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1 **CHARACTERIZATION OF BLACK SPOT RESISTANCE IN**
2 **DIPLOID ROSES WITH QTL DETECTION, META-ANALYSIS AND**
3 **CANDIDATE-GENE IDENTIFICATION**

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29

30 **Key message**

31 Two environmentally stable QTLs linked to black spot disease resistance in the *Rosa wichurana* genetic
32 background were detected, in different connected populations, on linkage groups 3 and 5. Co-localization between *R*-
33 genes and defense response genes was revealed via meta-analysis.

34 **Abstract**

35 The widespread rose black spot disease (BSD) caused by the hemibiotrophic fungus *Diplocarpon rosae* Wolf.
36 is efficiently controlled with fungicides. However, in the actual context of reducing agrochemical use, the demand for
37 rose bushes with higher levels of resistance has increased. Qualitative resistance conferred by major genes (*Rdr* genes)
38 has been widely studied but quantitative resistance to BSD requires further investigation. In this study, segregating
39 populations connected through the BSD resistant *Rosa wichurana* male parent were phenotyped for disease resistance
40 over several years and locations. A pseudo-testcross approach was used, resulting in six parental maps across three
41 populations. A total of 45 individual QTLs with significant effect on BSD resistance were mapped on the male maps
42 (on linkage groups (LG) B3, B4, B5 and B6), and 12 on the female maps (on LG A1, A2, A3, A4 and A5). Two major
43 regions linked to BSD resistance were identified on LG B3 and B5 of the male maps and were integrated into a
44 consensus map built from all three of the male maps. A meta-analysis was used to narrow down the confidence intervals
45 of individual QTLs from three populations by generating meta-QTLs. Two “hot spots” or meta-QTLs were found per
46 LG, enabling reduction of the confidence interval to 10.42 cM for B3 and 11.47 cM for B5. An expert annotation of
47 NBS-LRR encoding genes of the genome assembly of Hibrand et al. was performed and used to explore potential co-
48 localization with *R*-genes. Co-localization with defense response genes was also investigated.

49

50 **Keywords**

51 *Rosa*, quantitative resistance, natural infection, *Diplocarpon rosae*, QTL mapping, meta-analysis

52

53 **Conflict of interest**

54 All authors declare that they have no conflicts of interests.

55 **Ethical standards**

56 We declare that these experiments complied with the ethical standards in France.

57 **Availability of data and material**

58 Genetic maps and QTL tables are available as supplementary data.

59 **Author contribution**

60 DCLA participated in the phenotyping, performed the genetic and statistical analyses and wrote the paper.
61 VSF, FF and LHSO conceived the AC provided a technical support in the SSR genotyping and participated in the
62 phenotyping. TT coordinated the field trials and participated in the phenotyping. LVE and JB performed the manual
63 annotation and provided revision of the manuscript. YDO provided support in software Biomercator and the meta-
64 analysis approach. FF provided extensive revisions of the manuscript. SP, LHSO and VSF participated in the
65 phenotyping and provided extensive revisions of the manuscript. All authors read the final version of the manuscript
66 and approved its publication.

67

68 **Introduction**

69 Cultivated roses are among the most popular garden plants (Waliczek et al. 2015a; Wang et al. 2017). In
70 France, 16% of shrubs bought by the final consumers are garden roses, with a market value of 50.6 million Euros in
71 2017. Due in part to susceptibility to BSD, sales of garden roses in France declined 10% in 2017 compared with 2016
72 (VAL'HOR and FranceAgriMer 2017). As such, BSD causes large economic losses and is, therefore, considered the
73 most serious disease of cultivated roses grown outdoors.

74 BSD in roses, caused by the hemibiotrophic fungus *Diplocarpon rosae* Wolf, is globally distributed and
75 affects nearly all modern varieties. To date, 13 races have been reported (Carlson-Nilsson 2001; Gachomo et al. 2006;
76 Whitaker et al. 2007, 2010b; Zlesak et al. 2010; Zurn et al. 2018). Typical symptoms of this disease include dark
77 rounded spots with fringed margins on the adaxial side of the leaves followed by chlorosis around the lesion and

78 premature defoliation (Blechert and Debener 2005; Gachomo et al. 2006; Horst and Cloyd 2007). Reduced vigor in
79 susceptible varieties can be observed, sometimes leading to death due to increased susceptibility to other stresses, like
80 frost (Smith et al. 1989; Black et al. 1994). It is, then, important to study the rose-*Diplocarpon rosae* pathosystem.

81 The BSD fungus is obligate to the genus *Rosa*, though other *Diplocarpon* species are pathogenic on different
82 crop species in the *Rosaceae* genus (Horst and Cloyd 2007). *Diplocarpon rosae* is spread mainly through asexual
83 spores that are water-borne. During the infection process, the spores germinate, develop a germ tube with a melanized
84 appresorium and penetrate the leaf cuticle (Gachomo 2005; Gachomo et al. 2006, 2010; Gachomo and Kotchoni 2007).
85 During the biotrophic phase, subcuticular hyphae are formed followed by intercellular hyphae. Haustoria can be
86 observed in this first stage of infection (Gachomo 2005; Gachomo and Kotchoni 2007). Then, the pathogen switches
87 from a biotrophic lifestyle to a necrotrophic one and forms necrotrophic intracellular hyphae, followed in short order
88 by a production of acervuli and second-generation conidia. On susceptible plants, a new generation of conidia is
89 produced within nine days after inoculation (Gachomo 2005; Gachomo et al. 2006; Gachomo and Kotchoni 2007).
90 Conidia are then spread by water-splash to start a whole new infection process on other leaves. Effective infection
91 requires free water and humid conditions (Saunders 1966; Wiggers et al. 1997). Consequently, BSD is especially
92 problematic in areas with high annual precipitation and humidity (Debener 2017).

93 BSD is rarely observed in greenhouse production as humidity can be carefully regulated. Garden rose
94 multiplication and grafting are mainly done in the field, and rose bushes are generally used in gardens and landscaping
95 for aesthetic value and low maintenance requirements. Due to the perennial habit of garden roses and *D. rosae*
96 overwintering in fallen leaves, new infections can appear each year if the disease is not well managed (Münnekhoff et
97 al. 2017) and can impact final consumers such as private gardeners and public garden managers. BSD is traditionally
98 managed with fungicide applications. To reduce risk of chemical exposure, added costs and labor associated with this
99 type of management, today's consumers are increasingly asking for natural resistance in rose plants (Harp et al. 2009;
100 Zlesak et al. 2010, 2017; Waliczek et al. 2015b; Byrne et al. 2019). Moreover, European countries have adopted new
101 laws to preserve the environment that aim to decrease agrochemical use. For example in France, measures such as the
102 Ecophyto Plan (Labbé 2014) have forbidden the use of chemicals in public landscaping and private gardens since
103 January 2017 and 2019, respectively (Labbé 2014). These concerns have encouraged breeders and researchers to study
104 BSD and to develop varieties with sustainable and higher levels of resistance.

Indeed, genetic resistance is a critical challenge to successful disease management in an environmentally friendly and cost-effective manner. Researchers have studied the genetic resistance to BSD, helping to identify modern rose varieties and wild species with high levels of resistance (Wiggers et al. 1997; Carlson-Nilsson 2001; Boontiang 2003; Blechert and Debener 2005; Uggla and Carlson-Nilsson 2005; Harp et al. 2009; Schulz et al. 2009; Soufflet-Freslon et al. 2019). However, breeding for BSD resistance is complex due to the development of new pathogenic races and different ploidy levels in the genus *Rosa* (Debener et al. 1998; Uggla and Carlson-Nilsson 2005; Whitaker et al. 2007; Debener 2017). Four major loci associated with BSD resistance were identified mostly using detached leaf assays: *Rdr1* and *Rdr2* on chromosome 1 (Malek and Debener 1998; Yokoya et al. 2000; Malek et al. 2000; Kaufmann et al. 2003, 2010; Hattendorf et al. 2004; Whitaker et al. 2010a; Terefe-Ayana et al. 2011; Menz et al. 2018, 2020), *Rdr3* recently found to be located on chromosome 6 (Whitaker et al. 2010a; Zurn et al. 2020) and *Rdr4* possibly located on chromosome 5 (Zurn et al. 2018). Evidence of partial resistance to BSD was reported in several cases and seems to be race-non-specific (Xue and Davidson 1998; Shupert 2006; Whitaker and Hokanson 2009; Whitaker et al. 2010b; Allum et al. 2010; Dong et al. 2017). Quantitative resistance often confers a partial level of resistance to the plant by reducing pathogen multiplication, plant colonization, disease spread or symptom severity (Pilet-Nayel et al. 2017). This type of resistance is usually controlled by several genes and is associated with genomic regions termed Quantitative Trait Loci (QTLs). Over the last 20 years, many QTL experiments for disease resistance have been carried out on major crops (Lacape et al. 2010; Qi et al. 2011; Holland and Coles 2011; Yadava et al. 2012; Hamon et al. 2013; Semagn et al. 2013; Said et al. 2013; Pilet-Nayel et al. 2017). More recently, QTL analyses have been conducted on ornamental crops such as carnations, gerberas or roses (Yagi et al. 2006, 2012; Leus et al. 2015; Fu et al. 2017; Yan et al. 2019). On-going research suggests QTLs conferring resistance to BSD. Yan et al. (Yan et al. 2019) have identified a possible major QTL on LG 3, based on one year of phenotypic data and a pedigree based map of 15 diploid genotypes while Soufflet-Freslon et al. (Soufflet-Freslon et al. 2019) identified possible QTLs in two populations in France. These emerging studies aside, quantitative resistance to BSD has not been extensively studied, yet it remains a powerful tool to identify genomic regions involved in complex traits such as disease resistance.

The validity of QTL mapping results is influenced by many factors, including experimental conditions, choice of parents, rating scale, environmental conditions during the scored years, type and size of mapping populations, map density and statistical methods (Lanaud et al. 2009; Liu et al. 2009; Vasconcellos et al. 2017; Guo et al. 2018). Thus, QTL mapping of one trait across multiple populations and environments can frequently yield heterogeneous results

133 comprising different genomic positions and large confidence intervals. Further refinement of these intervals and
134 synthesis of all QTL information are difficult but necessary steps prior to QTL cloning attempts and MAS breeding
135 application. Meta-analysis is an effective approach to combine QTL results from independent studies and refine QTL
136 positions on a consensus genetic map (Goffinet and Gerber 2000; Veyrieras et al. 2007). This method was useful in
137 characterizing the genetic determinants of complex traits for a variety of crops such as drought stress in rice (Khowaja
138 et al. 2009), ear emergence in wheat (Griffiths et al. 2009), yield and anthesis silking in maize (Semagn et al. 2013),
139 yield associated traits in *Brassica juncea* (Yadava et al. 2012), seed weight and resistance to soybean cyst nematode
140 in soybean (Guo et al. 2006; Qi et al. 2011), partial resistance to *Aphanomyces euteiches* in pea (Hamon et al. 2013)
141 or fiber quality, yield, drought tolerance and disease resistance in cotton (Lacape et al. 2010; Said et al. 2013). With
142 plant genome sequences becoming increasingly available, it is now possible to apply comparative analysis between
143 genetic and physical maps to identify candidate genes underlying MetaQTLs. This approach has not yet been explored
144 for an ornamental crop such as roses.

145 The main objective of our study was to explore the genetic determinants of BSD resistance in *Rosa wichurana*
146 (RW). We identified QTLs linked to BSD resistance in RW using three different populations phenotyped over several
147 years and locations. We next evaluated the stability of these QTLs and their inheritance in different genetic
148 backgrounds. Finally, we explored sets of candidate genes at BSD resistance QTL locations using one of the recently
149 published rose genome assembly from Hibrand-Saint Oyant et al. in 2018.

150

151 **Material and methods**

152 **Mapping populations**

153 We used *R. wichurana* (RW) as a source of resistance. Indeed, RW was described to be highly resistant to
154 BSD (Debener et al. 1998; Yan et al. 2019). RW was crossed with different cultivars to develop three F1 progenies:

155 - OW population (151 individuals) was obtained from a cross between *R. chinensis* ‘Old Blush’ (OB),
156 susceptible to BSD, and RW (Lopez Arias et al. in press; Hibrand-Saint Oyant et al. 2018; Soufflet-Freslon et al. 2019),

157 - HW population (209 individuals) was generated from a cross between a dihaploid rose named H190 (Meynet
158 et al. 1994), susceptible to BSD, and RW (Soufflet-Freslon et al. 2019),

159 - FW population (96 individuals) resulted from a cross between the cultivar ‘The Fairy’ (TF) and RW
160 (Kawamura et al. 2015). In the Earth-Kind® Trials using detached leaf assay, TF was shown to be susceptible to
161 pathogen races 3, 8 and 9 (Zlesak et al. 2010).

162 The OW and FW populations were planted on their own roots in the field at INRA Horticulture Experimental
163 Facility (Beaucouzé, France). The HW population was grafted on to *Rosa canina* 'Laxa' rootstock and planted in three
164 French sites (Soufflet-Freslon et al. 2019):

- 165 - Nursery France Pilté (45270 Quiers-sur-Bezonde, Loiret, France), henceforth referred to as Bellegarde,
- 166 - Nursery/Breeder Meilland Richardier (Diémoz, Isère, France), henceforth referred to as Diémoz,
- 167 - Horticulture Experimental Facility (Beaucouzé, France), henceforth referred to as Angers.

168 Pruning was performed in November followed by a copper treatment to protect against canker. One to two applications
169 of the fungicide NIMROD® were made according to manufacturer’s recommendations in the Spring to prevent
170 powdery mildew development, and an aphicide spray was used if necessary. NIMROD® is not effective against *D.*
171 *rosae* and no broad-spectrum fungicide was used.

172 For the HW and FW populations, field trials were performed in a randomized complete block design
173 with three replicates. Due to production problems, only one replicate per individual for the OW population was used.
174

175 **Disease scoring and statistical analyses**

176 BSD was visually scored for each population two years after planting them in the field and at the peak of disease
177 (between July and September depending on the year). BSD was scored on the lower part of the plant using a visual
178 rating scale from 0 to 5 presented in Supplementary figure 1 (Marolleau et al. 2020; Soufflet-Freslon et al. 2019).
179 These scores correspond to a percentage of infected leaves and a degree of defoliation (scores 4 and 5). Disease
180 resistance or susceptibility on field trials was assessed using the visual rating scale described above. First, plants with
181 a score lower than 1 were considered “resistant”. Indeed, the response to the *D. rosae* infection seemed to prevent
182 pathogen development on the leaves or considerably reduce pathogen growth on the plant, leading to no visible
183 symptoms (score 0) or to the infection of a small portion of leaves (less than 25% of the lower part of the plant). Then,
184 plants with a score lower than 4 were considered “intermediate” as less than 75% of the lower part of the plant was
185 infected but no defoliation had yet occurred. Finally, susceptible plants were scored 4 to 5 with more than 75% of the

186 lower part of the plant showing symptoms and/or a sever defoliation at that time, meaning that the response to the
187 infection did not efficiently impair pathogen development.

188 The OW population was scored from 2014 to 2018 (Lopez Arias et al. in press), the HW population was scored from
189 2012 to 2014 (Soufflet-Freslon et al. 2019) and in 2018, and the FW population was scored in 2014 and 2018.

190 All phenotypic data were analyzed with Rstudio interface (version 1.1.463, <http://www.rstudio.com/>) of R
191 software (<http://www.r-project.org/>), version 3.5.1 (2018-07-02).

192 An overall mean for each population was calculated for each year of scoring to assess whether or not the
193 disease incidence was uniform over the years using a Kruskal-Wallis test (for OW and HW populations) and a
194 Wilcoxon test (for FW population).

195 The normality of residuals was tested using a Shapiro-Wilk test and the homogeneity of variance was assessed
196 with a Bartlett's test. However, in field situations, plants can die or disease scoring can be missing, resulting in
197 unbalanced experimental designs. Unlike analysis of variance (ANOVA), maximum likelihood methods, such as
198 Restricted Maximum Likelihood (REML), provide unbiased estimators without any demand on the design and balance
199 of data (Patterson and Thompson 1971; Corbeil and Searle 1976; Harville 1977; Lynch and Walsh 1998; Holland et
200 al. 2010). Based on the data distribution, REML was used in place of ANOVA to estimate variance components using
201 the package 'sommer' (Covarrubias-Pazaran 2019) in R. The broad-sense heritability was calculated for each
202 population based on the following formula:

203 $H^2 = \sigma_g^2 / (\sigma_g^2 + \frac{\sigma_{gxe}^2}{a} + \frac{\sigma_e^2}{ar})$, where σ_g^2 is the genotypic variance among populations, σ_{gxe}^2 is the variance of
204 the interaction between genotype and environment (year/location for HW and year for FW and OW), σ_e^2 is the residual
205 variance, a is the number of scoring years and r the number of replicates in each population.

206

207 **Genetic data and linkage mapping**

208 It is not possible to obtain homozygous parental lines in rose by self-fertilizing due to strong inbreeding
209 depression. As such, a "double pseudo-testcross strategy" developed for highly heterozygous plants (Grattapaglia and
210 Sederoff 1994; Weber et al. 2003; Fischer et al. 2004; Hibrand-Saint Oyant et al. 2007; Roman et al. 2015; Zurn et al.
211 2018; Bourke et al. 2018; Yan et al. 2019) was used in the current study. This strategy involves a controlled cross
212 between two genotypes, with heterozygous genetic markers originating from either parents, followed in their F1

213 generation. Multiple maximum likelihood mapping was conducted using JoinMap V4.1(Van Ooijen 2011) using the
214 CP (Cross population = outbreed full-sib family) population setting. In this analysis, molecular markers can segregate
215 in one or both parents, with maps comprising dominant and co-dominant markers calculated separately for each parent
216 followed by construction of an integrated consensus map.

217 Parental linkage maps for FW and HW populations were constructed from previously published data
218 (Kawamura et al. 2015; Roman et al. 2015). Constructed maps were checked for apparent genotyping errors and/or
219 poor fitting loci by looking at aberrant number of double crossing, high values of ‘Nearest Neighbor fit’ (N.N fit) and
220 genotype probabilities (-Log10(P)). When outstanding loci were found, genotyping was controlled either with
221 SNP/probeset categories according to cluster properties or raw genotyping from GeneMapper software and removed
222 when necessary. Maps were then re-calculated. The consensus map released by (Spiller et al. 2011) was used to check
223 LG names and whole LG inversions for consistency.

224 Parental linkage maps for the OW population were developed using previously reported single nucleotide
225 polymorphism (SNP) marker data (Hibrand-Saint Oyant et al. 2018). Short sequence repeat (SSR) markers previously
226 genotyped in this population were also included (Lopez Arias et al. in press) and used as common markers for the
227 Meta-QTL analysis. Parental maps were calculated using JoinMap 4.1 (Van Ooijen 2011) but due to insufficient
228 “anchor loci” (i.e. makers heterozygous in both parents) an integrated map could not be obtained for this population.
229 Following calculation of pair-wise recombination frequencies, seven LGs were identified using the logarithm of odds
230 (LOD) score of independence between pairs of loci at a threshold of 4. Due to a large number of markers per LG (from
231 171 to 1,134 markers), the maximum-likelihood mapping algorithm method was used to order markers on LGs. Indeed,
232 this method is more suitable than regression mapping for large marker datasets (Cheema and Dicks 2009). The
233 maximum-likelihood mapping algorithm method was carried out under default JoinMap calculation settings (i.e.
234 simulated annealing chain length of 10,000 with an acceptance probability threshold of 0.25, Gibbs sampling for
235 estimation of multipoint recombination frequencies with a burn-in chain length of 10,000 and a chain length per Monte
236 Carlo EM algorithm of 1,000). The same procedure previously described was carried out to identify and remove
237 markers with genotyping errors and poor fitting.

238

239 **QTL mapping**

240 QTL mapping was performed using the parental maps for each population (OW, FW and HW) and data from
241 different years were analyzed separately. The R/QTL package (Broman and Sen 2009; Broman and Wu 2019) was
242 used to map QTLs and specific analyses were carried out for each set of phenotypic data according to the distribution
243 of disease scores. For all populations, scoring years and locations, a “one dimensional QTL scan” was carried out using
244 different specific models that best fit the data using the package R/QTL on the Rstudio interface (Broman and Sen
245 2009).

246 For data distributed normally, a three-step strategy was employed using a normal model for simple interval
247 mapping (SIM) and composite interval mapping (CIM). First, the multiple imputation method was used to overcome
248 issues with missing data as it fills in all missing genotype data even at sites between markers on a defined grid along
249 LGs (Broman and Sen 2009). For this, the function ‘sim.gen’ was used with 200 imputations and a step size of 1cM.
250 Next, using the previous simulated data, a genome scan with a single QTL model (SIM) was performed with the
251 function ‘scanone’ (parameters: normal model and imputation method). Finally, a permutation test with 1,000
252 permutations of the data was used to identify genome-wide significance thresholds for declaring the presence of a QTL
253 (Doerge and Churchill 1996). When QTLs were identified, CIM was performed to improve further QTL detections by
254 including a marker at the peak of QTL with large effect as covariate (Broman and Sen 2009).

255 For data exhibiting a substantial peak at zero, the mapping strategy was based on a two-part model used to
256 better characterize the influence of a QTL presence on BSD (Broman 2003; Broman and Sen 2009; Holland and Coles
257 2011). For this approach, the phenotypic data were analyzed in two parts. First, individuals with scoring values above
258 zero were analyzed using a normal phenotype model. Second, the trait was considered as binary (0 and >0) (Broman
259 2003; Broman and Sen 2009). The two-part model performs the following three calculations, each with a resulting
260 LOD score: (1) the hypothesis that a given QTL increased the probability that an individual had a null phenotype
261 ($LOD\pi$), and so was resistant (which can also be referred as the penetrance of the disease); (2) the hypothesis that a
262 detected QTL influenced the average phenotype among individuals with non-null phenotypes ($LOD\mu$), so it affected
263 the severity of the disease; (3) the probability of having a QTL at a given position ($LOD\mu,\pi$) (simply the sum of LOD
264 scores from the preceding analyses).

265 To characterize detected QTLs, approximate 95% Bayesian credible intervals, phenotypic variation and QTL
266 effects were estimated using the functions bayesint, makeqtl/fitqtl and effectplot respectively.

267

268 **Meta-QTL analysis**

269 The meta-QTL analysis was conducted with Biomercator v4.2.2 software (Arcade et al. 2004; Sosnowski et
270 al. 2012). The total number of QTLs per LG for all three populations was recorded. LGs with more than three QTLs
271 and with QTLs from all the populations were considered for the meta-analysis. Input map files and QTL files for
272 Biomercator v4.2.2 were prepared for the male parent map of each population according to its requirements.

273 Using the male map of OW population as the reference linkage map to fix locus order, a consensus male map
274 was constructed using ConsMap (based on a weighted least square (WLS) strategy). To identify meta-QTLs, we
275 pursued the approach proposed by Goffinet and Gerber in 2000. Due to the fact that our mapping populations share a
276 common male parent and because the same plants were phenotyped across years, our data are not completely
277 independent. In simulation tests, the Goffinet approach proved to be robust, obviating the need for further manipulation
278 of non-independent data (Goffinet and Gerber 2000). The method first tests the likelihood of QTL grouping in
279 maximum four groups and then selects the optimum number of groups using an ‘Akaike’ information criterion (AIC)
280 (Arcade et al. 2004; Sosnowski et al. 2012). Estimated positions and confidence intervals (CI) of all consensus QTLs
281 were provided and the resulting meta-QTLs were projected on the previously constructed consensus map using
282 QTLProj.

283

284 **NB-encoding genes and candidate-gene mining**

285 In version 4.2.2 of Biomercator, genetic maps can be linked to genome annotation using anchor markers.
286 Genes underlying QTL or meta-QTL confidence intervals (CI) can be listed and basic gene ontology (GO) term
287 representation within CI, chromosome or whole genome can be applied. In this study, we compared the lists of genes
288 underlying meta-QTLs for the recently released rose genome sequence (Hibrand-Saint Oyant et al. 2018).

289 To detect potential candidate-genes, a detailed analysis of NBS-LRR genes was performed. Protein sequences
290 from Rosa chinensis (Hibrand-Saint Oyant et al. 2018) were scanned for the presence of R-gene-related domains using
291 the hmmsearch algorithm in HMMER v3.1b2 (Finn et al. 2015). These domains included NB-ARC (PF00931), TIR
292 (PF01582, PF13676) and LRR (PF00560, PF07723, PF07725, PF12799, PF13306, PF13516, PF13855, PF14580)
293 domains as defined in the Pfam database (Finn et al. 2016). Only proteins with an NB-ARC domain hit longer than 20
294 amino acid residues and with E-value $< 1 \times 10^{-5}$ were retained for subsequent analysis. These sequences were

295 scanned for the presence of additional, non-canonical domains. The presence of coiled-coil domains was determined
296 for each protein using ncoils with the arguments “-c -w -win 21 -min_P 0.75” and “-c -w -win 28 -min_P 0.75” (Lupas
297 et al. 1991). Custom python scripts were developed to parse, tile and filter the scan output to obtain detailed domain
298 configuration for each protein sequence. NB-ARC domains were extracted from each sequence according to the
299 hmmcan results, and used for subsequent phylogenetic analysis. NB-ARC sequences were coalesced into homology
300 groups using USEARCH with the arguments “-cluster_agg %s -id 0.8 -linkage min” (Edgar 2010). A multiple sequence
301 alignment was constructed for each homology group using MUSCLE (Edgar 2004), and consensus sequences obtained
302 using HMMBUILD and HMMEMIT in HMMER v3.1b2. A multiple sequence alignment was constructed from all
303 consensus sequences using MUSCLE and converted to the PHYLIP format (Felsenstein 1989). RaxML was used to
304 construct the phylogeny (Stamatakis 2014), using 100 bootstrap replicates and an NB-ARC consensus sequence from
305 *Arabidopsis thaliana* as outgroup, with the arguments “-m PROTCATDAYHOFF -T 24 -f a -x 98 -p f -N 100”.
306 Chromosomal positions for candidate *R*-genes were used to construct a physical map of *R*-gene distribution within the
307 genome, using CIRCOS (Krzywinski et al. 2009).

308

309

Results

310

Disease scoring and statistical analyses

311

BSD was recorded in all three studied populations over several environments (years and locations) under natural infection in fields with no chemical treatment. Across all scoring years, the parents RW and TF were found resistant to BSD with a mean score of 0.50 and 0.33, respectively. The H190 female parent was classified as intermediate with a mean score of 3.44 for all locations whereas OB had a mean score of 4.7 and was classified as susceptible to BSD.

316

For the OW population, the mean annual BSD scores from 2014 to 2018 were not significantly different from each other ($H=7.2759$, 4 d.f., $P=0.122$, see Supplementary figure 2) indicating that the disease impact on the OW population was homogeneous over 2014-2015-2016-2017 and 2018. The disease scores in the OW population ranged from 0 to the maximum score 5. The median of 2018 scoring was higher than for other years. Residuals for the OW population showed a distribution close to normal ($W=0.99509$, $P=0.02045$) but the homogeneity of variance across years was not validated by a Bartlett's test ($K=298.1$, 9 d.f., $P<0.001$).

322 For the FW population, BSD scores in 2014 were significantly different from those in 2018 ($Z=-12.648$, 5
323 d.f., $P<0.001$, see Supplementary figure 2). In general, the FW population was more resistant than the two other
324 populations with scores ranging from 0 to 4. Additionally, FW was the only population showing no defoliation due to
325 disease. The phenotypic distribution of the FW population showed a peak at 0 and the residuals did not follow a normal
326 distribution ($W=0.93557$, $P<0.001$). However, homogeneity of variance across years was validated ($K=298.1$, 9 d.f.,
327 $P<0.001$).

328 For the HW population, the mean of BSD scores in different locations was significantly different ($H=476.52$,
329 2 d.f., $P<0.001$, data not shown), so all three locations were considered separately. In the three locations (Angers,
330 Bellegarde and Diémoz), BSD was scored over several years (four, three and three years respectively) and infection
331 levels for each year within a location were significantly different from each other ($Ha=346.74$, 3 d.f., $P<0.001$;
332 $Hb=308.8$, 2 d.f., $P<0.001$ and $Hd=212.43$, 2 d.f., $P<0.001$; respectively, see Supplementary figure 2). BSD scores
333 ranged from 0 to 4 for Angers and Bellegarde, and no individual was found completely resistant in Diémoz in all
334 scoring years with BSD scores ranging from 0.67 to 4. A spike-like distribution was observed in 2018 in Angers, 2014
335 in Bellegarde and 2013 in Diémoz. Normality of residuals as well as homogeneity of variance were not validated
336 (respectively $W=0.99618$, $P<0.001$ and $K=35.799$, 9 d.f., $P<0.001$). Interestingly, scoring year 2012 was lower than
337 2013 and 2014 for all three locations, and for Angers in 2018, many individuals presented a high resistance. However,
338 the mean of BSD over the three years (2012, 2013 and 2014) was always the lowest in Angers, intermediate in
339 Bellegarde and the highest in Diémoz.

340 Since normality and variance homogeneity assumptions were not validated for all three populations, the
341 calculation of variance components was obtained using the REML method. The broad sense heritability of BSD
342 resistance was estimated to be 0.79, 0.86 and 0.65 for the OW, HW and FW populations, respectively, indicating that
343 BSD resistance is mainly controlled by genetic factors in all three populations. Moreover, the proportion of phenotypic
344 variance due to genetic effects, here the variance in response to *D. rosae* infection due to genetic background of the
345 individuals, seems to be higher for HW than for OW and lower for FW.

346

347 **Linkage mapping of parental maps**

348 Parent-based maps were constructed for the HW and FW populations using previously published data
349 (Kawamura et al. 2011, 2015; Roman et al. 2015). For both populations, seven LGs were defined and named according

350 to the rose integrated consensus map of (Spiller et al. 2011). For the HW population, the male map comprised 56
351 markers covering 418.58 cM, and the female map comprised 37 markers covering 313.89 cM. On LG6 of the female
352 map, only two markers were found heterozygous and were mapped. For the FW population, the male map comprised
353 94 markers covering 457.94 cM and the female map comprised 75 markers with a coverage of 369.91 cM.

354 For the OW population, we generated linkage maps with already published data by (Hibrand-Saint Oyant et
355 al. 2018) and SSR markers selected to facilitate meta-analysis. A total of 497 SNP and 36 SSR markers were mapped
356 on the male map. The resulting map comprises 402 unique loci assigned to seven LGs, designated B1-B7. The average
357 marker interval was 1.14 cM (Table 1 and Supplementary figure 4) and the entire map covered 453.62 cM. LGs range
358 in size from 42.6 (B3) to 84.34 cM (B2). A total of 692 SNP markers, 31 SSR markers and one gene (*NP* also known
359 as *RoAP2*, see Table 1 and Supplementary figure 3) were mapped in the female of the OW population. The resulting
360 map included 513 unique loci assigned to seven LGs (named A1-A7). The average distance between markers is 0.96
361 cM and LGs range in size from 33.42 (A2) to 97.65 cM (A5). The female map for the OW population is 473.85 cM in
362 total length.

363 Common markers were the ones shared by at least two populations. In total, 72 markers (41 common markers
364 found for the male maps and 31 for the female maps) were used as “bridge markers” to connect the OW, FW and HW
365 linkage maps (Table 1, listed on Supplementary table 1). The number of common markers per LG ranged from three
366 (B1-B6 and A1-A6-A7) to nine (B3) (Table 1). Of 41 markers shared by at least two of the male linkage map, 21 were
367 shared by all three male maps. Only eight markers were shared by the three female maps (Supplementary table 1).
368 There was at least one common marker between the three populations for all LGs of the male and the female (except
369 for A1) maps.

370

371 QTL analysis

372 First, QTL detections within populations were performed using the parental genetic maps and phenotypic data
373 of BSD resistance from the OW, HW and FW populations. In each population, individuals showed variable resistance
374 responses across environments and years, so locations and years were considered separately in QTL analysis
375 (Supplementary figure 2).

376 Two methods were adopted to perform QTL detection according to data distribution. Phenotypic data for the
377 OW population and the HW population, with the exception of Angers 2018, Bellegarde 2014 and Diémoz 2013

378 phenotypic data (Figure 1) were analyzed using a normal model for simple interval mapping (SIM) and composite
379 interval mapping (CIM). All other data exhibiting spike-like distribution were analyzed with a two-part model,
380 henceforth referred as “2p” (Broman 2003). In addition, a mean across years was applied for each population (and for
381 the HW population for each location separately). Then a normal method for QTL detection was used.

382 In total with the method for normally distributed phenotypes, 35 QTLs associated with BSD resistance were
383 detected for the male maps, and eight QTLs were detected for the female maps. For spike-like distributions, ten QTLs
384 were detected with the male maps and four with the female maps.

385 *Male maps*

386 For all three populations, across years and locations combined, a total of 45 QTLs with significant effects on
387 BSD resistance were identified on LGs B3, B4, B5 and B6 (Table 1 and Supplementary figures 5, 6, 7 and 8). QTLs
388 on B3 and B5 were found for all three populations, whereas QTLs on B4 and B6 were population-specific (OW and
389 HW, respectively).

390 QTLs on B3 were identified for all years and locations with both detection methods. Phenotypic variance
391 within-population explained by individual QTLs on B3 varied from 3.9% to 23.6% and the LOD values varied from
392 2.73 to 15.23 (Table 2). For the OW population, five marker peaks were found in a region from 4cM to 26cM for the
393 different years (Supplementary figure 5 and Table 2); for the HW population, five marker peaks were also found in a
394 region from 3 to 19cM for all scoring years and locations (Supplementary figures 7 and 8). For spike-like distributions,
395 2p model provides more information on the effect of the QTLs found. Indeed, for 2018 BSD scores of FW and HW in
396 Angers and 2014 BSD scores of HW in Bellegarde, both LOD scores calculated for the 2p model exceeded their
397 respective LOD thresholds (respectively Supplementary figures 6B, 8A and 8B, Table 2). This means that the QTLs
398 found on B3 affects the penetrance (appearance of the symptoms) as well as the severity of the disease. However, for
399 HW Diémoz 2013, only the LOD π reached its corresponding threshold meaning that the QTL found on B3 for 2013
400 affected only the penetrance. The 2p model gave a better precision on the QTL location on B3 from the beginning of
401 the LG to 9.67cM (Table 2).

402 QTLs on B5 were found repeatedly for each scoring year and location in the HW population (Supplementary
403 figures 7 and 8), and were year dependent in the OW population (detected for scoring years 2016, 2017 and 2018, see
404 Supplementary figure 5). A QTL on B5 was also detected on FW for scoring year 2018. The LOD peak values varied
405 from 3.43 to 12.14, and the phenotypic variance ranged from 2.89% to 19.82% (Table 2). For the OW population, two

406 close peaks were found for scoring years 2017, 2018 and the mean in a region from 8.71cM to 10cM. For all scoring
407 years and locations for the HW population, four marker peaks were found in a region from 23cM to 41cM
408 (Supplementary figures 7 and 8). Interestingly, in the OW population in 2016, the FW population in 2018, and for all
409 years and locations for the HW population, a second peak on the distal end of B5 can also be observed (Supplementary
410 figures 5, 6B, 7 and 8).

411 Two QTLs were identified on B4 in 2017 and with the mean across years for the OW population, explaining
412 5.1 to 7.6% of the phenotypic variance. The location of the B4 QTL was defined more precisely using BSD scores
413 averaged across years (10cM region) than a single year scores (entire LG based on 2017 data, see table 2).

414 QTLs with significant but small effects on BSD resistance were mapped on B6 in most years and locations
415 for the HW population as well as for the average BSD scores. These QTLs were population-specific and were only
416 detected when RW was crossed with H190 (Supplementary figures 7 and 8). The LOD peaks ranged from 2.6 to 5.92
417 explaining 3.6 to 4.63% of phenotypic variance (Table 2). For data from HW Angers 2018 and HW Bellegarde 2014,
418 the QTL on B6 affected the penetrance of the trait (Supplementary figure 8). No interactions between QTLs were
419 observed across years and locations (data not shown). As B6 and B4 QTLs had small effects on BSD resistance and
420 were population-specific and year-specific, they were not considered for the subsequent meta-analysis.

421 *Female maps*

422 No QTL common across all three populations was identified on the female maps (Table 3), but QTLs were
423 shared by pairs of populations. The OW and FW populations displayed a common QTL on A1, while for the HW and
424 FW populations displayed two common QTLs, both on A4.

425 In the OW population, a significant QTL on A1 was identified in 2017, explaining 6.53% of the total
426 phenotypic variance and was located at the end of the LG (Lopez Arias et al. in press).

427 For the FW population, three QTLs were detected with 2018 data using 2p method. These QTLs, located on
428 A1, A2 and A4, explained 4.06%, 2.57% and 3.61% of the phenotypic variance, respectively (Table 3). Interestingly,
429 QTLs on A1 and A4 had an effect on the penetrance of the trait (LOD 2.59 and 4.09 respectively; see Table 3) whereas
430 the QTL on A2 had an effect on both severity and penetrance (Supplementary figure 9A).

431 To position the QTL detected in the OW and FW populations on LG A1, markers at the confidence interval
432 limits and markers at the peak of the QTLs were positioned on a physical map (Supplementary figure 10). TIR-NB-
433 LRR (*TNL*) genes and cluster of genes from this regions identified by Menz et al. in 2020 were also mapped. Two

434 clusters of *TNL* genes, named cluster 1 (genes OB2_C to OB2_H) and cluster 2 (genes OB2_J to OB2_S), were
435 localized near the end of chromosome 1 (supplementary figure 10). The *RdrI* resistance gene from *Rosa multiflora* is
436 part of cluster 2 (Malek et al. 2000; Kaufmann et al. 2003; Hattendorf et al. 2004; Terefe-Ayana et al. 2011; Menz et
437 al. 2020). Importantly, the QTLs derived from the female parents TF and OB co-localized with both clusters of *TNL*
438 genes (Supplementary figure 10).

439 For the HW population, QTLs were identified on LG A3 in 2012 and 2014 in Angers, 2013 in Bellegarde,
440 2014 in Diémoz and the averages across years for each location explaining 4.4% to 5.8% of the phenotypic variation
441 (Table 3). One QTL explaining 5.91% of phenotypic variation was also identified on A3 in Bellegarde in 2014 using
442 the 2p model. This QTL had an effect on the penetrance of the trait (Supplementary figure 9B). Also in Bellegarde, a
443 QTL explaining 5.39% of the phenotypic variance was identified on A5 in 2012. In Diémoz, a QTL explaining 5.77%
444 of the phenotypic variance was identified on A4 in 2014 (Table 3).

445 For both male and female maps, further QTLs and epistasis between QTLs were investigated using a two
446 dimensional genome scan and no epistasis was significantly detected for any scoring year with normal distribution
447 (data not shown). The percent explained by all QTLs is, then, the sum of all the phenotypic variance explained by the
448 individual QTLs of each scoring years (Table 3).

449

450 **Meta-analysis**

451 A meta-analysis of B3 and B5 QTLs was conducted. First, a consensus male map across all populations was
452 constructed using 41 common markers (Table 1 and Supplementary table 1). In total, B3 comprised nine markers
453 common across the OW, FW and HW male maps and B5 comprised eight markers common across all male maps
454 (Table 1). LG3 and LG5 of the consensus map were represented in Figure 2. Secondly, QTLs of the original maps
455 were projected on the chosen reference map (OW population map) by the map-projection function of Biomercator
456 4.2.2. In total, 20 QTLs of BSD resistance were projected on the reference LG3 and 17 QTLs on the reference LG5
457 (Figure 2). The meta-QTL optimum number was ensured by the AIC. Two meta-QTLs were identified on both LG3
458 and LG5 (represented by two different colors on the LGs of figure 2). For LG3, the first meta-QTL (named Meta_1_3)
459 had a confidence interval (CI) of 2.72 cM and the second meta-QTL (named Meta_2_3) had a CI of 7.70 cM (Table 4
460 and Figure 2). The CI for the meta-QTL on LG5 (named Meta_1_5) was 3.95 cM and 7.52 cM for the second one
461 (Meta_2_5). The average CI of the 20 individual QTLs found in B3 was 20.1 cM whereas for both predicted meta-

462 QTLs together it was 10.42 cM. For B5, the individual QTL average CI was 26.62 cM and only 11.47 cM for both
463 predicted meta-QTLs (Figure 2 and Table 4). The CI were approximately twice as small with the meta-analysis, which
464 allowed us to be more precise in the location of QTLs linked to BSD resistance.

465 When looking at the meta-QTL contributions, we can see that the first meta-QTL (Meta_1_5) was represented
466 exclusively by OW population QTLs that showed large peaks at the beginning of the LG (except OWpop_RW_16B5
467 QTL that showed two distinct peaks separated by 30cM, see Supplementary figure 5) whereas the QTLs of HW and
468 FW populations contributed to the second meta-QTL (Meta_2_5). Curiously, individual QTLs with a wide interval
469 and double peaks separated by 10 to 30cM were detected on B5 (Supplementary figure 5 to 8). The configuration
470 suggests the presence of linked QTLs, requiring additional or alternative analytical approaches (Nakamichi et al. 2001;
471 Kao and Zeng 2010). Accordingly, we attempted a two-dimensional analytical approach for normally distributed data
472 but failed to separate more precisely the putatively linked QTLs in this region (data not shown).

473

474 **Gene mining from meta-QTL intervals and *NB*-encoding genes in *Rosa*
475 genome**

476 All SNP markers were mapped to the *Rosa chinensis* reference genome of Hibrand-Saint Oyant et al. (2018)
477 and were used to project the consensus genetic map onto the reference genome. The first meta-QTL on LG3, Meta_1_3,
478 corresponds to an approximately 2.86 Mb genome region encompassing 291 annotated genes. The second one,
479 Meta_2_3, represents a 3.5 Mb genome region comprising 450 annotated genes. On LG5, the first predicted meta-
480 QTL, Meta_1_5, represents 1.80 Mb comprising 271 annotated genes, while the second meta-QTL, Meta_2_5,
481 represents 6.06 Mb comprising 557 genes (Table 4).

482 We explored genes associated with predicted meta-QTLs, focusing specifically on potential disease resistance
483 genes. First, we annotated the predicted *NB*-encoding (Nucleotide Binding) genes in the rose genome, identifying 493
484 candidate *R*-genes (Supplementary table 2). Candidate *NB-LRR* genes were mapped onto the assembled
485 pseudochromosomes of *R. chinensis* (Figure 3). *NB*-encoding genes mapped to every chromosome of the rose genome.
486 Only nine genes mapped onto the unassembled scaffolds (rc00). Chromosome 1 contained the largest number of *NB*-
487 encoding genes (106). Overall, the mean number of *R*-genes per chromosome was 69. However, *NB*-encoding genes
488 were not homogeneously distributed across chromosomes, with clustering evident, especially on the distal end of
489 chromosomes 1, 5 and 7 (Figure 3).

490 On LG3, 11 automatically annotated R-genes and four manually annotated NBS-encoding genes
491 (*RC3G0136400*, *RC3G0136500*, *RC3G0136600*, *RC3G0145900*) co-localized with the first meta-QTL, Meta_1_3
492 (Table 4, Figure 3 and Supplementary table 2). The manual and the automated annotations identified nearly the same
493 number of NBS-encoding genes in the interval of the second B3 meta-QTL (Meta_2_3) encompassing four RGAs for
494 the automated annotation and three *NB*-coding genes (*RC3G0272000*, *RC3G0277900*, and *RC3G0280800*) for the
495 manual annotation (see table 4). In addition to these NBS-encoding genes, we investigated co-localizations of defense
496 response genes with the Meta-QTLs. Interestingly, a gene involved in response to fungal infection (*RC3G0142400*) is
497 associated with the meta-QTL Meta_1_3. This gene encodes an EMSY-LIKE 1 protein that is known to contribute to
498 RPP7-mediated and basal immunity against a specific strain Hiks1 of *Peronospora parasitica* in *Arabidopsis* (Tsuchiya
499 and Eulgem 2011), possibly by regulating chromatin states. Two genes encoding for P450 cytochrome also co-
500 localized with the first meta-QTL Meta_1_3. Cytochromes P450 monooxygenases (CYP) are known to be involved in
501 plant defense mechanisms as they mediate secondary metabolism compounds of the xenobiotic detoxification pathway.
502 For example, the CYP gene *CYP736B* in grapevine is involved in defense responses against *Xylella fastidiosa* and the
503 wheat *CYP72A* is involved in the defense responses to *Fusarium graminearum* (Schuler and Werck-Reichhart 2003;
504 Schuler et al. 2006). Similarly, in the Solanaceae, two cytochromes P450 participate in fungal pathogen resistance
505 (Morant et al. 2003) and a *Phytophthora infestans*-induced cytochrome P450 is associated with quantitative resistance
506 to late blight in potato (Trognitz et al. 2002). Moreover, a transcription factor from the WRKY family (*RC3G0261500*)
507 upstream of the NBS-encoding gene (*RC3G0261700*) also co-localize with the Meta_2_3. WRKY transcription factors
508 are known to play an important role in plant immunity and have been identified as major components of the resistance
509 to fungi (Yang et al. 2009; Pandey and Somssich 2009; Lui et al. 2017). A pathogenesis-related (PR) thaumatin gene
510 (*RC3G0264400*) was also found to co-localized with Meta_2_3. This gene codes for a PR-5 type protein (also called
511 TLP for thaumatin-like protein) that has been reported for its antifungal activity against various filamentous fungi (Chu
512 and Ng 2003; Ho et al. 2007; Singh et al. 2013; Zhang et al. 2018).
513 For LG B5, 17 QTLs were mapped on the consensus LG and two meta-QTL clusters were identified. The same genes
514 (*RC5G0059300*, *RC5G0061300*, and *RC5G0061600*) were annotated as *R*-genes with the expert annotation and the
515 automatic one for Meta_1_5 (Table 4). However, in Meta_2_5 region, five genes were not found to be *NB*-encoding
516 genes (*RC5G0227800*, *RC5G0228700*, *RC5G0231700*, *RC5G0232700*, *RC5G0245000*) with the expert annotation.
517 Interestingly, Meta_2_5 is close to the region where the newly identified *Rdr4* gene giving resistance to all races of *D.*

518 *rosae*, except the race 12, was located (Zurn et al. 2018). The meta-QTL, Meta_2_5, did not co-localize with the
519 possible location of *Rdr4* but the marker peak of the QTL found in 2016 for OW population co-localized with it (Lopez
520 Arias et al. in press) as well as the marker peak of the QTL found in Diémoz 2013 scoring year of HW population.
521 Moreover, a glucan synthase like gene (*RC5G0249400*; *GLS4* gene or also called *Cals8*), known to be involved in the
522 formation of callose-containing papillae in response to pathogen attack (Enrique et al.; Dong 2005; Enns et al. 2005;
523 Dong et al. 2008; Voigt and Somerville 2009; Ellinger et al. 2013; Voigt 2014, 2016), co-localized with Meta_2_5.
524 Finally, a cluster of ten genes coding for cytochrome P450 also co-localized with Meta_2_5.

525 **Discussion**

526 **Importance of environmental effects on BSD scores**

527 Since the expression of quantitative resistance can be affected by the environment, quantitative disease
528 resistance (QDR) is best studied under field conditions with phenotypic measurements collected over different
529 locations and years (Kelly and Vallejo 2006; Niks et al. 2015; Corwin and Kliebenstein 2017). In the current study, a
530 difference of inoculum pressure or fungal strains between locations (Soufflet-Freslon et al. 2019) could explain why,
531 for the HW population, the disease incidence was generally lower in Angers than in Bellegarde and Diémoz for a given
532 year (Supplementary figure 2C). On the other hand, the effects of environmental conditions such as temperature,
533 humidity or rainfall on BSD development in fields are well documented (Saunders 1966; Knight 1975; Gachomo
534 2005). In particular, (Saunders 1966) showed that climatic conditions play a critical role in the accumulation and spread
535 of *D. rosae* inoculum. Heavy rainfalls and temperature above 14°C during trigger inoculum accumulation and spread
536 of conidia from infected leaves (Saunders 1966). During the scoring period from 2012 to 2018, average precipitation
537 in August and September of a given year was consistently lower in Angers and Bellegarde than in Diémoz. Similarly,
538 for all populations, variation in disease impacts between years was observed, with low rainfall in August-September
539 correlating with lower BSD scores. Conversely, in wetter locations or years (e.g., Diémoz in 2013 and Bellegarde in
540 2014), more individuals presented disease symptoms with BSD score distributions skewed to the left (with a lot of
541 individuals presenting more symptoms than normal) like Diémoz. Specifically, the year 2013 (with a spike at score 4)
542 could be explained by heavy rainfalls in August-September. Similarly, Bellegarde in 2014 presenting similar rainfall
543 than Diémoz (97.25 mm) also showed a spike at score 4 and a distribution skewed to the left (Figure 1C).

545 **New QTLs detected on parental genetic maps**

546 Our main objective was to identify genomic regions conditioning resistance to *D. rosae*. We generated and
547 analyzed phenotypic BSD data gathered across seven years, three locations, and three genetic populations.

548 The three populations used in this study were originated from interspecific crosses. The highly heterozygous
549 nature of *Rosa* species is a complicating factor when it comes to genetic mapping. The pseudo-test cross mapping
550 approach (Grattapaglia and Sederoff 1994; Kirst et al. 2004; Adam-Blondon et al. 2016), developed for highly
551 heterozygous species, allows development of parental maps that are then combined into an integrated map. However,
552 (Gartner et al. 2013) showed that, although integrating homologous chromosomes that have been rearranged can
553 produce mathematically and statistically correct maps, they do not necessarily reflect the biological reality of
554 chromosomal rearrangements and meiotic recombination that had happened during the outbred cross. Therefore, even
555 if the gene position is highly conserved between species, genome rearrangements may exist in interspecific crosses.
556 This can lead to significant changes in collinearity between parental genomes (Lespinasse et al. 2000; Gartner et al.
557 2013). For example, recently released, independently generated rose genome assemblies suggest chromosome
558 rearrangements (Raymond et al. 2018; Hibrand-Saint Oyant et al. 2018; Smulders et al. 2019). In the current study, we
559 observed rearrangements between the parents OB and RW, especially on chromosome 3. For these reasons, we decided
560 to apply pseudo-test cross mapping approach without integrating the parental maps at the end. QTL analyses were then
561 carried out using two different methods of detection on separated parental maps.

562 Overall, many QTLs for resistance to BSD were detected in this study. Consistent with natural variation in
563 inoculum pressure, pathogen race, and environmental conditions encountered in field studies over several years, some
564 QTLs identified in this study were only found in a given population, location or year. For example, BSD resistance
565 QTLs on B6 were found specifically on the male map of the HW population across all environments (Table 2). Since
566 all three populations share the RW male parent, identification of the B6 QTLs only in the HW population for several
567 years and locations suggests that expression of these QTLs also depends on genetic background that is crossed with *R.*
568 *wichurana*. Moreover, the marker peak CTG623 of B6 QTL was found to co-localize with the possible location of
569 *Rdr3* (Zurn et al. 2020).

570 Importantly, other QTLs were more consistently detected across populations, locations, and years, suggesting a more
571 robust impact on disease resistance. First, a QTL on LG A1 was mapped in two populations (FW and OW)
572 (Supplementary figure 10), originating from the female parents TF and OB. This QTL co-localizes with a cluster of

573 NB-LRR genes, including the previously reported BSD resistance gene *Rdr1* (Lopez Arias et al. in press; Hattendorf
574 et al. 2004; Terefe-Ayana et al. 2011). This observation suggests the intriguing possibility that the underlying genetic
575 basis of the A1 QTL might be a canonical NB-LRR gene, in whole or in part. In addition, regarding the difference of
576 BSD score between both female parents (with OB very susceptible to BSD and TF resistant to it), we can hypothesize
577 that an allelic variation in the causal gene could originate a difference in the observed phenotype. Then, a QTL
578 conditioning BSD resistance on LG B4 was identified for two different environments and two different populations:
579 the OW population in Angers in 2017 (male map) and the HW population in Diémoz in 2014 (H190 female map; Table
580 2 and 3). Resistance conditioned by this QTL may be environment- and pathogen race-dependent. Finally, QTLs on
581 LGs B3 and B5 were found for all populations, years and locations in the male resistant parent RW but also in the
582 H190 female map (Table 2 and 3). At the moment, the apparent mapping of QTLs from these two parents, with a clear
583 difference in BSD resistance, on the same linkage groups could be explained by one of these two hypothesis: (1) RW
584 and H190 QTLs co-localized meaning that both parents shared the same resistance source and the difference observed
585 in the phenotype could be due to an allelic variation between them or (2) the QTLs originated from both parents do
586 not co-localize meaning that the resistance source is different. Unfortunately, the maps quality did not allow us to
587 determine precisely if the male and female QTLs on linkage group 3 and 5 co-localized (data not shown). However,
588 consistent expression of QTLs on linkage groups 3 and 5 across environments and genetic backgrounds suggest that
589 they are stable enough to be useful in the genetic improvement of rose resistance to *D. rosae*. In the end, we can see
590 with this study that separated maps allowed us to identify two main QTLs on B3 and B5 with large effect on the
591 resistance to BSD as well as small effect QTLs on parents that were considered tolerant or susceptible.

592

593 **QTLs characterization and two-part model result interpretation**

594 Substantial peaks in the distribution of genotype mean values are fairly common and represent one of the
595 principal departure from the assumption of normality required to perform QTL analysis (Lander and Botstein 1989).
596 When working with disease resistance, individuals may show high resistance so a peak at 0 can be observed. In this
597 case, the standard QTL detection approach behave poorly and can detect spurious QTLs in regions with low genetic
598 information (Broman 2003; Feenstra and Skovgaard 2004). To deal with this problem, Broman proposed in 2003 a
599 “Two-part model” that combines a binary analysis (absence *vs* presence) and a normal analysis for individuals with
600 non-null phenotype. The trait is divided in two components: penetrance and severity (Broman 2003; Broman and Sen

601 2009). That way, more information about the part of trait that is affected by the QTL can be obtained. This model has
602 so far been applied for reproductive barriers with male sterility in house mouse and ear tip masculinization in maize
603 (White et al. 2011, 2012; Holland and Coles 2011). In our study, we adapted when necessary the model used to perform
604 the QTL analyses, so data distributions with a substantial spike were analyzed with the two-part model. When both the
605 penetrance and the severity of the trait were affected by the QTLs, it meant that these positions have an effect on the
606 appearance of the BSD symptoms or penetrance (when treated as binomial; with no symptoms *vs* symptoms) as well
607 as the severity of symptoms (BSD score > 0).

608 The 2p model provided interesting information for the B3 and B5 QTLs found on the male parent maps. For
609 Angers 2018 data from the HW and FW populations, both the penetrance and the severity of the trait were affected by
610 the B3 QTLs, meaning that these regions impact both appearance of BSD symptoms and symptom severity.
611 Interestingly, for the B5 QTLs in both populations, only penetrance (absence/presence of the symptoms) was impacted.
612 For the resistant female parent TF, the A2 QTL impacts both the penetrance and the severity of the trait whereas the
613 A1 and A4 QTLs impact only penetrance.

614

615 **Meta-analysis and gene mining**

616 With recent progress in mapping algorithms and models that can handle a wide diversity of phenotypic data,
617 quantitative trait mapping has become the first step in the dissection of the genetic factors underlying complex and
618 quantitative traits such as disease resistance (Zhu and Zhao 2007; Rawat 2016). That way, many studies mapped
619 quantitative disease resistance loci of crop plants over the past decades (Lacape et al. 2010; Qi et al. 2011; Holland
620 and Coles 2011; Yadava et al. 2012; Hamon et al. 2013; Semagn et al. 2013; Said et al. 2013; Pilet-Nayel et al. 2017).
621 Cloning and functional validation of causal gene(s) or quantitative trait nucleotide polymorphism underlying QTLs
622 has been accomplished in maize (Yang et al. 2017) but remains a long and difficult process. Indeed, the biological
623 bases of QDR in the defense responses are still unknown, so several reviews proposed hypotheses of mechanisms
624 underlying Quantitative resistance loci (QRL) (Poland et al. 2009; St Clair 2010; Roux et al. 2014; Corwin and
625 Kliebenstein 2017).

626 First, one crucial step facilitating cloning and validation of causal genes is the QRL position refinement.
627 Towards this goal, in this study, we narrow the confidence interval of the most phenotypically stable and reproducible
628 QTLs on a common consensus map and perform a meta-analysis of the corresponding LGs, B3 and B5. Two meta-

629 QTL clusters were identified for both LG B3 and B5 (Figure 2 and Table 4). This method allowed us to refine the
630 genomic regions linked to BSD resistance and to study the influence of genetic background and environment on QRL
631 detection (Table 4). However, combination of QTL mapping results across several studies that differ with marker
632 density, linkage, sample size, etc. is still a challenge. Even though Goffinet and Gerber's method aims to resolve the
633 number of QTL and their location using a model selection, questions on the real number of QTL subsist. On one hand,
634 for LG B3, both clusters found during the meta-analysis can be either two real QTLs or an artefact due to the possible
635 rearrangement that happened in this region. For instance, not far from the meta-QTL Meta_1_3 on B3, a large
636 rearrangement was described between the two alleles in OB (corresponding to recurrent blooming locus and the
637 rearrangement of *copia*-like retrotransposon, Hibrand-Saint Oyant et al. 2018). On the other hand, on LG B5,
638 uncertainty remains on whether or not the QTLs located within the same genomic region are the same QTLs. Specially,
639 because individual QTLs present double LOD peaks characteristic of linked QTLs. Increasing the sample size of the
640 populations in future experiments may provide a better power to separate closely linked QTLs on LG B5. Therefore,
641 at this moment, only hypotheses can be made. For example: both clusters being completely new QTLs different from
642 the newly identified *Rdr4* resistance gene (Zurn et al. 2018) or the first meta-QTL Meta_1_5 being a new QTL and the
643 Meta_2_5 being *Rdr4* locus that did not co-localized with it due to map imprecisions.

644 Second, elucidating the molecular mechanisms underlying QRLs can assist breeders in developing cultivars
645 with more durable levels of resistance by “making more informed and prudent decisions” (Kelly and Vallejo 2006).
646 Indeed, it has been shown that QRLs can co-localize with major R-genes as well as defense response genes (Poland et
647 al. 2009; St Clair 2010; Roux et al. 2014; Corwin and Kliebenstein 2017). In this study, we used the meta-QTL physical
648 positions to inform gene mining efforts based on whole genome sequence data (Hibrand-Saint Oyant et al. 2018),
649 specifically searching for associations between defined genetic regions and NBS-LRR and defense response genes.
650 However, the resistance loci originated from RW and the genomic differences between both genotypes could impact
651 our efforts. Nevertheless, the use of the haploid OB genome sequence to identify candidate genes underlying BSD
652 resistance meta-QTLs has promise. Genes involved in pathogen recognition, signal transduction, transcription
653 modulation and detoxification pathways were identified in the chromosomal regions linked to BSD resistance.
654 Interestingly, Blechert and Debener in 2005 classified the interaction between *D. rosae* and the wild type *R. wichurana*
655 as type 7 meaning that the fungus germinates and penetrates the cuticle but is not capable of producing hyphal
656 structures on the host. Indeed, cell-wall appositions were observed on one to three cells resulting in visible necrotic

657 areas akin to hypersensitivity reactions (HR). Genes involved in the activation of cell death (WRKY, PR-proteins,
658 ROS pathway, etc.) as well as in detoxification pathways (with cytochrome P450) seem to be good candidates.

659 Thus, the possibility of RGAs being responsible for the observed resistance on RW is also not to be ruled out as they
660 are in the first line of biotic stress responses like the one observed for RW by Blechert and Debener (2005).

661 In this study, confidence intervals of chromosomal regions conditioning quantitative resistance to *D. rosae*
662 were reduced thanks to the meta-analysis approach. Unfortunately, at this stage of the study, no consistent markers
663 linked to BSD resistance have been identified as the CI regions and peaks of detected QTLs vary slightly over the
664 years and locations. A refinement of the QTL location of stable QTLs on B3 and B5 is needed prior to marker detection
665 for marker assisted breeding and/or causal gene identification. Using the genomic resources now available such as the
666 rose genome and the data provided in this article such as the manually annotated RGAs, the first hypothesis on the
667 genetic basis of QDR in Rose-*D. rosae* pathosystem were made. However, at this stage, only a large number of
668 candidate genes were identified. Further evidence supporting their involvement in the observed resistance of RW
669 genotype need to be provided so the potential candidate genes can be narrowed down to a number that can allow
670 experimental validation through qPCR expression profiles and/or gene inactivation. Finally, the large number of QTL
671 detected in this study, together with the fact that some QTL did not co-localize with known *Rdr* genes, suggests that
672 the number of QTL could be even larger than what has been detected with these limited populations, offering the
673 promise of wide spectrum of resistance sources to rose breeder and scientists.

674

675 Conclusion

676 In this study, we report the first discovery and genetic characterization of quantitative resistance to BSD. We
677 examined the contributions of a common resistant parent over several years, locations, and genetic populations. We
678 confirm the presence of a strong effect QTLs on LG B3 and B5 from the genotype *R. wichurana*, consistent with
679 complementary on-going research (Yan et al. 2019). The LG B3 and LG B5 QTLs are stable over years and effective
680 against a wide range of *D. rosae* races and across various environments (Lopez Arias et al. in press; Yan et al. 2019;
681 Soufflet-Freslon et al. 2019). We demonstrate a method to leverage meta-analyses to reduce CI of single QTLs. This
682 method was specifically chosen for its robustness to non-full independency and it allowed us to integrate data from
683 three different populations of perennial rose bushes. BSD data collected over seven years and multiple locations,

684 provided validation of QTLs on B3 and B5, demonstrating their stability and robustness. Genes underlying these QTLs
685 are potential breeding targets for the development of BSD resistant rose cultivars.

686

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- 1014

1015 **List of abbreviation**

1016 Black Spot Disease (BSD); Quantitative Trait Loci (QTLs); Marker Assisted Breeding (MAS); Linkage
1017 Groups (LG); *Rosa wichurana* (RW); *Rosa chinensis* 'Old blush' (OB); *Rosa hybrid* 'The Fairy' (TF); *Rosa chinensis*
1018 'Old blush' x *Rosa wichurana* population (OB population); *Rosa hybrid* 'The Fairy' x *Rosa wichurana* population
1019 (FW population); H190 x *Rosa wichurana* population (HW population); Analysis of Variance (ANOVA); Restricted

1020 Maximum Likelihood (REML); ‘Nearest Neighbor fit’ (N.N fit); Short Sequence Repeat (SSR); Single Nucleotide
1021 Polymorphism (SNP); Logarithm of Odds (LOD); Weighted Least Square (WLS); ‘Akaike’ Information Criterion
1022 (AIC); Confidence Intervals (CI); Centimorgans (cM); Gene Ontology (GO); Resistance gene (*R*-gene); Number of
1023 Petals (NP); Simple Interval Mapping (SIM); Composite Interval Mapping (CIM); Two-part model (2p model); TIR-
1024 NB-LRR (*TNL*); *NB*-encoding (Nucleotide Binding); Quantitative Disease Resistance (QDR); Quantitative resistance
1025 loci (QRL); Cytochromes P450 monooxygenases (CYP); Pathogenesis-Related (PR); Thaumatin-Like Protein (TLP)

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1026

1027 **Figure legends**

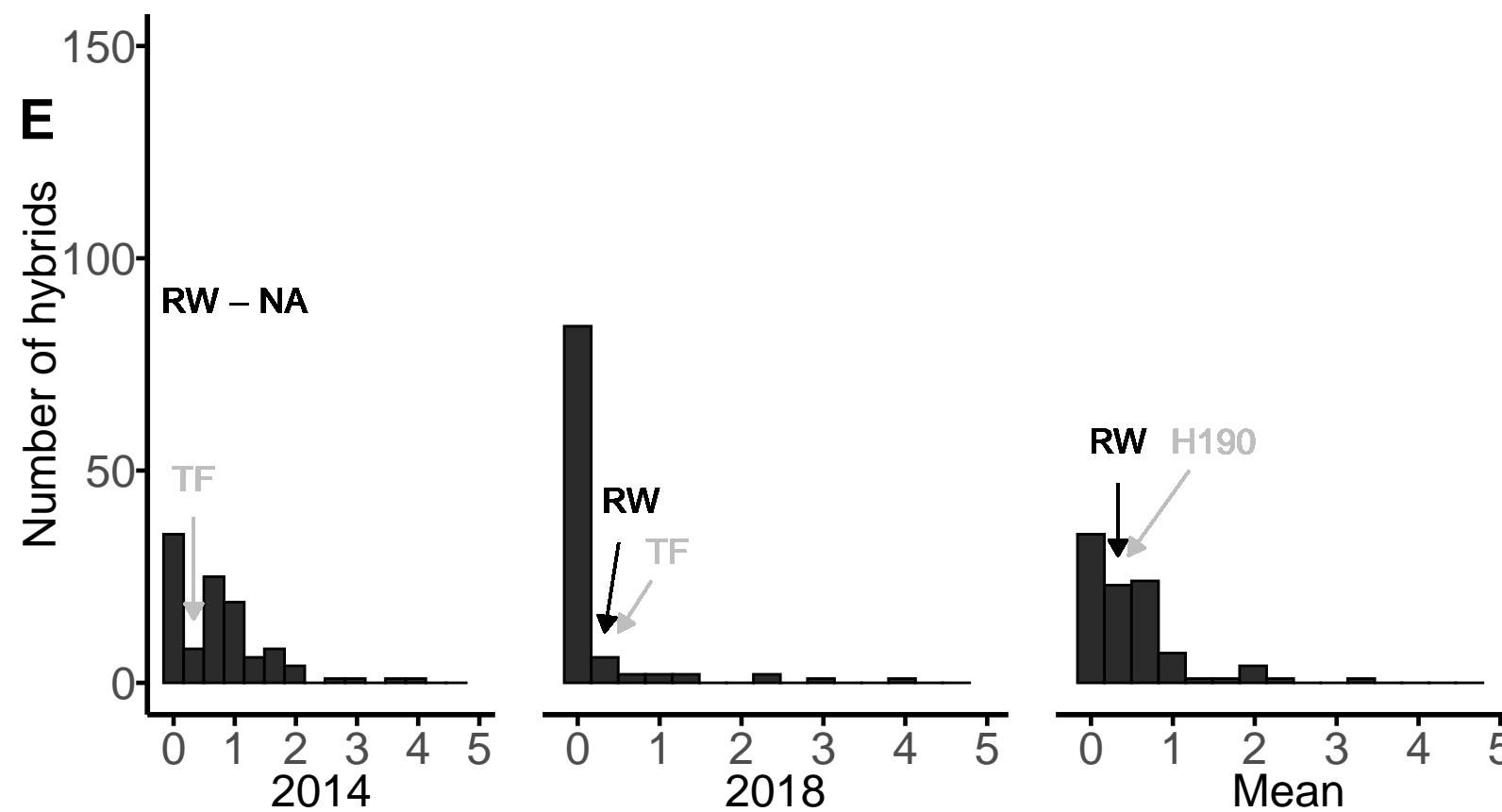
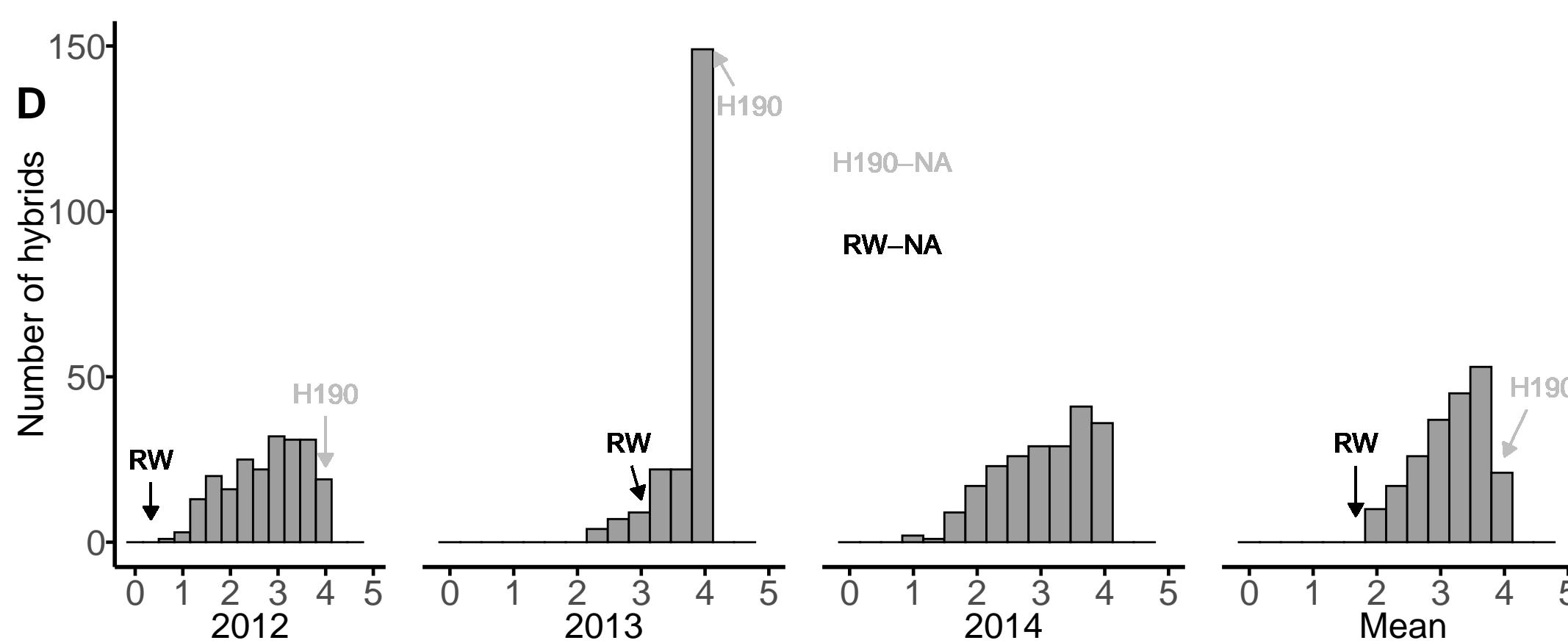
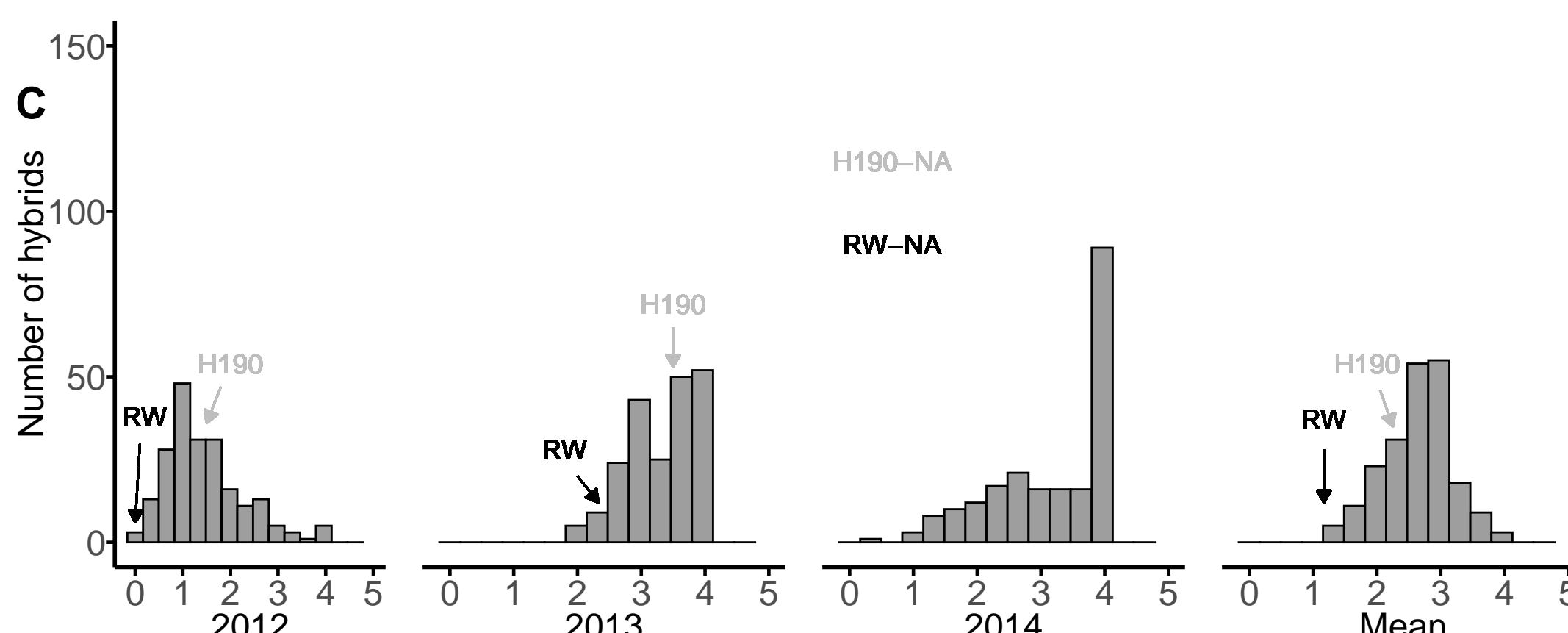
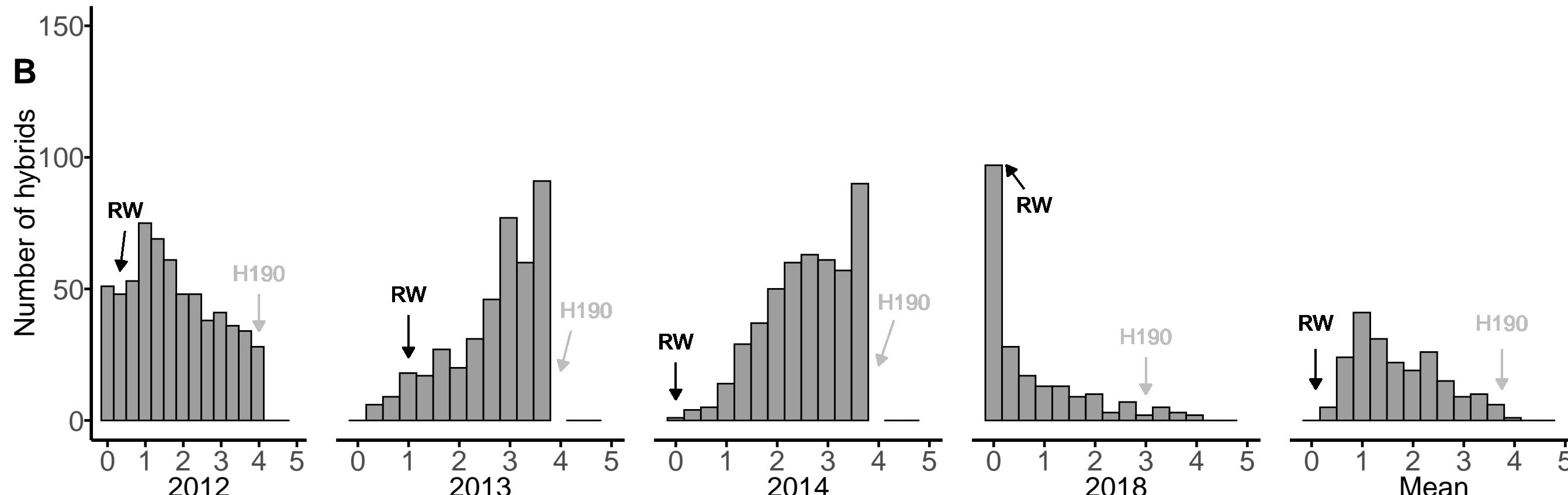
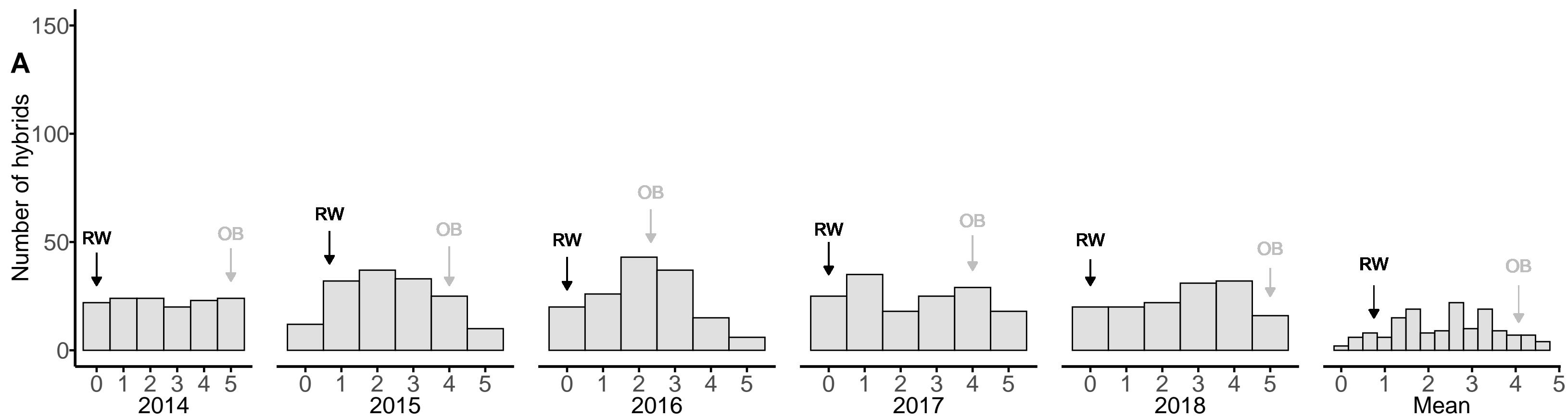
1028 **Fig. 1** Black spot disease scoring data distribution for all years and locations for the three populations

1029 A: Scoring data for different years for OW population in Angers, B: Scoring data for different years for HW population

1030 in Angers, C: Scoring data for different years for HW population in Bellegarde, D: Scoring data for different years for

1031 HW population in Diémoz, and E: Scoring data for different years for FW population in Angers.

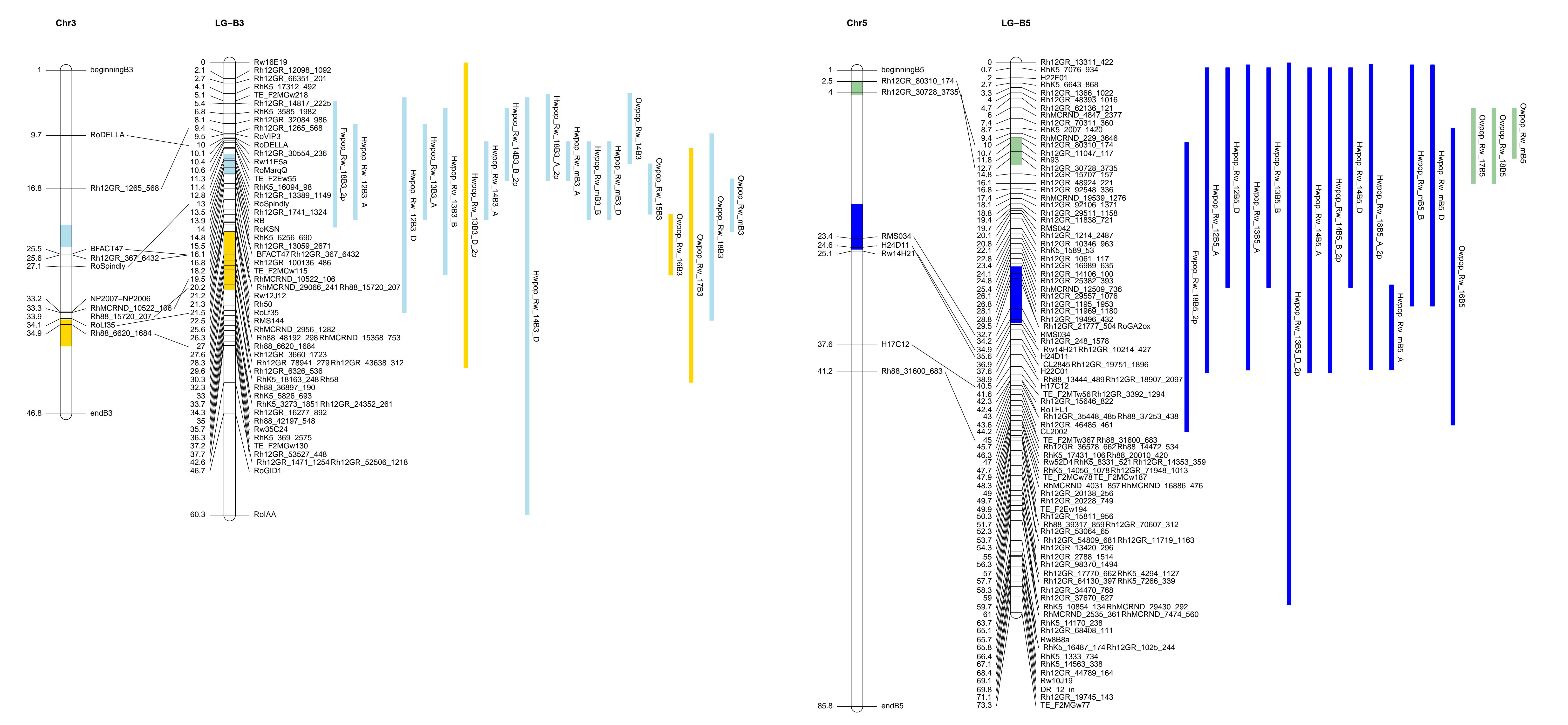
1032



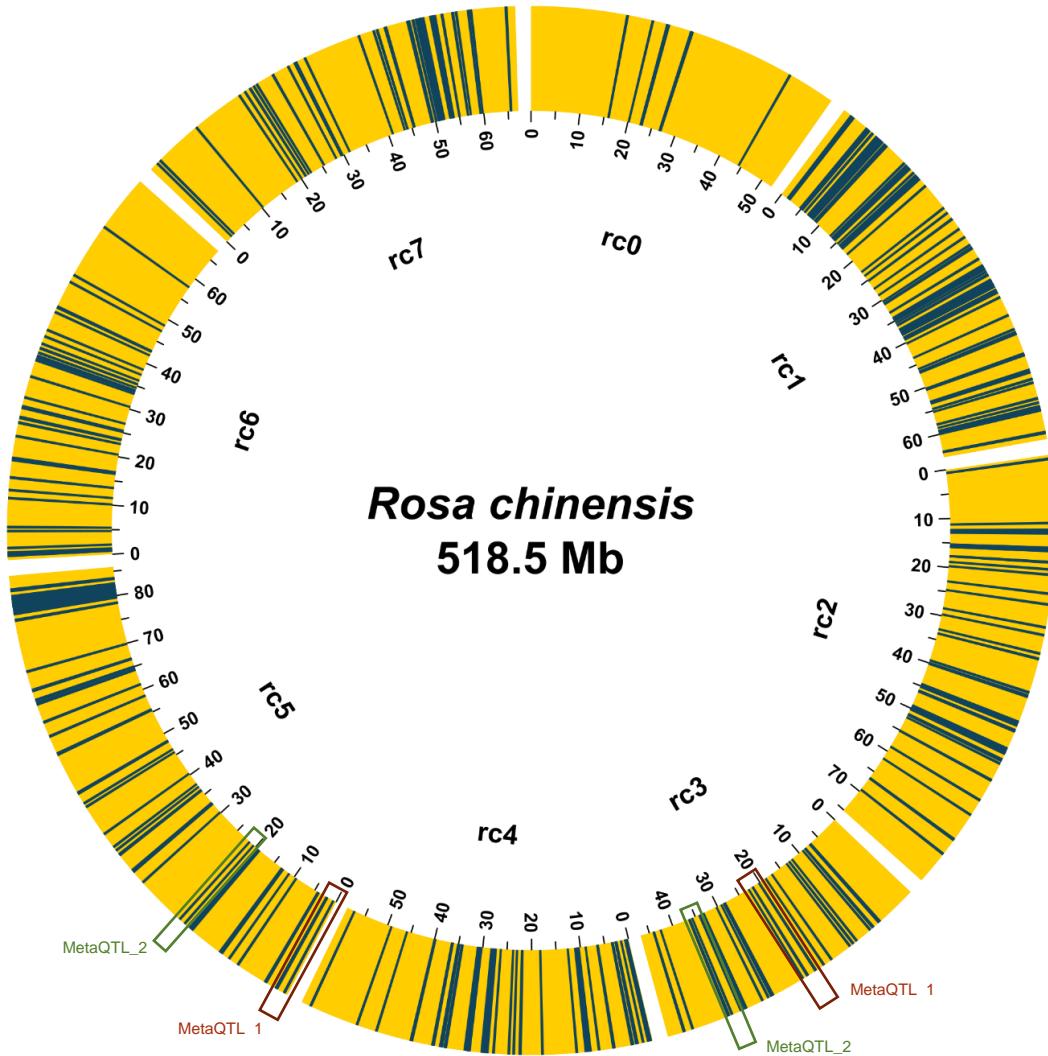
1033 **Fig. 2** Representation of individual QTLs and meta-QTLs associated with black spot disease resistance for OW, FW
1034 and HW rose populations on the male consensus map

1035 Names of markers are on the right and the genetic distances (in cM) on the left. The 19 and 17 QTLs detected on B3
1036 and B5, respectively, on all three populations are projected onto a newly built consensus map. QTL names are coded
1037 as follows: PopName_map_YearLG_Location_method. 95% Bayesian confidence intervals are displayed with vertical
1038 bars where the length is proportional to the interval width, and the QTL peak is represented by a line. Meta-QTLs are
1039 represented in plain color on the LGs.

1040



1041 **Fig. 3** Candidate R-genes placed on the pseudochromosomes of *Rosa chinensis* assembly and meta-QTL position
1042 Each pseudochromosome is represented by a yellow bar, with the positions of the *R*-genes indicated as blue lines.
1043



1044 **Table legends**

1045 **Table 1** Summary of the SSR and SNP-based linkage maps for OW population and the common markers with other
1046 populations

1047 Linkage groups (LG) names for the female map (A1 to A7) and for the male map (B1 to B7) were assigned according
1048 to Spiller et al. 2011. Several markers were mapped at the same locus so the number of unique loci is displayed and in
1049 the total number, the number of markers with different phases (called identicals) are displayed in parenthesis. One
1050 gene marker was used for the female map and is represented with (+1) on the table. *Marker was counted as common
1051 when at minimum two of the three populations shared this same marker.

1052

Table 1 Summary of the SSR and SNP-based linkage maps for OW population and the common markers with other populations

LG	Female map						LG	Male map						
	Number of markers			Number of loci	Average marker interval (cM)	Number of common markers*		Number of markers			Number of loci	Average marker interval (cM)	Number of common markers*	
	Length (cM)	SNP	SSR					Total (identicals)	SNP	SSR				
A1	71.71	115	2	117 (690)	0.91	3	B1	57.44	66	2	68 (171)	50	1.15	3
A2	33.42	69	3	72 (1100)	0.74	8	B2	84.34	90	7	97 (266)	65	1.30	8
A3	53.75	61	5 (+1)	68 (520)	1.01	5	B3	42.6	37	5	42 (518)	35	1.22	9
A4	58.79	41	5	46 (220)	1.47	4	B4	66.82	73	7	80 (371)	66	1.01	6
A5	97.68	148	7	155 (1007)	0.85	5	B5	71.12	83	7	90 (318)	74	0.96	8
A6	70.15	133	4	137 (1134)	0.77	3	B6	55.89	65	3	68 (210)	48	1.16	3
A7	88.36	126	5	131 (841)	0.98	3	B7	75.41	83	5	88 (217)	64	1.18	4
Total	473.85	692	31 (+1)	726 (5512)	0.96	31	Total	453.62	497	36	534 (2072)	402	1.14	41

Linkage groups (LG) names for the female map (A1 to A7) and for the male map (B1 to B7) were assigned according to Spiller et al. 2011. Several makers were mapped at the same locus so the number of unique loci is displayed and in the total number, the number of markers with different phases (called identicals) are displayed in parenthesis. One gene marker was used for the female map and is represented with (+1) on the table.

*Marker was count as common when minimum two of the three populations shared this same marker.

1053 **Table 2** Summary of QTL for black spot disease resistance in OW, FW and HW populations across multiple
1054 environments (years and locations) for male maps

1055 ^aNormal indicates a QTL mapping using a normal model with CIM analysis and 2p indicates a two-part model that
1056 studies consecutively a binary model and a normal one, so three LOD were calculated: LOD. π (penetrance, equivalent
1057 to binary model), LOD. μ (severity, equivalent to normal model for non-spike phenotypes) and LOD. π,μ (sum,
1058 complete model). ^bPermutation test giving the LOD threshold calculated using 1,000 permutations over which a QTL
1059 was significant. ^cLinkage group number with B for the male map. ^dProportion of phenotypic variation explained by
1060 the QTL. ^eConfidence interval calculated with the 95% Bayesian credible interval.

1061

1062

Table 2 Summary of QTL for black spot disease resistance in OW, FW and HW populations across multiple environments (years and locations) for male maps

Population	Method ^a	Location	Year	PT ^b	LG ^c	LOD ^a	Lod. π^a	Lod. μ^a	R ² (%) ^d	95% Bayes CI (in cM) ^e		Peak	
										Interval start	Interval end	Closest marker	Position (cM)
OW	normal	Angers	2014	2.6	B3	3.16			10.1	4.07	13.5	Rh12GR_1265_568	9.34
				2.6	B3	8.72			23.6	13.5	20.2	Rh12GR_367_6432	1613
				2.5	B3	6.79			17.9	20.2	28.3	Rh88_6620_1684	26.96
					B5	4.11			9.8	8.71	48.3	Rh88_31600_683	44.99
				2.6	B3	4.65			10.2	11.4	42.6	Rh88_15720_207	20.19
					B4	3.55			7.6	2	65.4	Rh12GR_14039_541	14.2
					B5	5.26			11.4	6.03	16.1	Rh12GR_80310_174	10.04
			2018	2.6	B3	3.17			8.8	9.44	34.3	RhMCRND_10522_106	19.52
					B5	3.43			9.3	6.03	16.1	Rh12GR_80310_174	10.04
			Mean	2.6	B3	11.18			22.1	15.46	22.49	Rh12GR_367_6432	16.33
					B4	3.02			5.1	13.95	23.6	Rh88_49087_478	20.9
					B5	5.42			11	6.03	12.74	Rh12GR_30728_3735	8.71
FW	2p	Angers	2018	2.15	B3	4.74	4.13	0.60	11.44	0	16.8	BFAC747	7.01
					B5	2.91	2.74	0.17	0.89	10.4	49	RoRGA2	29.34
HW	normal	Angers	2012	2.32	B3	7.67			15.74	3.97	16.7	RB	9.67
					B5	3.6			6.23	0	40.7	Rw14H21	25.13
				2.21	B3	8.56			16.02	3.97	16.7	RB	9.67
					B5	9.94			14.82	0	40.7	RMS034	32.18
					B6	2.87			3.6	0	62.5	CTG623	8.28
			2014	2.23	B3	7.54			12.99	6.3	16.7	RB	9.67
					B5	6.36			9.66	0	40.7	RMS034	25.13
			Mean	2.14	B3	15.23			21.43	6.3	11.5	RB	9.67
					B5	12.14			16.76	29.34	40.69	RMS034	32.18
					B6	3.12			4.22	0	20.88	CTG623	8.28
		Bellegarde	2013	2.30	B3	5.08			8.52	0	22.2	RoRGA/RoDELLA	3.97
					B5	9.86			19.6	0	29.3	Rw14H21	25.13

Table 2 (continued)

Population	Method ^a	Location	Year	PT ^b	LG ^c	LOD ^a	Lod. π ^a	Lod. μ ^a	R ² (%) ^d	95% Bayes CI (in cM) ^e		Peak	
										Interval start	Interval end	Closest marker	Position (cM)
HW	normal	Bellegarde	Mean	2.33	B3	5.23			8.41	6.3	16.66	RoMarQ	6.3
					B5	4.99			5.35	0	32.18	Rw14H21	25.13
			Diémoz	2012	B6	2.6			4.15	0	20.88	CTG623	8.28
					B3	3.72			7.19	0	28.7	Rw14H21	25.13
					B5	4.21			9.14	0	29.3	CTG623	8.28
		Mean	2014	2.21	B3	2.73			3.9	0	60.6	BFACT47	11.5
					B5	4.64			8.72	0	29.3	Rw14H21	25.13
					B6	2.96			4.17	0	38.3	CTG623	8.28
					B3	5.55			9.7	6.3	16.66	BFACT47	11.5
					B5	8.43			12.78	0	32.18	Rw14H21	25.13
2p	Angers	2018	3.03	B3	8.19	0.77	7.42	15.66	0	11.5	RoSpindly	8.96	
					B5	9.92	0.7	9.22	19.82	0	40.69	H24D11	30.08
					B6	3.13	0.64	2.48	2.35	0	62.5	CTG623	8.28
		Bellegarde	2014	2.96	B3	12.55	9.62	2.95	13.69	0	9.67	RoRGA	3.97
					B5	6.39	4.84	1.59	8.17	0	40.69	Rw14H21	25.13
					B6	4.87	4.7	0.17	2.76	0	20.88	CTG623	8.28
		Diémoz	2013	3.06	B3	4	0.87	3.13	8.96	0	60.63	RoLf35	19.08
					B5	5.98	0.16	5.82	11.93	0	72.49	H17C12	40.69

^a Normal indicates a QTL mapping using a normal model with CIM analysis and 2p indicates a two-part model that studies consecutively a binary model and a normal one, so three LOD were calculated: LOD. π (penetrance, equivalent to binary model), LOD. μ (severity, equivalent to normal model for non-spike phenotypes) and LOD. π . μ (sum, complete model).

^b Permutation test giving the LOD threshold calculated using 1,000 permutations over which a QTL was significant.

^c Linkage group number with B for the male map.

^d Proportion of phenotypic variation explained by the QTL.

^e Confidence interval calculated with the 95% Bayesian credible interval.

1063 **Table 3** Summary of QTL for black spot disease resistance in OW, FW and HW populations across multiple
1064 environments (years and locations) for female maps

1065 ^aNormal indicates a QTL mapping using a normal model with CIM analysis and 2p indicates a two-part model that
1066 studies consecutively a binary model and a normal one, so three LOD were calculated: LOD. π (penetrance, equivalent
1067 to binary model), LOD. μ (severity, equivalent to normal model for non-spike phenotypes) and LOD. π,μ (sum,
1068 complete model). ^bPermutation test giving the LOD threshold calculated using 1,000 permutations over which a QTL
1069 was significant. ^cLinkage group number with B for the male map. ^dProportion of phenotypic variation explained by
1070 the QTL. ^eConfidence interval calculated with the 95% Bayesian credible interval.

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Table 3 Summary of QTL for black spot disease resistance in OW, FW and HW populations across multiple environments (years and locations) for female maps

Population	Method ^a	Location	Year	PT ^b	LG ^c	LOD ^a	Lod. π ^a	Lod. μ ^a	R ² (%) ^d	95% Bayes CI (in cM) ^e			Peak	
										Interval Start	Interval End	Nearest marker		
OW	normal	Angers	2017	2.71	A1	4.12			6.53	42.89	60.3	Rh12GR_100474_250	54.3	
FW	2p	Angers	2018	2.10	A1	2.6	2.59	0.01	4.06	15.92	44.87	Rw34L6	35	
					A2	5.86	3.16	2.63	2.57	1.12	14.64	Rw59A12	1.12	
					A4	4.18	4.09	0.01	3.61	32.53	44.28	Rw53O21	44.28	
HW	normal	Angers	2012	2.04	A3	2.77			5.8	23.73	41.37	NP2007	33.71	
		Angers	2014	2.09	A3	2.3			4.44	23.73	41.37	NP2007	33.71	
		Bellegarde	2012	2.05	A5	2.51			5.39	0	36.04	H24D11	27.09	
	2p	Bellegarde	2013	1.95	A3	2.47			5.1	12.35	33.71	RoLf35H	23.73	
					Diémoz	2.08	A3	2.63		5.74	23.73	41.37	NP2007	33.71
						A4	2.87		5.77	0	37.36	Rw20l17	12.6	
	Diémoz	Mean	2.09	A3	2.17				4.4	23.73	41.37	NP2007	33.71	
									5.91	12.35	51.19	NP2006	33.71	

^a Normal indicates a QTL mapping using a normal model with CIM analysis and 2p indicates a two-part model that studies consecutively a binary model and a normal one, so three LOD were calculated: LOD. π (penetrance, equivalent to binary model), LOD. μ (severity, equivalent to normal model for non-spike phenotypes) and LOD. $\pi\cdot\mu$ (sum, complete model).

^b Permutation test giving the LOD threshold calculated using 1,000 permutations over which a QTL was significant.

^c Linkage group number with B for the male map.

^d Proportion of phenotypic variation explained by the QTL.

^e Confidence interval calculated with the 95% Bayesian credible interval.

1073 **Table 4** Meta-QTL genomic position and gene mining

1074 ^a Meta-QTL names using all the QTLs found with the normal and 2p method results. ^b Chromosome numbers from
1075 *Rosa chinensis* genome (Hibrand Saint-Oyant et al. 2018). ^c Genomic positions of the meta-QTLs after projection on
1076 *Rosa chinensis* genome (Hibrand Saint-Oyant et al. 2018). ^d Genes coding for disease resistance proteins from the
1077 automatic annotation of the genome. ^e Resistance gene analogs with NB-domain found with protein sequence scan
1078 (manual annotation). ^f Total number of annotated genes under meta-QTL intervals with Goffinet et al. (2000) method.

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Table 4 Meta-QTL genomic position and gene mining

Meta_QTL ^a	Chr ^b	Genetic position (cM)		Interval position (bp) ^c		Number of genes in the interval		
		start	end	start	end	RGAs_auto ^d	RGAs_manual ^e	Total ^f
Meta_1_3	3	12.17	14.89	21605249	24567362	11	4	291
Meta_2_3	3	22.51	30.21	34220246	37772912	4	3	450
Meta_1_5	5	9.68	13.63	2414969	4219224	3	3	271
Meta_2_5	5	27.14	34.66	18827666	24889549	5	9	557

^a Meta-QTL names using all the QTLs found with the normal and 2p method results.

^b Chromosome numbers from *Rosa chinensis* genome (Hibrand Saint-Oyant et al. 2018).

^c Genomic positions of the meta-QTLs after projection on *Rosa chinensis* genome (Hibrand Saint-Oyant et al. 2018).

^d Genes coding for disease resistance proteins from the automatic annotation of the genome.

^e Resistance gene analogs with *NB*-domain found with protein sequence scan (manual annotation).

^f Total number of annotated genes under meta-QTL intervals with Goffinet et al. (2000) method.

1081 **Additional files**

1082 **Supplementary tables**

1083 **Supp. Table 1** Common marker list for all populations for the female and male maps

1084 ^a Only SSR markers are listed. The markers shared by all three populations are displayed in green; ^b A1-A7 for the
1085 female maps and B1-B7 for the male maps.

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Supp. table 1 Common marker list for all populations for the female and male maps

Male maps					Female maps				
Markers ^a	LG ^b	OW	HW	FW	Markers ^a	LG ^b	OW	HW	FW
<u>RMS015</u>	B1	X	X	X	RMS015	A1	X		X
Rw25J16	B1		X	X	Rw32K24	A1	X		X
<u>Rw32K24</u>	B1	X	X	X	Rw25J16	A1		X	X
CTG329	B2		X	X	<u>RMS132</u>	A2	X	X	X
CTG356	B2	X	X		CTG356	A2	X		X
RMS129	B2	X		X	RMS147	A2		X	X
<u>RMS132</u>	B2	X	X	X	Rw59A12	A2		X	X
<u>RMS137</u>	B2	X	X	X	Rw23F13	A2		X	X
<u>RMS147</u>	B2	X	X	X	RMS137	A2		X	X
Rw23F13	B2	X		X	CTG329	A2		X	X
<u>Rw59A12</u>	B2	X	X	X	Rh80	A2		X	X
<u>BFACT47</u>	B3	X	X	X	BFACT47	A3	X	X	
RoAP2	B3		X	X	<u>Rh58</u>	A3	X	X	X
Rh50	B3		X	X	Rw35C24	A3	X		X
<u>Rh58</u>	B3	X	X	X	CTG21	A3	X		X
RMS144	B3	X		X	Rh50	A3		X	X
RoIAA	B3		X	X	Rog5	A4	X	X	
RoVIP3	B3		X	X	Rw55E12	A4	X	X	
<u>Rw16E19</u>	B3	X	X	X	CI3881	A4	X		X
<u>Rw35C24</u>	B3	X	X	X	<u>Rh98</u>	A4	X	X	X
<u>CI3881</u>	B4	X	X	X	H22F01	A5	X	X	
H20D08	B4	X	X		H24D11	A5	X	X	
H2F12	B4	X	X	X	<u>Rw14H21</u>	A5	X	X	X
Rog5	B4	X		X	<u>CL2845</u>	A5	X	X	X
<u>Rw53O21</u>	B4	X	X	X	Rw10J19	A5	X		X
<u>Rw55E12</u>	B4	X	X	X	Rw22A3	A6	X		X
<u>CL2845</u>	B5	X	X	X	Rw61F2	A6	X		X
H17C12	B5		X	X	<u>CTG623</u>	A6	X	X	X
H22C01	B5	X	X		<u>RMS003</u>	A7	X	X	X
<u>H22F01</u>	B5	X	X	X	Rw10M24	A7	X	X	
H24D11	B5	X		X	<u>Rw15D15</u>	A7	X	X	X
RMS034	B5	X		X					
<u>Rw10J19</u>	B5	X	X	X					
<u>Rw14H21</u>	B5	X	X	X					
<u>CTG623</u>	B6	X	X	X					
<u>Rw22A3</u>	B6	X	X	X					
Rw61F2	B6	X	X						
H10D03	B7	X	X						
<u>RMS003</u>	B7	X	X	X					
Rw10M24	B7	X		X					
<u>Rw15D15</u>	B7	X	X	X					

^a Only SSR markers are listed, the markers shared by all three populations are displayed in emphasized green; ^b A1-A7 for the female maps and B1-B7 for the male maps.

1088 **Supp. Table 2** NB-encoding genes information and position in Rose genome

1089 Summary of NB-encoding genes identified in manual annotations. Listed are gene ID names, chromosomal affiliation,
1090 end and start positions, classification (CC=Coiled Coil; LRR=Leucine Rich Repeat; NBS=Nucleotide Binding Site;
1091 TIR=Toll Interleukin Like Receptor); non-canonical domains (i.e., conserved protein domains that are atypical of
1092 NBS-LRR proteins); configuration of identified conserved NB-ARC subdomains; and detailed domain configurations,
1093 complete with reported e-values from a Pfam analysis.

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Gene ID	Chromosome	Start	End	Classification	Non-canonical domains	Configuration of subdomains within NB-ARC	Detailed domain configuration, including E-values from Pfam analysis
RC0G0129500	rc00	15921725	15925651	NBS-LRR		P-loop[465-473] Kin-2[546-553] RNBS-B[573-576] GPLP[629-635]	[440-721]NB-ARC:6.8e-40 [872-926]LRR_8:4.7e-07
RC0G0129700	rc00	15936605	15940195	NBS-LRR		P-loop[491-499] Kin-2[572-579] RNBS-B[599-605] GPLP[661-667]	[467-747]NB-ARC:1.3e-38 [908-964]LRR_8:9.6e-08
RC0G0157500	rc00	20165214	20168978	NBS		P-loop[100-108] Kin-2[181-188] RNBS-B[209-215] GPLP[276-282]	[76-370]NB-ARC:6.2e-73
RC0G0174400	rc00	22640609	22644651	NBS	RPW8	P-loop[186-194] Kin-2[267-274] RNBS-B[292-298] GPLP[347-353]	[4-135]RPW8:8.3e-22 [165-435]NB-ARC:1.7e-34
RC0G0176800	rc00	22873190	22878387	NBS-LRR	RPW8	P-loop[184-192] Kin-2[263-270] RNBS-B[288-294] GPLP[343-349]	[3-113]RPW8:7e-17 [165-429]NB-ARC:5.1e-34 [628-684]LRR_8:1.2e-05
RC0G0200900	rc00	26709295	26713250	NBS-LRR		P-loop[205-213] Kin-2[280-287] RNBS-B[310-316] GPLP[369-375]	[724-763]LRR_4:0.00046
RC0G0201600	rc00	26778236	26782002	NBS-LRR		P-loop[205-213] Kin-2[280-287] RNBS-B[310-316] GPLP[369-375]	[172-194]AAA_16:1.9e-05 [196-455]NB-ARC:2.2e-60 [576-613]LRR_8:0.0037
RC0G0202800	rc00	26907214	26909933	NBS-LRR		P-loop[116-124] Kin-2[191-198] RNBS-B[221-227] GPLP[280-286]	[83-105]AAA_16:0.00016 [107-367]NB-ARC:7e-63 [490-527]LRR_4:0.0038 [528-564]LRR_8:0.006
RC0G0283700	rc00	44426071	44428206	CC-NBS-LRR		P-loop[205-213] Kin-2[282-289] RNBS-B[313-319] GPLP[376-382]	[184-464]NB-ARC:1.4e-59 [574-623]LRR_8:2e-07 [630-652]LRR_4:8.3e-05
RC1G0009500	rc01	1503964	1506714	NBS		P-loop[26-34] Kin-2[104-111] RNBS-B[132-138] GPLP[191-197]	[2-263]NB-ARC:6.7e-37
RC1G0012400	rc01	1742358	1745854	CC-NBS-LRR		P-loop[201-209] Kin-2[277-284] RNBS-B[307-313] GPLP[368-374]	[170-191]AAA_16:0.00058 [192-453]NB-ARC:9.3e-64 [583-639]LRR_8:0.00043
RC1G0015400	rc01	1977225	1978112	NBS		P-loop[43-51] Kin-2[119-126] RNBS-B[149-155] GPLP[210-216]	[21-294]NB-ARC:2.3e-66
RC1G0035900	rc01	4772090	4776326	NBS-LRR		P-loop[204-212] Kin-2[279-286] RNBS-B[310-316] GPLP[371-377]	[174-420]NB-ARC:1.2e-48 [934-1038]LRR_4:0.0023
RC1G0036600	rc01	4825651	4829916	NBS-LRR		P-loop[200-208] Kin-2[274-281] RNBS-B[305-311] GPLP[366-372]	[950-1009]LRR_8:0.0013 [1009-1038]LRR_4:0.0023
RC1G0037000	rc01	4845477	4854130	NBS-LRR		P-loop[202-210] Kin-2[277-284] RNBS-B[308-314] GPLP[369-375]	[171-180]AAA_16:0.0022 [181-458]NB-ARC:3e-60 [877-922]LRR_8:0.00088 [961-1002]LRR_4:0.0015 [1009-1048]LRR_4:0.0053
RC1G0038100	rc01	4945293	4950173	NBS-LRR		P-loop[197-205] Kin-2[271-278] RNBS-B[304-310] GPLP[366-372]	[168-456]NB-ARC:3e-58 [584-638]LRR_8:9e-06
RC1G0038200	rc01	4997244	5004392	TIR-NBS-LRR		P-loop[227-235] Kin-2[301-308] RNBS-B[332-338] GPLP[390-396]	[18-189]TIR:9.3e-41 [206-459]NB-ARC:2.1e-34 [610-628]LRR_3:0.00055
RC1G0041300	rc01	5325468	5330421	NBS-LRR		P-loop[205-213] Kin-2[280-287] RNBS-B[309-315] GPLP[370-376]	[704-761]LRR_8:0.00073
RC1G0046400	rc01	6001575	6004952	NBS-LRR		P-loop[205-213] Kin-2[279-286] RNBS-B[308-314] GPLP[369-375]	[172-193]AAA_16:0.0076 [194-455]NB-ARC:5.5e-66 [583-635]LRR_8:3.8e-05
RC1G0046600	rc01	6015473	6021617	CC-NBS-LRR		P-loop[204-212] Kin-2[288-295] RNBS-B[317-323] GPLP[378-384]	[636-679]LRR_8:0.00045 [680-698]LRR_4:0.0018

RC1G0046700	rc01	6022946	6027291	NBS-LRR	P-loop[206-214] Kin-2[281-288] RNBS-B[310-316] GPLP[371-377]	[180-459]NB-ARC:4.1e-63 [584-621]LRR_4:0.0016 [622-635]LRR_4:0.0022	
RC1G0054000	rc01	6873096	6882290	NBS-LRR	P-loop[205-213] Kin-2[280-287] RNBS-B[310-316] GPLP[369-375]	[172-194]AAA_16:8.8e-05 [196-457]NB-ARC:4.1e-63 [579-616]LRR_4:0.0073	
RC1G0054700	rc01	6918760	6921635	NBS-LRR	P-loop[205-213] Kin-2[281-288] RNBS-B[311-317] GPLP[370-376]	[172-194]AAA_16:2.2e-05 [196-457]NB-ARC:3.5e-63 [580-634]LRR_8:4.1e-05 [634-654]LRR_8:0.00033	
RC1G0055000	rc01	7020069	7022309	NBS-LRR	P-loop[205-213] Kin-2[280-287] RNBS-B[310-316] GPLP[369-375]	[172-194]AAA_16:7.2e-06 [195-457]NB-ARC:5.7e-62 [579-633]LRR_8:8.9e-06	
RC1G0057100	rc01	7250515	7253199	CC-NBS-LRR	P-loop[199-207] Kin-2[273-280] RNBS-B[303-309] GPLP[361-367]	[172-194]AAA_16:7.2e-06 [195-457]NB-ARC:5.7e-62 [579-633]LRR_8:8.9e-06	
RC1G0057400	rc01	7348754	7351644	NBS-LRR	P-loop[203-211] Kin-2[278-285] RNBS-B[308-314] GPLP[367-373]	[170-192]AAA_16:1.3e-05 [194-454]NB-ARC:5.6e-63 [572-609]LRR_8:0.0065	
RC1G0057600	rc01	7392967	7394847	NBS-LRR	P-loop[106-114] Kin-2[180-187] RNBS-B[210-216] GPLP[268-274]	[73-95]AAA_16:5.5e-05 [96-356]NB-ARC:1.9e-59 [477-500]LRR_8:0.00043	
RC1G0058500	rc01	7430559	7433431	NBS-LRR	P-loop[201-209] Kin-2[276-283] RNBS-B[306-312] GPLP[369-375]	[501-541]LRR_4:4.9e-05	
RC1G0060200	rc01	7583456	7586325	NBS-LRR	P-loop[205-213] Kin-2[279-286] RNBS-B[309-315] GPLP[368-374]	[168-190]AAA_16:0.00032 [192-455]NB-ARC:1.1e-63	
RC1G0061100	rc01	7626425	7629494	NBS-LRR	P-loop[205-213] Kin-2[280-287] RNBS-B[310-316] GPLP[369-375]	[172-194]AAA_16:1.4e-05 [196-456]NB-ARC:2.9e-61 [579-633]LRR_8:7.2e-05	
RC1G0061900	rc01	7727136	7730004	CC-NBS-LRR	P-loop[205-213] Kin-2[280-287] RNBS-B[310-316] GPLP[369-375]	[172-194]AAA_16:2.1e-05 [195-456]NB-ARC:1.1e-63 [579-633]LRR_8:0.00012	
RC1G0064300	rc01	8054123	8056050	TIR-NBS	P-loop[133-141] Kin-2[211-218] RNBS-B[238-244] GPLP[297-303]	[640-653]LRR_8:0.0025	
RC1G0065800	rc01	8149862	8157268	NBS-LRR	P-loop[200-208] Kin-2[272-279] RNBS-B[302-308] GPLP[358-364]	[3-95]TIR:2.4e-07 [111-121]AAA_16:3.9e-06 [122-365]NB-ARC:1.4e-33	
RC1G0069700	rc01	8703984	8706776	NBS-LRR	P-loop[27-35] Kin-2[105-112] RNBS-B[132-138] GPLP[191-197]	[168-190]AAA_16:3.1e-05 [191-446]NB-ARC:7.1e-62 [570-608]LRR_4:3.9e-05	
RC1G0073500	rc01	9041245	9043098	TIR-NBS	P-loop[127-135] Kin-2[205-212] RNBS-B[232-238] GPLP[291-297]	[13-261]NB-ARC:2e-28 [409-427]LRR_3:1.8e-05 [477-500]LRR_4:0.00094 [501-557]LRR_8:0.0002 [557-581]LRR_8:0.004	
RC1G0074800	rc01	9109406	9111181	NBS	P-loop[27-35] Kin-2[105-112] RNBS-B[132-138] GPLP[191-197]	[2-93]TIR:9.3e-10 [107-117]AAA_16:4.2e-06 [118-306]NB-ARC:1.2e-24	
RC1G0102900	rc01	13141019	13142561	NBS-LRR	P-loop[35-43] Kin-2[110-117] RNBS-B[139-145] GPLP[196-202]	[18-258]NB-ARC:5.9e-30 [409-427]LRR_3:1.2e-05	
RC1G0105100	rc01	13684527	13694466	CC-NBS-LRR	RPW8	P-loop[904-912] Kin-2[985-992] RNBS-B[1009-1015] GPLP[1063-1069]	[14-284]NB-ARC:4.7e-57 [386-444]LRR_8:1.8e-07
RC1G0105300	rc01	13704406	13708236	CC-NBS-LRR	RPW8	P-loop[218-226] Kin-2[302-309] RNBS-B[328-333] GPLP[382-388]	[2-134]RPW8:3.7e-28 [172-435]NB-ARC:5e-35 [896-1145]NB-ARC:3.2e-27
RC1G0107900	rc01	14058276	14061495	CC-NBS-LRR		P-loop[199-207] Kin-2[274-281] RNBS-B[303-309] GPLP[364-370]	[2-111]RPW8:2.7e-13 [197-469]NB-ARC:3.1e-32 [732-788]LRR_8:0.0027

RC1G0110400	rc01	14418616	14420309	CC-NBS	P-loop[199-207] Kin-2[274-281] RNBS-B[304-310] GPLP[362-368]	[164-187]AAA_16:0.00012 [190-447]NB-ARC:2.5e-61
RC1G0116200	rc01	15333635	15336468	NBS-LRR	P-loop[194-202] Kin-2[270-277] RNBS-B[300-306] GPLP[361-367]	[171-446]NB-ARC:4.6e-63 [572-627]LRR_8:3.4e-05
RC1G0119600	rc01	15888685	15896466	CC-TIR-NBS-LRR	P-loop[358-366] Kin-2[433-440] RNBS-B[462-468] GPLP[523-529]	[23-193]TIR:1.8e-43 [332-612]NB-ARC:5.3e-66 [734-789]LRR_8:0.0025 [60-312]NB-ARC:7.8e-35 [501-540]LRR_4:0.0012 [541-559]LRR_4:0.0013 [605-646]LRR_4:0.00058
RC1G0122900	rc01	16293738	16299190	NBS-LRR	P-loop[81-89] Kin-2[155-162] RNBS-B[182-188] GPLP[241-247]	[17-273]NB-ARC:3.1e-35 [606-662]LRR_8:0.00016
RC1G0123100	rc01	16303980	16307600	NBS-LRR	P-loop[34-42] Kin-2[113-120] RNBS-B[140-146] GPLP[199-205]	[30-192]TIR:2.5e-44 [210-418]NB-ARC:9.7e-28
RC1G0126400	rc01	16721193	16724833	TIR-NBS	P-loop[231-239] Kin-2[306-313] RNBS-B[333-339] GPLP[391-397]	[22-187]TIR:2.2e-43 [206-477]NB-ARC:1.4e-52 [576-634]LRR_8:6.1e-06
RC1G0138100	rc01	18228736	18232954	TIR-NBS-LRR	P-loop[227-235] Kin-2[302-309] RNBS-B[331-337] GPLP[389-395]	[16-189]TIR:1.1e-46 [217-464]NB-ARC:6.7e-17 [584-632]MRP-S25:0.0048 [775-833]LRR_8:2.6e-05 [833-847]LRR_8:0.00033 [848-904]LRR_8:4.3e-06 [904-927]LRR_8:0.00037 [942-997]LRR_8:0.00036 [1264-1336]zf-RVT:3.6e-16
RC1G0164900	rc01	22907764	22914556	TIR-NBS-LRR	P-loop[224-232] Kin-2[306-313] RNBS-B[332-338] GPLP[396-402]	[172-194]AAA_16:0.00016 [196-454]NB-ARC:9.8e-63 [598-638]LRR_4:0.0077 [2-89]TIR:1.2e-10 [235-517]NB-ARC:2.5e-68
RC1G0173500	rc01	23919112	23922623	NBS-LRR	P-loop[205-213] Kin-2[278-285] RNBS-B[308-314] GPLP[367-373]	[170-451]NB-ARC:9.7e-66 [589-643]LRR_8:0.00012 [794-825]LRR_4:0.0019
RC1G0188800	rc01	25163338	25166861	CC-TIR-NBS	P-loop[262-270] Kin-2[337-344] RNBS-B[366-372] GPLP[427-433]	[103-370]NB-ARC:3.3e-70
RC1G0189200	rc01	25203533	25207311	NBS-LRR	P-loop[197-205] Kin-2[272-279] RNBS-B[301-307] GPLP[362-368]	[24-192]TIR:1.1e-43 [222-483]NB-ARC:2.8e-22 [634-651]LRR_3:4.2e-05
RC1G0202100	rc01	27188454	27191737	CC-NBS	P-loop[121-129] Kin-2[197-204] RNBS-B[224-230] GPLP[284-290]	[730-788]LRR_8:0.00017 [905-939]LRR_8:0.0056
RC1G0212800	rc01	28792198	28806550	TIR-NBS-LRR	P-loop[234-242] Kin-2[308-315] RNBS-B[340-346] GPLP[414-420]	[164-450]NB-ARC:2e-65
RC1G0222900	rc01	30353802	30356870	CC-NBS	P-loop[186-194] Kin-2[267-274] RNBS-B[295-301] GPLP[359-365]	[4-256]NB-ARC:2.5e-35 [408-463]LRR_8:0.001 [477-516]LRR_4:0.0044
RC1G0226800	rc01	30851240	30853319	NBS-LRR	P-loop[26-34] Kin-2[104-111] RNBS-B[131-137] GPLP[190-196]	[179-200]AAA_16:0.0038 [202-445]NB-ARC:1.4e-48 [524-548]LRR_8:7.3e-07
RC1G0227400	rc01	30924069	30929646	CC-NBS-LRR	P-loop[210-218] Kin-2[285-292] RNBS-B[316-322] GPLP[378-384]	[549-602]LRR_8:6.6e-07
RC1G0228100	rc01	31007694	31010755	CC-NBS-LRR	P-loop[197-205] Kin-2[272-279] RNBS-B[301-307] GPLP[362-368]	[171-451]NB-ARC:2.2e-65 [576-630]LRR_8:0.0063
RC1G0243000	rc01	33017453	33020902	NBS-LRR	P-loop[198-206] Kin-2[279-286] RNBS-B[307-313] GPLP[372-378]	[178-472]NB-ARC:7.6e-71
RC1G0243600	rc01	33043255	33047625	NBS	P-loop[270-278] Kin-2[351-358] RNBS-B[379-385] GPLP[444-450]	[250-544]NB-ARC:1.3e-71
RC1G0253600	rc01	34296194	34299052	NBS	P-loop[53-61] Kin-2[134-141] RNBS-B[163-169] GPLP[228-234]	[29-314]NB-ARC:6.1e-64
RC1G0255300	rc01	34455174	34458473	NBS-LRR	P-loop[197-205] Kin-2[278-285] RNBS-B[306-312] GPLP[371-377]	[174-471]NB-ARC:4.5e-67 [583-624]LRR_8:0.0071
RC1G0256100	rc01	34528453	34531707	NBS	P-loop[197-205] Kin-2[278-285] RNBS-B[306-312] GPLP[371-377]	[175-472]NB-ARC:8e-74
RC1G0256400	rc01	34538433	34541505	NBS	P-loop[197-205] Kin-2[278-285] RNBS-B[306-312] GPLP[371-377]	[173-471]NB-ARC:1.3e-66

RC1G0257500	rc01	34582155	34588844	NBS	P-loop[200-208] Kin-2[281-288] RNBS-B[309-315] GPLP[374-380]	[177-475]NB-ARC:5.7e-70
RC1G0258100	rc01	34682821	34686034	NBS	P-loop[168-176] Kin-2[249-256] RNBS-B[277-283] GPLP[342-348]	[146-443]NB-ARC:2.4e-70
RC1G0258500	rc01	34709625	34713095	NBS-LRR	P-loop[198-206] Kin-2[279-286] RNBS-B[307-313] GPLP[369-375]	[175-470]NB-ARC:1e-70 [803-834]LRR_4:0.0045
RC1G0260000	rc01	34855716	34858966	CC-NBS-LRR	P-loop[198-206] Kin-2[273-280] RNBS-B[302-308] GPLP[363-369]	[173-453]NB-ARC:1.5e-61 [573-624]LRR_8:5.5e-05
RC1G0260300	rc01	34910010	34911008	NBS	P-loop[63-71] Kin-2[138-145] RNBS-B[167-173] GPLP[228-234]	[40-305]NB-ARC:1.8e-63
RC1G0260800	rc01	34935325	34938804	CC-NBS-LRR	P-loop[260-268] Kin-2[335-342] RNBS-B[364-370] GPLP[425-431]	[234-516]NB-ARC:9.1e-64 [658-698]LRR_8:2.8e-05
RC1G0261200	rc01	34977136	34979891	NBS-LRR	P-loop[106-114] Kin-2[181-188] RNBS-B[210-216] GPLP[271-277]	[84-360]NB-ARC:9.7e-65 [476-530]LRR_8:9.5e-07 [530-553]LRR_4:0.0097
RC1G0261500	rc01	34992791	34995628	CC-NBS-LRR	P-loop[197-205] Kin-2[272-279] RNBS-B[301-307] GPLP[362-368]	[171-452]NB-ARC:6.2e-65 [570-624]LRR_8:2.9e-05 [624-653]LRR_4:0.00081
RC1G0263800	rc01	35482052	35484165	NBS-LRR	P-loop[1-8] Kin-2[75-82] RNBS-B[104-110] GPLP[165-171]	[1-254]NB-ARC:1.3e-61 [376-430]LRR_8:1.9e-06
RC1G0266700	rc01	35983205	35987660	TIR-NBS-LRR	P-loop[219-227] Kin-2[298-305] RNBS-B[325-331] GPLP[384-390]	[17-180]TIR:1.4e-45 [197-447]NB-ARC:1.8e-30 [611-666]LRR_8:0.00052
RC1G0267700	rc01	36085877	36095663	NBS-LRR	P-loop[1-8] Kin-2[79-86] RNBS-B[106-112] GPLP[165-171]	[769-808]LRR_8:0.00026
RC1G0274300	rc01	37005938	37008680	NBS-LRR	P-loop[157-165] Kin-2[232-239] RNBS-B[261-267] GPLP[324-330]	[1-227]NB-ARC:1.1e-28 [541-597]LRR_8:2.6e-05
RC1G0274700	rc01	37056770	37059016	NBS-LRR	P-loop[64-72] Kin-2[139-146] RNBS-B[168-174] GPLP[229-235]	[134-414]NB-ARC:8e-65 [537-575]LRR_4:0.00013 [576-594]LRR_8:0.00095
RC1G0276600	rc01	37308983	37312698	CC-TIR-NBS-LRR	P-loop[360-368] Kin-2[435-442] RNBS-B[464-470] GPLP[525-531]	[41-319]NB-ARC:1.4e-57 [439-494]LRR_8:3.6e-05
RC1G0277100	rc01	37347001	37349814	NBS-LRR	P-loop[194-202] Kin-2[278-285] RNBS-B[305-311] GPLP[369-375]	[23-193]TIR:5.6e-46 [329-350]AAA_16:0.0018 [351-617]NB-ARC:3.9e-68 [739-752]LRR_4:0.0075
RC1G0279800	rc01	37721000	37724162	TIR-NBS-LRR	P-loop[228-236] Kin-2[307-314] RNBS-B[334-340] GPLP[393-399]	[753-795]LRR_8:0.0023
RC1G0280200	rc01	37745457	37750723	TIR-NBS-LRR	P-loop[228-236] Kin-2[307-314] RNBS-B[334-340] GPLP[393-399]	[171-462]NB-ARC:2.5e-87 [580-636]LRR_8:0.0023 [848-888]LRR_4:0.0039
RC1G0280400	rc01	37798453	37800765	TIR-NBS-LRR	P-loop[128-136] Kin-2[207-214] RNBS-B[234-240] GPLP[293-299]	[23-188]TIR:6.8e-47 [204-457]NB-ARC:3e-30 [621-676]LRR_8:7.5e-05 [677-724]LRR_8:0.00036
RC1G0280700	rc01	37844788	37848991	TIR-NBS-LRR	P-loop[226-234] Kin-2[305-312] RNBS-B[332-338] GPLP[391-397]	[24-188]TIR:4.1e-44 [207-456]NB-ARC:5.1e-30 [621-639]LRR_3:0.0072
RC1G0280900	rc01	37882803	37884682	TIR-NBS	P-loop[226-234] Kin-2[305-312] RNBS-B[332-338] GPLP[391-397]	[779-830]LRR_8:0.00025
RC1G0281100	rc01	37889095	37900487	NBS-LRR	P-loop[65-73] Kin-2[144-151] RNBS-B[171-177] GPLP[230-236]	[2-87]TIR:1.9e-15 [104-356]NB-ARC:1.6e-33 [520-576]LRR_8:8.1e-05
RC1G0281700	rc01	37955383	37958948	CC-NBS-LRR	P-loop[180-188] Kin-2[255-262] RNBS-B[284-290] GPLP[346-352]	[22-183]TIR:8.7e-47 [202-456]NB-ARC:1.9e-33 [610-628]LRR_3:7.8e-05
RC1G0282300	rc01	38053236	38056766	CC-NBS-LRR	P-loop[180-188] Kin-2[255-262] RNBS-B[284-290] GPLP[346-352]	[22-183]TIR:1.3e-45 [202-457]NB-ARC:5.3e-34
						[43-295]NB-ARC:3.7e-30 [611-666]LRR_8:2.2e-07
						[154-435]NB-ARC:3.6e-62 [554-609]LRR_8:1.4e-05 [610-638]LRR_4:0.00029 [971-1024]LRR_8:0.0023
						[156-434]NB-ARC:2.2e-62 [554-609]LRR_8:1.5e-05 [610-

						637]LRR_4:0.00038 [972- 1025]LRR_8:0.0039
RC1G0283400	rc01	38244919	38248918	NBS-LRR	P-loop[65-73] Kin-2[144-151] RNBS-B[171-177] GPLP[230-236]	[41-298]NB-ARC:1.6e-30 [459- 478]LRR_3:0.0042 [616- 670]LRR_8:0.00028 [14-192]TIR:1.1e-47 [193- 207]AAA_16:0.0028 [208-446]NB- ARC:3.6e-24 [613-628]LRR_3:0.00089 [654-711]LRR_8:0.0042 [931- 987]LRR_8:8.9e-07
RC1G0288000	rc01	38848444	38859425	TIR-NBS-LRR	P-loop[218-226] Kin-2[296-303] RNBS-B[323-329] GPLP[379-385]	[5-257]NB-ARC:1.4e-34 [557- 579]LRR_4:0.0099 [580- 636]LRR_8:0.0078 [651- 689]LRR_4:0.0045 [821-875]LRR_8:7e-06 [182-449]NB-ARC:2.2e-66 [573- 628]LRR_8:6.5e-07 [190-458]NB-ARC:6.1e-55 [838- 898]LRR_8:0.00016 [1009- 1134]LRR_5:4.9e-05
RC1G0288100	rc01	38900986	38908393	NBS-LRR	P-loop[26-34] Kin-2[103-110] RNBS-B[130-136] GPLP[186-192]	[182-449]NB-ARC:2.2e-66 [573- 628]LRR_8:6.5e-07 [190-458]NB-ARC:6.1e-55 [838- 898]LRR_8:0.00016 [1009- 1134]LRR_5:4.9e-05
RC1G0292300	rc01	39326948	39330621	CC-NBS-LRR	P-loop[193-201] Kin-2[268-275] RNBS-B[297-303] GPLP[359-365]	[20-182]TIR:2.6e-43 [204-412]NB- ARC:6.6e-40
RC1G0300200	rc01	40223859	40231796	NBS-LRR	P-loop[202-210] Kin-2[277-284] RNBS-B[308-314] GPLP[369-375]	[151-415]NB-ARC:1.3e-43 [174-467]NB-ARC:7.2e-69 [621- 673]LRR_8:0.00042
RC1G0329000	rc01	43472577	43474189	TIR-NBS	P-loop[225-233] Kin-2[300-307] RNBS-B[329-335] GPLP[387-393]	[174-470]NB-ARC:2.8e-69 [767- 822]LRR_8:0.0085
RC1G0358000	rc01	45960816	45969304	NBS	P-loop[171-179] Kin-2[245-252] RNBS-B[269-275] GPLP[328-334]	[156-174]AAA_16:0.0039 [175-435]NB- ARC:5e-63
RC1G0363100	rc01	46493639	46504568	NBS-LRR	P-loop[194-202] Kin-2[275-282] RNBS-B[303-309] GPLP[368-374]	[1-229]NB-ARC:1.4e-23
RC1G0367100	rc01	46770348	46773547	NBS-LRR	P-loop[194-202] Kin-2[275-282] RNBS-B[303-309] GPLP[370-376]	[18-198]TIR:2.1e-47 [203-435]NB- ARC:2e-30 [587-642]LRR_8:0.0055
RC1G0400700	rc01	50256161	50257511	CC-NBS	P-loop[188-196] Kin-2[265-272] RNBS-B[294-300] GPLP[355-361]	[176-188]AAA_16:0.0056 [189-463]NB- ARC:4.3e-65 [587-642]LRR_8:3.2e-05
RC1G0404100	rc01	50508504	50510713	NBS-LRR	P-loop[1-8] Kin-2[76-83] RNBS-B[103-109] GPLP[162-163]	[174-184]AAA_16:0.00039 [186-459]NB- ARC:3.9e-64 [597-645]LRR_8:0.00017
RC1G0435000	rc01	53058281	53067880	TIR-NBS-LRR	P-loop[224-232] Kin-2[283-290] RNBS-B[310-316] GPLP[369-375]	[174-186]AAA_16:6.2e-05 [187-461]NB- ARC:6.8e-65 [560-578]LRR_4:0.002 [587- 627]LRR_4:0.00024
RC1G0441100	rc01	53471786	53475028	CC-NBS-LRR	P-loop[208-216] Kin-2[285-292] RNBS-B[314-320] GPLP[375-381]	[180-198]AAA_16:0.00011 [199-467]NB- ARC:9.4e-64 [620-660]LRR_4:1.3e-05
RC1G0454600	rc01	54629504	54632323	CC-NBS-LRR	P-loop[206-214] Kin-2[283-290] RNBS-B[312-318] GPLP[373-379]	[669-708]LRR_4:0.00022 [3-254]NB-ARC:2.8e-29 [430- 449]LRR_3:2e-05 [499- 540]LRR_4:0.00028 [673- 727]LRR_8:2.4e-05
RC1G0454800	rc01	54650760	54654953	CC-NBS-LRR	P-loop[206-214] Kin-2[283-290] RNBS-B[312-318] GPLP[373-379]	[3-255]NB-ARC:2.3e-30 [430- 449]LRR_3:3e-07 [674-728]LRR_8:1.7e-06
RC1G0461500	rc01	55237811	55240714	CC-NBS-LRR	P-loop[212-220] Kin-2[289-296] RNBS-B[318-324] GPLP[380-386]	[164-187]AAA_16:1.8e-05 [190-451]NB- ARC:1.5e-61 [566-576]LRR_8:0.00018
RC1G0497200	rc01	57900419	57903163	NBS-LRR	P-loop[26-34] Kin-2[104-111] RNBS-B[131-137] GPLP[188-194]	[577-616]LRR_4:3.8e-05 [617- 651]LRR_8:6.2e-05
RC1G0497800	rc01	57955390	57958437	NBS-LRR	P-loop[26-34] Kin-2[104-111] RNBS-B[131-137] GPLP[188-194]	
RC1G0510300	rc01	58639792	58643017	NBS-LRR	P-loop[199-207] Kin-2[274-281] RNBS-B[304-310] GPLP[362-368]	

RC1G0519100	rc01	59266796	59269332	NBS-LRR		P-loop[199-207] Kin-2[274-281] RNBS-B[304-310] GPLP[362-368]	[188-450]NB-ARC:2.2e-62 [556-569]LRR_8:0.00024 [570-624]LRR_8:1.1e-05 [624-643]LRR_8:0.0068
RC1G0522300	rc01	59490811	59493714	NBS-LRR		P-loop[213-221] Kin-2[295-302] RNBS-B[322-328] GPLP[388-394]	[203-481]NB-ARC:7.5e-77 [601-654]LRR_8:0.0052
RC1G0528100	rc01	59873875	59875920	TIR-NBS		P-loop[218-226] Kin-2[295-302] RNBS-B[322-328] GPLP[379-385]	[14-192]TIR:2.1e-47 [195-442]NB-ARC:1.3e-32
RC1G0528400	rc01	59891985	59893200	NBS		P-loop[19-27] Kin-2[96-103] RNBS-B[123-129] GPLP[180-186]	[5-238]NB-ARC:9.3e-33 [18-183]TIR:3.6e-44 [203-451]NB-ARC:1.6e-25 [618-637]LRR_3:4.4e-07
RC1G0528700	rc01	59911621	59918597	TIR-NBS-LRR	WRKY	P-loop[222-230] Kin-2[300-307] RNBS-B[327-333] GPLP[384-390]	[687-724]LRR_4:0.00096 [725-767]LRR_8:0.0075 [863-915]LRR_8:1.1e-06 [915-925]LRR_4:0.0054 [1275-1335]WRKY:1.3e-23 [18-197]TIR:1.1e-39 [201-446]NB-ARC:2.9e-28 [618-637]LRR_3:0.00013
RC1G0528900	rc01	59925434	59933238	TIR-NBS-LRR		P-loop[1131-1139] Kin-2[1209-1216] RNBS-B[1236-1242] GPLP[1291-1292]	[1107-1316]NB-ARC:4.4e-18 [1511-1530]LRR_3:3.7e-05 [1580-1623]LRR_4:0.0019 [1629-1684]LRR_8:0.00084
RC1G0579300	rc01	63596322	63598477	TIR-NBS		P-loop[124-132] Kin-2[202-209] RNBS-B[229-235] GPLP[288-294]	[4-98]TIR:2e-13 [104-357]NB-ARC:4e-38 [4-86]TIR:2.9e-12 [102-360]NB-ARC:3.2e-37 [503-558]LRR_8:0.00041 [685-727]LRR_4:0.0079
RC1G0579500	rc01	63622337	63626256	TIR-NBS-LRR		P-loop[124-132] Kin-2[203-210] RNBS-B[230-236] GPLP[289-295]	[18-197]TIR:3.9e-50 [206-455]NB-ARC:2.9e-35 [604-659]LRR_8:0.0039
RC1G0581100	rc01	63702553	63706461	CC-TIR-NBS-LRR		P-loop[224-232] Kin-2[302-309] RNBS-B[329-335] GPLP[388-394]	[4-254]NB-ARC:1.8e-38 [408-463]LRR_8:0.00074
RC1G0581200	rc01	63709713	63715148	NBS-LRR		P-loop[26-34] Kin-2[105-112] RNBS-B[132-138] GPLP[191-197]	[157-424]NB-ARC:8.9e-42 [1272-1282]TniB:0.0021 [1283-1554]NB-ARC:1e-42 [1671-1715]LRR_8:0.0054
RC2G0007300	rc02	645051	661704	CC-NBS-LRR	TniB	P-loop[176-184] Kin-2[253-260] RNBS-B[277-283] GPLP[337-343]	[1727-1784]LRR_8:0.0018
RC2G0007700	rc02	674151	678665	CC-NBS-LRR	TniB	P-loop[185-193] Kin-2[265-272] RNBS-B[289-295] GPLP[347-353]	[156-166]TniB:0.0043 [167-426]NB-ARC:1.8e-48 [608-663]LRR_8:0.0011
RC2G0134700	rc02	11227056	11230506	TIR-NBS-LRR		P-loop[226-234] Kin-2[300-307] RNBS-B[327-333] GPLP[386-392]	[20-200]TIR:5.5e-47 [211-454]NB-ARC:7.4e-36
RC2G0148100	rc02	12333147	12335759	NBS	RPW8	P-loop[208-216] Kin-2[282-289] RNBS-B[310-316] GPLP[374-380]	[23-98]RPW8:0.0034 [185-465]NB-ARC:1.3e-89
RC2G0151500	rc02	12581369	12586323	NBS-LRR		P-loop[135-143] Kin-2[212-219] RNBS-B[239-245] GPLP[300-306]	[107-125]AAA_16:0.00053 [126-367]NB-ARC:3.1e-29 [518-536]LRR_3:1.5e-05
RC2G0155400	rc02	12912578	12916217	CC-NBS-LRR		P-loop[193-201] Kin-2[275-282] RNBS-B[302-308] GPLP[365-371]	[610-667]LRR_8:6.9e-06 [765-822]LRR_8:0.0028
RC2G0179100	rc02	15325681	15329889	NBS-LRR	RPW8	P-loop[219-227] Kin-2[298-305] RNBS-B[324-330] GPLP[380-386]	[170-457]NB-ARC:1.8e-78 [574-630]LRR_8:1.6e-06 [631-647]LRR_8:0.00012
RC2G0179200	rc02	15342873	15347295	NBS-LRR	RPW8	P-loop[203-211] Kin-2[281-288] RNBS-B[307-313] GPLP[362-368]	[3-136]RPW8:3.2e-30 [183-447]NB-ARC:1.9e-25 [710-766]LRR_8:0.0032
RC2G0179300	rc02	15385324	15390125	NBS	RPW8	P-loop[239-247] Kin-2[318-325] RNBS-B[344-350] GPLP[396-402]	[21-157]RPW8:3.5e-31 [219-483]NB-ARC:7.5e-33
RC2G0179400	rc02	15392613	15396430	NBS-LRR	RPW8	P-loop[214-222] Kin-2[293-300] RNBS-B[319-325] GPLP[371-377]	[1-132]RPW8:3.5e-26 [194-457]NB-ARC:1.5e-34

RC2G0179500	rc02	15397426	15402277	NBS	RPW8	P-loop[215-223] Kin-2[294-301] RNBS-B[320-325] GPLP[374-380]	[6-137]RPW8:1e-23 [201-462]NB-ARC:2.9e-30
RC2G0179600	rc02	15402279	15405360	NBS-LRR		P-loop[54-62] Kin-2[134-141] RNBS-B[160-166] GPLP[215-221]	[38-302]NB-ARC:5.6e-27 [540-592]LRR_8:0.0028
RC2G0179800	rc02	15434947	15438315	CC-NBS-LRR	RPW8,Vps53_N	P-loop[231-239] Kin-2[310-317] RNBS-B[335-341] GPLP[389-395]	[5-140]RPW8:4.6e-28 [141-162]Vps53_N:0.0028 [211-475]NB-ARC:3.4e-33 [741-798]LRR_8:5.6e-05
RC2G0180500	rc02	15481969	15485440	CC-NBS-LRR	RPW8	P-loop[230-238] Kin-2[309-316] RNBS-B[334-340] GPLP[388-394]	[5-140]RPW8:1e-26 [210-474]NB-ARC:1.1e-31 [740-797]LRR_8:0.00019
RC2G0180800	rc02	15510723	15513360	CC-NBS	RPW8	P-loop[227-235] Kin-2[306-313] RNBS-B[331-337] GPLP[390-396]	[6-140]RPW8:3e-27 [207-476]NB-ARC:2.7e-30
RC2G0181000	rc02	15515501	15519519	NBS	RPW8	P-loop[213-221] Kin-2[290-297] RNBS-B[317-323] GPLP[372-378]	[8-133]RPW8:8.6e-22 [191-458]NB-ARC:7.2e-36
RC2G0181200	rc02	15537972	15543128	NBS-LRR	RPW8	P-loop[194-202] Kin-2[273-280] RNBS-B[299-305] GPLP[354-360]	[5-139]RPW8:1.4e-24 [175-441]NB-ARC:8.1e-35 [682-737]LRR_8:0.0017
RC2G0181300	rc02	15551313	15554880	CC-NBS	RPW8	P-loop[161-169] Kin-2[240-247] RNBS-B[266-272] GPLP[321-327]	[1-103]RPW8:1.4e-17 [142-407]NB-ARC:1.1e-32
RC2G0181700	rc02	15566602	15570265	CC-NBS	RPW8	P-loop[166-174] Kin-2[245-252] RNBS-B[271-277] GPLP[326-332]	[3-106]RPW8:3.9e-17 [149-412]NB-ARC:1.3e-31
RC2G0181800	rc02	15571593	15574784	NBS-LRR	RPW8	P-loop[199-207] Kin-2[278-285] RNBS-B[306-312] GPLP[361-367]	[11-121]RPW8:1.8e-19 [173-187]AAA_16:0.00063 [188-447]NB-ARC:1.6e-26 [699-746]LRR_8:0.0057
RC2G0183000	rc02	15720908	15732328	CC-NBS-LRR	RPW8,Pkinase_Tyr	P-loop[417-425] Kin-2[481-488] RNBS-B[507-513] GPLP[562-568]	[747-787]LRR_4:0.0016
RC2G0184000	rc02	15816412	15826862	CC-NBS-LRR	RPW8,zf-CCCH	P-loop[519-527] Kin-2[598-605] RNBS-B[623-629] GPLP[678-684]	[5-138]RPW8:6.5e-13 [183-310]RPW8:1.9e-19 [399-648]NB-ARC:4.3e-25 [887-945]LRR_8:0.0039
RC2G0184100	rc02	15828907	15835140	NBS	RPW8,Peptidase_C48	P-loop[196-204] Kin-2[275-282] RNBS-B[300-306] GPLP[355-361]	[1167-1476]Pkinase_Tyr:4.4e-35 [1558-1837]Pkinase_Tyr:1.2e-45
RC2G0199900	rc02	17674833	17684919	TIR-NBS-LRR		P-loop[260-268] Kin-2[334-341] RNBS-B[365-371] GPLP[426-432]	[12-144]RPW8:3.2e-12 [211-328]RPW8:6.9e-22 [439-463]zf-CCCH:2.9e-08 [498-763]NB-ARC:2.3e-41
RC2G0200100	rc02	17703046	17710202	TIR-NBS-LRR		P-loop[227-235] Kin-2[301-308] RNBS-B[332-338] GPLP[393-399]	[1015-1072]LRR_8:7.1e-05
							[6-140]RPW8:2.1e-33 [176-442]NB-ARC:1e-24 [1024-1231]Peptidase_C48:6e-30
							[56-227]TIR:2.8e-48 [232-241]AAA_16:0.0094 [242-491]NB-ARC:9.8e-33 [894-950]LRR_8:1.2e-05
							[1017-1054]LRR_4:3.1e-05 [1152-1204]LRR_8:0.00093 [1244-1280]LRR_8:3.3e-07 [1281-1313]LRR_4:0.00036 [1314-1324]LRR_8:0.0028
							[23-194]TIR:4.7e-47 [208-466]NB-ARC:9.1e-33 [716-774]LRR_8:0.0053
							[985-1022]LRR_4:0.0007 [1120-1173]LRR_8:0.0011 [1190-1249]LRR_8:5.5e-09 [1250-1282]LRR_4:0.00017 [1283-1293]LRR_8:0.0023

RC2G0200200	rc02	17718777	17727816	TIR-NBS-LRR	[23-194]TIR:7.8e-49 [205-467]NB-ARC:5e-31 [632-647]LRR_3:0.0018 [891-926]LRR_8:0.0065 [1011-1048]LRR_4:0.00013 [1219-1241]LRR_8:2.6e-06 [1242-1300]LRR_8:6e-12 [1301-1323]LRR_8:2.8e-10 [1324-1333]LRR_8:1.1e-06 [1334-1392]LRR_8:1.7e-09 [1393-1402]LRR_8:2.6e-09 [1403-1448]LRR_8:6e-10 [1449-1507]LRR_8:5.5e-11 [1511-1552]LRR_8:1.6e-05 [177-459]NB-ARC:2.8e-63 [562-572]LRR_8:0.0051 [573-629]LRR_8:0.00097 [1120-1159]LRR_4:0.0016 [67-333]NB-ARC:5.3e-50 [499-555]LRR_8:0.0016 [151-403]NB-ARC:8.4e-36 [591-628]LRR_8:0.0044 [628-652]LRR_8:0.0072 [148-167]AAA_16:0.0089 [168-355]NB-ARC:4.8e-24 [180-464]NB-ARC:5e-59 [584-640]LRR_8:0.00054 [254-525]NB-ARC:2.2e-69 [630-649]LRR_8:5.1e-07 [650-705]LRR_8:2.7e-09 [180-463]NB-ARC:3.5e-57 [585-639]LRR_8:0.0043 [30-306]NB-ARC:8.6e-43 [467-522]LRR_8:5.4e-08 [524-803]NB-ARC:3.9e-42 [958-1013]LRR_8:6.1e-05
RC2G0210900	rc02	18878750	18883160	NBS-LRR	P-loop[202-210] Kin-2[277-284] RNBS-B[308-314] GPLP[369-375]
RC2G0219600	rc02	19753419	19761438	NBS-LRR	P-loop[86-94] Kin-2[164-171] RNBS-B[188-194] GPLP[247-253]
RC2G0244600	rc02	22875094	22883763	NBS-LRR	P-loop[173-181] Kin-2[250-257] RNBS-B[274-280] GPLP[333-339]
RC2G0255900	rc02	24654280	24655778	NBS	P-loop[178-186] Kin-2[260-267] RNBS-B[288-294] GPLP[343-349]
RC2G0285900	rc02	28438869	28441360	CC-NBS-LRR	P-loop[206-214] Kin-2[281-288] RNBS-B[315-321] GPLP[376-382]
RC2G0294800	rc02	29720246	29724405	CC-NBS-LRR	P-loop[270-278] Kin-2[346-353] RNBS-B[375-381] GPLP[437-443]
RC2G0314400	rc02	32812925	32817044	NBS-LRR	P-loop[206-214] Kin-2[281-288] RNBS-B[315-321] GPLP[376-382]
RC2G0318800	rc02	33687657	33689879	NBS-LRR	P-loop[54-62] Kin-2[131-138] RNBS-B[159-165] GPLP[215-221]
RC2G0319100	rc02	33716915	33720694	CC-NBS-LRR	P-loop[549-557] Kin-2[629-636] RNBS-B[656-662] GPLP[716-722]
RC2G0350400	rc02	39412156	39414798	CC-NBS-LRR	P-loop[206-214] Kin-2[281-288] RNBS-B[315-321] GPLP[376-382]
RC2G0350700	rc02	39441734	39444415	NBS-LRR	P-loop[206-214] Kin-2[281-288] RNBS-B[315-321] GPLP[376-382]
RC2G0356300	rc02	39969343	39973621	NBS-LRR	P-loop[206-214] Kin-2[281-288] RNBS-B[315-321] GPLP[376-382]
RC2G0358600	rc02	40163047	40168495	NBS-LRR	P-loop[206-214] Kin-2[281-288] RNBS-B[315-321] GPLP[376-382]
RC2G0389900	rc02	44543234	44548635	CC-NBS-LRR	P-loop[208-216] Kin-2[283-290] RNBS-B[312-318] GPLP[375-381]
RC2G0392700	rc02	44882897	44887968	CC-NBS-LRR	P-loop[208-216] Kin-2[283-290] RNBS-B[312-318] GPLP[375-381]
RC2G0394600	rc02	45176707	45181083	NBS	P-loop[198-206] Kin-2[275-282] RNBS-B[305-311] GPLP[366-372]
RC2G0400800	rc02	46012932	46015626	CC-NBS-LRR	P-loop[208-216] Kin-2[283-290] RNBS-B[312-318] GPLP[375-381]
RC2G0401500	rc02	46046182	46047530	NBS-LRR	P-loop[1-8] Kin-2[75-82] RNBS-B[104-110] GPLP[167-173]

RC2G0401600	rc02	46049909	46052803	CC-NBS-LRR	P-loop[208-216] Kin-2[283-290] RNBS-B[312-318] GPLP[375-381]	[184-464]NB-ARC:1.6e-60 [562-584]LRR_8:9.4e-07 [585-641]LRR_8:4.1e-08 [780-833]LRR_8:0.0092 [85-367]NB-ARC:4.7e-63 [490-544]LRR_8:1e-08 [177-189]AAA_16:0.00095 [190-464]NB-ARC:1.8e-63 [562-584]LRR_8:1.5e-07 [585-640]LRR_8:1.2e-07 [186-465]NB-ARC:7.1e-62 [562-584]LRR_8:1.5e-07 [585-641]LRR_8:5.9e-08
RC2G0401900	rc02	46068087	46070552	NBS-LRR	P-loop[113-121] Kin-2[188-195] RNBS-B[217-223] GPLP[280-286]	[177-189]AAA_16:0.00095 [190-464]NB-ARC:1.8e-63 [562-584]LRR_8:1.5e-07 [585-640]LRR_8:1.2e-07 [186-465]NB-ARC:7.1e-62 [562-584]LRR_8:1.5e-07 [585-641]LRR_8:5.9e-08
RC2G0402100	rc02	46079724	46083075	CC-NBS-LRR	P-loop[208-216] Kin-2[283-290] RNBS-B[312-318] GPLP[375-381]	[185-463]NB-ARC:7.5e-62 [1-255]NB-ARC:1.3e-56 [354-376]LRR_8:2.9e-07 [377-433]LRR_8:1e-07
RC2G0402400	rc02	46117552	46120801	CC-NBS-LRR	P-loop[208-216] Kin-2[283-290] RNBS-B[312-318] GPLP[375-381]	[186-472]NB-ARC:7.2e-62 [567-623]LRR_8:2e-07 [631-654]LRR_4:0.00062 [1004-1069]CSD:7.6e-24
RC2G0403100	rc02	46146324	46149074	CC-NBS-LRR	P-loop[208-216] Kin-2[284-291] RNBS-B[313-319] GPLP[376-382]	[185-463]NB-ARC:7.5e-62 [1-255]NB-ARC:1.3e-56 [354-376]LRR_8:2.9e-07 [377-433]LRR_8:1e-07
RC2G0404000	rc02	46210483	46212510	NBS-LRR	P-loop[1-8] Kin-2[75-82] RNBS-B[104-110] GPLP[167-173]	[186-472]NB-ARC:7.2e-62 [567-623]LRR_8:2e-07 [631-654]LRR_4:0.00062 [1004-1069]CSD:7.6e-24
RC2G0422900	rc02	49299023	49302923	CC-NBS-LRR	P-loop[215-223] Kin-2[292-299] RNBS-B[321-327] GPLP[384-390]	[191-463]NB-ARC:8.4e-70 [179-455]NB-ARC:1.7e-63 [564-580]LRR_8:9.5e-06 [581-633]LRR_8:3.2e-07 [634-659]LRR_8:0.0019 [171-181]AAA_16:0.0028 [182-386]NB-ARC:7e-45
RC2G0424700	rc02	49551738	49556053	CC-NBS	P-loop[208-216] Kin-2[284-291] RNBS-B[313-319] GPLP[375-381]	[191-463]NB-ARC:8.4e-70 [179-455]NB-ARC:1.7e-63 [564-580]LRR_8:9.5e-06 [581-633]LRR_8:3.2e-07 [634-659]LRR_8:0.0019 [171-181]AAA_16:0.0028 [182-386]NB-ARC:7e-45
RC2G0425100	rc02	49561390	49564576	CC-NBS-LRR	P-loop[200-208] Kin-2[276-283] RNBS-B[305-311] GPLP[368-374]	[192-466]NB-ARC:3.4e-71 [587-642]LRR_8:1.4e-08 [657-697]LRR_4:0.0098 [199-472]NB-ARC:4.3e-64 [577-626]LRR_8:1.7e-07 [627-647]LRR_8:1.9e-07 [656-671]LRR_8:0.0036 [194-465]NB-ARC:2.6e-69 [588-643]LRR_8:6.7e-08 [194-465]NB-ARC:3.5e-69 [588-643]LRR_8:8e-08
RC2G0428200	rc02	49894772	49895982	CC-NBS	P-loop[203-211] Kin-2[279-286] RNBS-B[308-314] GPLP[371-377]	[176-463]NB-ARC:9.6e-83 [557-608]LRR_8:0.00031 [609-630]LRR_8:0.0021
RC2G0428600	rc02	49927478	49934703	CC-NBS-LRR	P-loop[209-217] Kin-2[285-292] RNBS-B[314-320] GPLP[376-382]	[199-472]NB-ARC:4.3e-64 [577-626]LRR_8:1.7e-07 [627-647]LRR_8:1.9e-07 [656-671]LRR_8:0.0036 [194-465]NB-ARC:2.6e-69 [588-643]LRR_8:6.7e-08 [194-465]NB-ARC:3.5e-69 [588-643]LRR_8:8e-08
RC2G0428800	rc02	49938166	49940232	CC-NBS-LRR	P-loop[216-224] Kin-2[292-299] RNBS-B[322-328] GPLP[384-390]	[176-463]NB-ARC:9.6e-83 [557-608]LRR_8:0.00031 [609-630]LRR_8:0.0021
RC2G0429900	rc02	50004991	50007661	CC-NBS-LRR	P-loop[210-218] Kin-2[286-293] RNBS-B[315-321] GPLP[377-383]	[5-245]NB-ARC:3.5e-61 [105-395]NB-ARC:6.5e-60 [497-543]LRR_8:3.1e-06 [544-562]LRR_8:1.2e-05 [184-448]NB-ARC:2.3e-59 [553-562]LRR_8:0.00013 [563-617]LRR_8:1.6e-05 [766-796]LRR_4:0.0049 [160-437]NB-ARC:3.9e-87 [518-535]LRR_9:0.0018 [536-594]LRR_8:1.1e-11 [595-624]LRR_4:0.00018 [181-203]AAA_16:9.6e-05 [204-467]NB-ARC:1.3e-60 [564-588]LRR_8:2.8e-05 [589-644]LRR_8:2.6e-06 [644-668]LRR_8:0.00052 [778-813]LRR_8:0.00043
RC2G0430300	rc02	50021196	50024246	CC-NBS-LRR	P-loop[210-218] Kin-2[286-293] RNBS-B[315-321] GPLP[377-383]	[182-201]AAA_16:0.00062 [202-468]NB-ARC:2.3e-59 [593-648]LRR_8:5.6e-06 [648-670]LRR_8:0.0023
RC2G0431500	rc02	50128154	50130890	NBS-LRR	P-loop[198-206] Kin-2[280-287] RNBS-B[307-313] GPLP[371-377]	[182-201]AAA_16:0.00062 [202-468]NB-ARC:2.3e-59 [593-648]LRR_8:5.6e-06 [648-670]LRR_8:0.0023
RC2G0432000	rc02	50213957	50215216	NBS	P-loop[18-26] Kin-2[100-107] RNBS-B[127-133] GPLP[191-197]	[182-201]AAA_16:0.00062 [202-468]NB-ARC:2.3e-59 [593-648]LRR_8:5.6e-06 [648-670]LRR_8:0.0023
RC2G0439500	rc02	51259407	51261938	NBS-LRR	P-loop[134-142] Kin-2[214-221] RNBS-B[243-249] GPLP[306-312]	[182-201]AAA_16:0.00062 [202-468]NB-ARC:2.3e-59 [593-648]LRR_8:5.6e-06 [648-670]LRR_8:0.0023
RC2G0441000	rc02	51485056	51489326	NBS-LRR	P-loop[194-200] Kin-2[271-278] RNBS-B[300-306] GPLP[359-365]	[182-201]AAA_16:0.00062 [202-468]NB-ARC:2.3e-59 [593-648]LRR_8:5.6e-06 [648-670]LRR_8:0.0023
RC2G0446800	rc02	52027088	52029827	CC-NBS-LRR	P-loop[182-190] Kin-2[260-267] RNBS-B[287-293] GPLP[347-353]	[182-201]AAA_16:0.00062 [202-468]NB-ARC:2.3e-59 [593-648]LRR_8:5.6e-06 [648-670]LRR_8:0.0023
RC2G0474400	rc02	55058308	55061000	CC-NBS-LRR	P-loop[214-222] Kin-2[287-294] RNBS-B[316-322] GPLP[378-384]	[182-201]AAA_16:0.00062 [202-468]NB-ARC:2.3e-59 [593-648]LRR_8:5.6e-06 [648-670]LRR_8:0.0023
RC2G0474900	rc02	55134538	55137227	CC-NBS-LRR	P-loop[215-223] Kin-2[288-295] RNBS-B[317-323] GPLP[379-385]	[182-201]AAA_16:0.00062 [202-468]NB-ARC:2.3e-59 [593-648]LRR_8:5.6e-06 [648-670]LRR_8:0.0023

RC2G0506600	rc02	58862239	58866940	NBS	DAGK_acc	P-loop[18-26] Kin-2[107-114] RNBS-B[148-154] GPL[221-227]	[11-247]NB-ARC:8.8e-20 [513-617]DAGK_acc:1.2e-10
RC2G0506700	rc02	58868511	58869206	NBS		P-loop[1-8] Kin-2[90-97] RNBS-B[131-137] GPL[202-208]	[1-221]NB-ARC:3e-19
RC2G0534600	rc02	61705745	61710532	NBS		P-loop[1-8] Kin-2[89-96] RNBS-B[118-124] GPL[180-186]	[1-268]NB-ARC:6.1e-57 [189-476]NB-ARC:7.9e-64 [574-608]LRR_8:0.0082 [610-651]LRR_8:0.0058
RC2G0587100	rc02	66525159	66528095	CC-NBS-LRR		P-loop[217-225] Kin-2[294-301] RNBS-B[325-331] GPL[387-393]	[188-474]NB-ARC:1.3e-60 [572-629]LRR_8:2.1e-07 [629-653]LRR_8:0.0015 [191-474]NB-ARC:7.7e-63 [574-631]LRR_8:1.2e-08 [631-652]LRR_8:2e-07
RC2G0588700	rc02	66625748	66630124	CC-NBS-LRR		P-loop[216-224] Kin-2[293-300] RNBS-B[324-330] GPL[385-391]	
RC2G0589000	rc02	66647790	66651098	CC-NBS-LRR		P-loop[215-223] Kin-2[292-299] RNBS-B[323-329] GPL[385-391]	
RC2G0620500	rc02	69511698	69514439	NBS-LRR		P-loop[185-193] Kin-2[258-265] RNBS-B[284-290] GPL[346-352]	[163-430]NB-ARC:2.5e-51
RC2G0620800	rc02	69557522	69560264	NBS-LRR		P-loop[185-193] Kin-2[258-265] RNBS-B[284-290] GPL[346-352]	[163-430]NB-ARC:2.4e-51 [177-459]NB-ARC:6.1e-61 [539-575]LRR_4:0.0021
RC3G0032000	rc03	6974322	6978370	NBS-LRR		P-loop[205-213] Kin-2[280-287] RNBS-B[311-317] GPL[372-378]	
RC3G0032300	rc03	7001366	7009066	NBS		P-loop[205-213] Kin-2[280-287] RNBS-B[311-317] GPL[372-378]	[177-378]NB-ARC:1.3e-42 [177-459]NB-ARC:8.2e-61 [539-574]LRR_4:0.0035 [843-903]LRR_8:0.00019
RC3G0034200	rc03	7189856	7196786	NBS-LRR		P-loop[205-213] Kin-2[280-287] RNBS-B[311-317] GPL[372-378]	[24-71]TIR:4.5e-10 [72-141]TIR:0.0014 [157-411]NB-ARC:4.7e-33 [706-738]LRR_8:0.00025
RC3G0042600	rc03	8370125	8377814	TIR-NBS-LRR		P-loop[181-189] Kin-2[260-267] RNBS-B[287-293] GPL[346-352]	
RC3G0044100	rc03	8494667	8497519	CC-NBS-LRR		P-loop[212-220] Kin-2[289-296] RNBS-B[318-324] GPL[379-385]	[181-192]AAA_16:0.00023 [193-467]NB-ARC:2.5e-63 [620-660]LRR_4:0.001 [23-193]TIR:2.9e-46 [327-344]AAA_16:0.00033 [345-613]NB-ARC:6.1e-66 [731-786]LRR_8:3.8e-05
RC3G0047600	rc03	9080520	9088487	TIR-NBS-LRR		P-loop[358-366] Kin-2[433-440] RNBS-B[462-468] GPL[523-529]	[44-320]NB-ARC:1.3e-49 [416-474]LRR_8:2.2e-11 [16-136]RPW8:9e-14 [159-445]NB-ARC:1.1e-33
RC3G0062300	rc03	11919385	11921083	NBS-LRR		P-loop[65-73] Kin-2[140-147] RNBS-B[169-175] GPL[229-235]	[5-111]RPW8:3.9e-13 [151-406]NB-ARC:7.5e-30
RC3G0070000	rc03	12642166	12647039	NBS	RPW8	P-loop[180-188] Kin-2[279-286] RNBS-B[305-311] GPL[360-366]	
RC3G0070100	rc03	12670256	12677491	NBS-LRR	RPW8	P-loop[166-174] Kin-2[243-250] RNBS-B[271-277] GPL[325-331]	
RC3G0075200	rc03	13340577	13343332	NBS		P-loop[177-185] Kin-2[251-258] RNBS-B[282-283] GPL[344-350]	[155-435]NB-ARC:2.7e-60
RC3G0098600	rc03	17063773	17066571	TIR-NBS		P-loop[206-214] Kin-2[284-291] RNBS-B[311-317] GPL[369-375]	[9-174]TIR:7.4e-48 [182-443]NB-ARC:4.8e-25 [600-615]LRR_3:0.0087
RC3G0111000	rc03	18591350	18592827	NBS-LRR		P-loop[35-43] Kin-2[110-117] RNBS-B[139-145] GPL[198-204]	[14-281]NB-ARC:1.9e-54 [385-443]LRR_8:2.4e-08 [7-100]TIR:2.2e-12 [113-346]NB-ARC:3.2e-36
RC3G0123500	rc03	20179686	20181286	TIR-NBS		P-loop[125-133] Kin-2[196-203] RNBS-B[223-229] GPL[282-288]	[22-205]TIR:5.5e-47 [208-217]AAA_16:0.0078 [218-468]NB-ARC:2.7e-34 [609-626]LRR_3:0.0038
RC3G0124000	rc03	20217168	20219331	TIR-NBS		P-loop[230-238] Kin-2[302-309] RNBS-B[329-335] GPL[388-394]	[22-205]TIR:7.5e-46 [219-456]NB-ARC:1.2e-33 [610-627]LRR_3:0.0008 [842-901]LRR_8:1.9e-05 [901-911]LRR_4:0.001 [1-101]RPW8:3.6e-18 [142-407]NB-ARC:1.3e-31
RC3G0124200	rc03	20245230	20250243	TIR-NBS-LRR		P-loop[230-238] Kin-2[302-309] RNBS-B[329-335] GPL[388-394]	[3-80]RPW8:1.3e-07 [122-385]NB-ARC:3.1e-30
RC3G0136400	rc03	21740920	21744430	NBS	RPW8	P-loop[161-169] Kin-2[240-247] RNBS-B[266-272] GPL[321-327]	
RC3G0136500	rc03	21762759	21766253	NBS	RPW8	P-loop[139-147] Kin-2[218-225] RNBS-B[244-250] GPL[299-305]	

RC3G0136600	rc03	21808068	21810533	NBS	P-loop[82-90] Kin-2[157-164] RNBS-B[187-193] GPL[240-244]	[62-325]NB-ARC:6.6e-20
RC3G0145900	rc03	22703075	22704352	CC-NBS	P-loop[178-186] Kin-2[267-274] RNBS-B[308-314] GPL[371-377]	[169-386]NB-ARC:3e-29
RC3G0199200	rc03	28299616	28301075	NBS-LRR	P-loop[65-73] Kin-2[140-147] RNBS-B[169-175] GPL[228-234]	[43-319]NB-ARC:3.1e-48 [413-447]LRR_8:5.3e-05
RC3G0200100	rc03	28424037	28425715	NBS-LRR	P-loop[35-43] Kin-2[110-117] RNBS-B[139-145] GPL[198-204]	[14-289]NB-ARC:8e-54 [383-441]LRR_8:1.1e-09
RC3G0200400	rc03	28514921	28516507	TIR-NBS	P-loop[127-135] Kin-2[202-209] RNBS-B[231-237] GPL[290-296]	[3-84]TIR:1.1e-07 [105-380]NB-ARC:1.6e-48
RC3G0200800	rc03	28549670	28551783	TIR-NBS	P-loop[160-168] Kin-2[235-242] RNBS-B[264-270] GPL[323-329]	[2-123]TIR:2.6e-27 [138-413]NB-ARC:1.4e-51
RC3G0201400	rc03	28584130	28585769	NBS-LRR	P-loop[36-44] Kin-2[111-118] RNBS-B[140-146] GPL[200-206]	[14-292]NB-ARC:1.4e-48 [385-443]LRR_8:1.4e-10
RC3G0207900	rc03	29140368	29142896	CC-NBS-LRR	P-loop[184-192] Kin-2[258-265] RNBS-B[287-293] GPL[344-350]	[15-89]RPW8:0.0049 [154-432]NB-ARC:1.6e-53 [551-605]LRR_8:4.2e-08
RC3G0216100	rc03	30235476	30237794	NBS-LRR	P-loop[74-82] Kin-2[145-152] RNBS-B[173-179] GPL[226-232]	[56-310]NB-ARC:5.7e-32
RC3G0242300	rc03	33188950	33190098	NBS	P-loop[205-213] Kin-2[280-287] RNBS-B[311-317] GPL[372-378]	[177-379]NB-ARC:4.9e-39
RC3G0242600	rc03	33200787	33209563	NBS	P-loop[204-212] Kin-2[279-286] RNBS-B[310-316] GPL[371-377]	[176-459]NB-ARC:9.7e-59 [1294-1344]Cyclin_N:6.4e-07
RC3G0243600	rc03	33281601	33296322	NBS-LRR	P-loop[200-208] Kin-2[274-281] RNBS-B[305-311] GPL[370-376]	[193-460]NB-ARC:1.7e-55 [532-586]LRR_8:0.00013 [878-936]LRR_8:0.0033 [975-1012]LRR_4:0.00067
RC3G0244300	rc03	33345473	33348282	NBS	P-loop[222-230] Kin-2[296-303] RNBS-B[327-333] GPL[388-394]	[194-465]NB-ARC:4.1e-53
RC3G0249600	rc03	33811859	33815053	NBS	P-loop[203-211] Kin-2[278-285] RNBS-B[309-315] GPL[370-376]	[171-181]AAA_16:9.4e-05 [182-457]NB-ARC:4.8e-62
RC3G0252800	rc03	34112771	34115901	NBS-LRR	P-loop[23-31] Kin-2[98-105] RNBS-B[129-135] GPL[190-196]	[2-280]NB-ARC:6.7e-60 [353-389]LRR_8:0.005
RC3G0272000	rc03	35710822	35716742	TIR-NBS-LRR	P-loop[227-235] Kin-2[305-312] RNBS-B[332-338] GPL[391-397]	[23-182]TIR:4.3e-50 [202-215]AAA_16:0.0022 [216-455]NB-ARC:3.6e-31 [609-626]LRR_3:6.9e-05
RC3G0277900	rc03	36251527	36255728	CC-NBS-LRR	P-loop[205-213] Kin-2[280-287] RNBS-B[311-317] GPL[372-378]	[726-782]LRR_8:0.0057 [863-918]LRR_8:0.00023
RC3G0280800	rc03	36402106	36405245	NBS-LRR	P-loop[204-212] Kin-2[279-286] RNBS-B[310-316] GPL[371-377]	[181-459]NB-ARC:9e-57
RC3G0357100	rc03	42585842	42591797	NBS-LRR	P-loop[79-87] Kin-2[164-171] RNBS-B[191-197] GPL[250-256]	[177-459]NB-ARC:7.4e-61 [876-934]LRR_8:0.00093
RC3G0380200	rc03	44011689	44014786	NBS-LRR	P-loop[212-220] Kin-2[291-298] RNBS-B[322-328] GPL[384-390]	[63-322]NB-ARC:3.2e-35 [664-719]LRR_8:0.00049
RC3G0380700	rc03	44048794	44052609	NBS-LRR	P-loop[208-216] Kin-2[289-296] RNBS-B[320-326] GPL[381-387]	[185-468]NB-ARC:3e-57 [627-660]LRR_8:0.00083
RC3G0380800	rc03	44079169	44082987	NBS-LRR	P-loop[214-222] Kin-2[293-300] RNBS-B[324-330] GPL[386-392]	[183-468]NB-ARC:1.6e-54 [574-600]LRR_8:0.0063 [605-635]LRR_4:0.00079 [651-682]LRR_4:0.0008 [1035-1129]LRR_5:0.0031 [1129-1158]LRR_4:0.0038
RC3G0380900	rc03	44084061	44085554	NBS	P-loop[207-215] Kin-2[286-293] RNBS-B[317-323] GPL[379-385]	[187-473]NB-ARC:5.7e-57 [603-647]LRR_8:0.0011 [648-665]LRR_4:0.0013 [1016-1134]LRR_5:5.2e-06
RC4G0003800	rc04	307316	310088	NBS-LRR	P-loop[6-14] Kin-2[82-89] RNBS-B[109-115] GPL[168-174]	[180-453]NB-ARC:4.5e-49
						[1-242]NB-ARC:9.9e-33 [440-496]LRR_8:3e-05 [536-558]LRR_8:0.0008 [559-589]LRR_4:0.00014 [637-696]LRR_8:6.8e-05

RC4G0004700	rc04	366404	371864	NBS-LRR	P-loop[81-89] Kin-2[157-164] RNBS-B[184-190] GPL[242-248]	[63-309]NB-ARC:3.3e-35 [493-524]LRR_4:0.0054 [666-704]LRR_4:0.001 [66-314]NB-ARC:1.7e-35 [582-638]LRR_8:0.0035 [653-709]LRR_8:0.0022 [724-780]LRR_8:0.0061 [795-851]LRR_8:0.0032 [913-969]LRR_8:0.0049 [1008-1062]LRR_8:0.0074 [1115-1156]LRR_4:0.0019 [2-234]NB-ARC:2.7e-36 [412-447]LRR_4:0.00031 [1-232]NB-ARC:5.5e-34 [420-455]LRR_4:0.004 [188-461]NB-ARC:3.5e-62 [591-617]LRR_8:0.00056 [618-658]LRR_4:0.00037 [794-826]LRR_4:0.00096 [29-190]TIR:5.3e-45 [205-215]AAA_16:0.00018 [216-456]NB-ARC:1.1e-36 [30-188]TIR:3.5e-45 [214-467]NB-ARC:4.5e-38 [649-691]LRR_4:9.7e-05 [694-727]LRR_4:0.0017 [789-845]LRR_8:5.3e-05 [1-233]NB-ARC:4.7e-34 [419-451]LRR_4:0.0058 [455-498]LRR_4:3.4e-07 [501-543]LRR_4:1.1e-05 [553-590]LRR_4:0.00034 [711-767]LRR_8:0.00048 [783-838]LRR_8:0.00016 [861-921]LRR_8:2e-06 [1-240]NB-ARC:4.6e-34 [411-452]LRR_4:0.00024 [456-498]LRR_4:3.4e-05 [502-545]LRR_4:6e-08 [548-583]LRR_4:0.00089 [643-698]LRR_8:0.0039 [714-767]LRR_8:0.0071
RC4G0006200	rc04	498278	503605	NBS-LRR	P-loop[81-89] Kin-2[154-161] RNBS-B[181-187] GPL[240-246]	
RC4G0009500	rc04	713187	716014	NBS-LRR	P-loop[2-10] Kin-2[75-82] RNBS-B[102-108] GPL[161-167]	
RC4G0018200	rc04	1569721	1571754	NBS-LRR	P-loop[6-14] Kin-2[81-88] RNBS-B[108-114] GPL[167-173]	
RC4G0026100	rc04	2528716	2531583	CC-NBS-LRR	P-loop[212-220] Kin-2[286-293] RNBS-B[315-321] GPL[376-382]	
RC4G0026700	rc04	2595101	2603424	TIR-NBS	P-loop[232-240] Kin-2[305-312] RNBS-B[332-338] GPL[391-397]	[30-188]TIR:3.5e-45 [214-467]NB-ARC:4.5e-38 [649-691]LRR_4:9.7e-05 [694-727]LRR_4:0.0017 [789-845]LRR_8:5.3e-05 [1-233]NB-ARC:4.7e-34 [419-451]LRR_4:0.0058 [455-498]LRR_4:3.4e-07 [501-543]LRR_4:1.1e-05 [553-590]LRR_4:0.00034 [711-767]LRR_8:0.00048 [783-838]LRR_8:0.00016 [861-921]LRR_8:2e-06 [1-240]NB-ARC:4.6e-34 [411-452]LRR_4:0.00024 [456-498]LRR_4:3.4e-05 [502-545]LRR_4:6e-08 [548-583]LRR_4:0.00089 [643-698]LRR_8:0.0039 [714-767]LRR_8:0.0071
RC4G0027200	rc04	2627151	2630401	TIR-NBS-LRR	P-loop[232-240] Kin-2[308-315] RNBS-B[335-341] GPL[394-400]	
RC4G0028300	rc04	2682384	2686107	NBS-LRR	P-loop[6-14] Kin-2[82-89] RNBS-B[109-115] GPL[168-174]	
RC4G0028800	rc04	2707114	2709934	NBS-LRR	P-loop[6-14] Kin-2[82-89] RNBS-B[109-115] GPL[168-174]	[767]LRR_8:0.0071
RC4G0032900	rc04	3293893	3296382	NBS	P-loop[178-186] Kin-2[252-259] RNBS-B[280-286] GPL[344-350]	[155-436]NB-ARC:1.9e-73
RC4G0034000	rc04	3377290	3379078	NBS	P-loop[178-186] Kin-2[232-239] RNBS-B[260-266] GPL[324-330]	[155-416]NB-ARC:5.7e-58
RC4G0034900	rc04	3445710	3448199	NBS	P-loop[178-186] Kin-2[252-259] RNBS-B[280-286] GPL[344-350]	[155-436]NB-ARC:1.7e-73 [169-465]NB-ARC:4.7e-74 [809-845]LRR_8:0.0017 [169-439]NB-ARC:1e-60 [766-799]LRR_4:0.0052
RC4G0058400	rc04	6390210	6394976	NBS-LRR	P-loop[193-201] Kin-2[274-281] RNBS-B[302-308] GPL[368-374]	[169-464]NB-ARC:7.3e-74 [810-842]LRR_4:0.00048
RC4G0059100	rc04	6456829	6460874	NBS-LRR	P-loop[193-201] RNBS-B[284-290] GPL[343-349]	[167-415]NB-ARC:1.7e-48 [629-664]LRR_8:0.0015
RC4G0059600	rc04	6519333	6524016	NBS-LRR	P-loop[193-201] Kin-2[274-281] RNBS-B[302-308] GPL[368-374]	[169-464]NB-ARC:7.3e-74 [810-842]LRR_4:0.00048
RC4G0076400	rc04	8903303	8907438	CC-NBS-LRR	P-loop[188-196] Kin-2[265-272] RNBS-B[289-295] GPL[348-354]	[167-415]NB-ARC:1.7e-48 [629-664]LRR_8:0.0015
RC4G0085600	rc04	10344840	10346607	CC-NBS	P-loop[178-186] Kin-2[255-262] RNBS-B[279-285] GPL[338-344]	[157-411]NB-ARC:1.9e-48 [167-413]NB-ARC:2.2e-44 [535-588]LRR_8:0.00012
RC4G0088100	rc04	10595425	10611786	CC-NBS-LRR	P-loop[186-194] Kin-2[263-270] RNBS-B[287-293] GPL[346-352]	[6-110]DUF677:0.00047 [177-439]NB-ARC:3.6e-46 [557-601]LRR_8:0.0036
RC4G0088900	rc04	10659086	10661392	CC-NBS-LRR	DUF677 P-loop[195-203] Kin-2[272-279] RNBS-B[296-302] GPL[355-361]	[635-670]LRR_4:0.0043

RC4G0089900	rc04	10762137	10766873	CC-NBS	P-loop[184-192] Kin-2[262-269] RNBS-B[286-292] GPLP[345-351]	[166-417]NB-ARC:2.6e-46 [112-378]NB-ARC:4.3e-44 [491-535]LRR_8:0.00064
RC4G0092500	rc04	11062966	11078607	NBS-LRR	P-loop[130-138] Kin-2[207-214] RNBS-B[231-237] GPLP[290-296]	[163-495]NB-ARC:1.1e-63 [623-667]LRR_8:0.0083
RC4G0101000	rc04	12580676	12583891	NBS-LRR	P-loop[186-194] Kin-2[315-322] RNBS-B[342-348] GPLP[402-408]	[20-188]TIR:6.3e-49 [201-458]NB-ARC:1.4e-33 [820-875]LRR_8:4e-07 [876-886]LRR_4:0.0011
RC4G0131400	rc04	18217613	18221438	TIR-NBS-LRR	P-loop[224-232] Kin-2[303-310] RNBS-B[330-336] GPLP[389-395]	[159-435]NB-ARC:3.2e-84 [532-569]LRR_8:8.9e-08 [579-614]LRR_8:0.00017
RC4G0150300	rc04	21839855	21844046	CC-NBS-LRR	P-loop[180-188] Kin-2[258-265] RNBS-B[285-291] GPLP[345-351]	[162-454]NB-ARC:3e-70 [618-670]LRR_8:0.00066 [783-817]LRR_4:0.0087
RC4G0150700	rc04	21950838	21954395	NBS-LRR	P-loop[186-194] Kin-2[267-274] RNBS-B[294-300] GPLP[359-365]	[326-588]NB-ARC:3.9e-48 [761-816]LRR_8:0.0091
RC4G0156700	rc04	22960778	22965591	CC-NBS-LRR	P-loop[346-354] Kin-2[423-430] RNBS-B[447-453] GPLP[506-512]	[163-184]AAA_16:5.3e-05 [185-448]NB-ARC:6.7e-63 [555-602]LRR_8:0.00015
RC4G0161100	rc04	23754452	23761269	NBS-LRR	P-loop[196-204] Kin-2[271-278] RNBS-B[301-307] GPLP[358-364]	[172-459]NB-ARC:1e-83 [576-631]LRR_8:7.2e-06
RC4G0177100	rc04	26269454	26272936	CC-NBS-LRR	P-loop[194-202] Kin-2[276-283] RNBS-B[303-309] GPLP[367-373]	[36-142]RPW8:3.5e-14 [241-508]NB-ARC:2.6e-33 [777-799]LRR_8:0.0087
RC4G0185400	rc04	27299484	27309739	CC-NBS-LRR	RPW8	P-loop[260-268] Kin-2[337-344] RNBS-B[367-373] GPLP[421-427] [800-838]LRR_4:0.0034 [17-264]NB-ARC:8.3e-34 [534-554]LRR_8:0.0054 [555-577]LRR_4:0.00055 [578-634]LRR_8:3.7e-07 [640-677]LRR_8:0.0021 [692-747]LRR_8:0.0019
RC4G0186600	rc04	27506043	27509702	NBS-LRR	P-loop[35-43] Kin-2[114-121] RNBS-B[141-147] GPLP[200-206]	[21-187]TIR:1.7e-47 [206-453]NB-ARC:1.8e-32 [608-663]LRR_8:0.0026 [748-770]LRR_4:0.0077 [771-815]LRR_8:0.00073 [816-855]LRR_4:1.2e-05 [856-872]LRR_8:1.3e-05 [987-1021]LRR_8:0.0082
RC4G0188900	rc04	27670968	27676905	TIR-NBS-LRR	P-loop[227-235] Kin-2[306-313] RNBS-B[333-339] GPLP[392-398]	[14-183]TIR:5.5e-47 [196-450]NB-ARC:1e-30 [833-873]LRR_4:0.00014 [173-182]AAA_16:0.0014 [183-460]NB-ARC:4.2e-60 [876-931]LRR_8:0.001
RC4G0191600	rc04	28026959	28031459	TIR-NBS-LRR	P-loop[219-227] Kin-2[298-305] RNBS-B[325-331] GPLP[384-390]	[1156-1195]LRR_4:0.0015 [1-234]NB-ARC:2.3e-30 [524-563]LRR_4:0.0015 [570-593]LRR_4:0.0045 [594-640]LRR_8:0.0025 [641-696]LRR_8:0.00059
RC4G0192500	rc04	28192080	28197651	NBS-LRR	P-loop[204-212] Kin-2[279-286] RNBS-B[310-316] GPLP[371-377]	[1-215]NB-ARC:1.4e-19 [488-543]LRR_8:0.00054 [580-636]LRR_8:0.00091 [672-727]LRR_8:0.0013 [169-461]NB-ARC:1.5e-59 [568-622]LRR_8:1.8e-05
RC4G0206200	rc04	30253977	30257175	NBS-LRR	P-loop[6-14] Kin-2[84-91] RNBS-B[111-117] GPLP[170-176]	[176-462]NB-ARC:7.5e-62 [521-571]LRR_8:1.8e-06 [895-919]LRR_8:0.00054 [920-978]LRR_8:0.00034 [991-1093]LRR_5:4.1e-07
RC4G0206500	rc04	30288798	30294008	NBS-LRR	P-loop[6-14] Kin-2[84-91] RNBS-B[111-117] GPLP[154-160]	
RC4G0208800	rc04	30532282	30535890	CC-NBS-LRR	P-loop[196-204] Kin-2[272-279] RNBS-B[303-309] GPLP[370-376]	
RC4G0210000	rc04	30659410	30664218	CC-NBS-LRR	P-loop[203-211] Kin-2[278-285] RNBS-B[309-315] GPLP[371-377]	

RC4G0211800	rc04	30991554	30994632	NBS	P-loop[201-209] Kin-2[276-283] RNBS-B[307-313] GPLP[366-372]	[175-419]NB-ARC:8.1e-50 [183-474]NB-ARC:2.1e-61 [577-608]LRR_8:0.0026 [609-647]LRR_8:0.00098	
RC4G0232800	rc04	34153012	34155878	NBS-LRR	P-loop[210-218] Kin-2[289-296] RNBS-B[320-326] GPLP[381-387]	[113-404]NB-ARC:4.5e-62 [773-813]LRR_4:0.0048 [113-404]NB-ARC:2.1e-58 [503-533]LRR_8:0.00042 [534-573]LRR_8:8.8e-05 [730-806]LRR_5:0.0015	
RC4G0233100	rc04	34202653	34205479	NBS-LRR	P-loop[140-148] Kin-2[219-226] RNBS-B[250-256] GPLP[311-317]	[113-402]NB-ARC:3.4e-60 [520-575]LRR_8:0.00017 [1-265]NB-ARC:4.1e-58 [387-436]LRR_4:0.00092 [437-452]LRR_8:0.008 [713-735]LRR_8:0.0008 [736-775]LRR_4:0.00023 [877-918]LRR_4:0.0094	
RC4G0233500	rc04	34258520	34261161	NBS-LRR	P-loop[140-148] Kin-2[219-226] RNBS-B[250-256] GPLP[311-317]		
RC4G0233700	rc04	34301613	34305036	NBS-LRR	P-loop[138-146] Kin-2[217-224] RNBS-B[248-254] GPLP[309-315]	[1-265]NB-ARC:4.1e-58 [387-436]LRR_4:0.00092 [437-452]LRR_8:0.008 [713-735]LRR_8:0.0008 [736-775]LRR_4:0.00023 [877-918]LRR_4:0.0094	
RC4G0238500	rc04	34800183	34810214	NBS-LRR	P-loop[5-13] Kin-2[83-90] RNBS-B[114-120] GPLP[175-181]		
RC4G0239200	rc04	34918326	34920024	NBS	P-loop[212-220] Kin-2[290-297] RNBS-B[321-327] GPLP[382-388]	[187-474]NB-ARC:2.5e-55 [62-353]NB-ARC:8.5e-60 [462-499]LRR_4:0.00048 [500-513]LRR_8:0.00064	
RC4G0239400	rc04	34935796	34938486	NBS-LRR	P-loop[89-97] Kin-2[168-175] RNBS-B[199-205] GPLP[260-266]	[1-269]NB-ARC:1.6e-58 [373-421]LRR_8:0.0023 [422-439]LRR_4:0.0024 [636-675]LRR_4:0.00071 [1-268]NB-ARC:1e-56 [381-422]LRR_4:0.0023 [423-436]LRR_8:0.0039	
RC4G0239800	rc04	35002789	35005494	NBS-LRR	P-loop[5-13] Kin-2[84-91] RNBS-B[115-121] GPLP[176-182]	[59-79]AAA_16:0.0025 [80-349]NB-ARC:6.6e-58 [183-473]NB-ARC:2.7e-61 [621-668]LRR_8:0.0074	
RC4G0240000	rc04	35027048	35030761	NBS-LRR	P-loop[5-13] Kin-2[83-90] RNBS-B[114-120] GPLP[175-181]		
RC4G0240400	rc04	35053190	35054891	NBS	P-loop[89-97] Kin-2[167-174] RNBS-B[198-204] GPLP[259-265]		
RC4G0248700	rc04	36192025	36195770	NBS-LRR	P-loop[209-217] Kin-2[287-294] RNBS-B[318-324] GPLP[380-386]	[183-472]NB-ARC:4.8e-64 [582-591]LRR_8:3.8e-05 [592-630]LRR_4:3.3e-05 [631-644]LRR_8:0.00032 [926-965]LRR_4:0.00016	
RC4G0249100	rc04	36239268	36244166	NBS-LRR	P-loop[210-218] Kin-2[288-295] RNBS-B[319-325] GPLP[380-386]	[182-471]NB-ARC:9.6e-64 [555-593]LRR_4:0.0017 [887-926]LRR_4:0.0021	
RC4G0249700	rc04	36295031	36299798	NBS-LRR	P-loop[209-217] Kin-2[287-294] RNBS-B[318-324] GPLP[379-385]	[182-472]NB-ARC:3.1e-64 [713-779]gag_pre-integrals:1.5e-14 [792-904]rve:1.3e-22 [1218-1461]RTV_2:2.1e-96 [1666-1718]LRR_8:0.00019 [1959-2044]LRR_5:0.0016 [2045-2084]LRR_4:0.0015	
RC4G0249900	rc04	36308849	36319578	NBS-LRR	gag_pre-integrals,rve, RVT_2	P-loop[209-217] Kin-2[287-294] RNBS-B[318-324] GPLP[379-385]	[183-473]NB-ARC:3.1e-64 [582-591]LRR_8:0.00096 [592-629]LRR_4:0.00034 [1043-1101]LRR_8:0.0022 [1126-1235]LRR_5:0.0031
RC4G0250200	rc04	36351503	36355784	NBS-LRR		[175-186]AAA_16:0.0074 [187-459]NB-ARC:5.2e-57	
RC4G0279600	rc04	39822263	39826573	NBS-LRR	P-loop[205-213] Kin-2[280-287] RNBS-B[311-317] GPLP[372-378]		
RC4G0280400	rc04	39888481	39889072	NBS	P-loop[1-8] Kin-2[75-82] RNBS-B[106-112] GPLP[167-173]	[1-176]NB-ARC:3.5e-34	
RC4G0281100	rc04	39962829	39966458	NBS	P-loop[205-213] Kin-2[280-287] RNBS-B[311-317] GPLP[372-378]	[177-460]NB-ARC:1.1e-57	

RC4G0281700	rc04	39977671	39984467	NBS-LRR	Apolipoprotein	P-loop[205-213] Kin-2[280-287] RNBS-B[311-317] GPLP[372-378]	[13-137]Apolipoprotein:0.0038 [177-460]NB-ARC:1.8e-57 [910-944]LRR_5:0.0061 [945-985]LRR_4:0.00054 [986-1011]LRR_5:0.0061
RC4G0338200	rc04	45846444	45850390	NBS		P-loop[1-8] Kin-2[78-85] RNBS-B[106-112] GPLP[171-177]	[1-268]NB-ARC:1.1e-66
RC4G0375900	rc04	49192413	49197402	CC-NBS-LRR	RPW8	P-loop[201-209] Kin-2[277-284] RNBS-B[306-312] GPLP[362-368]	[16-90]RPW8:0.005 [177-451]NB-ARC:4.1e-52 [568-618]LRR_8:2e-09
RC4G0479900	rc04	57383168	57385083	NBS		P-loop[83-91] Kin-2[164-171] RNBS-B[191-197] GPLP[252-258]	[61-332]NB-ARC:1.7e-32 [49-315]NB-ARC:3.4e-36 [600-658]LRR_8:0.00011 [741-797]LRR_8:0.00032 [916-971]LRR_8:0.00033
RC4G0480000	rc04	57386756	57392858	NBS-LRR		P-loop[71-79] Kin-2[149-156] RNBS-B[176-182] GPLP[236-242]	
RC5G0010300	rc05	599436	602538	NBS		P-loop[195-203] Kin-2[270-277] RNBS-B[301-302] GPLP[366-372]	[171-455]NB-ARC:9.2e-65
RC5G0010900	rc05	648214	651605	NBS		P-loop[185-193] Kin-2[259-266] RNBS-B[287-293] GPLP[351-357]	[162-446]NB-ARC:4.8e-73 [180-451]NB-ARC:7.4e-56 [545-597]LRR_8:1.9e-05 [885-945]LRR_8:0.00013
RC5G0030200	rc05	2012173	2016350	NBS-LRR		P-loop[193-201] Kin-2[269-276] RNBS-B[300-306] GPLP[365-371]	
RC5G0031700	rc05	2180099	2186355	CC-NBS-LRR		P-loop[211-219] Kin-2[284-291] RNBS-B[314-320] GPLP[376-382]	[188-463]NB-ARC:4e-58 [563-620]LRR_8:1e-05 [792-829]LRR_4:0.0093 [79-354]NB-ARC:2.5e-58 [454-478]LRR_8:1.5e-05 [479-517]LRR_4:6.5e-06
RC5G0032000	rc05	2200115	2202139	NBS-LRR		P-loop[102-110] Kin-2[175-182] RNBS-B[205-211] GPLP[267-273]	
RC5G0059300	rc05	4052738	4053379	NBS		P-loop[1-8] Kin-2[88-95] RNBS-B[115-121] GPLP[175-181]	[1-186]NB-ARC:9.2e-26 [14-308]NB-ARC:1.3e-46 [408-468]LRR_8:4.4e-09
RC5G0061300	rc05	4199023	4201464	NBS-LRR		P-loop[35-43] Kin-2[124-131] RNBS-B[151-157] GPLP[211-217]	
RC5G0061600	rc05	4224795	4228453	CC-NBS		P-loop[181-189] Kin-2[274-281] RNBS-B[301-307] GPLP[361-367]	[161-465]NB-ARC:1.5e-36 [77-247]TIR:5e-46 [253-279]AAA_16:0.0074 [280-529]NB-ARC:1.6e-20 [727-762]LRR_4:0.006 [868-924]LRR_8:0.0037 [985-1028]LRR_4:0.0002 [1029-1045]LRR_4:0.0058
RC5G0127700	rc05	9487723	9492155	TIR-NBS-LRR		P-loop[285-293] Kin-2[363-370] RNBS-B[390-396] GPLP[456-462]	[14-192]TIR:6.2e-47 [193-212]AAA_16:6.1e-05 [213-461]NB-ARC:3.7e-22 [635-650]LRR_3:0.0014 [4-266]NB-ARC:2e-46 [383-426]LRR_8:0.0019 [441-497]LRR_8:0.00096 [172-459]NB-ARC:1.2e-83 [577-633]LRR_8:6.4e-07 [172-460]NB-ARC:2.6e-80 [579-632]LRR_8:6.8e-07 [172-459]NB-ARC:2.3e-83 [576-632]LRR_8:3.2e-06 [173-459]NB-ARC:7.9e-85 [576-632]LRR_8:7.3e-06 [633-649]LRR_8:0.00054
RC5G0128100	rc05	9506935	9509502	TIR-NBS		P-loop[220-228] Kin-2[298-305] RNBS-B[325-331] GPLP[391-397]	
RC5G0149800	rc05	11250263	11252152	NBS-LRR		P-loop[23-31] Kin-2[100-107] RNBS-B[124-130] GPLP[184-190]	
RC5G0167000	rc05	12750787	12755732	NBS-LRR		P-loop[194-202] Kin-2[276-283] RNBS-B[303-309] GPLP[367-373]	
RC5G0169300	rc05	13053055	13055802	CC-NBS-LRR		P-loop[194-202] Kin-2[277-284] RNBS-B[304-310] GPLP[368-374]	
RC5G0169500	rc05	13080742	13083726	CC-NBS-LRR		P-loop[194-202] Kin-2[276-283] RNBS-B[303-309] GPLP[367-373]	
RC5G0169800	rc05	13105656	13115300	NBS-LRR		P-loop[194-202] Kin-2[276-283] RNBS-B[303-309] GPLP[367-373]	
RC5G0227800	rc05	18936361	18942066	TIR-NBS		P-loop[220-228] Kin-2[298-305] RNBS-B[326-332] GPLP[386-392]	[15-194]TIR:1.1e-48 [196-455]NB-ARC:5.7e-35 [618-634]LRR_3:0.0089

RC5G0228700	rc05	19071300	19075405	TIR-NBS-LRR	P-loop[220-228] Kin-2[300-307] RNBS-B[328-334] GPLP[386-392]	[15-185]TIR:2.1e-48 [197-457]NB-ARC:2.4e-29 [620-636]LRR_3:0.00036 [646-701]LRR_8:0.009 [713-745]LRR_8:0.0068	
RC5G0231700	rc05	19480303	19485750	TIR-NBS	P-loop[219-227] Kin-2[298-305] RNBS-B[326-332] GPLP[384-390]	[15-193]TIR:2.4e-49 [195-459]NB-ARC:1.8e-25 [620-635]LRR_3:0.00053 [175-458]NB-ARC:1.4e-65 [600-653]LRR_8:1.2e-05	
RC5G0245000	rc05	20532298	20535069	NBS-LRR	P-loop[196-204] Kin-2[274-281] RNBS-B[301-307] GPLP[365-371]	[14-177]TIR:7.4e-51 [200-460]NB-ARC:3.3e-26 [170-446]NB-ARC:3.4e-65 [538-595]LRR_8:1e-08 [609-665]LRR_8:1.4e-07	
RC5G0254700	rc05	21614563	21616935	TIR-NBS	P-loop[218-226] Kin-2[297-304] RNBS-B[324-330] GPLP[383-389]	[80-358]NB-ARC:1.1e-61 [479-517]LRR_4:0.00021 [525-562]LRR_4:0.0049 [177-454]NB-ARC:9.7e-61 [566-575]LRR_8:0.0081 [577-631]LRR_8:0.00027	
RC5G0327400	rc05	30163102	30167202	CC-NBS-LRR	P-loop[191-199] Kin-2[269-276] RNBS-B[296-302] GPLP[354-360]	[62-289]NB-ARC:1.4e-47 [175-452]NB-ARC:3e-64 [577-633]LRR_8:8.8e-06	
RC5G0343100	rc05	32481329	32483874	NBS-LRR	P-loop[106-114] Kin-2[181-188] RNBS-B[210-216] GPLP[271-277]	[4-88]RPW8:0.0071 [177-454]NB-ARC:8e-66 [575-616]LRR_8:0.00014 [176-453]NB-ARC:7.7e-62 [561-571]LRR_8:0.0013 [572-626]LRR_8:0.00047 [156-436]NB-ARC:1.3e-62 [552-573]LRR_8:3.2e-06 [574-632]LRR_8:2.4e-06	
RC5G0343400	rc05	32499168	32502401	CC-NBS-LRR	P-loop[203-211] Kin-2[278-285] RNBS-B[307-313] GPLP[368-374]	[4-88]RPW8:0.0014 [180-461]NB-ARC:1.2e-70 [588-626]LRR_4:8.7e-05	
RC5G0343500	rc05	32505090	32506001	NBS	P-loop[88-96] Kin-2[165-172] RNBS-B[194-200] GPLP[255-261]	[4-98]RPW8:1.4e-05 [181-433]NB-ARC:9.7e-43 [556-610]LRR_8:2e-05	
RC5G0343700	rc05	32507785	32512256	CC-NBS-LRR	P-loop[201-209] Kin-2[276-283] RNBS-B[305-311] GPLP[366-372]	[203-212]AAA_16:0.00014 [213-489]NB-ARC:4.2e-62 [608-641]LRR_4:0.00037 [156-433]NB-ARC:8.7e-63 [536-587]LRR_8:1.1e-05	
RC5G0346300	rc05	32787576	32790430	CC-NBS-LRR	RPW8	P-loop[203-211] Kin-2[278-285] RNBS-B[307-313] GPLP[368-374]	[5-246]NB-ARC:3.1e-29 [178-464]NB-ARC:1e-56 [586-639]LRR_8:0.0015 [172-459]NB-ARC:2e-80 [580-636]LRR_8:2.7e-06 [175-461]NB-ARC:1.3e-82 [587-643]LRR_8:4.5e-07 [172-459]NB-ARC:4.1e-81 [580-636]LRR_8:8.1e-06 [172-459]NB-ARC:4.1e-82 [580-636]LRR_8:6.7e-08 [37-204]TIR:3.7e-48 [221-476]NB-ARC:8.2e-29
RC5G0370200	rc05	36020158	36024058	CC-NBS-LRR		P-loop[202-210] Kin-2[277-284] RNBS-B[306-312] GPLP[367-373]	
RC5G0370400	rc05	36049700	36058870	CC-NBS-LRR		P-loop[182-190] Kin-2[257-264] RNBS-B[286-292] GPLP[347-353]	
RC5G0370800	rc05	36124042	36132140	NBS-LRR		P-loop[184-192] Kin-2[259-266] RNBS-B[288-294] GPLP[346-352]	
RC5G0371100	rc05	36172573	36178226	CC-NBS-LRR	RPW8	P-loop[206-214] Kin-2[281-288] RNBS-B[310-316] GPLP[370-376]	
RC5G0376400	rc05	36979080	36981422	CC-NBS-LRR	RPW8	P-loop[204-212] Kin-2[270-277] RNBS-B[299-305] GPLP[344-348]	
RC5G0380200	rc05	37680567	37683462	NBS-LRR		P-loop[234-242] Kin-2[310-317] RNBS-B[340-346] GPLP[401-407]	
RC5G0403300	rc05	40299954	40303988	CC-NBS-LRR		P-loop[182-190] Kin-2[257-264] RNBS-B[286-292] GPLP[347-353]	
RC5G0435500	rc05	45625860	45628523	NBS		P-loop[19-27] Kin-2[98-105] RNBS-B[125-131] GPLP[182-188]	
RC5G0441600	rc05	46313610	46317073	NBS-LRR		P-loop[206-214] Kin-2[281-288] RNBS-B[315-321] GPLP[376-382]	
RC5G0451400	rc05	48176707	48179831	NBS-LRR		P-loop[194-202] Kin-2[276-283] RNBS-B[303-309] GPLP[367-373]	
RC5G0451800	rc05	48195161	48198638	NBS-LRR		P-loop[197-205] Kin-2[279-286] RNBS-B[306-312] GPLP[370-376]	
RC5G0452200	rc05	48274304	48277639	NBS-LRR		P-loop[194-202] Kin-2[276-283] RNBS-B[303-309] GPLP[367-373]	
RC5G0452700	rc05	48338371	48341154	NBS-LRR		P-loop[194-202] Kin-2[276-283] RNBS-B[303-309] GPLP[367-373]	
RC5G0489900	rc05	55379318	55386672	TIR-NBS-LRR		P-loop[243-251] Kin-2[322-329] RNBS-B[349-355] GPLP[409-415]	

RC5G0490600	rc05	55468667	55471769	TIR-NBS-LRR	P-loop[199-207] Kin-2[276-283] RNBS-B[303-309] GPLP[362-368]	[36-165]TIR:2.1e-26 [175-189]AAA_16:0.00067 [190-432]NB-ARC:2.6e-28 [580-598]LRR_3:0.0002
RC5G0491400	rc05	55585356	55590552	TIR-NBS-LRR	P-loop[129-137] Kin-2[200-207] RNBS-B[227-233] GPLP[286-292]	[672-729]LRR_8:6.1e-06 [3-95]TIR:7.2e-12 [120-351]NB-ARC:9.2e-34 [503-520]LRR_3:0.0035 [756-815]LRR_8:6.2e-05
RC5G0511300	rc05	58633590	58636220	CC-NBS-LRR	P-loop[206-214] Kin-2[281-288] RNBS-B[315-321] GPLP[376-382]	[181-463]NB-ARC:1.2e-59 [584-605]LRR_8:0.0098 [606-645]LRR_4:0.0016
RC5G0511600	rc05	58675227	58680594	TIR-NBS-LRR	P-loop[175-183] Kin-2[250-257] RNBS-B[279-285] GPLP[338-344]	[2-131]TIR:1.2e-30 [153-429]NB-ARC:6e-52 [524-580]LRR_8:9.3e-09 [581-591]LRR_4:0.0015
RC5G0528800	rc05	61147231	61150828	NBS-LRR	P-loop[20-28] Kin-2[81-88] RNBS-B[110-116] GPLP[169-175]	[4-255]NB-ARC:1.1e-34 [377-435]LRR_8:4.4e-08
RC5G0529000	rc05	61157136	61161309	TIR-NBS-LRR	P-loop[219-227] Kin-2[280-287] RNBS-B[309-315] GPLP[368-374]	[14-187]TIR:1.1e-42 [199-459]NB-ARC:2.9e-36 [569-627]LRR_8:9.3e-06
RC5G0529400	rc05	61185509	61186618	NBS	P-loop[20-28] Kin-2[81-88] RNBS-B[110-116] GPLP[171-177]	[627-637]LRR_4:0.00059 [1-258]NB-ARC:1.5e-36
RC5G0550500	rc05	64286509	64289637	TIR-NBS-LRR	P-loop[231-239] Kin-2[306-313] RNBS-B[335-341] GPLP[403-409]	[22-193]TIR:6.3e-44 [211-489]NB-ARC:6.2e-48 [589-647]LRR_8:7.7e-10
RC5G0550800	rc05	64342396	64347751	CC-TIR-NBS-LRR	P-loop[317-325] Kin-2[391-398] RNBS-B[420-426] GPLP[478-484]	[101-274]TIR:1e-46 [296-567]NB-ARC:1.7e-50 [665-724]LRR_8:2.3e-09
RC5G0551300	rc05	64363055	64364261	TIR-NBS	P-loop[179-187] Kin-2[254-261] RNBS-B[283-289] GPLP[342-348]	[728-768]LRR_8:0.0006 [1209-1450]NAP:1.9e-68
RC5G0551600	rc05	64416135	64418578	TIR-NBS	P-loop[288-296] Kin-2[371-378] RNBS-B[400-406] GPLP[459-465]	[2-137]TIR:2.4e-29 [160-352]NB-ARC:2.8e-34
RC5G0551800	rc05	64429958	64436745	TIR-NBS-LRR	P-loop[232-240] Kin-2[307-314] RNBS-B[336-342] GPLP[395-401]	[78-249]TIR:5.8e-46 [267-548]NB-ARC:8.1e-46
RC5G0555100	rc05	64897229	64898989	TIR-NBS	P-loop[134-142] Kin-2[209-216] RNBS-B[236-242] GPLP[295-301]	[25-188]TIR:7.8e-44 [212-488]NB-ARC:2.2e-46 [586-643]LRR_8:6.3e-09
RC5G0555900	rc05	65041864	65043564	TIR-NBS	P-loop[125-133] Kin-2[200-207] RNBS-B[227-233] GPLP[286-292]	[650-666]LRR_4:0.0053
RC5G0568600	rc05	66603387	66605777	TIR-NBS	P-loop[227-235] Kin-2[299-306] RNBS-B[326-332] GPLP[385-391]	[20-109]TIR:2.8e-10 [121-372]NB-ARC:3.2e-34
RC5G0569800	rc05	66766343	66770979	TIR-NBS-LRR	P-loop[216-224] Kin-2[294-301] RNBS-B[321-327] GPLP[388-394]	[5-100]TIR:9.3e-12 [110-361]NB-ARC:9e-35
RC5G0600200	rc05	69891742	69900734	TIR-NBS-LRR	P-loop[232-240] Kin-2[307-314] RNBS-B[336-342] GPLP[395-401]	[20-186]TIR:1.4e-46 [213-455]NB-ARC:2.6e-35
RC5G0600300	rc05	69902585	69913939	CC-TIR-NBS-LRR	P-loop[233-241] Kin-2[308-315] RNBS-B[337-343] GPLP[396-402]	[11-181]TIR:1.4e-48 [186-208]AAA_16:0.0004 [209-457]NB-ARC:4e-25 [622-637]LRR_3:3.7e-05 [736-789]LRR_8:0.0062
RC5G0675300	rc05	78464769	78465971	TIR-NBS	P-loop[122-130] Kin-2[197-204] RNBS-B[226-232] GPLP[284-290]	[23-189]TIR:9.8e-42 [211-479]NB-ARC:5e-51 [574-632]LRR_8:8.5e-07 [645-685]LRR_4:0.00049 [686-700]LRR_8:0.0087
RC5G0675800	rc05	78567578	78569079	NBS-LRR	P-loop[20-28] Kin-2[95-102] RNBS-B[124-130] GPLP[181-187]	[18-190]TIR:1.8e-40 [213-480]NB-ARC:3.9e-53 [585-643]LRR_8:1.7e-08

RC5G0687100	rc05	79582027	79588091	TIR-NBS-LRR		P-loop[256-264] Kin-2[331-338] RNBS-B[360-366] GPLP[419-425]	[52-221]TIR:1.2e-40 [235-509]NB-ARC:5.6e-51 [608-665]LRR_8:2.7e-09
RC5G0687500	rc05	79603288	79605968	TIR-NBS-LRR	bHLH-MYC_N	P-loop[451-459] Kin-2[526-533] RNBS-B[555-561] GPLP[613-619]	[15-195]bHLH-MYC_N:7.5e-55 [242-407]TIR:1.6e-41 [430-702]NB-ARC:4.4e-52 [782-838]LRR_8:0.00037
RC5G0688900	rc05	79846207	79853071	TIR-NBS-LRR		P-loop[1076-1084] Kin-2[1151-1158] RNBS-B[1180-1186] GPLP[1238-1244]	[5-81]TIR:9.7e-07 [101-372]NB-ARC:3.9e-51 [470-526]LRR_8:1.2e-06 [1055-1330]NB-ARC:3e-46 [1421-1479]LRR_8:2.3e-09
RC5G0689200	rc05	79887787	79891821	TIR-NBS-LRR	bHLH-MYC_N	P-loop[454-462] Kin-2[529-536] RNBS-B[558-564] GPLP[616-622]	[16-195]bHLH-MYC_N:2.6e-53 [245-409]TIR:8e-41 [433-705]NB-ARC:9.5e-52 [804-862]LRR_8:1e-07 [876-930]LRR_8:0.0096 [1096-1128]LRR_4:0.0064
RC5G0689800	rc05	79921071	79925722	TIR-NBS-LRR		P-loop[284-292] Kin-2[359-366] RNBS-B[388-394] GPLP[446-452]	[76-241]TIR:2.8e-45 [264-530]NB-ARC:6.5e-49 [669-728]LRR_8:9.9e-09
RC5G0692400	rc05	80217334	80218912	NBS-LRR		P-loop[14-22] Kin-2[90-97] RNBS-B[119-125] GPLP[178-184]	[5-287]NB-ARC:3.4e-36 [378-434]LRR_8:2.2e-07 [435-445]LRR_4:0.00012 [446-464]LRR_4:0.00037 [465-480]LRR_8:0.0041
RC5G0693200	rc05	80412660	80413992	NBS		P-loop[35-43] Kin-2[110-117] RNBS-B[139-145] GPLP[196-202]	[14-286]NB-ARC:2.1e-54
RC5G0693300	rc05	80481072	80482660	NBS-LRR		P-loop[20-28] Kin-2[95-102] RNBS-B[124-130] GPLP[181-187]	[1-269]NB-ARC:4e-49 [370-427]LRR_8:6.9e-11
RC5G0693800	rc05	80551223	80552865	NBS-LRR		P-loop[16-24] Kin-2[91-98] RNBS-B[120-126] GPLP[178-184]	[4-265]NB-ARC:1.4e-46 [362-420]LRR_8:1.8e-10
RC5G0694500	rc05	80684718	80686586	NBS-LRR	TniB	P-loop[43-51] Kin-2[118-125] RNBS-B[147-153] GPLP[206-212]	[16-25]TniB:0.004 [26-288]NB-ARC:4.5e-52 [392-450]LRR_8:9e-09 [450-463]LRR_4:0.0039 [464-519]LRR_8:1.8e-07
RC5G0694800	rc05	80695805	80701646	NBS-LRR		P-loop[33-41] Kin-2[108-115] RNBS-B[137-143] GPLP[195-201]	[12-282]NB-ARC:1.3e-53 [381-439]LRR_8:1.8e-09
RC5G0695300	rc05	80730554	80736129	TIR-NBS-LRR		P-loop[229-237] Kin-2[304-311] RNBS-B[333-339] GPLP[392-398]	[23-190]TIR:6.4e-42 [210-477]NB-ARC:3.8e-55 [579-637]LRR_8:5e-05
RC5G0695400	rc05	80792576	80794250	NBS-LRR		P-loop[14-22] Kin-2[89-96] RNBS-B[118-124] GPLP[177-183]	[5-285]NB-ARC:1.5e-35 [377-433]LRR_8:1.3e-07 [434-444]LRR_4:0.00023 [445-463]LRR_4:0.0014 [464-479]LRR_8:0.0022
RC5G0697200	rc05	80998711	81009255	TIR-NBS-LRR		P-loop[465-473] Kin-2[540-547] RNBS-B[569-575] GPLP[628-634]	[259-425]TIR:8.5e-45 [447-719]NB-ARC:1.6e-48 [817-874]LRR_8:2.7e-08
RC5G0698000	rc05	81141362	81152942	TIR-NBS-LRR		P-loop[2668-2676] Kin-2[2743-2750] RNBS-B[2772-2778] GPLP[2830-2836]	[15-280]NB-ARC:5.1e-52 [384-440]LRR_8:1.6e-07 [456-510]LRR_8:0.00022 [988-1153]TIR:1.6e-41 [1172-1446]NB-ARC:3.7e-48 [1537-1698]TIR:6.4e-37 [1722-1990]NB-ARC:5.5e-51 [2088-2146]LRR_8:1.6e-06
RC5G0698100	rc05	81165421	81169898	TIR-NBS-LRR		P-loop[126-134] Kin-2[201-208] RNBS-B[230-236] GPLP[288-294]	[2649-2920]NB-ARC:6.5e-47 [3034-3090]LRR_8:4.7e-08
							[6-82]TIR:5.8e-06 [105-377]NB-ARC:5.8e-52 [476-534]LRR_8:7.6e-08 [768-800]LRR_4:0.0046

RC5G0699100	rc05	81344789	81350645	TIR-NBS-LRR	P-loop[222-230] Kin-2[297-304] RNBS-B[326-332] GPLP[384-390]	[18-194]TIR:4.5e-39 [200-472]NB-ARC:1.9e-53 [575-633]LRR_8:2.2e-07 [912-948]LRR_4:0.0089 [19-281]NB-ARC:4.7e-51 [385-443]LRR_8:4.2e-09 [457-512]LRR_8:3.7e-07
RC5G0699900	rc05	81493380	81497501	NBS-LRR	P-loop[36-44] Kin-2[111-118] RNBS-B[140-146] GPLP[199-205]	[17-182]TIR:7.7e-40 [258-420]TIR:4.4e-43 [441-732]NB-ARC:4.6e-39 [824-879]LRR_8:1.7e-07 [880-926]LRR_8:0.00097 [6-266]NB-ARC:6.3e-54 [364-408]LRR_8:7.3e-05
RC5G0700800	rc05	81678593	81683206	TIR-NBS-LRR	P-loop[461-469] Kin-2[536-543] RNBS-B[565-571] GPLP[624-630]	[68-232]TIR:5.2e-41 [251-524]NB-ARC:9.2e-51 [589-647]LRR_8:1.9e-10 [28-193]TIR:1.3e-38 [262-428]TIR:1.2e-44 [445-734]NB-ARC:5.2e-39 [828-884]LRR_8:8.9e-08 [885-895]LRR_4:0.00021 [896-905]LRR_4:0.0054
RC5G0700900	rc05	81694590	81695899	NBS-LRR	P-loop[16-24] Kin-2[91-98] RNBS-B[120-126] GPLP[178-184]	[74-239]TIR:9.8e-43 [258-529]NB-ARC:3.9e-53 [626-684]LRR_8:2.5e-05 [12-283]NB-ARC:4.9e-57 [381-438]LRR_8:4.2e-08 [448-484]LRR_8:0.00025 [1-273]NB-ARC:1.6e-50 [372-430]LRR_8:2.2e-10
RC5G0701600	rc05	81772931	81775477	TIR-NBS-LRR	P-loop[272-280] Kin-2[347-354] RNBS-B[376-382] GPLP[437-443]	[4-82]TIR:5.8e-06 [107-394]NB-ARC:3.4e-38 [492-548]LRR_8:0.00014 [3-251]NB-ARC:5.5e-27 [252-314]TIR:9.7e-08 [346-516]TIR:5.5e-27 [547-697]TIR:6.5e-26 [734-999]NB-ARC:3.8e-49 [1100-1156]LRR_8:1.1e-06 [2-88]TIR:1.5e-15 [104-294]NB-ARC:2.1e-21
RC5G0703200	rc05	81915928	81920392	TIR-NBS-LRR	P-loop[465-473] Kin-2[540-547] RNBS-B[569-575] GPLP[628-634]	[5-251]NB-ARC:7.3e-37 [23-183]TIR:3e-48 [199-454]NB-ARC:1.5e-30 [12-182]TIR:7.5e-50 [204-443]NB-ARC:4.2e-33 [666-725]LRR_8:0.0021 [997-1053]LRR_8:7.9e-06 [12-182]TIR:2.9e-49 [203-429]NB-ARC:1.4e-31 [642-682]LRR_4:0.0024 [831-886]LRR_8:2.7e-06 [12-192]TIR:9.5e-43 [198-212]AAA_16:3.3e-05 [213-452]NB-ARC:7.4e-31 [603-621]LRR_3:3.8e-06 [695-752]LRR_8:8.4e-06 [860-903]LRR_4:0.00025 [904-914]LRR_8:0.0015 [20-181]TIR:3.5e-34 [199-445]NB-ARC:5.1e-30 [595-613]LRR_3:0.004 [854-912]LRR_8:0.0001 [912-922]LRR_4:0.00053
RC5G0703900	rc05	82019665	82022336	TIR-NBS-LRR	P-loop[278-286] Kin-2[353-360] RNBS-B[382-388] GPLP[440-446]	[5-251]NB-ARC:7.3e-37 [23-183]TIR:3e-48 [199-454]NB-ARC:1.5e-30 [12-182]TIR:7.5e-50 [204-443]NB-ARC:4.2e-33 [666-725]LRR_8:0.0021 [997-1053]LRR_8:7.9e-06 [12-182]TIR:2.9e-49 [203-429]NB-ARC:1.4e-31 [642-682]LRR_4:0.0024 [831-886]LRR_8:2.7e-06 [12-192]TIR:9.5e-43 [198-212]AAA_16:3.3e-05 [213-452]NB-ARC:7.4e-31 [603-621]LRR_3:3.8e-06 [695-752]LRR_8:8.4e-06 [860-903]LRR_4:0.00025 [904-914]LRR_8:0.0015 [20-181]TIR:3.5e-34 [199-445]NB-ARC:5.1e-30 [595-613]LRR_3:0.004 [854-912]LRR_8:0.0001 [912-922]LRR_4:0.00053
RC5G0704100	rc05	82052760	82054580	NBS-LRR	P-loop[33-41] Kin-2[108-115] RNBS-B[137-143] GPLP[195-201]	[5-251]NB-ARC:7.3e-37 [23-183]TIR:3e-48 [199-454]NB-ARC:1.5e-30 [12-182]TIR:7.5e-50 [204-443]NB-ARC:4.2e-33 [666-725]LRR_8:0.0021 [997-1053]LRR_8:7.9e-06 [12-182]TIR:2.9e-49 [203-429]NB-ARC:1.4e-31 [642-682]LRR_4:0.0024 [831-886]LRR_8:2.7e-06 [12-192]TIR:9.5e-43 [198-212]AAA_16:3.3e-05 [213-452]NB-ARC:7.4e-31 [603-621]LRR_3:3.8e-06 [695-752]LRR_8:8.4e-06 [860-903]LRR_4:0.00025 [904-914]LRR_8:0.0015 [20-181]TIR:3.5e-34 [199-445]NB-ARC:5.1e-30 [595-613]LRR_3:0.004 [854-912]LRR_8:0.0001 [912-922]LRR_4:0.00053
RC5G0704400	rc05	82106576	82108154	NBS-LRR	P-loop[20-28] Kin-2[95-102] RNBS-B[124-130] GPLP[185-191]	[5-251]NB-ARC:7.3e-37 [23-183]TIR:3e-48 [199-454]NB-ARC:1.5e-30 [12-182]TIR:7.5e-50 [204-443]NB-ARC:4.2e-33 [666-725]LRR_8:0.0021 [997-1053]LRR_8:7.9e-06 [12-182]TIR:2.9e-49 [203-429]NB-ARC:1.4e-31 [642-682]LRR_4:0.0024 [831-886]LRR_8:2.7e-06 [12-192]TIR:9.5e-43 [198-212]AAA_16:3.3e-05 [213-452]NB-ARC:7.4e-31 [603-621]LRR_3:3.8e-06 [695-752]LRR_8:8.4e-06 [860-903]LRR_4:0.00025 [904-914]LRR_8:0.0015 [20-181]TIR:3.5e-34 [199-445]NB-ARC:5.1e-30 [595-613]LRR_3:0.004 [854-912]LRR_8:0.0001 [912-922]LRR_4:0.00053
RC5G0707000	rc05	82427759	82432941	TIR-NBS-LRR	P-loop[126-134] Kin-2[216-223] RNBS-B[245-251] GPLP[304-310]	[5-251]NB-ARC:7.3e-37 [23-183]TIR:3e-48 [199-454]NB-ARC:1.5e-30 [12-182]TIR:7.5e-50 [204-443]NB-ARC:4.2e-33 [666-725]LRR_8:0.0021 [997-1053]LRR_8:7.9e-06 [12-182]TIR:2.9e-49 [203-429]NB-ARC:1.4e-31 [642-682]LRR_4:0.0024 [831-886]LRR_8:2.7e-06 [12-192]TIR:9.5e-43 [198-212]AAA_16:3.3e-05 [213-452]NB-ARC:7.4e-31 [603-621]LRR_3:3.8e-06 [695-752]LRR_8:8.4e-06 [860-903]LRR_4:0.00025 [904-914]LRR_8:0.0015 [20-181]TIR:3.5e-34 [199-445]NB-ARC:5.1e-30 [595-613]LRR_3:0.004 [854-912]LRR_8:0.0001 [912-922]LRR_4:0.00053
RC5G0707800	rc05	82510963	82516475	TIR-NBS-LRR	P-loop[26-34] Kin-2[102-109] RNBS-B[129-135] GPLP[185-191]	[5-251]NB-ARC:7.3e-37 [23-183]TIR:3e-48 [199-454]NB-ARC:1.5e-30 [12-182]TIR:7.5e-50 [204-443]NB-ARC:4.2e-33 [666-725]LRR_8:0.0021 [997-1053]LRR_8:7.9e-06 [12-182]TIR:2.9e-49 [203-429]NB-ARC:1.4e-31 [642-682]LRR_4:0.0024 [831-886]LRR_8:2.7e-06 [12-192]TIR:9.5e-43 [198-212]AAA_16:3.3e-05 [213-452]NB-ARC:7.4e-31 [603-621]LRR_3:3.8e-06 [695-752]LRR_8:8.4e-06 [860-903]LRR_4:0.00025 [904-914]LRR_8:0.0015 [20-181]TIR:3.5e-34 [199-445]NB-ARC:5.1e-30 [595-613]LRR_3:0.004 [854-912]LRR_8:0.0001 [912-922]LRR_4:0.00053
RC5G0716100	rc05	83403364	83404578	TIR-NBS	P-loop[125-133] Kin-2[204-211] RNBS-B[231-237] GPLP[288-294]	[5-251]NB-ARC:7.3e-37 [23-183]TIR:3e-48 [199-454]NB-ARC:1.5e-30 [12-182]TIR:7.5e-50 [204-443]NB-ARC:4.2e-33 [666-725]LRR_8:0.0021 [997-1053]LRR_8:7.9e-06 [12-182]TIR:2.9e-49 [203-429]NB-ARC:1.4e-31 [642-682]LRR_4:0.0024 [831-886]LRR_8:2.7e-06 [12-192]TIR:9.5e-43 [198-212]AAA_16:3.3e-05 [213-452]NB-ARC:7.4e-31 [603-621]LRR_3:3.8e-06 [695-752]LRR_8:8.4e-06 [860-903]LRR_4:0.00025 [904-914]LRR_8:0.0015 [20-181]TIR:3.5e-34 [199-445]NB-ARC:5.1e-30 [595-613]LRR_3:0.004 [854-912]LRR_8:0.0001 [912-922]LRR_4:0.00053
RC5G0717400	rc05	83546016	83547738	NBS	P-loop[19-27] Kin-2[98-105] RNBS-B[125-131] GPLP[185-191]	[5-251]NB-ARC:7.3e-37 [23-183]TIR:3e-48 [199-454]NB-ARC:1.5e-30 [12-182]TIR:7.5e-50 [204-443]NB-ARC:4.2e-33 [666-725]LRR_8:0.0021 [997-1053]LRR_8:7.9e-06 [12-182]TIR:2.9e-49 [203-429]NB-ARC:1.4e-31 [642-682]LRR_4:0.0024 [831-886]LRR_8:2.7e-06 [12-192]TIR:9.5e-43 [198-212]AAA_16:3.3e-05 [213-452]NB-ARC:7.4e-31 [603-621]LRR_3:3.8e-06 [695-752]LRR_8:8.4e-06 [860-903]LRR_4:0.00025 [904-914]LRR_8:0.0015 [20-181]TIR:3.5e-34 [199-445]NB-ARC:5.1e-30 [595-613]LRR_3:0.004 [854-912]LRR_8:0.0001 [912-922]LRR_4:0.00053
RC5G0718200	rc05	83610483	83613250	TIR-NBS	P-loop[223-231] Kin-2[302-309] RNBS-B[329-335] GPLP[388-394]	[5-251]NB-ARC:7.3e-37 [23-183]TIR:3e-48 [199-454]NB-ARC:1.5e-30 [12-182]TIR:7.5e-50 [204-443]NB-ARC:4.2e-33 [666-725]LRR_8:0.0021 [997-1053]LRR_8:7.9e-06 [12-182]TIR:2.9e-49 [203-429]NB-ARC:1.4e-31 [642-682]LRR_4:0.0024 [831-886]LRR_8:2.7e-06 [12-192]TIR:9.5e-43 [198-212]AAA_16:3.3e-05 [213-452]NB-ARC:7.4e-31 [603-621]LRR_3:3.8e-06 [695-752]LRR_8:8.4e-06 [860-903]LRR_4:0.00025 [904-914]LRR_8:0.0015 [20-181]TIR:3.5e-34 [199-445]NB-ARC:5.1e-30 [595-613]LRR_3:0.004 [854-912]LRR_8:0.0001 [912-922]LRR_4:0.00053
RC6G0005500	rc06	717905	722131	TIR-NBS-LRR	P-loop[215-223] Kin-2[292-299] RNBS-B[319-325] GPLP[378-384]	[5-251]NB-ARC:7.3e-37 [23-183]TIR:3e-48 [199-454]NB-ARC:1.5e-30 [12-182]TIR:7.5e-50 [204-443]NB-ARC:4.2e-33 [666-725]LRR_8:0.0021 [997-1053]LRR_8:7.9e-06 [12-182]TIR:2.9e-49 [203-429]NB-ARC:1.4e-31 [642-682]LRR_4:0.0024 [831-886]LRR_8:2.7e-06 [12-192]TIR:9.5e-43 [198-212]AAA_16:3.3e-05 [213-452]NB-ARC:7.4e-31 [603-621]LRR_3:3.8e-06 [695-752]LRR_8:8.4e-06 [860-903]LRR_4:0.00025 [904-914]LRR_8:0.0015 [20-181]TIR:3.5e-34 [199-445]NB-ARC:5.1e-30 [595-613]LRR_3:0.004 [854-912]LRR_8:0.0001 [912-922]LRR_4:0.00053
RC6G0006000	rc06	738780	743774	TIR-NBS-LRR	P-loop[215-223] Kin-2[292-299] RNBS-B[319-325] GPLP[378-384]	[5-251]NB-ARC:7.3e-37 [23-183]TIR:3e-48 [199-454]NB-ARC:1.5e-30 [12-182]TIR:7.5e-50 [204-443]NB-ARC:4.2e-33 [666-725]LRR_8:0.0021 [997-1053]LRR_8:7.9e-06 [12-182]TIR:2.9e-49 [203-429]NB-ARC:1.4e-31 [642-682]LRR_4:0.0024 [831-886]LRR_8:2.7e-06 [12-192]TIR:9.5e-43 [198-212]AAA_16:3.3e-05 [213-452]NB-ARC:7.4e-31 [603-621]LRR_3:3.8e-06 [695-752]LRR_8:8.4e-06 [860-903]LRR_4:0.00025 [904-914]LRR_8:0.0015 [20-181]TIR:3.5e-34 [199-445]NB-ARC:5.1e-30 [595-613]LRR_3:0.004 [854-912]LRR_8:0.0001 [912-922]LRR_4:0.00053
RC6G0010700	rc06	1085292	1090720	TIR-NBS-LRR	P-loop[222-230] Kin-2[299-306] RNBS-B[326-332] GPLP[385-391]	[5-251]NB-ARC:7.3e-37 [23-183]TIR:3e-48 [199-454]NB-ARC:1.5e-30 [12-182]TIR:7.5e-50 [204-443]NB-ARC:4.2e-33 [666-725]LRR_8:0.0021 [997-1053]LRR_8:7.9e-06 [12-182]TIR:2.9e-49 [203-429]NB-ARC:1.4e-31 [642-682]LRR_4:0.0024 [831-886]LRR_8:2.7e-06 [12-192]TIR:9.5e-43 [198-212]AAA_16:3.3e-05 [213-452]NB-ARC:7.4e-31 [603-621]LRR_3:3.8e-06 [695-752]LRR_8:8.4e-06 [860-903]LRR_4:0.00025 [904-914]LRR_8:0.0015 [20-181]TIR:3.5e-34 [199-445]NB-ARC:5.1e-30 [595-613]LRR_3:0.004 [854-912]LRR_8:0.0001 [912-922]LRR_4:0.00053
RC6G0012000	rc06	1203564	1208147	TIR-NBS-LRR	P-loop[221-229] Kin-2[293-300] RNBS-B[320-326] GPLP[379-385]	[5-251]NB-ARC:7.3e-37 [23-183]TIR:3e-48 [199-454]NB-ARC:1.5e-30 [12-182]TIR:7.5e-50 [204-443]NB-ARC:4.2e-33 [666-725]LRR_8:0.0021 [997-1053]LRR_8:7.9e-06 [12-182]TIR:2.9e-49 [203-429]NB-ARC:1.4e-31 [642-682]LRR_4:0.0024 [831-886]LRR_8:2.7e-06 [12-192]TIR:9.5e-43 [198-212]AAA_16:3.3e-05 [213-452]NB-ARC:7.4e-31 [603-621]LRR_3:3.8e-06 [695-752]LRR_8:8.4e-06 [860-903]LRR_4:0.00025 [904-914]LRR_8:0.0015 [20-181]TIR:3.5e-34 [199-445]NB-ARC:5.1e-30 [595-613]LRR_3:0.004 [854-912]LRR_8:0.0001 [912-922]LRR_4:0.00053

RC6G0019700	rc06	1964771	1968620	NBS-LRR	P-loop[37-45] Kin-2[113-120] RNBS-B[145-151] GPLP[206-212]	[14-271]NB-ARC:5.9e-39 [437-452]LRR_3:0.0035 [577-630]LRR_8:0.0052	
RC6G0046600	rc06	4748698	4750511	TIR-NBS	P-loop[221-229] Kin-2[298-305] RNBS-B[325-331] GPLP[384-390]	[18-188]TIR:2.9e-47 [209-449]NB-ARC:1.5e-30	
RC6G0052000	rc06	5413192	5415967	NBS-LRR	P-loop[27-35] Kin-2[105-112] RNBS-B[132-138] GPLP[191-197]	[18-262]NB-ARC:7.6e-31 [409-427]LRR_3:1.9e-06 [501-557]LRR_8:1.9e-05 [646-669]LRR_8:0.0052 [670-713]LRR_4:0.00028	
RC6G0093200	rc06	10156940	10162501	CC-NBS-LRR	RPW8	P-loop[187-195] Kin-2[264-271] RNBS-B[293-299] GPLP[355-361]	[22-93]RPW8:0.00035 [166-445]NB-ARC:6.7e-57 [574-627]LRR_8:3.2e-05
RC6G0107000	rc06	11477082	11479066	NBS-LRR		P-loop[172-180] Kin-2[247-254] RNBS-B[279-285] GPLP[338-344]	[153-423]NB-ARC:2.8e-55 [524-583]LRR_8:1.6e-09 [592-629]LRR_8:0.00025
RC6G0123900	rc06	13531770	13533972	CC-NBS-LRR		P-loop[186-194] Kin-2[268-275] RNBS-B[295-301] GPLP[354-360]	[164-444]NB-ARC:1.8e-67 [544-601]LRR_8:1.3e-06 [618-670]LRR_8:2.4e-05
RC6G0124200	rc06	13557623	13561228	CC-NBS-LRR	YqeY	P-loop[222-230] Kin-2[304-311] RNBS-B[331-337] GPLP[390-396]	[109-162]YqeY:0.0033 [200-480]NB-ARC:1.1e-64 [581-637]LRR_8:5e-09 [655-708]LRR_8:0.0081
RC6G0157600	rc06	16429923	16432940	TIR-NBS		P-loop[117-125] Kin-2[196-203] RNBS-B[223-229] GPLP[283-289]	[4-79]TIR:1.8e-08 [95-354]NB-ARC:6.4e-34
RC6G0160400	rc06	16755259	16771333	TIR-NBS-LRR		P-loop[252-260] Kin-2[331-338] RNBS-B[358-364] GPLP[416-422]	[24-145]TIR:2.9e-40 [243-482]NB-ARC:1.7e-29 [687-726]LRR_4:0.0036
RC6G0160500	rc06	16774763	16779151	TIR-NBS-LRR		P-loop[217-225] Kin-2[296-303] RNBS-B[323-329] GPLP[382-388]	[11-177]TIR:6.2e-49 [193-446]NB-ARC:1.9e-31 [624-657]LRR_4:0.0065
RC6G0183500	rc06	20403767	20408944	TIR-NBS		P-loop[222-230] Kin-2[301-308] RNBS-B[328-334] GPLP[387-393]	[720-758]LRR_4:0.0014 [759-775]LRR_8:0.0041
RC6G0197000	rc06	22624488	22628680	TIR-NBS-LRR		P-loop[262-270] Kin-2[341-348] RNBS-B[368-374] GPLP[430-436]	[17-186]TIR:1.6e-48 [198-455]NB-ARC:1.9e-23
RC6G0197300	rc06	22658497	22666183	TIR-NBS-LRR		P-loop[229-237] Kin-2[308-315] RNBS-B[335-341] GPLP[394-400]	[33-189]TIR:8.8e-48 [250-494]NB-ARC:1.1e-29 [647-702]LRR_8:0.00061
RC6G0202400	rc06	23439171	23442402	TIR-NBS-LRR		P-loop[226-234] Kin-2[305-312] RNBS-B[332-338] GPLP[392-398]	[740-763]LRR_8:0.0017 [764-820]LRR_8:1.6e-05
RC6G0203300	rc06	23594062	23598587	NBS-LRR		P-loop[1-8] Kin-2[72-79] RNBS-B[102-108] GPLP[164-170]	[26-191]TIR:7.1e-43 [212-460]NB-ARC:4.6e-30 [635-673]LRR_4:0.0007
RC6G0214000	rc06	25147821	25151340	CC-NBS-LRR		P-loop[200-208] Kin-2[287-294] RNBS-B[316-322] GPLP[378-384]	[674-697]LRR_4:0.001 [730-767]LRR_4:0.0031 [768-785]LRR_8:0.0047
RC6G0216200	rc06	25400339	25403357	NBS-LRR	RPW8	P-loop[181-189] Kin-2[256-263] RNBS-B[285-291] GPLP[347-353]	[23-185]TIR:5.6e-45 [204-461]NB-ARC:6.1e-31 [655-693]LRR_4:0.00058

RC6G0224800	rc06	26889034	26894819	TIR-NBS-LRR	P-loop[221-229] Kin-2[299-306] RNBS-B[326-332] GPLP[383-389]	[15-195]TIR:3.9e-46 [197-445]NB-ARC:3.6e-32 [666-685]LRR_3:4.9e-05 [784-806]LRR_4:0.0076 [807-846]LRR_4:0.0045 [997-1037]LRR_4:0.0066 [1091-1131]LRR_4:0.0075 [1350-1405]LRR_8:9.9e-05 [29-194]TIR:2.1e-50 [210-221]ATPase_2:0.00028 [222-463]NB-ARC:1.8e-31 [615-634]LRR_3:0.00016 [755-811]LRR_8:0.0034 [865-920]LRR_8:0.0041 [173-458]NB-ARC:1.1e-83 [600-654]LRR_8:0.00027 [43-317]NB-ARC:3.6e-51 [413-470]LRR_8:4.5e-08 [199-464]NB-ARC:1.7e-68 [590-644]LRR_8:2.6e-09
RC6G0241800	rc06	30458368	30464847	TIR-NBS-LRR	P-loop[233-241] Kin-2[312-319] RNBS-B[339-345] GPLP[398-404]	
RC6G0256400	rc06	33268274	33273327	NBS-LRR	P-loop[193-201] Kin-2[275-282] RNBS-B[302-308] GPLP[366-372]	
RC6G0259700	rc06	33714369	33715887	NBS-LRR	P-loop[65-73] Kin-2[140-147] RNBS-B[169-175] GPLP[228-234]	
RC6G0262100	rc06	34010916	34013831	CC-NBS-LRR	P-loop[210-218] Kin-2[286-293] RNBS-B[315-321] GPLP[377-383]	
RC6G0265700	rc06	34555768	34566304	TIR-NBS-LRR	P-loop[227-235] Kin-2[306-313] RNBS-B[333-339] GPLP[392-398]	[23-189]TIR:4.2e-49 [209-459]NB-ARC:2.7e-31 [838-877]LRR_4:4.6e-05
RC6G0270900	rc06	35315757	35318664	TIR-NBS	P-loop[225-233] Kin-2[305-312] RNBS-B[332-338] GPLP[391-397]	[21-186]TIR:1.4e-50 [203-456]NB-ARC:6.1e-31
RC6G0271200	rc06	35365251	35371062	NBS	P-loop[35-43] Kin-2[115-122] RNBS-B[142-148] GPLP[201-207]	[13-266]NB-ARC:1.8e-31 [22-195]TIR:8.5e-47 [202-214]AAA_16:0.0025 [215-462]NB-ARC:9.4e-37 [620-639]LRR_3:4.4e-05 [665-705]LRR_4:0.0025 [900-940]LRR_4:0.0099 [209-498]NB-ARC:1.5e-84 [637-693]LRR_8:4.2e-06 [884-926]LRR_4:0.0037 [172-459]NB-ARC:1.9e-82 [571-627]LRR_8:5e-05 [628-645]LRR_8:0.00018 [160-429]NB-ARC:5.2e-50 [607-662]LRR_8:6.4e-05
RC6G0276500	rc06	36143986	36148656	TIR-NBS-LRR	P-loop[230-238] Kin-2[309-316] RNBS-B[336-342] GPLP[395-401]	
RC6G0284500	rc06	37427969	37431126	CC-NBS-LRR	P-loop[232-240] Kin-2[314-321] RNBS-B[341-347] GPLP[405-411]	
RC6G0290600	rc06	38547981	38551114	NBS-LRR	P-loop[194-202] Kin-2[276-283] RNBS-B[303-309] GPLP[367-373]	
RC6G0314900	rc06	41749290	41755946	CC-NBS-LRR	P-loop[180-188] Kin-2[254-261] RNBS-B[279-285] GPLP[339-345]	
RC6G0322100	rc06	42577765	42580401	TIR-NBS	P-loop[222-230] Kin-2[301-308] RNBS-B[328-334] GPLP[388-394]	[18-186]TIR:1e-46 [201-454]NB-ARC:2e-29 [613-631]LRR_3:0.0022 [1-231]NB-ARC:6.6e-24 [398-413]LRR_3:0.00056
RC6G0323100	rc06	42663725	42665265	NBS	P-loop[1-8] Kin-2[79-86] RNBS-B[106-112] GPLP[166-172]	
RC6G0323700	rc06	42727143	42728649	CC-NBS	P-loop[60-68] Kin-2[134-141] RNBS-B[161-167] GPLP[220-226]	[41-303]NB-ARC:8.7e-42 [16-180]TIR:6.1e-46 [196-447]NB-ARC:3e-33
RC6G0362300	rc06	47266486	47268853	TIR-NBS	P-loop[219-227] Kin-2[298-305] RNBS-B[325-331] GPLP[384-390]	
RC6G0374500	rc06	48557514	48566076	TIR-NBS	P-loop[218-226] Kin-2[297-304] RNBS-B[324-330] GPLP[383-389]	[16-185]TIR:3.5e-41 [201-456]NB-ARC:5e-33 [610-628]LRR_3:2.2e-05 [9-131]RPW8:2.8e-15 [197-455]NB-ARC:6.2e-35 [192-465]NB-ARC:1.9e-63 [589-644]LRR_8:1.5e-07
RC6G0478700	rc06	57862436	57865361	NBS	P-loop[213-221] Kin-2[290-297] RNBS-B[313-319] GPLP[370-376]	
RC7G0023600	rc07	1475070	1477290	NBS-LRR	P-loop[202-210] Kin-2[278-285] RNBS-B[312-318] GPLP[374-380]	
RC7G0033200	rc07	2131265	2134171	NBS-LRR	P-loop[85-93] Kin-2[159-166] RNBS-B[193-199] GPLP[254-260]	[53-67]AAA_16:0.00068 [68-342]NB-ARC:1.9e-62 [465-519]LRR_8:9.7e-05
RC7G0033400	rc07	2140917	2144390	CC-NBS-LRR	P-loop[204-212] Kin-2[278-285] RNBS-B[312-318] GPLP[373-379]	[172-183]AAA_16:0.0022 [184-462]NB-ARC:1.7e-64 [584-639]LRR_8:0.00017

RC7G0133900	rc07	10173706	10179266	TIR-NBS-LRR	P-loop[226-234] Kin-2[305-312] RNBS-B[332-338] GPLP[392-398]	[23-187]TIR:1.9e-47 [204-458]NB-ARC:1e-33 [604-630]LRR_8:0.0025 [631-666]LRR_4:0.00099
RC7G0225300	rc07	18963510	18972518	CC-NBS	P-loop[258-266] Kin-2[333-340] RNBS-B[357-363] GPLP[415-421]	[238-498]NB-ARC:7.4e-44 [160-416]NB-ARC:2.8e-38 [596-652]LRR_8:0.0068
RC7G0235900	rc07	20055775	20061940	CC-NBS-LRR	P-loop[179-187] Kin-2[256-263] RNBS-B[280-286] GPLP[338-344]	[164-425]NB-ARC:1.2e-44 [608-664]LRR_8:9.2e-05
RC7G0244700	rc07	21016051	21020571	CC-NBS-LRR	P-loop[184-192] Kin-2[260-267] RNBS-B[284-290] GPLP[343-349]	[2-260]NB-ARC:1.1e-42 [436-492]LRR_8:0.00016
RC7G0245500	rc07	21075666	21080081	NBS-LRR	P-loop[19-27] Kin-2[95-102] RNBS-B[119-125] GPLP[178-184]	[221-481]NB-ARC:4e-44 [657-713]LRR_8:0.00017
RC7G0252400	rc07	21761370	21763976	CC-NBS-LRR	P-loop[242-250] Kin-2[316-323] RNBS-B[340-346] GPLP[399-405]	[187-460]NB-ARC:1.4e-59
RC7G0257200	rc07	22347270	22350134	CC-NBS	P-loop[204-212] Kin-2[279-286] RNBS-B[310-316] GPLP[371-377]	[14-259]NB-ARC:1.4e-32 [46-213]TIR:5.4e-46 [228-491]NB-ARC:4.1e-37
RC7G0284000	rc07	25389959	25391583	NBS	P-loop[23-31] Kin-2[101-108] RNBS-B[128-134] GPLP[188-194]	[172-461]NB-ARC:1.1e-74 [576-598]LRR_8:0.0033 [599-649]LRR_8:0.00046
RC7G0284100	rc07	25432425	25434875	TIR-NBS	P-loop[251-259] Kin-2[330-337] RNBS-B[357-363] GPLP[417-423]	[177-463]NB-ARC:1.3e-76 [176-465]NB-ARC:2.8e-77 [605-655]LRR_8:0.0027
RC7G0309000	rc07	28256648	28259491	NBS-LRR	P-loop[195-203] Kin-2[277-284] RNBS-B[304-310] GPLP[366-372]	[173-462]NB-ARC:6.3e-76 [600-650]LRR_8:0.0027
RC7G0319700	rc07	29485761	29488529	NBS-LRR	P-loop[199-207] Kin-2[281-288] RNBS-B[308-314] GPLP[370-376]	[175-462]NB-ARC:1.8e-75 [600-650]LRR_8:0.0015
RC7G0319900	rc07	29491118	29495220	NBS-LRR	P-loop[199-207] Kin-2[281-288] RNBS-B[308-314] GPLP[370-376]	[171-458]NB-ARC:7.7e-75 [579-634]LRR_8:0.00019 [635-652]LRR_8:0.0016
RC7G0320000	rc07	29512402	29515306	NBS-LRR	P-loop[196-204] Kin-2[278-285] RNBS-B[305-311] GPLP[367-373]	[170-456]NB-ARC:4.6e-70 [171-458]NB-ARC:1.6e-75 [601-651]LRR_8:0.0043
RC7G0320100	rc07	29517534	29521547	NBS-LRR	P-loop[196-204] Kin-2[278-285] RNBS-B[305-311] GPLP[367-373]	[100-386]NB-ARC:6.6e-74 [507-562]LRR_8:9.1e-05 [563-580]LRR_8:0.0014
RC7G0320300	rc07	29539288	29542140	CC-NBS-LRR	P-loop[192-200] Kin-2[276-283] RNBS-B[303-309] GPLP[365-371]	[100-387]NB-ARC:2.6e-71 [507-562]LRR_8:4.6e-05 [563-580]LRR_8:0.0011
RC7G0320600	rc07	29549108	29551951	NBS	P-loop[192-200] Kin-2[274-281] RNBS-B[301-307] GPLP[363-369]	[190-463]NB-ARC:3.3e-72 [583-638]LRR_8:2.3e-05 [639-656]LRR_8:0.00045
RC7G0320900	rc07	29558456	29561305	CC-NBS-LRR	P-loop[192-200] Kin-2[276-283] RNBS-B[303-309] GPLP[365-371]	[181-347]NB-ARC:4.6e-49 [449-508]LRR_8:6.9e-10 [509-518]LRR_4:0.0021
RC7G0321100	rc07	29566741	29569691	NBS-LRR	P-loop[121-129] Kin-2[205-212] RNBS-B[232-238] GPLP[294-300]	[165-441]NB-ARC:2.1e-75 [17-188]TIR:5.6e-47 [209-479]NB-ARC:8.3e-51
RC7G0321400	rc07	29647957	29650613	NBS-LRR	P-loop[121-129] Kin-2[205-212] RNBS-B[232-238] GPLP[294-300]	[22-194]TIR:2.1e-51 [204-454]NB-ARC:1.5e-31 [607-626]LRR_3:0.00018
RC7G0321800	rc07	29682960	29685842	CC-NBS-LRR	P-loop[198-206] Kin-2[282-289] RNBS-B[309-315] GPLP[370-376]	[864-885]LRR_4:0.0079 [889-928]LRR_4:8.8e-05
RC7G0321900	rc07	29688306	29691152	NBS-LRR	P-loop[191-199] Kin-2[275-282] RNBS-B[302-308] GPLP[364-370]	[23-187]TIR:1.9e-47 [204-458]NB-ARC:1e-33 [604-630]LRR_8:0.0025 [631-666]LRR_4:0.00099
RC7G0322000	rc07	29706420	29708997	NBS-LRR	P-loop[101-109] Kin-2[176-183] RNBS-B[205-211] GPLP[263-269]	[177-458]NB-ARC:1.9e-75 [577-632]LRR_8:7.3e-06 [633-650]LRR_8:0.0011
RC7G0335300	rc07	31329692	31331125	NBS	P-loop[186-194] Kin-2[265-272] RNBS-B[292-298] GPLP[353-359]	[12-194]NB-ARC:2.1e-51 [204-454]NB-ARC:1.5e-31 [607-626]LRR_3:0.00018
RC7G0400300	rc07	40886140	40891483	CC-TIR-NBS	P-loop[230-238] Kin-2[305-312] RNBS-B[334-340] GPLP[393-399]	[172-461]NB-ARC:1.3e-76 [171-458]NB-ARC:1.6e-75 [601-651]LRR_8:0.0043
RC7G0416400	rc07	43459766	43467338	TIR-NBS-LRR	P-loop[226-234] Kin-2[304-311] RNBS-B[330-336] GPLP[389-395]	[177-463]NB-ARC:1.3e-76 [176-465]NB-ARC:2.8e-77 [605-655]LRR_8:0.0027

RC7G0421200	rc07	44042650	44045331	NBS-LRR		P-loop[16-24] Kin-2[91-98] RNBS-B[120-126] GPLP[179-185]	[6-261]NB-ARC:1.8e-46 [368-426]LRR_8:7.3e-08 [459-495]LRR_8:0.00084
RC7G0421300	rc07	44047157	44048711	TIR-NBS		P-loop[171-179] Kin-2[246-253] RNBS-B[275-281] GPLP[333-339]	[1-135]TIR:2.5e-32 [152-418]NB-ARC:3.3e-49
RC7G0429300	rc07	45382761	45384998	NBS-LRR		P-loop[1-8] Kin-2[75-82] RNBS-B[106-112] GPLP[168-174]	[1-257]NB-ARC:4.3e-59 [348-388]LRR_8:1.9e-05 [401-436]LRR_8:0.0072
RC7G0429700	rc07	45486721	45489588	CC-NBS-LRR	DUF3656	P-loop[210-218] Kin-2[285-292] RNBS-B[316-322] GPLP[378-384]	[15-79]DUF3656:0.0047 [185-467]NB-ARC:5.8e-63 [558-598]LRR_8:2.6e-05
RC7G0429900	rc07	45552832	45555696	CC-NBS-LRR		P-loop[210-218] Kin-2[285-292] RNBS-B[316-322] GPLP[378-384]	[611-646]LRR_8:0.0096 [183-467]NB-ARC:5.4e-62 [558-598]LRR_8:4.7e-06
RC7G0452100	rc07	49220915	49227770	CC-TIR-NBS-LRR		P-loop[233-241] Kin-2[308-315] RNBS-B[335-341] GPLP[394-400]	[27-195]TIR:2.8e-47 [209-464]NB-ARC:3.1e-36 [641-696]LRR_8:0.00042 [716-742]LRR_8:0.00015 [743-783]LRR_4:0.00012
RC7G0452700	rc07	49282300	49289216	TIR-NBS-LRR		P-loop[232-240] Kin-2[308-315] RNBS-B[335-341] GPLP[394-400]	[27-186]TIR:2.9e-48 [209-461]NB-ARC:1.9e-32 [612-668]LRR_8:0.00036 [754-809]LRR_8:0.00045 [825-865]LRR_4:0.0011
RC7G0454900	rc07	49474139	49476752	CC-NBS-LRR		P-loop[222-230] Kin-2[299-306] RNBS-B[330-336] GPLP[392-398]	[213-482]NB-ARC:2.3e-63 [571-613]LRR_8:3.2e-06 [614-656]LRR_8:0.00019
RC7G0460600	rc07	50106007	50108856	CC-NBS-LRR		P-loop[211-219] Kin-2[286-293] RNBS-B[317-323] GPLP[379-385]	[180-191]AAA_16:0.0042 [192-464]NB-ARC:6e-61 [595-649]LRR_8:4.7e-07
RC7G0461100	rc07	50173383	50178731	CC-NBS-LRR		P-loop[210-218] Kin-2[285-292] RNBS-B[317-323] GPLP[379-385]	[179-190]AAA_16:0.0083 [191-464]NB-ARC:1.8e-61 [596-651]LRR_8:1.1e-06
RC7G0463700	rc07	50685389	50689356	NBS-LRR		P-loop[64-72] Kin-2[139-146] RNBS-B[170-176] GPLP[232-238]	[36-319]NB-ARC:1.7e-61 [410-453]LRR_8:1.4e-06 [454-496]LRR_8:1.7e-06
RC7G0463900	rc07	50732972	50735776	NBS-LRR	DUF3656	P-loop[205-213] Kin-2[280-287] RNBS-B[311-317] GPLP[373-379]	[24-79]DUF3656:0.0054 [177-462]NB-ARC:9e-61 [557-598]LRR_8:9.7e-06
RC7G0464500	rc07	50812770	50814191	CC-NBS	DUF3656	P-loop[205-213] Kin-2[282-289] RNBS-B[313-319] GPLP[375-381]	[20-79]DUF3656:0.0027 [180-460]NB-ARC:2.5e-58
RC7G0465100	rc07	50857572	50862536	CC-NBS-LRR		P-loop[214-222] Kin-2[289-296] RNBS-B[320-326] GPLP[382-388]	[183-192]AAA_16:0.00042 [193-470]NB-ARC:1.6e-63 [561-604]LRR_8:2.3e-07
RC7G0465900	rc07	50945167	50948053	CC-NBS-LRR		P-loop[218-226] Kin-2[295-302] RNBS-B[326-332] GPLP[388-394]	[605-650]LRR_8:4.3e-06 [193-474]NB-ARC:2.1e-57 [567-608]LRR_8:1.2e-06 [625-659]LRR_8:0.0015
RC7G0466400	rc07	50969677	50971132	NBS		P-loop[184-192] Kin-2[266-273] RNBS-B[294-300] GPLP[360-366]	[174-374]NB-ARC:3.8e-25 [189-470]NB-ARC:1.3e-60 [557-599]LRR_8:1.9e-07 [607-650]LRR_8:0.0032
RC7G0466700	rc07	50980655	50990938	CC-NBS-LRR		P-loop[215-223] Kin-2[290-297] RNBS-B[321-327] GPLP[383-389]	[185-216]AAA_16:0.0077 [214-477]NB-ARC:4.3e-61 [571-603]LRR_8:0.00031
RC7G0467400	rc07	51045826	51049263	CC-NBS-LRR		P-loop[222-230] Kin-2[297-304] RNBS-B[328-334] GPLP[390-396]	[604-659]LRR_8:0.00027 [63-84]AAA_16:0.00016 [86-286]NB-ARC:2.1e-27
RC7G0468200	rc07	51139885	51140885	NBS		P-loop[96-104] Kin-2[178-185] RNBS-B[206-212] GPLP[272-278]	[21-79]DUF3656:0.0031 [179-454]NB-ARC:3.7e-60
RC7G0468400	rc07	51151640	51153007	CC-NBS	DUF3656	P-loop[205-213] Kin-2[282-289] RNBS-B[313-319] GPLP[375-381]	

RC7G0469000	rc07	51206574	51209390	CC-NBS-LRR	DUF3656	P-loop[204-212] Kin-2[281-288] RNBS-B[312-318] GPLP[374-380]	[19-79]DUF3656:0.005 [179-463]NB-ARC:8.6e-62 [560-615]LRR_8:2.6e-07 [616-640]LRR_8:8.9e-05 [186-469]NB-ARC:1.3e-63 [564-603]LRR_8:5.8e-06 [616-652]LRR_8:0.00051 [19-79]DUF3656:0.0072 [179-462]NB-ARC:7.9e-63 [554-595]LRR_8:2.1e-05 [603-647]LRR_8:0.0022 [186-469]NB-ARC:1.1e-61 [561-602]LRR_8:8.7e-07 [613-654]LRR_8:0.003 [63-84]AAA_16:0.00031 [86-286]NB-ARC:8.4e-26 [78-359]NB-ARC:5.3e-61 [464-521]LRR_8:2.7e-09 [22-79]DUF3656:0.0083 [173-204]AAA_16:0.0042 [201-467]NB-ARC:1.4e-63 [184-467]NB-ARC:4e-61 [561-603]LRR_8:6.7e-06 [604-649]LRR_8:6.7e-05 [185-477]NB-ARC:7.7e-58 [587-635]LRR_8:2.7e-09 [184-466]NB-ARC:4.8e-60 [576-623]LRR_8:1.7e-08 [631-655]LRR_4:0.0057 [31-308]NB-ARC:1.2e-57 [423-472]LRR_8:1.4e-08 [480-497]LRR_8:0.00047 [184-466]NB-ARC:4.7e-57 [577-626]LRR_8:1.2e-07 [183-465]NB-ARC:1.9e-61 [575-623]LRR_8:3e-09 [185-484]NB-ARC:8.8e-59 [595-643]LRR_8:7e-08 [651-674]LRR_4:0.002 [185-472]NB-ARC:4.5e-59 [582-598]LRR_8:6e-07 [599-654]LRR_8:5.2e-08 [183-466]NB-ARC:2e-61 [576-625]LRR_8:5.3e-07 [626-654]LRR_4:0.0031 [1-262]NB-ARC:9.7e-57 [373-422]LRR_8:1.1e-10 [423-446]LRR_4:0.00021 [35-314]NB-ARC:5.4e-60 [440-495]LRR_8:1.9e-06 [495-519]LRR_4:0.00038 [4-95]RPW8:0.0029 [223-502]NB-ARC:1.7e-65 [625-680]LRR_8:9.4e-05 [680-709]LRR_4:0.00049 [13-177]TIR:4.4e-47 [191-446]NB-ARC:5.8e-32 [643-701]LRR_8:0.00076 [1-84]TIR:5.7e-13 [104-359]NB-ARC:2.1e-37 [512-567]LRR_8:0.00046
RC7G0469600	rc07	51262264	51265140	CC-NBS-LRR		P-loop[214-222] Kin-2[289-296] RNBS-B[320-326] GPLP[382-388]	
RC7G0470500	rc07	51326238	51328673	CC-NBS-LRR	DUF3656	P-loop[204-212] Kin-2[282-289] RNBS-B[313-319] GPLP[375-381]	
RC7G0470700	rc07	51341530	51343590	CC-NBS-LRR		P-loop[214-222] Kin-2[289-296] RNBS-B[320-326] GPLP[382-388]	
RC7G0471000	rc07	51430939	51431977	CC-NBS		P-loop[96-104] Kin-2[178-185] RNBS-B[206-212] GPLP[272-278]	[78-359]NB-ARC:5.3e-61 [464-521]LRR_8:2.7e-09
RC7G0471600	rc07	51471327	51473867	NBS-LRR		P-loop[102-110] Kin-2[177-184] RNBS-B[208-214] GPLP[270-276]	[22-79]DUF3656:0.0083 [173-204]AAA_16:0.0042 [201-467]NB-ARC:1.4e-63 [184-467]NB-ARC:4e-61 [561-603]LRR_8:6.7e-06 [604-649]LRR_8:6.7e-05
RC7G0475200	rc07	51830046	51831773	CC-NBS	DUF3656	P-loop[210-218] Kin-2[287-294] RNBS-B[318-324] GPLP[380-386]	[185-477]NB-ARC:7.7e-58 [587-635]LRR_8:2.7e-09
RC7G0484900	rc07	53080293	53083711	CC-NBS-LRR		P-loop[210-218] Kin-2[287-294] RNBS-B[318-324] GPLP[380-386]	[184-466]NB-ARC:4.8e-60 [576-623]LRR_8:1.7e-08 [631-655]LRR_4:0.0057 [31-308]NB-ARC:1.2e-57 [423-472]LRR_8:1.4e-08 [480-497]LRR_8:0.00047
RC7G0486200	rc07	53255434	53258352	CC-NBS-LRR		P-loop[207-215] Kin-2[295-302] RNBS-B[326-332] GPLP[389-395]	[184-466]NB-ARC:4.8e-60 [576-623]LRR_8:1.7e-08 [631-655]LRR_4:0.0057 [31-308]NB-ARC:1.2e-57 [423-472]LRR_8:1.4e-08 [480-497]LRR_8:0.00047
RC7G0486400	rc07	53319282	53321738	CC-NBS-LRR		P-loop[208-216] Kin-2[284-291] RNBS-B[315-321] GPLP[378-384]	[183-465]NB-ARC:1.9e-61 [575-623]LRR_8:3e-09
RC7G0486600	rc07	53337335	53338855	NBS-LRR		P-loop[55-63] Kin-2[131-138] RNBS-B[162-168] GPLP[225-231]	[185-484]NB-ARC:8.8e-59 [595-643]LRR_8:7e-08 [651-674]LRR_4:0.002 [185-472]NB-ARC:4.5e-59 [582-598]LRR_8:6e-07 [599-654]LRR_8:5.2e-08
RC7G0486900	rc07	53398628	53401504	CC-NBS-LRR		P-loop[208-216] Kin-2[285-292] RNBS-B[316-322] GPLP[379-385]	[184-466]NB-ARC:4.7e-57 [577-626]LRR_8:1.2e-07 [183-465]NB-ARC:1.9e-61 [575-623]LRR_8:3e-09
RC7G0487800	rc07	53556508	53558706	CC-NBS-LRR		P-loop[207-215] Kin-2[283-290] RNBS-B[314-320] GPLP[377-383]	
RC7G0488000	rc07	53612846	53615618	CC-NBS-LRR		P-loop[209-217] Kin-2[304-311] RNBS-B[335-341] GPLP[397-403]	
RC7G0488200	rc07	53658690	53661166	CC-NBS-LRR		P-loop[209-217] Kin-2[290-297] RNBS-B[321-327] GPLP[384-390]	
RC7G0488400	rc07	53703331	53706225	CC-NBS-LRR		P-loop[207-215] Kin-2[284-291] RNBS-B[315-321] GPLP[378-384]	
RC7G0488900	rc07	53790542	53792110	CC-NBS-LRR		P-loop[1-8] Kin-2[81-88] RNBS-B[112-118] GPLP[175-181]	
RC7G0497000	rc07	54968789	54971929	NBS-LRR		P-loop[62-70] Kin-2[137-144] RNBS-B[166-172] GPLP[227-233]	
RC7G0497100	rc07	55007186	55010884	CC-NBS-LRR	RPW8	P-loop[250-258] Kin-2[325-332] RNBS-B[354-360] GPLP[415-421]	[4-95]RPW8:0.0029 [223-502]NB-ARC:1.7e-65 [625-680]LRR_8:9.4e-05 [680-709]LRR_4:0.00049
RC7G0507600	rc07	56734367	56738253	TIR-NBS-LRR		P-loop[214-222] Kin-2[293-300] RNBS-B[320-326] GPLP[379-385]	[13-177]TIR:4.4e-47 [191-446]NB-ARC:5.8e-32 [643-701]LRR_8:0.00076
RC7G0508000	rc07	56794636	56797637	TIR-NBS-LRR		P-loop[128-136] Kin-2[207-214] RNBS-B[234-240] GPLP[292-298]	[1-84]TIR:5.7e-13 [104-359]NB-ARC:2.1e-37 [512-567]LRR_8:0.00046

RC7G0511800	rc07	57337077	57340131	TIR-NBS-LRR	P-loop[252-260] Kin-2[331-338] RNBS-B[358-364] GPLP[417-423]	[48-210]TIR:2.7e-45 [228-482]NB-ARC:1.9e-32 [652-690]LRR_8:0.00054
RC7G0527800	rc07	59327412	59329960	CC-NBS	P-loop[179-187] Kin-2[255-262] RNBS-B[279-285] GPLP[338-344]	[160-422]NB-ARC:5.7e-44 [169-450]NB-ARC:1.3e-62 [581-635]LRR_8:2.3e-06
RC7G0530500	rc07	59779621	59782561	NBS-LRR	P-loop[197-205] Kin-2[272-279] RNBS-B[302-308] GPLP[363-369]	[96-267]TIR:7.1e-49 [276-535]NB-ARC:1.2e-37 [681-700]LRR_3:0.0004
RC7G0567300	rc07	65553075	65558854	TIR-NBS-LRR	P-loop[299-307] Kin-2[376-383] RNBS-B[402-408] GPLP[462-468]	[926-984]LRR_8:0.00057 [3-259]NB-ARC:1.9e-37 [500-523]LRR_8:0.0047 [524-580]LRR_8:0.0003 [642-700]LRR_8:0.00065
RC7G0567700	rc07	65614421	65619817	NBS-LRR	P-loop[26-34] Kin-2[103-110] RNBS-B[129-135] GPLP[189-195]	

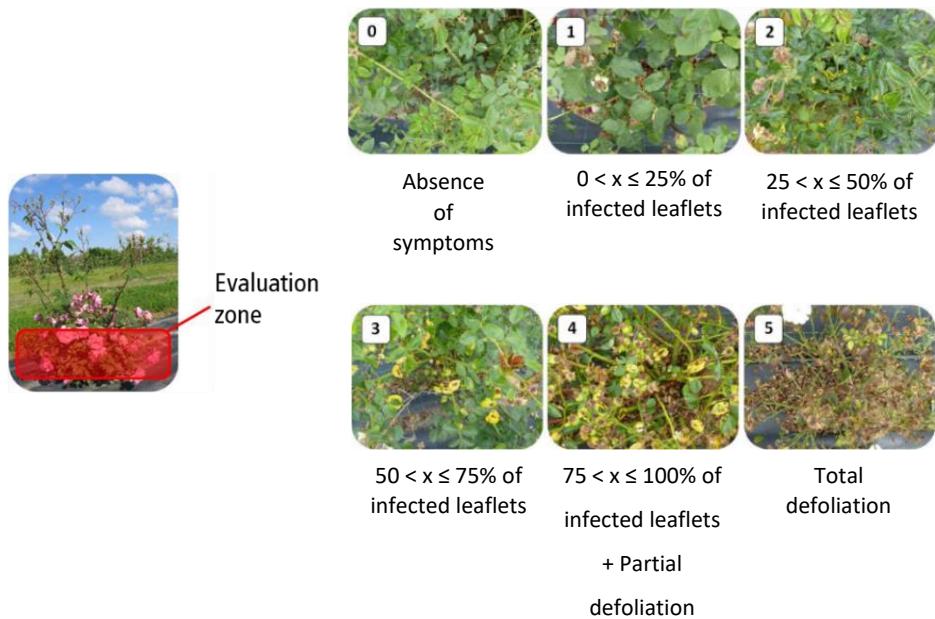
1096 **Supplementary figures**

1097 **Supp. Fig. 1** Evaluation zone and rating scale of black spot disease in rose

1098 From 0 (no symptoms) to 5 (total defoliation of the plant) with a score of 1 for less than 25% of infected leaflets, a
1099 score of 2 for infection between 25 and 50%, a score of 3 for infection between 50 and 75% of infected leaflets and 4
1100 for infection of 75% to 100% and partial defoliation.

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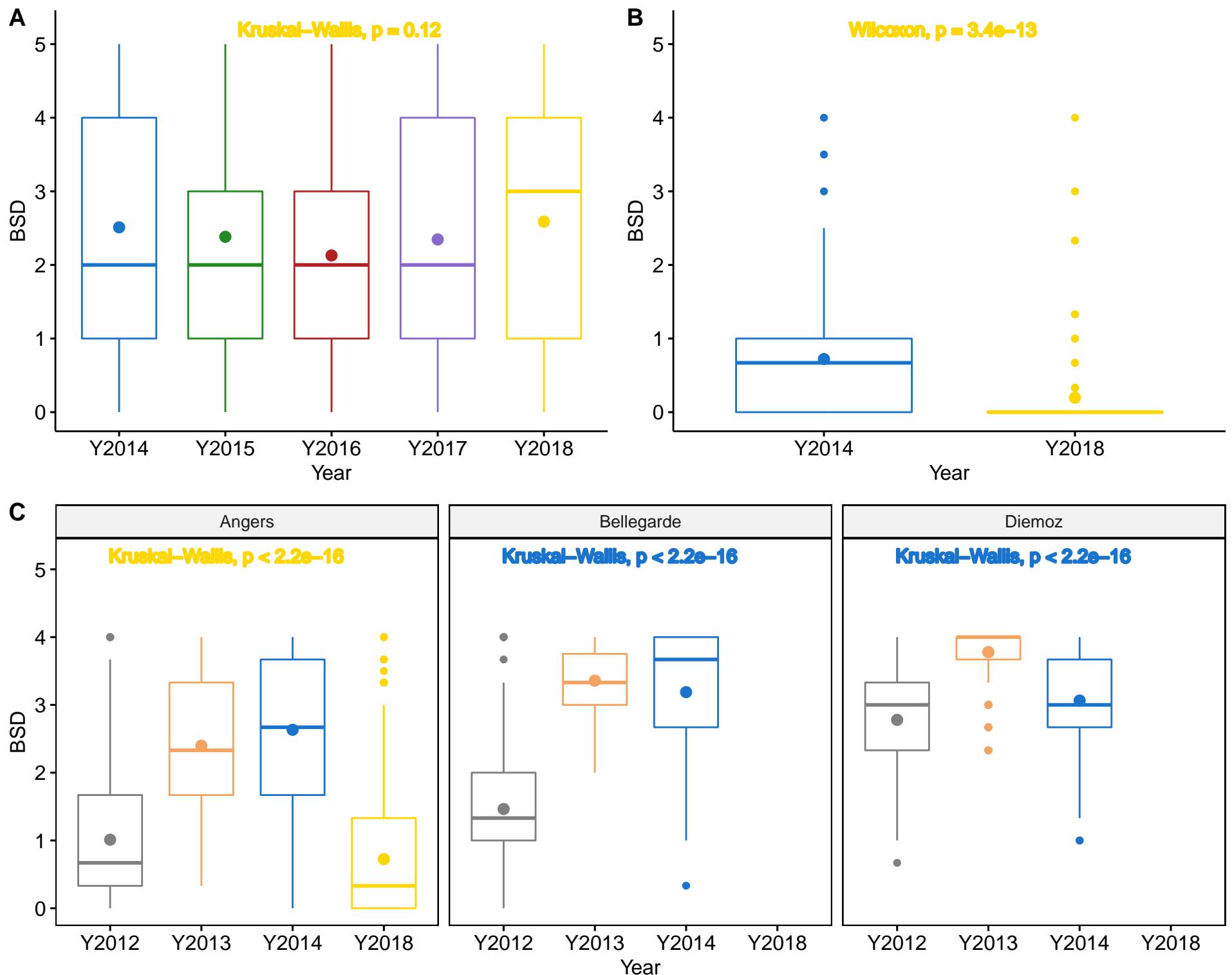


1103 **Supp. Fig. 2** Overall mean of black spot disease (BSD) scores for three rose populations over several locations and
1104 years under natural infections in field

1105 In the box plots, the boundaries of the box indicate the 25th percentile (on the lower part) and the 75th percentile (on
1106 the upper part). A thick line within the box marks the median, and a dot within the box marks the mean. Lines above
1107 and below the box indicate the 10th and 90th percentiles. Points above and below the whiskers indicate outliers outside
1108 the 10th and 90th percentiles. A: Data description for different years for OW population in Angers, B: Data description
1109 for different years for FW population in Angers, C: Data description for different years for HW population in Angers,
1110 Bellegarde and Diémoz. A Kruskal-Wallis test was used to compare the scoring years for HW and OW populations,
1111 and a Wilcoxon test was used to compare the two scoring years 2014-2018 for FW. For HW population, locations were
1112 considered separately. P-values of the tests are displayed on the graphs for all populations.

1113

1114



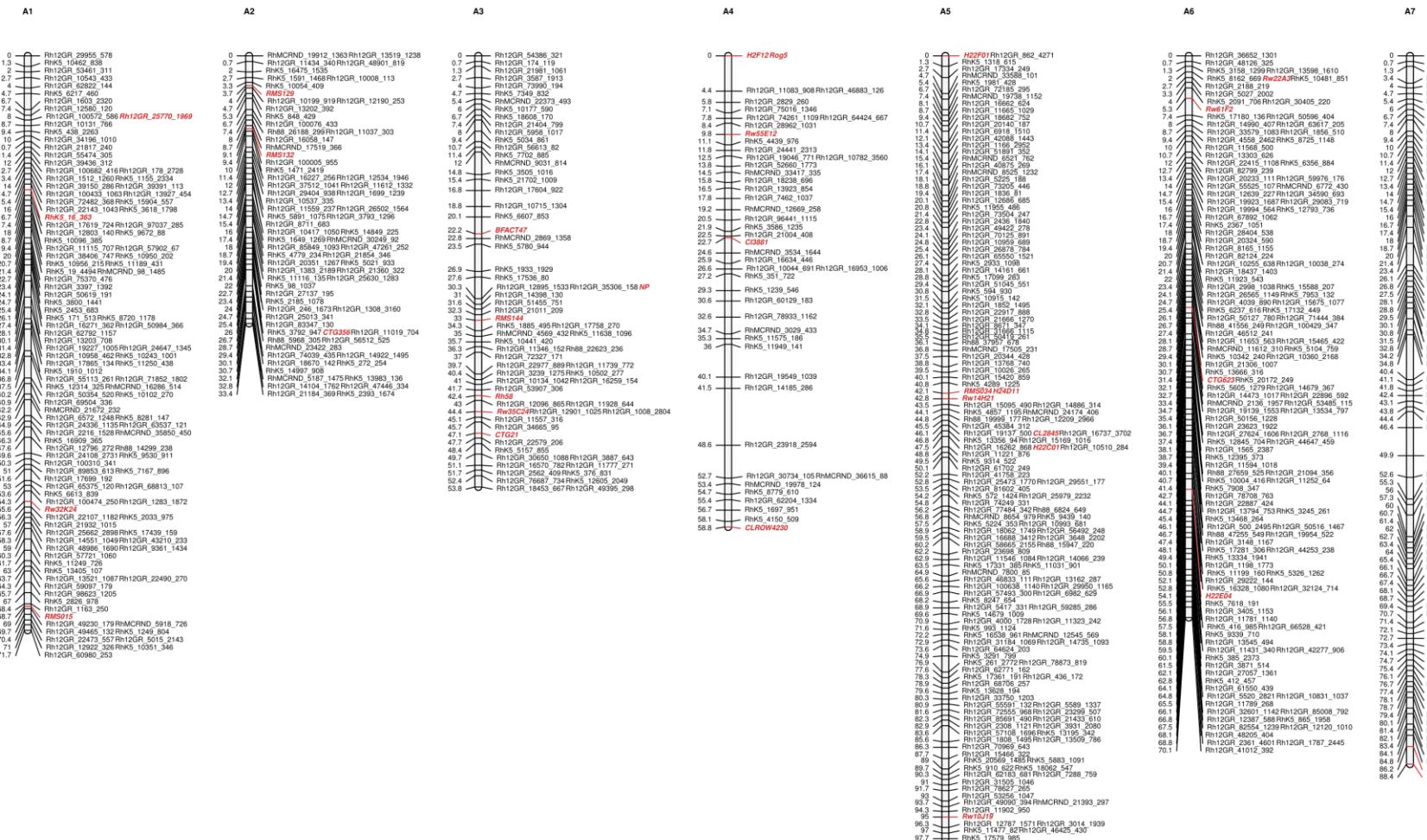
1115 **Supp. Fig. 3** Genetic linkage map of the male parent hybrid, *Rosa wichurana*, for OW population
1116 Linkage groups (LG) names for the male map (B1 to B7) are placed above the corresponding linkage groups according
1117 to Spiller et al. 2011. Locus names are indicated on the right side of each LG. When several markers were mapped at
1118 a same position, one or two markers were reported corresponding to the unique loci or markers with different phases.
1119 SSR markers are indicated in red. Genetic distances (cM) are indicated on the left side of each LG.
1120
1121



1122 **Supp. Fig. 4** Genetic linkage map of the female parent, *Rosa chinensis* ‘Old Blush’, for OW population
1123 Linkage groups (LG) names for the female map (A1 to A7) are placed above the corresponding linkage groups. Locus
1124 names are indicated on the right side of each LG. When several markers were mapped at the same position, one or two
1125 markers were reported corresponding to the unique loci or markers with different phases. SSR markers are indicated
1126 in red. Genetic distances (cM) are indicated on the left side of each LG.

1127

1128



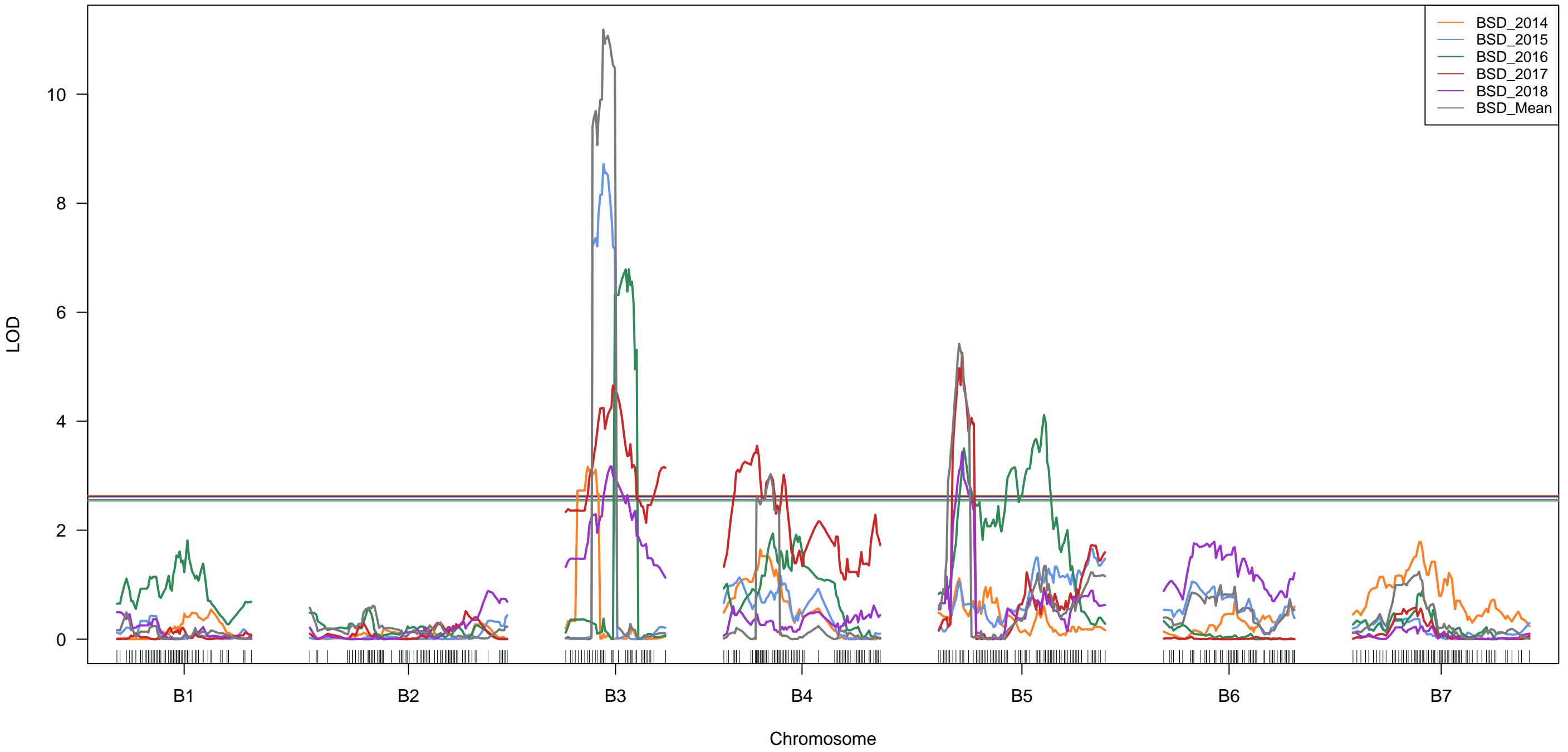
Supplementary figure 4: Genetic linkage map of the female parent, *Rosa chinensis* ‘Old Blush’, for OW population

1129 **Supp. Fig. 5** QTL mapping associated with black spot disease (BSD) resistance using a normal model with an CIM
1130 analysis for OW population for the male map

1131 Linkage groups are named as follows: “B” for the male map and the number of the linkage group. LOD score for each
1132 year and the mean of all years are calculated using a Composite Interval Mapping method (CIM) and are displayed
1133 with different colors. The same set of colors is used to represent the $\alpha=0.05$ LOD threshold for declaring significant
1134 QTL based on 1,000 permutations.

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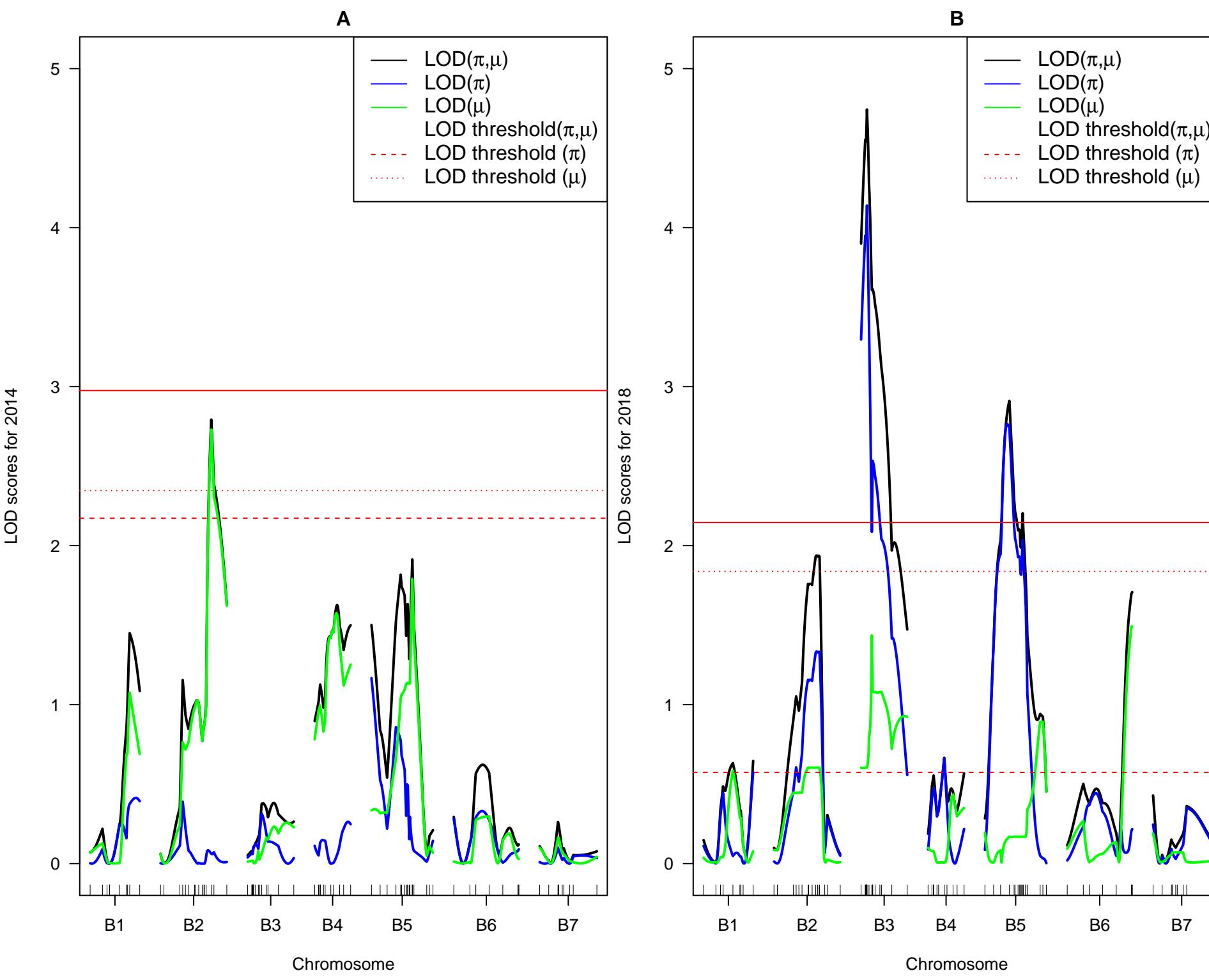


1137 **Supp. Fig. 6** QTL mapping associated with black spot disease resistance using a two-part model approach for non-
1138 normally distributed data of FW population for the male map

1139 A and B: LOD curves for the two-part model for 2014 (A) and 2018 (B); LOD. π (penetrance, equivalent to binary
1140 model) displayed in blue, LOD. μ (severity, equivalent to normal model for non-spike phenotypes) displayed in green
1141 and LOD. π,μ (sum, representing the complete model) displayed in black; LOD thresholds are displayed in red with
1142 $\alpha=0.05$ for declaring significant QTL based on 1,000 permutations.

1143

1144

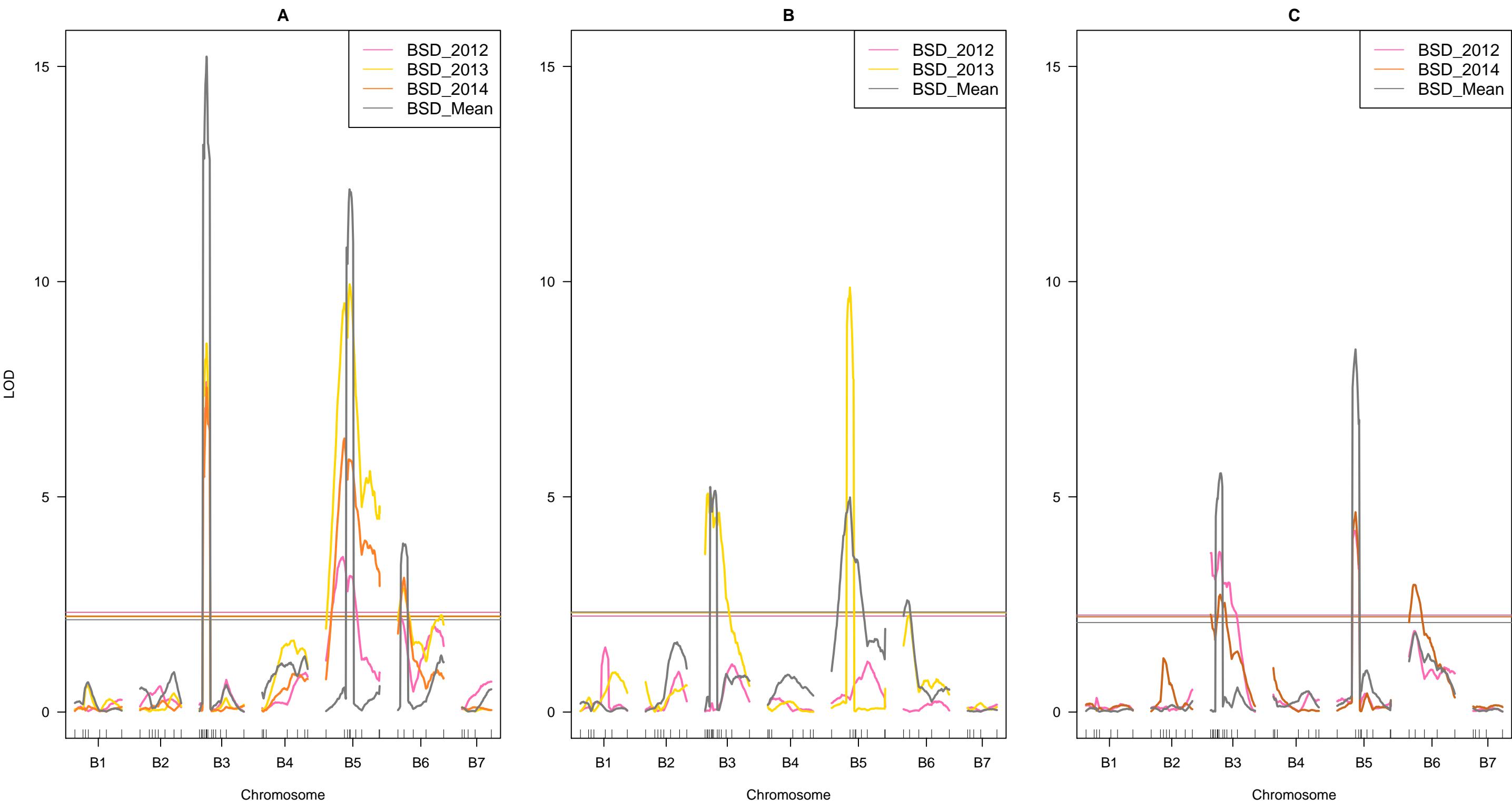


1145 **Supp. Fig. 7** QTL mapping associated with black spot disease (BSD) resistance for normally distributed data of HW
1146 population using a normal model with CIM analysis for the male map

1147 Linkage groups are named as follow: "B" for the male map and the number of the linkage group. For HW population,
1148 BSD was scored in three locations: (A) Angers, (B) Bellegarde and (C) Diémoz. LOD score for each year and the
1149 mean of all years were calculated using a Composite Interval Mapping (CIM) method. The same set of colors is used
1150 to represent the different scoring years in the different locations. $\alpha=0.05$ LOD threshold was used for declaring
1151 significant QTL based on 1,000 permutations.

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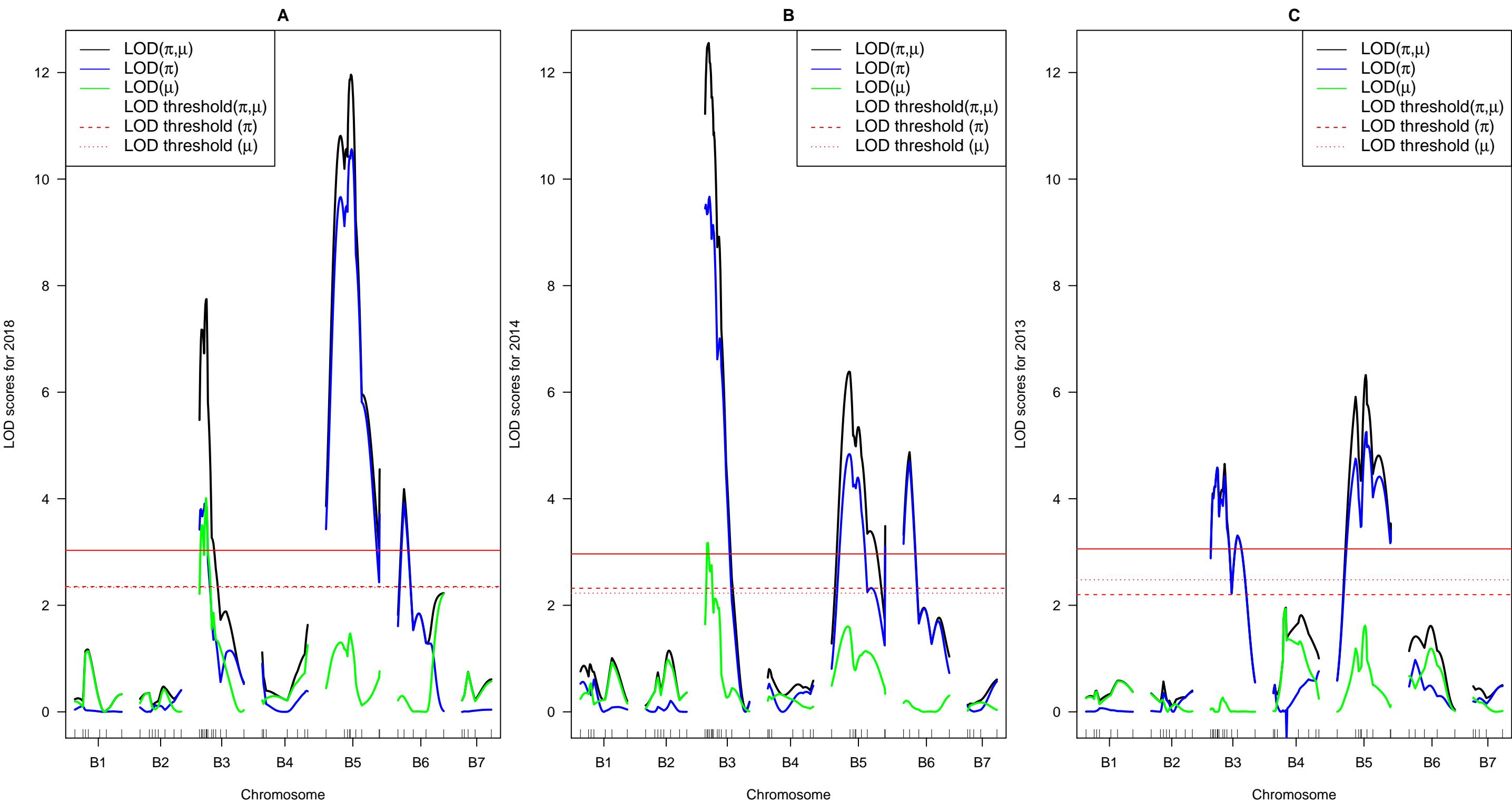


1154 **Supp. Fig. 8** QTL mapping with black spot disease (BSD) resistance using a two-part model approach for non-
1155 normally distributed data of HW population for the male map

1156 Linkage groups are named as follows: “B” for the male map and the number of the linkage group. A to C: LOD curves
1157 of the two-part model analysis for spike-like distribution of HW BSD scoring years (Angers-2018 (A), Bellegarde-
1158 2014 (B) and Diémoz-2013 (C)); LOD. π (penetrance, equivalent to binary model) displayed in blue, LOD. μ (severity,
1159 equivalent to normal model for non-spike phenotypes) displayed in green and LOD. π,μ (sum, representing the
1160 complete model) displayed in black; LOD thresholds are displayed in red with $\alpha=0.05$ for declaring significant QTL
1161 based on 1,000 permutations.

1162

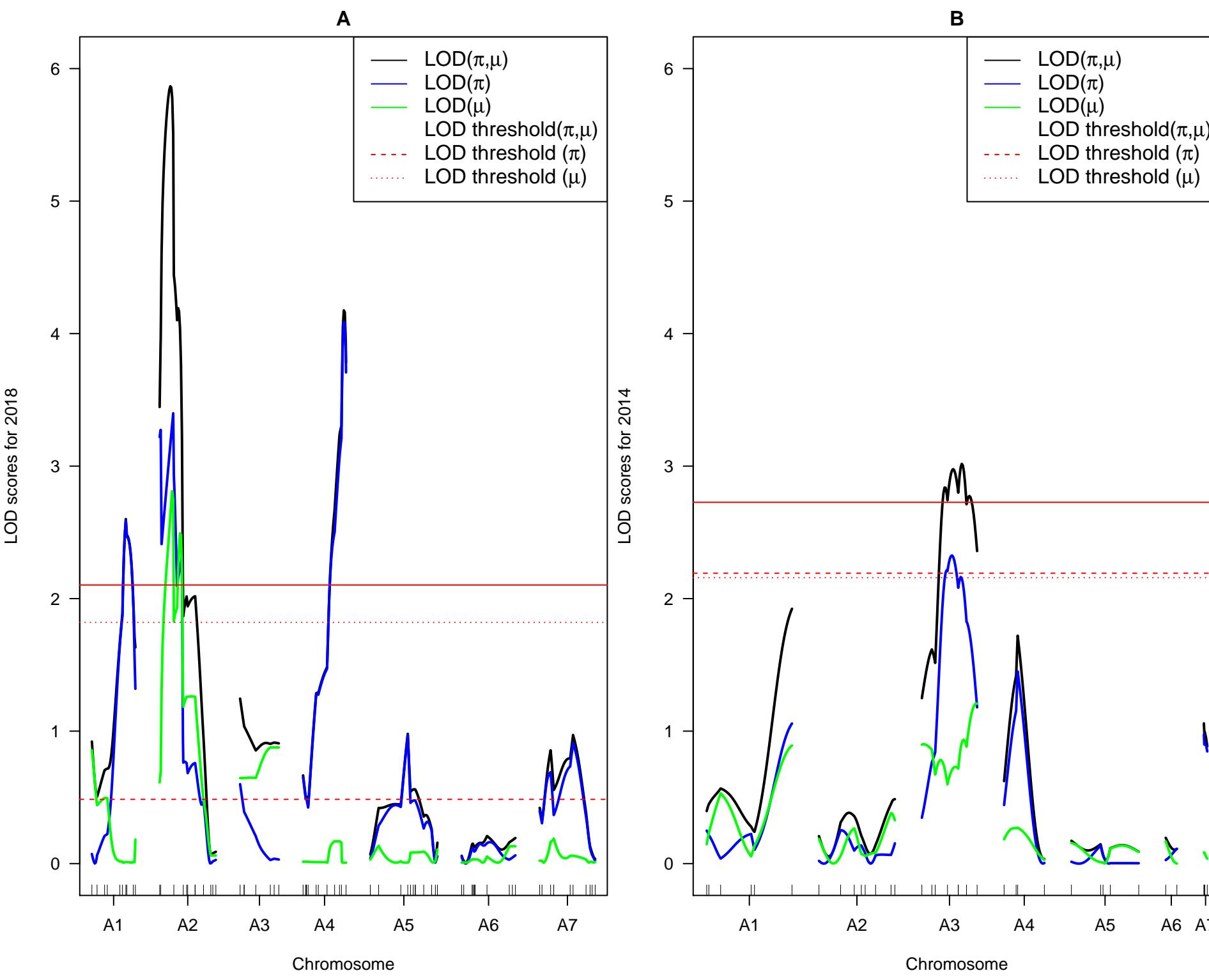
1163



1164 **Supp. Fig. 9** QTL mapping with black spot disease resistance using a two-part model approach for non-normally
1165 distributed data of FW and HW populations for the female maps
1166 A: LOD curves for the two-part model for FW population using 2018 scoring year in Angers; B: LOD curves for the
1167 two-part model for HW population using scoring year 2014 in Bellegarde; LOD. π (penetrance, equivalent to binary
1168 model) displayed in blue, LOD. μ (severity, equivalent to normal model for non-spike phenotypes) displayed in green
1169 and LOD. $\pi.\mu$ (sum, representing the complete model) displayed in black; LOD thresholds are displayed in red with
1170 $\alpha=0.05$ for declaring significant QTL based on 1,000 permutations.

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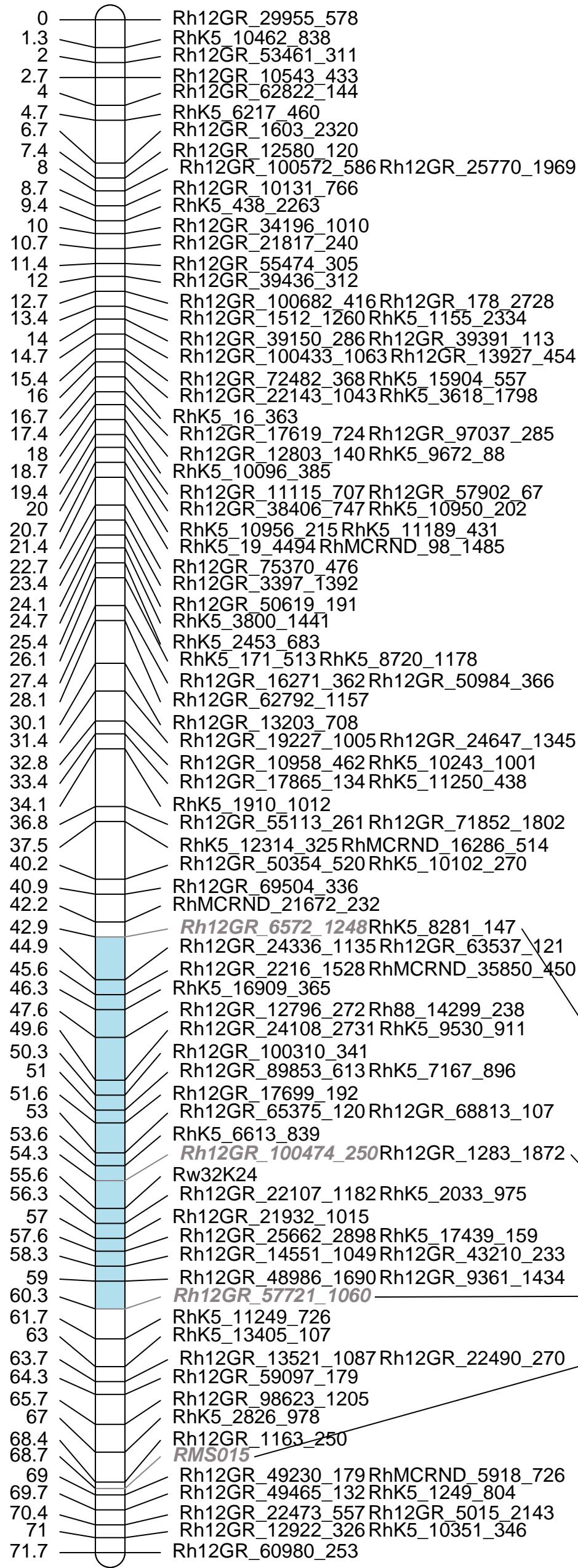


1173 **Supp. Fig. 10** Co-localization of the *Rdr1* genes cluster with the QTLs on A1 from OW and FW female maps
1174 Linkage groups (LG) names from female genetic maps are placed above the LG and named A1 - “population name”
1175 and the corresponding chromosome is placed in the middle. Names of markers are on the right and the genetic distances
1176 (in cM) on the left. For the chromosome from the physical map, physical distances are expressed in mega-base (Mb).
1177 TNLs genes and clusters (OB2-A, OB-B, Cluster1 and Cluster2, Menz et al. 2020) are shown in black. The markers
1178 peaks of each QTL are displayed in grey. The active form of *Rdr1* resistance gene (*muRdr1A*) is located on the cluster2
1179 (Menz et al. 2020). QTLs widest confidence intervals are represented in plain colors on the linkage groups: blue for
1180 the OW female map, yellow for the FW female map and green for the equivalent common widest region on the physical
1181 map.

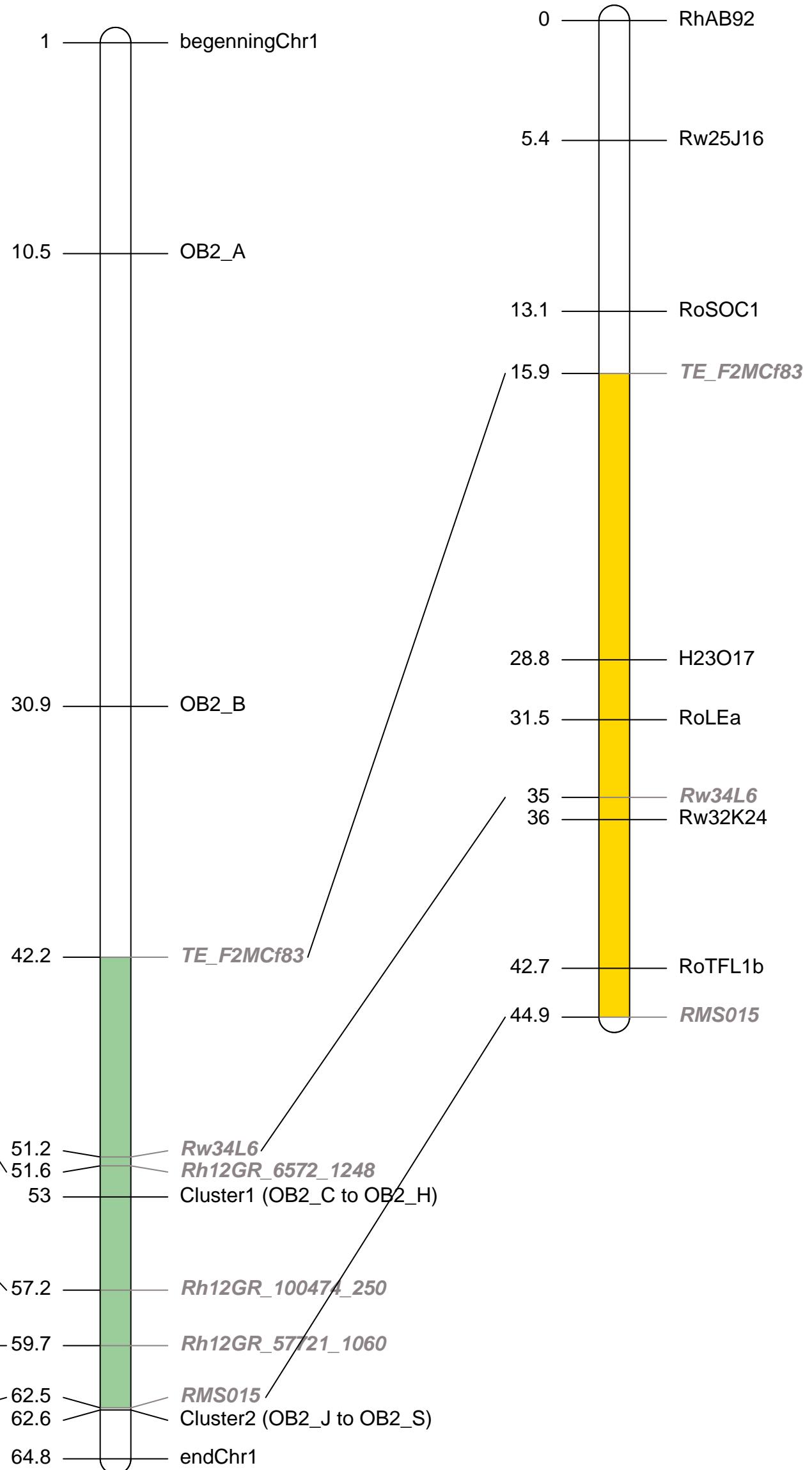
1182

1183

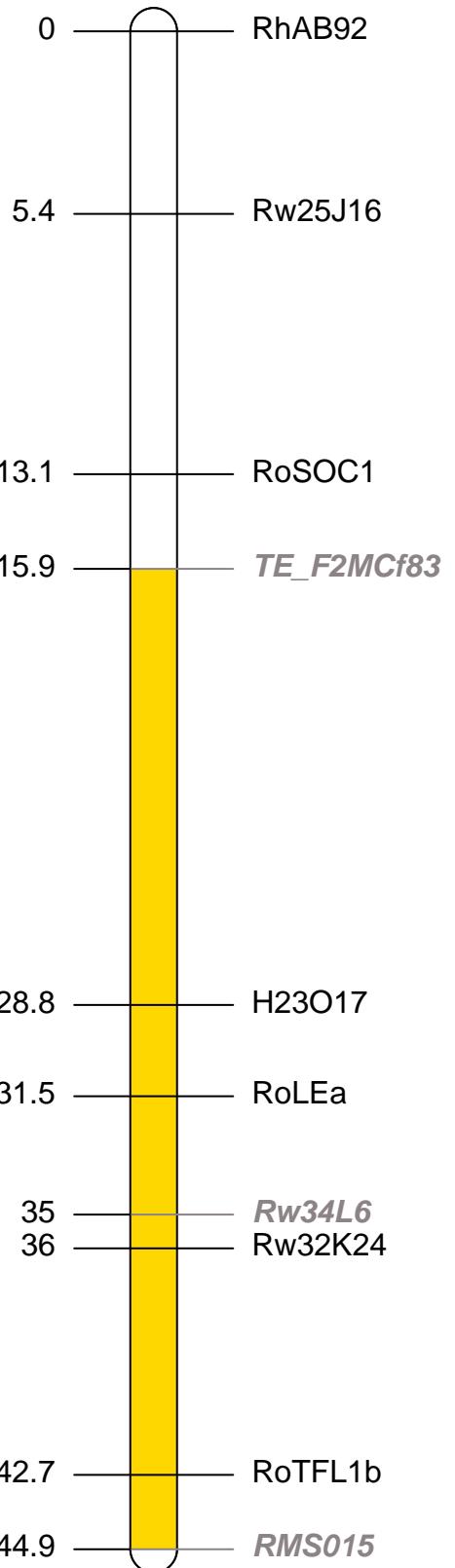
A1-OB



Chr1



A1-TF



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1192 **Material & correspondence**

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