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# High-resolution mapping of Ryd4Hb, a major resistance gene to Barley yellow dwarf virus from *Hordeum bulbosum*

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3 **Title:** High-resolution mapping of *Ryd4<sup>Hb</sup>*, a major resistance gene to *Barley yellow dwarf virus* from *Hordeum bulbosum*

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23 **Abstract**

24 Virus diseases are causing high yield losses in crops worldwide. The *Barley yellow dwarf virus* (BYDV)  
25 complex is responsible for one of the most widespread and economically important viral diseases of cereals.  
26 While no complete resistance gene has been uncovered in the primary gene pool of barley, sources of  
27 resistance were identified in the wild relative *Hordeum bulbosum*, representing the secondary gene pool of  
28 barley. One such locus, *Ryd4<sup>Hb</sup>*, has been previously introgressed into barley, and was allocated to  
29 chromosome 3H, but is tightly linked to a sublethality factor that prevents the incorporation and utilization  
30 of *Ryd4<sup>Hb</sup>* in barley varieties. To solve this problem, we fine-mapped *Ryd4<sup>Hb</sup>* and separated it from this  
31 negative factor. We narrowed the *Ryd4<sup>Hb</sup>* locus to a 66.5 kbp physical interval in the barley ‘Morex’  
32 reference genome. The region comprises one complete and one partial gene from the nucleotide-binding  
33 and leucine-rich repeat immune receptor family, typical of dominant virus resistance genes. The closest  
34 homolog to these two *Ryd4<sup>Hb</sup>* candidate genes is the wheat *Sr35* stem rust resistance gene. In addition to the  
35 fine mapping, we reduced the sublethality factor interval to 600 kbp in barley. Aphid feeding experiments  
36 demonstrated that *Ryd4<sup>Hb</sup>* provides a direct resistance to BYDV rather than a resistance to its vector. The  
37 presented results, including the high-throughput molecular markers, will permit a more targeted selection  
38 of the resistance in breeding, enabling the use of *Ryd4<sup>Hb</sup>* in barley varieties.

39 **Keywords**

40 High-resolution mapping, *Barley yellow dwarf virus*, disease resistance, barley, *Hordeum bulbosum*, *Ryd4<sup>Hb</sup>*

41 **Declarations**

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47 **Conflicts of interest/Competing interests** Neele Wedler, Viktor Korzun, Klaus Oldach, and Anja  
48 Maasberg-Prelle are employed at KWS SAAT SE & Co and KWS LOCHOW. The other authors declare no  
49 conflict of interest.

50 **Availability of data and material** The Exome capture sequencing datasets generated and/or analyzed  
51 in this study are deposited at EMBL-ENA under the project IDs PRJEB7909 and PRJEB65283.

52 **Authors' contributions** Brigitte Ruge-Wehling, Nils Stein, Neele Wedler, and Viktor Korzun  
53 conceived the project and acquired the funding. Brigitte Ruge-Wehling, Neele Wedler, Klaus Oldach, Anja  
54 Maasberg-Prelle, and Viktor Korzun designed and built the mapping populations. Brigitte Ruge-Wehling  
55 and Kristin Fischer performed the initial linkage mapping and broke the linkage between the resistance and  
56 the sublethality loci. Brigitte Ruge-Wehling and Antje Habekuß performed the phenotyping experiments.  
57 Neele Wedler did the exome capture experiment. Torsten Will performed and analyzed the aphid feeding  
58 experiments. H el ene Pidon performed the high-resolution mapping and the pangenome analysis and drafted  
59 the manuscript. Nils Stein supervised the project. All authors provided critical feedback and helped shape  
60 the manuscript.

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65 marker analysis.

66 **Key message (<30 words)**

67 We mapped *Ryd4<sup>Hb</sup>* in a 66.5 kpb interval in barley and dissociated it from a sublethality factor. These  
68 results will enable a targeted selection of the resistance in barley breeding.

## 69 **Introduction**

70 Virus diseases cause significant yield losses and represent an increasing threat to agricultural crop  
71 production worldwide (Oerke, 2006). Among them, *Barley yellow dwarf virus* (BYDV) complex is  
72 responsible for one of the most widespread and economically important viral diseases of cereals.  
73 Transmitted in a persistent and circulative manner by several species of aphids, BYDV causes dwarfing and  
74 leaf discoloration, leading to significant yield loss in major cereal crops, in particular barley, wheat, maize,  
75 and oats (Ali et al., 2018). In recent years, it has become increasingly important in winter barley with an  
76 incidence that could reach 70% and yield loss of up to 80% (Beoni et al., 2016; Dedryver et al., 2010; Ordon  
77 et al., 2009). As climate change scenarios predict longer and warmer autumns, which favor aphid  
78 infestations of winter crop fields, BYDV could become one of the most threatening diseases of cereal crops  
79 (Roos et al., 2011; Trebicki, 2020). Reduction of yield losses by insecticide-based vector control is possible  
80 in principle, but undesirable for ecological reasons. To ensure sustainable barley cultivation in the expanding  
81 infestation areas and thus secure yields and quality in the long term, the cultivation of virus resistant varieties  
82 would provide the best solution.

83 So far, three genes and some QTLs have been described as providing partial resistance or tolerance to BYDV  
84 in barley. The gene *ryd1*, providing recessive intermediate tolerance was identified by Suneson (1955) but  
85 is still not cloned (Niks et al., 2004). Its effectiveness is low and it is rarely used in breeding. *Ryd2* was  
86 identified from an Ethiopian barley landrace (Schaller et al., 1964). It provides field tolerance to the virus  
87 serotypes BYDV-PAV, BYDV-MAV, and BYDV-SGV (Baltenberger et al., 1987). Mapped close to the  
88 centromere of chromosome 3H (Collins et al., 1996), *Ryd2* is used in several breeding lines (Kosova et al.,  
89 2008) where it can reduce significantly the yield loss caused by BYDV (Beoni et al., 2016). The third gene,  
90 *Ryd3* was also identified from an Ethiopian barley landrace (Niks et al., 2004). The gene was mapped in the  
91 centromeric region of chromosome 6H but, despite fine mapping on more than 3,000 F<sub>2</sub> plants (Lüpken et  
92 al., 2014), the mapping interval is still large. *Ryd3* has been transferred to commercial varieties where it  
93 provides a quantitative resistance, improved when in combination with *Ryd2* (Riedel et al., 2011). QTLs on  
94 chromosomes 1H, 2H, 4H, 5H, and 7H have been reported, however, providing only a limited level of  
95 tolerance (Toojinda et al., 2000; Riedel et al., 2011; Hu et al., 2019). No complete resistance to BYDV or  
96 its aphid vectors is known in barley, and broadening the genetic basis of resistance is therefore needed to  
97 ensure a durable and stable production of winter barley fields.

98 The secondary genepool of barley, consisting of the species *Hordeum bulbosum*, has not yet been used to  
99 improve resistance to the BYDV complex. Michel (1996) identified resistance to BYDV in the tetraploid  
100 (2n=4x=28) *Hordeum bulbosum* accession A17 (Bu10/2) from the Botanical Garden of Montevideo,  
101 Uruguay. Plants of this accession remained ELISA-negative for BYDV after several inoculations with  
102 aphids charged with the virus isolates BYDV-PAV1 Aschersleben, BYDV-MAV1 Aschersleben, and  
103 CYDV (*Cereal yellow dwarf virus*)-RPV Dittersbach (Habekuß et al., 2004). A17 was used as a parent in  
104 interspecific crosses and backcrosses with *H. vulgare* cv. Igri to generate an *H. bulbosum* introgression to  
105 barley. Its resistance was described as complete, dominant, and monogenic, and the locus, assigned to  
106 chromosome 3H, was named *Ryd4<sup>Hb</sup>* (Scholz et al., 2009). Adversely, a recessive sublethality factor was  
107 cosegregating with *Ryd4<sup>Hb</sup>* in the respective introgression. A study revealed low aphid feeding on the *H.*  
108 *bulbosum* A17 accession, suggesting that resistance may not be acting directly on the virus but rather  
109 indirectly against the aphid vector (Schliephake et al., 2013).

110 The present study reports the fine mapping of the *Ryd4<sup>Hb</sup>* locus, the identification of candidate genes, and  
111 the description of aphids feeding behavior on susceptible and resistant introgression lines.

## 112 **Material and methods**

### 113 **Plant material**

114 BC<sub>2</sub>F<sub>5</sub> and BC<sub>2</sub>F<sub>6</sub> selected from BC<sub>2</sub>F<sub>4</sub> plants from the Scholz et al. (2009) population were used for the  
115 low-resolution linkage mapping and development of an introgression line lacking the sublethality factor.  
116 This population is later named LM\_Pop.

117 Two additional populations were generated to map *Ryd4<sup>Hb</sup>* at a higher resolution. FM\_Pop1 was derived  
118 from a BC<sub>2</sub>F<sub>7</sub> plant from LM\_Pop crossed successively with three different barley elite varieties. The  
119 pedigree of the 15 lineages that constitute FM\_Pop1 is presented in supplementary table 1. The donor of  
120 resistance in the FM\_Pop2 was a BC<sub>2</sub>F<sub>8</sub> derived from the BC<sub>2</sub>F<sub>6</sub> JKI-5215 homozygous for the *H. vulgare*  
121 (*Hv*)-allele in the sublethality factor locus. As for FM\_Pop1, it was crossed successively with two different  
122 barley elite varieties. The pedigree of the lines of four lineages that constitute FM\_Pop2 is presented in  
123 supplementary table 2. The F<sub>1</sub> plants from the successive crosses were checked with markers to ensure the  
124 presence of the *H. bulbosum* (*Hb*)-allele at the *Ryd4<sup>Hb</sup>* locus and were further selfed to obtain the F<sub>2</sub> lineages  
125 forming FM\_Pop1 and FM\_Pop2.

### 126 **Test of resistance to BYDV**

127 Five to ten *Rhopalosiphum padi* aphids of the biotype R07, that were reared on BYDV-PAV1 Aschersleben  
128 (PAV1-ASL) infected plants as described by Kern et al. (2022), were placed on each one-week-old seedlings  
129 to be phenotyped in an air-conditioned greenhouse (20 °C, 16 h photoperiod, 10 klx). The aphids were  
130 killed after two days using the insecticide Confidor®WG 70 (Bayer CropScience AG, Germany). Further  
131 cultivation of the plants was carried out. Five to six weeks after inoculation, leaf samples of 50 mg from  
132 two leaves were taken and tested by a double-antibody sandwich-enzyme-linked immunosorbent assay  
133 (DAS-ELISA) according to Clark & Adams (1977) using custom-made antibodies. The viral content was  
134 evaluated by measuring extinction at 405 nm on a microtitre plate reader (Opsys MR, ThermoLabsystems  
135 or Tecan Sunrise, Tecan) one hour after the addition of the enzyme substrate. Based on negative controls, a  
136 extinction threshold was set in each experiment, usually at 0.1, under which a plant was classified as  
137 resistant. Phenotyping tests for gene mapping were performed on ten to 15 seeds of progenies of each  
138 genotype.

### 139 **DNA extraction**

140 Genomic DNA from the LM-Pop was either isolated following a slightly modified protocol after Stein et  
141 al. (2001) or using the Biosprint 96 DNA Plant Kit (Qiagen) and the Biosprint 96 working station (Qiagen)  
142 following the manufacturer's instructions. DNA was dissolved in TE buffer, quantified via photometric  
143 approaches (NanoQuant, Tecan, Austria) and diluted to a working concentration of 10 ng/μl. DNA  
144 extractions of plants from FM\_Pop1 and FM\_Pop2 were carried out according to the protocol described in  
145 Milner et al. (2019).

### 146 **Marker development for low-resolution linkage mapping**

147 The EST-derived SSR anchor markers *GBM1050* and *GBM1059* (Scholz et al., 2009; Stein et al., 2007;  
148 Thiel et al., 2003; Varshney et al., 2007) were kindly provided by Prof. Andreas Graner (Leibniz Institute  
149 of Plant Genetics and Crop Plant Research, Gatersleben). The STS markers *GLMWG883* and *GLABC161*  
150 were derived from the sequence of RFLP probe *MWG883* (Rostoks et al., 2005; Szűcs et al., 2009) and  
151 barley anchor marker *ABC161* (Close et al., 2009), respectively. Orthology of the interval on the rice  
152 chromosome 1 using the mapping of the anchor marker *ABC161* at 40.43 Mbp on said chromosome allowed

153 for the development of 18 tentative consensus (TC) markers polymorphic between Hv and Hb on  
154 chromosome 3HL.

155 Additional polymorphisms between the *H. bulbosum* and *H. vulgare* genomes for marker development were  
156 identified by RNASeq and Massive analysis of cDNA-ends (MACE). To this end, 1,000 plants from BC<sub>2</sub>F<sub>5</sub>  
157 of LM\_Pop were screened with the TC marker *TC173485*. Among them, 200 plants homozygous for the *H.*  
158 *bulbosum* allele, considered resistant, and 200 plants homozygous for the *H. vulgare* allele, considered  
159 susceptible, were selected. In total, 100 plants of each category were inoculated by aphids carrying the  
160 isolate BYDV-PAV1, and an equal amount of plants were infested with control aphids without virus titer in  
161 a separate climate chamber. 1h, 4h, 8h, and 24h after inoculation plant material of 25 genotypes per category  
162 and treatment was harvested and sent to GenXPro (Frankfurt am Main, Germany) for RNA isolation and  
163 sequencing. RNASeq and MACE were performed as described in Santos et al. (2018) and Braun et al.  
164 (2019), respectively. In short, the raw data was cleaned off adapter sequences using the software TagDust  
165 (Lassmann et al., 2009). All RNAseq datasets were combined to create a reference library. Assembly was  
166 performed using the software Trinity (Grabherr et al., 2011). The reads of the individual libraries were  
167 hereafter mapped to the reference library and single nucleotide polymorphisms (SNPs) were identified using  
168 the software SNVMix (Goya et al., 2010). SNPs between the *H. bulbosum* and *H. vulgare* genomes were  
169 identified and sequences 100 bps up- and downstream of each SNP were determined. Annotation of the  
170 SNP-containing sequences was done by using the database Swiss-Prot (Boeckmann et al., 2003).

171 Additional polymorphisms were retrieved from exome capture sequencing, performed according to Wendler  
172 et al. (2014) on the *H. bulbosum* parent A17 (Wendler et al., 2015) and the BC<sub>2</sub>F<sub>4</sub> plant 5194/5, homozygous  
173 for the 3HL-*H. bulbosum* introgression and mapped on the first barley genome assembly (International  
174 Barley Genome Sequencing Consortium, 2012). Single nucleotide variants between *H. vulgare* and *H.*  
175 *bulbosum* were called with samtools (SNP call score <200). Variants located within 200 bp of the end of a  
176 reference sequence contig or supported by less than fivefold sequence read coverage were excluded from  
177 further evaluation. The flanking sequences (50–60 bp) of variant positions were used for marker assay  
178 development.

179 The primer design for PCR markers was carried out using Primer 3 (Untergasser et al., 2012). Conversion  
180 of SNPs in CAPS markers was done by using SNP2CAPS (Thiel et al., 2004). All markers used for the low-  
181 resolution linkage mapping are described in supplementary table 3.

### 182 **Marker development for high-resolution linkage mapping**

183 Exome capture data of the *H. bulbosum* A17 parent and of the BC<sub>2</sub>F<sub>4</sub> plant 5194/5 was remapped onto the  
184 barley reference genome MorexV3 (Mascher et al., 2021) together with the exome capture data of 13 barley  
185 varieties from (Russell et al., 2016) (cultivars ‘Barke’, ‘Bonus’, ‘Borwina’, ‘Bowman’, ‘Foma’, ‘Gull’,  
186 ‘Harrington’, ‘Haruna-Nijo’, ‘Igri’, ‘Kindred’, ‘Morex’, ‘Step toe’, and ‘Vogelsanger Gold’). Reads  
187 mapping and variant calling were performed as described in Milner et al., (2019). The SNP matrix was  
188 filtered on the following criteria: heterozygous and homozygous calls had to have a minimum mapping  
189 quality score of three and five, respectively, and be supported by a minimum of ten reads. SNP sites were  
190 retained if they had less than 20% missing data and less than 20% heterozygous calls. SNPs that were within  
191 the *Ryd4<sup>Hb</sup>* 20 Mbp interval defined by the low-resolution linkage mapping, homozygous for one allele in  
192 all barley varieties and for the other allele in A17 and the BC<sub>2</sub>F<sub>4</sub> introgression line, were retained.

193 For six SNPs, a 100 bp sequence containing the SNP in its center was provided to LGC genomics (Berlin,  
194 Germany) for KASPar marker production (Supplementary table 4). Within the sublethality factor interval,

195 ten more SNPs were retrieved and sequences of 100 bp around each one were sent to 3CR Bioscience  
196 (Welwyn Garden City, UK) for PACE assay design (Supplementary table 5). Primers were ordered from  
197 Metabion (Germany) and mixed according to 3CR Bioscience (Welwyn Garden City, UK)  
198 recommendations.

199 Thirteen CAPS markers (Supplementary table 6) were developed using NEBcutter (Vincze et al., 2003) to  
200 identify the cutting enzyme and Primer 3 (Untergasser et al., 2012) to design the PCR primers.

### 201 **Genotyping assays**

202 For PCR of SSR, STS, and CAPS markers were carried out in a volume of 10µL containing 50-100ng of  
203 DNA, 1X PCR buffer (Qiagen), 0.5 mM of each primer, 0.5 U of Taq DNA polymerase (Qiagen), and 0.2  
204 mM of dNTPs. PCR amplification was carried out with an initial 10 min step at 95°C, followed by a  
205 touchdown profile of ten cycles at 95°C for 30 seconds, 60°C for 30 seconds with a 0.5°C reduction per  
206 cycle, and 72°C for 1 minute, followed by 35 cycles at 95°C for 30 seconds, 55°C for 30 seconds then 72°C  
207 for 1 minute, and a last step of 7 minutes at 72°C. For CAPS markers, a 5 µl aliquot of the PCR product was  
208 digested in 10 µL with 1 U of restriction enzyme and 1x of the appropriate digestion buffer at the temperature  
209 recommended by the manufacturer. Pre- and post-digestion PCR products were separated on 2.5 % agarose  
210 gels followed by ethidium bromide staining or in 10% polyacrylamide gels followed by silver nitrate  
211 staining according to Budowle et al. (1991).

212 Detection of SNPs as genetic markers were performed by high-resolution melt analysis (HRM) by using the  
213 Rotor Gene Technology (Qiagen). PCR was carried out in 20 µl volume containing 20 ng template DNA, 1  
214 x buffer (Promega), 2.5 mM MgCl<sub>2</sub>, 0.8 mM dNTP mix, 0.5 µM of each primer, 1 x EvaGreen Dye  
215 (Biotium, Inc.) and 0.3 U *Taq* DNA polymerase (Promega). A touchdown PCR protocol was conducted  
216 with a temperature gradient from 60–50°C. The melt curve analysis was conducted by ramping from 65 C  
217 to 95 C with a 0.1 C decrease per capture.

218 Genotyping assays with KASPar and PACE markers were carried out as described in Pidon et al. (2020).

### 219 **Genetic linkage analysis**

220 LM\_Pop was genotyped with 4 EST-derived SSR anchor markers, 18 TC-markers, 6 MACE-SNP, 13 STS-  
221 markers derived from MACE (denoted as MACE\_b), 9 markers derived from RNA-seq experiment, and 3  
222 markers derived from exome capture. Linkage analysis was performed using the JoinMap® 4.1 software  
223 (Van Ooijen, 2006). Genetic maps were displayed and edited in MapChart2.2 (Voorrips, 2002).

### 224 **Pangenome comparison**

225 The flanking markers and the *Ryd4<sup>Hb</sup>* interval in the MorexV3 genome were searched on the 19 other  
226 assemblies of the barley pangenome (Jayakodi et al., 2020) using BLAST+ (Camacho et al., 2009). The  
227 resulting intervals were extracted and reannotated through a combination of alignments of the Morex  
228 candidate genes to them, the search for the presence of conserved domains using NCBI *conserved domains*  
229 (S. Lu et al., 2019), and NLRs annotation with NLR-Annotator (Steuernagel et al., 2020). The interval  
230 structures were compared using Easyfig with blastn (Sullivan et al., 2011).

### 231 **Aphids feeding experiment**

232 In order to test if *Ryd4<sup>Hb</sup>* provides resistance to aphids, a resistant and a susceptible progeny of the  
233 heterozygous lines at *Ryd4Hb* locus EP\_16-271\_3\_206 and EP\_16-460\_5\_228 were selected. The  
234 susceptible progenies EP\_16-271\_3\_206\_2 and EP\_16-460\_5\_228\_2 were carrying Hv alleles at both  
235 *Ryd4\_CAPS19* and *Ryd4\_CAPS24*, while the resistant lines EP\_16-271\_3\_206\_4 and EP\_16-

236 460\_5\_228\_6 were recombining in the interval and carrying a Hb allele at Ryd4\_CAPS24 or  
237 Ryd4\_CAPS19, respectively. The feeding behavior of 12 to 16 adult apterouse non-viruliferous *R. padi*  
238 (clone R07) of random age was observed on an individual healthy plant of the respective genotypes per  
239 aphid by using the electrical penetration graph (EPG) technique (Tjallingii, 1978). Plants for EPG  
240 experiments were reared in a greenhouse and were used at a 3-4 leaf stage where aphids were placed on the  
241 lower side of the second leaf. Aphids were reared as described before (Kern et al., 2022). Aphids starved  
242 for 1 hour before they were placed on the leaf. The recording started when all aphids were prepared. The  
243 observation period was set to 8 hours and recording was started after all aphids were placed. For data  
244 acquisition, the GIGA-8 EPG amplifier and EPG stylet software (EPG Systems, Wageningen, The  
245 Netherlands) were used and data were analyzed with the EPG stylet analysis module. Waveforms were  
246 annotated according to Tjallingii (1978) and Tjallingii & Esch (1993). Subsequently, selected parameters  
247 were analyzed by using an Excel workbook (Alvarez et al., 2021). Recordings of aphids that fell from the  
248 leaf or escaped during the experiment were not used.

## 249 **Results**

### 250 **Low-resolution linkage mapping of *Ryd4<sup>Hb</sup>***

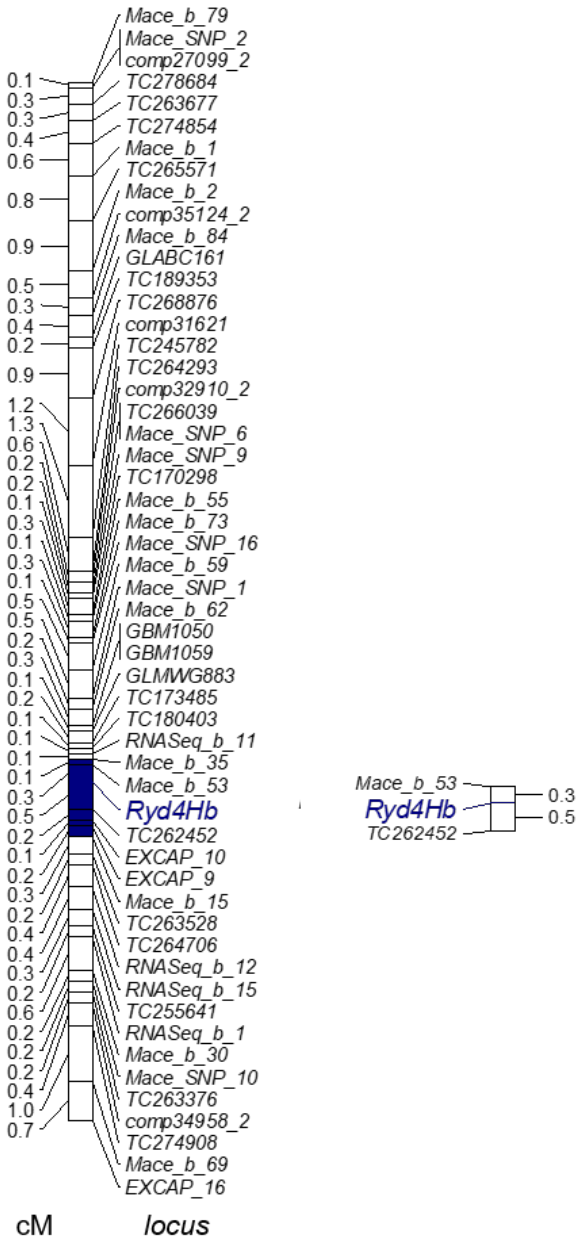
251 From LM\_Pop, 1,125 BC<sub>2</sub>F<sub>5</sub> and BC<sub>2</sub>F<sub>6</sub> were used for the low-resolution linkage mapping of *Ryd4<sup>Hb</sup>*.  
252 Phenotyping of progenies revealed 570 resistant, 276 susceptible plants, and 279 plants that died at early  
253 stages. This high mortality rate was expected due to the recessively inherited sublethality factor very closely  
254 linked to *Ryd4<sup>Hb</sup>*. This locus prevents normal plant development, resulting in plant death (Figure 1). Because  
255 of the close linkage between the two loci, we considered that all plants that died in the BC<sub>2</sub>F<sub>5</sub> and BC<sub>2</sub>F<sub>6</sub>  
256 families could be defined as homozygous resistant, while the resistant plants that survived would be  
257 heterozygous at *Ryd4<sup>Hb</sup>*. The phenotype distribution would indeed fit the expected 1:2:1 ratio of homozygous  
258 resistant, heterozygous resistant, and homozygous susceptible genotypes for a dominant monogenic  
259 inheritance of *Ryd4<sup>Hb</sup>* resistance (Chi-Square Goodness of Fit Test:  $\chi^2= 0.216$ ,  $p=0.90$ ), confirming the  
260 previous observation for that locus on the BC<sub>2</sub>F<sub>4</sub> generation (Scholz et al., 2009).





261  
262 **Fig. 1** Five months-old homozygous resistant plants either carrying a sublethality factor (left) or vital (right).  
263 The growth of plants homozygous at the sublethality factor is greatly reduced compared to plants carrying  
264 the resistance locus without the sublethality factor. They died before reaching heading.

265 The population was genotyped with 53 co-dominant markers and the linkage mapping was performed on  
266 the 1,014 individuals with a low amount of missing data. The introgression size was estimated to be 18.7  
267 cM limited distally by the marker EXCAP\_16 and proximally by the marker MACE\_b\_79 (Figure 2). The  
268 resistance locus *Ryd4<sup>Hb</sup>* is flanked by the MACE marker Mace\_b\_53 and the TC marker TC262452 with a  
269 genetic distance of 0.3 cM proximally and 0.5 cM distally, respectively. Moreover, the 200 BC<sub>2</sub>F<sub>5</sub> plants  
270 screened with TC262452 and phenotyped by DAS-ELISA showed a perfect cosegregation of the TC262452  
271 marker data with the resistance: the 100 plants carrying at least one Hb allele at the TC173485 marker had  
272 an extinction <0.1 whereas the 100 plants homozygous for the Hv allele had an extinction >0.5.

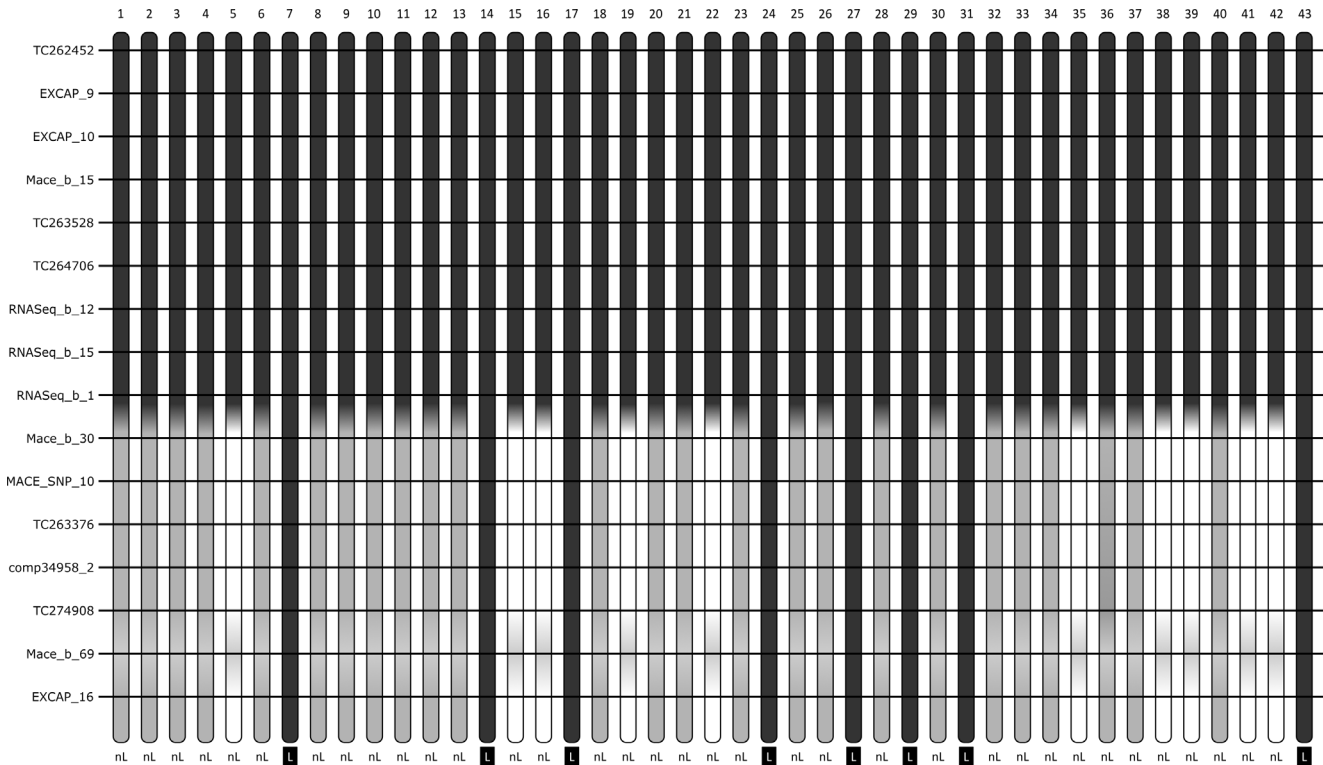


273  
 274 **Fig. 2** Linkage map of chromosome 3HL carrying *Ryd4<sup>Hb</sup>*. The extent of the *Ryd4<sup>Hb</sup>* locus is represented in  
 275 blue (1), marker bracket around *Ryd4<sup>Hb</sup>* displaying the flanking markers (2)

276 **Development of an introgression line without sublethality factor**

277 The exploitation of *Ryd4<sup>Hb</sup>* for breeding programs requires the selection of homozygous resistant and vital  
 278 (by opposition with sublethal) plants. To select recombinants lacking the sublethality factor, 12,133 BC<sub>2</sub>F<sub>6</sub>  
 279 plants of LM\_Pop were screened with markers TC262452 and Mace\_b\_53. Among those, 3,103 plants were  
 280 homozygous for Hb-alleles, 6,020 heterozygous (Hb/Hv), and 3,010 homozygous for *H. vulgare* (Hv) at  
 281 *Ryd4<sup>Hb</sup>* locus, confirming the 1:2:1 segregation (Chi-Square Goodness of Fit Test:  $\chi^2 = 2.14$ ,  $p = 0.34$ ). The  
 282 3,103 plants homozygous for Hb-alleles were propagated and the progenies were checked for resistance. A  
 283 single progeny, denoted as JKI-5215, was both completely resistant and vital. Marker analysis revealed that  
 284 this population was segregating for Hb- and Hv-alleles distally from *Ryd4<sup>Hb</sup>*.

285 The JKI-5215 population, made of 43 BC<sub>2</sub>F<sub>7</sub> plants from JKI-5215 progeny, was genotyped with all 16  
286 markers that mapped distally from *Ryd4<sup>Hb</sup>*. Markers TC262452 to RNASeq\_b\_1 were homozygous for Hb-  
287 alleles whereas Mace\_b\_30 and all the remaining markers distally located were segregating in a 1:2:1  
288 fashion (Figure 3). The recombination occurred within the initial 3HL introgression and resulted in a  
289 reduced Hb-segment of 3.4 cM and all progenies are completely vital. A BC<sub>2</sub>F<sub>8</sub> from the family JKI-5215  
290 homozygous for the Hv-segment in the sublethality factor interval was selfed and used as the resistant donor  
291 for the FM\_Pop2.



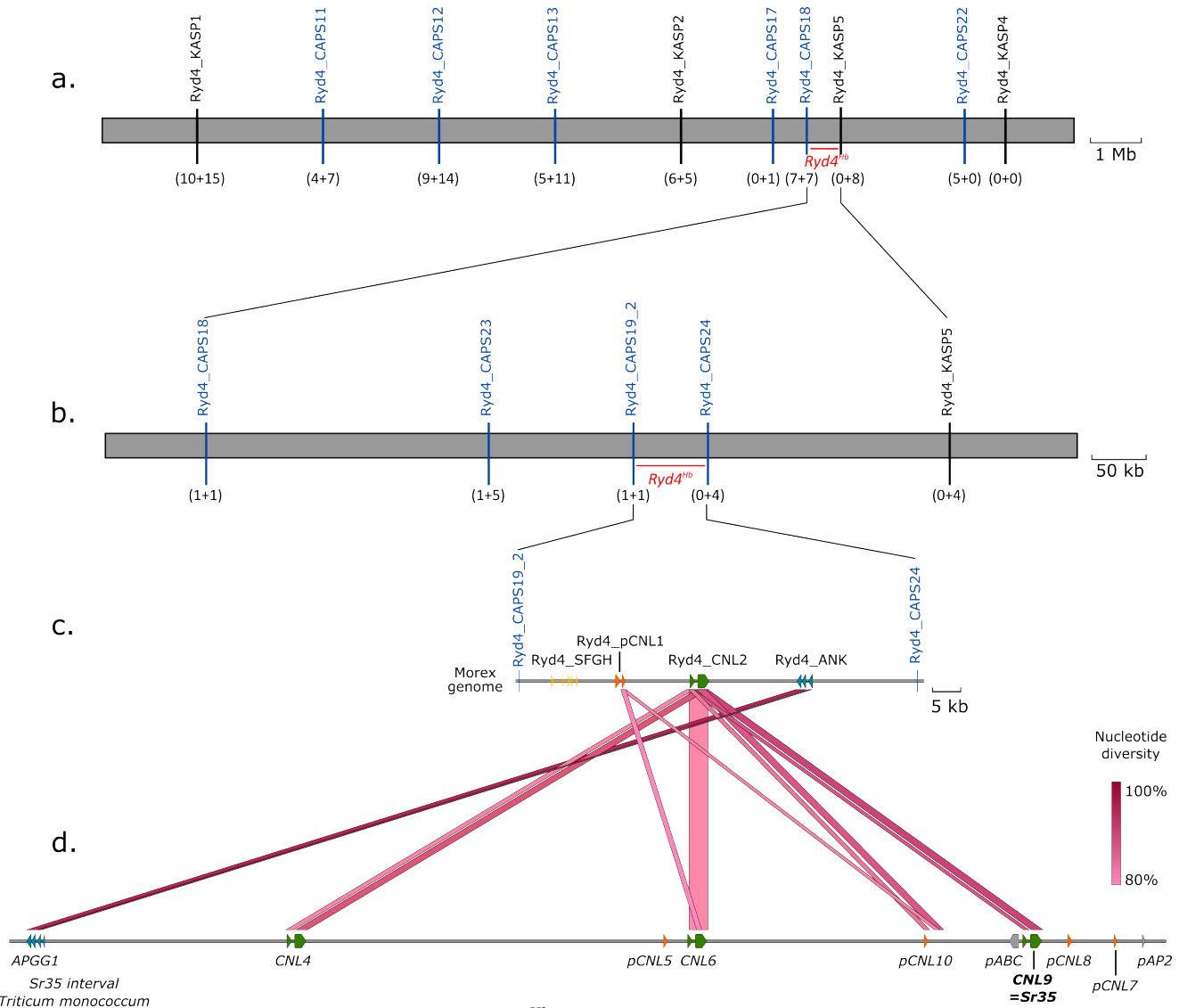
292 **Fig. 3** Characterization of 43 plants from the family JKI-5215 characterized by reduced introgressed Hb-  
293 fragment without sublethality factor. Each vertical bar represents one offspring from JKI-5215. White,  
294 black, and grey fragments represent Hb fragments, Hv fragments, and heterozygous genotypes at the  
295 markers indicated on the right side, respectively. The light grey fragments at the dominant marker  
296 Mace\_b\_69 are either Hv or heterozygous genotypes. The phenotype is indicated below the figure as ‘nL’  
297 for vital plants and ‘L’ for sublethal ones.

### 298 **High-resolution mapping of *Ryd4<sup>Hb</sup>* in two F<sub>2</sub> populations**

299 To precisely map *Ryd4<sup>Hb</sup>*, 5,589 F<sub>2</sub> plants from FM\_Pop1 and 10,155 F<sub>2</sub> plants from FM\_Pop2 were  
300 genotyped with two KASPar markers to identify recombination at the locus. Plants from FM\_Pop1 were  
301 screened with Ryd4\_KASP1 and Ryd4\_KASP4, and plants from FM\_Pop2 with Ryd4\_KASP1 and  
302 Ryd4\_KASP5. Indeed, Ryd4\_KASP4 is located in the sublethality factor interval and was segregating in  
303 FM\_Pop1, but not in FM\_Pop2 where it was fixed Hv in its resistant donor. We identified 46 and 68  
304 recombinant plants in FM\_Pop1 and FM\_Pop2, corresponding to 0.82% and 0.67% of recombination,  
305 respectively. The positions of the SNPs of the markers Ryd4\_KASP1, Ryd4\_KASP4 and Ryd4\_KASP5  
306 were identified in the GBS data from 92 recombinant inbred lines of the cross ‘Barke’ x ‘Morex’ (Mascher  
307 et al., 2013). A distance of 15 cM was observed between the markers Ryd4\_KASP1 and Ryd4\_KASP4, and  
308 of 12.6 cM between Ryd4\_KASP1 and Ryd4\_KASP5, indicating by definition a 15% and 12.6% probability  
309 of recombination in these intervals, respectively. The observed rate of recombination at the *Ryd4<sup>Hb</sup>* locus is

310 therefore about 20-times lower than expected for the same genetic interval in a pure intraspecific barley  
311 cross.

312 Recombinants were phenotyped on 15 offsprings and genotyped with the 13 CAPS markers. The resulting  
313 interval for *Ryd4<sup>Hb</sup>* was 66.5 kbp-long in MorexV3 genome between the coordinates 592,685,940 and  
314 592,752,329 flanked by CAPS19\_2 and CAPS24, describing an interval comprising six recombination  
315 events (Figure 4, Supplementary table 7). Four genes are annotated with high confidence on the MorexV3  
316 genome in that interval: HORVU.MOREX.r3.3HG0318400, an S-formylglutathione hydrolase,  
317 HORVU.MOREX.r3.3HG0318420, a partial nucleotide-binding and leucine-rich repeat immune receptors  
318 (NLR) with a coiled-coil domain (CNL) lacking LRR domain which is likely a pseudogene,  
319 HORVU.MOREX.r3.3HG0318450, a complete CNL, and HORVU.MOREX.r3.3HG0318470, an ankyrin-  
320 repeat-containing gene. Those genes will later be referred to as *Ryd4\_SFGH*, *Ryd4\_pCNL1*, *Ryd4\_CNL2*,  
321 and *Ryd4\_ANK*, respectively. The genes' homology revealed that locus *Ryd4<sup>Hb</sup>* is syntenic to the *Triticum*  
322 *monococcum* locus *Sr35*, conferring resistance to wheat stem rust (Saintenac et al., 2013). The candidate  
323 genes present a high similarity to one of the *Sr35* candidate genes. In particular, the translation of the  
324 complete *Ryd4\_CNL2* gene sequence from the MorexV3 reference genome shows 83% identity with the  
325 SR35 protein while the respective coding sequence shows 88.7% nucleotide identity. The *Ryd4<sup>Hb</sup>* interval  
326 also overlaps almost completely the ones of the *Rph13* leaf rust resistance gene from the *H. vulgare* ssp.  
327 *spontaneum* Hs2986 (Jost et al., 2020) and of the *Jmv2* resistance gene to the *Japanese soil-borne wheat*  
328 *mosaic virus* from the barley cultivar 'Sukai Golden' (Okada et al., 2022). *Rph13* is located on chr3H  
329 between the coordinates 592,658,337 and 592,786,929 on MorexV3 (128.6 kbp). Comparing the number  
330 of recombinants, the size of the interval in which they occurred, and the size of the mapping population for  
331 *Rph13* and *Ryd4<sup>Hb</sup>* (4 recombinant in 128.6 kbp out of 719 plants and 6 recombinants plants in 66.5 kbp out  
332 of 15,774, respectively), the recombination rate observed in the *Ryd4<sup>Hb</sup>* populations is 7.5 times lower than  
333 observed in the intraspecific cross used to map *Rph13*.

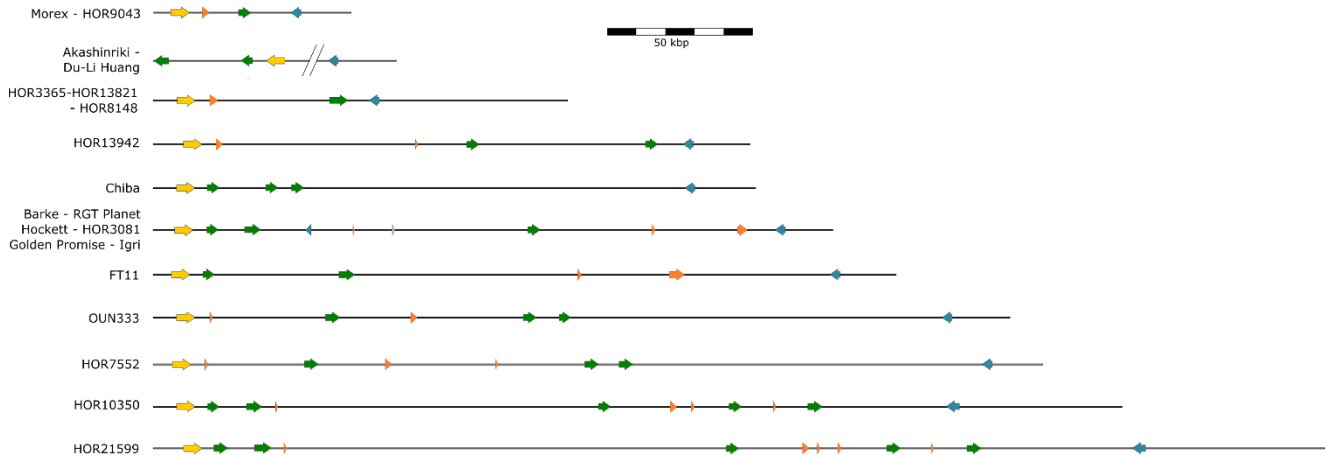


334 **Fig. 4** High-resolution mapping of the *Ryd4<sup>Hb</sup>* locus. (a) High-resolution mapping in the 5,589 F<sub>2</sub> plants  
 335 from FM\_Pop1 and 10,155 plants of FM\_Pop2. The numbers in brackets show the sum of individual  
 336 recombinants between the resistance locus and the corresponding marker in FM\_Pop1 and FM\_Pop2,  
 337 respectively. (b) Marker saturation of the 18 recombinant plants at *Ryd4<sup>Hb</sup>* locus. Recombinants from  
 338 FM\_Pop1 that died are excluded. (c) Candidate genes in the 66.5 kbp final *Ryd4<sup>Hb</sup>* interval. (d) Comparison  
 339 of *H. vulgare* 'Morex' and *T. monococcum* DV92 orthologous genes (only fragments with more than  
 340 80% nucleotide identity are shown).

#### 341 *Ryd4<sup>Hb</sup>* locus diversity in the barley pangenome

342 The orthologous intervals of the MorexV3 *Ryd4<sup>Hb</sup>* region were retrieved from 19 additional diverse genome  
 343 assemblies of the barley pangenome (Jayakodi et al., 2020) (supplementary table 8). We then annotated  
 344 them using a combination of methods: mapping the 'Morex' genes, searching for NLR genes with NLR-  
 345 Annotator (Steuernagel et al., 2020), and confirmation of the absence of additional conserved domains with  
 346 NCBI conserved domains (S. Lu et al., 2019). The analysis revealed a very large divergence of the *Ryd4<sup>Hb</sup>*  
 347 interval in the different genotypes (Figure 5, supplementary figure 1). The shortest orthologous interval is  
 348 the one of MorexV3. The largest is the one of the accession 'HOR 21599', 406 kbp-long and containing 10  
 349 NLRs, of which five are complete. The interval in the cultivars 'Akashinriki' and 'Du-Li Huang' is affected

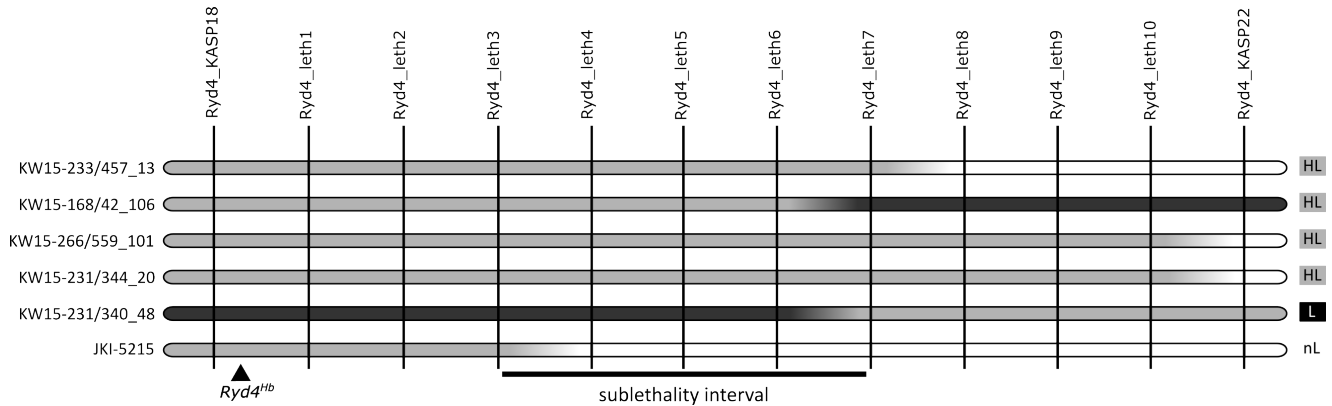
350 by a large inversion of around 600 kbp. The observed diversity between haplotypes is mainly explained by  
351 the presence of different repetitive elements and duplications. The degree of divergence in the *H. vulgare*  
352 gene pool in this interval suggests that an even greater diversity and divergence may be anticipated for the  
353 corresponding region in the *H. bulbosum* genome.



354 **Fig. 5** Graphical representation of the haplotype size and gene composition in the barley pangenome. Grey  
355 horizontal bars represent the dimension of the interval; forward slashes represent the breakpoint due to the  
356 large inversion in Akashinriki and Du-Li Huang. The interval between them is around 400 kbp-long and is  
357 not homologous to ‘Morex’ interval. Arrows represent genes; yellow genes are S-formylglutathione  
358 hydrolase, orange genes are partial NLRs, green genes are complete NLRs, and blue genes are ankyrin-  
359 repeats-containing genes.

### 360 Mapping of the sublethality factor

361 To better understand why the *H. bulbosum* locus is causing the sublethality, we used recombinants identified  
362 in the frame of *Ryd4<sup>Hb</sup>* mapping to pinpoint the responsible factor more precisely. The low-resolution linkage  
363 mapping located it distally from the marker *RNASeq\_b\_1*, which corresponds to position 594,019,595 on  
364 chromosome 3H of the MorexV3 genome. To precise its interval, ten PACE markers were designed between  
365 *Ryd4\_KASP18* and *Ryd4\_KASP22* (supplementary table 5), and used to genotype plants recombining in  
366 the interval. Six recombination events were available: the one of JKI-5215 that we mapped using 24 non-  
367 recombinant F<sub>2</sub> plants from lineage EP\_16-460 of FM\_Pop2, and the ones of five F<sub>2</sub> plants from FM\_Pop1  
368 recombining between *Ryd4\_KASP5* and *Ryd4\_C22*, of which four vital plant and the sublethal plant  
369 KW15\_231/340\_48 which died before heading (figure 5). The genotyping of 24 non-recombinant FM\_Pop2  
370 F<sub>2</sub> plants confirmed that the JKI-5215 recombination event occurred between *Ryd4\_KASP5* and  
371 *Ryd4\_CAPS22* (Figure 5), and more precisely between markers *Ryd4\_leth2* and *Ryd4\_leth3* (594,034,042  
372 to 594,290,776 bp). The genotyping and phenotyping of thirty-two F<sub>3</sub> plants from each of the four vital  
373 plants recombining between *Ryd4\_KASP5* and *Ryd4\_C22* placed the sublethality factor proximally of  
374 marker *Ryd4\_leth7*. This was confirmed by the genotyping of the sublethal plant KW15\_231/340\_48 from  
375 FM\_Pop1 which was identified as recombinant between *Ryd4\_leth6* and *Ryd4\_leth7* (Figure 6). The  
376 sublethality factor could therefore be assigned to a 483 kbp-interval between markers *Ryd4\_leth3* and  
377 *Ryd4\_leth7* (594,290,776-594,773,972 bp on chromosome 3H of MorexV3). This interval is annotated with  
378 15 high-confidence genes described in table 1. Among those genes, one or several could be essential genes  
379 for plant development with no orthologs in the corresponding region of the *H. bulbosum* genome.



380 **Fig. 6** Graphical representation of the genotype of lines recombining in the sublethality interval. Genotypes  
 381 of KW15-233/457\_13, KW15-168/41\_106, KW15-266/59\_101, and KW15-231/344\_20 are inferred from  
 382 those of 32 of their offsprings. The genotype of JKI-5215 is reconstructed from those of 24 F<sub>2</sub> plants of  
 383 FM\_Pop2 from the lineage EP\_16-460. Markers are depicted as vertical black lines and genotypes as  
 384 horizontal bars. White, black, and grey segments represent Hv, Hb, and heterozygotes genotypes,  
 385 respectively. Phenotypes are described on the right as sublethal (L), sublethality segregating in the progeny  
 386 (HL), and vital (nL). For better readability, marker positions are not to scale.

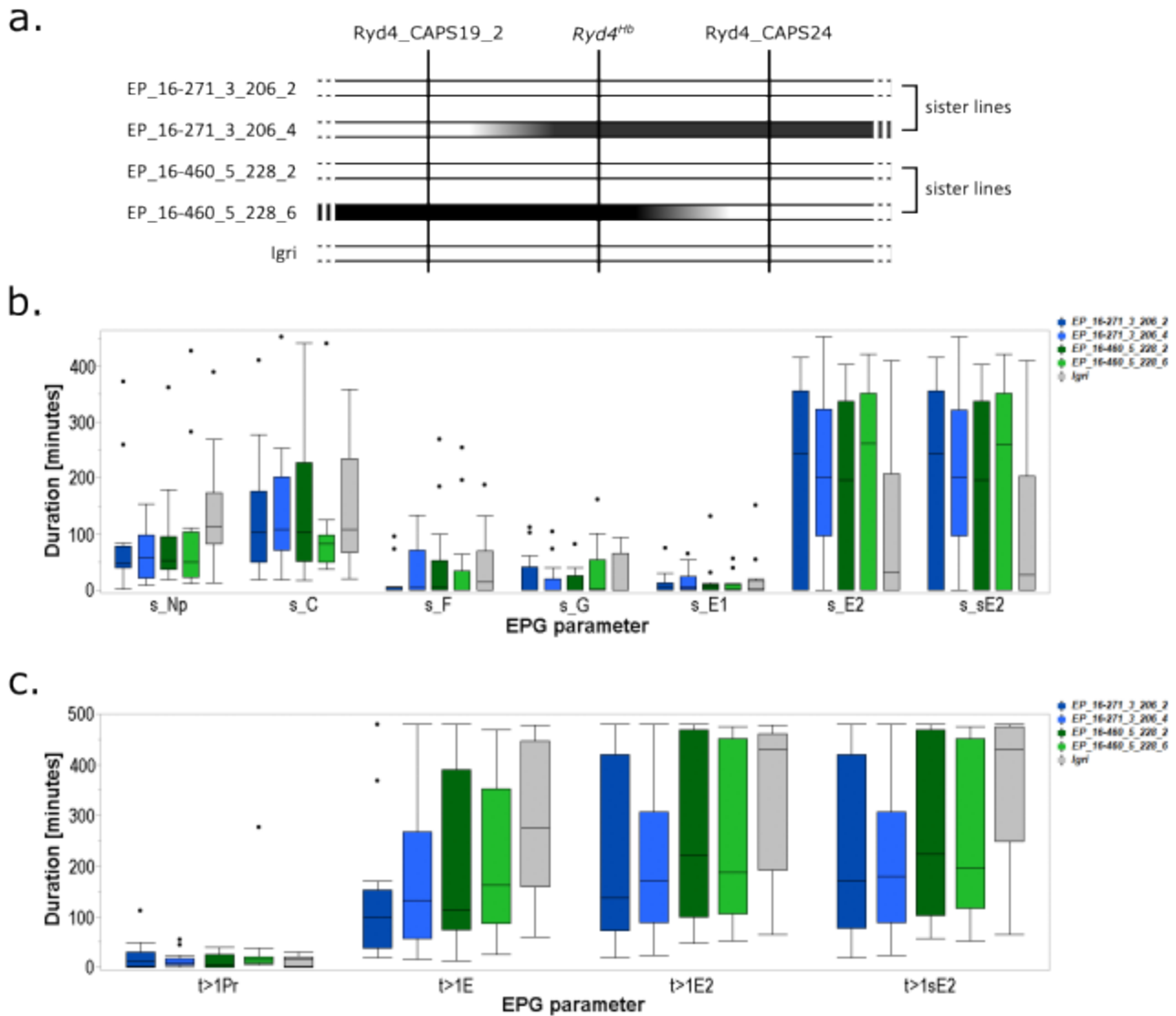
Gene name	Start	Stop	Annotation
HORVU.MOREX.r3.3HG0319200	594,288,404	594,295,050	B3 domain-containing protein
HORVU.MOREX.r3.3HG0319210	594,376,497	594,377,229	B3 domain-containing protein
HORVU.MOREX.r3.3HG0319220	594,404,110	594,405,348	Werner Syndrome-like exonuclease
HORVU.MOREX.r3.3HG0319240	594,551,247	594,553,562	B3 domain-containing protein
HORVU.MOREX.r3.3HG0319250	594,556,937	594,557,242	Ultraviolet-B-repressible protein
HORVU.MOREX.r3.3HG0319270	594,615,615	594,620,408	B3 domain-containing protein
HORVU.MOREX.r3.3HG0319280	594,622,773	594,626,954	Beta-1,3-glucanase
HORVU.MOREX.r3.3HG0319300	594,699,354	594,701,563	Beta-1,3-glucanase
HORVU.MOREX.r3.3HG0319310	594,712,025	594,712,888	F-box protein
HORVU.MOREX.r3.3HG0319320	594,721,495	594,725,844	RecA
HORVU.MOREX.r3.3HG0319330	594,731,099	594,738,322	Sentrin-specific protease
HORVU.MOREX.r3.3HG0319340	594,744,042	594,747,817	voltage-dependent L-type calcium channel subunit
HORVU.MOREX.r3.3HG0319350	594,748,418	594,749,859	Annexin
HORVU.MOREX.r3.3HG0319360	594,764,653	594,766,566	Amino acid permease
HORVU.MOREX.r3.3HG0319370	594,772,628	594,783,366	Acetyl-CoA carboxylase

387 **Table 1** High-confidence genes annotated in the sublethality interval on MorexV3 reference genome.  
 388 Coordinates refer to chromosome 3H.

### 389 *Ryd4<sup>Hb</sup>* does not prevent aphid feeding

390 Resistance to insect-transmitted viruses can either be a direct resistance to the virus or an indirect one,  
 391 through resistance to the vector. To test if *Ryd4<sup>Hb</sup>* provides resistance to its aphid vector, we monitored the  
 392 feeding of 12 to 16 aphids by EPG on five lines: two susceptible F<sub>4</sub> lines (EP\_16-271\_3\_206\_2 and  
 393 EP\_16\_460\_5\_228\_2), their two resistant sister lines (EP\_16-271\_3\_206\_4 and EP\_16\_460\_5\_228\_6) and  
 394 the susceptible barley cultivar ‘Igrı’ which was the susceptible parent of LM-Pop and JKI-5215 (Figure 7a).  
 395 As none of the selected EPG parameters showed a normal distribution according to a Shapiro-Wilk test with  
 396 a p-value threshold of 0.05, we selected the Kruskal-Wallis test for multiple comparison. No significant  
 397 differences between the lines were observed for the selected parameters s\_Np ( $\chi^2=6.78$ , df=4, p=0.148),  
 398 s\_C ( $\chi^2=2.35$ , df=4, p=0.671), s\_F ( $\chi^2=4.64$ , df=4, p=0.327), s\_G ( $\chi^2=2.96$ , df=4, p=0.565), s\_E1 ( $\chi^2=1.35$ ,  
 399 df=4, p=0.854), s\_E2 ( $\chi^2=3.16$ , df=4, p=0.534) and s\_sE2 ( $\chi^2=3.52$ , df=4, p=0.474) (Figure 7b,

400 supplementary table 9). The most divergent line was Igri, with an increased median duration for s\_Np and  
 401 decreased median durations for s\_E2 and s\_sE2, probably due to differences in the genetic background with  
 402 the other lines.



403 **Fig. 7** Aphid feeding behaviour on resistant and susceptible lines **a.** Graphical representation of the lines  
 404 used to test the aphid feeding behaviour on resistant and susceptible lines. Loci are depicted as vertical black  
 405 lines and genotypes as horizontal bars. White and black, segments represent Hv and Hb genotypes,  
 406 respectively. **b.** Duration of the different feeding events on the five lines summed up by type. s\_Np: total  
 407 duration of all non-probing events. s\_C: total duration of pathway phase. s\_F: total duration of penetration  
 408 problems. s\_G: total duration of xylem drinking. s\_E1: total duration of secretion of watery saliva. s\_E2:  
 409 total duration of phloem sap ingestion. s\_sE2: total duration of sustained phloem sap ingestion. **c.** Duration  
 410 ... Lines in the box plots indicate the median, and whiskers show the upper and lower 1,5xIQR (interquartile  
 411 range) with dots indicating outliers.

412  
 413 In addition to these general parameters, parameters associated with epidermis (t>1Pr) and mesophyll located  
 414 (t>1E) but also sieve element located (t>1E2, t>1sE2) defense responses were inspected. Igri showed the



415 longest median durations for reaching the sieve elements ( $t > 1E$ ) and to reach ingestion ( $t > 1E2$  and  $t > 1sE2$ ).  
416 However, none of the parameters  $t > 1Pr$  ( $\chi^2=3.83$ ,  $df=4$ ,  $p=0.43$ ),  $t > 1E$  ( $\chi^2=6.32$ ,  $df=4$ ,  $p=0.176$ ),  $t > 1E2$   
417 ( $\chi^2=3.43$ ,  $df=4$ ,  $p=0.489$ ) and  $t > sE2$  ( $\chi^2=5.42$ ,  $df=4$ ,  $p=0.247$ ) differs significantly between the tested lines  
418 (Figure 7c, supplementary table 9).

## 419 **Discussion**

420 BYDV is a major threat to barley cultivation that is expected to increase in the following years, as autumns  
421 become longer and warmer in Northern Europe (Roos et al., 2011; Trebicki, 2020), thus breeding for BYDV  
422 resistance will become an even higher priority. So far only partial resistance has been discovered in the *H.*  
423 *vulgare* primary genepool (Baltenberger et al., 1987; Collins et al., 1996; Lüpken et al., 2014; Niks et al.,  
424 2004; Schaller et al., 1964; Suneson, 1955). Here, we report the high-resolution mapping of *Ryd4<sup>Hb</sup>*, the first  
425 resistance gene to BYDV in barley, originating from the wild relative and secondary genepool species *H.*  
426 *bulbosum*. We mapped the gene in a 66.5 kbp-interval of the MorexV3 barley reference genome despite the  
427 linkage of the resistance locus to a sublethality factor and the reduced recombination between *H. vulgare*  
428 and *H. bulbosum* genomes.

429 At the *Ryd4<sup>Hb</sup>* locus, four genes are annotated with high confidence on the MorexV3 genome, including two  
430 genes from the CNL family, one pseudogene, and one likely to be functional. CNL genes are part of the  
431 larger NLR family which are the most common class of resistance genes to biotic stress. They are coding  
432 for intracellular proteins that form complexes (Wang et al., 2019) recognizing, directly or indirectly,  
433 pathogen effector molecules and inducing local cell death in response. More than 30 NLR genes conferring  
434 resistance to viruses have been cloned so far (Boualem et al., 2016; Sett et al., 2022) and more are candidates.  
435 An *H. bulbosum* homolog of *Ryd4\_pCNL1* or *Ryd4\_CNL2* is therefore a very likely candidate for *Ryd4<sup>Hb</sup>*.  
436 The *Ryd4<sup>Hb</sup>* locus is orthologous to the *Sr35* resistance locus from the wheat wild relative *Triticum*  
437 *monococcum* (Saintenac et al., 2013). *Sr35* is coding for a CNL protein that shares 83% identity with the  
438 translated *H. vulgare* sequence of *Ryd4\_CNL2* and provides resistance to the fungal pathogen *Puccinia*  
439 *graminis* f. sp. *tritici* causing wheat stem rust. This interval was also identified as candidate for the *Rph13*  
440 resistance gene to leaf rust in the *H. vulgare* spp. *spontaneum* accession ‘PI 531849’ (Jost et al., 2020), and,  
441 overlaps with the large interval of the *Jmv2* resistance gene to the *Japanese soil-borne wheat mosaic virus*  
442 from the barley cultivar ‘Sukai Golden’ (Okada et al., 2022). Interestingly, the best homolog of *Sr35* in rice  
443 is LOC\_Os11g43700, which was identified as a resistance gene to the *Rice yellow mottle virus* in the African  
444 rice species *Oryza glaberrima* (Pidon et al., 2017; Bonnamy et al., 2023). It is not rare that closely related  
445 NLRs provide resistance to different classes of pathogens. A good example is the potato NLRs genes GPA2  
446 and RX1 which provide resistance against the nematode *Globodera pallida* and potato virus X, respectively,  
447 and share 88% of their amino acid sequence (Van Der Vossen et al., 2000). The comparison of the *Ryd4<sup>Hb</sup>*  
448 interval in the barley pangenome (Jayakodi et al., 2020) demonstrated a very large diversity at this locus,  
449 including NLR duplications. NLRs genes are indeed frequently under diversifying selection and tend to  
450 evolve and duplicate by interallelic recombination between orthologs and by unequal crossing-over (Baggs  
451 et al., 2017; Chen et al., 2010; Ding et al., 2007; Guo et al., 2011; Li et al., 2010; Michelmore & Meyers,  
452 1998; Zhou et al., 2004). The *Sr35/Ryd4<sup>Hb</sup>* locus is one of those very diverse and dynamic loci that could be  
453 described as R gene factories. Together with the homology with other resistance loci, this locus’ NLR  
454 diversity pleads for *Ryd4<sup>Hb</sup>* to be a CNL. However, in addition to the CNL genes, an *H. bulbosum* ortholog  
455 of the *Ryd4\_ANK* could also be a good candidate. Indeed, the structure of the encoded protein is close to the  
456 one of *Arabidopsis* ACCELERATED CELL DEATH 6 (ACD6) protein. ACD6 confers enhanced resistance  
457 to bacterial pathogens, including *Pseudomonas syringae*, by increasing the level of salicylic acid and

458 inducing spontaneous cell death (Rate et al., 1999; Dong, 2004; H. Lu et al., 2003, 2005). We also cannot  
459 exclude that *Ryd4<sup>Hb</sup>* resistance is due to presence/absence variation of a gene in the primary and the  
460 secondary gene pool of barley, thus the resistance gene from *H. bulbosum* may have no ortholog in the *H.*  
461 *vulgare* interval. Cloning of *Ryd4<sup>Hb</sup>* would therefore most likely require a *de novo* genome assembly of the  
462 *Ryd4<sup>Hb</sup>* interval in a resistant genotype (introgression line of *H. vulgare* or resistance donor genotype of  
463 *H. bulbosum*).

464 Resistance to insect-transmitted viruses, like the one provided by *Ryd4<sup>Hb</sup>*, can either be a direct resistance  
465 to the virus or a resistance to the vector, which would in effect prevent infection and therefore provide  
466 indirect virus resistance. The melon NLR *Vat* resistance gene is the model of this indirect resistance. VAT  
467 provides resistance to *Aphis gossypii* and to all the viruses it transmits tested so far, including the *Cucumber*  
468 *mosaic virus* (Boissot et al., 2016). It recognizes an effector from *A. gossypii* and triggers the hypersensitive  
469 response, stopping at the same time any viral infection that may have occurred. BYDV cannot be inoculated  
470 to barley mechanically, so only resistance to the aphid vector was tested. A previous study showed that *R.*  
471 *padi* aphids were feeding less and having a shorter salivation time on the *Ryd4<sup>Hb</sup>* *H. bulbosum* resistance  
472 donor A17 compared to the BYDV-susceptible *H. bulbosum* line A21, suggesting that this could be the  
473 reason for A17 BYDV resistance (Schliephake et al., 2013). However, our study showed no differences in  
474 aphid feeding patterns on closely related resistant and susceptible lines, accompanied by an absence of  
475 BYDV infection in the resistant lines, suggesting that the preliminary observation on the *H. bulbosum* donor  
476 was probably due to A17 genetic background rather than *Ryd4<sup>Hb</sup>*. *Ryd4<sup>Hb</sup>*, therefore, provides direct  
477 resistance to BYDV.

478 *Ryd4<sup>Hb</sup>* is a prime example of the importance of crop wild relatives serving as genetic resources and gene  
479 donors in breeding schemes to achieve efficient and durable disease resistance. The advantage of using a  
480 crop wild relative in prebreeding schemes as a unique source of resistance, however, comes at a cost:  
481 reduced frequency of recombination and/or hybrid incompatibility leading to fertility or lethality problems.  
482 In the case of the *Ryd4<sup>Hb</sup>* locus, recombination is 7.5 times less than in the intraspecific barley cross used to  
483 map *Rph13*. To fine map the gene despite this handicap, we screened very large mapping populations with  
484 high throughput genotyping technologies. At the *Ryd4<sup>Hb</sup>* locus, this negative linkage drag was strongly  
485 materialized by a sublethality factor characterized by the reduced growth and early death of introgression  
486 lines carrying the Hb allele at homozygous state at this locus. By screening a large number of plants for  
487 recombination, we managed to break the linkage, producing a resistance donor without the sublethality  
488 factor, that could be included in breeding schemes. We mapped the sublethality factor to a 600 kbp interval  
489 on MorexV3 genome. The observed phenotype suggested that sublethal plants are possibly lacking an  
490 essential gene, or a few genes, for development, therefore that one of the genes of the *H. vulgare* interval  
491 has no ortholog in the donor *H. bulbosum* genome. Among the 15 genes annotated with high confidence in  
492 the interval, B3 domain-containing proteins are part of a large transcription factor superfamily whose  
493 members are playing key roles in various stages of plant development, from embryogenesis to seed  
494 maturation (Swaminathan et al., 2008). F-box containing proteins are central part of the ubiquitin–26S  
495 proteasome system and are thus key for different processes like phytohormone signaling, plant development,  
496 cell cycle, or self-incompatibility (Stefanowicz et al., 2015). RecA proteins are maintaining DNA integrity  
497 during meiosis by initiating double-strand break repair (Emmenecker et al., 2023). Annexins are widely  
498 involved in regulating plant processes, from growth and development to responses to stresses (Wu et al.,  
499 2022). One of the corresponding genes in the MorexV3 interval could be missing in the A17 haplotype and  
500 explain the observed phenotype.

501 The results of this study would be helpful to breed barley varieties with an effective resistance to BYDV.  
502 We identified recombinants with a strongly reduced *H. bulbosum* fragment that can be used in breeding  
503 schemes, removing almost completely the negative linkage drag. The markers closely linked to the  
504 resistance can then be used in marker-assisted and genomic selection, postponing the tedious resistance  
505 evaluation to the last breeding step. Knowing that *Ryd4<sup>Hb</sup>* is a direct resistance gene to BYDV would also  
506 make it possible to establish the best strategy to avoid resistance breaking. Such a strategy could be  
507 pyramiding it with partial resistance or tolerance sources like *Ryd2* and *Ryd3*. Such resistant varieties would  
508 make a major contribution to sustainable barley cultivation.

509  
510 **Supplementary figure 1** Comparison of *Ryd4<sup>Hb</sup>* in *H. vulgare* pangenome modify from Easyfig 2.2.5  
511 output. Only fragments with more than 80% nucleotide identity are shown.

512

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