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## Development of a high-density genetic linkage map and identification of quantitative trait loci (QTLs) associated with *Botrytis cinerea* resistance in strawberry (*Fragaria × ananassa* Duch.)

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**Abstract:** Over the centuries, strawberry fruit quality has greatly improved through various selection studies. The discovery of genes and genomic positions related to traits such as fruit quality and resistance to diseases and pests has been accelerated by new biotechnological methods. The objectives of this study are (i) to construct single nucleotide polymorphism (SNP) F<sub>1</sub> array-based high-throughput genetic linkage groups for the 'Fortuna × Rubygem' F<sub>1</sub> population, and (ii) to detect quantitative trait loci (QTL) regions associated with *Botrytis cinerea* resistance in leaf and fruit traits of strawberry. A total of 945 and 984 SNPs were mapped in the 'Fortuna' maternal and the 'Rubygem' paternal maps, respectively. The lengths of the linkage groups (LGs) and the average length of 'Fortuna' were calculated to be 1814 cM and 55.0 cM, respectively. The total length of 'Rubygem' was determined to be 2170 cM, with an average length of 65.7 cM. The average marker densities for the 'Fortuna' and 'Rubygem' linkages per cM were recorded as 0.58 and 0.53 markers, respectively. The 'Fortuna' female produced a mean of 28.64 markers per LG, while the 'Rubygem' male linkage groups had approximately 30 markers per LG. Five significant QTLs associated with resistance to *B. cinerea* in the leaves were identified in both parents. QTLs associated with resistance in strawberry fruits were found within a total of three LGs in different positions. The compressive genetic linkage maps developed in 'Fortuna × Rubygem' population can be used in genetic and QTL studies for important agronomical traits. The identified QTLs associated with *Botrytis cinerea* resistance may be preferred for use in future strawberry breeding programs to carry out marker-assisted selection.

**Key words:** Strawberry, *Botrytis cinerea*, quantitative trait loci (QTL), genetic mapping, *Fragaria × ananassa*

### 1. Introduction

Horticulture plants are highly diverse and have been recognized for their health benefits to humans. They contain a high concentration of nonnutritive, nutritive, and bioactive compounds, such as flavonoids, phenolics, anthocyanins, and phenolic acids, as well as nutritive compounds, such as sugars, essential oils, carotenoids, vitamins, and minerals. (Ercisli et al., 2010; Benjak et al., 2005; Celik et al., 2007; Erturk et al., 2012; Durul and Aktaş, 2023; Orman, 2023; Özkan, 2023; Wu et al., 2023).

Strawberry is one of the temperate climate fruit species with high adaptability and can be cultivated in

a wide ecological region from Ecuador to Siberia. It is one of 23 species in the Rosaceae family, which includes cherry, apple, and rose, and it belongs to the genus *Fragaria* (Shulaev et al., 2008). Commercially cultivated strawberries are octoploid (2n = 8x = 56), with a haploid chromosome number of n = 7 (Davis et al., 2007), and they constitute a significant portion of global production (Amil-Ruiz et al., 2011). The octoploid chromosomal scale reference genome of the Camarosa cultivar (*Fragaria × ananassa* Duchesne) has been released, with an estimated genome size of 813.4 Mb (Edger et al., 2019).

Strawberries are among the most important and highly nutritious fruits for human health due to their high

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content of vitamin C, minerals, folates, and antioxidants (Giampieri et al., 2014). Several studies have indicated that consuming strawberries offers numerous health benefits, such as preventing aging, Alzheimer's disease, obesity, and various heart and cancer-related diseases (Zhang et al., 2008; Silva et al., 2010).

Developing a high-throughput linkage map is crucial for detecting quantitative trait loci (QTLs) associated with agronomically important traits in strawberries. Over the last decade, the IStraw 90 K and IStraw35 384HT Axiom SNP arrays have been improved through the RosBREED project, supported by the cooperation of international researchers (Bassil et al., 2015; Verma et al., 2017; Karci et al., 2022). Thus, these arrays can facilitate the identification of the QTLs and provide high-quality genome scanning with reduced costs for octoploid strawberry breeding programs all over the world.

The primary objectives of plant breeding programs are the development of disease-resistant cultivars and the improvement of existing cultivars (Faedi et al., 2004). Diseases caused by pathogens, in particular, limit strawberry production and are a major challenge in strawberry breeding. Therefore, identifying promising cultivars with resistance to diseases has become a crucial goal in strawberry breeding programs due to the widespread negative effects of these diseases. There are numerous postharvest diseases, such as *B. cinerea*, *Penicillium* spp., *Mucor* spp., *Rhizopus stolonifer*, *Colletotrichum* spp., etc., which not only cause economic losses but also produce mycotoxins that can affect human health if consumed. In particular, *B. cinerea* can significantly reduce yield and postharvest quality in Türkiye and other strawberry growing regions worldwide (Braun and Sutton, 1987; Sutton, 1998). Strawberries may suffer mechanical damage during harvest and storage due to their soft flesh, which can also lead to rot afterward. This damage increases their susceptibility to postharvest diseases. Developing superior cultivars resistant to gray mold in strawberry breeding is a challenging process. To date, strong genetic sources with natural resistance have not been identified, and there are significant differences in disease resistance among strawberry cultivars and genotypes. Despite challenges arising from the complex genetic structure of the strawberry genome, significant progress has been made in QTL mapping in plants using DNA markers and advanced bioinformatic methods.

The developing of a genetic map is an initial step in separating whole subgenomes and performing marker-assisted breeding in *F. × ananassa*. In the last decade, the whole genome chromosomal sequences of diploid *F. vesca* were first released (Shulaev et al., 2011). A high-resolution genotyping based on SNP in *F. × ananassa*, IStraw90 Axiom array, was developed by Bassil et al.

(2015). The construction of high-resolution SNP linkage groups based on the Axiom array in the  $F_1$  strawberry populations included 6594 and 8407 SNPs in previous findings, respectively (Bassil et al., 2015; Sargent et al., 2015). Additionally, double digest restriction-associated DNA sequencing (ddRAD-seq) and diversity array (DART-seq) technologies have been performed for high-throughput linkage maps in strawberries (Davik et al., 2015; Sánchez-Sevilla et al., 2015). The publication of the *F. × ananassa* reference genome is highly valuable for the fast and more cost-effective identification of single nucleotide polymorphisms (SNPs) at the genome level in the development of high-density linkage maps (Hossain et al., 2019; Labadie et al., 2022). To date, QTLs with either minor or major effects on traits related to resistance to pathogens such as *Verticillium dahliae* (Antanaviciute et al., 2015), *Colletotrichum acutatum* (Salinas et al., 2019), and *Phytophthora cactorum* (Nellist et al., 2019) have been detected in strawberries.

The aims of the present research are as follows: (i) the development of high-resolution genetic linkage maps using SNP markers obtained from Fana array (Axiom), and (ii) the detection of QTLs associated with gray mold disease caused by *Botrytis cinerea* using the 'Fortuna × Rubygem'  $F_1$  population in strawberry.

## 2. Material and methods

### 2.1. Plant material and DNA extraction

Susceptibility across *B. cinerea* of *F. × ananassa* Duch. cultivars 'Fortuna' and 'Rubygem' was identified in the PRIMA Med-Berry project. In the current paper, the tolerant 'Fortuna' and sensitive 'Rubygem' strawberry cultivars were used as female and male parents, respectively, for the construction of the  $F_1$  population. Intraspecific  $F_1$  accessions were used in the current study for developing linkage maps and performing QTL analysis. The crosses between 'Fortuna' and 'Rubygem' ('Fortuna × Rubygem') were performed in 2019. The leaf samples from 164  $F_1$  hybrids were collected for DNA isolation from Yaltır Agricultural Products Inc. (Adana, Türkiye).

The genomic DNA samples were isolated using the CTAB (cetyltrimethylammonium bromide) method (Doyle and Doyle, 1987), with several minor modifications according to Kafkas et al. (2005). The quality of the genomic DNA samples was assessed using 0.8% agarose gel electrophoresis. DNA concentration was measured using both agarose gel electrophoresis and fluorometer (Qubit, Invitrogen).

### 2.2. Phenotyping of gray mold resistance

Phenotypic observations of *B. cinerea* in the 'Fortuna × Rubygem'  $F_1$  individuals and their parents were performed. These observations were carried out on the leaves and fruits of  $F_1$  strawberry progenies. The levels

of *B. cinerea* infection in the fruits and leaves of cultivars were determined, and *B. cinerea* was cultured following the methods described by Siedliska et al. (2018). Both trials for *B. cinerea* resistance on leaves (BC\_L) and fruits (BC\_F) in the 'Fortuna × Rubygem' F<sub>1</sub> strawberry population were evaluated for each individual. Histograms depicting the frequencies of leaf and fruit measurements were created to illustrate the distribution of these traits.

### 2.3. SNP genotyping with Fana Axiom array

An intraspecies linkage map of 'Fortuna × Rubygem' F<sub>1</sub> population was created using the Fana Axiom array, which is composed of 49,483 Affymetrix SNP markers, including 5919 markers from the previous 35K SNP diploid *F. vesca* array and 43,664 from the 90K SNP octoploid array (cultivar Camarosa). Variant calling was conducted using the Affymetrix Power Tools (APT) software. SNP classification was divided into six categories using the default parameters of the APT software, as described by Nagano et al. (2017).

### 2.4. Development of genetic linkage maps

The genetic maps of the 'Fortuna × Rubygem' F<sub>1</sub> strawberry population were created using multilocus ordering algorithm in the MultiPoint program (Mester et al., 2003). The poly high-resolution SNPs (PHR-SNPs) for each linkage were organized into multiple linkage groups (LGs) using the color map method (Kiss et al., 1998). This method involved comparing graphical genotypes derived from segregation data. During the mapping of the color process, reciprocal genotypes were transformed into coupling genotypes. The reliability of all LGs was confirmed using the logarithm of odds (LOD) threshold of 2.0 with the Grouping Module of MultiPoint 3.3 (MultiQTL Ltd, Haifa, Israel). The frequencies of recombination distances in the linkage were expressed in centimorgans (cM). We employed the Kosambi mapping function (Kosambi, 2016) and a regression mapping algorithm for the development of the map. The final visualization of these linkage groups was created using MapChart v2.2 on the Windows platform (Voorrips, 2002). In the segregation description, if both parents were heterozygous (hk × hk), the markers were referred to as 'common.' If one parent was heterozygous (nn × np (male) and lm × ll (female)), the markers were termed as 'parental.'

### 2.5. QTL analysis

A general interval mapping approach was used to identify QTL through a comprehensive genome-wide scan (Korol et al., 1998). A mixture-model strategy was employed using MultiQTL software with ML algorithms (Korol et al., 2001). Initially, a single-QTL model was established and evaluated for significance for each combination of trait and chromosome. Subsequently, the significance of all effects was evaluated by considering the false discovery rate to

control for experimental-wise significance (Benjamini and Hochberg, 1995). The identified QTL effects were denoted according to the nomenclature outlined by McIntosh et al. (2001). It is worth noting that, in several instances, a notable colocalization of QTL was observed for different traits, indicating potential pleiotropic effects of the corresponding QTL or tight linkage among multiple QTL. These situations were challenging to resolve due to the number of samples used in the current study (n = 164).

## 3. Results

### 3.1. Development of a high-density genetic linkage map

A total of 49,483 SNPs based on the Fana Axiom array were categorized with six classifications: polymorphic or nonpolymorphic natures in accessions. Specifically, 28,697 SNPs (58.0%) were classified as poly high resolution (PHR, codominant segregation), 12,949 SNPs (26.2%) as no minor homozygote (NMH, dominant segregation), 5586 SNPs (11.3%) as mono high resolution (MHR) (AA or BB), 469 SNPs (0.9%) as off-target variant (OTV), 671 SNPs (1.4%) as call rate below threshold (CRBT), and 1111 SNPs (2.2%) as others (Table 1). After filtering according to MAF < 0.05, missing data > 5%, and SNPs of replicates of the parents, 24,415 PHR-SNPs, 3419 NMH-SNPs, and 233 MHR loci were mapped onto 33 LGs (Tables 1 and 2).

Finally, 1946 SNP markers were used to map 33 linkage groups, with a length of 1814 cM in the 'Fortuna' map and 2170 cM in the 'Rubygem' map, integrated with Fana Axiom array (Table 2; Figure 1). In 'Fortuna,' a total of 681 common (hk × hk, 1:2:1) and 270 parental (lm × ll, 1:1) markers were identified, accounting for 71.61% and 28.39%, respectively. The lengths of the linkage groups varied, ranging from 3.4 cM (LG32) to 116.8 cM (LG9), with an average length of 55.0 cM. The map resolution was characterized by an average marker density of one marker every 0.59 cM, with the longest marker interval observed in LG22, which was 3.36 cM. In 'Rubygem,' 691 common (hk × hk, 1:2:1) and 304 parental (nn × np, 1:1) markers were recorded, accounting for 69.45% and 30.55%, respectively. The shortest linkage group was calculated as 12.1 cM in LG14, while the longest was detected as 199.1 cM in LG9. The average marker density of 'Rubygem' map was 0.54 cM, and the average marker distance was found to be 2.19 markers per cM. Details of the linkage group-wise markers, marker densities, and genetic distances for the 'Fortuna × Rubygem' F<sub>1</sub> population were provided in Table 1, and the SNP positions and their linkage groups were presented in Supplementary Table S1.

### 3.2. Phenotyping of the traits and QTL mapping

The phenotypic parameters assessed in the F<sub>1</sub> population showed variations among plants; BC\_L and BC\_F were observed in both the 2021 and 2022 growing seasons. The frequency distribution for *B. cinerea* resistance showed

**Table 1.** Classification of detected SNPs.

Classes	Number of raw SNPs	Ratio (%)	Number of mapped SNPs	Mapped ratio (%)
PHR	28,697	58.0	24,415	49.3
NMH	12,949	26.2	3419	6.9
MHR	5586	11.3	233	0.5
OTV	469	0.9	-	-
CRBT	671	1.4	-	-
Other	1111	2.2	-	-
<b>Total</b>	<b>49,483</b>	<b>100</b>	<b>28,067</b>	<b>56.7</b>

MHR: mono high resolution; CRBT: call rate below threshold; NMH: no minor homozygote; OTV: off-target variant; PHR: poly high resolution (PHR).

Most of the used SNPs were derived from PHR.

**Table 2.** Linkage group lengths, number of mapped markers, marker density (markers per cM), and average distance between markers in the 'Fortuna' and 'Rubygem' maps.

LGs	Fortuna				Rubygem			
	LG Lengths (cM)	Number of mapped markers	Marker density (marker/cM)	Average marker distance (cM/marker)	LG Lengths (cM)	Number of mapped markers	Marker density (marker/cM)	Average marker distance (cM/marker)
1	38.9	17	0.44	2.29	52.2	25	0.48	2.09
2	48.8	34	0.70	1.44	28.8	24	0.83	1.20
3	107.4	49	0.46	2.19	98.0	51	0.52	1.92
4	106.1	65	0.61	1.63	86.2	55	0.64	1.57
5	106.3	42	0.40	2.53	147.8	48	0.32	3.08
6	54.5	35	0.64	1.56	43.1	18	0.42	2.39
7	15.4	7	0.45	2.20	30.0	18	0.60	1.67
8	84.0	32	0.38	2.63	69.0	29	0.42	2.38
9	116.8	64	0.55	1.83	199.1	43	0.22	4.63
10	64.4	29	0.45	2.22	25.7	18	0.70	1.43
11	104.9	48	0.46	2.19	149.3	25	0.17	5.97
12	79.5	35	0.44	2.27	76.3	17	0.22	4.49
13	54.0	37	0.69	1.46	81.1	34	0.42	2.39
14	16.5	12	0.73	1.38	12.1	9	0.74	1.34
15	22.9	17	0.74	1.35	17.4	15	0.86	1.16
16	44.1	30	0.68	1.47	110.7	53	0.48	2.09
18	71.5	34	0.48	2.10	61.4	22	0.36	2.79
19	19.8	6	0.30	3.30	84.8	21	0.25	4.04
20	86.3	43	0.50	2.01	91.9	52	0.57	1.77
21	23.8	10	0.42	2.38	30.0	16	0.53	1.88
22	23.5	7	0.30	3.36	27.4	17	0.62	1.61
24	48.7	32	0.66	1.52	71.9	40	0.56	1.80
25	89.0	27	0.30	3.30	79.7	33	0.41	2.42
26	90.9	57	0.63	1.59	91.3	60	0.66	1.52
27	90.8	37	0.41	2.45	88.6	52	0.59	1.70
28	46.3	20	0.43	2.32	42.3	18	0.43	2.35
29	19.7	17	0.86	1.16	27.1	18	0.66	1.51
30	31.5	26	0.83	1.21	47.6	36	0.76	1.32



Table 2. (Continued.)

31	17.3	15	0.87	1.15	74.6	39	0.52	1.91
32	3.4	4	1.18	0.85	23.4	18	0.77	1.30
33	36.2	24	0.66	1.51	36.7	27	0.74	1.36
39	8.1	8	0.99	1.01	18.9	11	0.58	1.72
40	42.7	31	0.73	1.38	45.3	33	0.73	1.37
Total	1814	951			2170	995		
Mean	55.0	28.82	0.59	1.92	65.7	30.15	0.54	2.19

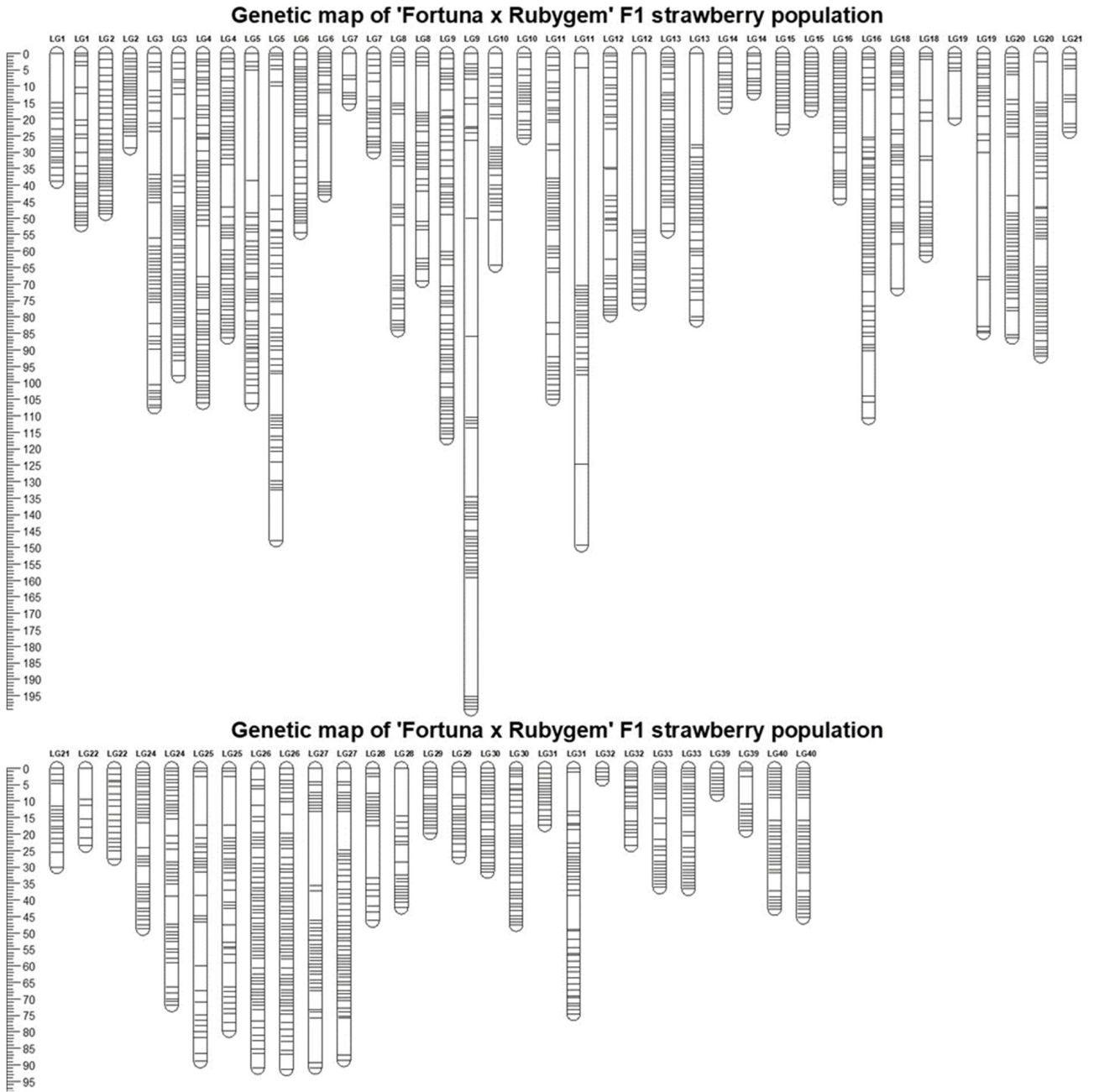
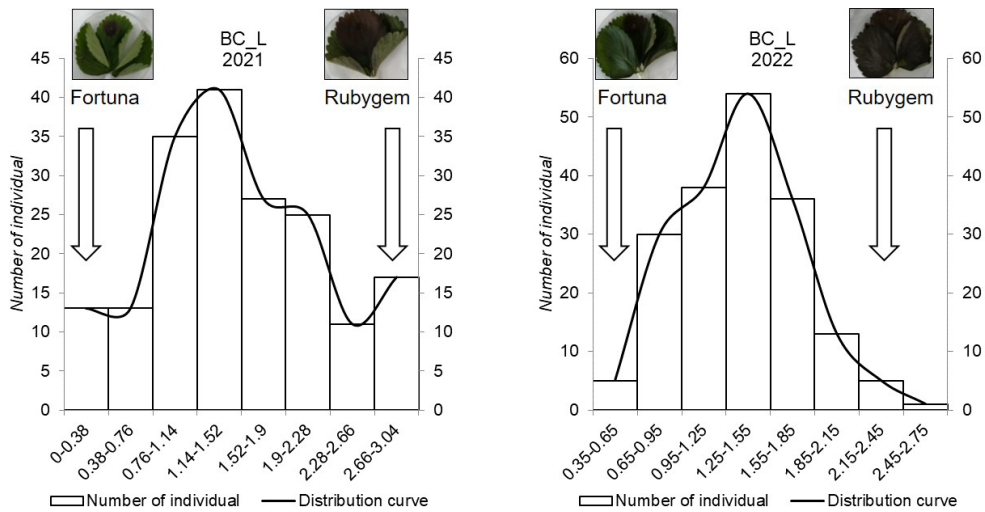


Figure 1. SNP-based linkage map of the *F. × ananassa* mapping population derived from the 'Fortuna × Rubygem' F1 strawberry population.

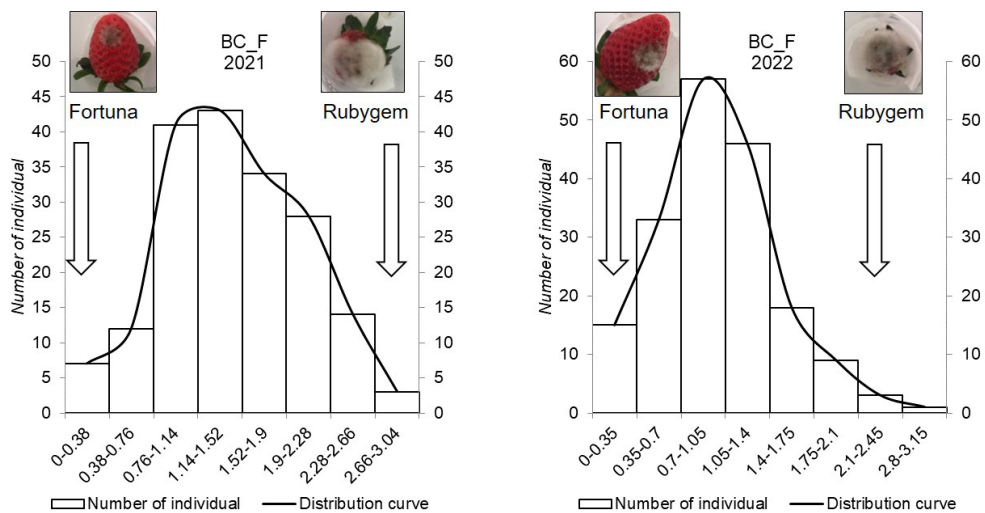
the expected normal distribution among plants. The resistant ‘Fortuna’ and susceptible ‘Rubygem’ parents exhibited extreme responses to *Bortytis* in trials on both leaves and fruits, resulting in a wide range of variation within the population. The distribution histograms and curves showing the range of resistance degrees in *B. cinerea* parents are provided in Figures 2 and 3.

We identified three significant QTLs located in ‘Fortuna’ and five QTL regions and associated loci on linkage groups in LG6, LG16, and LG33 related to the *B. cinerea* resistance on leaves (BC\_L), using F<sub>1</sub> population derived from crossing ‘Fortuna × Rubygem’ (Table 3; Figure 4). In ‘Fortuna,’ the significant linked loci in LG6, LG16, and LG33 were

determined as Ax-184251409, Ax-123614760, and Ax-166505239 at 25.31, 36.65, and 0.00 cM, respectively. These markers were found to correspond to the chr4D, chr6, and chr3 in the strawberry genomes. Although the loci Ax-184251409, Ax-123614760, and Ax-166505239 were identified in both the ‘Fortuna’ and ‘Rubygem’ maps, the loci Ax-184297806 and Ax-184047067 were only found in ‘Rubygem’ at 72.36 and 25.53 cM, respectively (Table 3). The highest associated loci (Ax-184047067) on LG16, with the highest LOD score of 2.90 ( $p < 0.005$ ), was calculated and explained the highest proportion (9.80%) of phenotypic variation ( $r^2$ ) among the identified QTLs. The determined QTL region was detected between the flanking markers Ax-184033341 and Ax-184231551



**Figure 2.** Frequency distribution of score of resistance to *B. cinerea* in strawberry leaves in the Fortuna maternal and Rubygem paternal and their progenies.

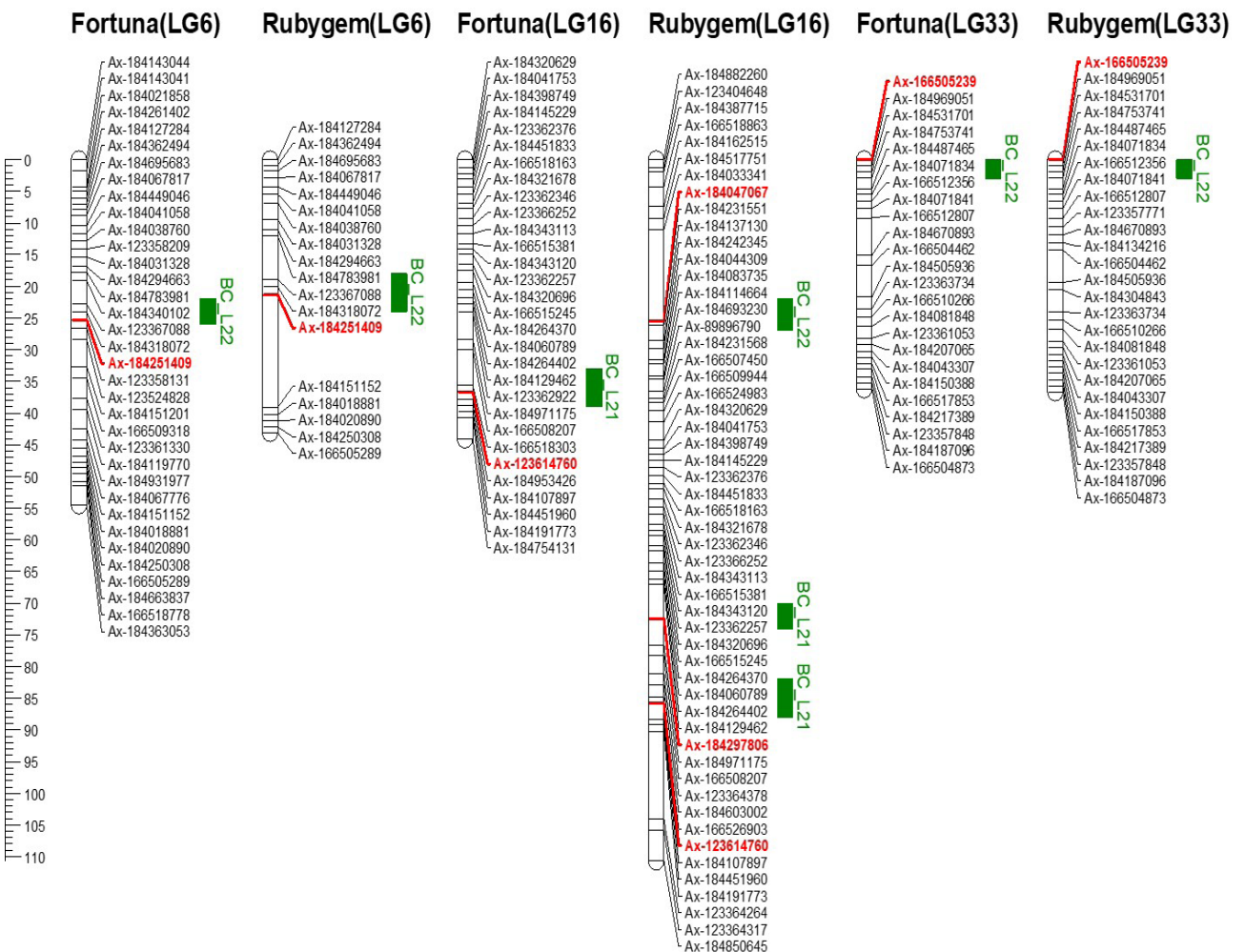


**Figure 3.** Frequency distribution of score of resistance to *B. cinerea* in strawberry fruits in the Fortuna maternal and Rubygem paternal and their progenies.



**Table 3.** Marker positions, panels, corresponding chromosomes (Chrs), LOD score, phenotypic variance (PV%), segregations, and significance of markers linked to resistance to *B. cinerea* in strawberry leaves (BC\_L) from the ‘Fortuna × Rubygem’ population.

Fortuna											
Trait	Years	LGs	Position (cM)	Panels	Chrs	Physical position (Mb)	LOD	PV%	Linked loci	Segregation	Significance (p)
Resistance to <i>Botrytis cinerea</i> on leaf (BC_L)	2021	16	36.65	iStraw35	6	5808306	1.70	5.10	Ax-123614760	hk × hk	0.006
	2022	33	0.00	iStraw35	3	25825109	2.20	5.70	Ax-166505239	hk × hk	0.009
	2022	6	25.31	Fana_Array	4D	9740764	2.10	5.90	Ax-184251409	hk × hk	0.005
Rubygem											
Trait	Years	LGs	Position (cM)	Panels	Chrs	Physical position (Mb)	LOD	PV%	Linked loci	Segregation	Significance (p)
Resistance to <i>Botrytis cinerea</i> on leaf (BC_L)	2021	16	72.36	Fana_Array	6A	26330375	2.20	7.00	Ax-184297806	nn × np	0.018
	2021	16	85.84	iStraw35	6	5808306	1.70	5.10	Ax-123614760	hk × hk	0.006
	2022	33	0.00	iStraw35	3	25825109	2.20	5.70	Ax-166505239	hk × hk	0.009
	2022	6	21.38	Fana_Array	4D	9740764	2.10	5.90	Ax-184251409	hk × hk	0.005
	2022	16	25.53	Fana_Array	6A	13163884	2.90	9.80	Ax-184047067	nn × np	0.005



**Figure 4.** QTL regions associated with resistance to *B. cinerea* in strawberry leaves.

(11.00–26.10 cM) on linkage group 16 of the ‘Rubygem’ map. The range of the flanking markers for this QTL was identified on the chr6 within the 13 Mb physical position of the first subgenome in the strawberry genome.

The significant loci associated with resistance to *B. cinerea* in fruits of the ‘Fortuna × Rubygem’ F<sub>1</sub> strawberry population were identified over two consecutive years. The linked loci were found in LG5, LG20, and LG28 in ‘Fortuna,’ while associated loci were identified in LG20 in ‘Rubygem’ (Table 4; Figure 5). In ‘Fortuna,’ the significantly linked loci in LG5, LG20, and LG28 were Ax-184547649, Ax-123360550, and Ax-184191302, located at 103.21, 49.39, and 37.01 cM, respectively. The alignment of these markers corresponded to the chr3A, chr2, and chr6B in strawberry genomes, respectively. The locus associated with Ax-123360550 was found in LG20 on both maps within the chr2 iStraw35 genome. In ‘Rubygem,’ a total of two QTL regions were identified in LG20, with Ax-184051916, and Ax-123360550 located at 47.21 and 50.76 cM, corresponding to chr2D and chr2, respectively. The range of the flanking markers on LG20 and the identified locus in both parents (Ax-123360550) were found within the chr2 iStraw35 genome on three Mb physical positions (Table 4; Figure 5). Additionally, the investigation of the regions controlling resistance to *B. cinerea* demonstrated that the ‘Fortuna’ and ‘Rubygem’ parents have distinct resistance mechanisms due to their extreme responses to *B. cinerea*, with ‘Fortuna’ being tolerant and ‘Rubygem’ sensitive. When compared to the ‘Rubygem’ map, the QTL intervals on LG5 and LG28, which correspond to chr3A and chr6B in ‘Fortuna,’ might be influenced by *B. cinerea*.

The detected loci associated with BC\_L and BC\_F were annotated to the latest versions of the *F. × ananassa* and *F. vesca* strawberry genomes using an updated gene information file. Although the markers were not classified as nonsynonymous or synonymous due to incomplete gene

information (gff), the marker/genes associated with genomic regions from strawberry genomes were obtained from the Genome Database for Rosaceae (GDR). The Ax-184251409 marker linked to BC\_L was located on the subgenome of chr4 and was found to control the *FxaC\_14g19050* gene. The other linked marker, Ax-184297806, was identified in the first subgenome of the chr6 within the *FxaC\_21g50810* gene, which is responsible for BC\_L. Ax-184297806 marker located gene plays a role in the synthesis cellular component related to nuclear factor kappa-B-binding protein (IPR024867). The markers linked to BC\_F, such as Ax-184051916 and Ax-184191302, were detected on the last subgenome of the chr2 and the second subgenome of the chr6, respectively. These markers were identified within the *FxaC\_6g23420* and *FxaC\_23g50910* corresponding genes (Supplementary Table S2).

**3.3. Distribution of SNPs to Fana array**

In total, 33 LGs were distributed to seven HGs according to the combined *F. vesca* and *F. × ananassa* genome, Fana Axiom array. The number of linkage groups overlapping with HGs was detailed for both parents. Three of the seven HGs (HG1, HG3, HG7) consisted of four LGs; the other three HGs (HG2, HG4, HG5) were matched with five LGs; and the remaining HG, HG6, comprised six LGs in both the ‘Fortuna’ and ‘Rubygem’ maps. The highest level of synteny was found in subgenome II (SGII) and a total 274 SNPs was mapped to *F. vesca* genome, in ‘Fortuna’ map. In ‘Rubygem,’ the highest collinearity was observed in SGI and SGII, with a total of 184 and 180 SNPs, respectively. Additionally, a total of 837 PHR, 64 NMH, and 2 OTV markers in ‘Fortuna,’ and 857 PHR, 92 NMH, and 2 OTV markers in ‘Rubygem’ were successfully mapped (Table 5). Detailed information about the comparative analysis of homoeologous linkage groups across *F. vesca* and Fana array was presented in Supplementary Table S3.

**Table 4.** Marker positions, panels, corresponding chromosomes (Chrs), LOD score, phenotypic variance (PV%), segregations, and significance of markers linked to resistance to *B. cinerea* in strawberry fruits (BC\_F) from the ‘Fortuna × Rubygem’ population.

<b>Fortuna</b>												
Trait	Year	LGs	Position (cM)	Panels	Chrs	Physical position (Mb)	LOD	PV%	Linked loci	Segregation	Significance (p)	
<i>Botrytis cinerea</i> on fruit (BC_F)	2022	5	103.21	Fana_Array	3A	26978746	3.30	9.10	Ax-184547649	lm × ll	0.003	
	2022	20	49.39	iStraw35	2	3189628	2.50	7.60	Ax-123360550	hk × hk	0.002	
	2022	28	37.01	Fana_Array	6B	30561696	2.40	6.70	Ax-184191302	lm × ll	0.002	
<b>Rubygem</b>												
Trait	Year	LGs	Position (cM)	Panels	Chrs	Physical position (Mb)	LOD	PV%	Linked loci	Segregation	Significance (p)	
<i>Botrytis cinerea</i> on fruit (BC_F)	2022	20	47.21	Fana_Array	2D	14876565	3.83	10.90	Ax-184051916	nn × np	<0.001	
	2022	20	50.76	iStraw35	2	3189628	2.50	7.60	Ax-123360550	hk × hk	0.002	

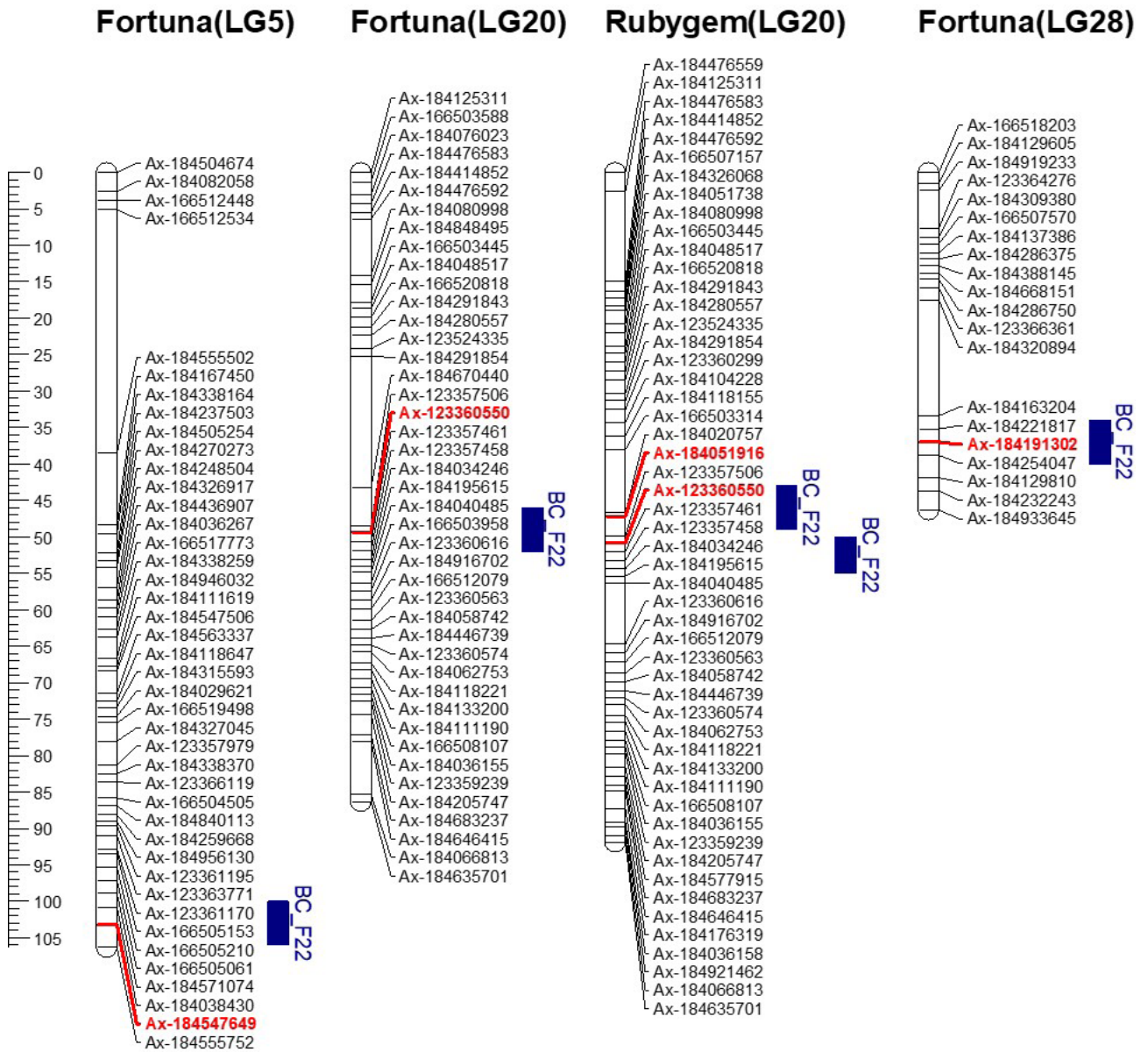


Figure 5. QTL intervals associated with resistance to *B. cinerea* in strawberry fruits.

Table 5. Number of markers in HGs mapped to subgenomes (SGI, SGII, SGIII, SGIV) using *F. vesca* and Fana array with PHR, NMH, and OTV classifications.

Fortuna		Number of markers					Total map length (cM)	Mean map length (cM)	Number of markers		
HG	Number of LGs	<i>F. × ananassa</i>				<i>F. vesca</i>			PHR	NMH	OTV
		SGI	SGII	SGIII	SGIV						
1	4	5	43	17	14	28	198.38	1.74	97	10	1
2	5	33	24	27	21	49	327.92	2.10	149	8	-
3	4	28	36	4	32	45	291.23	1.79	138	8	-
4	5	24	20	24	6	27	250.91	2.30	99	2	-
5	5	17	20	24	24	45	252.68	1.83	119	10	1

Table 5. (Continued.)

6	6	27	21	28	21	50	270.22	1.79	138	10	-
7	4	29	14	11	27	30	222.30	1.83	95	16	-
<b>Total</b>	33	163	178	135	145	274	1813.64	13.38	835	64	2
<b>Rubygem</b>											
HG	Number of LGs	Number of markers					Total map length (cM)	Mean map length (cM)	Number of markers		
		<i>F. × ananassa</i>		<i>F. vesca</i>					PHR	NMH	OTV
		SGI	SGII	SGIII	SGIV						
1	4	7	44	23	15	35	257.02	1.97	111	13	-
2	5	43	28	34	27	54	335.52	1.77	167	20	-
3	4	34	40	5	28	46	315.96	1.93	144	11	-
4	5	15	25	17	18	29	240.70	2.20	97	8	-
5	5	19	15	18	23	41	311.92	2.53	105	10	1
6	6	40	21	18	26	48	414.95	2.45	140	20	1
7	4	26	7	20	20	30	293.04	2.61	93	10	-
<b>Total</b>	33	184	180	135	157	283	2169.11	15.46	857	92	2

#### 4. Discussion

In the current study, 28,067 out of 49,483 SNP loci were mapped to the reference genome. After applying several filtering parameters, a total of 33 linkage groups with 1946 SNPs were observed in ‘Fortuna × Rubygem’  $F_1$  strawberry population. The lengths of both maps in this population were calculated to be 1814 and 2170 cM, respectively. Several previous studies have revealed that the lengths of linkage maps and the number of mapped loci vary among different strawberry species based on the sequencing platforms used (Bassil et al., 2015; Mahoney et al., 2016; Hossain et al., 2019). The distance of the locus per cM in SNP-based linkage maps was calculated to be 0.91 in diploid *F. vesca*. Although the average marker distance was detected as 2.43 and 2.71 cM/marker in *F. vesca* ssp. *bracteata* (Tenessen et al., 2014), this value was identified as 0.91 cM/marker in ancestral *F. iinumae* (Mahoney et al., 2016). Recently, Hossain et al. (2019) published a high-resolution genetic map developed using ddRAD-seq SNPs in *F. × ananassa*, revealing that the average marker distance was 2.22 cM/marker. The researchers also addressed the marker density as 0.50, while the marker density in the current study was found to be 0.58 and 0.53 in the maternal and parental maps, respectively. Additionally, the average marker distances were identified as 1.92 cM/marker for the ‘Fortuna’ map and 2.19 cM/marker for the ‘Rubygem’ map in this study. In total, 31 linkage groups were created using the S1 population of octoploid strawberries for the separation of loci-specific subgenomes of *F. × ananassa* and the development of a linkage map (Nagano et al., 2017). The total length of the ‘Reikou’ linkage map in the S1 population was determined to be 2,816 cM. Previous studies by Bassil et al. (2015) and Sargent et al. (2015) reported shorter maps compared to

the S1 population derived from ‘Reikou’ cultivar. Nagano et al. (2017) mapped a total of 8588 SNPs distributed among subgenomes. These mapped SNP loci were found to be higher than in the previous linkage mapping studies due to the larger number of mapped SNP loci. Specifically, Bassil et al. (2015), Sargent et al. (2015), and Hossain et al. (2019) mapped 6593, 8407, and 1268 SNPs, respectively. The sequencing platform and calling errors affect the number of loci and the total lengths of LGs depending on the genetic variation between parents. The high-density linkage map, which is well-covered with subgenomes and includes accurately called variants, increases the chances of detecting loci associated with traits in QTL analysis.

The distinct findings in developing the genetic mapping in *F. × ananassa* observed variations in the number of LGs and lengths (Bassil et al., 2015; Sargent et al., 2015; Davik et al., 2015; Nagano et al., 2017). In previous studies, the number of linkage groups was calculated to be more than the seven homoeologous groups with four subgenomes, similar to the findings in the current report. Generally, polymorphic loci were expected to segregate into distinct genotypes based on their subgenome specificity. If variations in linkage groups and lengths are observed in genetic maps, there are possible reasons for this situation. First, the Axiom array system sometimes misclassified nonspecific loci, and biparental linkage maps were developed using the Axiom array in octoploid *F. × ananassa* (Davik et al., 2015; Nagano et al., 2017). Consequently, the linked loci were spread across the linkage map without clear differentiation from nonspecific loci. The researchers stated that the linkage groups with Axiom array might have been missed from the linkage map due to the monomorphic structure among subgenomes, and that discrepancies with the *F. vesca* genome could be



attributed to assembly errors or incompleteness. Overall, the studies concluded that subgenome-specific sequences were randomly distributed across the *F. × ananassa* genome, with notable differences among the subgenomes in the number of LGs and their lengths (Bassil et al., 2015; Sargent et al., 2015; Davik et al., 2015; Nagano et al., 2017).

Similar results were observed in the current paper compared to the expected outcomes. However, this report utilized a more comprehensive version of the *F. × ananassa* octoploid strawberry genome cultivar 'Camarosa,' published by Edger et al. (2019), which includes homoeologous chromosomes and subgenomes. The complex genome structure of strawberry, including its octoploid ploidy and the genome of *F. × ananassa*, has been published recently. It has become clear that many genomic processes still need to be explored in future research. This study illustrates the constraints faced in performing genome and functional annotations of the linked loci. As mentioned in the previous section, addressing major challenges such as population structure with genomic inheritance, applied sequencing platforms, errors during assembly, and incomplete subgenomic fragments should be priority research areas in strawberry breeding studies.

*B. cinerea* is difficult to control with various fungicides because it is an airborne pathogen active throughout the year. Furthermore, the host-pathogen relationships are complex, and these pathogens rapidly develop resistance mechanisms to fungicides due to the repeated application of certain chemicals (Williamson et al., 2007; Cosseboom et al., 2019; Zhang et al., 2019; Caseys et al., 2021). Early diagnosis of fungal contamination in strawberries is crucial, as it directly affects producers and consumers through its effects on storage, transportation, and marketing, and product safety (Siedliska et al., 2018). The resistance mechanisms of *B. cinerea* are quantitative (Finkers et al., 2007; Williamson et al., 2007; Seijo et al., 2008; Petrasch et al., 2019; Caseys et al., 2021). Identifying the genes responsible for resistance to complex diseases, such as *B. cinerea*, is a lengthy process due to the complex genomic structures of necrotrophic pathogens such as *B. cinerea* and the wide genetic variation in resistance or susceptibility to diseases among strawberry cultivars and genotypes. To address this challenge, a report on the genome-wide resistance to gray mold in strawberries was performed by Petrasch et al. (2022). They identified the QTLs associated with gray mold in five full-sibling families using the 50 K Axiom SNP array developed by Hardigan et al. (2020). A total of nine QTLs were detected in various populations, with the highest significance based on LOD scores. These QTLs were distributed across pseudochromosomes 3, 4, 5, and 7 within different subgenomes. Given that these identified QTLs were characterized as minor and exhibited small effects, it suggests that the genes responsible for

gray mold susceptibility may be controlled by polygenes. On the other hand, a biparental population derived from the tolerant 'Fortuna' and sensitive 'Rubygem' cultivars exhibited a wide range of polymorphism for *B. cinerea* in this study. In the more southern regions, the strawberry cultivar 'Fortuna,' which was improved in California, has been introduced into both public and private breeding programs in Florida (Mezzetti et al., 2018). However, 'Fortuna' and 'Rubygem' were not challenging enough to pose a serious problem for *B. cinerea*, and there has been no comprehensive study on *B. cinerea* in the literature (Herrington et al., 2007). In the current report, the response of 'Fortuna' and 'Rubygem' cultivars to *B. cinerea* infection in leaves and fruits was identified, along with putative genomic regions and QTLs, in an  $F_1$  population for the first time. Additionally, the commercial strawberry cultivars 'Fortuna' and 'Rubygem' were recorded as resistant and sensitive to *B. cinerea* for the first time thanks to the present project. The candidate-associated loci for *B. cinerea*, using the genetic variability of the parents, were identified in distinct LGs corresponding to different nonspecific and subgenome-specific regions. On the other hand, QTLs in 'Fortuna' linked by *B. cinerea* on fruits have two additional distinct locations that overlap with chr3A and chr6B homoeologous. However, the common responsible interval in LG20, which is collinear with chr2 and its subgenome, was detected in both maps. Thus, we hypothesized that the transfer of *B. cinerea*-controlling genes or genomic fragments from parents to  $F_1$  plants during meiosis, in crosses related to resistance, was predominantly inherited from the 'Fortuna' parent.

SNP markers within the genes associated with resistance to *B. cinerea cinerea* can affect phenotypes directly or indirectly. Nonsynonymous SNPs (nsSNPs) result in a change in the amino acid sequence of the protein encoded by the gene. These variations can contribute to phenotypic diversity and influence plant traits within QTL regions (Wang et al., 2017; Rifat et al., 2022). Synonymous SNPs (sSNPs) do not change the amino acid sequence of the encoded protein due to the degeneracy of the genetic code. However, sSNPs can still affect QTL and plant traits through regulatory regions, RNA stability, splicing, and linked variations. sSNPs can occur within regulatory regions of a gene, such as promoter or enhancer regions (PS et al., 2017; Karıcı, 2023). To describe SNPs according to their positions, the genome annotations for the highest correlated markers associated with gray mold were performed using *F. × ananassa* transcriptome genome database. While only a few markers could be defined, most of them were not detected through gene ontology and biochemical compound analyses. In addition, reports on similar topics in the literature have not classified SNPs according to genome annotation results, such as exonic,

intronic, intergenic, etc. (Davik et al., 2015; Nagano et al., 2017; Hossain et al., 2019). The potential causes of this annotation issue were investigated, including the possibility that the subgenome-specific transcriptome sequences were incomplete or that the .gff file had been rearranged during the research on the complete genic information in strawberries.

In plants, the probability of selecting superior genotypes in terms of features such as disease resistance, which involve complex genetic mechanisms, is relatively low. Genetic linkage mapping and QTL studies associated with key traits provide valuable genetic information for understanding complex traits, such as resistance to *B. cinerea*. Therefore, developing candidate markers associated with these traits, understanding the genetic mechanisms, and identifying the genomic positions of such complex traits will provide valuable information for breeders and geneticists to accelerate progress in strawberry breeding programs (Kim et al., 2014). The investigations aimed to control pre- and postharvest processes by combining the classical and modern breeding approaches, thereby saving time and labor from field to market and reducing significant product loss due to *B. cinerea*.

## 5. Conclusion

This study is one of the first QTL studies conducted using a high-density genetic map to investigate resistance

to *B. cinerea* using the F<sub>1</sub> population derived from the crossbreeding of 'Fortuna' and 'Rubygem' strawberry cultivars. In terms of resistance to *B. cinerea*, after inoculations and assessments performed on leaves and fruits in 2021 and 2022, linked loci in different LGs were identified in the 'Fortuna' and 'Rubygem' maps. The obtained data will be valuable for understanding the resistance mechanism of *B. cinerea* and will support breeding programs that enable marker-assisted selection in strawberries.

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## Conflict of interest

The authors declare that they have no conflict of interest.

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**Supplementary Table S1.** SNP positions and their linkage groups in the Fortuna and Rubygem maps.

<b>Fortuna (LG1)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	<b>Rubygem (LG1)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184066134	0.00	hk × hk	Ax-184097055	0.00	nn × np
Ax-184520797	15.05	hk × hk	Ax-184348673	0.61	nn × np
Ax-184040107	16.59	hk × hk	Ax-123366843	2.45	nn × np
Ax-184962606	18.00	lm × ll	Ax-184066134	3.79	hk × hk
Ax-184553826	19.85	lm × ll	Ax-184597978	10.41	nn × np
Ax-184862772	23.08	hk × hk	Ax-184465269	12.24	nn × np
Ax-184369318	25.23	hk × hk	Ax-184520797	20.20	hk × hk
Ax-184024948	26.15	hk × hk	Ax-184040107	21.74	hk × hk
Ax-123356937	27.21	lm × ll	Ax-184085497	24.60	nn × np
Ax-184520776	28.61	hk × hk	Ax-184862772	25.68	hk × hk
Ax-184246091	29.53	hk × hk	Ax-184301543	30.16	hk × hk
Ax-166510687	31.38	hk × hk	Ax-184930078	34.28	nn × np
Ax-123360076	32.30	hk × hk	Ax-166520237	36.46	hk × hk
Ax-184894660	33.22	hk × hk	Ax-184193966	39.24	hk × hk
Ax-184085471	34.65	lm × ll	Ax-184604639	40.15	hk × hk
Ax-166510731	37.09	lm × ll	Ax-123361820	41.07	hk × hk
Ax-184110000	38.92	lm × ll	Ax-184369318	42.61	hk × hk
<b>Fortuna (LG2)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184024948	43.53	hk × hk
Ax-166520479	0.00	lm × ll	Ax-184520776	45.39	hk × hk
Ax-184852772	1.86	lm × ll	Ax-184246091	46.31	hk × hk
Ax-184380313	4.35	lm × ll	Ax-166510687	48.16	hk × hk
Ax-166509495	6.79	lm × ll	Ax-123360076	49.08	hk × hk
Ax-184485232	8.62	lm × ll	Ax-184894660	50.00	hk × hk
Ax-123367440	11.06	lm × ll	Ax-184117015	50.92	hk × hk
Ax-184465000	12.89	lm × ll	Ax-184561649	52.15	hk × hk
Ax-184124530	14.73	lm × ll	<b>Rubygem (LG2)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184290760	16.59	lm × ll	Ax-123360030	0.00	hk × hk
Ax-123356945	18.44	lm × ll	Ax-184058266	1.54	hk × hk
Ax-184358642	20.28	lm × ll	Ax-166502594	2.46	hk × hk
Ax-184302807	22.72	lm × ll	Ax-184484983	3.99	hk × hk
Ax-184546079	24.56	lm × ll	Ax-166517541	4.91	hk × hk
Ax-166510620	26.40	lm × ll	Ax-166502583	6.14	hk × hk
Ax-123360030	27.60	hk × hk	Ax-184584393	7.36	hk × hk
Ax-184058266	29.13	hk × hk	Ax-184358682	8.28	hk × hk
Ax-166502594	30.05	hk × hk	Ax-184268441	9.20	hk × hk
Ax-184484983	31.59	hk × hk	Ax-166517535	10.12	hk × hk
Ax-166517541	32.51	hk × hk	Ax-166510426	11.04	hk × hk
Ax-166502583	33.73	hk × hk	Ax-184413843	11.96	hk × hk
Ax-184584393	34.96	hk × hk	Ax-166502708	12.88	hk × hk
Ax-184358682	35.88	hk × hk	Ax-166519654	14.10	hk × hk
Ax-184268441	36.80	hk × hk	Ax-184424691	15.64	hk × hk
Ax-166517535	37.72	hk × hk	Ax-184235637	16.84	nn × np
Ax-166510426	38.63	hk × hk	Ax-166502787	18.67	nn × np
Ax-184413843	39.55	hk × hk	Ax-184235657	19.89	hk × hk

Ax-166502708	40.47	hk × hk	Ax-166502512	20.81	hk × hk
Ax-166519654	41.70	hk × hk	Ax-166503146	22.04	hk × hk
Ax-184424691	43.23	hk × hk	Ax-166519765	22.96	hk × hk
Ax-184235657	44.77	hk × hk	Ax-166509450	23.88	hk × hk
Ax-166502512	45.69	hk × hk	Ax-166502499	25.11	nn × np
Ax-166503146	46.92	hk × hk	Ax-184257018	28.78	nn × np
Ax-166519765	47.84	hk × hk	<b>Rubygem (LG3)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-166509450	48.75	hk × hk	Ax-184091701	0.00	hk × hk
<b>Fortuna (LG3)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-123394608	2.84	hk × hk
Ax-184091701	0.00	hk × hk	Ax-184070945	4.72	hk × hk
Ax-123394608	2.84	hk × hk	Ax-184026067	8.17	nn × np
Ax-184291352	4.19	lm × ll	Ax-184530193	8.78	nn × np
Ax-184070945	5.46	hk × hk	Ax-184651192	10.61	nn × np
Ax-184360303	11.23	lm × ll	Ax-184166492	12.44	nn × np
Ax-184530241	13.07	lm × ll	Ax-184117750	19.81	nn × np
Ax-184258193	14.95	lm × ll	Ax-184863021	36.91	nn × np
Ax-166503536	17.45	lm × ll	Ax-184051593	38.74	nn × np
Ax-184577476	21.14	lm × ll	Ax-184280172	40.57	nn × np
Ax-184125012	22.36	lm × ll	Ax-184030860	42.40	nn × np
Ax-166507168	23.59	lm × ll	Ax-184336893	46.47	hk × hk
Ax-184903334	36.77	lm × ll	Ax-166520781	47.69	hk × hk
Ax-184336893	38.12	hk × hk	Ax-166527183	48.61	hk × hk
Ax-166520781	39.35	hk × hk	Ax-166511361	49.53	hk × hk
Ax-166527183	40.27	hk × hk	Ax-184873885	50.48	hk × hk
Ax-166511361	41.19	hk × hk	Ax-184710012	51.43	hk × hk
Ax-184873885	42.14	hk × hk	Ax-166503364	52.35	hk × hk
Ax-184710012	43.08	hk × hk	Ax-184140659	53.58	hk × hk
Ax-166503364	44.00	hk × hk	Ax-184020776	54.73	nn × np
Ax-184140659	45.24	hk × hk	Ax-184765972	56.57	nn × np
Ax-184538721	55.99	hk × hk	Ax-123364729	58.40	nn × np
Ax-166503838	58.47	hk × hk	Ax-166520594	59.01	nn × np
Ax-184054966	59.69	hk × hk	Ax-184773144	60.84	nn × np
Ax-184865531	60.92	hk × hk	Ax-184062528	62.06	nn × np
Ax-166503905	62.15	hk × hk	Ax-184538721	63.28	hk × hk
Ax-166509686	63.07	hk × hk	Ax-166503838	65.76	hk × hk
Ax-123365316	64.30	hk × hk	Ax-184054966	66.98	hk × hk
Ax-166511960	65.52	hk × hk	Ax-184865531	68.21	hk × hk
Ax-123360444	66.44	hk × hk	Ax-166503905	69.44	hk × hk
Ax-123614850	67.67	hk × hk	Ax-166509686	70.36	hk × hk
Ax-184280386	68.90	hk × hk	Ax-123365316	71.58	hk × hk
Ax-184392880	70.12	hk × hk	Ax-166511960	72.81	hk × hk
Ax-166521357	71.35	hk × hk	Ax-123360444	73.73	hk × hk
Ax-166512001	72.89	hk × hk	Ax-123614850	74.96	hk × hk
Ax-166517737	73.81	hk × hk	Ax-184280386	76.19	hk × hk
Ax-166503851	74.73	hk × hk	Ax-184392880	77.41	hk × hk
Ax-184236612	75.66	hk × hk	Ax-166521357	78.64	hk × hk

Ax-184258475	82.03	lm × ll	Ax-166512001	80.18	hk × hk
Ax-184860797	85.78	hk × hk	Ax-166517737	81.10	hk × hk
Ax-166521798	87.32	hk × hk	Ax-166503851	82.02	hk × hk
Ax-184381951	88.24	hk × hk	Ax-184236612	82.95	hk × hk
Ax-184195344	89.80	hk × hk	Ax-184071114	85.49	nn × np
Ax-184446431	100.68	lm × ll	Ax-184635467	86.71	nn × np
Ax-184530439	102.51	lm × ll	Ax-184071116	87.93	nn × np
Ax-184024248	103.12	lm × ll	Ax-184860797	89.18	hk × hk
Ax-123357499	104.34	lm × ll	Ax-166521798	90.71	hk × hk
Ax-184521843	104.95	lm × ll	Ax-184381951	91.64	hk × hk
Ax-123360642	106.78	lm × ll	Ax-184195344	93.19	hk × hk
Ax-166521403	107.39	lm × ll	Ax-166521382	97.97	nn × np
<b>Fortuna (LG4)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	<b>Rubygem (LG4)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184926966	0.00	lm × ll	Ax-123363703	0.00	hk × hk
Ax-184217804	1.85	lm × ll	Ax-184142542	1.54	hk × hk
Ax-1841616841	2.47	lm × ll	Ax-166512510	2.46	hk × hk
Ax-184119402	3.69	lm × ll	Ax-184671130	4.65	hk × hk
Ax-166512900	5.52	lm × ll	Ax-184896074	7.17	hk × hk
Ax-166521742	7.35	lm × ll	Ax-166504673	8.33	nn × np
Ax-184373109	7.96	lm × ll	Ax-184134658	10.66	hk × hk
Ax-184896062	9.20	lm × ll	Ax-184506427	11.82	nn × np
Ax-184941528	11.05	lm × ll	Ax-184059469	12.96	hk × hk
Ax-166517789	12.90	lm × ll	Ax-123363725	14.19	hk × hk
Ax-184571848	15.96	lm × ll	Ax-123524746	15.11	hk × hk
Ax-123363703	17.11	hk × hk	Ax-123366965	16.33	hk × hk
Ax-184142542	18.64	hk × hk	Ax-123357862	17.25	hk × hk
Ax-166512510	19.56	hk × hk	Ax-184448614	19.10	hk × hk
Ax-184671130	21.76	hk × hk	Ax-184197457	20.94	hk × hk
Ax-184896074	24.28	hk × hk	Ax-123360505	22.17	hk × hk
Ax-12335774	25.44	lm × ll	Ax-184586392	23.40	hk × hk
Ax-123615253	26.05	lm × ll	Ax-123360537	24.32	hk × hk
Ax-184134658	29.54	hk × hk	Ax-123365409	25.55	hk × hk
Ax-184059469	32.64	hk × hk	Ax-123524547	26.46	hk × hk
Ax-123363725	33.87	hk × hk	Ax-184142657	27.80	nn × np
Ax-123524746	34.79	hk × hk	Ax-123501886	29.11	hk × hk
Ax-123366965	36.01	hk × hk	Ax-184187654	30.65	hk × hk
Ax-123357862	36.93	hk × hk	Ax-166517763	31.88	hk × hk
Ax-184448614	38.78	hk × hk	Ax-184861291	33.73	hk × hk
Ax-184197457	40.62	hk × hk	Ax-184593430	46.67	nn × np
Ax-123360505	41.85	hk × hk	Ax-184548535	49.74	nn × np
Ax-184586392	43.08	hk × hk	Ax-123357919	52.09	hk × hk
Ax-123360537	44.00	hk × hk	Ax-184134832	53.01	hk × hk
Ax-123365409	45.23	hk × hk	Ax-123367042	54.24	hk × hk
Ax-123524547	46.15	hk × hk	Ax-184448788	55.16	hk × hk
Ax-123501886	47.68	hk × hk	Ax-184029726	56.08	hk × hk
Ax-184187654	49.22	hk × hk	Ax-184304287	59.80	hk × hk



Ax-166517763	50.45	hk × hk	Ax-123614608	61.03	hk × hk
Ax-184861291	52.30	hk × hk	Ax-184151010	62.57	hk × hk
Ax-184099337	67.77	lm × ll	Ax-184478694	63.81	hk × hk
Ax-123357919	70.13	hk × hk	Ax-166505049	64.72	hk × hk
Ax-184134832	71.05	hk × hk	Ax-123614604	65.64	hk × hk
Ax-123367042	72.27	hk × hk	Ax-123357907	66.87	hk × hk
Ax-184448788	73.19	hk × hk	Ax-184642140	68.41	hk × hk
Ax-184029726	74.11	hk × hk	Ax-184072288	70.25	hk × hk
Ax-184304287	77.83	hk × hk	Ax-184023686	71.48	hk × hk
Ax-123614608	79.06	hk × hk	Ax-184052504	72.40	hk × hk
Ax-184178268	81.28	lm × ll	Ax-184082245	73.32	hk × hk
Ax-184151010	82.45	hk × hk	Ax-123615215	74.55	hk × hk
Ax-184478694	83.68	hk × hk	Ax-184077147	75.48	hk × hk
Ax-166505049	84.60	hk × hk	Ax-123357889	76.72	hk × hk
Ax-123614604	85.52	hk × hk	Ax-123357651	77.95	hk × hk
Ax-123357907	86.74	hk × hk	Ax-184178317	79.49	hk × hk
Ax-184642140	88.28	hk × hk	Ax-184159941	80.71	hk × hk
Ax-184072288	90.13	hk × hk	Ax-123367008	81.63	hk × hk
Ax-184023686	91.36	hk × hk	Ax-184458891	82.55	hk × hk
Ax-184052504	92.27	hk × hk	Ax-166526738	83.78	hk × hk
Ax-184082245	93.19	hk × hk	Ax-184167827	84.70	hk × hk
Ax-123615215	94.43	hk × hk	Ax-184457798	86.24	hk × hk
Ax-184077147	95.36	hk × hk	<b>Rubygem (LG5)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-123357889	96.59	hk × hk	Ax-184406089	0.00	nn × np
Ax-123357651	97.82	hk × hk	Ax-166521769	0.61	nn × np
Ax-184178317	99.36	hk × hk	Ax-166521747	1.83	nn × np
Ax-184159941	100.59	hk × hk	Ax-123357810	3.66	nn × np
Ax-123367008	101.51	hk × hk	Ax-184082058	4.91	hk × hk
Ax-184458891	102.43	hk × hk	Ax-184055716	8.67	nn × np
Ax-166526738	103.66	hk × hk	Ax-166512534	9.87	hk × hk
Ax-184167827	104.58	hk × hk	Ax-184555502	43.32	hk × hk
Ax-184457798	106.11	hk × hk	Ax-166518742	47.38	nn × np
<b>Fortuna (LG5)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-166519683	51.05	nn × np
Ax-184504674	0.00	lm × ll	Ax-184382855	53.49	nn × np
Ax-184082058	2.63	hk × hk	Ax-184514053	54.10	nn × np
Ax-166512448	3.88	lm × ll	Ax-166504767	55.93	nn × np
Ax-166512534	5.09	hk × hk	Ax-184226803	57.76	nn × np
Ax-184555502	38.53	hk × hk	Ax-184338138	58.98	nn × np
Ax-184167450	48.37	hk × hk	Ax-184486796	61.42	nn × np
Ax-184338164	49.59	hk × hk	Ax-184167450	63.95	hk × hk
Ax-184237503	52.07	hk × hk	Ax-184338164	65.18	hk × hk
Ax-184505254	53.30	hk × hk	Ax-184436863	67.85	nn × np
Ax-184270273	54.23	hk × hk	Ax-184237503	73.06	hk × hk
Ax-184248504	57.02	hk × hk	Ax-184505254	74.30	hk × hk
Ax-184326917	58.56	hk × hk	Ax-184270273	75.22	hk × hk
Ax-184436907	59.78	hk × hk	Ax-184206347	79.18	nn × np

Ax-184036267	61.01	hk × hk	Ax-184248504	83.30	hk × hk
Ax-166517773	62.55	hk × hk	Ax-184326917	84.83	hk × hk
Ax-184338259	63.78	hk × hk	Ax-184436907	86.07	hk × hk
Ax-184946032	66.60	lm × ll	Ax-184036267	87.29	hk × hk
Ax-184111619	67.83	lm × ll	Ax-166517773	88.83	hk × hk
Ax-184547506	68.44	lm × ll	Ax-184338259	90.06	hk × hk
Ax-184563337	71.54	hk × hk	Ax-184104720	92.80	nn × np
Ax-184118647	72.46	hk × hk	Ax-184045820	94.63	nn × np
Ax-184315593	73.38	hk × hk	Ax-184028301	96.46	nn × np
Ax-184029621	74.61	hk × hk	Ax-184514166	97.07	nn × np
Ax-166519498	75.52	hk × hk	Ax-184563337	109.70	hk × hk
Ax-184327045	77.99	hk × hk	Ax-184118647	110.62	hk × hk
Ax-123357979	81.29	lm × ll	Ax-184315593	111.54	hk × hk
Ax-184338370	82.52	lm × ll	Ax-184029621	112.77	hk × hk
Ax-123366119	83.60	hk × hk	Ax-166519498	113.69	hk × hk
Ax-166504505	85.75	lm × ll	Ax-184327045	116.15	hk × hk
Ax-184840113	86.85	hk × hk	Ax-123360751	117.25	nn × np
Ax-184259668	88.08	hk × hk	Ax-184036290	119.69	nn × np
Ax-184956130	89.02	hk × hk	Ax-123366119	120.77	hk × hk
Ax-123361195	89.64	hk × hk	Ax-184167599	124.00	nn × np
Ax-123363771	90.98	lm × ll	Ax-184840113	129.64	hk × hk
Ax-123361170	92.81	lm × ll	Ax-184259668	130.88	hk × hk
Ax-166505153	93.42	lm × ll	Ax-184956130	131.81	hk × hk
Ax-166505210	95.26	lm × ll	Ax-123361195	132.44	hk × hk
Ax-166505061	97.10	lm × ll	Ax-184118742	147.76	nn × np
Ax-184571074	98.93	lm × ll	<b>Rubygem (LG6)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184038430	100.76	lm × ll	Ax-184127284	0.00	hk × hk
Ax-184547649	103.21	lm × ll	Ax-184362494	0.92	hk × hk
Ax-184555752	106.29	lm × ll	Ax-184695683	1.84	hk × hk
<b>Fortuna (LG6)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184067817	2.76	hk × hk
Ax-184143044	0.00	lm × ll	Ax-184449046	4.29	hk × hk
Ax-184143041	1.83	lm × ll	Ax-184041058	5.52	hk × hk
Ax-184021858	4.27	lm × ll	Ax-184038760	6.75	hk × hk
Ax-184261402	4.88	lm × ll	Ax-184031328	9.54	hk × hk
Ax-184127284	6.06	hk × hk	Ax-184294663	11.08	hk × hk
Ax-184362494	6.98	hk × hk	Ax-184783981	12.00	hk × hk
Ax-184695683	7.90	hk × hk	Ax-123367088	18.92	hk × hk
Ax-184067817	8.81	hk × hk	Ax-184318072	20.14	hk × hk
Ax-184449046	10.35	hk × hk	Ax-184251409	21.38	hk × hk
Ax-184041058	11.58	hk × hk	Ax-184151152	39.08	hk × hk
Ax-184038760	12.81	hk × hk	Ax-184018881	40.31	hk × hk
Ax-123358209	14.08	lm × ll	Ax-184020890	41.23	hk × hk
Ax-184031328	15.36	hk × hk	Ax-184250308	42.15	hk × hk
Ax-184294663	16.90	hk × hk	Ax-166505289	43.07	hk × hk
Ax-184783981	17.82	hk × hk	<b>Rubygem (LG7)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184340102	19.13	lm × ll	Ax-184374551	0.00	nn × np

Ax-123367088	22.84	hk × hk	Ax-166505951	1.83	nn × np
Ax-184318072	24.07	hk × hk	Ax-184179296	3.66	nn × np
Ax-184251409	25.31	hk × hk	Ax-184208839	6.10	nn × np
Ax-123358131	26.56	lm × ll	Ax-184127871	8.54	nn × np
Ax-123524828	28.40	lm × ll	Ax-184056248	13.15	hk × hk
Ax-184151201	32.70	lm × ll	Ax-184120491	14.30	nn × np
Ax-166509318	34.54	lm × ll	Ax-184680336	16.74	hk × hk
Ax-123361330	37.60	lm × ll	Ax-166505694	17.96	nn × np
Ax-184119770	39.43	lm × ll	Ax-184407731	18.57	nn × np
Ax-184931977	42.50	lm × ll	Ax-166513805	19.79	nn × np
Ax-184067776	44.34	lm × ll	Ax-166505728	21.01	nn × np
Ax-184151152	45.57	hk × hk	Ax-89887612	22.84	nn × np
Ax-184018881	46.80	hk × hk	Ax-184088218	25.28	nn × np
Ax-184020890	47.72	hk × hk	Ax-184049603	26.65	hk × hk
Ax-184250308	48.64	hk × hk	Ax-184295691	27.58	hk × hk
Ax-166505289	49.56	hk × hk	Ax-123363850	28.50	hk × hk
Ax-184663837	50.78	lm × ll	Ax-184273227	30.03	hk × hk
Ax-166518778	51.39	lm × ll	<b>Rubygem (LG8)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184363053	54.48	lm × ll	Ax-123358325	0.00	hk × hk
<b>Fortuna (LG7)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-166506074	1.23	hk × hk
Ax-184056248	0.00	hk × hk	Ax-184088130	2.46	hk × hk
Ax-184680336	6.65	hk × hk	Ax-166523312	3.68	hk × hk
Ax-89807530	7.87	lm × ll	Ax-184306829	17.84	hk × hk
Ax-184049603	11.99	hk × hk	Ax-184892540	18.77	hk × hk
Ax-184295691	12.91	hk × hk	Ax-123358292	19.69	hk × hk
Ax-123363850	13.83	hk × hk	Ax-184385635	20.62	hk × hk
Ax-184273227	15.37	hk × hk	Ax-184765414	21.90	nn × np
<b>Fortuna (LG8)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-166514035	23.73	nn × np
Ax-123358325	0.00	hk × hk	Ax-123367139	27.18	hk × hk
Ax-166506074	1.23	hk × hk	Ax-166526808	28.10	hk × hk
Ax-184088130	2.46	hk × hk	Ax-184507372	29.95	hk × hk
Ax-166523312	3.68	hk × hk	Ax-123358002	30.87	hk × hk
Ax-123358335	15.28	lm × ll	Ax-166505539	32.07	nn × np
Ax-184179228	15.89	lm × ll	Ax-184396373	33.28	hk × hk
Ax-184151808	17.11	lm × ll	Ax-166513491	34.48	nn × np
Ax-184498292	18.34	lm × ll	Ax-166522868	35.09	nn × np
Ax-184306829	27.06	hk × hk	Ax-166513588	38.14	nn × np
Ax-184892540	27.99	hk × hk	Ax-166505579	39.97	nn × np
Ax-123358292	28.91	hk × hk	Ax-184127724	41.80	nn × np
Ax-184385635	29.84	hk × hk	Ax-166519178	51.11	hk × hk
Ax-166514050	31.12	lm × ll	Ax-184229250	52.33	hk × hk
Ax-166519197	32.34	lm × ll	Ax-166523089	53.56	hk × hk
Ax-184229386	34.17	lm × ll	Ax-184969929	62.28	hk × hk
Ax-123367139	45.87	hk × hk	Ax-184046462	63.52	hk × hk
Ax-166526808	46.79	hk × hk	Ax-166517948	64.44	hk × hk
Ax-184507372	48.64	hk × hk	Ax-184904797	65.35	hk × hk

Ax-123358002	49.56	hk × hk	Ax-184922833	69.02	nn × np
Ax-184396373	52.06	hk × hk	<b>Rubygem (LG9)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-166519178	67.62	hk × hk	Ax-184073411	0.00	hk × hk
Ax-184229250	68.85	hk × hk	Ax-184364841	3.15	hk × hk
Ax-166523089	70.08	hk × hk	Ax-166519691	4.38	hk × hk
Ax-184698856	71.24	lm × ll	Ax-184558446	5.30	hk × hk
Ax-184072655	71.86	lm × ll	Ax-184408977	6.22	hk × hk
Ax-184093835	74.31	lm × ll	Ax-184121293	7.77	hk × hk
Ax-184374324	76.14	lm × ll	Ax-166506785	13.61	nn × np
Ax-184619882	77.36	lm × ll	Ax-184088894	15.44	nn × np
Ax-184969929	80.98	hk × hk	Ax-184100820	22.18	nn × np
Ax-184046462	82.22	hk × hk	Ax-184408944	22.79	nn × np
Ax-166517948	83.14	hk × hk	Ax-184053287	24.01	nn × np
Ax-184904797	84.05	hk × hk	Ax-166524427	26.45	nn × np
<b>Fortuna (LG9)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184889266	50.01	hk × hk
Ax-123358346	0.00	hk × hk	Ax-184580901	85.80	hk × hk
Ax-184073411	1.54	hk × hk	Ax-184440420	110.37	hk × hk
Ax-184364841	4.69	hk × hk	Ax-184672057	111.29	hk × hk
Ax-166519691	5.92	hk × hk	Ax-184073182	112.21	hk × hk
Ax-184558446	6.84	hk × hk	Ax-123453619	113.75	hk × hk
Ax-184408977	7.76	hk × hk	Ax-184965393	134.64	hk × hk
Ax-184121293	9.30	hk × hk	Ax-184128504	136.18	hk × hk
Ax-166524334	11.15	hk × hk	Ax-184516889	137.11	hk × hk
Ax-166506955	17.13	lm × ll	Ax-184106976	138.04	hk × hk
Ax-184534218	18.97	lm × ll	Ax-166526864	139.27	hk × hk
Ax-184210109	19.59	lm × ll	Ax-184307764	140.49	hk × hk
Ax-184750677	21.42	lm × ll	Ax-166515123	141.41	hk × hk
Ax-123363930	23.25	lm × ll	Ax-184853724	144.83	hk × hk
Ax-184128820	25.08	lm × ll	Ax-166515165	146.70	hk × hk
Ax-184180436	26.91	lm × ll	Ax-184364220	147.32	nn × np
Ax-184387091	29.36	lm × ll	Ax-184965362	148.64	hk × hk
Ax-184918717	32.43	lm × ll	Ax-123358041	149.56	hk × hk
Ax-184199960	34.28	lm × ll	Ax-123358020	150.79	hk × hk
Ax-184859637	37.96	lm × ll	Ax-184100476	151.71	hk × hk
Ax-184170994	39.80	lm × ll	Ax-166514928	153.24	hk × hk
Ax-184274406	40.41	lm × ll	Ax-166527285	154.47	hk × hk
Ax-184517220	42.27	lm × ll	Ax-184701194	156.01	hk × hk
Ax-184230747	42.88	lm × ll	Ax-123361836	156.93	hk × hk
Ax-184107228	44.10	lm × ll	Ax-123358486	157.85	hk × hk
Ax-184889266	45.32	hk × hk	Ax-123367179	159.08	hk × hk
Ax-123358397	46.54	lm × ll	Ax-184044070	195.12	hk × hk
Ax-184580901	48.98	hk × hk	Ax-184035035	196.04	hk × hk
Ax-184689046	60.14	lm × ll	Ax-184839590	196.97	hk × hk
Ax-184558250	61.36	lm × ll	Ax-166514792	198.20	hk × hk
Ax-166504043	62.58	lm × ll	Ax-184965499	199.12	hk × hk
Ax-184680668	64.41	lm × ll	<b>Rubygem (LG10)</b>	<b>Positions (cM)</b>	<b>Segregation</b>

Ax-184073182	70.62	hk × hk	Ax-184036926	0.00	hk × hk
Ax-123453619	72.15	hk × hk	Ax-123363994	1.23	hk × hk
Ax-184319321	73.36	lm × ll	Ax-123483068	4.85	nn × np
Ax-184128546	75.20	lm × ll	Ax-184460765	6.68	nn × np
Ax-184508191	75.81	lm × ll	Ax-166518015	9.01	hk × hk
Ax-184274034	77.04	lm × ll	Ax-166514461	9.92	hk × hk
Ax-166527290	79.50	lm × ll	Ax-166506487	10.84	hk × hk
Ax-184905261	81.94	lm × ll	Ax-184021947	11.76	hk × hk
Ax-166506237	83.77	lm × ll	Ax-166510135	12.68	hk × hk
Ax-184152660	84.99	lm × ll	Ax-166502931	13.60	hk × hk
Ax-184508165	86.84	lm × ll	Ax-123524238	14.52	hk × hk
Ax-184658321	88.69	lm × ll	Ax-184077980	15.44	hk × hk
Ax-184965393	89.88	hk × hk	Ax-184341599	17.62	hk × hk
Ax-184128504	91.42	hk × hk	Ax-89905703	20.44	hk × hk
Ax-184516889	92.35	hk × hk	Ax-184199370	21.67	hk × hk
Ax-184106976	93.28	hk × hk	Ax-166509628	23.22	hk × hk
Ax-166526864	94.51	hk × hk	Ax-184549876	24.76	hk × hk
Ax-184307764	95.73	hk × hk	Ax-184273795	25.67	hk × hk
Ax-166515123	96.65	hk × hk	<b>Rubygem (LG11)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184853724	100.07	hk × hk	Ax-166508054	0.00	hk × hk
Ax-166515165	101.31	hk × hk	Ax-166527323	4.38	hk × hk
Ax-166506825	104.52	hk × hk	Ax-166524986	70.43	hk × hk
Ax-166506818	105.45	hk × hk	Ax-184028983	71.66	hk × hk
Ax-184965362	106.37	hk × hk	Ax-184211719	72.58	hk × hk
Ax-123358041	107.29	hk × hk	Ax-166507438	73.50	hk × hk
Ax-123358020	108.52	hk × hk	Ax-184254345	74.73	hk × hk
Ax-184100476	109.44	hk × hk	Ax-184130027	75.65	hk × hk
Ax-166514928	110.98	hk × hk	Ax-123366305	76.57	hk × hk
Ax-166527285	112.21	hk × hk	Ax-166515651	78.11	hk × hk
Ax-184701194	113.74	hk × hk	Ax-123358922	79.33	hk × hk
Ax-123361836	114.66	hk × hk	Ax-184137874	80.25	hk × hk
Ax-123358486	115.58	hk × hk	Ax-184431973	81.17	hk × hk
Ax-123367179	116.81	hk × hk	Ax-123362315	82.40	hk × hk
<b>Fortuna (LG10)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184122503	83.32	hk × hk
Ax-184842287	0.00	lm × ll	Ax-166524788	84.86	hk × hk
Ax-184209268	4.39	lm × ll	Ax-184201600	86.09	hk × hk
Ax-184841120	6.24	lm × ll	Ax-184633306	89.03	nn × np
Ax-184161284	7.48	lm × ll	Ax-166507291	90.91	nn × np
Ax-184052989	9.95	lm × ll	Ax-184638794	92.74	nn × np
Ax-184607909	11.79	lm × ll	Ax-184377825	95.41	hk × hk
Ax-184565466	13.64	lm × ll	Ax-123367326	96.33	hk × hk
Ax-166523497	15.47	lm × ll	Ax-123614395	97.56	hk × hk
Ax-123363932	16.08	lm × ll	Ax-184452822	124.67	hk × hk
Ax-184036926	18.58	hk × hk	Ax-184276429	149.33	hk × hk
Ax-123363994	19.81	hk × hk	<b>Rubygem (LG12)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-166518015	28.49	hk × hk	Ax-184553002	0.00	hk × hk

Ax-166514461	29.41	hk × hk	Ax-184233625	53.78	hk × hk
Ax-166506487	30.33	hk × hk	Ax-166518440	54.70	hk × hk
Ax-184021947	31.25	hk × hk	Ax-166527724	55.93	hk × hk
Ax-166510135	32.16	hk × hk	Ax-184333694	57.52	hk × hk
Ax-166502931	33.08	hk × hk	Ax-166510086	60.07	hk × hk
Ax-123524238	34.00	hk × hk	Ax-184116067	61.01	hk × hk
Ax-184077980	34.92	hk × hk	Ax-184032046	62.59	hk × hk
Ax-184341599	37.11	hk × hk	Ax-184603313	63.82	hk × hk
Ax-89905703	39.92	hk × hk	Ax-166516760	64.74	hk × hk
Ax-184199370	41.16	hk × hk	Ax-123363034	65.66	hk × hk
Ax-166509628	42.70	hk × hk	Ax-184019080	68.10	nn × np
Ax-184549876	44.24	hk × hk	Ax-123366735	69.93	nn × np
Ax-184273795	45.16	hk × hk	Ax-123363341	71.76	nn × np
Ax-123361879	46.29	lm × ll	Ax-123358774	72.37	nn × np
Ax-184088523	48.12	lm × ll	Ax-184311244	74.20	nn × np
Ax-123364070	50.57	lm × ll	Ax-123363299	76.03	nn × np
Ax-184162406	64.42	lm × ll	<b>Rubygem (LG13)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
<b>Fortuna (LG11)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-123357522	0.00	hk × hk
Ax-166508054	0.00	hk × hk	Ax-166508541	27.69	hk × hk
Ax-166510114	1.22	lm × ll	Ax-184733779	28.62	hk × hk
Ax-166527323	3.72	hk × hk	Ax-184146591	31.44	hk × hk
Ax-184254173	4.99	lm × ll	Ax-184115957	32.98	hk × hk
Ax-123362725	8.68	lm × ll	Ax-166518928	33.90	hk × hk
Ax-184287223	10.51	lm × ll	Ax-184378749	35.13	hk × hk
Ax-166507833	11.73	lm × ll	Ax-166508593	36.67	hk × hk
Ax-166516081	14.17	lm × ll	Ax-184069827	37.59	hk × hk
Ax-166507736	16.61	lm × ll	Ax-184389787	38.51	hk × hk
Ax-166525311	17.22	lm × ll	Ax-123614460	39.74	hk × hk
Ax-184309805	18.44	lm × ll	Ax-184333861	40.96	hk × hk
Ax-184035359	20.29	lm × ll	Ax-123364455	42.20	hk × hk
Ax-184654222	20.90	lm × ll	Ax-184389798	43.44	hk × hk
Ax-166507637	27.64	lm × ll	Ax-184212705	44.36	hk × hk
Ax-184527065	29.47	lm × ll	Ax-184146611	45.90	hk × hk
Ax-166524986	37.89	hk × hk	Ax-184919896	47.14	hk × hk
Ax-184028983	39.11	hk × hk	Ax-166508657	48.49	nn × np
Ax-184211719	40.03	hk × hk	Ax-184244358	49.81	hk × hk
Ax-166507438	40.95	hk × hk	Ax-184244356	50.74	hk × hk
Ax-184254345	42.18	hk × hk	Ax-184333874	51.98	hk × hk
Ax-184130027	43.10	hk × hk	Ax-184255378	54.14	hk × hk
Ax-123366305	44.02	hk × hk	Ax-166508709	56.77	nn × np
Ax-166515651	45.56	hk × hk	Ax-184510761	59.28	hk × hk
Ax-123358922	46.79	hk × hk	Ax-184876289	60.20	hk × hk
Ax-184137874	47.71	hk × hk	Ax-184463860	61.42	hk × hk
Ax-184431973	48.63	hk × hk	Ax-166508861	65.13	nn × np
Ax-123362315	49.86	hk × hk	Ax-184333919	66.96	nn × np
Ax-184122503	50.78	hk × hk	Ax-184664346	68.79	nn × np



Ax-166524788	52.31	hk × hk	Ax-184202450	71.24	nn × np
Ax-184201600	53.54	hk × hk	Ax-184699875	72.44	hk × hk
Ax-184377825	58.58	hk × hk	Ax-184575548	74.85	nn × np
Ax-123367326	59.50	hk × hk	Ax-184622261	79.81	nn × np
Ax-123614395	60.73	hk × hk	Ax-184299746	81.06	nn × np
Ax-184243498	62.08	lm × ll	<b>Rubygem (LG14)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184095668	65.13	lm × ll	Ax-166515010	0.00	nn × np
Ax-123359777	66.35	lm × ll	Ax-184046933	0.61	nn × np
Ax-184452822	81.76	hk × hk	Ax-184073436	2.91	hk × hk
Ax-123364810	85.22	lm × ll	Ax-166514384	4.76	hk × hk
Ax-184410821	91.96	lm × ll	Ax-166506458	7.54	hk × hk
Ax-184751951	93.79	lm × ll	Ax-184180593	8.46	hk × hk
Ax-184399867	95.04	lm × ll	Ax-184688951	9.68	hk × hk
Ax-184749697	96.29	lm × ll	Ax-184171208	11.22	hk × hk
Ax-184713473	97.54	lm × ll	Ax-123358566	12.14	hk × hk
Ax-184421586	98.79	lm × ll	<b>Rubygem (LG15)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184399839	100.65	lm × ll	Ax-184073586	0.00	hk × hk
Ax-184222311	102.48	lm × ll	Ax-184053449	1.23	hk × hk
Ax-184276429	103.67	hk × hk	Ax-166508104	2.45	hk × hk
Ax-166507072	104.86	lm × ll	Ax-184901326	3.38	hk × hk
<b>Fortuna (LG12)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-123364350	4.70	nn × np
Ax-184682130	0.00	lm × ll	Ax-184353989	6.03	hk × hk
Ax-166517081	0.62	lm × ll	Ax-184129215	6.95	hk × hk
Ax-184902312	2.47	lm × ll	Ax-123362814	8.49	hk × hk
Ax-184890462	4.30	lm × ll	Ax-184297420	9.71	hk × hk
Ax-123363199	7.36	lm × ll	Ax-184938206	10.94	hk × hk
Ax-184553002	9.56	hk × hk	Ax-123363787	12.17	hk × hk
Ax-184693726	10.65	lm × ll	Ax-184320383	13.40	hk × hk
Ax-184277600	12.48	lm × ll	Ax-166518160	14.94	hk × hk
Ax-184155566	14.31	lm × ll	Ax-184073961	15.85	hk × hk
Ax-184202708	16.16	lm × ll	Ax-123362731	17.39	hk × hk
Ax-166517211	18.61	lm × ll	<b>Rubygem (LG16)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-123614800	19.22	lm × ll	Ax-184882260	0.00	nn × np
Ax-123363254	21.05	lm × ll	Ax-123404648	1.24	nn × np
Ax-166508724	22.88	lm × ll	Ax-184387715	1.85	nn × np
Ax-184664459	34.68	lm × ll	Ax-166518863	4.29	nn × np
Ax-184483937	35.29	lm × ll	Ax-184162515	7.35	nn × np
Ax-184288733	43.29	lm × ll	Ax-184517751	9.19	nn × np
Ax-184096209	44.51	lm × ll	Ax-184033341	11.03	nn × np
Ax-123359374	46.34	lm × ll	Ax-184047067	25.53	nn × np
Ax-123364415	48.17	lm × ll	Ax-184231551	26.14	nn × np
Ax-123367562	50.00	lm × ll	Ax-184137130	28.58	nn × np
Ax-184732247	50.61	lm × ll	Ax-184242345	29.80	nn × np
Ax-123359593	51.85	lm × ll	Ax-184044309	31.63	nn × np
Ax-123359604	53.68	lm × ll	Ax-184083735	32.24	nn × np
Ax-184644685	62.41	lm × ll	Ax-184114664	34.07	nn × np

Ax-184233625	67.62	hk × hk	Ax-184693230	34.68	nn × np
Ax-166518440	68.54	hk × hk	Ax-89896790	36.51	nn × np
Ax-166527724	69.77	hk × hk	Ax-184231568	37.73	nn × np
Ax-184333694	71.36	hk × hk	Ax-166507450	38.34	nn × np
Ax-166510086	73.91	hk × hk	Ax-166509944	39.56	nn × np
Ax-184116067	74.85	hk × hk	Ax-166524983	41.39	nn × np
Ax-184032046	76.43	hk × hk	Ax-184320629	44.34	hk × hk
Ax-184603313	77.66	hk × hk	Ax-184041753	45.57	hk × hk
Ax-166516760	78.58	hk × hk	Ax-184398749	46.48	hk × hk
Ax-123363034	79.50	hk × hk	Ax-184145229	47.40	hk × hk
<b>Fortuna (LG13)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-123362376	48.63	hk × hk
Ax-123550204	0.00	lm × ll	Ax-184451833	49.86	hk × hk
Ax-123357522	1.11	hk × hk	Ax-166518163	51.09	hk × hk
Ax-184233353	2.24	lm × ll	Ax-184321678	52.01	hk × hk
Ax-123359715	3.48	lm × ll	Ax-123362346	53.55	hk × hk
Ax-123363294	4.09	lm × ll	Ax-123366252	54.78	hk × hk
Ax-184567869	5.93	lm × ll	Ax-184343113	56.00	hk × hk
Ax-123363274	7.76	lm × ll	Ax-166515381	57.54	hk × hk
Ax-184030453	12.07	lm × ll	Ax-184343120	58.46	hk × hk
Ax-184255312	12.68	lm × ll	Ax-123362257	59.38	hk × hk
Ax-184432853	13.92	lm × ll	Ax-184320696	60.92	hk × hk
Ax-166508541	15.17	hk × hk	Ax-166515245	61.84	hk × hk
Ax-184733779	16.09	hk × hk	Ax-184264370	63.69	hk × hk
Ax-123615172	17.34	lm × ll	Ax-184060789	64.91	hk × hk
Ax-184146591	19.98	hk × hk	Ax-184264402	66.15	hk × hk
Ax-184115957	21.52	hk × hk	Ax-184129462	67.07	hk × hk
Ax-166518928	22.44	hk × hk	Ax-184297806	72.36	nn × np
Ax-184378749	23.67	hk × hk	Ax-184971175	76.72	hk × hk
Ax-166508593	25.21	hk × hk	Ax-166508207	78.25	hk × hk
Ax-184069827	26.13	hk × hk	Ax-123364378	81.07	nn × np
Ax-184389787	27.05	hk × hk	Ax-184603002	82.92	nn × np
Ax-123614460	28.27	hk × hk	Ax-166526903	84.75	nn × np
Ax-184333861	29.50	hk × hk	Ax-123614760	85.84	hk × hk
Ax-123364455	30.74	hk × hk	Ax-184107897	88.31	hk × hk
Ax-184389798	31.97	hk × hk	Ax-184451960	89.23	hk × hk
Ax-184212705	32.89	hk × hk	Ax-184191773	90.15	hk × hk
Ax-184146611	34.44	hk × hk	Ax-123364264	103.97	nn × np
Ax-184919896	35.68	hk × hk	Ax-123364317	105.80	nn × np
Ax-184244358	37.52	hk × hk	Ax-184850645	110.70	nn × np
Ax-184244356	38.46	hk × hk	<b>Rubygem (LG18)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184333874	39.70	hk × hk	Ax-123363256	0.00	hk × hk
Ax-184255378	41.86	hk × hk	Ax-184234181	0.92	hk × hk
Ax-184182741	43.18	lm × ll	Ax-184139018	1.84	hk × hk
Ax-184510761	44.43	hk × hk	Ax-184183409	14.23	hk × hk
Ax-184876289	45.34	hk × hk	Ax-184639739	17.90	nn × np
Ax-184463860	46.57	hk × hk	Ax-184245168	20.34	nn × np

Ax-184699875	51.59	hk × hk	Ax-184050952	31.22	hk × hk
Ax-184244421	54.01	lm × ll	Ax-184203138	32.46	hk × hk
<b>Fortuna (LG14)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184054324	45.02	hk × hk
Ax-184153130	0	lm × ll	Ax-184368411	46.56	hk × hk
Ax-184073436	1.16	hk × hk	Ax-184164873	48.40	hk × hk
Ax-166514384	3.01	hk × hk	Ax-184234292	49.63	hk × hk
Ax-166506458	5.79	hk × hk	Ax-184484014	50.75	nn × np
Ax-184180593	6.71	hk × hk	Ax-184890536	51.94	hk × hk
Ax-184688951	7.94	hk × hk	Ax-184164903	52.87	hk × hk
Ax-184171208	9.47	hk × hk	Ax-184412478	53.78	hk × hk
Ax-123358566	10.39	hk × hk	Ax-184174048	54.70	hk × hk
Ax-166505359	11.57	lm × ll	Ax-166517369	55.91	nn × np
Ax-184588222	13.40	lm × ll	Ax-166509031	57.74	nn × np
Ax-184308485	14.63	lm × ll	Ax-184131357	58.35	nn × np
Ax-123362015	16.47	lm × ll	Ax-184289445	60.18	nn × np
<b>Fortuna (LG15)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184203245	61.40	hk × hk
Ax-184073586	0	hk × hk	<b>Rubygem (LG19)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184053449	1.23	hk × hk	Ax-184175094	0.00	nn × np
Ax-166508104	2.45	hk × hk	Ax-184682395	1.85	nn × np
Ax-184901326	3.38	hk × hk	Ax-166520403	3.71	nn × np
Ax-184353989	5.55	hk × hk	Ax-166510119	4.32	nn × np
Ax-184129215	6.47	hk × hk	Ax-184110273	6.17	nn × np
Ax-123362814	8.01	hk × hk	Ax-184597686	7.40	nn × np
Ax-184297420	9.24	hk × hk	Ax-123366835	9.87	nn × np
Ax-184938206	10.47	hk × hk	Ax-184040182	10.49	nn × np
Ax-123363787	11.69	hk × hk	Ax-184402874	11.73	nn × np
Ax-184320383	12.92	hk × hk	Ax-184369675	12.96	nn × np
Ax-166518176	14.24	lm × ll	Ax-166502963	14.20	nn × np
Ax-166518160	15.57	hk × hk	Ax-166502928	16.05	nn × np
Ax-184073961	16.49	hk × hk	Ax-184604879	19.10	nn × np
Ax-123362731	18.03	hk × hk	Ax-166510694	24.61	nn × np
Ax-123362724	21.69	lm × ll	Ax-184380159	26.44	nn × np
Ax-184033320	22.91	lm × ll	Ax-184037941	29.98	hk × hk
<b>Fortuna (LG16)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184894543	67.79	hk × hk
Ax-184320629	0	hk × hk	Ax-184289829	68.71	hk × hk
Ax-184041753	1.23	hk × hk	Ax-184561359	82.98	nn × np
Ax-184398749	2.15	hk × hk	Ax-184090851	84.20	nn × np
Ax-184145229	3.07	hk × hk	Ax-166510812	84.81	nn × np
Ax-123362376	4.30	hk × hk	<b>Rubygem (LG20)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184451833	5.52	hk × hk	Ax-184476559	0.00	nn × np
Ax-166518163	6.75	hk × hk	Ax-184125311	2.63	hk × hk
Ax-184321678	7.67	hk × hk	Ax-184476583	15.03	hk × hk
Ax-123362346	9.21	hk × hk	Ax-184414852	16.26	hk × hk
Ax-123366252	10.44	hk × hk	Ax-184476592	17.19	hk × hk
Ax-184343113	11.67	hk × hk	Ax-166507157	18.39	nn × np
Ax-166515381	13.21	hk × hk	Ax-184326068	19.00	nn × np

Ax-184343120	14.12	hk × hk	Ax-184051738	20.83	nn × np
Ax-123362257	15.04	hk × hk	Ax-184080998	22.04	hk × hk
Ax-184320696	16.58	hk × hk	Ax-166503445	23.88	hk × hk
Ax-166515245	17.50	hk × hk	Ax-184048517	24.80	hk × hk
Ax-184264370	19.35	hk × hk	Ax-166520818	26.03	hk × hk
Ax-184060789	20.58	hk × hk	Ax-184291843	27.26	hk × hk
Ax-184264402	21.81	hk × hk	Ax-184280557	28.48	hk × hk
Ax-184129462	22.74	hk × hk	Ax-123524335	30.33	hk × hk
Ax-123362922	24.07	lm × ll	Ax-184291854	31.25	hk × hk
Ax-184971175	28.43	hk × hk	Ax-123360299	32.49	nn × np
Ax-166508207	29.97	hk × hk	Ax-184104228	34.32	nn × np
Ax-166518303	35.55	lm × ll	Ax-184118155	36.15	nn × np
Ax-123614760	36.65	hk × hk	Ax-166503314	37.98	nn × np
Ax-184953426	37.76	lm × ll	Ax-184020757	46.60	nn × np
Ax-184107897	38.84	hk × hk	Ax-184051916	47.21	nn × np
Ax-184451960	39.76	hk × hk	Ax-123357506	49.84	hk × hk
Ax-184191773	40.68	hk × hk	Ax-123360550	50.76	hk × hk
Ax-184754131	44.06	lm × ll	Ax-123357461	51.99	hk × hk
<b>Fortuna (LG18)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-123357458	53.22	hk × hk
Ax-123363256	0	hk × hk	Ax-184034246	54.44	hk × hk
Ax-184234181	0.92	hk × hk	Ax-184195615	55.36	hk × hk
Ax-184139018	1.84	hk × hk	Ax-184040485	56.28	hk × hk
Ax-166519356	3.07	lm × ll	Ax-123360616	64.67	hk × hk
Ax-166516965	3.68	lm × ll	Ax-184916702	65.92	hk × hk
Ax-166516902	5.51	lm × ll	Ax-166512079	67.15	hk × hk
Ax-166508587	6.12	lm × ll	Ax-123360563	68.69	hk × hk
Ax-184725570	7.34	lm × ll	Ax-184058742	69.92	hk × hk
Ax-184717950	9.17	lm × ll	Ax-184446739	71.14	hk × hk
Ax-184876507	9.78	lm × ll	Ax-123360574	72.06	hk × hk
Ax-184173948	11.00	lm × ll	Ax-184062753	72.98	hk × hk
Ax-184183409	13.44	hk × hk	Ax-184118221	74.52	hk × hk
Ax-166508563	18.34	lm × ll	Ax-184133200	75.44	hk × hk
Ax-184050952	23.11	hk × hk	Ax-184111190	76.67	hk × hk
Ax-184203138	24.35	hk × hk	Ax-166508107	77.89	hk × hk
Ax-184278066	27.80	lm × ll	Ax-184036155	78.81	hk × hk
Ax-184079862	28.41	lm × ll	Ax-123359239	79.73	hk × hk
Ax-184193178	29.63	lm × ll	Ax-184205747	81.58	hk × hk
Ax-184545032	30.85	lm × ll	Ax-184577915	82.80	nn × np
Ax-166508925	31.46	lm × ll	Ax-184683237	84.00	hk × hk
Ax-123364491	32.68	lm × ll	Ax-184646415	84.92	hk × hk
Ax-123366710	33.91	lm × ll	Ax-184176319	87.28	nn × np
Ax-166526582	37.59	lm × ll	Ax-184036158	89.11	nn × np
Ax-184054324	39.77	hk × hk	Ax-184921462	89.72	nn × np
Ax-184368411	41.31	hk × hk	Ax-184066813	90.98	hk × hk
Ax-184164873	43.15	hk × hk	Ax-184635701	91.92	hk × hk
Ax-184234292	44.38	hk × hk	<b>Rubygem (LG21)</b>	<b>Positions (cM)</b>	<b>Segregation</b>

Ax-184116502	46.63	lm × ll	Ax-184092264	0.00	hk × hk
Ax-184890536	51.40	hk × hk	Ax-166503256	1.85	hk × hk
Ax-184164903	52.32	hk × hk	Ax-184045723	3.69	hk × hk
Ax-184412478	53.24	hk × hk	Ax-166503347	4.61	hk × hk
Ax-184174048	54.16	hk × hk	Ax-184158310	11.47	nn × np
Ax-166527072	57.78	lm × ll	Ax-123360383	12.65	hk × hk
Ax-184203245	71.53	hk × hk	Ax-184687404	13.88	hk × hk
<b>Fortuna (LG19)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184026058	14.79	hk × hk
Ax-184037941	0	hk × hk	Ax-184026057	15.96	nn × np
Ax-166502853	1.18	lm × ll	Ax-184167327	17.79	nn × np
Ax-184454870	3.01	lm × ll	Ax-184759695	18.40	nn × np
Ax-184894543	4.40	hk × hk	Ax-184020063	19.62	nn × np
Ax-184289829	5.32	hk × hk	Ax-184635868	21.45	nn × np
Ax-184174353	19.80	lm × ll	Ax-184259249	22.65	hk × hk
<b>Fortuna (LG20)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184032587	25.44	hk × hk
Ax-184125311	0	hk × hk	Ax-123357310	29.99	nn × np
Ax-166503588	1.27	lm × ll	<b>Rubygem (LG22)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184076023	3.11	lm × ll	Ax-123361598	0.00	nn × np
Ax-184476583	4.28	hk × hk	Ax-184136011	1.83	nn × np
Ax-184414852	5.52	hk × hk	Ax-184296003	3.66	nn × np
Ax-184476592	6.44	hk × hk	Ax-123500179	4.27	nn × np
Ax-184080998	14.10	hk × hk	Ax-184318822	5.49	nn × np
Ax-184848495	15.35	lm × ll	Ax-184199167	7.93	nn × np
Ax-166503445	17.79	hk × hk	Ax-184262614	9.76	nn × np
Ax-184048517	18.71	hk × hk	Ax-184031516	11.59	nn × np
Ax-166520818	19.94	hk × hk	Ax-123358654	14.03	nn × np
Ax-184291843	21.17	hk × hk	Ax-123361276	15.86	nn × np
Ax-184280557	22.39	hk × hk	Ax-184179621	17.69	nn × np
Ax-123524335	24.24	hk × hk	Ax-184653104	19.52	nn × np
Ax-184291854	25.16	hk × hk	Ax-123367218	21.35	nn × np
Ax-184670440	43.19	lm × ll	Ax-123367208	22.59	hk × hk
Ax-123357506	48.47	hk × hk	Ax-184152192	23.82	nn × np
Ax-123360550	49.39	hk × hk	Ax-123363926	24.97	hk × hk
Ax-123357461	50.62	hk × hk	Ax-184918795	27.44	hk × hk
Ax-123357458	51.84	hk × hk	<b>Rubygem (LG24)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184034246	53.07	hk × hk	Ax-123364138	0.00	hk × hk
Ax-184195615	53.99	hk × hk	Ax-184544039	0.92	hk × hk
Ax-184040485	54.91	hk × hk	Ax-184053939	2.15	hk × hk
Ax-166503958	56.34	lm × ll	Ax-184400179	3.37	hk × hk
Ax-123360616	57.44	hk × hk	Ax-184130421	4.29	hk × hk
Ax-184916702	58.68	hk × hk	Ax-184039668	5.84	hk × hk
Ax-166512079	59.92	hk × hk	Ax-184031965	6.76	hk × hk
Ax-123360563	61.46	hk × hk	Ax-184065292	8.30	hk × hk
Ax-184058742	62.68	hk × hk	Ax-184172975	9.83	hk × hk
Ax-184446739	63.91	hk × hk	Ax-184122827	11.06	hk × hk
Ax-123360574	64.83	hk × hk	Ax-123364271	11.98	hk × hk

Ax-184062753	65.75	hk × hk	Ax-184333457	12.90	hk × hk
Ax-184118221	67.29	hk × hk	Ax-123367097	13.82	hk × hk
Ax-184133200	68.21	hk × hk	Ax-184053964	15.36	hk × hk
Ax-184111190	69.43	hk × hk	Ax-166507597	20.38	nn × np
Ax-166508107	70.66	hk × hk	Ax-184069694	22.82	nn × np
Ax-184036155	71.58	hk × hk	Ax-184934058	24.65	nn × np
Ax-123359239	72.50	hk × hk	Ax-123364932	28.36	hk × hk
Ax-184205747	74.35	hk × hk	Ax-184971864	29.29	hk × hk
Ax-184683237	77.13	hk × hk	Ax-184779729	30.48	nn × np
Ax-184646415	78.05	hk × hk	Ax-184057459	31.70	nn × np
Ax-184066813	85.33	hk × hk	Ax-123359071	32.90	hk × hk
Ax-184635701	86.27	hk × hk	Ax-184065325	34.11	nn × np
<b>Fortuna (LG21)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184754120	35.28	hk × hk
Ax-184092264	0	hk × hk	Ax-184288063	38.82	nn × np
Ax-166503256	1.85	hk × hk	Ax-166516034	47.44	hk × hk
Ax-184045723	3.69	hk × hk	Ax-166516204	48.36	hk × hk
Ax-166503347	4.61	hk × hk	Ax-184689714	49.59	hk × hk
Ax-123360383	12.60	hk × hk	Ax-123525443	50.51	hk × hk
Ax-184687404	13.82	hk × hk	Ax-166525342	51.74	hk × hk
Ax-184026058	14.74	hk × hk	Ax-184400373	52.66	hk × hk
Ax-184259249	21.40	hk × hk	Ax-184061381	54.81	hk × hk
Ax-184303805	22.62	lm × ll	Ax-123366428	55.73	hk × hk
Ax-184032587	23.77	hk × hk	Ax-184288146	57.58	hk × hk
<b>Fortuna (LG22)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184894028	59.12	hk × hk
Ax-184273447	0	lm × ll	Ax-166525571	66.40	nn × np
Ax-166506636	9.32	lm × ll	Ax-184069553	68.23	nn × np
Ax-184363728	11.16	lm × ll	Ax-184025680	70.06	nn × np
Ax-184060279	15.46	lm × ll	Ax-123485715	70.67	nn × np
Ax-123367208	17.97	hk × hk	Ax-184321901	71.93	nn × np
Ax-123363926	21.06	hk × hk	<b>Rubygem (LG25)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184918795	23.53	hk × hk	Ax-123367129	0.00	hk × hk
<b>Fortuna (LG24)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184072581	0.92	hk × hk
Ax-184222589	0	lm × ll	Ax-166523016	2.45	hk × hk
Ax-123364138	1.23	hk × hk	Ax-166506092	17.15	hk × hk
Ax-184544039	2.15	hk × hk	Ax-123358289	21.19	hk × hk
Ax-184053939	3.38	hk × hk	Ax-184093694	22.25	nn × np
Ax-184400179	4.61	hk × hk	Ax-166517968	23.32	hk × hk
Ax-184130421	5.53	hk × hk	Ax-184564766	24.25	hk × hk
Ax-184039668	7.08	hk × hk	Ax-184059776	25.79	hk × hk
Ax-184031965	7.99	hk × hk	Ax-184169379	27.64	hk × hk
Ax-184065292	9.53	hk × hk	Ax-123364775	28.55	hk × hk
Ax-184172975	11.07	hk × hk	Ax-184052674	29.47	hk × hk
Ax-184122827	12.29	hk × hk	Ax-123361566	30.39	hk × hk
Ax-123364271	13.21	hk × hk	Ax-184120048	31.62	hk × hk
Ax-184333457	14.13	hk × hk	Ax-184557066	34.06	nn × np
Ax-123367097	15.05	hk × hk	Ax-184488644	37.11	nn × np



Ax-184053964	16.60	hk × hk	Ax-184151435	40.73	hk × hk
Ax-184929209	24.16	lm × ll	Ax-184428489	41.65	hk × hk
Ax-123364932	26.63	hk × hk	Ax-184059749	42.57	hk × hk
Ax-184971864	27.55	hk × hk	Ax-123367086	47.53	nn × np
Ax-123359071	28.47	hk × hk	Ax-184059738	52.81	hk × hk
Ax-184754120	29.70	hk × hk	Ax-184077358	54.12	nn × np
Ax-166516034	35.24	hk × hk	Ax-184082430	54.73	nn × np
Ax-166516204	36.16	hk × hk	Ax-184059732	56.56	nn × np
Ax-184689714	37.39	hk × hk	Ax-123358218	58.95	hk × hk
Ax-123525443	38.31	hk × hk	Ax-184105987	66.28	hk × hk
Ax-166525342	39.54	hk × hk	Ax-184112877	67.83	hk × hk
Ax-184400373	40.45	hk × hk	Ax-184506904	69.38	hk × hk
Ax-184061381	42.61	hk × hk	Ax-184038790	71.24	hk × hk
Ax-123366428	43.53	hk × hk	Ax-184208122	73.09	hk × hk
Ax-184609768	44.75	lm × ll	Ax-184261460	74.50	nn × np
Ax-184288146	45.97	hk × hk	Ax-184317536	77.20	hk × hk
Ax-184894028	47.51	hk × hk	Ax-184586727	79.68	hk × hk
Ax-166525427	48.74	lm × ll	<b>Rubygem (LG26)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
<b>Fortuna (LG25)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184075097	0.00	nn × np
Ax-123367129	0	hk × hk	Ax-166510726	1.83	nn × np
Ax-184072581	0.92	hk × hk	Ax-184109780	3.66	nn × np
Ax-166523016	2.45	hk × hk	Ax-184075087	4.88	hk × hk
Ax-166506092	17.15	hk × hk	Ax-123359978	6.10	nn × np
Ax-123358289	21.19	hk × hk	Ax-184568972	7.30	hk × hk
Ax-166517968	23.04	hk × hk	Ax-184224274	9.15	hk × hk
Ax-184564766	23.96	hk × hk	Ax-184061931	10.07	hk × hk
Ax-184059776	25.51	hk × hk	Ax-184464881	14.12	hk × hk
Ax-184169379	27.35	hk × hk	Ax-184967624	19.79	hk × hk
Ax-123364775	28.27	hk × hk	Ax-184312710	21.03	hk × hk
Ax-184052674	29.19	hk × hk	Ax-123363529	21.95	hk × hk
Ax-123361566	30.11	hk × hk	Ax-184065984	23.19	hk × hk
Ax-184120048	31.34	hk × hk	Ax-184773592	24.41	hk × hk
Ax-184120024	38.71	lm × ll	Ax-166511006	27.20	hk × hk
Ax-184151435	44.76	hk × hk	Ax-123366844	29.05	hk × hk
Ax-184428489	45.68	hk × hk	Ax-184193751	30.58	hk × hk
Ax-184059749	46.60	hk × hk	Ax-123357155	31.50	hk × hk
Ax-184059738	60.06	hk × hk	Ax-184058000	33.36	hk × hk
Ax-123358218	67.49	hk × hk	Ax-123357147	34.90	hk × hk
Ax-166523248	71.07	lm × ll	Ax-184335312	36.44	hk × hk
Ax-184105987	74.97	hk × hk	Ax-184256794	37.36	hk × hk
Ax-184112877	76.52	hk × hk	Ax-184080133	38.58	hk × hk
Ax-184506904	78.07	hk × hk	Ax-184939793	39.50	hk × hk
Ax-184038790	79.93	hk × hk	Ax-184018056	40.42	hk × hk
Ax-184208122	81.78	hk × hk	Ax-184402222	41.96	hk × hk
Ax-184317536	86.49	hk × hk	Ax-184267665	43.18	hk × hk
Ax-184586727	88.96	hk × hk	Ax-184894598	44.10	hk × hk

<b>Fortuna (LG26)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184848261	45.65	hk × hk
Ax-184075087	0	hk × hk	Ax-184085367	47.19	hk × hk
Ax-184568972	3.48	hk × hk	Ax-184725726	48.11	hk × hk
Ax-184224274	5.33	hk × hk	Ax-184862738	49.03	hk × hk
Ax-184061931	6.25	hk × hk	Ax-184610934	50.26	hk × hk
Ax-184040043	11.26	lm × ll	Ax-184193820	51.48	hk × hk
Ax-184464881	14.80	hk × hk	Ax-184109872	52.41	hk × hk
Ax-184124024	15.98	lm × ll	Ax-184854346	53.65	hk × hk
Ax-184967624	19.60	hk × hk	Ax-184545572	54.88	hk × hk
Ax-184312710	20.83	hk × hk	Ax-184131966	55.80	hk × hk
Ax-123363529	21.76	hk × hk	Ax-184301327	57.03	hk × hk
Ax-184065984	22.99	hk × hk	Ax-184147744	57.95	hk × hk
Ax-184773592	24.22	hk × hk	Ax-184085402	60.75	hk × hk
Ax-166511006	27.00	hk × hk	Ax-166519952	62.60	hk × hk
Ax-123366844	28.85	hk × hk	Ax-184070419	63.83	hk × hk
Ax-184193751	30.39	hk × hk	Ax-123356973	64.75	hk × hk
Ax-123357155	31.30	hk × hk	Ax-184193854	65.67	hk × hk
Ax-184058000	33.16	hk × hk	Ax-184569119	67.20	hk × hk
Ax-123357147	34.71	hk × hk	Ax-184763256	68.13	hk × hk
Ax-184335312	36.24	hk × hk	Ax-123359936	69.05	hk × hk
Ax-184256794	37.16	hk × hk	Ax-166510437	70.29	hk × hk
Ax-184080133	38.39	hk × hk	Ax-184184081	71.21	hk × hk
Ax-184939793	39.31	hk × hk	Ax-166510611	72.13	hk × hk
Ax-184018056	40.23	hk × hk	Ax-184413541	73.39	hk × hk
Ax-184402222	41.76	hk × hk	Ax-184062002	74.59	nn × np
Ax-184267665	42.99	hk × hk	Ax-184030672	77.06	hk × hk
Ax-184894598	43.91	hk × hk	Ax-166517529	79.22	hk × hk
Ax-184848261	45.45	hk × hk	Ax-184346735	81.38	hk × hk
Ax-184085367	47.00	hk × hk	Ax-184576258	82.97	hk × hk
Ax-184725726	47.92	hk × hk	Ax-184256987	85.57	hk × hk
Ax-184862738	48.83	hk × hk	Ax-184165544	86.82	hk × hk
Ax-184610934	50.06	hk × hk	Ax-166510346	91.28	hk × hk
Ax-184193820	51.29	hk × hk	<b>Rubygem (LG27)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184109872	52.21	hk × hk	Ax-184062384	0.00	hk × hk
Ax-184854346	53.45	hk × hk	Ax-123357237	4.20	hk × hk
Ax-184545572	54.69	hk × hk	Ax-184724124	5.13	hk × hk
Ax-184131966	55.61	hk × hk	Ax-184103763	7.31	hk × hk
Ax-184301327	56.83	hk × hk	Ax-184935342	8.23	hk × hk
Ax-184147744	57.75	hk × hk	Ax-184091572	9.15	hk × hk
Ax-184085402	60.55	hk × hk	Ax-184091574	10.38	hk × hk
Ax-166519952	62.41	hk × hk	Ax-184291206	11.30	hk × hk
Ax-184070419	63.64	hk × hk	Ax-184945296	12.22	hk × hk
Ax-123356973	64.55	hk × hk	Ax-184257988	13.14	hk × hk
Ax-184193854	65.47	hk × hk	Ax-184504029	24.73	nn × np
Ax-184569119	67.01	hk × hk	Ax-184257923	25.95	nn × np
Ax-184763256	67.93	hk × hk	Ax-166511170	26.56	nn × np

Ax-123359936	68.86	hk × hk	Ax-184097511	27.78	nn × np
Ax-166510437	70.09	hk × hk	Ax-184132456	29.00	nn × np
Ax-184184081	71.02	hk × hk	Ax-184871148	30.83	nn × np
Ax-166510611	71.94	hk × hk	Ax-184029397	32.66	nn × np
Ax-184413541	73.19	hk × hk	Ax-184562215	34.49	nn × np
Ax-184030672	76.70	hk × hk	Ax-184569816	36.72	hk × hk
Ax-166517529	78.86	hk × hk	Ax-184018835	38.25	hk × hk
Ax-184346735	81.02	hk × hk	Ax-184645936	39.38	nn × np
Ax-184576258	82.60	hk × hk	Ax-166512038	41.21	nn × np
Ax-184256987	85.21	hk × hk	Ax-184117506	43.04	nn × np
Ax-184165544	86.45	hk × hk	Ax-166509680	44.87	nn × np
Ax-166510346	90.91	hk × hk	Ax-184503940	46.70	nn × np
<b>Fortuna (LG27)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-123357443	47.82	hk × hk
Ax-184062384	0	hk × hk	Ax-123360891	48.94	nn × np
Ax-123357237	4.20	hk × hk	Ax-184214989	50.29	hk × hk
Ax-184724124	5.13	hk × hk	Ax-166521289	51.52	hk × hk
Ax-184103763	7.31	hk × hk	Ax-166527442	52.44	hk × hk
Ax-184935342	8.23	hk × hk	Ax-166508115	53.98	hk × hk
Ax-184091572	9.15	hk × hk	Ax-184702999	55.21	hk × hk
Ax-184091574	10.38	hk × hk	Ax-184392268	56.74	hk × hk
Ax-184291206	11.30	hk × hk	Ax-184175340	57.66	hk × hk
Ax-184945296	12.22	hk × hk	Ax-184085849	58.58	hk × hk
Ax-184257988	13.14	hk × hk	Ax-184257763	59.50	hk × hk
Ax-184569816	35.74	hk × hk	Ax-184605063	60.43	hk × hk
Ax-184018835	37.27	hk × hk	Ax-184029378	61.35	hk × hk
Ax-123357443	46.26	hk × hk	Ax-184140436	62.58	hk × hk
Ax-184214989	47.19	hk × hk	Ax-184091610	63.50	hk × hk
Ax-166521289	48.41	hk × hk	Ax-184117628	64.73	hk × hk
Ax-166527442	49.33	hk × hk	Ax-184117630	65.65	hk × hk
Ax-166508115	50.87	hk × hk	Ax-184042760	67.49	hk × hk
Ax-184702999	52.10	hk × hk	Ax-166503810	68.41	hk × hk
Ax-184392268	53.64	hk × hk	Ax-184456160	69.64	hk × hk
Ax-184175340	54.55	hk × hk	Ax-184032406	70.56	hk × hk
Ax-184085849	55.47	hk × hk	Ax-184280010	72.79	nn × np
Ax-184257763	56.39	hk × hk	Ax-184937252	74.02	nn × np
Ax-184605063	57.32	hk × hk	Ax-184530181	75.26	nn × np
Ax-184029378	58.24	hk × hk	Ax-184117680	75.88	nn × np
Ax-184140436	59.47	hk × hk	Ax-123366900	87.04	hk × hk
Ax-184091610	60.39	hk × hk	Ax-184036013	88.58	hk × hk
Ax-184117628	61.62	hk × hk	<b>Rubygem (LG28)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184117630	62.54	hk × hk	Ax-184354681	0.00	nn × np
Ax-184042760	64.39	hk × hk	Ax-166515609	14.41	nn × np
Ax-166503810	65.30	hk × hk	Ax-184181383	16.24	nn × np
Ax-184456160	66.53	hk × hk	Ax-166507416	18.07	nn × np
Ax-184032406	67.46	hk × hk	Ax-166518203	20.70	hk × hk
Ax-184086017	73.23	lm × ll	Ax-184129605	22.24	hk × hk

Ax-184521533	73.85	lm × ll	Ax-184919233	23.16	hk × hk
Ax-184623841	75.70	lm × ll	Ax-184462066	28.52	nn × np
Ax-123366900	89.28	hk × hk	Ax-123364276	32.42	hk × hk
Ax-184036013	90.82	hk × hk	Ax-184309380	33.65	hk × hk
<b>Fortuna (LG28)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-166507570	34.58	hk × hk
Ax-166518203	0	hk × hk	Ax-184137386	35.81	hk × hk
Ax-184129605	1.54	hk × hk	Ax-184286375	36.73	hk × hk
Ax-184919233	2.46	hk × hk	Ax-184388145	37.64	hk × hk
Ax-123364276	7.62	hk × hk	Ax-184668151	38.56	hk × hk
Ax-184309380	8.85	hk × hk	Ax-184286750	39.48	hk × hk
Ax-166507570	9.78	hk × hk	Ax-123366361	40.71	hk × hk
Ax-184137386	11.00	hk × hk	Ax-184320894	42.25	hk × hk
Ax-184286375	11.92	hk × hk	<b>Rubygem (LG29)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184388145	12.84	hk × hk	Ax-184045652	0.00	hk × hk
Ax-184668151	13.76	hk × hk	Ax-184415141	1.23	hk × hk
Ax-184286750	14.68	hk × hk	Ax-184226382	2.45	hk × hk
Ax-123366361	15.91	hk × hk	Ax-166510204	8.13	hk × hk
Ax-184320894	17.45	hk × hk	Ax-184269793	9.05	hk × hk
Ax-184163204	33.35	lm × ll	Ax-184141205	11.52	hk × hk
Ax-184221817	35.18	lm × ll	Ax-123366983	12.44	hk × hk
Ax-184191302	37.01	lm × ll	Ax-184585208	13.98	hk × hk
Ax-184254047	38.84	lm × ll	Ax-184337692	14.90	hk × hk
Ax-184129810	41.89	lm × ll	Ax-184393425	15.82	hk × hk
Ax-184232243	43.72	lm × ll	Ax-166503869	17.04	hk × hk
Ax-184933645	46.25	lm × ll	Ax-184281005	18.27	hk × hk
<b>Fortuna (LG29)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184025139	19.19	hk × hk
Ax-184045652	0	hk × hk	Ax-166521364	20.42	hk × hk
Ax-184415141	1.23	hk × hk	Ax-123360634	21.34	hk × hk
Ax-184226382	2.45	hk × hk	Ax-184062820	22.87	hk × hk
Ax-184205830	3.69	lm × ll	Ax-184216180	25.23	nn × np
Ax-166510204	4.92	hk × hk	Ax-184302880	27.06	nn × np
Ax-184269793	5.84	hk × hk	<b>Rubygem (LG30)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184141205	8.32	hk × hk	Ax-123358731	0.00	nn × np
Ax-123366983	9.23	hk × hk	Ax-184120699	0.61	nn × np
Ax-184585208	10.77	hk × hk	Ax-184088599	1.84	nn × np
Ax-184337692	11.69	hk × hk	Ax-166515138	2.45	nn × np
Ax-184393425	12.61	hk × hk	Ax-184210106	4.91	nn × np
Ax-166503869	13.84	hk × hk	Ax-166506945	6.14	nn × np
Ax-184281005	15.07	hk × hk	Ax-184241903	6.75	nn × np
Ax-184025139	15.98	hk × hk	Ax-184331327	7.97	nn × np
Ax-166521364	17.21	hk × hk	Ax-166506943	9.80	nn × np
Ax-123360634	18.13	hk × hk	Ax-166506183	11.63	nn × np
Ax-184062820	19.67	hk × hk	Ax-184107433	13.46	nn × np
<b>Fortuna (LG30)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-123365966	17.42	hk × hk
Ax-184280872	0	lm × ll	Ax-184353830	18.64	hk × hk
Ax-123365966	1.32	hk × hk	Ax-123361799	19.87	hk × hk

Ax-184353830	2.54	hk × hk	Ax-123361809	21.10	hk × hk
Ax-123361799	3.77	hk × hk	Ax-184083576	22.02	hk × hk
Ax-123361809	5.00	hk × hk	Ax-184342739	22.94	hk × hk
Ax-184083576	5.92	hk × hk	Ax-184893255	23.86	hk × hk
Ax-184342739	6.84	hk × hk	Ax-184461491	25.40	hk × hk
Ax-184893255	7.76	hk × hk	Ax-166506608	27.24	hk × hk
Ax-184461491	9.29	hk × hk	Ax-184136945	29.09	hk × hk
Ax-166506608	11.14	hk × hk	Ax-184558719	30.32	hk × hk
Ax-184136945	12.99	hk × hk	Ax-184658720	31.25	hk × hk
Ax-184558719	14.22	hk × hk	Ax-184481206	32.49	hk × hk
Ax-184658720	15.15	hk × hk	Ax-123357048	34.65	hk × hk
Ax-184481206	16.39	hk × hk	Ax-184297344	36.82	hk × hk
Ax-123357048	18.55	hk × hk	Ax-123358553	37.73	hk × hk
Ax-184297344	20.71	hk × hk	Ax-184041680	38.65	hk × hk
Ax-123358553	21.63	hk × hk	Ax-123366038	39.57	hk × hk
Ax-184041680	22.55	hk × hk	Ax-123358590	41.11	hk × hk
Ax-123366038	23.47	hk × hk	Ax-123358547	42.03	hk × hk
Ax-123358590	25.01	hk × hk	Ax-184699322	43.26	hk × hk
Ax-123358547	25.93	hk × hk	Ax-184028843	44.79	hk × hk
Ax-184699322	27.16	hk × hk	Ax-184050084	45.71	hk × hk
Ax-184028843	28.69	hk × hk	Ax-184121566	46.63	hk × hk
Ax-184050084	29.61	hk × hk	Ax-166514730	47.55	hk × hk
Ax-184121566	30.53	hk × hk	<b>Rubygem (LG31)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-166514730	31.45	hk × hk	Ax-166508807	0.00	nn × np
<b>Fortuna (LG31)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-166508818	1.22	nn × np
Ax-184090415	0	hk × hk	Ax-184233903	13.02	nn × np
Ax-184846918	1.54	hk × hk	Ax-123359583	14.24	nn × np
Ax-184883066	3.08	hk × hk	Ax-184544750	16.68	nn × np
Ax-184116238	4.30	hk × hk	Ax-166508692	17.29	nn × np
Ax-184422804	5.22	hk × hk	Ax-166518380	18.51	nn × np
Ax-184568315	6.15	hk × hk	Ax-184090415	22.63	hk × hk
Ax-184029133	7.07	hk × hk	Ax-184846918	24.17	hk × hk
Ax-123364445	7.99	hk × hk	Ax-184883066	25.70	hk × hk
Ax-184780967	8.92	hk × hk	Ax-184116238	26.93	hk × hk
Ax-184597081	10.15	hk × hk	Ax-184422804	27.85	hk × hk
Ax-166519604	11.07	hk × hk	Ax-184568315	28.78	hk × hk
Ax-184029134	12.61	hk × hk	Ax-184029133	29.70	hk × hk
Ax-184277733	14.46	hk × hk	Ax-123364445	30.62	hk × hk
Ax-123363395	15.59	hk × hk	Ax-184780967	31.55	hk × hk
Ax-184411516	17.26	lm × ll	Ax-184597081	32.78	hk × hk
<b>Fortuna (LG32)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-166519604	33.70	hk × hk
Ax-184431612	0	hk × hk	Ax-184029134	35.24	hk × hk
Ax-184089521	1.23	hk × hk	Ax-184277733	37.08	hk × hk
Ax-184442071	2.47	hk × hk	Ax-123363395	38.62	hk × hk
Ax-184388475	3.40	hk × hk	Ax-184668968	48.89	nn × np
<b>Fortuna (LG33)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184860262	49.50	nn × np



Ax-166505239	0	hk × hk	Ax-184057718	51.96	nn × np
Ax-184969051	0.92	hk × hk	Ax-184131064	54.40	nn × np
Ax-184531701	1.85	hk × hk	Ax-123359620	56.23	nn × np
Ax-184753741	2.77	hk × hk	Ax-123359716	56.84	nn × np
Ax-184487465	4.61	hk × hk	Ax-184234034	58.67	nn × np
Ax-184071834	5.53	hk × hk	Ax-123363004	60.50	nn × np
Ax-166512356	6.45	hk × hk	Ax-166517490	61.72	nn × np
Ax-184071841	7.67	hk × hk	Ax-123358007	63.55	nn × np
Ax-166512807	9.22	hk × hk	Ax-184967147	65.39	nn × np
Ax-184670893	15.12	hk × hk	Ax-123364522	67.23	nn × np
Ax-166504462	16.67	hk × hk	Ax-166509021	69.06	nn × np
Ax-184505936	21.70	hk × hk	Ax-166509590	69.67	nn × np
Ax-123363734	23.54	hk × hk	Ax-123364150	71.50	nn × np
Ax-166510266	24.78	hk × hk	Ax-123359672	72.11	nn × np
Ax-184081848	26.31	hk × hk	Ax-184223643	73.33	nn × np
Ax-123361053	28.16	hk × hk	Ax-184898312	74.55	nn × np
Ax-184207065	29.08	hk × hk	<b>Rubygem (LG32)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184043307	30.31	hk × hk	Ax-184060953	0.00	nn × np
Ax-184150388	31.24	hk × hk	Ax-184050503	0.61	nn × np
Ax-166517853	32.16	hk × hk	Ax-123359261	1.83	nn × np
Ax-184217389	33.08	hk × hk	Ax-123359265	2.44	nn × np
Ax-123357848	34.31	hk × hk	Ax-123362883	3.66	nn × np
Ax-184187096	35.23	hk × hk	Ax-184309621	5.49	nn × np
Ax-166504873	36.15	hk × hk	Ax-123362894	6.10	nn × np
<b>Fortuna (LG39)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-123367498	7.32	nn × np
Ax-166514015	0	hk × hk	Ax-184668275	8.54	nn × np
Ax-184418266	1.54	hk × hk	Ax-123364813	10.37	nn × np
Ax-184240252	2.76	hk × hk	Ax-123359337	11.59	nn × np
Ax-184228500	3.71	hk × hk	Ax-123356929	12.20	nn × np
Ax-166505819	4.96	hk × hk	Ax-184431612	16.05	hk × hk
Ax-184250834	5.89	hk × hk	Ax-184089521	17.28	hk × hk
Ax-184374524	6.82	hk × hk	Ax-184442071	18.52	hk × hk
Ax-123357996	8.05	hk × hk	Ax-184388475	19.45	hk × hk
<b>Fortuna (LG40)</b>	<b>Positions (cM)</b>	<b>Segregation</b>	Ax-184122221	20.79	nn × np
Ax-184877607	0	hk × hk	Ax-184309707	23.35	nn × np
Ax-166505233	0.93	hk × hk	<b>Rubygem (LG33)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184327486	1.84	hk × hk	Ax-166505239	0.00	hk × hk
Ax-184206852	2.76	hk × hk	Ax-184969051	0.92	hk × hk
Ax-123366944	3.99	hk × hk	Ax-184531701	1.85	hk × hk
Ax-184052168	4.91	hk × hk	Ax-184753741	2.77	hk × hk
Ax-184457909	5.83	hk × hk	Ax-184487465	4.61	hk × hk
Ax-166512645	6.75	hk × hk	Ax-184071834	5.53	hk × hk
Ax-123357972	7.98	hk × hk	Ax-166512356	6.45	hk × hk
Ax-184756836	8.90	hk × hk	Ax-184071841	7.67	hk × hk
Ax-184168267	15.95	hk × hk	Ax-166512807	9.22	hk × hk
Ax-184477718	17.49	hk × hk	Ax-123357771	10.63	nn × np

Ax-184578616	18.41	hk × hk	Ax-184670893	11.85	hk × hk
Ax-123366933	19.33	hk × hk	Ax-184134216	13.07	nn × np
Ax-184055459	20.56	hk × hk	Ax-166504462	14.34	hk × hk
Ax-166522559	21.48	hk × hk	Ax-184505936	19.36	hk × hk
Ax-166510269	23.01	hk × hk	Ax-184304843	20.55	nn × np
Ax-184248990	24.25	hk × hk	Ax-123363734	24.04	hk × hk
Ax-123365613	25.18	hk × hk	Ax-166510266	25.28	hk × hk
Ax-184141912	26.41	hk × hk	Ax-184081848	26.82	hk × hk
Ax-166505041	27.34	hk × hk	Ax-123361053	28.67	hk × hk
Ax-184186719	28.26	hk × hk	Ax-184207065	29.58	hk × hk
Ax-184206730	29.17	hk × hk	Ax-184043307	30.81	hk × hk
Ax-184031116	30.71	hk × hk	Ax-184150388	31.74	hk × hk
Ax-184259939	31.63	hk × hk	Ax-166517853	32.66	hk × hk
Ax-184416020	37.14	hk × hk	Ax-184217389	33.58	hk × hk
Ax-184641557	38.98	hk × hk	Ax-123357848	34.81	hk × hk
Ax-184505573	39.90	hk × hk	Ax-184187096	35.73	hk × hk
Ax-184877566	40.82	hk × hk	Ax-166504873	36.65	hk × hk
Ax-123357726	41.75	hk × hk	<b>Rubygem (LG39)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
Ax-184248885	42.68	hk × hk	Ax-184273320	0.00	nn × np
			Ax-184188968	0.61	nn × np
			Ax-184022487	2.44	nn × np
			Ax-166514015	10.85	hk × hk
			Ax-184418266	12.39	hk × hk
			Ax-184240252	13.62	hk × hk
			Ax-184228500	14.56	hk × hk
			Ax-166505819	15.81	hk × hk
			Ax-184250834	16.74	hk × hk
			Ax-184374524	17.67	hk × hk
			Ax-123357996	18.90	hk × hk
			<b>Rubygem (LG40)</b>	<b>Positions (cM)</b>	<b>Segregation</b>
			Ax-184877607	0.00	hk × hk
			Ax-166505233	0.93	hk × hk
			Ax-184327486	1.84	hk × hk
			Ax-184206852	2.76	hk × hk
			Ax-123366944	3.99	hk × hk
			Ax-184052168	4.91	hk × hk
			Ax-184457909	5.83	hk × hk
			Ax-166512645	6.75	hk × hk
			Ax-123357972	7.98	hk × hk
			Ax-184756836	8.90	hk × hk
			Ax-184168267	15.95	hk × hk
			Ax-184477718	17.49	hk × hk
			Ax-184578616	18.41	hk × hk
			Ax-123366933	19.33	hk × hk
			Ax-184055459	20.56	hk × hk
			Ax-166522559	21.48	hk × hk

			Ax-166510269	23.01	hk × hk
			Ax-184248990	24.25	hk × hk
			Ax-123365613	25.18	hk × hk
			Ax-184141912	26.41	hk × hk
			Ax-166505041	27.34	hk × hk
			Ax-184186719	28.26	hk × hk
			Ax-184206730	29.17	hk × hk
			Ax-184031116	30.17	hk × hk
			Ax-184259939	31.63	hk × hk
			Ax-184416020	37.14	hk × hk
			Ax-184641557	38.98	hk × hk
			Ax-184505573	39.90	hk × hk
			Ax-184877566	40.82	hk × hk
			Ax-123357726	41.75	hk × hk
			Ax-184248885	42.68	hk × hk
			Ax-184126175	44.09	nn × np
			Ax-184048893	45.31	nn × np

**Supplementary Table S2.** List of linked markers, gene IDs, and functional information associated with linked loci.

Markers related to leaf	Panel	Chr	Pos	Allel A	Allel B	Gene ID	New ID	GO	KEGG	Go description	IPR description
Ax-184251409	Fana_SNP	Fvb4-4	9740764	A	G	Fvb4-4-snap-gene-97.34	FxaC_14g19050	-	-		Region of a membrane-bound protein predicted to be embedded in the membrane.
Ax-184047067	Fana_SNP	Fvb6-1	13163884	C	T	-	-	-	-	-	-
Ax-184297806	Fana_SNP	Fvb6-1	26330375	A	G	Fvb6-1-snap-gene-263.45	FxaC_21g50810	GO:0031011	IPR02486Z	Cellular Component:Ino80 complex	Nuclear factor related to kappa-B-binding protein
Ax-123614760	iStraw35	Fvb6	5808306	-	CAG						
Ax-166505239	iStraw35	Fvb3	25825109	C	T						
Markers related to fruit	Panel	Chr	Pos								
Ax-184547649	Fana_SNP	Fvb3-1	26978746	C	T						
Ax-184051916	Fana_SNP	Fvb2-4	14876565	G	T	Fvb2-4-snap-gene-148.38	FxaC_6g23420		IPR022552		Uncharacterized protein family Ycf55
Ax-123360550	iStraw35	Fvb2	13650030	A	C						
Ax-184191302	Fana_SNP	Fvb6-2	30561696	C	T	snap_masked-Fvb6-2-processed-gene-305.35	FxaC_23g50910				

**Supplementary Table S3.** Number of markers defined in each LG corresponding to chromosomes (Chrs) of *F. vesca* and *F. × ananasa*.

LG	Fortuna					Rubygem									
	<i>F. vesca</i>		Chrs	Fana array			LG	<i>F. vesca</i>		Fana array					
	Chrs	Number of markers		1	2	3		4	Chrs	Number of markers	1	2	3	4	
1	1	3		2	13		1	1	5			19			
2	1	14			1	13	2	1	12			1	1	8	
19	1	1	4			1	19	1	7			6	1	7	
26	1	10	1	41	3		26	1	11			1	42	3	
3	2	21	3	24		1	3	2	19			3	27	1	
20	2	14			27	1	20	2	16			1		34	
21	2	2				7	21	2	3			39		12	
27	2	6	30				27	2	10					1	
29	2	5				12	29	2	5				1	12	
40	2	1					40	2	1						
4	3	23	1	2	2	32	4	3	21			1	2	1	28
5	3	6	27		1		5	3	8			33		3	
33	3	7					33	3	8				16		
40	3	9		20	1		40	3	9				22	1	
6	4	6	23		2	1	6	4	2			14		1	1
7	4	1				5	7	4	4						14
8	4	10			19		8	4	11					13	
25	4	7		19			25	4	8				24		
39	4	3	1	1	3		31	4	1						
9	5	18		19	23	1	39	4	3			1	1	3	3
10	5	12	15			1	9	5	12					13	16
14	5	4				7	10	5	8					8	1
22	5	3	2	1	1		14	5	4					10	
30	5	8				15	22	5	5					1	



