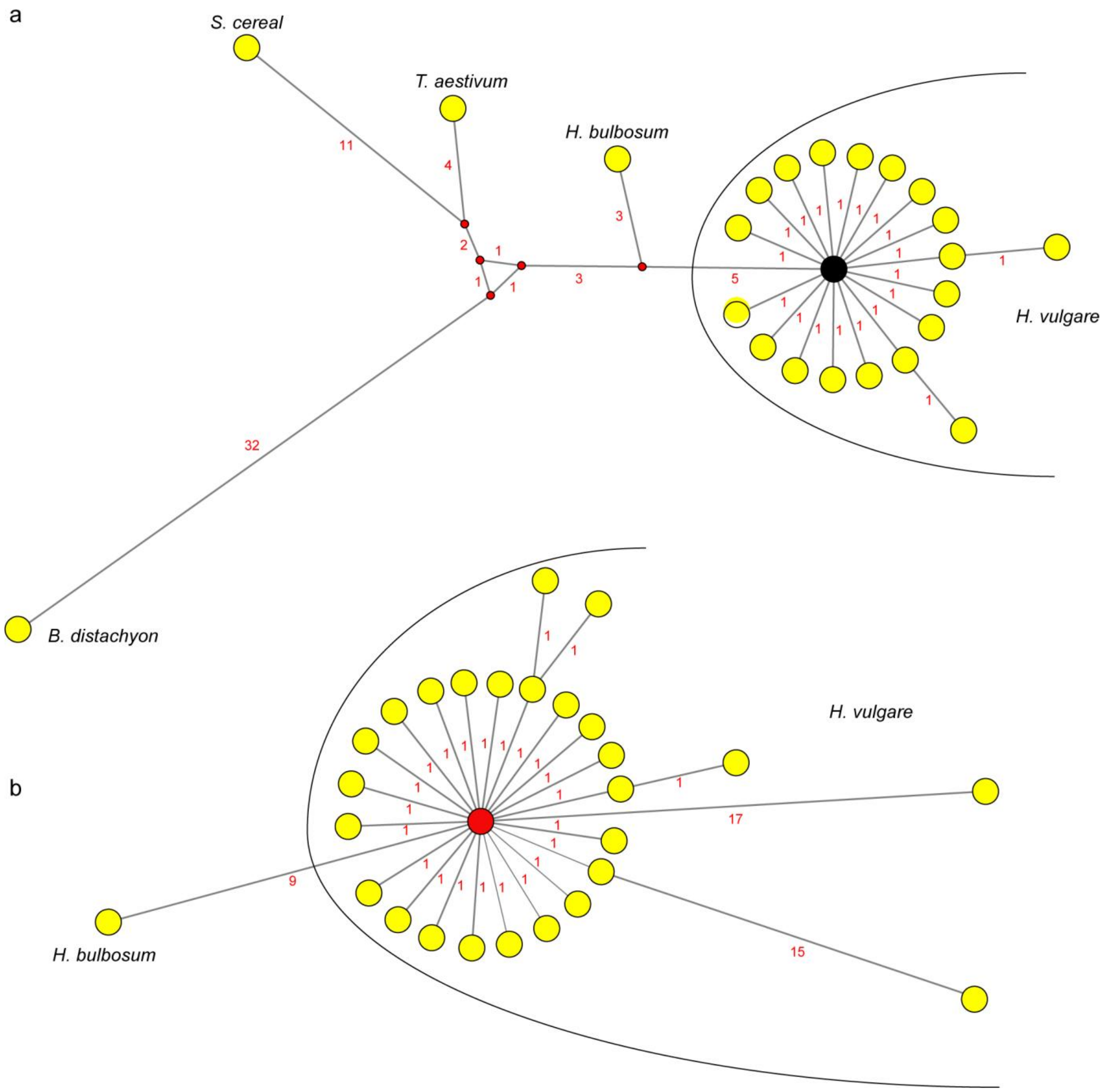


Figure 3-11 Median-joining network derived from *HvPDIL5-1* haplotypes in comparison to the putative orthologs of *B. distachyon*, *S. cereale*, *T. aestivum* and *H. bulbosum*. The distance in nucleotide substitution and deletion between haplotypes is indicated by numbers. The number of accessions in particular haplotypes is not shown. (a) MJ network constructed with deletion-excluded algorithm. The number of haplotypes is reduced since the deletions are not considered. The previously identified haplotype I with deletion-considered algorithm is shown with black color, but it is grouped together with a few haplotypes. (b) MJ network constructed with deletion-considered algorithm. The orthologs in *B. distachyon*, *S. cereale* and *T. aestivum* and the haplotype XXVIII (*rym11-a*) are excluded as the higher sequence difference. The red cycle represents haplotype I.

3.3.2 Geographical distribution and origin of *rym11*

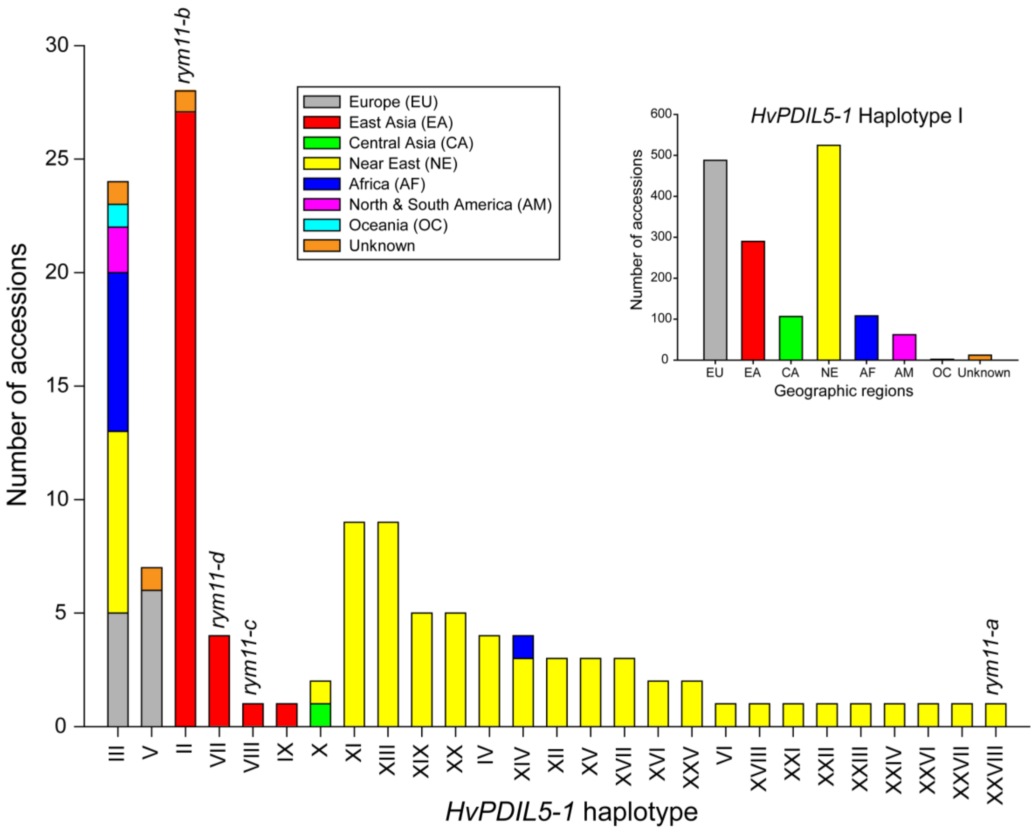


Figure 3-12 Geographic distribution of *HvPDIL5-1* haplotypes. The height of bars displays the number of accessions carrying the particular haplotype. Information for major haplotype I is shown independently on the insertion of the upper right panel.

Relying on geographic references of the analyzed accessions, the geographic distribution of 28 identified exon haplotypes was analyzed (Figure 3-12). Twenty-three out of total 28 haplotypes originated from Near East, where domesticated barley originated around 10,000 years ago (Purugganan and Fuller 2009), and nineteen haplotypes were exclusively found in this region. Four haplotypes (II, VII, VIII and IX) were particularly occurring in East Asia, and Haplotype V was specific for barley accessions collected from Georgia. Ancient haplotype I was present in basically all geographic origins (Figure 3-13, a), while haplotype III was found in several regions but not Central and East Asia (Figure 3-12). Except for the single barley landrace ‘HOR1363’ (*rym11-a,* collected from Turkey), the remaining three resistance alleles (*rym11-b*, *-c* and *-d*) were exclusively detected in accessions from East Asia (Figure 3-12 and Figure 3-13, b). These alleles were found in 34 domesticated barleys, but in none of the wild barleys, implying that resistance alleles of *rym11* likely originated in domesticated barley and not in wild barley. The breeding line ‘Russia57’ carrying *rym11-b* was provided by Okayama University, but exact geographical origin information was missing. No naturally occurring accession with true European origin was found carrying a functional *rym11* resistance allele (Figure 3-12). Therefore, *rym11* resistance alleles were predominantly observed in accession with origin from East Asia in winter-type six-rowed barley (Figure 3-14). As a conclusion, the resistance alleles of *rym11* likely have independently evolved in domesticated barleys during adaptation to *Bymovirus* infested environments in East Asia.

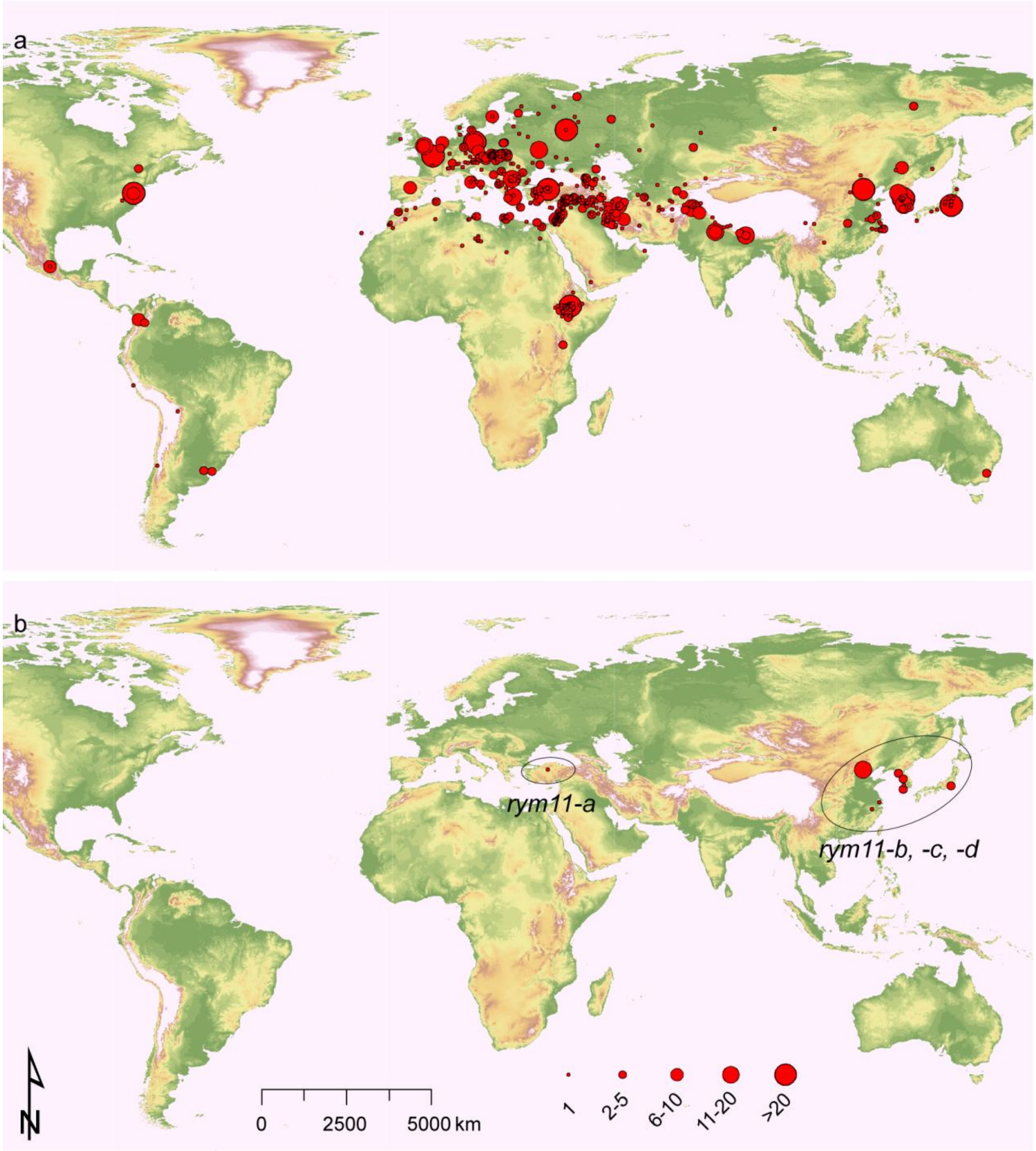


Figure 3-13 Geographic distribution of *rym11* alleles and its ancestral haplotype. Geographic information system (GIS)-based topographical maps for the susceptible potentially ancestral haplotype-I and the combination of 4 resistance alleles (*rym11-a*, *b*, *c*, and *d*) are shown. (a)

Geographic distribution of accessions carrying haplotype-I. (b) distribution of accession carrying either one of the resistance conferring *rym11* alleles. The size of filled cycles is proportional to the number of accessions of each particular site. For accessions without geo-reference information the capital state of the source country was arbitrarily chosen as collecting site which is explaining circles in regions that do not in fact represent barley cultivation area.

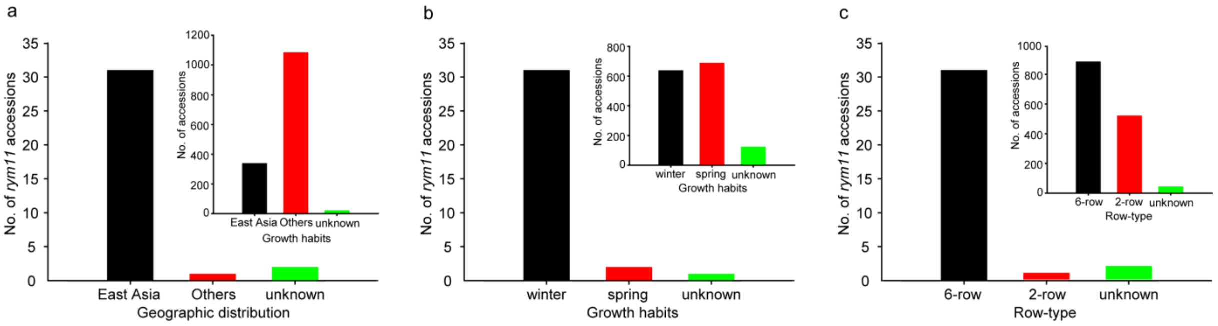


Figure 3-14 Geographic distribution (a), growth habit (b) and row-type (c) of 34 domesticated barleys carrying resistance conferring alleles at the *rym11* locus. Data is shown for all accessions in the respective upper right insertions of panels (a), (b) and (c).

3.4 Diagnostic markers for *rym11* functional alleles

In a summary of surveying natural and induced diversity of *HvPDIL5-1*, six alleles conferring resistance were identified that either were complete knock-outs without any detectable transcript, carrying frame shifts or pre-stop mutations of *HvPDIL5-1* (Figure 3-15, a). *rym11* was described to confer immunity to all known European strains of *Bymovirus* (Bauer et al. 1997; Habekuß et al. 2008; Kanyuka et al. 2004; Nissan-Azzouz et al. 2005). Therefore it should provide a strong candidate for resistance breeding in European barley. A set of PCR-based allele-specific markers could be derived for detecting the resistance alleles (Figure 3-15, b and Table 3-6). Markers detecting size-polymorphisms were produced to identify alleles *rym11-a* and *rym11-b.* CAPS markers were designed for alleles *rym11-c* and *rym11-d* and dCAPS markers were developed for two induced alleles *rym11-9699* and *rym11-10253*. As an example, the marker M-rym11-b may generate 240-bp and 223-bp fragments in susceptible and *rym11-b* carrying cultivars, respectively. The 17 bp size difference can be separated in 4% agarose gel. PCR products of marker M-rym11-c cleaved by restriction endonuclease *Dde*I results in a single fragment (619 bp) in susceptible cultivars, but two bands (441 and 178 bp) in *rym11-c* containing cultivar. In case of marker M-rym11-a that may theoretically produce double fragments (541 bp and 1946 bp) in the artificial heterozygous DNA pool, this primer pair frequently amplify the smaller fragment (541 bp) rather than the large one (1,916 bp). It is advised for convinced result to in use with the marker M-rym11-b to select the genotypes carrying *rym11-a* allele.

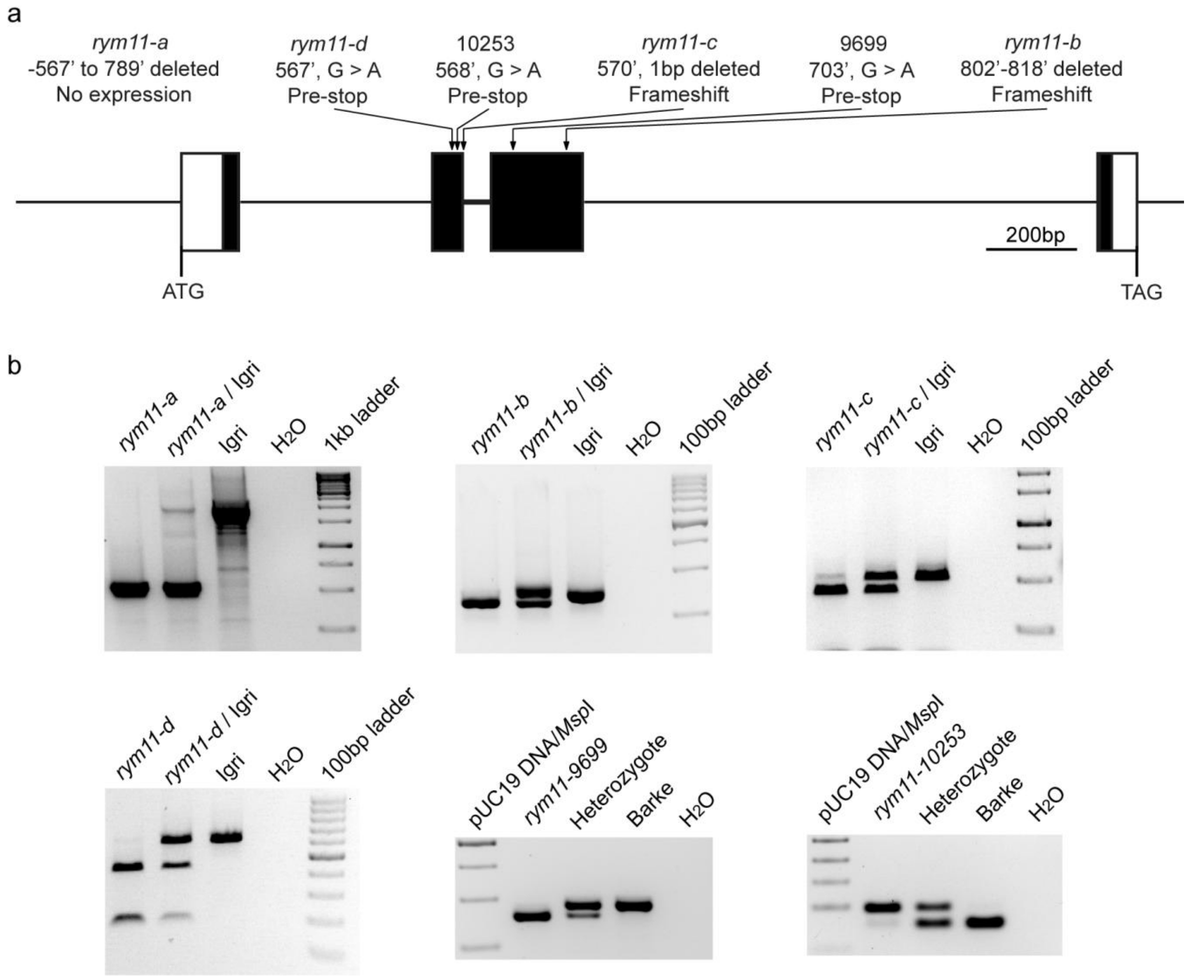


Figure 3-15 Diagnostic markers for *rym11*. (a) Graphical representation of the functional-exchanged variations at the *HvPDIL5-1* locus. (b) Diagnostic markers for the resistance *rym11* alleles. PCR amplification was conducted in homozygote, (Natural or artificial) heterozygote and wild type.

The established markers were surveyed for their diagnostic values in a subset of 1,816 natural accessions (57 accessions, randomly selected, Table 3-7). Three resistance alleles *rym11-a*, *rym11-c* and *rym11-10253* were not found in this sub-collection by using markers M-*rym11-a*, M-*rym11-c* and M-*rym11-10253*, respectively (Table 3-7). *rym11-b* was detected in 10 accessions and *rym11-d* was exclusively found in the single accession HOR11141. Interestingly, *rym11-b* carrying genotypes also could be detected by using the marker M-*rym11-9699*, which can produce 223-bp, 258-bp and 281-bp fragments in genotypes carrying *rym11-b*, *rym11-9699* and wild type *HvPDIL5-1*, respectively. Re-sequencing of *HvPDIL5-1* in these 57 natural accessions revealed perfect consistency between the diagnostic marker screening and Sanger-sequencing results (Table 3-7). Therefore, the six diagnostic markers can be potentially exploited in marker assisted selection of *rym11* in barley breeding.

Table 3-6 Diagnostic markers for the resistance alleles of *rym11*

Markers	Susceptibility (bp)	Resistance (bp)	Comments
M-*rym11-a*	1916	541	1,5% agarose gel, 40 min for electrophoresis
M-*rym11-b*	240	223	4% agarose gel, 1,5-2 h for electrophoresis
M-*rym11-c*	517, 58, 41	435, 81, 58, 44	*MseI* digestion, 1,5% agarose gel, 40 min for electrophoresis
M-*rym11-d*	619	441, 178	*DdeI* digestion, 1,5% agarose gel, 40 min for electrophoresis
M-*rym11-Till-9699*	281	258, 23	*DdeI* digestion, 3% agarose gel, 1,5-2 hour for electrophoresis
M-*rym11-Till-10253*	88, 18	106	*NcoI* digestion, 4% agarose gel, 1,5-2 hour for electrophoresis

Table 3-7 Tests of diagnostic markers in natural populations

Number	Accessions	M-rym11-a	M-rym11-b	M-rym11-c	M-rym11-d	M-rym11-9699[a]	M-rym11-10253	Haplotypes of *HvPDIL5-1*
1	HOR976	wt	wt	wt	wt	Wt	wt	*I*
2	HOR2363	wt	*rym11-b*	wt	wt	*rym11-b*	wt	*II, rym11-b*
3	HOR3130	wt	wt	wt	wt	Wt	wt	*I*
4	HOR3296	wt	wt	wt	wt	Wt	wt	*I*
5	HOR3298	wt	wt	wt	wt	Wt	wt	*IV*
6	HOR3299	wt	*rym11-b*	wt	wt	*rym11-b*	wt	*II, rym11-b*
7	HOR3500	wt	wt	wt	wt	Wt	wt	*I*
8	HOR4219	missing	wt	wt	missing	Wt	wt	*I*
9	HOR4224	wt	wt	wt	wt	Wt	wt	*I*
10	HOR5734	wt	wt	wt	wt	Wt	wt	*I*
11	HOR7259	wt	wt	wt	wt	Wt	missing	*I*
12	HOR9288	wt	*rym11-b*	wt	wt	*rym11-b*	wt	*II, rym11-b*
13	HOR11024	wt	*rym11-b*	wt	wt	*rym11-b*	wt	*II, rym11-b*
14	HOR11027	wt	*rym11-b*	wt	wt	*rym11-b*	wt	*II, rym11-b*
15	HOR11078	wt	wt	wt	wt	Wt	wt	*I*
16	HOR11079	wt	wt	wt	wt	Wt	wt	*I*
17	HOR11088	wt	wt	wt	wt	Wt	wt	*I*
18	HOR11091	wt	wt	wt	wt	Wt	wt	*I*
19	HOR11096	wt	wt	wt	wt	Wt	wt	*I*
20	HOR11098	wt	wt	wt	wt	Wt	wt	*I*
21	HOR11099	missing	*rym11-b*	wt	wt	*rym11-b*	wt	*II, rym11-b*
22	HOR11132	wt	wt	wt	wt	Wt	wt	*I*
23	HOR11139	wt	wt	wt	wt	Wt	wt	*I*
24	HOR11140	wt	wt	wt	wt	Wt	wt	*I*
25	HOR11141	wt	wt	wt	*rym11-d*	Wt	wt	*VII, rym11-d*
26	HOR11143	wt	wt	wt	wt	Wt	wt	*I*
27	HOR11524	wt	wt	wt	wt	Wt	wt	*I*
28	HOR11525	wt	wt	wt	wt	Wt	wt	*I*
29	HOR11527	wt	wt	wt	wt	Wt	wt	*I*
30	HOR11529	wt	wt	wt	wt	Wt	wt	*I*
31	HOR11540	wt	wt	wt	wt	Wt	wt	*I*
32	HOR11543	wt	wt	wt	wt	Wt	wt	*I*
33	HOR11545	wt	wt	wt	wt	Wt	wt	*I*
34	HOR11546	wt	wt	wt	wt	Wt	wt	*I*
35	HOR11551	wt	wt	wt	wt	Wt	wt	*I*
36	HOR11564	wt	wt	wt	wt	Wt	wt	*I*
37	HOR11568	wt	wt	wt	wt	Wt	wt	*I*
38	HOR11586	wt	wt	wt	wt	Wt	wt	*I*
39	HOR11590	wt	wt	wt	wt	Wt	wt	*I*
40	HOR11591	wt	wt	wt	wt	Wt	wt	*I*
41	HOR11594	wt	*rym11-b*	wt	wt	*rym11-b*	wt	*II, rym11-b*
42	HOR11600	wt	*rym11-b*	wt	wt	*rym11-b*	wt	*II, rym11-b*
43	HOR11602	wt	wt	wt	wt	Wt	wt	*I*
44	HOR11604	wt	wt	wt	wt	Wt	wt	*I*
45	HOR11610	wt	wt	wt	wt	Wt	wt	*I*
46	HOR11611	wt	wt	wt	wt	Wt	wt	*I*
47	HOR11614	wt	wt	wt	wt	Wt	wt	*I*
48	HOR11641	wt	wt	wt	wt	Wt	wt	*I*
49	HOR11670	wt	wt	wt	wt	Wt	wt	*I*
50	HOR11681	wt	wt	wt	wt	Wt	wt	*I*
51	HOR11706	wt	wt	wt	wt	Wt	wt	*I*
52	HOR11711	wt	wt	wt	wt	Wt	wt	*I*

53	HOR11851	wt	wt	wt	wt	Wt	wt	*I*
54	HOR11861	wt	wt	wt	wt	Wt	wt	*I*
55	HOR11862	wt	wt	wt	wt	Wt	wt	*I*
56	HOR11597	wt	*rym11-b*	wt	wt	*rym11-b*	wt	*II, rym11-b*
57	HOR11598	wt	*rym11-b*	wt	wt	*rym11-b*	wt	*II, rym11-b*
Reliability of diagnostic markers		100%	100%	100%	100%	100%	100%	

[a] 223bp for *rym11-b*, 258bp for *rym11-9699* and 281bp for wild type (wt).

3.5 Phylogenetic analysis of PDI gene family

HvPDIL5-1 belongs to the protein disulfide isomerase (PDI) gene family that contains >10 different members in eukaryotic species, e.g. 20 members in human (*H. sapiens*) (Ellgaard and Ruddock 2005; Houston et al. 2005; Kozlov et al. 2010). In general, the family members carry 1 to 3 thioredoxin (TRX) domains with catalytic motif (Cys-x-x-Cys) that determines the formation of native disulfide bond (Ellgaard and Ruddock 2005; Kozlov et al. 2010). Independent of their redox activities, PDIs play possibly also a role in correct protein folding via mediating the formation, breakage and rearrangement of disulfide bonds. Therefore, PDIs are recognized as chaperones, involved in the quality control for correct folding of proteins (Hayano et al. 1995; Maattanen et al. 2010).

Table 3-8 Protein disulfide isomerase (PDI) like proteins in barley

Identifier	Accessions	cDNA	Amino acid	Signal pepetide	Transmembrane	TRX domain	SP-value[a]	C-terminal tetrapeptide
HvPDIL1-1	AK357991.1	1542	513	1'-25'	None	41'-144', 396'-483'	0.969	KDEL
HvPDIL1-2	AK368066.1	1554	517	1'-24'	None	38'-141', 379'-481'	0.971	RDEL
HvPDIL1-3	AK370108.1	1764	587	1'-25'	None	100'-199', 439'-541'	0.958	KDEL
HvPDIL1-4	AK366963.1	1635	544	1'-23'	7'-24'	73'-172', 410'-511'	0.929	KDEL
HvPDIL2-1	AK249580.1	1104	367	1'-30'	11'-28'	33'-134', 150'-253'	0.968	AFSS
HvPDIL2-2	AK359586.1	1305	434	1'-18'	None	25'-125', 155'-260'	0.935	KEEL
HvPDIL2-3	AK353639.1	1323	440	1'-22'	5'-27'	29'-129', 165'-267'	0.963	NDEL
HvPDIL5-1	AK250421.1	456	151	1'-32'	13'-32'	34'-135'	0.941	EDEL
HvPDIL5-2	AK251979.1	1245	415	1'-26'	378'-400'	36'-133'	0.976	VHDE
HvPDIL5-3	AK249445.1	1257	418	1'-26'	380-402'	44'-141'	0.978	AHQE
HvPDIL5-4	AK251501.1	1458	485	None	20'-42', 447'-469'	144'-258'	0.232	GKDI
HvAPRL1	AK373140.1	1377	458	None	None	347'-454'	0.048	NTLR
HvAPRL3	AK374493.1	966	321	1'-27'	None	67'-166'	0.884	NELR
HvQSOXL1	AK362034.1	1524	507	1'-19'	471'-493'	34'-154'	0.888	KNWN

[a] SP-value indicates the reliability of putative sub-cellular localization.

By using the published nucleotide / protein sequences of putative PDI-like (PDIL) genes of *A. thaliana*, rice and maize (Houston et al. 2005), 14 barley PDIL genes were identified by sequence homology search to fl-cDNAs and whole genome shotgun sequence (WGS) assembly information of cv. ‘Morex’, ‘Barke’ and ‘Bowman’ (IBSC 2012; Matsumoto et al. 2011). Barley PDIL proteins consist of 151 to 587 amino acids (AA) and contain 1 to 2 active TRX domains (Table 3-8). Except for two members HvPDIL5-4 and HvAPRL1, the remaining 12 PDIL proteins are potentially localized in or directed to the endoplasmic reticulum (ER). This was revealed by *de* *novo* prediction of ER retention signals by utilizing the online software TargetP 1.1. The majority of family members contains specific C'-terminal tetrapeptides like KDEL, RDEL, KDEL, NDEL, EDEL etc., which are associated to ER-retention of the respective proteins (Ellgaard and Ruddock 2005).

HvPDIL5-1 encodes the smallest protein of barley PDILs and contains a single TRX domain and ER-retention signal (EDEL) (Table 3-7). In comparison to human PDIL genes, it is the closest homolog to ERp16 (also called ERp18, ERp19 or hLTP19), which contains also a single TRX domain and an EDEL-motif, respectively (Jeong et al. 2008). Based on homology search of HvPDIL5-1 in public databases, 18 homologous genes in plants and 30 genes in animals were obtained (Table 3-9). A majority of the homologous proteins are putatively part of the secretory pathway with a higher reliability and a larger proportion of members containing the ER-associated motifs (Table 3-9). A phylogenetic tree was constructed for *PDIL5-1* on the basis of 17 deduced proteins of different species from all evolutionary and organizational stages (e.g. unicellulate and multicellulate organisms, algae / primitive land plants / higher vascular plants etc.). It shows two separated major groups: plant group and animal group (Figure 3-16, a), implying that the differentiation of this gene occurred along with the divergence of the plant and animal kingdoms. Higher sequence identity is found within the plant and animal branch inside the TRX domain. Among monocotyledonous and dicotyledonous plants, the putatively active TRX domains are highly conserved with a tendency for differentiation of C'- and N'- terminal peptides. A few amino acids inside the functional domain are shared in plants and animals (Figure 3-17), e.g. the active center (Cys-x-x-Cys), implying the possibility of similar protein structure and function. The three-dimensional (3D) structure of homologous proteins of a protist *Capsaspora owczarzaki ATCC 30864* (EFW40541), a unicellulate algae *C. reinhardtii* (XP_001699351.1) and barley PDIL5-1 could be simulated in reference to the human protein ERp18 (PDB: 2k8vA) (Rowe et al. 2009). This illustrated that the predicted overall 3D structure is conserved between the homologous proteins across all kingdoms (Figure 3-16, b). It may therefore be concluded that PDIL5-1 homologs share structure, putative function and sub-cellular localization and thus potentially could have served in many organisms as a substrate for interactions to virus life cycles.

Table 3-9 The homologous genes of *HvPDIL5-1* in plants and animals

Entry	Species	Active center	C'-terminal tetrapeptide	SP value[b]	Protein accession	Amino acids
Plants						
NP_001239828.1	*Glycine max*	CKHC	NKEL[a]	0.945	NP_001239828.1	147
AFK35873.1	*Lotus japonicus*	CKHC	DKEL[a]	0.988	AFK35873.1	149
XP_003597187.1	*Medicago truncatula*	CKYC	DKEI[a]	0.803	XP_003597187.1	161
VvPDIL5-1	*Vitis vinifera*	CKHC	EKDL[a]	0.974	XP_002264005.2	151
XP_002526354.1	*Ricinus communis*	CKHC	YTIS	0.964	XP_002526354.1	132
AtPDIL5-1	*Arabidopsis thaliana*	CKHC	DKEL[a]	0.978	NP_172274.1	146
XP_002313546.1	*Populus trichocarpa*	CKHC	DKDL[a]	0.974	XP_002313546.1	147
ZmPDIL5-1	*Zea mays*	CKHC	LEAD	0.910	NP_001105760.1	150
XP_002465423.1	*Sorghum bicolor*	CKHC	LQAD	0.933	XP_002465423.1	150
NP_001049781.1	*Oryza sativa*	CKHC	LQDS	0.964	NP_001049781.1	147
BdPDIL5-1	*Brachypodium distachyon*	CKHC	QDEL[a]	0.950	XP_003558171.1	151
HvPDIL5-1	*Hordeum vulgare*	CKHC	EDEL[a]	0.941	AK250421.1	151
TaPDIL6-1	*Triticum aestivum*	CKHC	EDEL[a]	0.947	CBG91910.1	151
ABK26945.1	*Picea sitchensis*	CKHC	NALL	0.970	ABK26945.1	143
XP_001765606.1	*Physcomitrella patens subsp. patens*	CGHC	KSEE	0.903	XP_001765606.1	133
XP_002973548.1	*Selaginella moellendorffii*	CGHC	NDSL	0.955	XP_002973548.1	140
EFN50563.1	*Chlorella variabilis*	CGHC	LTTA	0.934	EFN50563.1	136
XP_001699351.1	*Chlamydomonas reinhardtii*	CGHC	TTEA	0.953	XP_001699351.1	139
XP_002952241.1	*Volvox carteri f. nagariensis*	CGHC	TSDS	0.957	XP_002952241.1	139
Animals						
CBK24051	*Blastocystis hominis*	CPAC	SYVC	0.952	CBK24051	162
EFW40541	*Capsaspora owczarzaki ATCC 30864*	CGAC	HAEL[a]	0.956	EFW40541	187
EKX45660	*Guillardia theta CCMP2712*	CGAC	KEEL[a]	0.970	EKX45660	188
XP_001900093.1	*Brugia malayi*	CHAC	KSDL[a]	0.957	XP_001900093.1	216
ADY44560.1	*Ascaris suum*	CKAC	RTRA	0.980	ADY44560.1	158
NP_496599.1	*Caenorhabditis elegans*	CHAC	KKEL[a]	0.783	NP_496599.1	186
EFZ15491.1	*Solenopsis invicta*	CPTC	TKRK[a]	0.799	EFZ15491.1	180
XP_001746532.1	*Monosiga brevicollis MX1*	CGAC	HFNI	0.959	XP_001746532.1	157
EFN82717.1	*Harpegnathos saltator*	CPTC	PKES	0.678	EFN82717.1	164
EGI62790	*Acromyrmex echinatior*	CPTC	EMKK	0.582	EGI62790	177
ELU04453	*Capitella teleta*	CGAC	FDEL[a]	0.912	ELU04453	169
NveTXNDC12	*Nematostella vectensis*	CGAC	GDEL[a]	0.741	XP_001635954.1	170
EHJ76926.1	*Danaus plexippus*	CSAC	QFDV	0.450	EHJ76926.1	161
XP_003491621.1	*Bombus impatiens*	CPSC	TLLH	0.912	XP_003491621.1	198
XP_003251492.1	*Apis mellifera*	CPSC	TLIH	0.536	XP_003251492.1	197
XP_002431962.1	*Pediculus humanus corporis*	CGAC	KFPD	0.105	XP_002431962.1	147
XP_003372511.1	*Trichinella spiralis*	CPAC	KSEL[a]	0.933	XP_003372511.1	203
CBY24266	*Oikopleura dioica*	CGAC	HEEL[a]	0.778	CBY24266	148
SpuTXNDC12	*Strongylocentrotus purpuratus*	CGAC	NDEL[a]	0.961	XP_791682.2	161
XP_002602566.1	*Branchiostoma floridae*	CGAC	DLTT	0.943	XP_002602566.1	147
DrTXNDC12	*Danio rerio*	CGAC	GDEL[a]	0.924	NP_001018660.1	172
SsaTXNDC12	*Salmo salar*	CGAC	EDEL[a]	0.912	NP_001139851.1	171
XlERp19	*Xenopus laevis*	CGAC	IDEL[a]	0.936	NP_001080756.1	168
XP_003411133.1	*Loxodonta africana*	CGAC	EDEL[a]	0.880	XP_003411133.1	172
MmTXNDC12	*Mus musculus*	CGAC	QDEL[a]	0.895	NP_079610.1	170
RnTXNDC12	*Rattus norvegicus*	CGAC	QDEL[a]	0.895	NP_001094310.1	170
BsTXNDC12	*Bos taurus*	CGAC	EDEL[a]	0.882	NP_001015536.1	172
MfaTXNDC12	*Macaca fascicularis*	CGAC	EDEL[a]	0.910	EHH49903.1	172
HsERp18	*Homo sapiens*	CGAC	EDEL[a]	0.915	NP_056997.1	172
XP_002750865.1	*Callithrix jacchus*	CGAC	EDEL[a]	0.899	XP_002750865.1	174

[a] The motifs are slightly associated to ER-retention of the respective proteins according to L.Eligaard & L.W.Ruddock (2005) and Houston et al. (2005). [b] SP-value indicates the reliability of putative ER-localization.

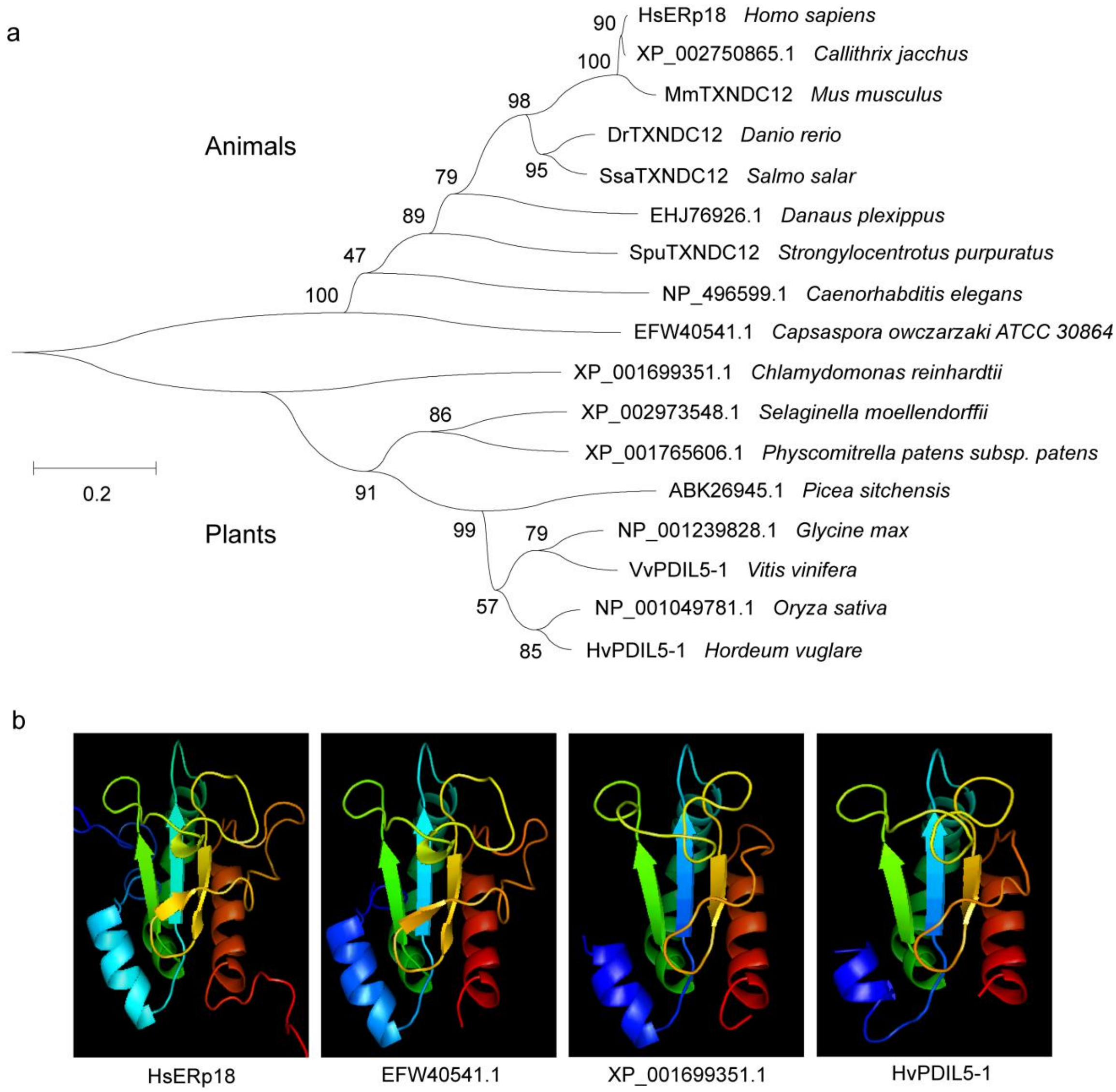


Figure 3-16 Phylogenetic analysis of *HvPDIL5-1*. (a) A phylogenetic tree of HvPDIL5-1 and its homologous proteins was derived by analysis of 17 homologous proteins. (b) Three-dimensional model of the homologous proteins in *Capsaspora owczarzaki ATCC 30864*, *C. reinhardtii* and *H. vulgare*. Simulation of 3D protein structure was achieved based on sequence homology to human HsERp18 (PDB code: 2k8vA).

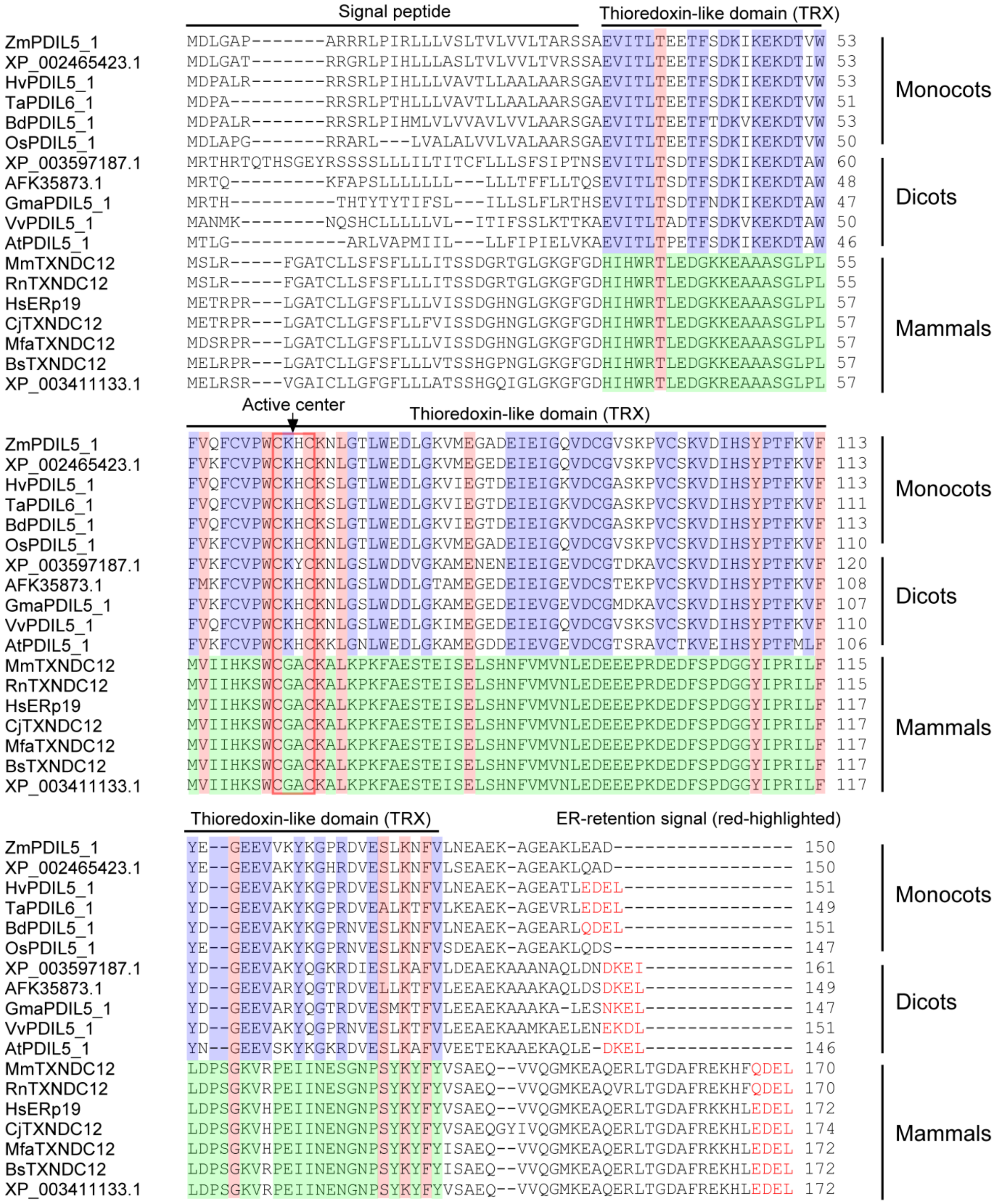


Figure 3-17 Multiple alignment of deduced protein sequences of *HvPDIL5-1* and its homologs in monocots, dicots and mammals. The identical amino acids inside TRX-like domain among plants and mammals, within plants, and within mammals are highlighted by pink, blue and green background, respectively. The putative ER-retention signal is highlighted in red. Signal peptide, TRX-like domain and active center are indicated as shown.

4. Discussion

The soil-borne barley yellow mosaic virus disease seriously affects winter barley production in East Asia and Europe. Virus particles are transmitted to the root system of susceptible barley cultivars via the *Oomycete Polymyxa graminis* and this mode of transmission prohibits plant protection by application of pesticides. Therefore, exploiting natural virus resistance in modern plant breeding is the practical way to prevent potential yield losses in cultivars. In the present thesis two naturally occurring *Bymovirus* resistance genes were targeted. Firstly, it was the aim to perform genetic mapping of the partial resistance gene *rym7*. Secondly, the causal gene *HvPDIL5-1* underlying *rym11*-based *Bymovirus* resistance was identified by map-based cloning and functionally verified by mutant and transgene analysis. It is a member of the highly conserved protein disulfide isomerase (PDI) gene family, and constitutes a novel susceptibility factor to plant viruses. Furthermore, by surveying of a large geographically referenced collection of wild and domesticated barleys, natural variation of *HvPDIL5-1* was revealed to provide multiple independent functional alleles of the resistance gene *rym11*. As part of the work a set of allele-specific PCR-based genetic markers were developed for *rym11*. Since *rym11* confers broad-spectrum resistances to all identified European strains of *Barley yellow mosaic virus* and *Barley mild mosaic virus* (Habekuß et al. 2008; Kanyuka et al. 2004; Nissan-Azzouz et al. 2005) it can be expected that these results will have an important impact on virus resistance breeding.

4.1 *PROTEIN DISULFIDE ISOMERASE 5-1* is a new *Bymovirus* susceptibility factor in barley and highly conserved between plants and animals

This work identified a novel susceptibility factor - *HvPDIL5-1* of the highly conserved protein disulfide isomerase (PDI) gene family to the *Bymovirus* disease of barley. The role of the wild type form of the gene as a susceptibility factor required to establish the *Bymovirus* infection was independently confirmed by (i) TILLING for chemically induced mutants, (ii) transgenic complementation of susceptibility in a genotype carrying a resistance conferring allele of the gene, and by (iii) surveying natural genetic diversity combined with allelic crossing. The gene is highly conserved in plant species but the biological role of the protein in plants is yet to be determined (Houston et al. 2005). The PDI gene family usually contains more than ten members in different eukaryotic species; e.g. there are 20 genes in *H. sapiens* and 18 in rice (Ellgaard and Ruddock 2005; Houston et al. 2005; Kozlov et al. 2010). The major function of PDILs was determined to contribute to formation of native disulfide bonds by induction, oxidization and isomerization, all catalyzed by the functional thioredoxin (TRX) domain (Ellgaard and Ruddock 2005; Kozlov et al. 2010). Independent of the redox activities, PDIs also play a role as chaperones in the quality check systems for correct protein folding (Maattanen et al. 2010). According to its high amino acid sequence conservation to human ERp16, which represents an endoplasmic reticulum-resident thiol-disulfide oxidoreductase fulfilling chaperone activities (Ellgaard and Ruddock 2005; Jeong et al. 2008; Kozlov et al. 2010; Maattanen et al. 2010), it may be concluded that the plant homologs have retained this function. Thus HvPDIL5-1 could have been recruited by *Bymovirus* in barley to act as cellular chaperone (protein folding, stabilization or facilitating transport) during its infection and/or replication cycle (Figure 4-1). Virus proteins or virus-required components could be generated via HvPDIL5-1-assisted protein folding and/or assembling. Otherwise, that leads to degradation of virus protein precursor by 26S-proteosome complex system (Ellgaard and Helenius 2003; Gao and Luo 2006), hence blocking virus replication in general and resulting in complete recessive resistance to *Bymovirus* (Figure 4-1). Other chaperones like heat shock protein 70 (Hsp70), Hsp90 and DNA-J-like proteins have been described for similar putative functions of interaction between plants and several genera of plant viruses (Verchot 2012). Functional motifs and protein structure of HvPDIL5-1 and its homologous proteins in plants and animals are highly conserved, even between evolutionary less or more derived eukaryotic species. As a consequence of determining *HvPDIL5-1* as a susceptibility factor to the *Potyvirus*-related *Bymovirus* in barley, members of the PDI gene family may have a similar role in other plant / virus interactions. This is especially important given the fact that already the highly conserved members of the eukaryotic translation initiation factor family (eIF4E, eIFiso4E, eIF4G, eIFiso4G) were determined repeatedly as susceptibility factors in numerous different plant species / *Potyvirus* (or related viruses) interactions (Robaglia and Caranta 2006).

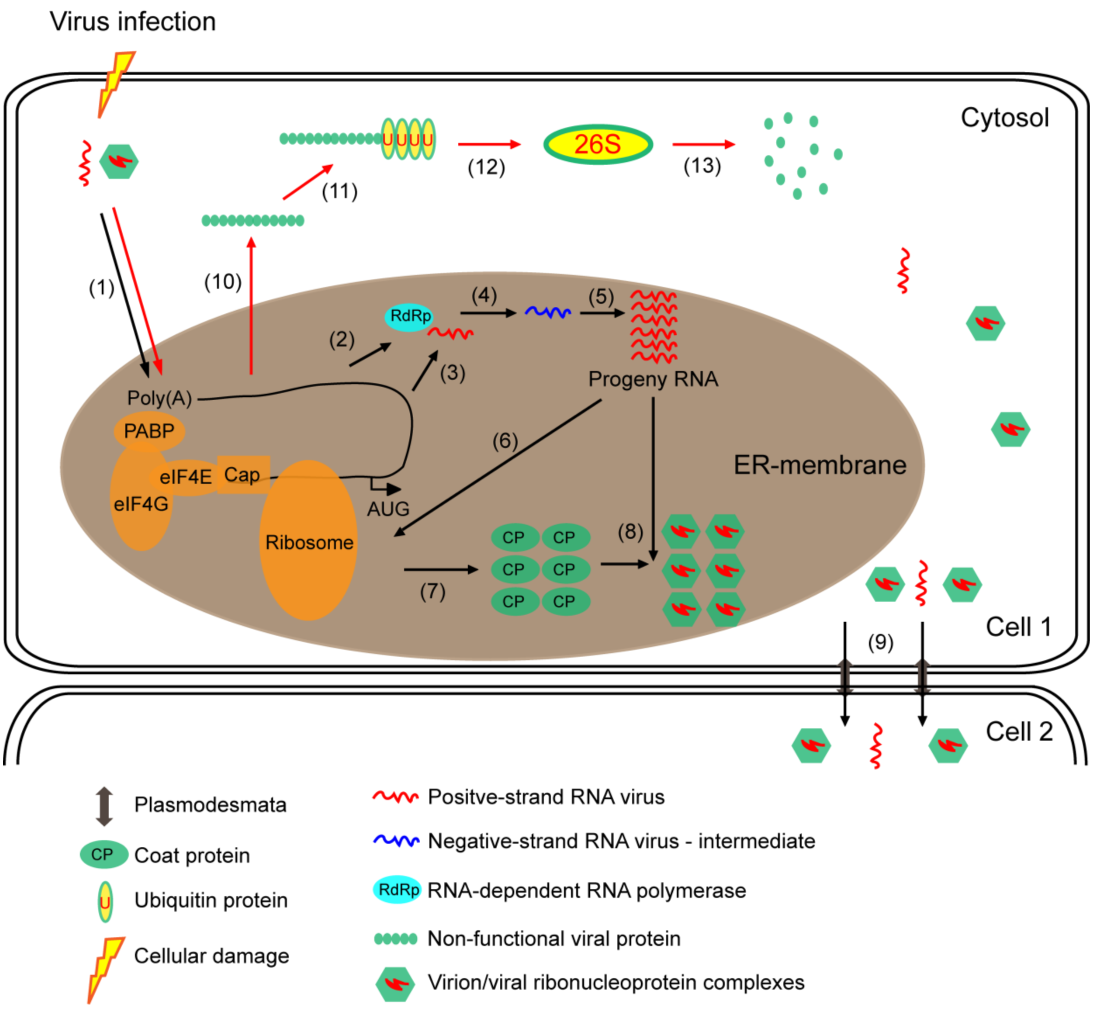


Figure 4-1 Schematic overview of a model of *Bymovirus* replication and local movement in interaction to plant encoded susceptibility factors. Steps of successful viral replication in susceptible host genotype and *rym11*-carrying genotype were shown by black (1 to 9) and red arrows (1, 10 to 13), respectively. In susceptible genotype, *Bymovirus* typically enters plant cell through cellular damage (yellow lightning bolt) consisting of fungus-directed natural inoculation and artificially mechanical inoculation. Viral RNA genome is transported to rough endoplasmic reticulum (ER) (1), and translates viral polyprotein by cooperating with cellular proteins (Whitham and Wang 2004), e.g. the eukaryotic translation initiation complex. The protein precursors are modified subsequently by cleavage, folding, assembly or disassembly for generating functional viral proteins such as RNA-dependent RNA polymerase (RdRp, also called NIb) (2). Positive-strand RNA formerly applied for translation is released through inhibition of viral translation (3) and applied as a template to synthesize the intermediate negative-strand RNA in cooperation with the newly produced RdRp (4). The temporarily negative ssRNA is used as a template to multiple the progeny positive ssRNA (5), which were applied for translating progeny viral proteins (6-7), and also used in combination with the synthesized coat protein (CP) for encapsidation of virion/viral ribonucleoprotein complex (8). Cell-to-cell movement is initiated by translocation of the accumulated virus genome and proteins through plasmodesmata from the infected cell to neighbors (9). In *rym11*-carrying genotypes as occurred in susceptible genotypes, virus components may enter host cells via cellular damage releasing the nucleic acid (1) and

translating the precursor of viral protein. However, due to loss of wild type functional *HvPDIL5-1*, the correct folding and/or assembling of the synthesized polyproteins is blocked. The mis-folded viral proteins are subjected for degradation via 26S-proteosome complex in cytoplasm (10-13). As lack of RdRp, initial multiplication of virus RNA genome is blocked, therefore resulting in immunity to *Bymovirus*.

Members of the plant PDI-like gene family have not been reported so far as *senso stricto* susceptibility factors to any plant viruses and little is known about PDILs and virus interactions in plants. It was shown that knockdown of gene expression by virus-induced gene-silencing (VIGS) of two PDI-like gene family members in tobacco, *NtERp57* and *NtP5,* partially decreased *N*-gene mediated resistance to *Tobacco mosaic virus* (TMV) (Caplan et al. 2009). Although this provides a hint for plant PDI-like genes / virus interactions, these examples do not indicate for the two genes a role as susceptibility factors. The situation is different in animals. PDI gene family members, particularly cell-surface PDIL proteins, may participate in the infection process of multiple human and animal viruses (e.g. HIV) (Bi et al. 2011; Calderon et al. 2011; Fenouillet et al. 2007; Gilbert et al. 2006; Jain et al. 2007, 2008; Magnuson et al. 2005; Ou and Silver 2006; Schelhaas et al. 2007; Walczak and Tsai 2011; Wan et al. 2012; Wang et al. 2010). Non-specific inhibition of PDI activity suppressed the PDI-mediated redox environment of plasma membranes (Jain et al. 2007) and therefore interfered with HIV envelope protein-directed cell fusions (Ou and Silver 2006). Knock-down of specific PDI members could influence the infectivity of several viruses, e.g. HIV, Newcastle disease virus and mouse polyomavirus (Gilbert et al. 2006; Jain et al. 2008; Ou and Silver 2006). In *H. sapiens*, knockdown of PDI, ERp29, ERp57 and ERp72 inhibited the accumulation of viral particles under cell culture conditions (Magnuson et al. 2005; Schelhaas et al. 2007; Walczak and Tsai 2011). Together with the novel findings in barley it may be postulated that PDILs could generally be important components for virus infection and/or replication in animals as well as also plants.

4.2 Naturally occurring diversity of *Bymovirus* resistance could represent the consequence of adaptation to virus infested environments

Up to date, Sixteen genetic loci conferring resistance to the *Bymovirus* disease were reported in the primary gene-pool of barley comprising the two *H. vulgare* sub-species *vulgare* and *spontaneum* (Kai et al. 2012; Ordon et al. 2005). A higher proportion (14/16) of the resistance genes (expect *Rym17* and *rym18*) was originally identified in genotypes collecting from virus-infested environments East Asia and Europe (Kühne 2009), probably implying a correlation on geographic distribution of resistance genes and the *Bymovirus* disease. In addition, the majority (9/16) of resistance genes (*rym1*, *rym2*, *rym3*, *rym5*, *rym6*, *rym11*, *rym12*, *rym13*, *rym15*) was initially discovered in East Asian barley accessions whereas five resistance genes only (*rym4*, *rym7*, *rym8*, *rym9* and *rym10*) were found in European barleys (Ordon et al. 2005). Interestingly, during the presented screening for diversity in the gene *HvPDIL5-1* a higher allelic diversity was found in accessions originating from East Asia. So far, five isolates of *Bymovirus* were identified and serologically differentiated in Europe (Habekuß et al. 2008; Hariri et al. 2000; Kanyuka et al. 2004; Meyer and Dessens 1996; Peerenboom et al. 1996; Shi et al. 1995; Timpe and Kuhne 1994), while dozens of strains / variations on genome sequences were observed in East Asian countries (Chen et al. 1999; Lee et al. 1996; Lee et al. 2006; Nishigawa et al. 2008; Nomura et al. 1996; Park et al. 2005; Zheng et al. 1999). Therefore, the larger diversity of naturally occurring resistance alleles in East Asia genotypes in comparison to those originating from Europe is associated to higher pathogen diversity and thus just may reflect a stronger need for adapting to virus infested environments in East Asia.

Unlocking naturally occurring genetic diversity of *HvPDIL5-1* by re-sequencing a large geographically referenced collection of wild and domesticated barleys also revealed local adaptation of barley against the *Bymovirus* threat throught revealing association of the resistance alleles and virus distribution. Natural variation of *HvPDIL5-1* was also determined in wild barleys. However, no resistance conferring haplotypes could be detected. This is indicating that the resistance alleles of *HvPDIL5-1* were not present in the wild barley gene pool implying that *Bymovirus* plays no role in the life cycle of *H. spontaneum* and its original environment. Re-sequencing of *HvPDIL5-1* in domesticated barleys revealed four resistance alleles (*rym11-a*, *-b*, *-c* and *-d*) in 34 barley accessions. Except *rym11-a*, which was found in a single barley landrace from Turkey, all remaining resistance alleles (*rym11-b*, *-c* and *-d*) in 32 landraces / cultivars were exclusively found from East Asia. Approximately 9.2% (32/347) of accessions carry *rym11* conferring *Bymovirus* resistance. This provided a strong hint that the origin of resistance alleles is an adaptive effect of barley / *Bymovirus* interaction given that in East Asia also a greater pathogen diversity was reported than in Europe (Chen et al. 1999; Habekuß et al. 2008; Hariri et al. 2000; Kanyuka et al. 2004; Lee et al. 1996; Lee et al. 2006; Meyer and Dessens 1996; Nishigawa et al. 2008; Nomura et al. 1996; Park et al. 2005; Peerenboom et al. 1996; Shi et al. 1995; Timpe and Kuhne 1994; Zheng et al. 1999). This situation for *HvPDIL5-1* was somewhat reflected by analysis of genetic diversity in the *rym4*/*rym5* resistance gene *HvEIF4E* (Hofinger et al. 2011). The haplotype diversity of *HvEIF4E* was considerably higher in East Asian accessions (0.787) rather than those collected from Europe and other geographic regions (0.564 worldwide). This was in contrast to a comparatively lower degree of general genetic diversity in East Asian accessions (East Asia, 0.185; Worldwide, 0.291). This could be interpreted that natural variation of *HvEIF4E* was influenced by local environmental conditions, e.g. the higher *Bymovirus* diversity (Chen et al. 1999; Lee et al. 1996; Lee et al. 2006; Nishigawa et al. 2008; Nomura et al. 1996; Park et al. 2005; Zheng et al. 1999). Therefore, both genes *rym4*/*rym5* and *rym11* show patterns of adaptive genetic diversity correlated with *Bymovirus* resistance.

Overall, naturally occurring diversity of *Bymovirus* resistance genes and the resistance alleles of *rym4*/*rym5* and *rym11* could represent the consequence of adaptation to virus infested environments. Thus, extensive screening of barley resources from *Bymovirus* containing barley growing regions or habitats (e.g. East Asian countries) can possibly provide additional naturally occurring novel alleles and genes conferring resistances (Gotz and Friedt 1993; Ordon et al. 1993; Ordon and Friedt 1993).

4.3 Barley resistance breeding requires access to multiple sources of naturally occurring resistance

The barley yellow mosaic virus disease may cause serious damage of winter barley production (Plumb et al. 1986). Under natural conditions virus infection proceeds through the barley root system by the soil-borne plasmodiophorid *Polymyxa graminis*, prohibiting plant protection by help of chemical treatment. Thus, resistance breeding is the only practical way to avoid yield losses. *rym4* and *rym5* were the predominant source of resistance for barley breeding over the past twenty years (Kühne 2009), but *rym4*/*rym5*-based resistance has been overcome by several strains of BaMMV and

BaYMV (Habekuß et al. 2008; Kanyuka et al. 2004; Kashiwazaki et al. 1989; Kühne et al. 2003). Thus novel, longer lasting or more durable sources of resistance are required for resistance breeding. It was shown that the formerly *rym1* and *rym11* showed identical phenotypes under the infection of different virulent strains, and were genetically allocated to similar genetic position on chromosome 4HL in close proximity to the centromere (Habekuß et al. 2008; Kanyuka et al. 2004; Konishi et al. 1997; Nissan-Azzouz et al. 2005). By re-sequencing *HvPDIL5-1* in *rym1*-carrying accessions and by testing for resistance in F_1 plants derived from crosses between *rym1* and *rym11* containing genotypes provided evidence that both resistance loci are alleles of the same functional gene *HvPDIL5-1*. *rym1*/*rym11* confer complete resistance to all virulent European isolates (Habekuß et al. 2008; Kanyuka et al. 2004; Nissan-Azzouz et al. 2005) and also Japanese strains of *Bymovirus* (Konishi and Kaiser-Alexnat 2000; Konishi et al. 2002) thus *rym1*/*11* could efficiently replace the central importance of *rym4*/*rym5* in barley breeding in Japan and Europe. Due to lack of phenotypic data upon infection with isolates from China or Korea, it remains to be determined if the same locus could be of similar importance for breeding in these regions. In this study, unlocking naturally occurring resistances in a large collection of landraces and cultivars revealed frequent distribution of the resistant *rym11* alleles in East Asia, but not in Europe. Since *rym11* has not been knowingly used in registered cultivars in Europe there has been so far no environmental selection pressure on virus populations which could have led to natural variations of the virus genome. Therefore it may be reasonable to expect that *rym1*/*rym11* can provide an alternative source of complete and durable resistance in European cultivation system. Its application in cultivars may represent an alternative protection against the *Bymovirus* disease in Europe.

As plants with monogenic resistance, e.g. *rym4*/*rym5* (Graner and Bauer 1993; Pellio et al. 2005) generally cause a higher selection pressure on pathogen populations and could promote the rapid appearance of resistance breaking isolates, e.g. BaYMV-2, BaMMV-Sil and BaMMV-Teik (Habekuß et al. 2008; Kanyuka et al. 2004; Kühne et al. 2003), pyramiding of several resistance genes in a single genotype is considered a promising strategy to obtain durable resistance (Werner et al. 2005, 2007). For example, *rym9* confers resistance (or partial) to all virulent isolates of BaMMV but not to BaYMV (Bauer et al. 1997; Habekuß et al. 2008; Kanyuka et al. 2004). But the combination of *rym4*, *rym9* and *rym11* completely stops virus infection of BaMMV and BaYMV (Werner et al. 2005). The work provided by the present thesis identified the functional gene *HvPDIL5-1* conferring *rym11*-based resistance and indeed developed the allele-specific perfect markers. The efforts will allow now to precisely select the resistance conferring *rym11* alleles on chromosome 4HL thus facilitating the pyramidization together with *rym4*/*rym5* on chromosome 3HL, which is derived from allelic mutation of *HvEIF4E* (Kanyuka et al. 2005; Stein et al. 2005). The resistance locus *rym7* was allocated to a 9.9 cM interval, but pyramidizaiton between this locus and other resistance genes (e.g., *rym1*/*rym11* and *rym4*/*rym5*) may require perfect markers to avoid the linkage drag and accelerate the breeding process.

4.4 Barley physical map is a fundamental and information-enriched platform for gene identification

Gene discovery by chromosome walking and map-based cloning used to be a laborious and time-consuming task in barley. The efficiency for gene identification is dependent on genetic/physical resolution (e.g. chromosomal localization, recombination frequency). For instance, by using 5,232 gametes, the stem rust resistance gene *Rpg5* was delimited to a 70 kb interval on chromosome 5HL distal (Brueggeman et al. 2008) in comparison to, however, the >500 kb region on 2HL proximally to centromere of the gene *Vrs1* controlling spike development by using nearly two-fold of individuals (9,831 gametes) (Komatsuda et al. 2007). It was shown and demonstrated by fluorescent *in situ* hybridisation of single copy probes that a small genetic distance around the centromere can translate into a large physical distance (Ma et al. 2010) expanding possibly over the length of half a chromosome arm. Therefore, the published barley genetic and physical map of barley genome may facilitate by basically omitting the need of performing any additional steps of chromosome walking for isolating barley genes in particularly centromeric and peri-centromeric regions of chromosomes, where a large number of functional genes were revealed (IBSC 2012).

The present work by identifying the functional gene underlying *rym11* conferring resistance represented an example for cloning barley genes relying on an intermediate version of the published physical map of barley (IBSC 2012). Firstly, sequence homology of the original flanking (C_1030750_B and C_1012894_B) and co-segregating markers (C_205243_B) in comparison to the physical and sequence assembly of the barley genome allowed anchoring between genetic and physical maps of *rym11*, therefore opening the possibilities for efficiently utilizing the sequence sources for target marker development to narrow down the genetic interval between new flanking markers C5B4C and C2B18S2. Then, constructing the physical map of *rym11* was facilitated by integrating the generated BAC contigs anchoring with the flanking markers or screening BAC libraries of cultivar ‘Morex’. The entire sequences of physical contig were achieved by applying available BAC sequences or sequencing of MTP-analyzed BAC clones. Moreover, the physical and sequence assembly of barley genome illustrated the barley gene spaces by WGS-assembly and sequencing transcriptomes. This allows predicting the functional gene for *rym11* by PCR amplification of parental DNA samples and sequencing of the annotated genes, which are allocated in the physical interval. In case of contig analysis of *rym11*, the physical distance between the original flanking markers C_1030750_B and C_1012894_B expands approximately 3 Mbp non-redundant sequences. To reach the goal by iterative steps of chromosome walking would have been incomparably more time intensive and laborious. Therefore, the example of contig assembly at the *rym11* locus supported by the ordered, information-enriched scaffold of the physical map (IBSC 2012) illustrates perfectly the future potential of gene isolation in barley, thus map-based cloning in barley will become easier and applicable.

4.5 Rapid, robust and cost-efficient strategy for marker saturation in barley

In this study, a strategy for marker saturation was followed for future high-density and high-resolution genetic mapping of the partial resistance gene *rym7.* On the basis of a previously defined mapping interval around *rym7* (Graner et al. 1999a) recently published genomic resources were tapped for straightforward selection and establishing of candidate genetic markers. PCR-based transcript-derived markers provide the basis for highly efficient and rapid marker saturation and the preliminary investigation of gene-based variation. Recently published marker resources including EST-SSR markers (Varshney et al. 2007), EST-SNP/STS markers (Stein et al. 2007; Sato et al. 2009), zipper-derived STS-markers (Mayer et al. 2011), and a 9k-iSelect SNP assay (Comadran et al. 2012) were used for selection and polymorphism survey of markers assigned to the target interval on chromosome 1H close to the centromere. 49 polymorphic candidate markers were revealed ready-to-use for high-resolution mapping of *rym7*. This result demonstrates how recently established barley genomic resources facilitate the effort of marker selection and development in barley in general.

In addition to ten obtained mapped markers the physical, genetic and sequence resources recently published for barley (IBSC 2012) also allow implementing novel strategies for marker detection or development which rely on the power of Next Generation Sequencing (NGS) technology. Methods like RNA sequencing (RNAseq) of multiple genotypes (IBSC 2012), exome-captured re-sequencing (Mascher et al. 2013b) as well as whole genome shotgun (WGS) survey sequencing (IBSC 2012) can reveal almost unlimited sequence polymorphisms by sequence read mapping to the published draft reference sequence assembly of the barley genome (IBSC 2012). Due to the provided integration of genetic and physical genome information this is opening the possibility for direct marker selection on the genome level and even in the target genomic region. This was principally demonstrated for instance by whole-genome survey sequencing of population individuals. This approach was originally applied to anchor a physical map (Mascher et al. 2013a), and revealed >5 millions of SNPs genome-wide. Sequencing of population individuals is limited in use because of extremely high cost, but sequencing of parental genotypes for polymorphisms in conjunction with designing custom marker assays for genotyping the populations is needed to be performed. Genotyping-by-sequencing of complexity reduction in pooled-DNA samples of population individuals by means of a *PstI*/*MspI* double-digestion is an alternative for rapid marker development, and may produce tens of thousands of SNP markers (Poland et al. 2012). This strategy integrating polymorphism detection and genotyping in a single sequencing step is recommending as a rapid and cost-efficient strategy for marker saturation and finally producing intermediate amount of genetic markers. Altogether, marker development is straightforward and therefore no longer the limited step for gene identification by map-based cloning in barley.

4.6 Outlook

The work reported in this thesis identified the functional gene underlying *rym11*-based naturally occurring resistance, and evaluated its natural variation, geographic distribution and origin. The recessive resistance locus is conferred by loss-of-function of a novel susceptibility factor *HvPDIL5*-1, a protein which is highly conserved but was never described as susceptibility factor in other plants and animals. This work provided a hint that plant PDIs may provide host factors involved in virus lifecycles. According to the putative redox activity and ER-retention, *HvPDIL5-1* likely acts as chaperone for correct protein folding of virus proteins or virus-required host proteins. The biological function of *HvPDIL5-1* and underlying molecular mechanism for virus infection could not yet be demonstrated and require additional molecular and biochemical experimentations including protein characterization, protein-protein interaction studies as well as the analysis of virus induced transcriptome. The gene *rym11* confers immunity to all European *Bymovirus* strains, but the response to East Asian virulent isolates is unclear and remains to be determined. In addition low-resolution mapping of a second resistance gene *rym7* could be accomplished and enlarged mapping populations could be constructed. The established resources will allow to perform the next steps towards high-resolution mapping and map-based cloning of the resistance locus *rym7*.

5. Summary

The barley yellow mosaic virus disease seriously threatens winter barley production in Europe and East Asia, and improving natural resistance to *Bymovirus* in cultivars is the only practical way to prevent yield loss. The project within this thesis attempted to perform genetic mapping of *rym7* conferring partial resistance to BaMMV, and identify the functional gene underlying *rym11*-based broad-spectrum resistance to all European virulent strains of *Bymovirus*.

Relying on the published barley genomic resources, *rym7* was allocated to a 9.9 cM interval of chromosome 1H closely linked to centromere as was previously reported by Graner *et al.* (1999). This work demonstrated how to combine the genomic resources for efficient and rapid marker saturation. The archived markers and enlarged populations will facilitate high-resolution mapping and isolation of this gene.

rym11 was previously assigned by Lüpken *et al.* (2013) to a 0.074cM interval of chromosome 4HL proximately to the centromere. The present thesis reported construction of a physical map at *rym11* locus, identification of the underlying functional gene *HvPDIL5-1*, as well as functional verification by TILLING for EMS-induced resistance alleles, transgene-induced susceptibility and by allelic test via phenotyping F_1 hybrids between genotypes carrying natural resistance alleles. Re-sequencing of the entire open reading frame (ORF) of *HvPDIL5-1* in a large collection of wild and domesticated barleys revealed natural variation, geographic distribution and origin of *rym11*. Four naturally occurring resistance alleles (*rym11-a*, *-b*, *-c* and *-d*) out of total 28 haplotypes were identified, and may be evolved from the ancestral haplotype I by natural variation and artificial selection. A larger diversity of *rym11*-based resistance alleles was observed in East-Asian accessions, possibly due to higher pathogen diversity in this region. The user-friendly co-dominant diagnostic markers for four naturally occurring resistance alleles and two EMS-induced alleles (*rym11-9699* and *rym11-10253*) were develop and may provide the precise selection of the resistance *rym11* alleles in barley resistance breeding. The particular member of PDI gene family may exist in the majority of plants and animals, and represents overall high conservation of protein structures across kingdoms. This work within the thesis proved that *HvPDIL5-1*, member of highly conserved PDI gene family, provides a susceptibility factor to viruses in eukaryotic species.

6. Zusammenfassung

Die Gerste-Gelbmosaik Erkrankung stellt ein wichtiges Problem für die Winter-Gerste Produktion in Europa und Ost-Asien dar. Eine Verbesserung der natürlichen Resistenz von Gerste-Kultivaren gegenüber den Erregern, verschiedenen Stämmen der Bymoviren, stellt die einzige praktikable Möglichkeit dar, Ernteausfälle zu verhindern oder zu reduzieren. Die vorliegende Doktorarbeit hatte daher zum Ziel, einerseits den, partielle BaMMV-Resistenz vermittelnden, Lokus *rym7* genetisch zu kartieren, und andererseits das dem, gegen alle virulenten europäischen Bymovirus-Stämme Resistenz-vermittelnde, Resistenzlokus *rym11* zugrundeliegende Gen zu isolieren und funktionell zu charakterisieren.

Unter Berücksichtigung der neuesten für Gerste publizierten und verfügbaren, genomischen Ressourcen, konnte das Gen *rym7* in einem 9,9 cM großen Intervall auf Gerste-Chromosom 1H, in engster Kopplung zum genetischen Zentromer und in Übereinstimmung zu einer vorangegangen Publikation (Graner et al. 1999), lokalisiert werden. Die vorliegende Arbeit demonstriert, mit welcher Effizienz, auf Basis der neuen genomischen Ressourcen, in kurzer Zeit genetische Abschnitte mit neuen molekularen Markern gesättigt werden können. Die etablierten Marker und die erweiterten Kartierungspopulationen werden die hoch-auflösende Kartierung sowie die Isolierung des Gens zukünftig ermöglichen.

Das Gen *rym11* wurde kürzlich in einem 0,074 cM Intervall auf Gerste Chromosom 4HL, in Nähe zum Zentromer, kartiert (Lüpken *et al.* 2013). In der vorliegenden Doktorarbeit wurde zunächst eine, den Resistenzlokus überspannende, physikalische Karte erstellt und das zugrundeliegende Kandidatengen *HvPDIL5-1* identifiziert. Daraufhin konnte dieses Kandidatengen durch TILLING, Komplementation durch Transformation und durch Allelietests zwischen unabhängigen funktionellen Allelen, als das funktionelle Gen *rym11* bestätigt werden. Der gesamte offene Leserahmen (open reading frame, ORF) des Gens *HvPDIL5-1* wurde in einer umfangreichen Sammlung genetischer Ressourcen für Gerste resequenziert. Für diese Sammlung an Genotypen lagen Informationen ihrer Herkunft vor, so dass ein detailliertes Bild der vorhandenen genetischen Diversität dieses Gens sowie die Herkunft funktioneller, resistenzvermittelnder Allele ermittelt werden konnte. Es wurden vier natürliche, resistenzvermittelnde Allele (*rym11-a*, *-b*, -

c and *-d*) aus insgesamt 28 Exon-basierten Haplotypen identifiziert. Alle Allele konnten als direkte, durch natürliche Variation und Selektion entstandene, Derivate des möglicherweise ursprünglichen Haplotyps I eingeordnet werden. In Gerste-Herkünften aus Ostasien wurde insgesamt ein höherer Anteil und eine höhere Diversität an resistenzvermittelnden *HvPDIL5-1* Allelen festgestellt. Dies wurde als Folge einer höheren Pathogendiversität und eines höheren Pathogendrucks in Ost-Asien interpretiert. Es konnten für alle resistenzvermittelnden Allele anwendungsfreundliche, kodominante, molekulare Marker entwickelt werden, deren Einsatz eine präzise Selektion der Allele in der Gerste-Züchtung erleichtern wird. Das identifizierte Gen *HvPDIL5-1* ist Mitglied einer größeren Genfamilie, die, in hoher Konservierung der Proteinsequenz, in der Mehrzahl der Tier- und Pflanzenarten zu finden ist. Die Ergebnisse dieser Doktorarbeit zeigen erstmals, dass dieser Vertreter der Proteindisulfidisomerase-Genfamilie als Anfälligkeit-vermittelnder Faktor in Eukaryoten wirken kann.

7. References

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8. Eidesstattliche erklärung

Herr Ping Yang

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Germany

Hiermit erkläre ich, dass mit dieser wissenschaftlichen Arbeit noch keine vergeblichen Promotionsversuche unternommen wurden.

Die eingereichte Dissertation mit dem Thema: “ Map-based cloning of susceptibility factors for *Bymovirus* in barley (*H. vulgare L.*)” habe ich selbständig und nur unter Verwendung der angegeben Literatur und Hilfsmittel angefertigt. Des Weiteren erkläre ich, dass keine Strafverfahren gegen mich anhängig sind.

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Ping Yang

9. Curriculum Vitae

Family name: Yang, **First name:** Ping
Address: Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstr. 3, 06466, Gatersleben, Stadt Seeland, Germany
Phone number: +49 (0)394825594
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Date of Birth: 11/04/1984
Place of Birth: Nanchuan city / Chongqing municipality / China
Nationality: Chinese **Gender:** Male **Marital status:** Married

Education:

- **Ph.D.** Enrolled at Martin Luther University, Halle, Germany, and the thesis was prepared at: Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany (Sep. 2010 - present)
- **M.Sc.** Biochemistry and molecular biology**,** Sichuan Agricultural University (SAU), Ya'an, China (Sep. 2007 - Jul. 2010), and the dissertation was prepared at: Institute of Genetics and Developmental Biology (IGDB), Chinese Academy of Sciences (CAS), Beijing, China (Jun. 2008 – Jul. 2010)
- **B.Sc.** Biotechnology**,** Sichuan Agricultural University (SAU), Ya'an, China (Sep. 2003 - Jul. 2007), and the dissertation was prepared at: Crop Research Institute, Sichuan Academy of Agricultural Sciences, Chengdu, China

Academic researches:

- Map-based cloning of susceptibility factors for *Bymovirus* in barley (PhD thesis) (Sep. 2010 - Dec. 2013)
- Isolation and chromosomal mapping of the nitrate and phosphate related genes in common wheat (Master dissertation) (Jun. 2008 - Jul. 2010)
- Construction of wheat genetic map with SRAP markers (Jul. 2007 - Feb. 2008)
- Genetic diversity of domesticated barley varieties by SRAP Markers (Bachelor dissertation) (Feb. 2007 - Jun. 2007)

Honors and awards:

- *Summa cum laude* (Excellent/Best) of PhD thesis defense, Martin-Luther-University, Halle, Germany (Jan. 2014)
- The prize of best poster, The 11th International Barley Genetics Symposium (IBGS), Hangzhou, China (Apr. 2012)
- The prize for outstanding academic discussion, Annual meeting of state key laboratory of plant cell and chromosome engineering, Beijing, China, (Jun. 2010)
- The tuition scholarship, Sichuan Agriculture University (SAU) (2007-2010)

- Outstanding student volunteer of social practice (SAU) (2005-2006)
- The second level of faculty scholarship (SAU) (2003-2007)

Patents:

- **Ping Yang**, Thomas Lüpken, Frank Ordon, Nils Stein. Mittel zur Selektion und/oder Erzeugung von gegen Gelbmosaikvirose resistenter Gerste. (2013) PAT 1448 (Under evaluation).

Publications:

1, **Ping Yang**, Frank Ordon, Nils Stein. On the allelic state of bymovirus resistance genes on barley chromosome 4HL, submitted.
2, **Ping Yang**, Thomas Lüpken, Antje Habekuß, Götz Hensel, Benjamin Kilian, Ruvini Ariyadasa, Axel Himmelbach, Jochen Kuhmlehn, Frank Ordon, Nils Stein. *PROTEIN DISULFIDE ISOMERASE LIKE 5-1* is a susceptibility factor to plant viruses. Proceeding of the National Academy of Sciences of the United States of America (2014), doi: 10.1073/pnas.1320362111.
3, **Ping Yang**, Dragan Perovic, Antje Habekuß, Rounan Zhou, Andreas Graner, Frank Ordon, Nils Stein. Gene-based high-density mapping of *rym7* (*rmm7*) conferring resistance to *Barley mild mosaic virus* (BaMMV). Molecular breeding (2013), 32(1): 27-37.
4, **Ping Yang**, Xianjun Liu, Xinchun Liu, Wuyun Yang, Zongyun Feng. Diversity analysis of the developed qingke (Hulless barley) cultivars representing different growing regions of the Qinghai-Tibet Plateau in China using sequence-related amplified polymorphism (SRAP) markers. African Journal of Biotechnology (2010), 9(50): 8530-8538.
5, **Yang Ping**, Liu Xianjun, Liu Xinchun, Li Jun, Wang Xiwen, He Shoupu, Li Gang, Yang Wuyun, Feng Zongyun. Genetic diversity analysis of the developed qingke (Hulless barley) varieties from the plateau regions of Sichuan Province in China revealed by SRAP markers. Hereditas (Beijing) (2008), 30(1): 115-122. (Chinese with English abstract)
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Conferences - oral presentation:

- **Ping Yang.** Isolation, distribution and origin of *rym11* conferring broad-spectrum resistance to the *Bymovirus* disease. International Advances in Plant Virology 2013, Sportspark, University of East Anglia, Norwich, UK.

- **Ping Yang**. Unlocking barley genetic resources for isolation, distribution and origin of *rym11* conferring broad-spectrum resistance to the Bymovirus disease. 7th International Triticeae Symposium (7ITS), Chengdu, China, 2013.
- **Ping Yang**. Isolation, distribution and origin of *rym11* conferring broad-spectrum resistances to the Bymovirus disease. PLANT 2030 Status Seminar-2013, Potsdam, Germany, 2013.
- **Ping Yang**. *HvRym11*, a novel susceptibility factor conferring immunity to the *Bymovirus* disease. The 10th Genome Research Working Group Conference of the GPZ, Halle, Germany, 2012.
- **Ping Yang**. Positional isolation and functional analysis of *rym11* conferring immunity to BaMMV and BaYMV. Plant Science Student Conference, Gatersleben, Germany, 2012.

Conferences - poster:

- **Ping Yang**, Axel Himmelbach, Neele Wendler, Martin Mascher, Antje Habekuß, Frank Ordon, Nils Stein. Genotyping-by-sequencing accelerates the genetic mapping of the resistance gene *rym7* in barley. 7th International Triticeae Symposium (7ITS), Chengdu, China, 2013.
- **Ping Yang**, Thomas Lüpken, Antje Habekuß, Ariyadasa Ruvini, Axel Himmelbach, Benjamin Kilian, Frank Ordon, Nils Stein. *HvRym11*, a novel susceptibility factor of the *Bymovirus*-barley interaction. Plant & Animal genome XXI conference, San Diego, USA, 2013.
- **Ping Yang**, Thomas Lüpken, Ariyadasa Ruvini, Antje Habekuß, Axel Himmelbach, Benjamin Kilian, Frank Ordon, Nils Stein. Positional isolation and functional investigation of *rym11* conferring immunity to BaMMV and BaYMV. The 11th International Barley Genetics Symposium, HangZhou, China, 2012. (The prize of best poster)
- **Ping Yang**, Thomas Lüpken, Ariyadasa Ruvini, Antje Habekuß, Axel Himmelbach, Benjamin Kilian, Frank Ordon, Nils Stein. Positional isolation and functional investigation of *rym11* conferring immunity to BaMMV and BaYMV. PLANT 2030 Status Seminar, Potsdam, Germany, 2012.
- **Ping Yang**, Dragan Perovic, Antje Habekuß, Ruonan Zhou, Andreas Graner, Frank Ordon, Nils Stein. Towards map-based cloning of the gene *rym7* (*rmm7*) conferring partial resistance to *Barley Mild Mosaic Virus* (BaMMV) disease. Plant Science Student Conference, Halle, Germany, 2011.

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Ping Yang

Appendix Tables:

Appendix Table 1 Geo-referenced wild and domesticated barleys

Serial number	Accession name	Haplotype number of HvPDIL5-1-cds	Taxonomy	Status	Growth habit	Row type	Region	FAO country code	Latitude	Longitude
1	BCC1565	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	ALB	41,325556	19,819722
2	BCC1591	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	ALB	41,331650	19,831800
3	HOR12797	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	ALB	41,331650	19,831800
4	HOR12798	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	ALB	41,331650	19,831800
5	HOR1281	*missing*	*Hordeum vulgare*	Landrace	Spring	6	EU	ALB	41,116667	20,683333
6	HOR1381	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	ALB	41,150000	20,550000
7	HOR739	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	ALB	41,452500	19,566667
8	HOR740	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	ALB	41,454444	20,533333
9	HOR741	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	ALB	41,333333	19,831111
10	HOR749	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	ALB	41,816667	20,492500
11	HOR756	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	ALB	40,787778	20,189167
12	HOR772	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	ALB	42,294722	19,541111
13	FT783	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	ALB	41,331650	19,831800
14	BCC1471	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	ARM	40,183333	44,516667
15	HOR4157	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	ARM	40,183333	44,516667
16	BCC1324	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	AUT	48,208174	16,373819
17	BCC1341	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	AUT	48,208174	16,373819
18	BCC1407	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	48,208331	16,373064
19	BCC1409	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	48,208331	16,373064
20	BCC1431	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	48,208331	16,373064
21	BCC1440	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	48,208331	16,373064
22	BCC1529	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	AUT	48,208331	16,373064
23	HOR1	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	AUT	48,208174	16,373819
24	HOR10094	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	AUT	48,500000	14,764167
25	HOR10630	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	AUT	47,128889	10,955833
26	HOR10632	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	AUT	48,533333	14,183333
27	HOR108	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	48,200000	16,350000
28	HOR1320	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	AUT	48,208174	16,373819
29	HOR2346	*missing*	*Hordeum vulgare*	Landrace	Spring	6	EU	AUT	47,000000	11,600000
30	HOR3305	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	AUT	48,208174	16,373819
31	HOR3777	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	47,028889	12,868611
32	HOR3950	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	47,006389	13,166667
33	HOR3952	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	46,978889	14,196667
34	HOR3955	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	47,009167	13,605556
35	HOR3958	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	47,096667	13,601667
36	HOR3959	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	AUT	47,272222	12,644722
37	HOR3960	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	AUT	47,028889	12,887500
38	HOR3961	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	AUT	47,800000	13,033333
39	HOR828	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	48,200000	16,350000
40	HOR9853	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	48,500000	14,764167
41	HOR9855	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	48,150000	14,664167
42	HOR9856	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	AUT	48,150000	14,664167
43	FT704	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	AUT	48,208174	16,373819
44	BCC1339	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	BEL	50,850340	4,351710
45	HOR3313	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	BEL	50,850340	4,351710
46	HOR3314	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	BEL	50,850340	4,351710

47	HOR4140	*/*	*Hordeum vulgare*	Cultivar	Winter	6	EU	BEL	50,850340	4,351710
48	BCC1561	*/*	*Hordeum vulgare*	Landrace	Spring	6	EU	BGR	42,697222	23,323333
49	BCC1562	*/*	*Hordeum vulgare*	Landrace	Spring	6	EU	BGR	40,103333	29,358056
50	BCC1579	*/*	*Hordeum vulgare*	Cultivar	Winter	6	EU	BGR	42,697839	23,321670
51	HOR11224	*/*	*Hordeum vulgare*	Cultivar	Winter	6	EU	BGR	42,697839	23,321670
52	HOR13449	*/*	*Hordeum vulgare*	Landrace	Winter	6	EU	BGR	42,252222	22,981389
53	HOR13450	*/*	*Hordeum vulgare*	Landrace	Winter	2	EU	BGR	42,697839	23,321670
54	HOR13453	*missing*	*Hordeum vulgare*	Landrace	Winter	2	EU	BGR	42,697839	23,321670
55	HOR13458	*/*	*Hordeum vulgare*	Landrace	Winter	2	EU	BGR	42,697839	23,321670
56	HOR3199	*/*	*Hordeum vulgare*	Landrace	Winter	6	EU	BGR	42,697839	23,321670
57	HOR3500	*/*	*Hordeum vulgare*	Cultivar	Winter	6	EU	BGR	42,697839	23,321670
58	HOR372	*/*	*Hordeum vulgare*	Landrace	Spring	6	EU	BGR	43,503889	24,072222
59	HOR380	*/*	*Hordeum vulgare*	Landrace	Spring	6	EU	BGR	43,239167	25,302500
60	HOR383	*/*	*Hordeum vulgare*	Landrace	Spring	6	EU	BGR	43,854444	25,958611
61	HOR386	*/*	*Hordeum vulgare*	Landrace	Spring	6	EU	BGR	42,134167	24,953333
62	HOR396	*/*	*Hordeum vulgare*	Landrace	Spring	6	EU	BGR	42,314444	27,766944
63	HOR4380	*/*	*Hordeum vulgare*	Landrace	Winter	6	EU	BGR	42,697839	23,321670
64	HOR4383	*/*	*Hordeum vulgare*	Landrace	Winter	6	EU	BGR	42,697839	23,321670
65	HOR4386	*/*	*Hordeum vulgare*	Cultivar	Winter	6	EU	BGR	42,697839	23,321670
66	HOR4914	*/*	*Hordeum vulgare*	Cultivar	Winter	6	EU	BGR	42,697839	23,321670
67	HOR4919	*/*	*Hordeum vulgare*	Cultivar	Winter	6	EU	BGR	42,697839	23,321670
68	FT782	*/*	*Hordeum vulgare*	Landrace	Spring	6	EU	BGR	42,697839	23,321670
69	BCC1467	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	BLR	42,697222	23,323333
70	HOR3388	*/*	*Hordeum vulgare*	Landrace	Winter	6	EU	BLR	53,900000	27,566667
71	BCC1361	*/*	*Hordeum vulgare*	Cultivar	Winter	2	EU	CHE	46,947922	7,444608
72	HOR12154	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	CHE	46,716667	9,216667
73	HOR12166	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	CHE	46,666667	8,766667
74	HOR12206	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	CHE	46,800000	9,216667
75	HOR3011	*/*	*Hordeum vulgare*	Cultivar	Spring	6	EU	CHE	46,947922	7,444608
76	FT411	*/*	*Hordeum vulgare*	Landrace	Unknown	2	EU	CHE	46,947922	7,444608
77	BCC1379	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	CZE	50,088611	14,421389
78	BCC1414	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	CZE	50,088611	14,421389
79	BCC1421	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	CZE	50,088611	14,421389
80	BCC1432	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	CZE	50,088611	14,421389
81	BCC1436	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	CZE	48,816667	15,466667
82	BCC1437	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	CZE	48,816667	15,466667
83	BCC1439	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	CZE	50,088611	14,421389
84	BCC1444	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	CZE	50,088611	14,421389
85	HOR7344	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	CZE	48,433333	18,000000
86	HOR7380	*/*	*Hordeum vulgare*	Landrace	Spring	6	EU	CZE	49,519722	18,832222
87	HOR7387	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	CZE	49,416667	18,226111
88	BCC1376	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	DNK	55,675706	12,578744
89	BCC1392	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	DNK	55,675706	12,578744
90	BCC1418	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	DNK	55,675706	12,578744
91	HOR4750	*/*	*Hordeum vulgare*	Cultivar	Spring	2	EU	DNK	55,676097	12,568337
92	HOR4815	*/*	*Hordeum vulgare*	Landrace	Spring	6	EU	DNK	56,250000	9,500000
93	BCC1521	*/*	*Hordeum vulgare*	Cultivar	Winter	6	EU	ESP	40,416775	-3,703790
94	BCC1522	*/*	*Hordeum vulgare*	Cultivar	Winter	2	EU	ESP	40,416775	-3,703790
95	BCC1523	*/*	*Hordeum vulgare*	Cultivar	Winter	6	EU	ESP	40,416775	-3,703790
96	BCC1572	*/*	*Hordeum vulgare*	Landrace	Winter	6	EU	ESP	40,416775	-3,703790
97	HOR11188	*/*	*Hordeum vulgare*	Landrace	Unknown	2	EU	ESP	40,416775	-3,703790

98	HOR13500	/	*Hordeum vulgare*	Landrace	Spring	2	EU	ESP	40,416775	-3,703790
99	HOR3938	/	*Hordeum vulgare*	Landrace	Spring	6	EU	ESP	28,291389	-16,628889
100	FT521	/	*Hordeum vulgare*	Landrace	Spring	6	EU	ESP	40,416775	-3,703790
101	BCC1448	/	*Hordeum vulgare*	Landrace	Spring	6	EU	FIN	60,166667	24,933333
102	BCC1450	/	*Hordeum vulgare*	Landrace	Spring	6	EU	FIN	60,166667	24,933333
103	BCC1453	/	*Hordeum vulgare*	Landrace	Spring	6	EU	FIN	60,166667	24,933333
104	HOR9901	/	*Hordeum vulgare*	Landrace	Spring	2	EU	FIN	61,923889	25,748056
105	BCC1312	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	FRA	48,856614	2,352222
106	BCC1320	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	FRA	48,856614	2,352222
107	BCC1321	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	FRA	48,856614	2,352222
108	BCC1340	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	FRA	48,856614	2,352222
109	BCC1345	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	FRA	48,856614	2,352222
110	BCC1349	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	FRA	48,856614	2,352222
111	BCC1350	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	FRA	48,856614	2,352222
112	BCC1353	/	*Hordeum vulgare*	Cultivar	Winter	2	EU	FRA	48,856614	2,352222
113	BCC1355	/	*Hordeum vulgare*	Landrace	Winter	6	EU	FRA	48,856614	2,352222
114	BCC1370	/	*Hordeum vulgare*	Landrace	Spring	2	EU	FRA	48,856614	2,352222
115	BCC1371	/	*Hordeum vulgare*	Landrace	Spring	2	EU	FRA	48,856614	2,352222
116	BCC1377	/	*Hordeum vulgare*	Landrace	Spring	2	EU	FRA	48,856614	2,352222
117	BCC1380	/	*Hordeum vulgare*	Landrace	Spring	2	EU	FRA	48,856614	2,352222
118	BCC1400	/	*Hordeum vulgare*	Landrace	Spring	2	EU	FRA	48,856614	2,352222
119	BCC1423	/	*Hordeum vulgare*	Landrace	Spring	2	EU	FRA	48,856614	2,352222
120	BCC1430	/	*Hordeum vulgare*	Landrace	Spring	2	EU	FRA	48,856614	2,352222
121	BCC1445	/	*Hordeum vulgare*	Landrace	Spring	2	EU	FRA	45,583000	7,650000
122	BCC1447	/	*Hordeum vulgare*	Landrace	Spring	2	EU	FRA	48,856614	2,352222
123	HOR10058	/	*Hordeum vulgare*	Landrace	Spring	6	EU	FRA	45,432222	6,556944
124	HOR1133	/	*Hordeum vulgare*	Landrace	Spring	6	EU	FRA	46,216667	2,213611
125	HOR13514	/	*Hordeum vulgare*	Landrace	Spring	2	EU	FRA	48,856614	2,352222
126	HOR2917	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	FRA	48,856614	2,352222
127	HOR2919	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	FRA	48,856614	2,352222
128	HOR2920	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	FRA	48,856614	2,352222
129	HOR2921	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	FRA	48,856614	2,352222
130	HOR2922	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	FRA	48,856614	2,352222
131	HOR3177	/	*Hordeum vulgare*	Cultivar	Winter	2	EU	FRA	48,856614	2,352222
132	HOR8260	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	FRA	48,856614	2,352222
133	HOR976	/	*Hordeum vulgare*	Landrace	Winter	6	EU	FRA	48,856614	2,352222
134	HOR9919	/	*Hordeum vulgare*	Landrace	Spring	2	EU	FRA	45,432222	6,305694
135	BCC1313	/	*Hordeum vulgare*	Cultivar	Winter	2	EU	GBR	51,507335	-0,127683
136	BCC1315	/	*Hordeum vulgare*	Cultivar	Winter	2	EU	GBR	51,507335	-0,127683
137	BCC1373	/	*Hordeum vulgare*	Landrace	Spring	2	EU	GBR	51,509389	0,118319
138	BCC1378	/	*Hordeum vulgare*	Landrace	Spring	2	EU	GBR	51,509389	0,118319
139	BCC1381	/	*Hordeum vulgare*	Landrace	Spring	2	EU	GBR	51,509389	0,118319
140	BCC1382	/	*Hordeum vulgare*	Landrace	Spring	2	EU	GBR	51,509389	0,118319
141	BCC1383	/	*Hordeum vulgare*	Landrace	Spring	2	EU	GBR	51,509389	0,118319
142	BCC1404	/	*Hordeum vulgare*	Landrace	Spring	2	EU	GBR	51,509389	0,118319
143	BCC1405	/	*Hordeum vulgare*	Landrace	Spring	2	EU	GBR	51,509389	0,118319
144	BCC1408	/	*Hordeum vulgare*	Landrace	Spring	2	EU	GBR	51,509389	0,118319
145	BCC1415	/	*Hordeum vulgare*	Landrace	Spring	2	EU	GBR	51,509389	0,118319
146	BCC1428	/	*Hordeum vulgare*	Landrace	Spring	2	EU	GBR	51,509389	0,118319
147	BCC1442	/	*Hordeum vulgare*	Landrace	Spring	2	EU	GBR	51,509389	0,118319
148	HOR10855	/	*Hordeum vulgare*	Cultivar	Winter	2	EU	GBR	51,507335	-0,127683

149	HOR22	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	GBR	51,507335	-0,127683
150	FT417	*I*	*Hordeum vulgare*	Cultivar	Spring	2	EU	GBR	51,507335	-0,127683
151	FT426	*I*	*Hordeum vulgare*	Cultivar	Unknown	2	EU	GBR	51,507335	-0,127683
152	FT445	*I*	*Hordeum vulgare*	Cultivar	Unknown	2	EU	GBR	51,507335	-0,127683
153	HOR10357	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	43,045556	42,729722
154	HOR10360	*VI*	*Hordeum vulgare*	Landrace	Spring	6	EU	GEO	43,050000	42,716667
155	HOR10463	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	42,916389	43,011389
156	HOR10645	*missing*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	42,546667	45,678611
157	HOR10741	*V*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	42,650000	45,150000
158	HOR10749	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	45,366667	45,616667
159	HOR10754	*V*	*Hordeum vulgare*	Landrace	Spring	6	EU	GEO	45,366667	45,616667
160	HOR10774	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	42,716667	45,350000
161	HOR10972	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	41,710000	42,990000
162	HOR10973	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	41,710000	42,990000
163	HOR11320	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	42,300000	43,350000
164	HOR9607	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	42,300000	43,350000
165	HOR9612	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	43,033333	42,729722
166	HOR9614	*V*	*Hordeum vulgare*	Landrace	Spring	6	EU	GEO	43,045556	42,729722
167	HOR9615	*V*	*Hordeum vulgare*	Landrace	Spring	6	EU	GEO	43,045556	42,729722
168	HOR9619	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	43,045556	42,729722
169	HOR9626	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	42,916389	43,011389
170	HOR9630	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	42,459444	43,087778
171	HOR9816	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	42,100000	42,800000
172	HOR9869	*V*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	42,916389	43,011389
173	HOR9871	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GEO	42,916389	43,011389
174	FT559	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	GEO	41,709981	44,792998
175	FT560	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	GEO	41,709981	44,792998
176	BCC1302	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	DEU	52,519171	13,406091
177	BCC1304	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	DEU	52,519171	13,406091
178	BCC1307	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	DEU	52,519171	13,406091
179	BCC1309	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	DEU	52,519171	13,406091
180	BCC1316	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	DEU	52,519171	13,406091
181	BCC1318	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	DEU	52,519171	13,406091
182	BCC1325	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
183	BCC1326	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
184	BCC1328	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
185	BCC1334	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
186	BCC1344	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
187	BCC1367	*III*	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	52,518611	13,408056
188	BCC1384	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	52,518611	13,408056
189	BCC1386	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	52,518611	13,408056
190	BCC1391	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	52,518611	13,408056
191	BCC1401	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	52,518611	13,408056
192	BCC1403	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	52,518611	13,408056
193	BCC1411	*III*	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	52,518611	13,408056
194	BCC1413	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	52,518611	13,408056
195	BCC1417	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	52,518611	13,408056
196	BCC1419	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	52,518611	13,408056
197	BCC1424	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	52,518611	13,408056
198	BCC1425	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	52,518611	13,408056
199	BCC1433	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	49,452778	11,077778

200	BCC1441	/	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	49,383333	6,833333
201	BCC1443	/	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	54,515278	9,569722
202	BCC1507	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
203	BCC1510	/	*Hordeum vulgare*	Cultivar	Winter	2	EU	DEU	52,519171	13,406091
204	BCC1524	/	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	48,537222	12,152222
205	BCC1558	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
206	BCC1568	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
207	BCC1570	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
208	HOR10861	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
209	HOR1116	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
210	HOR1117	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
211	HOR13	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
212	HOR13169	/	*Hordeum vulgare*	Cultivar	Winter	2	EU	DEU	52,519171	13,406091
213	HOR13170	/	*Hordeum vulgare*	Cultivar	Winter	2	EU	DEU	52,519171	13,406091
214	HOR1326	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
215	HOR1329	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
216	HOR1361	/	*Hordeum vulgare*	Landrace	Winter	6	EU	DEU	52,519171	13,406091
217	HOR14037	/	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	51,195556	10,461389
218	HOR14364	/	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	51,195556	10,461389
219	HOR15961	/	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	51,195556	10,461389
220	HOR1868	/	*Hordeum vulgare*	Landrace	Spring	6	EU	DEU	51,195556	10,461389
221	HOR2041	/	*Hordeum vulgare*	Cultivar	Winter	2	EU	DEU	52,519171	13,406091
222	HOR2048	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
223	HOR2072	/	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	51,185556	10,471389
224	HOR2195	/	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	51,185556	10,471389
225	HOR2212	/	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	51,175556	10,491389
226	HOR2269	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
227	HOR2276	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
228	HOR2962	/	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	51,195556	10,461389
229	HOR3064	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
230	HOR32	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
231	HOR3242	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
232	HOR3244	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
233	HOR3246	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
234	HOR3247	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
235	HOR3248	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
236	HOR3251	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
237	HOR354	/	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	51,175556	10,461389
238	HOR357	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
239	HOR3757	/	*Hordeum vulgare*	Landrace	Spring	2	EU	DEU	51,175556	10,491389
240	HOR3799	/	*Hordeum vulgare*	Cultivar	Spring	6	EU	DEU	52,519171	13,406091
241	HOR4	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
242	HOR9817	/	*Hordeum vulgare*	Cultivar	Spring	2	EU	DEU	52,519171	13,406091
243	Igri	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	DEU	52,519171	13,406091
244	Naturel	/	*Hordeum vulgare*	Cultivar	Winter	2	EU	DEU	52,519171	13,406091
245	FT416	/	*Hordeum vulgare*	Cultivar	Spring	2	EU	DEU	52,519171	13,406091
246	FT418	/	*Hordeum vulgare*	Cultivar	Winter	2	EU	DEU	52,519171	13,406091
247	FT427	/	*Hordeum vulgare*	Cultivar	Unknown	2	EU	DEU	52,519171	13,406091
248	FT430	/	*Hordeum vulgare*	Cultivar	Unknown	2	EU	DEU	52,519171	13,406091
249	FT433	/	*Hordeum vulgare*	Cultivar	Unknown	2	EU	DEU	52,519171	13,406091
250	FT442	/	*Hordeum vulgare*	Cultivar	Spring	2	EU	DEU	52,519171	13,406091

251	FT443	*III*	*Hordeum vulgare*	Cultivar	Spring	2	EU	DEU	52,519171	13,406091
252	FT593	*I*	*Hordeum vulgare*	Cultivar	Spring	2	EU	DEU	52,519171	13,406091
253	FT700	*I*	*Hordeum vulgare*	Landrace	Unknown	6	EU	DEU	52,519171	13,406091
254	HOR1019	*missing*	*Hordeum vulgare*	Landrace	Winter	6	EU	GRC	37,983716	23,729310
255	HOR1020	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	GRC	37,983716	23,729310
256	HOR1022	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	GRC	37,983716	23,729310
257	HOR1023	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	GRC	37,983716	23,729310
258	HOR1030	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	GRC	37,983716	23,729310
259	HOR1122	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GRC	35,266667	25,616667
260	HOR1127	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GRC	37,666667	22,183333
261	HOR1356	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	GRC	37,983716	23,729310
262	BCC1566	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GRC	40,313889	21,797222
263	HOR1943	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GRC	37,666667	22,183333
264	HOR2281	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	GRC	37,983716	23,729310
265	HOR2674	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GRC	35,266667	25,616667
266	HOR676	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	GRC	35,266667	25,616667
267	HOR713	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	GRC	37,666667	22,183333
268	HOR723	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	GRC	37,983716	23,729310
269	HOR725	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GRC	37,666667	22,183333
270	HOR753	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GRC	38,316667	23,761667
271	HOR869	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GRC	35,328889	25,138333
272	HOR883	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GRC	37,666667	22,183333
273	HOR937	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GRC	39,074167	21,824167
274	HOR979	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	GRC	37,983716	23,729310
275	HOR981	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	GRC	37,983716	23,729310
276	HOR983	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	GRC	37,983716	23,729310
277	HOR992	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	GRC	37,983716	23,729310
278	HOR996	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	GRC	37,983716	23,729310
279	FT360	*I*	*Hordeum spontaneum*	Wild	Winter	2	EU	GRC	36,250000	28,166667
280	FT361	*I*	*Hordeum spontaneum*	Wild	Winter	2	EU	GRC	36,400000	28,166667
281	FT784	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	GRC	37,983716	23,729310
282	HOR182	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	HRV	45,100000	15,200000
283	BCC1332	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	HUN	47,497912	19,040235
284	BCC1338	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	HUN	47,497912	19,040235
285	BCC1356	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	HUN	47,497912	19,040235
286	BCC1358	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	HUN	47,497912	19,040235
287	BCC1397	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	HUN	47,500000	19,050000
288	BCC1398	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	HUN	47,500000	19,050000
289	HOR3085	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	HUN	47,497912	19,040235
290	HOR3759	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	HUN	47,162222	19,503056
291	BCC1389	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	IRL	53,342500	-6,265833
292	BCC1303	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	ITA	41,901514	12,460774
293	BCC1587	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	ITA	41,901514	12,460774
294	BCC1589	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	ITA	41,883333	12,483333
295	BCC1590	*I*	*Hordeum vulgare*	Landrace	Winter	2	EU	ITA	41,901514	12,460774
296	BCC1596	*I*	*Hordeum vulgare*	Landrace	Winter	2	EU	ITA	41,901514	12,460774
297	HOR10364	*III*	*Hordeum vulgare*	Landrace	Spring	6	EU	ITA	39,083611	16,372778
298	HOR10778	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	ITA	41,901514	12,460774
299	HOR10782	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	ITA	41,901667	13,882500
300	HOR10937	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	ITA	42,550000	12,983333
301	HOR11123	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	ITA	45,871944	10,301667

302	HOR12750	/	*Hordeum vulgare*	Landrace	Spring	2	EU	ITA	41,901514	12,460774
303	HOR12832	/	*Hordeum vulgare*	Landrace	Spring	6	EU	ITA	41,901514	12,460774
304	HOR2285	/	*Hordeum vulgare*	Landrace	Winter	6	EU	ITA	41,901514	12,460774
305	HOR9308	*missing*	*Hordeum vulgare*	Landrace	Spring	6	EU	ITA	41,442778	14,950833
306	HOR9309	/	*Hordeum vulgare*	Landrace	Spring	6	EU	ITA	41,442778	14,950833
307	HOR9702	/	*Hordeum vulgare*	Landrace	Spring	6	EU	ITA	40,390556	15,087500
308	FT395	/	*Hordeum vulgare*	Cultivar	Unknown	6	EU	ITA	41,901514	12,460774
309	FT785	/	*Hordeum vulgare*	Landrace	Spring	2	EU	ITA	41,901514	12,460774
310	BCC1472	/	*Hordeum vulgare*	Landrace	Spring	2	EU	LTU	54,683333	25,266667
311	HOR4720	/	*Hordeum vulgare*	Landrace	Spring	2	EU	LVA	56,648333	23,713889
312	HOR3226	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	MDA	47,026859	28,841551
313	BCC1310	/	*Hordeum vulgare*	Cultivar	Winter	2	EU	NLD	52,370216	4,895168
314	BCC1336	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	NLD	52,370216	4,895168
315	BCC1357	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	NLD	52,370216	4,895168
316	BCC1368	/	*Hordeum vulgare*	Landrace	Spring	2	EU	NLD	52,370197	4,890444
317	BCC1374	/	*Hordeum vulgare*	Landrace	Spring	2	EU	NLD	52,370197	4,890444
318	BCC1387	/	*Hordeum vulgare*	Landrace	Spring	2	EU	NLD	52,370197	4,890444
319	BCC1394	/	*Hordeum vulgare*	Landrace	Spring	2	EU	NLD	52,370197	4,890444
320	BCC1395	/	*Hordeum vulgare*	Landrace	Spring	2	EU	NLD	52,370197	4,890444
321	BCC1420	/	*Hordeum vulgare*	Landrace	Spring	2	EU	NLD	52,370197	4,890444
322	BCC1422	/	*Hordeum vulgare*	Landrace	Spring	2	EU	NLD	52,370197	4,890444
323	BCC1452	/	*Hordeum vulgare*	Landrace	Spring	6	EU	NLD	52,370197	4,890444
324	HOR16	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	NLD	52,370216	4,895168
325	HOR17	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	NLD	52,370216	4,895168
326	HOR18	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	NLD	52,370216	4,895168
327	FT419	/	*Hordeum vulgare*	Cultivar	Spring	2	EU	NLD	52,370216	4,895168
328	BCC1333	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	POL	52,229676	21,012229
329	BCC1372	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	52,216667	21,033333
330	BCC1385	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	52,216667	21,033333
331	BCC1582	/	*Hordeum vulgare*	Landrace	Winter	6	EU	POL	52,229676	21,012229
332	HOR10249	/	*Hordeum vulgare*	Landrace	Spring	6	EU	POL	52,406111	21,331667
333	HOR10410	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	52,406111	21,331667
334	HOR10600	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,509444	19,112778
335	HOR10635	*missing*	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	52,406111	21,331667
336	HOR3078	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EU	POL	52,229676	21,012229
337	HOR3211	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	POL	52,229676	21,012229
338	HOR3212	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	POL	52,229676	21,012229
339	HOR7484	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,409722	20,302778
340	HOR7515	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,409722	20,302778
341	HOR7519	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,421389	20,952778
342	HOR7531	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,480278	22,069444
343	HOR7537	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,335000	22,410278
344	HOR7540	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,615556	22,428611
345	HOR7542	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,330556	22,285278
346	HOR8808	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	50,244167	21,776111
347	HOR8812	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,480278	22,069444
348	HOR8813	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,533333	21,966667
349	HOR8816	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,623889	20,947778
350	HOR8817	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,623889	20,947778
351	HOR8818	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,623889	20,947778
352	HOR8825	/	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,623889	20,947778

353	HOR8826	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	POL	49,421389	20,959167
354	HOR8827	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,633333	20,600000
355	HOR8828	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,633333	20,600000
356	HOR8832	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,393333	20,187222
357	HOR8833	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,508333	20,243333
358	HOR8834	*missing*	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,508333	20,243333
359	HOR8854	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	POL	49,633333	20,600000
360	BCC1360	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	ROM	44,437711	26,097367
361	BCC1559	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EU	ROM	44,437711	26,097367
362	BCC1578	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	ROM	44,437711	26,097367
363	BCC1585	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	ROM	44,437711	26,097367
364	HOR1340	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	ROM	44,437711	26,097367
365	HOR1391	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	ROM	45,943056	24,966667
366	HOR9450	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	ROM	46,781389	23,083056
367	HOR9453	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	ROM	46,777222	23,599722
368	BCC1363	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	RUS	55,751242	37,618422
369	BCC1364	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	RUS	55,751242	37,618422
370	BCC1455	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	RUS	59,933333	30,266667
371	BCC1456	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	RUS	58,600000	49,650000
372	BCC1457	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	RUS	55,750000	37,616667
373	BCC1458	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	RUS	56,833333	60,583333
374	BCC1459	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	RUS	45,033333	38,983333
375	BCC1461	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	RUS	54,966667	73,383333
376	BCC1463	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	RUS	45,333333	134,666667
377	BCC1479	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	RUS	64,550000	40,533333
378	BCC1480	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	RUS	64,550000	40,533333
379	BCC1481	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	RUS	61,783333	34,350000
380	BCC1482	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	RUS	58,600000	49,650000
381	BCC1483	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	RUS	59,216667	39,900000
382	BCC1484	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	RUS	57,766667	40,933333
383	BCC1485	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	RUS	51,533333	46,000000
384	BCC1487	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	RUS	42,975000	47,501944
385	BCC1488	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	RUS	55,751242	37,618422
386	BCC1490	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	RUS	62,033333	129,733333
387	BCC1491	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	RUS	62,033333	129,733333
388	BCC1504	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	RUS	56,000000	92,933333
389	BCC1512	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	RUS	55,751242	37,618422
390	BCC1513	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	RUS	55,751242	37,618422
391	BCC1517	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	RUS	55,751242	37,618422
392	BCC1518	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	RUS	55,751242	37,618422
393	HOR11190	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	RUS	55,751242	37,618422
394	HOR13161	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	RUS	55,751242	37,618422
395	HOR2446	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	RUS	55,751242	37,618422
396	HOR3098	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	RUS	55,751242	37,618422
397	HOR3230	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	RUS	55,751242	37,618422
398	HOR3232	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	RUS	55,751242	37,618422
399	HOR3233	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	RUS	55,751242	37,618422
400	HOR3296	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	RUS	55,751242	37,618422
401	HOR3318	*III*	*Hordeum vulgare*	Cultivar	Winter	6	EU	RUS	55,751242	37,618422
402	HOR3369	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	RUS	55,751242	37,618422
403	HOR3386	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	RUS	55,751242	37,618422

404	HOR3395	/	*Hordeum vulgare*	Landrace	Winter	6	EU	RUS	55,751242	37,618422
405	HOR3397	/	*Hordeum vulgare*	Landrace	Winter	6	EU	RUS	55,751242	37,618422
406	HOR3438	*missing*	*Hordeum vulgare*	Landrace	Winter	6	EU	RUS	55,751242	37,618422
407	HOR3450	/	*Hordeum vulgare*	Landrace	Winter	6	EU	RUS	55,751242	37,618422
408	HOR3451	/	*Hordeum vulgare*	Landrace	Winter	6	EU	RUS	55,751242	37,618422
409	HOR3458	/	*Hordeum vulgare*	Landrace	Winter	6	EU	RUS	55,751242	37,618422
410	HOR3474	/	*Hordeum vulgare*	Landrace	Winter	6	EU	RUS	55,751242	37,618422
411	HOR4104	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	RUS	55,751242	37,618422
412	HOR4198	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	RUS	55,751242	37,618422
413	HOR7439	/	*Hordeum vulgare*	Cultivar	Spring	2	EU	RUS	55,751242	37,618422
414	HOR9292	/	*Hordeum vulgare*	Cultivar	Winter	6	EU	RUS	55,751242	37,618422
415	FT774	/	*Hordeum vulgare*	Landrace	Spring	2	EU	RUS	55,751242	37,618422
416	HOR7335	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,854722	17,677222
417	HOR7336	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,740556	17,400000
418	HOR7337	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,563333	18,663056
419	HOR7338	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,563333	18,663056
420	HOR7339	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,563333	18,663056
421	HOR7340	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,563333	18,663056
422	HOR7343	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,563333	18,663056
423	HOR7350	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,483333	19,666667
424	HOR7351	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,483333	19,666667
425	HOR7353	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,483333	19,666667
426	HOR7354	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,483333	19,666667
427	HOR7355	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,591389	20,097222
428	HOR7357	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,238889	20,109444
429	HOR7358	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,238889	20,109444
430	HOR7360	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,043611	21,333056
431	HOR7361	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,043611	21,333056
432	HOR7362	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,061667	21,581667
433	HOR7363	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,061667	21,581667
434	HOR7364	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,061667	21,581667
435	HOR7365	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,061667	21,581667
436	HOR7369	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,140278	19,292778
437	HOR7370	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,363889	19,527778
438	HOR7372	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,394722	19,401389
439	HOR7373	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,369167	19,185833
440	HOR7374	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,369167	19,185833
441	HOR7375	/	*Hordeum vulgare*	Landrace	Spring	6	EU	SVK	49,367500	19,185833
442	HOR7377	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,357222	18,892778
443	HOR7389	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,800000	19,677778
444	HOR7390	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,738333	20,139167
445	HOR7391	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,061667	21,581667
446	HOR7393	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,800000	19,677778
447	HOR8615	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,821667	20,988056
448	HOR8627	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,325556	20,827778
449	HOR8629	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,325556	20,827778
450	HOR8630	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,325556	20,827778
451	HOR8633	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,528056	22,141111
452	HOR8634	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,528056	22,141111
453	HOR8635	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,528056	22,141111
454	HOR8636	/	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,991111	22,438056

455	HOR8638	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,967500	22,481389
456	HOR8641	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,967500	22,314444
457	HOR8643	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,967500	22,314444
458	HOR8646	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,209444	22,049167
459	HOR8647	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,306111	21,651667
460	HOR8648	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,349722	21,663333
461	HOR8649	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,362222	21,738333
462	HOR8651	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,329167	21,731944
463	HOR8675	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,801944	18,113889
464	HOR8679	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,987500	22,151944
465	HOR9636	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,000000	18,000000
466	HOR9641	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,000000	18,000000
467	HOR9642	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,000000	18,000000
468	HOR9658	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,915000	17,816667
469	HOR9660	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,915000	17,816667
470	HOR9662	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,000000	18,000000
471	HOR9670	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,883333	17,816667
472	HOR9673	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,000000	18,000000
473	HOR9675	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,000000	18,000000
474	HOR9680	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,916667	18,500000
475	HOR9681	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,916667	18,500000
476	HOR9682	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,737222	19,605556
477	HOR9684	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,737222	19,605556
478	HOR9685	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	48,804167	19,388889
479	HOR9692	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,150000	18,215278
480	HOR9693	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,150000	18,215278
481	HOR9695	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,224722	18,488889
482	HOR9696	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,224722	18,488889
483	HOR9700	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SVK	49,244167	18,465000
484	BCC1390	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SWE	59,325000	18,050000
485	BCC1396	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SWE	59,325000	18,050000
486	BCC1399	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SWE	59,325000	18,050000
487	BCC1402	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SWE	59,325000	18,050000
488	BCC1410	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SWE	59,325000	18,050000
489	BCC1412	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SWE	59,325000	18,050000
490	BCC1416	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SWE	59,325000	18,050000
491	HOR1732	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	SWE	59,350000	18,066667
492	BCC1465	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	UKR	48,002778	37,805278
493	BCC1466	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	UKR	46,483333	30,733333
494	BCC1474	*/*	*Hordeum vulgare*	Landrace	Spring	6	EU	UKR	44,933347	34,099928
495	BCC1493	*/*	*Hordeum vulgare*	Landrace	Spring	6	EU	UKR	46,483333	30,733333
496	BCC1505	*/*	*Hordeum vulgare*	Landrace	Spring	6	EU	UKR	48,464444	35,046111
497	BCC1506	*/*	*Hordeum vulgare*	Landrace	Spring	2	EU	UKR	46,483333	30,733333
498	HOR13163	*/*	*Hordeum vulgare*	Cultivar	Winter	2	EU	UKR	50,450100	30,523400
499	HOR3322	*/*	*Hordeum vulgare*	Landrace	Winter	6	EU	UKR	50,450100	30,523400
500	HOR3338	*/*	*Hordeum vulgare*	Landrace	Winter	6	EU	UKR	50,450100	30,523400
501	HOR3347	*/*	*Hordeum vulgare*	Landrace	Winter		EU	UKR	50,450100	30,523400
502	HOR3350	*/*	*Hordeum vulgare*	Landrace	Winter	2	EU	UKR	50,450100	30,523400
503	HOR3351	*missing*	*Hordeum vulgare*	Landrace	Winter	2	EU	UKR	50,450100	30,523400
504	HOR3354	*/*	*Hordeum vulgare*	Landrace	Winter	2	EU	UKR	50,450100	30,523400
505	HOR3355	*missing*	*Hordeum vulgare*	Landrace	Winter	6	EU	UKR	50,450100	30,523400

506	HOR3357	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	UKR	50,450100	30,523400
507	HOR4163	*I*	*Hordeum vulgare*	Landrace	Winter	6	EU	UKR	50,450100	30,523400
508	FT420	*missing*	*Hordeum vulgare*	Cultivar	Unknown	6	EU	UKR	50,450100	30,523400
509	BCC1359	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	YUG	44,820556	20,462222
510	BCC1434	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	YUG	43,866667	18,416667
511	BCC1519	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	YUG	44,820556	20,462222
512	BCC1520	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EU	YUG	44,820556	20,462222
513	BCC1541	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	YUG	44,820556	20,462222
514	HOR308	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	YUG	44,820556	20,462222
515	HOR3204	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EU	YUG	44,820556	20,462222
516	HOR4016	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	YUG	43,866667	18,416667
517	HOR4017	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	YUG	43,866667	18,416667
518	HOR742	*I*	*Hordeum vulgare*	Landrace	Spring	6	EU	YUG	43,866667	18,416667
519	HOR757	*I*	*Hordeum vulgare*	Landrace	Spring	2	EU	YUG	43,966667	21,233333
520	BCC421	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	CHN	33,027089	119,707031
521	BCC423	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	CHN	30,713503	103,403319
522	BCC424	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
523	BCC427	*I*	*Hordeum vulgare*	Landrace	Spring	2	EA	CHN	30,967778	112,231389
524	BCC431	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EA	CHN	39,902627	116,401287
525	BCC432	*I*	*Hordeum vulgare*	Landrace	Spring	2	EA	CHN	43,644028	115,664064
526	BCC434	*I*	*Hordeum vulgare*	Landrace	Spring	2	EA	CHN	30,967778	112,231389
527	BCC436	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	CHN	45,750000	126,633333
528	BCC438	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	CHN	45,750000	126,633333
529	BCC439	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	CHN	45,750000	126,633333
530	BCC445	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	CHN	45,750000	126,633333
531	BCC446	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	CHN	45,750000	126,633333
532	BCC447	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	CHN	45,750000	126,633333
533	BCC453	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter		EA	CHN	39,902627	116,401287
534	BCC454	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
535	BCC455	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
536	BCC456	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
537	BCC457	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
538	BCC458	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
539	BCC459	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
540	BCC460	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
541	BCC461	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
542	BCC462	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
543	BCC463	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
544	BCC464	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
545	BCC465	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
546	BCC466	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
547	BCC467	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
548	BCC468	*VII,rym11-d*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
549	BCC469	*VII,rym11-d*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
550	BCC470	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
551	BCC471	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
552	BCC474	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
553	BCC475	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
554	BCC477	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
555	BCC478	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
556	BCC479	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287

557	BCC480	*I*	*Hordeum vulgare*	Cultivar	Winter		EA	CHN	39,902627	116,401287
558	BCC482	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
559	BCC483	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
560	BCC484	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
561	BCC502	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	CHN	36,086667	120,341389
562	BCC514	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
563	BCC520	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
564	BCC947	*missing*	*Hordeum vulgare*	Cultivar	Winter		EA	CHN	39,902627	116,401287
565	FT364	*I*	*Hordeum spontaneum*	Wild	Winter	2	EA	CHN	25,808333	106,075000
566	FT365	*I*	*Hordeum spontaneum*	Wild	Winter	2	EA	CHN	31,000000	101,150000
567	FT388	*I*	*Hordeum agriocrithon*	*Agriocrithon*	Unknown	6	EA	CHN	39,902627	116,401287
568	FT389	*I*	*Hordeum agriocrithon*	*Agriocrithon*	Unknown	2	EA	CHN	39,902627	116,401287
569	FT390	*I*	*Hordeum agriocrithon*	*Agriocrithon*	Unknown	6	EA	CHN	39,902627	116,401287
570	FT392	*I*	*Hordeum agriocrithon*	*Agriocrithon*	Unknown	6	EA	CHN	39,902627	116,401287
571	FT403	*I*	*Hordeum vulgare*	Landrace	Unknown	6	EA	CHN	39,902627	116,401287
572	FT519	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	CHN	39,902627	116,401287
573	FT548	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
574	HOR11030	*VII,rym11-d*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
575	HOR11031	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
576	HOR11042	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
712	HOR11141	*VII,rym11-d*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
577	HOR11521	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
578	HOR11523	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
579	HOR11524	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	32,066667	118,766667
580	HOR11525	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	32,066667	118,766667
581	HOR11526	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
582	HOR11531	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
583	HOR11532	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
584	HOR11533	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	31,300000	120,616667
585	HOR11534	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
586	HOR11535	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
587	HOR11536	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
588	HOR11537	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	29,883333	121,766667
589	HOR11538	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	29,466667	121,866667
590	HOR11539	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	29,216667	119,866667
591	HOR11540	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	29,466667	121,866667
592	HOR11541	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	33,000000	120,000000
593	HOR11542	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
594	HOR11543	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	33,000000	120,000000
595	HOR11544	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	29,500000	120,900000
596	HOR11545	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	28,850000	120,733333
597	HOR11546	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	29,150000	121,033333
598	HOR11547	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
599	HOR11548	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
600	HOR11549	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
601	HOR11550	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
602	HOR11551	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	30,683333	121,016667
603	HOR11564	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	CHN	39,100000	112,983333
604	HOR11565	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
605	HOR11566	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
606	HOR11568	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	CHN	31,863889	117,280556

607	HOR11573	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
608	HOR11574	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
609	HOR11575	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
610	HOR11647	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
611	HOR11648	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	CHN	39,902627	116,401287
612	HOR11649	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
613	HOR11650	*II, rym11-b*	*Hordeum vulgare*	Landrace	Winter	6	EA	CHN	39,902627	116,401287
614	HOR11651	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
615	HOR11652	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
616	HOR11653	*II, rym11-b*	*Hordeum vulgare*	Landrace	Winter	6	EA	CHN	39,902627	116,401287
617	HOR11654	*I*	*Hordeum vulgare*	Cultivar	Winter		EA	CHN	39,902627	116,401287
618	HOR11655	*II, rym11-b*	*Hordeum vulgare*	Landrace	Winter	6	EA	CHN	39,902627	116,401287
619	HOR11656	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
620	HOR11657	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
621	HOR11804	*IX*	*Hordeum vulgare*	Landrace	Winter	6	EA	CHN	30,250000	81,166667
622	HOR11903	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	45,000000	125,000000
623	HOR11904	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
624	HOR11905	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
625	HOR11906	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
626	HOR11907	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
627	HOR11908	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
628	HOR11909	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
629	HOR11910	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
630	HOR11911	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
631	HOR11912	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
632	HOR11913	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
633	HOR11914	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
634	HOR11915	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
635	HOR11916	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
636	HOR11917	*I*	*Hordeum vulgare*	Cultivar	Winter		EA	CHN	39,902627	116,401287
637	HOR11918	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
638	HOR11919	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
639	HOR11920	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
640	HOR11921	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
641	HOR11922	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
642	HOR11923	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
643	HOR11924	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
644	HOR11925	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
645	HOR11926	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
646	HOR11927	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
647	HOR11928	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
648	HOR11960	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
649	HOR11961	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
650	HOR11963	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
651	HOR11964	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
652	HOR12229	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
653	HOR12295	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
654	HOR12303	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
655	HOR12304	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
656	HOR12305	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
657	HOR12306	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287

658	HOR12307	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
659	HOR12308	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
660	HOR12396	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
661	HOR12731	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
662	HOR12732	*II, rym11-b*	*Hordeum vulgare*	Landrace	Winter	6	EA	CHN	39,902627	116,401287
663	HOR12737	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
664	HOR12738	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
665	HOR12739	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
666	HOR12806	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
667	HOR12807	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EA	CHN	39,902627	116,401287
668	HOR12808	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EA	CHN	39,902627	116,401287
669	HOR12809	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EA	CHN	39,902627	116,401287
670	HOR12810	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EA	CHN	39,902627	116,401287
671	HOR13399	*I*	*Hordeum vulgare*	Cultivar	Winter	2	EA	CHN	39,902627	116,401287
672	HOR13467	*II, rym11-b*	*Hordeum vulgare*	Landrace	Winter	6	EA	CHN	39,902627	116,401287
673	HOR22155	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
674	HOR2279	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
675	HOR2352	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
676	HOR2355	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
677	HOR2360	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
678	HOR2363	*II, rym11-b*	*Hordeum vulgare*	Landrace	Winter	6	EA	CHN	39,902627	116,401287
679	HOR3299	*II, rym11-b*	*Hordeum vulgare*	Landrace	Winter	6	EA	CHN	39,902627	116,401287
680	HOR4196	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
681	HOR4553	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
682	HOR9288	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
683	HOR9483	*VIII, rym11-c*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	29,483333	118,733333
684	HOR9484	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	CHN	39,902627	116,401287
685	BCC586	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
686	BCC593	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
687	BCC595	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
688	BCC596	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
689	BCC602	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
690	BCC607	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
691	BCC610	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
692	BCC618	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
693	BCC619	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
694	BCC620	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
695	BCC621	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	36,750000	139,750000
696	BCC622	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
697	BCC623	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
698	BCC625	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	JPN	36,648611	138,194167
699	BCC626	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
700	BCC631	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
701	BCC639	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
702	BCC642	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	JPN	31,596536	130,557117
703	BCC647	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
704	BCC648	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	39,983333	141,216667
705	BCC649	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
706	BCC650	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
707	BCC651	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
708	BCC657	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706

709	BCC660	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	34,083333	134,533333
710	HOR11132	/	*Hordeum vulgare*	Cultivar	Spring	2	EA	JPN	35,689488	139,691706
711	HOR11133	/	*Hordeum vulgare*	Cultivar	Spring	6	EA	JPN	35,689488	139,691706
713	HOR11143	/	*Hordeum vulgare*	Cultivar	Spring	2	EA	JPN	35,689488	139,691706
714	HOR11247	/	*Hordeum vulgare*	Cultivar	Spring	6	EA	JPN	35,689488	139,691706
715	HOR11277	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
716	HOR11285	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
717	HOR11286	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
718	HOR11300	/	*Hordeum vulgare*	Cultivar	Spring	6	EA	JPN	35,689488	139,691706
719	HOR11527	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
720	HOR11529	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,750000	139,750000
721	HOR11530	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,750000	139,500000
722	HOR11670	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	37,500000	140,250000
723	HOR11678	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	31,616667	130,533333
724	HOR11681	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
725	HOR11683	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
726	HOR11684	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
727	HOR11689	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
728	HOR11690	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
729	HOR11693	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
730	HOR11694	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
731	HOR11700	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
732	HOR11701	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
733	HOR11704	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
734	HOR11706	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,500000	139,500000
735	HOR11707	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
736	HOR11776	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	37,500000	139,000000
737	HOR11851	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
738	HOR11852	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
739	HOR11861	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
740	HOR11862	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
741	HOR11865	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
742	HOR11867	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	36,000000	138,000000
743	HOR11869	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
744	HOR11874	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
745	HOR12337	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
746	HOR12344	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
747	HOR12353	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
748	HOR12361	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
749	HOR12362	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
750	HOR12363	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
751	HOR12366	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
752	HOR12370	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
753	HOR12381	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
754	HOR12393	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706
755	HOR12442	/	*Hordeum vulgare*	Cultivar	Winter	2	EA	JPN	35,689488	139,691706
756	HOR12448	/	*Hordeum vulgare*	Cultivar	Winter	2	EA	JPN	35,689488	139,691706
757	HOR12469	*missing*	*Hordeum vulgare*	Cultivar	Winter	2	EA	JPN	35,689488	139,691706
758	HOR12506	/	*Hordeum vulgare*	Cultivar	Winter	2	EA	JPN	35,689488	139,691706
759	HOR12726	/	*Hordeum vulgare*	Landrace	Winter	6	EA	JPN	34,500000	136,000000
760	HOR4224	/	*Hordeum vulgare*	Cultivar	Winter	6	EA	JPN	35,689488	139,691706

761	HOR4245	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	JPN	35,689488	139,691706
762	HOR9546	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	JPN	35,689488	139,691706
763	BCC661	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
764	BCC662	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
765	BCC666	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	KOR	37,565653	126,978136
766	BCC667	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	KOR	37,565653	126,978136
767	BCC669	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
768	BCC670	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
769	BCC671	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
770	BCC672	*I*	*Hordeum vulgare*	Cultivar	Unknown	6	EA	KOR	37,566535	126,977969
771	BCC675	*I*	*Hordeum vulgare*	Landrace	Spring	2	EA	KOR	37,565653	126,978136
772	BCC676	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
773	BCC677	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
774	BCC678	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
775	BCC679	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
776	BCC680	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
777	BCC681	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
778	BCC682	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
779	BCC683	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
780	BCC684	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
781	BCC685	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
782	BCC688	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
783	BCC689	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
784	BCC690	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
785	BCC691	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
786	BCC693	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
787	BCC694	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
788	BCC695	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	KOR	35,270833	128,663056
789	BCC696	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
790	BCC697	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
791	BCC699	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
792	BCC701	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
793	BCC703	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
794	BCC704	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
795	BCC707	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
796	BCC710	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
797	BCC713	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
798	BCC714	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
799	BCC716	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
800	BCC717	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
801	BCC718	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	KOR	37,250000	127,000000
802	BCC719	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	KOR	37,565653	126,978136
803	BCC720	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
804	BCC722	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
805	BCC729	*I*	*Hordeum vulgare*	Landrace	Spring	6	EA	KOR	35,270833	128,663056
806	BCC730	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
807	HOR11580	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	36,750000	128,000000
808	HOR11581	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	36,750000	128,000000
809	HOR11582	*missing*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	34,750000	127,000000
810	HOR11586	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	35,750000	127,250000
811	HOR11590	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	35,750000	127,250000

812	HOR11591	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	35,750000	127,250000
813	HOR11592	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	35,750000	127,250000
814	HOR11594	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	34,750000	127,000000
815	HOR11597	*II, rym11-b*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	34,750000	127,000000
816	HOR11598	*II, rym11-b*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	34,750000	127,000000
817	HOR11600	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter		EA	KOR	35,750000	127,250000
818	HOR11602	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	35,750000	127,250000
819	HOR11604	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	35,750000	127,250000
820	HOR11610	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	35,750000	127,250000
821	HOR11611	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	34,750000	127,000000
822	HOR11612	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	35,750000	127,250000
823	HOR11613	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	35,750000	127,250000
824	HOR11614	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	35,750000	127,250000
825	HOR11629	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	36,333333	128,750000
826	HOR11630	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	36,333333	128,750000
827	HOR11631	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	36,333333	128,750000
828	HOR11634	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	36,333333	128,750000
829	HOR11640	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	36,333333	128,750000
830	HOR11641	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	35,250000	128,500000
831	HOR11711	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,600000	127,250000
832	HOR11722	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,600000	127,250000
833	HOR11728	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
834	HOR11732	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
835	HOR11738	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
836	HOR11756	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,600000	127,250000
837	HOR11759	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,600000	127,250000
838	HOR11877	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
839	HOR11881	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
840	HOR11889	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
841	HOR11890	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
842	HOR11894	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
843	HOR11896	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
844	HOR12775	*missing*	*Hordeum vulgare*	Landrace	Winter	6	EA	KOR	37,566667	127,000000
845	HOR3130	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	36,750000	128,000000
846	HOR3151	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	KOR	37,566535	126,977969
847	FT524	*I*	*Hordeum vulgare*	Landrace	Spring		EA	KOR	37,566535	126,977969
848	BCC725	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	PRK	39,014861	125,776363
849	HOR11019	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	PRK	39,014861	125,776363
850	HOR11024	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Spring	6	EA	PRK	39,014861	125,776363
851	HOR11027	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Spring	6	EA	PRK	39,014861	125,776363
852	HOR11036	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	PRK	39,014861	125,776363
853	HOR11048	*I*	*Hordeum vulgare*	Cultivar	Spring	6	EA	PRK	39,014861	125,776363
854	HOR11051	*I*	*Hordeum vulgare*	Cultivar	Unknown	6	EA	PRK	39,014861	125,776363
855	HOR11056	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	PRK	39,014861	125,776363
856	HOR11060	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	PRK	39,014861	125,776363
857	HOR11076	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	PRK	39,014861	125,776363
858	HOR11078	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	PRK	39,014861	125,776363
859	HOR11079	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	PRK	39,014861	125,776363
860	HOR11080	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	PRK	39,014861	125,776363
861	HOR11084	*I*	*Hordeum vulgare*	Cultivar	Unknown	6	EA	PRK	39,014861	125,776363
862	HOR11088	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	PRK	39,014861	125,776363

863	HOR11091	*I*	*Hordeum vulgare*	Cultivar	Unknown	6	EA	PRK	39,014861	125,776363
864	HOR11096	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	PRK	39,014861	125,776363
865	HOR11098	*I*	*Hordeum vulgare*	Cultivar	Winter	6	EA	PRK	39,014861	125,776363
866	HOR11099	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Unknown	6	EA	PRK	39,014861	125,776363
867	HOR12800	*I*	*Hordeum vulgare*	Landrace	Winter	6	EA	PRK	39,014861	125,776363
868	BCC1	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	34,533056	69,166111
869	BCC2	*missing*	*Hordeum vulgare*	Landrace	Spring	2	CA	AFG	34,533056	69,166111
870	BCC3	*missing*	*Hordeum vulgare*	Landrace	Spring	2	CA	AFG	34,633000	65,750000
871	BCC6	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	34,533056	69,166111
872	FT278	*I*	*Hordeum spontaneum*	Wild	Winter	2	CA	AFG	36,667000	65,754000
873	FT279	*I*	*Hordeum spontaneum*	Wild	Winter	2	CA	AFG	35,750000	69,000000
874	FT280	*I*	*Hordeum spontaneum*	Wild	Winter	2	CA	AFG	34,333333	62,200000
875	FT450	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	34,528455	69,171703
876	FT516	*I*	*Hordeum spontaneum*	Wild	Winter	2	CA	AFG	36,953000	65,124000
877	FT568	*I*	*Hordeum spontaneum*	Wild	Winter	2	CA	AFG	34,500000	63,183000
878	FT716	*I*	*Hordeum vulgare*	Landrace	Unknown	6	CA	AFG	34,528455	69,171703
879	FT762	*I*	*Hordeum vulgare*	Landrace	Spring	2	CA	AFG	34,528455	69,171703
880	HOR1431	*I*	*Hordeum vulgare*	Landrace	Spring	2	CA	AFG	35,000000	71,150389
881	HOR1463	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	35,883333	71,180000
882	HOR1544	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	35,000000	71,150389
883	HOR1553	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	35,316667	70,900000
884	HOR1675	*I*	*Hordeum vulgare*	Landrace	Spring	2	CA	AFG	35,000000	71,150389
885	HOR1703	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	31,616944	65,716944
886	HOR1707	*I*	*Hordeum vulgare*	Landrace	Spring	2	CA	AFG	35,883333	71,500000
887	HOR1712	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	35,000000	71,150389
888	HOR1751	*I*	*Hordeum vulgare*	Landrace	Spring	2	CA	AFG	35,000000	71,150389
889	HOR1758	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	35,000000	71,150389
890	HOR1790	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	35,000000	71,150389
891	HOR1794	*I*	*Hordeum vulgare*	Landrace	Spring	2	CA	AFG	35,000000	71,150389
892	HOR1800	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	35,000000	71,150389
893	HOR1804	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	35,000000	71,150389
894	HOR1805	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	35,000000	71,150389
895	HOR1826	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	35,883333	71,180000
896	HOR1838	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	35,883333	71,180000
897	HOR1842	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	35,883333	71,180000
898	HOR1968	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	35,000000	71,150389
899	HOR4219	*I*	*Hordeum vulgare*	Landrace	Winter	6	CA	AFG	34,528455	69,171703
900	HOR7259	*I*	*Hordeum vulgare*	Landrace	Winter	6	CA	AFG	34,528455	69,171703
901	HOR8265	*missing*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	34,366667	62,166667
902	HOR9551	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	AFG	34,533056	69,166111
903	BCC524	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,666667	77,216667
904	BCC525	*missing*	*Hordeum vulgare*	Cultivar	Unknown	6	CA	IND	28,635308	77,224960
905	BCC526	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,666667	77,216667
906	BCC527	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,666667	77,216667
907	BCC532	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,666667	77,216667
908	BCC533	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,666667	77,216667
909	BCC535	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,666667	77,216667
910	BCC538	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,666667	77,216667
911	BCC551	*I*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,666667	77,216667
912	BCC565	*I*	*Hordeum vulgare*	Cultivar	Winter	6	CA	IND	28,635308	77,224960
913	BCC567	*I*	*Hordeum vulgare*	Cultivar	Winter	6	CA	IND	28,635308	77,224960

914	BCC570	*/*	*Hordeum vulgare*	Cultivar	Winter	6	CA	IND	28,635308	77,224960
915	BCC571	*/*	*Hordeum vulgare*	Cultivar	Winter	6	CA	IND	28,635308	77,224960
916	BCC577	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,666667	77,216667
917	BCC579	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,666667	77,216667
918	BCC581	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,666667	77,216667
919	FT522	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,635308	77,224960
920	HOR11403	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	31,100000	77,166667
921	HOR11799	*missing*	*Hordeum vulgare*	Landrace	Winter	6	CA	IND	30,050000	80,366667
922	HOR11821	*/*	*Hordeum vulgare*	Landrace	Winter	6	CA	IND	29,833333	79,500000
923	HOR1849	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,635308	77,224960
924	HOR8379	*/*	*Hordeum vulgare*	Landrace	Winter	6	CA	IND	28,635308	77,224960
925	HOR8393	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	32,433333	76,450000
926	HOR8395	*/*	*Hordeum vulgare*	Landrace	Winter	6	CA	IND	28,635308	77,224960
927	HOR8399	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	IND	28,635308	77,224960
928	BCC1468	*/*	*Hordeum vulgare*	Landrace	Spring	2	CA	KAZ	51,166667	71,416667
929	BCC1469	*/*	*Hordeum vulgare*	Landrace	Spring	2	CA	KAZ	51,166667	71,416667
930	BCC1494	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	KAZ	50,283056	57,166667
931	FT776	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	KAZ	51,166667	71,433333
932	BCC1497	*/*	*Hordeum vulgare*	Landrace	Spring	2	CA	KGZ	42,874722	74,612222
933	FT520	*/*	*Hordeum vulgare*	Landrace	Spring	2	CA	KGZ	51,166667	71,433333
934	FT777	*/*	*Hordeum vulgare*	Landrace	Spring	2	CA	KGZ	51,166667	71,433333
935	BCC737	*/*	*Hordeum vulgare*	Landrace	Winter	6	CA	NPL	27,700000	85,333333
936	BCC732	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	NPL	27,716667	85,316667
937	BCC741	*missing*	*Hordeum vulgare*	Landrace	Winter	6	CA	NPL	27,700000	85,333333
938	BCC744	*/*	*Hordeum vulgare*	Cultivar	Winter	6	CA	NPL	27,700000	85,333333
939	BCC745	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	NPL	27,716667	85,316667
940	BCC746	*/*	*Hordeum vulgare*	Landrace	Winter	6	CA	NPL	27,700000	85,333333
941	BCC747	*missing*	*Hordeum vulgare*	Landrace	Winter	6	CA	NPL	27,700000	85,333333
942	BCC748	*/*	*Hordeum vulgare*	Landrace	Winter	6	CA	NPL	27,700000	85,333333
943	BCC759	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	NPL	27,716667	85,316667
944	BCC761	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	NPL	28,356111	83,736111
945	BCC763	*/*	*Hordeum vulgare*	Cultivar	Winter	6	CA	NPL	27,700000	85,333333
946	BCC766	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	NPL	28,356111	83,736111
947	BCC768	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	NPL	28,356111	83,736111
948	BCC770	*/*	*Hordeum vulgare*	Landrace	Winter	6	CA	NPL	27,700000	85,333333
949	BCC776	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	NPL	27,700000	85,333333
950	BCC777	*/*	*Hordeum vulgare*	Landrace	Winter	6	CA	NPL	27,700000	85,333333
951	BCC778	*/*	*Hordeum vulgare*	Landrace	Winter	6	CA	NPL	27,700000	85,333333
952	BCC780	*/*	*Hordeum vulgare*	Landrace	Winter	6	CA	NPL	27,700000	85,333333
953	HOR7078	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	NPL	27,700000	85,333333
954	FT535	*/*	*Hordeum vulgare*	Landrace	Unknown	6	CA	NPL	27,700000	85,333333
955	FT561	*/*	*Hordeum vulgare*	Landrace	Winter	6	CA	NPL	27,700000	85,333333
956	FT689	*/*	*Hordeum vulgare*	Landrace	Unknown	6	CA	NPL	27,700000	85,333333
957	BCC173	*/*	*Hordeum vulgare*	Landrace	Unknown	6	CA	PAK	36,133333	73,233333
958	BCC182	*/*	*Hordeum vulgare*	Landrace	Unknown	6	CA	PAK	36,300000	73,366667
959	HOR7566	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	PAK	33,719150	73,039089
960	HOR7583	*X*	*Hordeum vulgare*	Landrace	Spring	6	CA	PAK	33,719150	73,039089
961	HOR7658	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	PAK	33,719150	73,039089
962	HOR7673	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	PAK	33,719150	73,039089
963	HOR7695	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	PAK	33,719150	73,039089
964	HOR7697	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	PAK	33,719150	73,039089

965	FT409	*/*	*Hordeum vulgare*	Cultivar	Unknown	6	CA	PAK	33,719150	73,039089
966	FT410	*/*	*Hordeum vulgare*	Landrace	Unknown	6	CA	PAK	33,719150	73,039089
967	FT551	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	PAK	33,719150	73,039089
968	BCC218	*/*	*Hordeum vulgare*	Landrace	Unknown	6	CA	TJK	38,560000	68,773889
969	BCC219	*/*	*Hordeum vulgare*	Landrace	Unknown	6	CA	TJK	38,560000	68,773889
970	BCC1500	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	TJK	38,560000	68,773889
971	FT554	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	TJK	38,536667	68,780000
972	FT778	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	TJK	38,536667	68,780000
973	FT789	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	TJK	38,536667	68,780000
974	BCC1503	*missing*	*Hordeum vulgare*	Landrace	Spring	6	CA	TKM	37,941667	58,383611
975	HOR4170	*/*	*Hordeum vulgare*	Landrace	Winter	6	CA	TKM	37,933333	58,366667
976	FT370	*/*	*Hordeum spontaneum*	Wild	Winter	2	CA	TKM	37,950000	58,390000
977	FT376	*/*	*Hordeum spontaneum*	Wild	Winter	2	CA	TKM	35,275833	62,341667
978	FT566	*/*	*Hordeum spontaneum*	Wild	Winter	2	CA	TKM	38,417000	56,683000
979	FT567	*/*	*Hordeum spontaneum*	Wild	Winter	2	CA	TKM	41,050000	61,883300
980	FT725	*/*	*Hordeum vulgare*	Landrace	Unknown	6	CA	TKM	37,933333	58,366667
981	FT779	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	TKM	37,933333	58,366667
982	BCC1470	*/*	*Hordeum vulgare*	Landrace	Spring	2	CA	UZB	39,654167	66,959722
983	BCC1476	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	UZB	39,654167	66,959722
984	BCC1498	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	UZB	39,654167	66,959722
985	FT523	*/*	*Hordeum vulgare*	Landrace	Spring	6	CA	UZB	41,266667	69,216667
986	BCC1548	*/*	*Hordeum vulgare*	Landrace	Spring	6	NE	CYP	35,116667	33,400000
987	FT362	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	CYP	35,145800	33,400000
988	FT363	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	CYP	34,983299	34,016701
989	FT715	*/*	*Hordeum vulgare*	Landrace	Unknown	6	NE	CYP	35,166667	33,366667
990	FT235	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,850000	48,900000
991	FT236	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,500000	48,800000
992	FT237	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	33,550000	46,216667
993	FT238	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,000000	53,000000
994	FT239	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,000000	53,000000
995	FT240	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,000000	53,000000
996	FT241	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	35,700000	51,420000
997	FT242	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	34,083333	49,800000
998	FT243	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	30,516667	49,833333
999	FT244	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,550000	48,816667
1000	FT245	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,550000	48,816667
1001	FT246	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,533333	48,816667
1002	FT247	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,550000	48,816700
1003	FT248	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,675894	48,579156
1004	FT282	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,000000	48,550000
1005	FT284	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	30,283000	57,083000
1006	FT285	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	33,550000	46,216667
1007	FT286	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	30,066667	50,833333
1008	FT330	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	30,359167	50,792500
1009	FT331	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	33,233333	48,566667
1010	FT332	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	33,816667	48,183333
1011	FT333	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	35,983000	59,483000
1012	FT339	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,000000	53,000000
1013	FT344	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	36,621667	53,033333
1014	FT345	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	36,621667	53,033333
1015	FT346	*/*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	30,516667	49,833333

1016	FT347	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,550000	49,833333
1017	FT348	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,550000	48,816667
1018	FT349	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,550000	48,816667
1019	FT350	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,533333	48,816667
1020	FT351	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,533333	48,816667
1021	FT352	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,533333	48,816667
1022	FT353	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,533333	48,816667
1023	FT354	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,550000	48,816667
1024	FT355	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,533333	48,816667
1025	FT378	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,000000	53,000000
1026	FT423	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,000000	53,000000
1027	FT436	*III*	*Hordeum vulgare*	Cultivar	Unknown	6	NE	IRN	35,696111	51,423056
1028	FT509	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	37,066667	45,466667
1029	FT510	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,533333	48,816667
1030	FT514	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	36,621667	53,033333
1031	FT517	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,850000	48,900000
1032	FT526	*VI*	*Hordeum vulgare*	Landrace	Winter	6	NE	IRN	35,696111	51,423056
1033	FT527	*I*	*Hordeum vulgare*	Landrace	Unknown	6	NE	IRN	35,696111	51,423056
1034	FT528	*I*	*Hordeum vulgare*	Landrace	Unknown	6	NE	IRN	35,696111	51,423056
1035	FT529	*I*	*Hordeum vulgare*	Landrace	Winter	6	NE	IRN	35,696111	51,423056
1036	FT550	*I*	*Hordeum vulgare*	Landrace	Unknown	6	NE	IRN	35,696111	51,423056
1037	FT564	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	36,750000	45,717000
1038	FT569	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	34,617000	46,950000
1039	FT605	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,850000	48,900000
1040	FT611	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	35,500000	51,250000
1041	FT612	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,550000	49,833333
1042	FT613	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,550000	49,830000
1043	FT614	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,550000	49,833333
1044	FT616	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	32,189220	48,257785
1045	FT618	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	36,266701	47,766701
1046	FT655	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	36,750000	45,716670
1047	FT656	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,283330	48,716670
1048	FT657	*XIII*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	29,608056	52,524722
1049	FT658	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	35,366670	43,200000
1050	FT660	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	36,750000	45,700000
1051	FT661	*XIII*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	38,500000	47,200000
1052	FT675	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	35,696111	51,423056
1053	FT677	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRN	31,533333	48,816667
1054	FT800	*I*	*Hordeum vulgare*	Landrace	Spring	6	NE	IRN	35,696111	51,423056
1055	FTblack	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	IRN	35,696111	51,423056
1056	FTwhite	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	IRN	35,696111	51,423056
1057	HOR2777	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	37,633333	47,800000
1058	HOR2785	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	35,600000	51,866667
1059	HOR2792	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	30,516667	50,850000
1060	HOR2795	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	32,550000	49,833333
1061	HOR2797	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	32,550000	48,816667
1062	HOR2800	*I*	*Hordeum vulgare*	Landrace	Spring	6	NE	IRN	31,533333	48,816667
1063	HOR2807	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	32,550000	50,850000
1064	HOR2808	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	33,566667	50,850000
1065	HOR2809	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	33,566667	50,850000
1066	HOR2815	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	35,600000	48,816667

1067	HOR2819	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	35,600000	48,816667
1068	HOR2820	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	35,600000	48,816667
1069	HOR2828	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	34,583333	48,816667
1070	HOR2829	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	34,583333	48,816667
1071	HOR2833	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	34,583333	48,816667
1072	HOR2835	*I*	*Hordeum vulgare*	Landrace	Spring	6	NE	IRN	34,583333	48,816667
1073	HOR2838	*missing*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	31,533333	48,816667
1074	HOR2841	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	37,633333	46,783333
1075	HOR2844	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	37,633333	46,783333
1076	HOR2849	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	37,633333	46,783333
1077	HOR2853	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	38,650000	46,783333
1078	HOR2857	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	36,616667	49,833333
1079	HOR2867	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	37,633333	58,983333
1080	HOR2872	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	35,600000	51,866667
1081	HOR3298	*IV*	*Hordeum vulgare*	Landrace	Winter	6	NE	IRN	32,550000	50,850000
1082	KC70115	*missing*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	35,696111	51,423056
1083	TN3826	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	35,696111	51,423056
1084	TN4792	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRN	35,696111	51,423056
1085	TN6396	*I*	*Hordeum vulgare*	Landrace	Spring	6	NE	IRN	35,696111	51,423056
1086	BCC93	*I*	*Hordeum vulgare*	Landrace	Winter	2	NE	IRQ	33,333333	44,383333
1087	FT229	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	36,400000	44,150000
1088	FT230	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	35,033333	45,716667
1089	FT231	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	35,583333	43,000000
1090	FT232	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	36,416667	41,650000
1091	FT233	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	33,330000	44,400000
1092	FT234	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	33,330000	44,400000
1093	FT283	*XII*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	36,400000	44,200000
1094	FT446	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	35,536667	44,831944
1095	FT507	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	36,383333	43,416667
1096	FT508	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	33,330000	44,400000
1097	FT515	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	36,400000	44,150000
1098	FT562	*I*	*Hordeum vulgare*	Landrace	Winter		NE	IRQ	33,325000	44,422000
1099	FT595	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	36,333333	42,166667
1100	FT603	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	36,350000	43,133333
1101	FT604	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	36,083333	43,166667
1102	FT637	*XII*	*Hordeum spontaneum*	Wild	Winter	2	NE	IRQ	35,033333	45,716667
1103	HOR10484	*III*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRQ	33,315556	44,391944
1104	HOR10607	*I*	*Hordeum vulgare*	Landrace	Spring	6	NE	IRQ	33,325000	44,422000
1105	HOR10609	*I*	*Hordeum vulgare*	Landrace	Spring	6	NE	IRQ	36,166389	43,256944
1106	HOR10610	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRQ	36,443333	43,256667
1107	HOR10620	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRQ	34,833333	42,000000
1108	HOR10627	*I*	*Hordeum vulgare*	Landrace	Spring	6	NE	IRQ	34,833333	42,000000
1109	HOR10651	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	IRQ	36,443333	43,256667
1110	FT001	*XIII*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	30,934060	34,865820
1111	FT002	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	30,933480	34,865270
1112	FT005	*IV*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	30,933190	34,864850
1113	FT006	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,411780	34,877720
1114	FT007	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,413990	34,880180
1115	FT008	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,414860	34,880440
1116	FT010	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,834370	35,305290
1117	FT011	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,834730	35,304790

1118	FT013	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,926130	35,469150
1119	FT015	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,926160	35,468400
1120	FT016	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,926160	35,468400
1121	FT017	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,068640	35,398410
1122	FT018	*XXIV*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,068730	35,399370
1123	FT020	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,068630	35,400730
1124	FT024	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,343040	35,517060
1125	FT027	*XVIII*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,282900	35,548360
1126	FT028	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,282450	35,548370
1127	FT031	*III*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,698340	34,585050
1128	FT033	*III*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,697880	34,584900
1129	FT037	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,401210	34,472990
1130	FT038	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,401970	34,472710
1131	FT042	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	30,889990	34,631460
1132	FT045	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,672920	35,436720
1133	FT046	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,674860	35,435440
1134	FT047	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,674860	35,435440
1135	FT050	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,852260	35,679600
1136	FT051	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,852380	35,679630
1137	FT052	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,852980	35,679090
1138	FT053	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,779130	35,660720
1139	FT054	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,779280	35,660120
1140	FT055	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,780320	35,659690
1141	FT058	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,690110	35,662090
1142	FT059	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,689860	35,662320
1143	FT060	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,689610	35,661760
1144	FT062	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,347760	35,122910
1145	FT063	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,347080	35,122680
1146	FT064	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,346960	35,123260
1147	FT065	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,347320	35,123710
1148	FT067	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,537280	34,890360
1149	FT070	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,538590	34,889690
1150	FT072	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,437030	34,887480
1151	FT078	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,917960	35,019880
1152	FT079	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,917940	35,021360
1153	FT082	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,617690	34,932270
1154	FT084	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,616670	34,932370
1155	FT086	*XIV*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,647810	34,967270
1156	FT087	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,647600	34,967750
1157	FT089	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,685720	35,171390
1158	FT090	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,685920	35,170530
1159	FT091	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,685600	35,171260
1160	FT092	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,684820	35,170630
1161	FT094	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,956730	34,972670
1162	FT095	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,956360	34,972210
1163	FT099	*XVII*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,549190	35,339640
1164	FT101	*XVII*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,548750	35,339980
1165	FT102	*XVII*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,548620	35,339100
1166	FT103	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,463280	35,433850
1167	FT104	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,463180	35,434410
1168	FT108	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,747570	35,638920

1169	FT109	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,747140	35,638690
1170	FT110	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,746690	35,638530
1171	FT112	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,745800	35,638100
1172	FT113	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,875390	35,544080
1173	FT116	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,874190	35,542930
1174	FT117	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,873550	35,542500
1175	FT123	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,822040	35,503270
1176	FT125	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,821030	35,507250
1177	FT129	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,715770	34,975670
1178	FT130	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,715020	34,975320
1179	FT133	*XV*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,773470	35,447220
1180	FT135	*XV*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,771820	35,448570
1181	FT137	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,578370	35,470670
1182	FT141	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,579250	35,472850
1183	FT142	*XV*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	30,571580	34,676970
1184	FT144	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	30,571760	34,679570
1185	FT145	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	30,571720	34,676410
1186	FT147	*XIII*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	30,845380	34,744400
1187	FT148	*XIII*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	30,845050	34,744880
1188	FT151	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	30,844360	34,746950
1189	FT152	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,596860	34,898840
1190	FT153	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,596250	34,898960
1191	FT155	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,595280	34,899220
1192	FT158	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,925890	35,531070
1193	FT159	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,925920	35,531890
1194	FT162	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,910280	35,605640
1195	FT165	*XXI*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,910790	35,604650
1196	FT166	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,943990	35,701550
1197	FT167	*XXVII*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,943370	35,700440
1198	FT168	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,942850	35,700290
1199	FT169	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,070340	35,769550
1200	FT170	*XXV*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,070840	35,769420
1201	FT172	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,229360	35,730740
1202	FT173	*XXVI*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,230400	35,731000
1203	FT175	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,251120	35,645530
1204	FT178	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,250000	35,646110
1205	FT181	*III*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,140570	35,630040
1206	FT183	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,139360	35,629960
1207	FT184	*XXV*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,146470	35,629700
1208	FT185	*XVI*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,131070	35,556370
1209	FT186	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,131470	35,556630
1210	FT187	*XVI*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,132580	35,557590
1211	FT189	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,987760	35,190310
1212	FT190	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,986660	35,191240
1213	FT194	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,986890	35,192050
1214	FT196	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,046350	35,248780
1215	FT197	*XXII*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,045780	35,248770
1216	FT200	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,872630	35,502040
1217	FT202	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,874350	35,502220
1218	FT205	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,839610	35,009220
1219	FT207	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,839080	35,009370

1220	FT208	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,838910	35,010780
1221	FT212	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,690880	35,013160
1222	FT213	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,690710	35,012650
1223	FT217	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,772040	35,112400
1224	FT218	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,771950	35,112920
1225	FT219	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,287180	35,763540
1226	FT220	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,287340	35,762990
1227	FT221	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,973600	35,423930
1228	FT222	*XIV*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,974290	35,423860
1229	FT223	*I*	*Hordeum agriocrithon*	*Agriocrithon*	Unknown		NE	ISR	32,066158	34,777819
1230	FT224	*I*	*Hordeum vulgare*	Landrace	Unknown		NE	ISR	32,066158	34,777819
1231	FT225	*I*	*Hordeum vulgare*	Landrace	Unknown		NE	ISR	32,066158	34,777819
1232	FT226	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	ISR	32,066158	34,777819
1233	FT227	*I*	*Hordeum vulgare*	Cultivar	Unknown	6	NE	ISR	32,066158	34,777819
1234	FT228	*missing*	*Hordeum vulgare*	Cultivar	Unknown	2	NE	ISR	32,066158	34,777819
1235	FT287	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,000000	34,916667
1236	FT288	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,683333	35,000000
1237	FT294	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,583333	35,050000
1238	FT312	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,850000	34,966667
1239	FT313	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,400000	34,600000
1240	FT314	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,766667	35,000000
1241	FT319	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,350000	35,516667
1242	FT327	*XIII*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	30,916667	35,050000
1243	FT334	*XIII*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,066667	34,850000
1244	FT337	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,016667	35,616667
1245	FT338	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	33,000000	35,416667
1246	FT340	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,500000	34,700000
1247	FT341	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,300000	35,016667
1248	FT372	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,683333	35,000000
1249	FT383	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,770000	35,230000
1250	FT384	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,770000	35,230000
1251	FT385	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,770000	35,230000
1252	FT386	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,770000	35,230000
1253	FT387	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,770000	35,230000
1254	FT393	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	32,742608	35,445311
1255	FT394	*XIV*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,774733	35,048508
1256	FT553	*I*	*Hordeum vulgare*	Landrace	Winter		NE	ISR	32,066158	34,777819
1257	FT639	*XIII*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	31,801790	35,476590
1258	FT646	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	ISR	30,571930	34,677630
1259	HOR11370	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	ISR	31,779167	35,223611
1260	HOR11371	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	ISR	31,779167	35,223611
1261	HOR11373	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	ISR	31,779167	35,223611
1262	HOR11374	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	ISR	31,779167	35,223611
1263	FT267	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	JOR	31,700000	35,950000
1264	FT269	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	JOR	32,633333	35,700000
1265	FT272	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	JOR	32,216667	36,050000
1266	FT275	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	JOR	32,016667	36,016667
1267	FT276	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	JOR	32,583333	35,666667
1268	FT434	*I*	*Hordeum vulgare*	Cultivar	Spring	2	NE	JOR	31,956578	35,945695
1269	FT511	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	JOR	32,050000	35,783333
1270	FT549	*I*	*Hordeum vulgare*	Landrace	Spring		NE	JOR	31,956578	35,945695

1271	FT570	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	JOR	32,083000	35,716667
1272	FT571	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	JOR	32,650000	35,717000
1273	FT572	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	JOR	30,667000	35,633000
1274	FT626	*XXIII*	*Hordeum spontaneum*	Wild	Winter	2	NE	JOR	32,100000	35,666667
1275	FT627	*III*	*Hordeum spontaneum*	Wild	Winter	2	NE	JOR	32,016667	35,900000
1276	FT274	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	LBN	33,450000	35,316667
1277	FT630	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	LBN	33,466667	35,866667
1278	FT631	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	LBN	33,933333	36,100000
1279	FT671	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	LBN	33,833333	35,916667
1280	FT672	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	LBN	33,616667	35,816667
1281	FT673	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	LBN	33,433333	35,750000
1282	FT699	*I*	*Hordeum vulgare*	Landrace	Unknown	6	NE	LBN	33,888629	35,495479
1283	BCC167	*I*	*Hordeum vulgare*	Landrace	Unknown	6	NE	OMN	22,666667	-57,333333
1284	FT786	*I*	*Hordeum vulgare*	Landrace	Spring	6	NE	OMN	23,610000	58,540000
1285	BCC190	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	SYR	36,833333	40,072222
1286	BCC192	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	SYR	36,383333	38,959722
1287	BCC195	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	SYR	33,816667	36,544167
1288	BCC197	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	SYR	36,116667	36,463056
1289	FT268	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	35,167222	38,881389
1290	FT270	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	33,654167	36,836111
1291	FT273	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	34,935000	36,736667
1292	FT421	*I*	*Hordeum vulgare*	Cultivar	Unknown	2	NE	SYR	33,511100	36,306400
1293	FT438	*I*	*Hordeum vulgare*	Cultivar	Winter	2	NE	SYR	33,511100	36,306400
1294	FT439	*I*	*Hordeum vulgare*	Cultivar	Winter	2	NE	SYR	33,511100	36,306400
1295	FT512	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	35,605556	35,820833
1296	FT513	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	33,976667	36,591389
1297	FT544	*I*	*Hordeum vulgare*	Landrace	Spring		NE	SYR	33,511100	36,306400
1298	FT545	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	SYR	33,511100	36,306400
1299	FT558	*I*	*Hordeum vulgare*	Landrace	Winter	2	NE	SYR	33,511100	36,306400
1300	FT563	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	33,483000	36,317000
1301	FT574	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	33,511100	36,306400
1302	FT582	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	37,092500	42,098889
1303	FT583	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	37,037778	41,215556
1304	FT584	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	36,966944	40,497500
1305	FT585	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	37,082222	40,998611
1306	FT586	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	36,820278	40,880556
1307	FT587	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	36,483889	37,770000
1308	FT588	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	34,822500	36,474167
1309	FT589	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	35,028889	37,006944
1310	FT590	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	35,013333	36,702500
1311	FT592	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	37,073767	41,085567
1312	FT628	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	32,596389	36,378889
1313	FT629	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	32,866667	36,696667
1314	FT632	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	SYR	37,077778	42,070556
1315	FT788	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	SYR	33,511100	36,306400
1316	HOR12828	*I*	*Hordeum vulgare*	Landrace	Spring	6	NE	SYR	31,005000	47,441944
1317	HOR12829	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	SYR	36,338333	36,833333
1318	HOR12830	*I*	*Hordeum vulgare*	Landrace	Unknown	6	NE	SYR	36,701389	38,086528
1319	HOR4469	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	SYR	32,685000	36,033333
1320	FT249	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,850833	40,047500
1321	FT250	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,850000	40,033333

1322	FT251	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	39,666667	31,166667
1323	FT252	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,250000	44,483333
1324	FT253	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,250000	44,483333
1325	FT254	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,716667	37,116667
1326	FT255	*XX*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,838889	36,932500
1327	FT256	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,751944	37,475278
1328	FT257	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,785000	37,476389
1329	FT258	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,925556	37,470833
1330	FT259	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,760000	37,629722
1331	FT261	*XIX*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,229444	37,517222
1332	FT262	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,780833	37,283333
1333	FT263	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,008611	37,133889
1334	FT264	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,945556	36,925000
1335	FT266	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,867222	36,950000
1336	FT281	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,850833	40,047500
1337	FT343	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,500000	40,850000
1338	FT373	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,786556	39,748019
1339	FT374	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,786556	39,748019
1340	FT375	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,786556	39,748019
1341	FT451	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	TUR	39,920770	32,854110
1342	FT452	*XIX*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,325278	37,157778
1343	FT454	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,255833	36,467222
1344	FT455	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,255833	36,467222
1345	FT456	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,247500	36,524722
1346	FT458	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,493333	38,876667
1347	FT459	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,493333	38,876667
1348	FT460	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,493333	38,876667
1349	FT461	*IV*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,493333	38,876667
1350	FT462	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,778333	39,780000
1351	FT463	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,771944	39,734167
1352	FT464	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,714167	39,734167
1353	FT465	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,661944	39,713611
1354	FT466	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,607500	39,728056
1355	FT468	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,585556	39,743333
1356	FT469	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,552500	39,701667
1357	FT470	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,331944	40,771389
1358	FT472	*XII*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,678611	37,865000
1359	FT473	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,658333	37,786667
1360	FT474	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,658333	37,786667
1361	FT478	*I*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1362	FT479	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1363	FT481	*I*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1364	FT490	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1365	FT492	*I*	*Hordeum vulgare*	Cultivar	Unknown	2	NE	TUR	39,920770	32,854110
1366	FT493	*I*	*Hordeum vulgare*	Cultivar	Unknown	2	NE	TUR	39,920770	32,854110
1367	FT494	*I*	*Hordeum vulgare*	Cultivar	Unknown	2	NE	TUR	39,920770	32,854110
1368	FT503	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1369	FT504	*I*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1370	FT505	*I*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1371	FT506	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,247500	36,524722
1372	FT518	*I*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110

1373	FT525	*I*	*Hordeum vulgare*	Landrace	Winter		NE	TUR	39,920770	32,854110
1374	FT530	*IV*	*Hordeum vulgare*	Landrace	Unknown	6	NE	TUR	39,920770	32,854110
1375	FT532	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	TUR	39,920770	32,854110
1376	FT533	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1377	FT534	*I*	*Hordeum vulgare*	Landrace	Unknown	6	NE	TUR	39,920770	32,854110
1378	FT536	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	TUR	39,920770	32,854110
1379	FT537	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	TUR	39,920770	32,854110
1380	FT538	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	TUR	39,920770	32,854110
1381	FT539	*I*	*Hordeum vulgare*	Landrace	Spring	6	NE	TUR	39,920770	32,854110
1382	FT540	*I*	*Hordeum vulgare*	Landrace	Spring	6	NE	TUR	39,920770	32,854110
1383	FT541	*I*	*Hordeum vulgare*	Landrace	Unknown	6	NE	TUR	39,920770	32,854110
1384	FT542	*I*	*Hordeum vulgare*	Landrace	Winter	2	NE	TUR	39,920770	32,854110
1385	FT543	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	TUR	39,920770	32,854110
1386	FT546	*I*	*Hordeum vulgare*	Landrace	Winter	2	NE	TUR	39,920770	32,854110
1387	FT547	*III*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1388	FT555	*X*	*Hordeum vulgare*	Landrace	Spring	6	NE	TUR	39,920770	32,854110
1389	FT556	*I*	*Hordeum vulgare*	Landrace	Winter		NE	TUR	39,920770	32,854110
1390	FT557	*I*	*Hordeum vulgare*	Landrace	Unknown		NE	TUR	39,920770	32,854110
1391	FT565	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,850000	40,033333
1392	FT576	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,250000	44,483333
1393	FT577	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,133333	44,516667
1394	FT578	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	40,650000	43,100000
1395	FT579	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,983333	39,966667
1396	FT580	*XIII*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,816667	41,866667
1397	FT581	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,966667	41,716667
1398	FT619	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,881944	37,351111
1399	FT620	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,691111	37,464444
1400	FT621	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,853611	37,521389
1401	FT622	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,853611	37,521389
1402	FT623	*XX*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,267500	37,520278
1403	FT624	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,920833	37,181667
1404	FT625	*III*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,877500	37,057778
1405	FT662	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,691111	37,464444
1406	FT663	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,035278	37,607500
1407	FT664	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,088056	37,710556
1408	FT665	*XX*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,191944	37,459722
1409	FT666	*XIX*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,280833	37,245833
1410	FT667	*XX*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,253056	37,333056
1411	FT668	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,322778	37,467222
1412	FT669	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,968333	37,185556
1413	FT670	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,992222	36,932222
1414	FT681	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	39,920770	32,854110
1415	FT684	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,850833	40,047500
1416	FT728	*XIX*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,325278	37,157778
1417	FT729	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,287778	37,189444
1418	FT730	*XIX*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,329444	37,274722
1419	FT731	*XX*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,423889	37,281389
1420	FT732	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,255833	36,467222
1421	FT733	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,255833	36,467222
1422	FT734	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,410278	38,778611
1423	FT735	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,791944	39,955000

1424	FT736	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,791944	39,955000
1425	FT737	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,821389	39,992778
1426	FT738	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,839167	39,723056
1427	FT739	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,839167	39,723056
1428	FT741	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,681389	41,452500
1429	FT743	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,711111	37,942222
1430	FT744	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,658333	37,786667
1431	FT746	*missing*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,978611	36,728056
1432	FT747	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,866111	36,951944
1433	FT751	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	36,950000	40,000556
1434	FT756	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,133889	39,840833
1435	FT757	*I*	*Hordeum spontaneum*	Wild	Winter	2	NE	TUR	37,133889	39,840833
1436	FT802	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1437	FT803	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1438	HOR1000	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1439	HOR1001	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1440	HOR1002	*I*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1441	HOR1003	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1442	HOR1041	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1443	HOR1042	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1444	HOR1043	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1445	HOR1044	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1446	HOR1045	*XI*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1447	HOR1046	*missing*	*Hordeum vulgare*	Landrace	Spring	6	NE	TUR	39,920770	32,854110
1448	HOR1047	*XI*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1449	HOR1048	*XI*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1450	HOR1049	*I*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1451	HOR1050	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1452	HOR1051	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1453	HOR1052	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1454	HOR1053	*missing*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1455	HOR1054	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1456	HOR1055	*XI*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1457	HOR1056	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1458	HOR1057	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1459	HOR1058	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1460	HOR1059	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1461	HOR1060	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1462	HOR1061	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1463	HOR1062	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1464	HOR1065	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1465	HOR1066	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1466	HOR1067	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1467	HOR1068	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1468	HOR1069	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1469	HOR1070	*XI*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1470	HOR1071	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1471	HOR1072	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1472	HOR1073	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1473	HOR1074	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1474	HOR1075	*I*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110

1475	HOR1076	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1476	HOR1077	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1477	HOR1078	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1478	HOR1079	*I*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1479	HOR1080	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1480	HOR1081	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1481	HOR1082	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1482	HOR1083	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1483	HOR1085	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1484	HOR1086	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1485	HOR1087	*I*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1486	HOR1088	*missing*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1487	HOR1089	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1488	HOR1090	*missing*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1489	HOR1091	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1490	HOR1092	*I*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1491	HOR1093	*missing*	*Hordeum vulgare*	Landrace	Winter	2	NE	TUR	39,920770	32,854110
1492	HOR1094	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1493	HOR1095	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1494	HOR1096	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1495	HOR1097	*XI*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1496	HOR1098	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1497	HOR1099	*XI*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1498	HOR1100	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1499	HOR1101	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1500	HOR1102	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1501	HOR1103	*I*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1502	HOR1104	*I*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1503	HOR1105	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1504	HOR1106	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1505	HOR1107	*XI*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1506	HOR1108	*XI*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1507	HOR12252	*I*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1508	HOR12253	*I*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1509	HOR12254	*missing*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1510	HOR1362	*I*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1511	HOR1363	*XXVIII, rym11-a*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1512	HOR1415	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	36,450000	37,516667
1513	HOR1740	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,883333	28,783333
1514	HOR2237	*I*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1515	HOR23	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1516	HOR4078	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	37,456667	30,581667
1517	HOR4093	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	37,456667	30,581667
1518	HOR4103	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1519	HOR4109	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1520	HOR4116	*I*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1521	HOR4117	*I*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1522	HOR4118	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1523	HOR4119	*I*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1524	HOR4120	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1525	HOR4127	*I*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110

1526	HOR4128	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1527	HOR4129	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1528	HOR4130	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1529	HOR4131	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1530	HOR4132	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1531	HOR4133	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1532	HOR4134	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1533	HOR4136	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1534	HOR4137	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1535	HOR4138	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1536	HOR4207	*/*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1537	HOR4223	*/*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1538	HOR4228	*/*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1539	HOR4229	*/*	*Hordeum vulgare*	Landrace	Winter	6	NE	TUR	39,920770	32,854110
1540	HOR4321	*/*	*Hordeum vulgare*	Landrace	Winter	2	NE	TUR	39,920770	32,854110
1541	HOR441	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	40,050000	29,566667
1542	HOR4520	*/*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1543	HOR4523	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1544	HOR4524	*/*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1545	HOR4525	*/*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1546	HOR4526	*/*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1547	HOR4527	*/*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1548	HOR4528	*/*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1549	HOR4529	*/*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1550	HOR4530	*/*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1551	HOR4531	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1552	HOR4532	*/*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1553	HOR4580	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1554	HOR4604	*/*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1555	HOR4605	*/*	*Hordeum vulgare*	Cultivar	Winter	2	NE	TUR	39,920770	32,854110
1556	HOR4727	*/*	*Hordeum vulgare*	Landrace	Spring	6	NE	TUR	39,916667	32,850000
1557	HOR509	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	38,987500	29,385833
1558	HOR526	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	36,737222	29,918889
1559	HOR527	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	36,737222	29,918889
1560	HOR572	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	40,233333	32,683333
1561	HOR634	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	36,450000	37,516667
1562	HOR655	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	37,918611	29,860556
1563	HOR6931	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1564	HOR7266	*/*	*Hordeum vulgare*	Cultivar	Winter	6	NE	TUR	39,920770	32,854110
1565	HOR7964	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,783333	30,516667
1566	HOR7969	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	38,000000	37,000000
1567	HOR7970	*missing*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,916667	32,833333
1568	HOR7977	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,783333	30,516667
1569	HOR7978	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	38,750000	29,416667
1570	HOR7985	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	38,750000	29,416667
1571	HOR7988	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1572	HOR7995	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1573	HOR7997	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1574	HOR8000	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1575	HOR8006	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	38,750000	29,416667
1576	HOR8011	*/*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	41,733333	27,216667

1577	HOR8027	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1578	HOR8050	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	38,750000	30,666667
1579	HOR8068	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1580	HOR8074	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1581	HOR8084	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1582	HOR8092	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1583	HOR8093	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1584	HOR8099	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,416667	29,983333
1585	HOR8102	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1586	HOR8108	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1587	HOR8113	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,416667	29,983333
1588	HOR8117	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1589	HOR8119	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1590	HOR8120	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1591	HOR8125	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1592	HOR8158	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,416667	29,983333
1593	HOR8160	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,250000	29,500000
1594	HOR8173	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1595	HOR8176	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1596	HOR8180	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1597	HOR8183	*missing*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1598	HOR8194	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,920770	32,854110
1599	HOR902	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	41,292778	36,331111
1600	HOR930	*I*	*Hordeum vulgare*	Landrace	Spring	2	NE	TUR	39,916667	32,850000
1601	FT414	*I*	*Hordeum vulgare*	Landrace	Unknown	2	NE	YEM	15,352029	44,207456
1602	HOR10092	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	DZA	36,700000	3,216667
1603	HOR4146	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	DZA	40,895833	40,563333
1604	HOR4150	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	DZA	36,700000	3,216667
1605	FT402	*I*	*Hordeum vulgare*	Landrace	Unknown	6	AF	DZA	36,752887	3,042048
1606	HOR819	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	EGY	26,816667	30,802222
1607	HOR8659	*I*	*Hordeum vulgare*	Landrace	Winter	6	AF	EGY	31,193333	29,904167
1608	HOR8658	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	EGY	31,193333	29,904167
1609	FT379	*I*	*Hordeum spontaneum*	Wild	Winter	2	AF	EGY	30,050000	31,250000
1610	FT380	*I*	*Hordeum spontaneum*	Wild	Winter	2	AF	EGY	31,350000	27,233300
1611	FT401	*I*	*Hordeum vulgare*	Landrace	Unknown	2	AF	EGY	30,044420	31,235712
1612	FT437	*I*	*Hordeum vulgare*	Cultivar	Spring	2	AF	EGY	30,044420	31,235712
1613	FT712	*I*	*Hordeum vulgare*	Cultivar	Unknown	6	AF	EGY	30,044420	31,235712
1614	HOR10258	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	ETH	7,850000	36,083333
1615	HOR10259	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	ETH	7,850000	36,083333
1616	HOR10307	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	6,166667	36,616667
1617	HOR10308	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	8,650000	39,066667
1618	HOR10310	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	8,000000	38,833333
1619	HOR10324	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	6,400000	38,300000
1620	HOR10328	*III*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	6,800000	38,250000
1621	HOR10334	*I*	*Hordeum vulgare*	Landrace	Spring	Deficiens	AF	ETH	9,100000	37,316667
1622	HOR10338	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,000000	37,450000
1623	HOR10350	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	8,450000	36,350000
1624	HOR10421	*I*	*Hordeum vulgare*	Landrace	Spring	Deficiens	AF	ETH	8,650000	39,066667
1625	HOR10497	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1626	HOR10508	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	6,800000	38,250000
1627	HOR10509	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	6,800000	38,250000

1628	HOR10761	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	ETH	6,000000	38,250000
1629	HOR10800	*I*	*Hordeum vulgare*	Landrace	Spring	Deficiens	AF	ETH	6,000000	38,250000
1630	HOR2932	*III*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1631	HOR3285	*III*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,016667	38,733333
1632	HOR4732	*missing*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1633	HOR5005	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1634	HOR5082	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1635	HOR5188	*missing*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,000000	35,500000
1636	HOR5342	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	12,583333	39,500000
1637	HOR5402	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1638	HOR5428	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,583333	41,866667
1639	HOR5593	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	8,985833	37,850000
1640	HOR5689	*III*	*Hordeum vulgare*	Landrace	Spring	2	AF	ETH	9,033333	38,700000
1641	HOR5702	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	ETH	7,666667	36,833333
1642	HOR5732	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1643	HOR5734	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,083333	36,550000
1644	HOR5753	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1645	HOR5771	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1646	HOR5800	*III*	*Hordeum vulgare*	Landrace	Spring	Deficiens	AF	ETH	9,022736	38,746799
1647	HOR5811	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	ETH	9,683333	39,533333
1648	HOR5845	*I*	*Hordeum vulgare*	Cultivar	Spring	2	AF	ETH	9,022736	38,746799
1649	HOR5865	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,150000	39,033333
1650	HOR5895	*I*	*Hordeum vulgare*	Landrace	Spring	Deficiens	AF	ETH	6,200000	38,700000
1651	HOR5939	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	8,533333	34,800000
1652	HOR6145	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1653	HOR6243	*missing*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,250000	41,250000
1654	HOR6252	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	8,766667	38,933333
1655	HOR6253	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	8,766667	38,933333
1656	HOR6360	*III*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	7,466667	36,883333
1657	HOR6460	*I*	*Hordeum vulgare*	Landrace	Spring	Deficiens	AF	ETH	7,550000	36,616667
1658	HOR6514	*I*	*Hordeum vulgare*	Landrace	Spring	Labile	AF	ETH	8,650000	39,066667
1659	HOR6698	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1660	HOR7410	*I*	*Hordeum vulgare*	Cultivar	Spring	Deficiens	AF	ETH	9,022736	38,746799
1661	HOR7722	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1662	HOR7725	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1663	HOR7732	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1664	HOR7737	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1665	HOR7744	*I*	*Hordeum vulgare*	Landrace	Spring	Labile	AF	ETH	9,022736	38,746799
1666	HOR7869	*I*	*Hordeum vulgare*	Landrace	Spring	Deficiens	AF	ETH	9,022736	38,746799
1667	HOR7875	*I*	*Hordeum vulgare*	Landrace	Spring	Deficiens	AF	ETH	9,022736	38,746799
1668	HOR7877	*I*	*Hordeum vulgare*	Landrace	Spring	Deficiens	AF	ETH	9,022736	38,746799
1669	HOR7935	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	ETH	9,022736	38,746799
1670	HOR7939	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	ETH	8,633333	38,050000
1671	HOR7956	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	ETH	9,066667	38,483333
1672	HOR8946	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1673	HOR9001	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1674	HOR9158	*I*	*Hordeum vulgare*	Landrace	Spring	Labile	AF	ETH	9,022736	38,746799
1675	HOR9164	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1676	HOR9203	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1677	HOR9374	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,022736	38,746799
1678	HOR9920	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	ETH	9,016667	38,733333

1679	FT408	*I*	*Hordeum vulgare*	Landrace	Unknown	2	AF	ETH	9,022736	38,746799
1680	FT412	*III*	*Hordeum vulgare*	Landrace	Unknown	2	AF	ETH	9,022736	38,746799
1681	FT435	*I*	*Hordeum vulgare*	Cultivar	Spring	2	AF	ETH	9,022736	38,746799
1682	FT404	*missing*	*Hordeum vulgare*	Landrace	Unknown	2	AF	KEN	-1,292066	36,821946
1683	FT714	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	KEN	-1,292066	36,821946
1684	BCC118	*I*	*Hordeum vulgare*	Landrace	Unknown	6	AF	LBY	26,466667	14,383333
1685	HOR10098	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	31,864722	11,793056
1686	HOR10110	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	26,254167	14,286111
1687	HOR10111	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	26,166667	15,116667
1688	HOR10123	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	27,566667	14,354722
1689	HOR10124	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	31,950000	12,016667
1690	HOR10140	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	24,964167	10,167500
1691	HOR10162	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	LBY	32,480000	21,126389
1692	HOR10169	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	LBY	32,480000	21,126389
1693	HOR10170	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	32,480000	21,126389
1694	HOR10280	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	LBY	26,803056	13,533333
1695	HOR2766	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	23,311111	21,856667
1696	HOR9725	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	32,017778	21,741667
1697	HOR9827	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	32,766667	13,983333
1698	HOR9828	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	32,766667	13,983333
1699	HOR9830	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	32,766667	13,983333
1700	HOR9836	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	27,033333	14,433333
1701	HOR9860	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	32,516667	13,166667
1702	HOR9879	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	32,537778	21,575833
1703	HOR9880	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	LBY	32,690556	21,907500
1704	HOR9883	*I*	*Hordeum vulgare*	Landrace	Spring	2	AF	LBY	32,017778	21,741667
1705	HOR9885	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	32,763611	22,639167
1706	HOR9887	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	32,763611	22,639167
1707	HOR9924	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	LBY	32,530000	13,000000
1708	FT356	*I*	*Hordeum spontaneum*	Wild	Winter	2	AF	LBY	32,483300	21,120800
1709	FT357	*XIV*	*Hordeum spontaneum*	Wild	Winter	2	AF	LBY	32,766701	21,716700
1710	FT358	*I*	*Hordeum spontaneum*	Wild	Winter	2	AF	LBY	32,090811	21,327064
1711	FT764	*I*	*Hordeum vulgare*	Landrace	Unknown	6	AF	LBY	32,876174	13,187507
1712	BCC126	*I*	*Hordeum vulgare*	Landrace	Unknown	6	AF	MAR	29,666667	-8,283333
1713	BCC129	*I*	*Hordeum vulgare*	Landrace	Unknown	6	AF	MAR	33,633333	-6,283333
1714	BCC131	*I*	*Hordeum vulgare*	Landrace	Unknown	6	AF	MAR	32,050000	3,050000
1715	BCC149	*I*	*Hordeum vulgare*	Landrace	Winter	6	AF	MAR	34,433333	-4,650000
1716	BCC161	*I*	*Hordeum vulgare*	Landrace	Unknown	6	AF	MAR	34,950000	-2,333333
1717	HOR13416	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	MAR	31,050000	-8,833333
1718	HOR13419	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	MAR	30,466667	-9,366667
1719	HOR13420	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	MAR	30,883333	-9,050000
1720	HOR13428	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	MAR	30,700000	-8,854444
1721	HOR4029	*I*	*Hordeum vulgare*	Landrace	Spring	6	AF	MAR	32,000000	-5,000000
1722	FT359	*I*	*Hordeum spontaneum*	Wild	Winter	2	AF	MAR	34,020000	-6,830000
1723	FT400	*I*	*Hordeum vulgare*	Landrace	Unknown	6	AF	MAR	34,015049	-6,832720
1724	FT447	*I*	*Hordeum vulgare*	Landrace	Unknown	6	AF	MAR	34,015049	-6,832720
1725	FT448	*I*	*Hordeum vulgare*	Landrace	Unknown	6	AF	MAR	34,015049	-6,832720
1726	FT775	*I*	*Hordeum vulgare*	Landrace	Unknown	6	AF	MAR	34,015049	-6,832720
1727	FT428	*I*	*Hordeum vulgare*	Cultivar	Spring	2	AM	ARG	-34,603723	-58,381593
1728	FT429	*I*	*Hordeum vulgare*	Cultivar	Spring	2	AM	ARG	-34,603723	-58,381593
1729	FT431	*III*	*Hordeum vulgare*	Cultivar	Unknown	2	AM	ARG	-34,603723	-58,381593

1730	FT432	*III*	*Hordeum vulgare*	Cultivar	Winter	2	AM	ARG	-34,603723	-58,381593
1731	BCC892	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	BOL	-19,047778	-65,259722
1732	BCC801	*I*	*Hordeum vulgare*	Landrace	Spring	2	AM	CAN	5,411556	-75,698444
1733	BCC852	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	CAN	5,411556	-75,698444
1734	BCC881	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	CAN	5,411556	-75,698444
1735	BCC888	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	CAN	5,411556	-75,698444
1736	BCC903	*I*	*Hordeum vulgare*	Landrace	Spring	2	AM	CAN	5,411556	-75,698444
1737	BCC929	*I*	*Hordeum vulgare*	Landrace	Spring	2	AM	CAN	5,411556	-75,698444
1738	HOR3074	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	CAN	45,421530	-75,697193
1739	HOR3264	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	CAN	45,421530	-75,697193
1740	BCC899	*I*	*Hordeum vulgare*	Landrace	Spring	2	AM	CHL	-33,450000	-70,666667
1741	BCC844	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	COL	4,598889	-74,080833
1742	BCC921	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	COL	4,598889	-74,080833
1743	BCC806	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	MEX	19,419444	-99,145556
1744	BCC812	*I*	*Hordeum vulgare*	Landrace	Spring	2	AM	MEX	19,419444	-99,145556
1745	BCC857	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	MEX	19,419444	-99,145556
1746	BCC868	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	MEX	19,419444	-99,145556
1747	BCC869	*I*	*Hordeum vulgare*	Landrace	Spring	2	AM	MEX	19,419444	-99,145556
1748	BCC900	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	MEX	19,419444	-99,145556
1749	FT265	*missing*	*Hordeum vulgare*	Cultivar	Unknown	6	AM	MEX	19,432608	-99,133208
1750	BCC927	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	PER	-12,035000	-77,018611
1751	BCC807	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	URY	-34,866667	-56,166667
1752	BCC860	*I*	*Hordeum vulgare*	Landrace	Spring	2	AM	URY	-34,866667	-56,166667
1753	BCC861	*I*	*Hordeum vulgare*	Landrace	Spring	2	AM	URY	-34,866667	-56,166667
1754	BCC814	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	USA	38,895000	-77,036667
1755	BCC817	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	USA	38,895000	-77,036667
1756	BCC818	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	USA	38,895000	-77,036667
1757	BCC833	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366
1758	BCC846	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	USA	38,895000	-77,036667
1759	BCC847	*I*	*Hordeum vulgare*	Landrace	Spring	2	AM	USA	38,895000	-77,036667
1760	BCC851	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366
1761	BCC875	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	USA	38,895000	-77,036667
1762	BCC893	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	USA	38,895000	-77,036667
1763	BCC907	*I*	*Hordeum vulgare*	Landrace	Spring	2	AM	USA	38,895000	-77,036667
1764	BCC913	*I*	*Hordeum vulgare*	Landrace	Spring	2	AM	USA	38,895000	-77,036667
1765	BCC938	*missing*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	37,000000	-80,000000
1766	BCC942	*I*	*Hordeum vulgare*	Landrace	Spring	6	AM	USA	38,895000	-77,036667
1767	HOR10031	*I*	*Hordeum vulgare*	Landrace	Winter	6	AM	USA	38,895112	-77,036366
1768	HOR2469	*I*	*Hordeum vulgare*	Cultivar	Unknown	6	AM	USA	38,895112	-77,036366
1769	HOR2755	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366
1770	HOR2757	*I*	*Hordeum vulgare*	Cultivar	Spring	6	AM	USA	38,895112	-77,036366
1771	HOR29	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366
1772	HOR3093	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366
1773	HOR3108	*I*	*Hordeum vulgare*	Cultivar	Winter	2	AM	USA	38,895112	-77,036366
1774	HOR3125	*I*	*Hordeum vulgare*	Cultivar	Winter	2	AM	USA	38,895112	-77,036366
1775	HOR3131	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366
1776	HOR3136	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366
1777	HOR3150	*I*	*Hordeum vulgare*	Cultivar	Winter	2	AM	USA	38,895112	-77,036366
1778	HOR3152	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366
1779	HOR3155	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366
1780	HOR4114	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366

1781	HOR4609	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366
1782	HOR9522	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366
1783	HOR9525	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366
1784	HOR9526	*I*	*Hordeum vulgare*	Cultivar	Winter	6	AM	USA	38,895112	-77,036366
1785	FT422	*I*	*Hordeum vulgare*	Cultivar	Spring	2	AM	USA	38,895112	-77,036366
1786	FT424	*I*	*Hordeum vulgare*	Cultivar	Unknown	6	AM	USA	38,895112	-77,036366
1787	FT425	*I*	*Hordeum vulgare*	Cultivar	Unknown	6	AM	USA	38,895112	-77,036366
1788	FT727	*I*	*Hordeum vulgare*	Cultivar	Unknown	2	AM	USA	38,895112	-77,036366
1789	FT805	*I*	*Hordeum vulgare*	Cultivar	Spring	6	AM	USA	38,895112	-77,036366
1790	FT806	*I*	*Hordeum vulgare*	Cultivar	Spring	6	AM	USA	38,895112	-77,036366
1791	FT808	*I*	*Hordeum vulgare*	Cultivar	Spring	2	AM	USA	38,895112	-77,036366
1792	FT809	*I*	*Hordeum vulgare*	Cultivar	Spring	6	AM	USA	38,895112	-77,036366
1793	FT440	*I*	*Hordeum vulgare*	Cultivar	Spring	2	OC	AUS	-35,308235	149,124224
1794	FT441	*III*	*Hordeum vulgare*	Cultivar	Spring	2	OC	AUS	-35,308235	149,124224
1795	FT415	*I*	*Hordeum vulgare*	Landrace	Unknown	6	OC	AUS	-35,308235	149,124224
1796	Russia57	*II, rym11-b*	*Hordeum vulgare*	Cultivar	Winter	2	Unknown			
1797	HOR11139	*I*	*Hordeum vulgare*	Cultivar	Spring	2	Unknown			
1798	HOR11140	*I*	*Hordeum vulgare*	Cultivar	Spring	2	Unknown			
1799	HOR13406	*I*	*Hordeum vulgare*	Landrace	Spring	6	Unknown			
1800	HOR1662	*I*	*Hordeum vulgare*	Cultivar	Winter	6	Unknown			
1801	HOR1962	*I*	*Hordeum vulgare*	Landrace	Spring	6	Unknown			
1802	HOR26	*I*	*Hordeum vulgare*	Cultivar	Winter	6	Unknown			
1803	HOR2944	*I*	*Hordeum vulgare*	Cultivar	Spring	6	Unknown			
1804	HOR3205	*I*	*Hordeum vulgare*	Cultivar	Winter	6	Unknown			
1805	FT277	*I*	*Hordeum spontaneum*	Wild	Winter	2	Unknown			
1806	FT366	*I*	*Hordeum spontaneum*	Wild	Winter	2	Unknown			
1807	FT367	*I*	*Hordeum spontaneum*	Wild	Winter	2	Unknown			
1808	FT368	*I*	*Hordeum spontaneum*	Wild	Winter	2	Unknown			
1809	FT369	*I*	*Hordeum spontaneum*	Wild	Winter	2	Unknown			
1810	FT396	*V*	*Hordeum vulgare*	Cultivar	Unknown	6	Unknown			
1811	FT398	*I*	*Hordeum vulgare*	Landrace	Unknown	6	Unknown			
1812	FT407	*I*	*Hordeum vulgare*	Landrace	Unknown	2	Unknown			
1813	FT413	*I*	*Hordeum vulgare*	Landrace	Unknown	6	Unknown			
1814	FT680	*I*	*Hordeum spontaneum*	Wild	Winter	2	Unknown			
1815	FT685	*III*	*Hordeum vulgare*	Cultivar	Unknown		Unknown			
1816	FT721	*I*	*Hordeum vulgare*	Landrace	Unknown	2	Unknown			

Note: Africa (AF), Europe (EU), East Asia (EA), Central Asia (CA), Near East (NE), North and South America (AM), Oceania (OC)

Appendix Table 2 The primers used in this study

Order	Identifier	Forward	Reverse	Comments
rym7 works				
1	k09483	TCGCAGATCGCCTCTAAAAC	GACCGTACCTGACGAGCAAG	Polymorphic
2	k03235	TTTACACACGCCACCAACAT	CAAGGGTGGGTATAGCAGGA	Monomorphic
3	k01339	CAACCCAGCTACAGGGTGAT	CGTCATGTGCGTTCACCTAC	Monomorphic
4	k00690	CATGGACCGACAGATGACAC	AGTGCAGAGACGACACCAGA	No sequence
5	k08186	AAATCCTGCTCACCTCCTCC	TACAGGGGAAAATGGCAGAC	Monomorphic
6	k04911	CATCAGGGGAAGGTGAAAAA	CAAGGAGGTTGGTTTCCTGA	Polymorphic
7	k02167	ACTCCGGCATGTGACCTAAC	AGGGGAGTATGTCGCAGTTG	Monomorphic
8	k01042	ATCAACGGTTTACAGCAGGG	GCTGTGTGAGCGTCTACCAA	Monomorphic

9	k04311	AGGAACGCAGACAAGCATCT	ATGACTCCAAGAGCAAAGCG	Polymorphic
10	k04311-1	TTTGCAGCACGGGGGTAGATT	AGGAACGCAGACAAGCATCT	dCAPs marker
11	k03373	ACTAGAACAGGCAGGCCTCA	AATCAGGCTCAGGACAGGAA	Monomorphic
12	k08165	CTGGAGACCTCATCATGTGC	AGCGCATAGCCACTGTTCTT	Monomorphic
13	k09850	GCGAGTTGGTGAAAGTTGGT	ATCGTCTGGATGCAATTGGT	No PCR product
14	k07951	TCTTCCCCAAATCTGAGCAT	CAGAAGCCGCAGAAGAAGAA	Polymorphic
15	k06232	TCTTCCAGCAAATGTTCAGGT	TCGAGGAAGAAGATGGATGC	Polymorphic
16	k03631	CTGAACCCCACTGGATCTTG	GGTATTGGTTCCAAACACCG	Monomorphic
17	k08546	CTCATGGAGATTTGCCGTTT	GGCAGTGTTTCTTCGGTTGT	Polymorphic
18	k01492	GCTACATCCGAGGAGAGTGC	ACGAACAGTACCCGCAGAGT	Monomorphic
19	k02563	ATGCTACAAACGCCAGGTTC	GGAACATCTGTGGCTCCTTC	Polymorphic
20	k00782	TTTCTGTAATCCACCCAGCC	CTCGCCTTACCGTGGAGATA	Monomorphic
21	k06493	TGGAAACGAGCAACATGCTA	GGCCATTACCACCATTGTTC	Polymorphic
22	k05001	CCAATCTCCCCACCTTTTCT	AAGAAGGTCTTGCTTTCGCA	Polymorphic
23	k04899	CTTCGTACTCTGCCCTGGAG	CCTCGACTACGAACAGGAGC	Monomorphic
24	k00341	AGACAGAGCGGCAGATTCAT	GGATGCCTTTTTCCATGCTA	Monomorphic
25	k08483	CAGCTTCTTTTCTGCTGCCT	TGGATATGCATTTGCACGAG	Polymorphic
26	k02190	GATAGCAAACCGAAATCCCA	CCCTACCTCCTGTCGATGAG	Monomorphic
27	k02301	TCAGATTTGCTGTAGTGCCG	CACAACGTCACCAAGGACTG	Monomorphic
28	k02306	GTCCACAATCCCTCGAAAAA	CCATCCCCTCTGTAAGGTCA	Monomorphic
29	k06814	GGCTCCCAAGAAACATTACAA	TTGGAATACCGGAAGAGCAG	Polymorphic
30	k03070	CAATTCAGATAAGGCGGCAT	ATGAGCCGAAGCAGGAGTTA	Not specific
31	k07909	AAGAAAGCAACCTGCCACAT	CACAGTTTCTCTGCGAGGTG	Monomorphic
32	k04280	TGGGCTCATAGCAAAGAGGT	AGCAGAAGTCTCAAGCTGCC	Monomorphic
33	k00079	CCACAAGACCTTGCAACAGA	TGAAACAGCCACTGAGGTCTT	Monomorphic
34	k07676	CAACGGAAAGGGCAAAGATA	GAGCAAGGTGCTGGACATCT	Monomorphic
35	k03861	ACGATCGATCAAAAGGACCA	AATCCGACGAAATCAACGAG	Monomorphic
36	k07510	AGAGCAGCAGATACCGCTTG	CGACTCAGTTGAGAATGCCA	No sequence
37	k09911	TGTTTTTCCATGCAGGTTTG	ATCTGCCCACTGGAGATCAG	Polymorphic
38	k09911-1	AAATCGCTAGGAGCTCGGCGACT	TGATGACGCTAGTGGTCTACC	dCAPs marker
39	k08853	CGTTGTACCGAGCAGAGACA	ATGCTCGGAGTGCTTTGACT	Monomorphic
40	k00527	GAAGACCATGTAGGGGACGA	TGAAGGAAGGTGACGAGCTT	No PCR product
41	k01268	AACTTCGAACAAGCCTGGTG	CGAACTTCTATCCCTGTGTGC	Monomorphic
42	k05079	GACGGTCCACTCGATGTTTT	TCAAAAGTGGTAGCTGCACG	Monomorphic
43	k03009	CTGAGCACGCAACACCTTTA	CGTCGAGACTGCAGGTGATA	Monomorphic
44	k02023	TTACAAGAATGCAACGCGAC	GTGCAACCATGTTTGGATCA	Polymorphic
45	k09761	ACGGCATGCATTAAACAACA	GCTGAAGCTGTGGTATGGGT	Polymorphic
46	k01527	CATCCAGCACAAAACACTGG	TTCCTGGTGGAGGTCAAGTC	Polymorphic
47	k08348	AATAGGGGATACAGGGGCAC	GTCATGTTCGGCATGTGTTC	Polymorphic
48	k02939	GCGCCATGTAGACAAGGATT	GAAGATGGTGTCCAAGGTGC	Monomorphic
49	k06372	TTGCAACTCATGACCAGAGC	GAAAGTGCTCCAACGGAAAG	Polymorphic
50	k08045	TCTCCACTCCCCAGTACCAG	CACTGATATCTCCGGATGCC	Polymorphic
51	k02456	GTGACAACAGATGTCGGTGC	ACCTCTGCCTCCAGTTGATG	No PCR product
52	k05374	AGCCTGTCTTTGTGGCTGAT	CAAATTGGCCGCTCAGTTAT	Polymorphic
53	k04452	CACATTGTACAACGCCAAGG	AGCACCTCCTCCAGTCATTG	Polymorphic
54	k04669	AATGCAAGGCACAAGTGATG	TACAGGGGTTGCAACTAGCC	Monomorphic
55	k06478	CCAATGCTCATTCGTCAAGA	GCGATGGAAGTCCAAGCTAC	Polymorphic
56	k03269	TGGGGGTGATTAATGGCTAA	CTCAGATTCTGCTGAACCCC	Polymorphic
57	k00727	CTGTTTTAGCTCTGCCAGCC	AGAAGAGGAAAACGGAAGGG	Polymorphic

58	GBS0060	TGTCGGTATACACAATTCGCC	TGGGCATGCAGGAGTTCTT	Monomorphic
59	GBS0079	TTATTCCGAATACAAGCCGTTC	CCCGTCTTCGAGGAGTTGTT	Polymorphic
60	GBS0103	GAGGATGATGGGGCTGACTA	TCCTTCGTTCAGAATTTGGG	Polymorphic
61	GBS0125	TTGTCGATCCCGTCGCTTAT	TCTTCTCATGGACACTTCCGA	Polymorphic
62	GBS0131	AAGATACTCCACACCGACCG	GGGTGGGGAACTTTGATCTC	Monomorphic
63	GBS0237	ACTGCATACCCTTCTGCTGTTG	CCAATAACTCAGAGGCAAGCC	Polymorphic
64	GBS0267	TTGCCTTCCAGTGTACCAGCA	CCAGTGCCCAGACGTTGATT	Monomorphic
65	GBS0306	CCGTGAAGAAGACCTCCCG	GGGTCCGTTGTACGGCTG	Monomorphic
66	GBS0342	CATCTAGCAGCATCCATGGG	ACCAGTTTGCCACCCGTC	No sequence
67	GBS0361	AGCAGCATCCTCAGTGCCAA	GCGACACGACCCTGAACG	No sequence
68	GBS0371	AGTGCCAATCCGGTTACACG	GGATGCCCTCAAGCACCTTC	Polymorphic
69	GBS0383	CGGCTTGACCACTCCAAATC	CAGGGTTAAGGCCCAAGCA	Polymorphic
70	GBS0403	CCCTCCGTTTCAAAATAAGTGTC	TCTCCTGGTTGAACGCTACAGA	Polymorphic
71	GBS0450	AACTGCAAACTCTCGCCACA	TCTGTCCAACAACCAGCCTTC	Monomorphic
72	GBS0455	TTTCCAAACTTCTGACAACATTCA	CCTGTCGTCGAAGGGAAAGG	No PCR product
73	GBS0469	AGGAACCAAGATTTCATAGCGG	CCATGGACATCCCGCCTC	Polymorphic
74	GBS0507	CAAGTTTGGGCCGGTCATAC	TTGCAGCCACACCAAATAGC	Polymorphic
75	GBS0528	AGGCACAGCACCAGAACACA	CGCAAGTACCAGAAGAGCACC	Polymorphic
76	GBS0546	AACTCTCGTGTCAATGCCGA	CAACGTATTGCAAGGTCGCA	Polymorphic
77	GBS0554	ATGGAGCCCCTCCCAACTAC	GTAGACGTCCAGCACCTCGAT	Monomorphic
78	GBS0582	CTGGAGAAACCAGCCTATGGA	CCAGGCAATGCTCATGAATG	Polymorphic
79	GBS0626	CCAACTCTGGTGTCAATGGCT	GCAGTTGCCATGTGTTGCAG	Polymorphic
80	GBS0687	ACCCACATCAAGCGCTAACAA	TGCATGTTATCTGCACTGAAGG	Polymorphic
81	GBS0738	CATGGGAATGGGATCGTACC	CCACGAACTTGGACAGCCA	Polymorphic
82	GBS0765	GGCCCTTGCATATATCCATCG	TCATGCACCTGATTTCTTCCC	Polymorphic
83	GBS0821	TCGCACCATTGACCTTTCTG	CGGTTCCGCTTAACAGCAC	Polymorphic
84	GBS0853	GCCCCCTTGATGATAAGTACG	TGCTCTGATTGGGTGTGCAT	Polymorphic
85	GBM1007	GTTCCGGTTTCTTTCGGTC	GTTAGCTATGGTGCGGTGTG	Polymorphic
86	GBM1029	AGAACCAACAAGCCCTTCCT	AGAAGACGCGATCCTCTTGA	Polymorphic
87	GBM1032	GGATGACATGGCTTTGCTTT	TCGTAGGCGTTCTTGGTTTT	Polymorphic
88	GBM1042	CACACAAGATCTCTCACGGC	TCCCTGACCAAACCAAGTTC	Polymorphic
89	TC134653	GAATCTACGGGCAACTTGGA	TACCAAATCGACTTCCTGGC	Polymorphic
90	Bmac32	CCATCAAAGTCCGGCTAG	GTCGGGCCTCATACTGAC	Polymorphic
91	Bmag347	CTGGGATTGGATCACTCTAA	AAAACAAGTACTGAAAATAGGAGA	Polymorphic
92	GMS21	CTATCACACGACGCAACATG	CCTGAGAAAGAAAGCGCAAC	Polymorphic
93	1H_0938	ACCACAGCATGTGTGCTCTC	TCAACTTTGTCCCAGTGTTCAG	Monomorphic
94	1H_0940	TCGGTCTTCTTCCTGCTCTC	TCAACTTCAGCACCTTCCTC	No PCR product
95	1H_0941	CCGAATGCCAGCATTTCTAT	ACGCATGCGACACTCATTTA	Monomorphic
96	1H_0942	GAACGGAGGGAGCAGTAGATT	ATCAGCCGTGGTGATCTTGT	Polymorphic
97	1H_0943	CATCCTCATCCACGGGTACT	TTGGATTCATACCAGCCACA	Monomorphic
98	1H_0944	CGTCGGTTCTGGGCTATTAC	CATCACCATTTGTGTCCACCT	Un-determined
99	1H_0946	CCGGTCAGATAGGAAGAACC	ATTGACGACGAAACCAGAGG	Un-determined
100	1H_0947	GTGGTGATCGCAGGTCTCTT	GGAGGAGCCAACGATAGTGA	Un-determined
101	1H_0948	AAGTGCTGGGAGACAGTGGT	GTGACTCCTTGCACCTTGCT	Un-determined
102	1H_0949	ATGCATGGTGAAGCACTGAA	TGCTGCTGCTATTACGTCCT	No PCR product
103	1H_0952	TGGCAAACATTTGGACACTG	GGTCGAAGTCTTGGGAACTG	No PCR product
104	1H_0954	AAGAGCTCCAGGCTTCCAAC	GGATTGCTGTGTGCTATGGA	Monomorphic
105	1H_0955	ATGTGATGATCGGCATTCTG	TCCTATGCCAAGATCAAACC	Monomorphic
106	1H_0956	TCTTCTATGGGCCTGCCTAA	GATTTATGGCATCGCTCCTC	Monomorphic

107	1H_0957	CTCGCCCTTGTTTGCTAAAG	ATGGAGGGATGTCAACCAGA	Monomorphic
108	1H_0958	GGTGTTTCATGGTCTCATGTGT	AAACTCGGGAGTGCCTTGTA	Monomorphic
109	1H_0959	TCTGAGCTCGGCTACCTTGT	TGAGAGGGACATTGGGACAT	Monomorphic
110	1H_0961	ATTGGAGGCATGTTTCAAGG	TTTGTTCTCGTTGCGCGTAT	Un-determined
111	1H_0964	CCATTCTTTGGCTTTGGTTC	AGATTGGAGACAGGCTGTGG	Un-determined
112	1H_0967	CGAATGGGTGAAGCAACATA	TGTCAAGAGCCTCTGCTTCA	No PCR product
113	1H_0968	TGGCAGATTTGTGTCGGAAA	TATTGCGGGAAGAGTGATCC	No PCR product
114	1H_0970	TCCTTCTGGTAACGCTCCTC	GAGTTCTTCCAGCGCGATAA	Un-determined
115	1H_0971	CAAACAGGGAGCTTTCTGGA	TCCTTCCAGTGCTTCCCTTC	Monomorphic
116	1H_0972	ACCTCCAGAACGACATGGTG	TATCTTGGACATCGCCTCCT	Un-determined
117	1H_0973	AAGCAAAGAGCTCCCAACAA	AGCTGTTCCTTCCCATACCC	Monomorphic
118	1H_0977	GTCTAGCAAGTGGCGAAAGG	AGCCGCATGGTAGGTGTACT	Monomorphic
119	1H_0979	TATGAAGCACTCCACGTTGC	GCCTGGATTCAACCAACTCT	No PCR product
120	1H_0982	GCATGAGGTAGCGTTGGATT	GCAGGTTTCTCCCATTCTGA	No PCR product
121	1H_0983	TTTCCCGTTTCTCTGCTGAT	TTGCAACGGTTAACGAACAG	Monomorphic
122	1H_0984	TCCACGAAGAACGACCAGAT	GATGATCCTAGTGCCCTCGT	Un-determined
123	1H_0985	ACCTCTTCTGCAAGCCTCCT	ACATGGGTGTCAATGTGCAG	Monomorphic
124	1H_0986	CAAGCAATCCAAGGCTTCTC	CTCCGCCTACCAATTTACCC	Monomorphic
125	1H_0987	CCTAGGCATGTCACAGTGGA	CTGGGAAATGGAATCAAGGA	Monomorphic
126	1H_0988	CCAGAAATAACTCGGCAACA	GCAGGTTCAGGAACCAGACT	Monomorphic
127	1H_0989	GCAATATTTGTCGCCAGAAC	TGTCCGGGAAGGAACTACTG	Monomorphic
128	1H_0990	GCTTGGAGCAGTTGCTTCTT	TGACAGCATCTGCTTCTTCCT	Monomorphic
129	1H_0991	CGCTCTCCTCCATGATTTGT	GACAACCGACCAACCAACAG	No PCR product
130	1H_0993	GCAGATGTGGGTAGCTGCTT	GACCTGATTGAGAAGGCGATA	Polymorphic
131	1H_0995	TATGCAGCCTAGGGTTGCTC	TTTGGTCCATAGGCAGTGAA	Monomorphic
132	1H_0996	GATCACGATGTGGAAGACGA	GATTAATCGTGCCATTGCTG	No PCR product
133	1H_0997	ACGAGCATGGGAAGGGTGAT	TGAGGAACCTCATGGAGTCG	Un-determined
134	1H_0998	GATCCTCGACCTCTCCAACA	AAGAGGCCGGTGAAGCTATT	Un-determined
135	1H_0999	GAGTTATCGCAATATGCTCTCC	GTGATGCACCTTTGAGCAGA	Un-determined
136	1H_1001	ACTGCCTATGCTTGGGATTG	CCTCGAAGTCGGTACCATGT	Un-determined
137	1H_1002	TTGCAAGCAGTAATGGAGGA	ACCGGAACATCGTCAAGCTC	Monomorphic
138	1H_1003	TGTAACCGTGCAAGTTCCAT	TCCCTTGCTTGCCTTGTATT	Monomorphic
139	1H_1004	CATTTACGACCATTGGCACA	GGGACTCCAAACAACCTTTG	No PCR product
140	1H_1005	AGCTCGAATAGACACGGTTCA	CCGGAAATGAATAAGGACCA	Un-determined
141	1H_1006	CCACCATTGCTTACGACCTT	CTCTACGTTCGCTCCGTCAT	Monomorphic
142	1H_1006_n1	TGATGGCTTATGAGAAGGGC	CTCTACGTTCGCTCCGTCAT	Polymorphic
143	1H_1007	TTCGGATTTACAAGGCGATG	GTTGGTCAGACCGGACGTTT	Polymorphic
144	1H_1009	GGATTATGGTTGCACAACTG	GCACATGGAGAAGACATGGTT	Un-determined
145	1H_1010	TAGGGAGATTTGGCGACATT	AGAAGCAACGCAAGACGAAT	Monomorphic
146	1H_1013	AGGTGTGAGCATTGCTTGTG	TGTCAATGGAAGAGGAAAGG	Polymorphic
147	1H_1016	AGCTAACGGAGTAGGGCAAA	AGAGAAGGGTGGGTTGGTGT	Un-determined
148	1H_1020	TGAAATTGTCTGCCGTTCAG	CGGAGACGATGTAGGTGGAA	Monomorphic
149	1H_1021	CCTCCAGATTCACGCTCTTC	GATTGATTGATCCCGATGCT	Un-determined
150	1H_1024	CATAGTACTCCCTCCGTACCAAA	GTTTGCCACCCTTCAATGAT	Monomorphic
151	1H_1025	CCTTCTTCCCGACCTCATTC	CCTCATCATCCTCCGGAATAC	Un-determined
152	1H_1026	CAGGTGCTGTTGCAGACATT	AAGCCCAAGTATACCCACACA	Monomorphic
153	1H_1027	GACACGAAAGCGGGTTAGAA	GGTTTCGACATGGCTTCTCC	Un-determined
154	1H_1028	AGAAGGGCCTAACAGGCAAC	CATTTGGACACCAGGGAAAG	Monomorphic
155	1H_1029	ACGACATCCTGCTTCTCCAC	ACGCATCGTCTCCATGAACT	Un-determined

156	1H_1030	AGTCCATGAGTCTGGCGTCT	CATGCAGAGGCTGTACGAGA	No PCR product
157	1H_1031	TGGTGAAGCAACTGAAGGAG	CGGAGGGAGTAATATAGATGG	Monomorphic
158	1H_1035	TTTGTTCCATCCGTGTTGGT	CCACTTCGTCATCTTCCACA	Monomorphic
159	1H_1036	CCATGAGTGCGAATACACGA	TGCATATTAGCTCACACACCTG	Monomorphic
160	1H_1038	GAGGGAAGCAGGGATGAAAC	CGGCTTTGTGGTCCAATATG	Monomorphic
161	1H_1039	TCGCACATGAGCTATTGACC	GTGCAATGCGTGAGGTACAG	Un-determined
162	1H_1041	GAAACGGCCGATAACCTCTT	AGCCTTCTCATGAAGGTTGG	Monomorphic
163	1H_1043	TTCAACTGGAGACAGAGAACCA	AGGCAAACATAGCCATCACTC	Monomorphic
164	1H_1045	GCTTCCACCGTGTTCTTAAA	CGTCAAGAACTTCCCGAGAG	Monomorphic
165	1H_1047	CCACGACAAACACCAACATC	TTTGCGACATCTTCAGTTGG	Monomorphic
166	1H_1048	GAAAGTCAAGCGCCAAATGT	CGGTTAAAGCTGGCACTCAT	Monomorphic
167	1H_1049	GCTTTGGTACCATGGCTTCT	CAAGGGCTACATGTTTGGTG	No PCR product
168	1H_1051	CGTCTCCGTGAGATCCTTCT	AGAACCAGGTTGGCATTGAT	Polymorphic
169	1H_1052	AAACGCACCACAACAGATCA	AGAGGGATGTGCAATTCTGA	No PCR product
170	1H_1053	GTAGCTGTTGGACACGGTGA	TCATCATCCACAACCTGCAC	Un-determined
171	1H_1054	AAGAAACGGACGGAGGGAAG	GGCCCTTGTGCTATTCAATTC	Un-determined
172	1H_1055	CAAGCCTTTGCCATGAAGAC	CCCTGAGTGCTCCACTTTCT	Monomorphic
173	1H_1056	CGCTCAACTTGTGATATGACCT	GCCTAGCATTCATCAGTCGAA	Monomorphic
174	1H_1057	GATGGGTGACACTGGTGATG	ACATGTGTGGCATCGTCTTC	Monomorphic
175	1H_1058	TGAAGCTGCTAGTGCTTGCT	TTTGGTGTGCATCAGTGCAT	Monomorphic
176	1H_1060	CATGAAGACGAGCCTCCAAC	AGCAAGACAGATGCAGAGGA	Monomorphic
177	1H_1062	CGCTTGATGGAGATTGTGTC	TGAGCTCCTAGTTTCAGCATACC	Monomorphic
178	1H_1064	CAAACTGCCACAAAGAAAGC	GCAAATAACATGCTTGGTAGCC	Monomorphic
179	1H_1065	AAACTCTGAACCGTAGCGTAGC	GATCTGGAAGTCCGAATCGT	Polymorphic, Not linked to rym7
180	1H_1066	AGTACCGTGGATCCGGAAGT	CATCGTAATTTCCGGCTTGT	No PCR product
181	1H_1068	GCTCTTCCGATCTGGTTCTG	CCATCATAAGGCCCATATCC	No PCR product
182	1H_1070	TGATGCTGAGGATGACAAGC	TCGAGGAAGTGGGCTAGAAA	Monomorphic
183	1H_1071	AATGGGAGAGTCCGAACACA	TTGGGAGACTGCACTACTGTTC	Monomorphic
184	1H_1074	TTCCGATCTATTGGCACCAC	ACGCTCTTCCGATCTCTTTG	No PCR product
185	1H_1075	GAGAATTAACGGGAGCCACA	CGTATTTGTCGATCCAGGAAG	Un-determined
186	1H_1079	GTCAAGGTCGTAGCCGATGT	CAGAGTTTCAGCTGGGCTTC	Polymorphic
187	1H_1081	GTTTGTGAGTTCACCCTTGA	CGTAACATTGTTGCCACGAC	Monomorphic
188	1H_1084	ACCAGTGAAATCCCTTGTGC	TAACAGTGCGGACATTCCAA	Monomorphic
189	1H_1085	CCACAAGTCTGTTCTTGGGATT	TCGTCGTCAGAGTCTAGTCACC	Monomorphic
190	1H_1087	GACGCACAGGGTATCGTCTA	CCCAACATTTCATTCGAGGT	Monomorphic
191	1H_1089	TCACAGTAGAAGCTGGTGATGG	TTTCGGATCTCATGACGTTG	No PCR product
192	1H_1091	GATAAGTGTTTCCGGTCGAAAG	TTGACGAATGCAGAGAAGGA	No PCR product
193	1H_1095	AAACAAATCGACAGCGTGGT	TGTCGCAAACAGCTTCTGTC	Monomorphic
194	1H_1096	CAACTCACCAGAAAGCAGCA	GTCCCTCTTATCGGCCATCT	Monomorphic
195	1H_1097	GGCTAATTCCTCAGCAATCC	GACGTGTGCATCGAGAGGTA	Monomorphic
196	1H_1098	GGCTCACCACTGAAGCCTTA	CCATGTCCAGATCGAGGATT	Monomorphic
197	1H_1099	CGATTTCTACTTCCGCCTCA	AAACGAGTCCGTGGACCTTC	Polymorphic
198	1H_1100	GAGACGTCCCAGTCGAAGAA	TCAGCTCACGTCCACTCCAA	Monomorphic
199	1H_1102	TCTTTCAAACGCACGCACTA	GAGACATGCTAGCAAATGATGC	No PCR product
200	1H_1103	CGGGTGAATACAGGAACTAA	AAGTAGGCTAACACTGGAAGTGC	Un-determined
201	1H_1104	GCCGTGTTAGTGTCTATTCAACC	TGCACAGTAGAGGCATCAGG	Un-determined
202	1H_1109	TGTAAGCCATGCTCAGTTGC	ATGAGCACCTGCAGAGCAAA	Monomorphic
203	1H_1112	GACATGCTGGCAGAAACAAA	GCTTTCGAGAAATCGAGGTG	Polymorphic
204	1H_1115	TGTCTTCCCATACTTGTTGC	GAGAATGCAACATCAGAAGG	No PCR product

205	1H_1116	TTACCTGCAGCGTCTTTGTG	CGGGTGTTATCTTCCTGCAT	Polymorphic
206	1H_1117	CGACGTGCATGTGGATTAAC	TGGCATAGATCAGCAACCAA	No PCR product
207	1H_1118	AGGGCCACTTATGTTTCTGG	CGAGAATTGCATGCTGAGAA	Monomorphic
208	1H_1119	GCTTTGTGGGCACACTGAAA	CAATGCCTTGCGCTGTAACT	Monomorphic
209	1H_1122	GGGCACATTCTTCCTCCTTT	ACAAGAGCAGGTGAGTGCAT	Monomorphic
210	1H_1127	CCAACAGGAGCAAATTGTGA	GACACAGGCCAGCTTTCTTC	Monomorphic
211	1H_1130	GTCATCGCAACAACAACCAG	CTCATGGAGATTTGCCGTTT	Un-determined
212	1H_1131	GGAGCCAAGCTAATGAGAGC	GCAAACATCTCTCACAGAATGC	No PCR product
213	1H_1132	GGCTAGGCTAACACCTGCAA	GCTGCATGCATCTCTTGAAT	No PCR product
214	1H_1133	GACTAAGTGTGCACCGCACTA	GTGGTCATCGCAACGAAGTT	No PCR product
215	1H_1135	CCGACGTTGGACTTGAAGTAG	CACACAAGCAGCACACACAC	Monomorphic
216	1H_1136	CGTGAAAGCTACCAGGACCA	GCATGGATGAGATCATTAGGG	Un-determined
217	1H_1137	GTAAGCAGTGTGGCAACAGG	GTGCCATTTCGATCGTCACT	Un-determined
218	1H_1138	CGCCATCTTTGGAGGATTAG	CCGCGTAGAACAACAAACAA	Un-determined
219	1H_1143	GAGAGGGAGGACAGTTTCCA	CCAAACCCTAACCCTACCAC	No PCR product
220	eIF4E-iso-1-803	CTTCCTTTCCCTTCGGCGGCT	TCAACGTGAGCATGACAAGTT	Monomorphic, 802 bp
221	eIF4E-iso-749-1352	TCAACAGTCCCGTGGTACTTC	CCAAACCATCGCAACATATC	Polymorphic, 602 bp
222	eIF4E-iso-1331-1989	CCCAAACCATCGCAACATAT	GGACTAAGACTGCCAGTAATG	Monomorphic, 657 bp
223	eIF4E-iso-1922-2707	TGGTGTTGTCTCTAGTGTCC	GTTACTGTCCATCCTCTATGC	Monomorphic, 785 bp
224	eIF4E-iso-2604-3138	GGCTAATCTTTGTGGTGCTGC	TGGAAGGAGGTTATTGACTAC	Monomorphic, 515 bp
225	eIF4E-iso-3105-3512	GACATTGGCAAGAAATGGAAG	CACCTCATGTGGGAAGTTTGA	Monomorphic, 430 bp
rym11 works				
226	P5-1-1	AGATGTGTGTCTCAGGTCTCCAT	GGCCCTACCTATCACAACACTAA	987 bp
227	P5-1-2	CCGTAGACATCCAGGTGTTCTT	TACGGCTGCATGGATGTAGTTTA	905 bp
228	P5-1-3	CTTGATGACTGAAGCATACAGGA	GATCGGAGGGAGTAGGGATTATT	999 bp
229	P5-1-4	CTACGCATAGAACCTGTCTCTGA	GTGTATCCATATTCCGCTATTGGT	1019 bp
230	P5-1-5	TTCCTTGTCCAACAACTACTCCT	AGCTCAAGATGTCTTCTCAGGAT	928 bp
231	P5-1-6	CGTCACTTTATATTGCTCCTGTG	GCCTCCATCCTTGATTGAACT	1075 bp
232	P5-2-7	AGATAACCTTTCCCACTTGGTGT	GATTAGGAATCTCGAGGGAGAGA	987 bp
233	P5-2-8	ACTTCTTGAACTTGTCCGAAACC	AACAAGGAAAGTTAAGCGAGTGG	992 bp
234	P5-2-9	GAATCCATGTGTGTCCATTACAG	ACTCTTGTGCGATGACTTCTAGG	995 bp
235	P5-2-10	CTTCTTCTCTGGCTATGAAGTGC	AGAAGGAAACAGAGGAAGAGAGG	971 bp
236	P5-2-11	CAACAACTTCGTGATTTGATCC	GAAAGGTCCAATTTAACGAGGAG	957 bp
237	P5-2-12	GCTATACCCTCTCCAATGTCCTT	CCCACCGTAGAGTTAATGATTTG	978 bp
238	P5-2-13	CAACTTGAAATCCATGGGTAGAC	CTCATCACGCCATTAACCTGTAT	998 bp
239	P5-2-14	TAGTAGTTGAGTTCTCCGGCAGT	TGACATGGATCGAGACTAGGATT	1008 bp
240	P5-2-15	CCTAACCATGCTCCCAAATACAT	CATAGCAAGCACGACATTCATAG	976 bp
241	P5-2-16	GGAGAGGATCATCAATAATGTGG	GATGTTGAAAGTGGGAAGTTGAG	1006 bp
242	P5-2-17	GTCACATTTCTTGTAGCCCTGTT	CAATTCCAAGCAAAGTGTGGTAG	956 bp
243	P5-2-18	GTTGGGTGCAAGTTCGTTATTT	CCCAACGAGAGCATCATAAAG	1091 bp
244	P5-3-19	AGTGTTCCGGTTCCTCTAGTTGT	ATAGCCAGAATGCCACTATGAGA	1008 bp
245	P5-3-20	TCAACCATACGAACTTCTCCTGT	AGGATTGGTTAGAGTTGGCCTTA	965 bp
246	P5-3-21	CTTGCCAAGTTTCACCTCAATAC	CCTCGTCAAGAACGTGATCTATT	1015 bp
247	P5-3-22	ATGGTGTCCGTACTTTCGCTAC	TAGCTTGTCGTGGTACCTAATGG	1019 bp
248	P5-3-23	TTCAGCATGGTGGTGCTATTAT	TATCCCTCACAGGTGGTATGTTT	1000 bp
249	P5-3-24	TCCACTTCTTCTGAGTAGCCAAT	GCATGCACTGTATCTGTACCTGA	994 bp
250	P5-3-25	GCACAATAAATCAAACCACCAC	GGGAGTATCGATGATGTTCTTATTG	829 bp
251	P5-3-26	CATCACTATTGCGCCTCTTCTAT	CTCAGCCTGACTGAACAGAGACT	1000 bp
252	P5-3-27	ATTGCTCCTCCCTCATCTAAGTC	AGTAGGCCGTAGTAAAGGGTTTG	1006 bp

253	P5-4-28	GCCTGACTGAACAGAGACTTGAT	CATCACTATTGCGCCTCTTCTAT	998 bp
254	P5-4-29	CCTCCATAGATAGGTCACCCTTT	AGGGAGGGACGGCTTATATAGTT	1003 bp
255	P5-4-30	AGTGCAAGTCTTGGATTAGCAAC	TCACCTTACTTGAATAGGCTGGA	1000 bp
256	P5-4-31	TCCTCGATCGGAGTAAGAACC	TTTCACGGTGGCATTCTTCTT	1080 bp
257	P5-4-32	ATGATTCGTCATCAGAGTTGACC	GTGATGTGATGCCTTGTGATG	948 bp
258	P5-4-33	ACTTTCGACCAGTAACCCACAA	GAGTCCTTGACGACACACTGATA	1015 bp
259	P5-5-34	GATACAAAGAACATCGTGGTTGAC	AATCTGCGTATCTTCCCACAGTA	987 bp
260	P5-5-35	GTGGAGCGTAAGGAAGTAGGAAT	CAGAGGACGGATGACAATTACTC	996 bp
261	P5-5-36	GCTGCTGGAGGATCTTAAAGAAA	CACGTCAGACACGACTCTTCTGT	1101 bp
262	P5-5-37	AAGTCAACACCAAACCAGCAAT	TGTATGGCTACACACGGAATG	1001 bp
263	P5-5-38	TTAGCCCTAAGAATTCCGCTACT	ACACAAGATCCCGTGGCTTAC	1097 bp
264	P5-5-39	CCCTAATACATCGACTGCTTCAC	GACAATCGTACAGGAAAGGCTTA	999 bp
265	P5-5-40	CCTGTTGAGTCCCTCTATTCCTC	CTAACAACAACTAGCGTGGAAGC	1073 bp
266	P5-5-41	CCGGATCTGAGATAGGAGGTA	CCACAAGATCCAATCTAGAGCAT	972 bp
267	P5-5-42	GGGTTATTCTCAAGATGGGTGTT	ACCCAACAAGCCTATCAGGTAAT	1014 bp
268	P5-5-43	GGCTACCTCCTCTCTTGTATGG	GTGACTCCTATTGGTACTTGTAAGG	1014 bp
269	P5-5-44	CCGGACAGAGAATTGACGTATTA	TCCTGTGCTTCTCTGAGTTGTTT	1074 bp
270	P5-5-45	GCCCAAGCTATAAGTGTTATCGT	TTTCTGAAATAGAGAGCTAGTCAGG	1110 bp
271	P5-5-46	GCGATCCGATATACGGTTTAGA	GATTATTAGTCGGACGTTTGTCG	1009 bp
272	P5-9-47	AGGCAACTTCTCCTTGTTTGA	CTTTCACAACTGTTTAGTGGTTCC	1019 bp
273	P5-9-48	GCTATCCCACCATCCAACTAAG	CTCGGCTTGTTGGAAATATGC	1157 bp
274	P5-9-49	ATCGTCAGTCAGATCGAGGAGTA	GATAGAGGGCAAGAAGCACTACA	958 bp
275	P5-9-50	ATAATCCTCCCAATCCAAGAGAG	GTGGTACACCAGCCCTTAGTTG	1027 bp
276	P5-9-51	GCTATTCTTGGTGTTGTTTCTCG	CCATGATAGCAACAATCCATAGG	1036 bp
277	P5-9-52	CTTGTGTGACTTCTGTGCTTCAC	CGAGGATATATAGGCGGAAGAAG	1042 bp
278	P5-10-53	ACGATTCACCGTACTCGATACAC	GAACTCTGGACAATCCTTCTGG	990 bp
279	P5-10-54	CAAACACCTAGAAGTGCAAGGAC	CCGGGTAAGACATGGTAGGTT	1021 bp
280	P5-10-55	CTTGGCGTAGATTTGCTTGATA	CCAAAGCAAGCTATCACTACCAT	894 bp
281	P5-10-56	AATACTGGGTGTCTCCTCCTCAT	CAAGGAGATGAGCTTGGTATGAT	967 bp
282	P5-10-57	GGTGAAACCCTAAGGCAACTAAT	GAGTACAATCAATGGATCCCTACAA	1020 bp
283	P5-10-58	CCTCGTCCAGTCTAATAGGTATCTC	CCACTCATTCTAGCTCCCATCT	1110 bp
284	P5-11-59	GTCTCGATCCTGGCAGACTCTAT	AGAAGGGAGGTTAGAAATCATCG	974 bp
285	P5-11-60	TCTTCATCACTTTCGAGTGTGTC	GATTTGGTGTAAGCAGGAGTGAG	1004 bp
286	P5-11-61	GTATTGTTTCTAAGGCCGAGGAC	GAAGCTATCTGCGCTATTGTCAT	998 bp
287	P5-11-62	AGCCAGCATAAGCTCATCTACAC	CTTGCCCTTCTATCTATCACTGC	990 bp
288	P5-11-63	GGAATTTATAGGCGGAAGAGGTA	CACATGGTGTTCAATAGTGATGTC	1008 bp
289	P5-11-64	AAGATACATGGAGGAGGAGGAGA	ACTTATCGGTGGCATGATAGGTA	996 bp
290	P5-11-65	GAAGAATGAAGATGGTGTGAACC	AACAGACTGAAGAACGAATGGAC	1003 bp
291	P5-11-66	CCATTCTTCCTCCTCCTTATCTC	GCCATTCTGTCAACTGACTAACA	996 bp
292	P5-11-67	TGCGTAGACCACCATAACCTATT	GTGTTCATTCCTCACTTCCTCTG	1019 bp
293	P5-11-68	CCAACGCTTGTCCTGATAAATAG	GTCAGCCGATAACATTCTGAGG	1014 bp
294	P2-22-69	GGGTCAATATGGAAGGAGGAC	GGCAAATACATTTAAGGCACGA	989 bp
295	P2-22-70	GGAAGCAGTTGCAGACACAAT	ACATTGCCAACCTTGCTTAGA	1001 bp
296	P2-22-71	GATGCATAATCAACCCGAGTG	AGTGACTTGGACCTTGTGGTG	1001 bp
297	P2-22-72	GTACATTGGCCGAAGTTGAAG	CAAATCATACGGTCCCATGAC	999 bp
298	P2-22-73	CCTATTAATTGTGGGCTGCAA	CACACTACATATGGCGGCAGT	988 bp
299	P2-22-76	ACACCAAGTGGGATGGTGAC	CGCGATTGATAGGACTTTGG	872 bp
300	P2-22-77	GAGCGTAGTTGGCTTGACTTG	AATGAGTATGCCATCCGTGAG	996 bp
301	P2-22-78	TACCGATGCAACTCTGGTTTC	CACAGGTGTTATCTGCGGAGT	999 bp

302	P2-22-79	TCAACGCCTTGTACGACTTCT	TTTCATGCCTCGGTAATATGC	997 bp
303	P2-22-80	TACAAGAGAACGGCGGATATG	GGTCTTCACATACCCGAGTGA	998 bp
304	P2-22-81	ACTCAGCCTTGATTCGGAAAT	GAACGACTCCGACAACAGAAA	993 bp
305	P2-23-82	CAGTAGTTGGTGAGCGGACTT	GCCTCGAGCCTTCTTCTTATC	605 bp
306	P2-23-83	CGCGATGGTTATTTCCTACAA	GAATGAATGCCTCTCGCAGT	506 bp
307	P2-23-84	TCTGGAAACTTCCGTGTGAAC	GATCGGTAACTACCTCGGTGA	604 bp
308	P2-23-85	GTTGAGTGATGCCTTTGTGCT	GCTATGTGCTCCACATCCATT	607 bp
309	P2-23-86	CAGCTGGCTGACGTCTTAGAT	TCGGACAACCGTGAACTTATC	587 bp
310	P2-23-87	TGGGAATTTAGCAAAGGAAGTG	GTGATTACCACGTGCACAACC	608 bp
311	P2-23-88	CGCTAGACACATCGACATCAA	ACCATTCCGAACAGGAAGATT	599 bp
312	P2-23-89	GCCACACCTTGACGGTATCTA	TGGGAACCAACATCATAGCAT	601 bp
313	P2-23-90	AAATCATACGGTCCCATGACA	GGCAATCAGACTATGCAGCTT	609 bp
314	P2-23-91	GGAGTCATTCAAACCCTCCTC	GGCCCTATTTGATGATGTCCT	596 bp
315	P2-16-92	AACAGATGGCAGATCGTGATT	AACTATCTGGCCCATAACTCCA	801 bp
316	P2-16-93	ACGACCTCCTCTCTCTCAACC	TCACGTTGTGTTACGATCAGC	967 bp
317	P2-16-94	CACATCTCCCACTCTGCTCTC	CATCACGGATCATCAAATCCT	946 bp
318	P2-17-95	TACACCAACCGTGGAAAGGTA	GGACACCTCAACGAGGATACA	951 bp
319	P2-17-96	GCAACAATCACGAAGGACAAT	AGTTGGCTCATTGGTGACAAG	957 bp
320	P2-17-97	TGGGTGGAACTATTGGACTGA	AGCTCAACCGTGTGTCTCAAG	935 bp
321	P2-17-98	GATGAGGAGGTTGGCATCATA	AGAATAAGCCTCGGAAAGTGG	943 bp
322	P2-17-99	AATGACGGTAAAGGCATGTTG	TTCCTATGATGCGAGGTTGTC	952 bp
323	P2-17-100	TGGCCAATCTTTCATGTTAGG	CGTGTTAGTGGGCAAATCAGT	957 bp
324	P2-17-101	AAGTATGTCTGCCTCGCACAT	AACAAACCAGCAGGAGTGAGA	949 bp
325	P2-17-102	AAACAGAACACCTCACACGAAA	GAGGACGTCATGAGTTTGAGC	951 bp
326	P2-18-104	CAGCCTCTCAAGCATTAGCTG	CCCATTCTTTCCTGGATGTTT	949 bp
327	P2-18-106	TTGTAGACCACCCACGTCTTT	GTTCTTTCCTTCCTGGACCTG	951 bp
328	P2-18-107	ATGTGCGAGGCAGACATACTT	GTTGTGGGTGACTTGGTGTTC	951 bp
329	P2-18-108	GCAAGAAGCCACAACCTAACA	TCCATTTGGATGAAACTGAGG	943 bp
330	P2-18-109	TCATGGTATTGGGAACCTTCA	ACCAACGTGGAGCTAGTCAAA	939 bp
331	P2-18-110	CGTGAGAATTCCAGCACTAGC	CAGCCTTCAGAGAGGATCAAG	965 bp
332	P5-8/9-111	GGATTGCCATACAAGAGATGC	CGTATGGTGAACCGCTATGTT	897 bp
333	P5-8/9-112	CCCTCAATGACTTTGTGAAGC	GGATCCTCTGCAGCTTCTTCT	902 bp
334	P5-8/9-113	GGCCACTTGTACACAAGGAAA	CGACAGATGATACACGCGTAA	900 bp
335	P5-8/9-114	GGCAACACATTGATGGAGATC	GTTGAAGTCCCGGTTCTAAGC	898 bp
336	P5-8/9-115	AGAAGCTCGATGATGCACTGT	CTTACCACCGCTGTGCTACAT	899 bp
337	P5-8/9-116	AAGAGAGACATTGCACCGGTA	GTATCCATGGACGAGATTGCA	880 bp
338	C5B2C	GAATCCATGTGTGTCCATTACAG	ACTCTTGTGCGATGACTTCTAGG	Genetic markers
339	C5B3C	TTCAGCATGGTGGTGCTATTAT	TATCCCTCACAGGTGGTATGTTT	Genetic markers
340	C5B4C	AGTGCAAGTCTTGGATTAGCAAC	TCACCTTACTTGAATAGGCTGGA	Genetic markers
341	C5B6D3	GTATCCGCCTTCTCCTCGTC	CGGTCAAAACTCGCATTGTA	Genetic markers
342	C5B6D4	TTCCACTTACGGAAGGTTCG	AACAGCGTGGTTTTGGTTTC	Genetic markers
343	C5B6coD1	GGAGCTCCTACATGCTGCTC	TTGCAACTTCTTCGCCATC	Genetic markers
344	C5B6coD2	CGTTGCTGTGAAGGATCTGA	GCATTGGCCTAGATGGTGAT	Genetic markers
345	C5B11C	TCTTCATCACTTTCGAGTGTGTC	GATTTGGTGTAAGCAGGAGTGAG	Genetic markers
346	C5B11S	AGCTCCGTGTTGGTGGTTAG	GCTTGTACCCGCCTTCTATTC	Genetic markers
347	C2B23C18	CAGCTGGCTGACGTCTTAGAT	TCGGACAACCGTGAACTTATC	Genetic markers
348	C2B23C22	CGCTAGACACATCGACATCAA	ACCATTCCGAACAGGAAGATT	Genetic markers
349	C2B22C4	GTACATTGGCCGAAGTTGAAG	CAAATCATACGGTCCCATGAC	Genetic markers
350	C2B22C7	ACCATTCCGAACAGGAAGATT	AAATTCCCTAACCGGAGGACT	Genetic markers

351	C2B22S9	GAGCGTAGTTGGCTTGACTTG	AATGAGTATGCCATCCGTGAG	Genetic markers
352	C2B17S8	AAACAGAACACCTCACACGAAA	GAGGACGTCATGAGTTTGAGC	Genetic markers
353	C2B17S7	AAGTATGTCTGCCTCGCACAT	AACAAACCAGCAGGAGTGAGA	Genetic markers
354	C2B17S1	TACACCAACCGTGGAAAGGTA	GGACACCTCAACGAGGATACA	Genetic markers
355	C2B17_9	CTATGTGCAGGCCATTTAAGC	ACATGCGAAAGCCAAGATTT	965 bp
356	C2B18S2	TGGGTCTCGGGATACCACTAT	AGCCGAGCTAGCCACTTTAAC	958 bp
357	C2B20/21_1	ATCGAGAGAATCACGGAAGAAG	GTGACTTGATTTCCACACCTGA	552 bp
358	C2B20/21_2	ACCCGACAGAGATTACAAGCAT	GTCCTCTTTGCAGCAAGAAGTT	541 bp
359	C2B22_6	CACACATTCTCGTGGAAAGGT	TGTCTATGTGCTTTGCTGGTG	995 bp
360	C2B22_7	ACCATTCCGAACAGGAAGATT	AAATTCCCTAACCGGAGGACT	997 bp
361	Bac_11L_1	CCAAACTAGAGGCACTTGTGG	GGTTATGGTGGTCTACGCAAG	569 bp
362	Bac_11L_2	CGCCCATCACTTATGTATTGC	TCCATGACCTTTCCCAAACTA	497 bp
363	Bac_11R_11	TACATCTCAACCTTCCGCTTG	TAGAACAGTGCGGATCGTACC	553 bp
364	C5B11/10_3	ATGTCACCACCATTGCTTACAC	ACAACTTGGTGTTCTCAGTGGA	547 bp
365	C5B10/11_1	GAAGCAGAAGAAATGTGTCGTG	ATTCAGAACGGAGGTGATCCT	502 bp
366	C5B10/11_2	AGGAGATTACGGTGGCCTTAG	CCAGTCTTTGACCAATTGAGC	501 bp
367	C5B10/9_1	CTTCTTCTTCCTCCCGATTCTT	GATGTGTGCGCGATTTAGTCT	576 bp
368	C5B10/9_2	ATCCACATCGGATAGACCTGAT	AGTGCTCATTCCTCATTTCCTC	567 bp
369	C5B8/9_C3_4	GGCAACACATTGATGGAGATC	GTTGAAGTCCCGGTTCTAAGC	898 bp
370	C5B8/9_C3_5	AGAAGCTCGATGATGCACTGT	CTTACCACCGCTGTGCTACAT	899 bp
371	C5B7/8_1	TACTCTACCCTCGAAATCTGCTG	AAGATGGGCTATTACCGTCTCAG	1046 bp
372	C5B7/8_2	GAGGCTCTTCAAGCCGTAACT	CACTGCTGTCTGAGCTCCTCTA	994 bp
373	C5B7/6_1	CAACCCACTCTCTCCTCGAA	ATGCTCCTCGTCACCTCATC	524 bp
374	C5B7/6_2	AAGTGGTACGCTAAATCCGTTG	TAGTAGTGGGCTTATGGCAACC	543 bp
375	C5B6/5_1	GACGAATGTAGTGCAACTCTGC	CCTACCGAATGAAGGAAACAAG	546 bp
376	C5B6/5_2	GTGAGCGCCTAGAATAGGAGAA	CTCCATGTCTCCTCATCAACAC	551 bp
377	C5B5/4_1	ATCACACCATGCTTCACACTTC	AGTGAATATCATGGCCCTCAAC	550 bp
378	C5B5/4_2	CTAAAGCTCCTGGAAGCAGGTA	CTTCTCCCAATTCAAGACAAGG	558 bp
379	Bac_11L_3	TGGGAAAGGTCATGGAAATCT	TTTAGTGAAAGGTCGCTGTCG	553 bp
380	Bac_11L_4	ACTGAGGGAGTTCGGGACTAA	GATTCAATGTCCGCAACAAGT	535 bp
381	Bac_11L_5	GCCTTGAAGACCAAGCATGTA	AGAGGAGGGTTAGGTCATGGA	566 bp
382	Bac_11L_6	AGCCCTCATTACCGAGGAATA	AGGTCAAATCTGATCCCTTCC	526 bp
383	Bac_11L_7	ATGTCATGTGCCCAAGGATAA	ATCCTTTAGACCCTCCACCAA	570 bp
384	Bac_11L_8	TAACGGGTGAACACATCCTTC	GCGAAGCAAGAGACAATTTGA	568 bp
385	Bac_11L_9	ATTCCAACGCTTGTCCTGATA	AGGTTCGCAAGTAAGAGTGGA	541 bp
386	Bac_11R_10	GTTGTATGCCTGCTGTGGATT	TCGGACTTCCATTGTTCATTC	563 bp
387	Bac_11R_12	GACTTGTCAGTCGGCTCACTC	GACGACCACGAGATGATTGAT	544 bp
388	Bac_11R_13	ATCAATCATCTCGTGGTCGTC	CTCGTTTGTTGCAAGTCAGTG	545 bp
389	Bac_11R_14	TGATGCACCACTAGGAGACTTG	TCAACATCCGCTATAGTGTCAA	597 bp
390	Bac_11R_15	GCGGATGTTGATTCCTACTAGC	TGCATGACAAGAATTGTGACC	557 bp
391	Bac_11R_16	GGAGCCAGCATGAGAAGAAG	GCAATCAGTCAAACAGCCATA	530 bp
392	Bac_11R_17	ATGCCACCGATAAGTGAAGAA	AAAGGCTTTCCTTGTGTTTGC	543 bp
393	Bac_11R_18	ACAGGATGCAAACACAAGGAA	TGTGCAGTTTGGAGAACATGA	528 bp
394	Bac_11R_19	ATTGAAACATGGTGCATCCTC	CAAGAGAGATACGTGGGTTAGGA	555 bp
395	Bac_23_20	AAGTGCCTTCTCCGTCTAGGA	GGTCTCCACTTTCACCAACAA	547 bp
396	Bac_23_21	CGTGTGGATGCTATGATGTTG	AGGAGTCCGTCCTGGATACAT	530 bp
397	Bac_23_22	AAACAAGAGCAGGACGTATGG	AAGAGGGCCATGTCTTCATTT	548 bp
398	Bac_23_23	GAAGAAACCAACCACTTCTCG	TGTGCTTACTCACCATCTCCA	541 bp
399	Bac_23_24	TGGCAAAGCTTATTCCTCTCC	CTTGGTTAGAGGCACCCATTT	532 bp

400	Bac_23_25	AAATGGGTGCCTCTAACCAAG	GAAGGATGTGTTCACCCGTTA	531 bp
401	Bac_23_26	TGGCCTCCTTCATGGAATAGT	TGGGAGTTTGATCCATAACCA	581 bp
402	C2B20_21_3	CAGGTGCGGTGTAGTTGTTCTA	CCAAGCCTATAATGAGCCGTAA	550 bp
403	C2B20_21_4	CTAGAATTGGTCGTGGATCTCC	CCAGGAACAAGCTTAATTGGAC	549 bp
404	C2B20_21_5	GGCGTCTATAAAGCCATGATGT	ATGGAAGTTTCCTCCTTCCATC	537 bp
405	C2B20_21_6	CGTATGGACTCACTCAGACAGC	GATCTCTCCGCCAAGTATCATC	550 bp