Genome-wide identification of putative disease resistance genes (R genes) in carrot (*Daucus carota* subsp. *sativus*) by homology-based gene prediction

Anastassia Boudichevskaia[1], Thomas Berner[2], Jens Keilwagen[2], Frank Dunemann[3]*

[1]KWS SAAT SE & Co. KGaA, Grimsehlstr. 31, 37574 Einbeck, Germany

[2]Julius Kühn-Institut (JKI), Federal Research Centre for Cultivated Plants, Institute for Biosafety in Plant Biotechnology, Erwin-Baur-Str. 27, 06484 Quedlinburg, Germany

[3]Julius Kühn-Institut (JKI), Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Horticultural Crops, Erwin-Baur-Str. 27, 06484 Quedlinburg, Germany

*correspondence to: frank.dunemann@julius-kuehn.de

Abstract

The cultivated carrot (*Daucus carota* ssp. *sativus)* is one of the most important root vegetable crops grown worldwide. Carrots are highly susceptible to several pests and diseases, and disease resistance is currently among the main breeding aims. The inheritance of resistance has been reported for a few carrot foliar diseases and root-knot nematodes, but no functionally characterized resistance gene (R gene) has yet been linked as a candidate gene to any resistance locus in carrot. Knowledge about the inventory of NLR genes (nucleotide-binding leucine-rich repeat receptors) and other R genes encoding transmembrane proteins such as receptor-like proteins (RLPs) and kinases (KIN) would be necessary to associate major QTLs (quantitative trait loci) identified by bi-parental QTL analyses or GWAS (genome-wide association analysis) with functional candidate R genes. In this study, we describe a combination of a genome-wide inventory of putative full-length carrot R genes based on a homology-based gene prediction approach called GeMoMa and subsequent classification by usage of the recent version of PRGdb 4.0 database (Calle-Garcia et al. 2022). A total of 320 putative carrot R genes were identified and bioinformatically characterized, including 72 newly identified gene models, that have not yet been annotated in the currently available carrot whole genome sequence. Based on the DRAGO 3 pipeline, totally 137 putative NLR genes were found, whereas 162 putative functional RLP and KIN genes were identified in the carrot genome. About one third of the R genes was found to be organized in clusters consisting only of NLR, RLP or KIN genes. To determine the evolutionary relationships of carrot R gene predictions, we generated a phylogenetic tree based on the alignment of all 320 R proteins. Three large clades (NLR, RLP and KIN) and a small clade (RLK) were identified, which reflect well the classification obtained after DRAGO 3 analysis. The presented carrot R gene inventory might be useful for resistance gene isolation, the development of (functional) molecular markers and resistance breeding in carrot.

Keywords: Carrot genome, resistance gene, annotation, gene prediction, R gene inventory, R gene map, gene cluster

Background

The cultivated carrot (*Daucus carota* ssp. *sativus)* is one of the most important root vegetable crops grown worldwide. Carrot production can be affected by a wide range of pests and pathogens. At least five diseases of carrot are caused by bacterial pathogens, 36 by fungal and oomycete pathogens, two by phytoplasmas, and 13 by viruses (Du Toit et al. 2019). Additionally, seven genera of nematodes and several insect and mite pests can impair carrot cultivation (Du Toit et al. 2019). Among the most important foliar diseases are leaf blight caused by the fungus *Alternaria dauci*, leaf spot disease (*Cercospora carotae*), bacterial blight (*Xanthomonas hortorum* pv. *carotae*), and powdery mildew (*Erysiphe heraclei*) (Davis and Raid 2002). The most widespread soilborne root pathogens of carrot are cavity spot (caused by several species of *Pythium*), white mold (*Sclerotinia sclerotiorum*), and root-knot nematodes (various species of *Meloidogyne*) (Davis and Raid 2002). Storage diseases are mainly caused by necrotrophic fungi, such as *Botrytis cinerea* (gray mold), and *Mycocentrospora acerina* (liquorice rot disease).

Despite the numerous biotic stress factors that can impact carrot growth and storage, comparatively less is known about putative resistances and, therefore, about the genetics of resistances. The inheritance of resistance has been reported for a few carrot foliar diseases and root-knot nematodes. For instance, monogenic resistance to two foliar diseases, *Cercospora* leaf spot and powdery mildew, was reported, but resistance genes have not yet been mapped (Simon 2019). Several quantitative trait loci (QTLs) for leaf blight resistance (*Alternaria dauci*) were identified by Le Clerc et al. (2015, 2019). For resistance to the root knot nematode *Meloidogyne javanica* two loci called as *Mj-1* and *Mj-2* were mapped on carrot chromosome 8 at different positions (Ali et al. 2014, Parsons et al. 2015). With a single exception, no predicted or functionally characterized resistance gene (R gene) has been associated yet as a candidate gene with any resistance in carrot. A cluster consisting of four putative R genes spanning a region of only 50 kb co-localized in the same region of chromosome 8 as the *Mj-1* locus (Iorizzo et al. 2016). The occurrence of the first carrot whole genome sequence (Iorizzo et al. 2016) and the progress made in candidate gene identification by SNP-based genome-wide association analyses (GWAS) of carrot natural substances (Keilwagen et al. 2017, Ellison et al. 2018) implicate such approaches also for carrot disease resistance research. As a first basis, a preliminary characterization of the carrot R gene inventory in the carrot genome has yielded a large number of more than 600 putative R gene sequences (Iorizzo et al. 2016).

As plants are immobile, they have evolved two major types of disease resistance, basal defense and R gene mediated defense (Gururani et al. 2012). Basal defense, which can be a constituent of both non-host and host resistance, provides the first line of defense to the infection by a wide range of pathogens. R gene-mediated pathogen resistance is mainly based on effector molecules encoded by Avr (avirulence) genes of the pathogen, which are delivered directly into the plant cells during initial stage of infection. The effectors found in viral pathogens, bacteria, oomycetes, fungi, nematodes or insects cause a plant pathogen to elicit a resistance response in a host plant. These receptors coded by R genes are mainly intracellular, and they can specifically interact with pathogen effectors coded by the Avr genes following the gene-for-gene relationship model (Borelli et al. 2018). Plant R genes have been identified from numerous species through genetic approaches, and these loci are associated with resistance to a wide spectrum of pathogens. Although plants are confronted by such a large variety of pathogens with different modes of pathogenesis (e.g., biotrophs versus necrotrophs), most R genes belong to a limited set of proteins that are made up of a conserved set of domains, whose organization is used to define them (Dangl and Jones 2001, Hammond-Kosack and Parker 2003). Through a comprehensive review, Kourelis and van der Horn (2018) identified a number of 314 cloned functional

plant R genes. Only 128 of the 314 gene products have a proposed mechanism, and the majority of these R genes encode cell surface or intracellular receptors (Kourelis and van der Horn 2018).

More than two thirds of plant disease resistance genes encode nucleotide-binding leucine-rich repeat receptors (NLRs), and most plant genomes carry a repertoire of hundreds of NLR genes (Van de Weyer et al. 2019). Based on their N-terminal structures, these R proteins can be further divided into two subclasses: TIR-NBS-LRR (TNL) that possesses a domain homologous to the Toll and interleukin-1 receptor (TIR), and non-TNL. Most non-TNL R proteins have a coiled-coil (CC) structure at the N terminal and are often called CC-NBS-LRR (CNL) R proteins (Wei et al 2018). The LRRs (Leucine rich repeats) represent the components that play an important role in recognition specificity, and these domains are present in the majority of R proteins (Jones 2001). There are a few further classes including groups that contain neither LRRs nor NBS domains but other functional domains, such as an intracellular serine-threonine kinase domain (Gururani et al. 2012). Transmembrane receptor proteins containing kinase and LRR domains, such as receptor-like proteins (RLP) and the receptor-like kinases (RLK), are also involved (Osuna-Cruz 2018). In the last years, several online omics platforms have been offered to facilitate the exploration, inventory and use of plant resistance genes. Among these platforms, the Pathogen Recognition Genes database (PRGdb) (Sanseverino et al. 2010) represents a user-friendly reference site and repository for plant geneticists interested in structure and putative function of genes involved in plant disease resistance.

In this study, we describe a combination of a genome wide inventory of predicted full-length carrot R genes based on a homology-based gene prediction approach called GeMoMa (Keilwagen et al. 2016) and usage of the PRGdb 4.0 database (Calle-Garcia et al. 2022) for classifying the predicted genes. A total of 320 putative carrot R genes were identified and bioinformatically characterized, including 72 gene models that have not yet been annotated in the current version of the carrot genome presented by Iorizzo et al. (2016).

Methods

For detecting resistance genes in carrot, homology-based gene prediction was utilized using a wide range of resistance genes from diverse plant species. Based on publicly available sequences of 110 known plant resistance genes, we collected the information about resistance transcript isoforms from eight reference genome annotations including *Arabidopsis thaliana*, *Glycine max*, *Malus domestica*, *Populus trichocarpa*, *Solanum lycopersicum*, *Solanum tuberosum*, *Sorghum bicolor*, and *Vitis vinifera.* In total, 810 putative R gene sequences selected from the reference genomes were used for homology-based gene prediction using the software GeMoMa. GeMoMa (version 1.4.3) was run for each reference species in combination with RNA-seq evidence (Keilwagen et al. 2017, 2018). The predictions of all reference species were combined using the module GAF yielding 602 gene predictions for carrot. The Integrative Genomics Viewer (IGV) (Robinson et al. 2011) was used as a visualization tool for the interactive exploration of predicted transcripts and annotated *Daucus* genome loci (DCAR sequences, Iorizzo et al. 2016). After this first round of screening, 375 gene models were selected for a second round of analysis to examine if the gene models are indeed complete. Translated protein sequences were analyzed manually by a BLAST P search at NCBI using the non-redundant protein sequence database, and only predicted full-length sequences with putative R gene function were selected for the final R gene inventory. DRAGO 3, the tool for automatic annotation and prediction of plant resistance genes implemented in PRGdb 4.0 database was used to identify the LRR, Kinase, NBS and TIR domains from 60 HMM modules created for this purpose using HMMER v3 package (Calle-Garcia et al. 2022). DRAGO 3 is also able to detect CC and TM domains using COILS 2.2 and TMHMM 2.0c

programs (Calle-Garcia et al. 2022). A phylogenetic analysis of 320 deduced *Daucus carota* R proteins was performed with MEGA-X after multiple sequence alignment by MUSCLE. Neighbor-joining method and n=1000 replicates for bootstrapping were applied. The software *MapChart* 2.2. (Plant Research International, Biometris, Wageningen, Netherlands) was used for R gene map visualization. R genes were considered clustered if at least three genes from the classes NLR, RLP or KIN were located within a genomic region < 200 kb.

Results and Discussion

The objective of this research was to conduct a genome-wide (re)-identification of R genes in the cultivated carrot. Initially, we predicted 602 putative R gene models after GeMoMa analysis. After manual evaluation using the IGV browser and elimination of too short and obviously fragmentary sequences, followed by BLAST P-based analyses for full-length CDS and predicted functions, 320 putative R gene models remained (Suppl. Table 1). Among these predicted genes, 72 of them (23%) have been newly identified since they have not yet been annotated in the current version of the carrot genome (Iorizzo et al. 2016). In addition, some new R gene clusters, such as the six-gene cluster at the beginning of chromosome Chr_3 (*DcRG_082 - DcRG_87*) or the four-gene cluster on Chr_7 (*DcRG_233 - DcRG_236*) were detected. Based on the DRAGO 3 pipeline, 137 putative NLR genes (43%) were found, whereas 172 putative genes encoding transmembrane proteins (54%) were identified in the carrot genome (Table 1). Among the NLR genes, the largest sub-class is the NBS-LRR (NL) type, followed by the TIR-NBS-LRR (TNL) type (Table 1). A few genes showing rare or unknown domain combinations such as CK or CL (Osuna-Cruz et al. 2018) were indeed genes possibly involved in plant resistance. For instance, genes *DcRG_169* and *DcRG_192* (CTNL class) were predicted in the *D. carota* genome as TMV resistance protein N-like isoforms X1 and X2 (Table 2). Only two genes (*DcRG_079* and *DcRG_222*) were not classified by DRAGO domain recognition but were predicted by BLAST as putative EDR2s (Table 2). These carrot genes are similar (amino acid identity ~ 80%) to the *A. thaliana EDR2* resistance gene (AT4G19040, Vorwerk et al. 2007). Because loss-of-function mutations in the *EDR2* gene confer enhanced disease resistance to powdery mildew in *A. thaliana, EDR2* probably functions as a negative regulator of powdery mildew resistance (Vorwerk et al. 2007). In the work of Iorizzo et al. (2016), MATRIX-R pipeline was used to automatically retrieve, annotate, and classify carrot R genes. Based on this pipeline, 634 putative R genes were predicted, which is comparable to the 602 gene models detected after GeMoMa analysis. However, based on sequence analyses of a random sample, we noticed that not all predicted sequences appeared to represent putative functional R genes (data not shown). In the study of Iorizzo et al. (2016), 295 R genes were assigned to the NLR classes of cytoplasmic proteins, and 339 genes were classified as transmembrane receptors. The NLR sub-class with the highest number of genes was the NL class (63 genes), which is in accordance with our finding of 64 NL genes in this sub-class (Table 1). The proportion of the NLRs at the total number of R genes was 46%, which is similar to the value found after GeMoMa (43%).

Over the past two decades, sequencing technologies have been rapidly developed and used to assess plant-microbe interactions (Lee et al. 2015). Their use enables genome-wide analyses of NLR genes based on the NB-ARC domain (Meyers et al. 2005). Because of their importance in ecology and breeding, there has been much interest in defining inventories of NLR genes at different taxonomic levels. These efforts have revealed that the number of NLR genes across species varies from less than a hundred to over a thousand (van de Weyer et al. 2019). The number of NLR genes in flowering plants is largely variable without any clear correlation to the phylogeny, suggesting species-specific mechanisms in NLR genes expansion and/or contraction (Jacob et al. 2013). *Arabidopsis thaliana* has

159 NLR genes including 43 CNLs and 83 TNLs (Guo et al. 2011). Solanaceae plants carry more than twice the number of NLR genes than *Arabidopsis* and possess more CNLs than TNLs (Lee et al. 2015). As reviewed by Jacob et al. (2013), species with large numbers of NLRs are rice and grape with each about 460 NLR genes. Nearly 1000 NLR genes have been identified in apple, although its genome size is only approximately 740 Mb (Velasco et al. 2010). Furthermore, there is also variation in the gene copy numbers of the two subclasses, TIR-type NLRs (TNL) and non-TIR-type NLRs (CNL). In our study, we observed a CNL-type NLR to TNL-type NLR ratio of 1:2. The same ratio was found in Brassicaceae species, in potato and grapevine it was 4:1, whereas a ratio of 1:1 has been reported for apple (Borelli et al. 2018). The importance of the NLR-type R genes for plant disease resistance is also documented by the number of cloned R genes. Out of the more than 300 cloned genes, 61% encode NLRs, but only 19% of the cloned R genes encode RLPs and RLKs (Kourelis and van der Horn 2018).

The predicted carrot R genes are not evenly distributed over the nine chromosomes. The number of R genes varied between only 19 on chromosome Chr_6 and 52 on Chr_3 (Table 3). As demonstrated by the R gene map presented in Figure 1, some genomic regions appear to have no or a fewer number of R genes. Especially dense R gene regions were observed on chromosomes Chr_1 (lower end), Chr_2 (whole chromosome), Chr_3 (upper and lower part), Chr_4 (middle part), Chr_5 (lower end), Ch_7 (lower half), Chr_8 (lower half), and Chr_9 (whole chromosome). NLRs, RLPs and kinases (KIN) showed a clear tendency for clustering (Figure 1, Suppl. Table 1). The size of clusters is rather variable. The largest cluster on Chr_8 contains 11 NLRs within an interval of about 250 kb, and the second-largest NLR cluster was found on Chr_7 with 9 genes within a 340 kb-interval. Both clusters are heterogenous and contain a mixture of diverse NLRs, i.e. NL, CNL, TN, and TNL. Smaller homogenous NLR clusters were also found, as for instance the TNL-gene cluster on Chr_2 or the NL-cluster on Chr_3 (Suppl. Table 1). The in total 8 RLP and 7 KIN clusters (Table 3) were, with two exceptions on Chr_1 and Chr_9, homogenously in terms that they do not contain genes from the cytoplasmic NLR sub-classes. The three largest RLP clusters with each seven genes are located on chromosomes Chr_1, Chr_3 and Chr_5. NLR genes are known to be unevenly located in plant genomes and are often found in multigene clusters (Meyers et al. 2003). This clustered distribution likely arose by tandem duplications and further sequence divergence and depicts a large genetic reservoir for evolution of new specificities to pathogens (Duplessis et al. 2009). The homogeneous cluster type is most probably generated by tandem duplication, whereas the heterogenous cluster type is derived from ectopic duplications, transpositions, and/or large-scale segmental duplications with subsequent local rearrangements (Jacob et al. 2013). In the carrot genome, also other major R gene classes such as RLP and KIN were found to be organized in gene clusters.

To determine the evolutionary relationships of carrot R gene predictions, we generated a phylogenetic tree based on the alignment of all 320 deduced R proteins. Three large clades (NLR, RLP and KIN) and a small clade (RLK) were identified (Fig. 2). The predicted classification of the R genes is well represented by the phylogenetic relationships. Only a single predicted NL gene (*DcRG_010*) was placed among the RLP genes. The three genes with the unknown domain combination CK (*DcRG_101*, *DcRG_218* and DcRG_253) were assigned to the KIN clade, and the single CL gene was assigned to the RLP clade, respectively. The two EDR2 genes are closely related to the two CNL genes *DcRG_093* and *DcRG_158* and function in this phylogenetic analysis like an outgroup (Fig. 2). The similarity of the sequences of clustered R genes is often reflected by their positions in the phylogenetic tree (Fig. 2). Examples are the NLR cluster on Chr_2, which contains the six NL genes *DcRG_041* - *DcRG_046,* and the eleven-gene cluster on Chr_8 with the six genes *DcRG_269* - *DcRG_274*, which also formed a common NL sub-group. The other five genes from this cluster, however, were grouped in a common

TNL gene sub-group at a different position in the phylogenetic tree (Fig. 2). There are also some RLP and KIN gene clusters that obviously contain structurally similar R genes. For instance, RLP genes *DcRG_113* - *DcRG_119* (Chr_3) and KIN genes *DcRG_258* - *DcRG_262* (Chr_8) were located each in the same sub-group after phylogenetic analysis indicating common evolutionary origins.

Conclusion

The presented carrot R gene inventory consisting of more than 300 putative functional genes might be useful for resistance research and resistance breeding in carrot. Studies on the genotypic and phenotypic variability of resistances against several carrot diseases, supplemented by bi-parental QTL analyses or GWAS based on larger carrot genotype collections, may identify major QTLs and associated candidate R genes. In case of conventional breeding for resistance, introgression of resistance genes from resistant wild carrot relatives by repeated backcrossing is a long-lasting process. The use of molecular markers developed directly from R genes or R gene clusters might strongly support the backcrossing program. In addition, a deeper knowledge about the structure and function of isolated R gene candidates might be used in future for biotechnological approaches, such as CRISPR/Cas9-based genome editing, with the aim to generate new or to integrate known resistance alleles in the genome of the cultivated carrot.

Author's contributions

AB, TB, and JK performed the bioinformatic analyses. FD performed the evaluation and classification of predictions and compiled the carrot R gene inventory. FD drafted the manuscript. AB, JK, and FD contributed to the discussion and interpretation of results and read and approved the final manuscript.

References

Ali A, Matthews WC, Cavagnaro PF, Iorizzo M, Roberts PA, Simon PW (2014) Inheritance andmapping of *Mj-2*, a new source of root-knot nematode (*Meloidogyne javanica*) resistance in carrot. J Heredity 105:288–291

Andolfo G, Ercolano MR (2015) Plant innate immunity multicomponent model. Front Plant Sci. 6:987–994

Borelli GM, Mazzucotelli E, Marone D, Crosatti C, Michelotti V, Valè G, Mastrangelo AM (2018) Regulation and Evolution of NLR Genes: A close interconnection for plant immunity. Int J Mol Sci 19: 1662, DOI: 10.3390/ijms19061662

Calle-Garcia J, Guadagno A, Paytuvi-Gallart A, Saera-Vila A, Amoroso CG, D'Esposito D, Andolfo G, Cigliano RA, Sanseverino W, Ercolano MR (2022) PRGdb 4.0: an updated database dedicated to genes involved in plant disease resistance process. Nucleic Acids Research 50:D1483–D1490, DOI: 10.1093/nar/gkab1087

Dangl JL, Jones JD (2001) Plant pathogens and integrated defense responses to infection. Nature 411:826–833

Davis RM, Raid RN (eds) (2002) Compendium of umbelliferous crop diseases. American Phyto-pathological Society, APS Press, St. Paul, USA, 75pp.

Duplessis S, Major I, Martin F, Séguin A (2009) Poplar and pathogen interactions: Insights from *Populus g*enome-wide analyses of resistance and defense gene families and gene expression Profiling. Critical Reviews in Plant Science 28:309–334, DOI: 10.1080/07352680903241063

Du Toit LJ, Le Clerc V, Briard M (2019) Genetics and Genomics of Carrot Biotic Stress. In: Simon P, Iorizzo M, Grzebelus D, Baranski R, editors. The Carrot Genome. Cham: Springer Nature Switzerland. 2019. p. 317 -367, DOI: 10.1007/978-3-030-03389-7_18

Ellison SL, Luby CH, Corak KE, Coe KM, Senalik D, Iorizzo M, et al. (2018) Carotenoid presence is associated with the *Or* gene in domesticated carrot. Genetics 210:1497-1508

Guo YL, Fitz J, Schneeberger K, et al. (2011) Genome-wide comparison of nucleotide-binding site-leucine-rich repeat-encoding genes in *Arabidopsis*. Plant Physiology 157:757–769
Gururani MA, Venkatesh J, Upadhyaya CP, Nookaraju A, Pandey SK, Park SW (2012) Plant disease resistance genes: Current status and future directions. Physiological and Molecular Plant Pathology 78:51e65, DOI: 10.1016/j.pmpp.2012.01.002
Hammond-Kosack KE, Parker JE (2003) Deciphering plant-pathogen communication: fresh perspectives for molecular resistance breeding. Current Opinions in Biotechnology 14:177–193
Iorizzo M, Ellison S, Senalik D, Zeng P, Satapoomin P, et al. (2016) A high-quality carrot genome assembly provides new insights into carotenoid accumulation and asterid genome evolution. Nature Genetics 48:657-666
Jacob F, Vernaldi S, Maekawa T (2013) Evolution and conservation of plant NLR functions. Front Immun 4:Article 297, DOI: 10.3389/fimmu.2013.00297
Jones JD (2001) Putting knowledge of plant disease resistance genes to work. Current Opinions in Plant Biology 4:281e7
Keilwagen J, Wenk M, Erickson JL, Schattat MH, Grau J, Hartung F (2016) Using intron position conservation for homology-based gene prediction. Nucleic Acids Research 44:e89, DOI: 10.1093/nar/gkw092
Keilwagen J, Lehnert H, Berner T, Budahn H, Nothnagel T, Ulrich D, Dunemann F (2017) The terpene synthase gene family of carrot (*Daucus carota* L.): Identification of QTLs and candidate genes associated with terpenoid volatile compounds. Front Plant Sci 8:1930, DOI: 10.3389/fpls.2017.01930
Keilwagen J, Hartung F, Paulini M, Twardziojk SO, Grau J (2018) Combining RNA-seq data and homology-based gene prediction for plants, animals and fungi. BMC Bioinformatics 19:189
Kourelis J, van der Hoorn RAL (2018) Defended to the nines: 25 years of resistance gene cloning identifies nine mechanisms for R protein function. The Plant Cell 30:285-299,
DOI: 10.1105/tpc.17.00579
Le Clerc V, Marques S, Suel A, Huet S, Hamama L, Voisine L, Auperpin E, Jourdan M, Barrot L, Prieur R (2015) QTL mapping of carrot resistance to leaf blight with connected populations: stability across years and consequences for breeding. Theor Appl Genet 128:2177–2187
Le Clerc V, Aubert C, Cottet V, Yovanopoulos C, Piquet M, Suel A, et al. (2019) Breeding for carrot resistance to *Alternaria dauci* without compromising taste. Molecular Breeding 39:59,
DOI: 10.1007/s11032-019-0966-7
Lee H-A, Yeom S-I (2015) Plant NB-LRR proteins: tightly regulated sensors in a complex manner. Briefings in Functional Genomics 14:233–242, DOI: 10.1093/bfgp/elv012
Meyers BC, Kozik A, Griego A, Kuang H, Michelmore RW (2003) Genome-wide analysis of NBS-LRR-encoding genes in *Arabidopsis.* Plant Cell 15:809–834
Meyers BC, Kaushik S, Nandety RS (2005) Evolving disease resistance genes. Current Opinion in Plant Biology 8:129–134
Osuna-Cruz CM, Paytuvi-Gallart A, Di Donato A, Sundesha V, Andolfo G, Cigliano RA, Sanseverino W, Ercolano MR (2018) PRGdb 3.0: a comprehensive platform for prediction and analysis of plant disease resistance genes. Nucleic Acids Research 46, Database issue D1197–D1201, DOI: 10.1093/nar/gkx1119
Parsons J, Matthews WC, Iorizzo M, Roberts PA, Simon PW (2015) *Meloidogyne incognita* nematode resistance QTL in carrot. Molecular Breeding 35:114
Robinson JT, Thorvaldsdóttir H, Winckler W, Guttman M, Lander ES, Gatz G, et al. (2011) Integrative Genomics Viewer. Nature Biotechnology 29:24-26, DOI: 10.1038/nbt.1754
Sanseverino W, Roma G, De Simone M, Faino L, Melito S, Stupka E, Frusciante L, Ercolano MR (2010) PRGdb: a bioinformatics platform for plant resistance gene analysis. Nucleic Acids Research 38: D814–D821
Simon PW (2019) Classical and molecular carrot breeding. In: Simon P, Iorizzo M, Grzebelus D, Baranski R, editors. The Carrot Genome. Cham: Springer Nature Switzerland. 2019. p. 137-147,
DOI: 10.1007/978-3-030-03389-7_9
Van de Weyer A-L, Monteiro F, Furzer OJ, Nishimura MT, Cevik V, Witek K, Jones JD, et al. (2019) A species-wide inventory of NLR genes and alleles in *Arabidopsis thaliana.* Cell 178:1260–1272,
DOI: 10.1016/j.cell.2019.07.038

Velasco R, Zharkikh A, Affourtit J, Dhingra A, Cestaro A, Kalyanaraman A, Fontana P, Bhatnagar SK, Troggio M, et al. (2010) The genome of the domesticated apple (*Malus* x *domestica* Borkh.). Nature Genetics 42:833–839
Vorwerk S, et al. (2007) EDR2 negatively regulates salicylic acid-based defenses and cell death during powdery mildew infections of *Arabidopsis thaliana*. BMC Plant Biology 7:35
Wei WC, Chen J, Kuang H, et al. (2018) Dramatic number variation of R genes in Solanaceae species accounted for by a few R gene subfamilies. PLoS ONE 11:e0148708, DOI:10.1371/ journal.pone.0148708

Table 1. Predicted putative R genes identified in the carrot genome

R protein type	Class	No. of genes
NLR		
CC-NBS-LRR	CNL	19
TIR-NBS-LRR	TNL	40
NBS-LRR	NL	64
CC-NBS	CN	1
TIR-NBS	TN	10
NBS	N	3
Transmembrane protein		
Receptor-like kinase	RLK	10
Receptor-like protein	RLP	82
Kinase	KIN	80
Unknown domain combination[2)]	CK, CL, CTNL	9
Other[2)]		
Enhanced disease resistance 2	EDR2	2
		320

[1)] according to PRGdb 4.0 database (Calle-Garcia et al. 2022)

[2)] for details, see Table 2

Table 2. R genes with unknown domain combinations (CK, CL, CTNL) or no domain recognition (EDR2) by DRAGO 3 predicted with highest max. score by NCBI BLAST P (best hit)

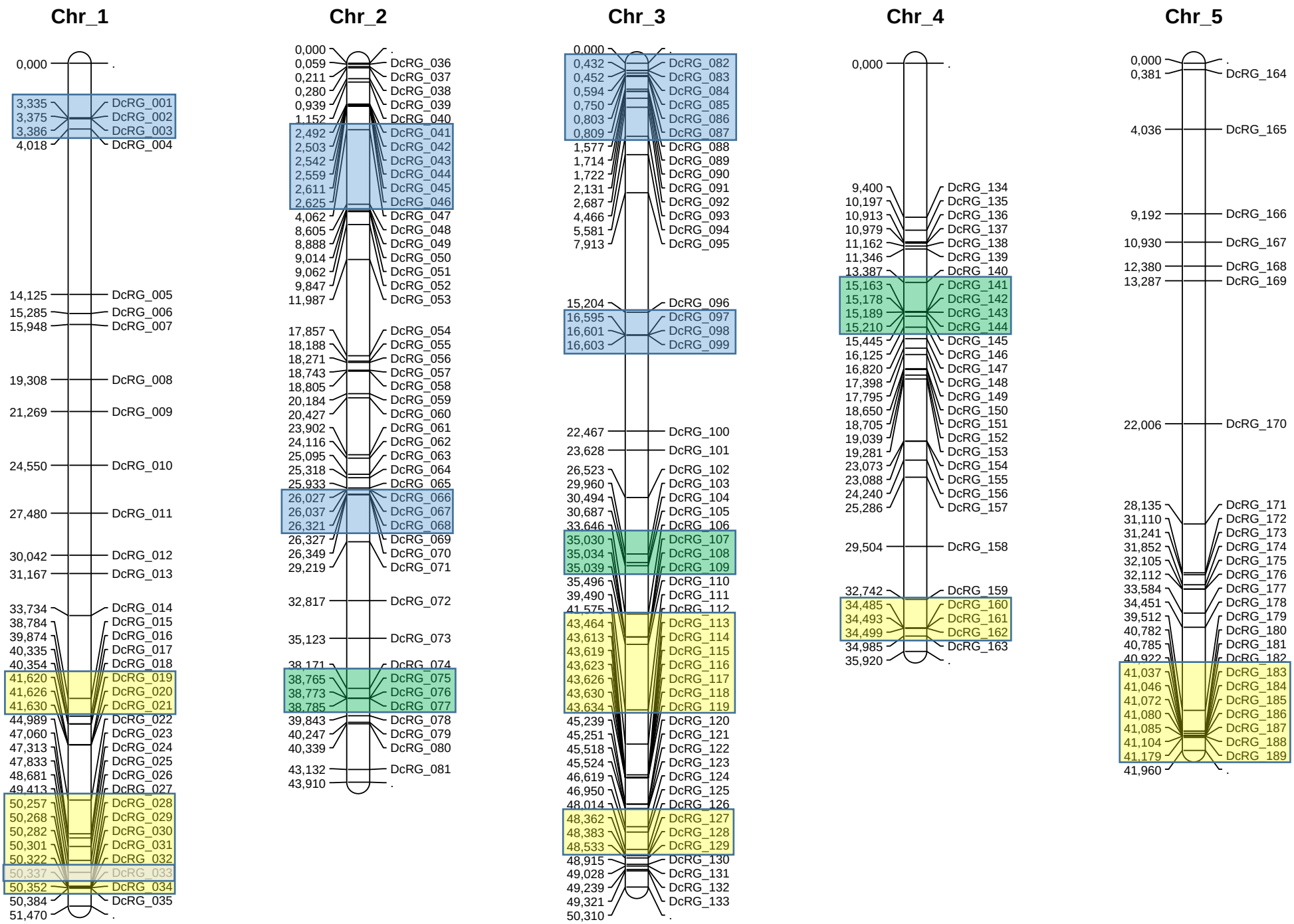
Gene name	Chromosome	Class	Locus name	Prediction NCBI BLAST P (*D. carota* ssp. *sativus*)	Max. Score	Sequence ID
DcRG_002	Chr_1	CTNL	NA[1)]	TMV resistance protein N-like isoform X3	2270	XP_017226921.1
DcRG_006	Chr_1	CTNL	DCAR_001436	Disease resistance protein TAO1-like	1477	XP_017224931.1
DcRG_011	Chr_1	CTNL	DCAR_002255	TMV resistance protein N-like	2292	XP_017230126.1
DcRG_033	Chr_1	CL	DCAR_004675	Receptor-like protein 12	1410	XP_017255570.1
DcRG_079	Chr_2	EDR2	DCAR_008189	Protein ENHANCED DISEASE RESISTANCE 2 isoform X1	1448	XP_017237032.1
DcRG_101	Chr_3	CK	NA[1)]	Wall-associated receptor kinase-like 20	1200	XP_017237511.1
DcRG_169	Chr_5	CTNL	DCAR_017232	TMV resistance protein N-like isoform X1	1283	XP_017222904.1
DcRG_192	Chr_6	CTNL	DCAR_022321	TMV resistance protein N-like isoform X2	2292	XP_017254942.1
DcRG_218	Chr_7	CK	DCAR_024644	Serine/threonine-protein kinase PBS1-like	872	XP_017218963.1
DcRG_222	Chr_7	EDR2	DCAR_024947	Protein ENHANCED DISEASE RESISTANCE 2-like	1449	XP_017219098.1
DcRG_253	Chr_8	CK	DCAR_028743	Probable serine/threonine-protein kinase NAK	770	XP_017222609.1

[1)] NA - not annotated in carrot genome vers.2

Table 3. Number of predicted R genes on carrot chromosomes and number of R gene clusters according to the inventory list (Suppl. Table 1)

		No. of R gene clusters[1)]		
Chromosome	**No. of R genes**	**NLR**	**RLP**	**KIN**
Chr_1	35	1	2	0
Chr_2	46	2	0	1
Chr_3	52	2	2	1
Chr_4	30	0	1	1
Chr_5	26	0	1	0
Chr_6	19	0	0	0
Chr_7	27	1	1	2
Chr_8	33	1	0	1
Chr_9	40	2	1	1
unknown	2			
	320	**9**	**8**	**7**

[1)] three or more genes, 200 kb interval definition (see Methods)


Chr_1
0,000 .
3,335 DcRG_001
3,375 DcRG_002
3,386 DcRG_003
4,018 DcRG_004
14,125 DcRG_005
15,285 DcRG_006
15,948 DcRG_007
19,308 DcRG_008
21,269 DcRG_009
24,550 DcRG_010
27,480 DcRG_011
30,042 DcRG_012
31,167 DcRG_013
33,734 DcRG_014
38,784 DcRG_015
39,874 DcRG_016
40,335 DcRG_017
40,354 DcRG_018
41,620 DcRG_019
41,626 DcRG_020
41,630 DcRG_021
44,989 DcRG_022
47,060 DcRG_023
47,313 DcRG_024
47,833 DcRG_025
48,681 DcRG_026
49,413 DcRG_027
50,257 DcRG_028
50,268 DcRG_029
50,282 DcRG_030
50,301 DcRG_031
50,322 DcRG_032
50,337 DcRG_033
50,352 DcRG_034
50,384 DcRG_035
51,470 .
Chr_2
0,000 .
0,059 DcRG_036
0,211 DcRG_037
0,280 DcRG_038
0,939 DcRG_039
1,152 DcRG_040
2,492 DcRG_041
2,503 DcRG_042
2,542 DcRG_043
2,559 DcRG_044
2,611 DcRG_045
2,625 DcRG_046
4,062 DcRG_047
8,605 DcRG_048
8,888 DcRG_049
9,014 DcRG_050
9,062 DcRG_051
9,847 DcRG_052
11,987 DcRG_053
17,857 DcRG_054
18,188 DcRG_055
18,271 DcRG_056
18,743 DcRG_057
18,805 DcRG_058
20,184 DcRG_059
20,427 DcRG_060
23,902 DcRG_061
24,116 DcRG_062
25,095 DcRG_063
25,318 DcRG_064
25,933 DcRG_065
26,027 DcRG_066
26,037 DcRG_067
26,321 DcRG_068
26,327 DcRG_069
26,349 DcRG_070
29,219 DcRG_071
32,817 DcRG_072
35,123 DcRG_073
38,171 DcRG_074
38,765 DcRG_075
38,773 DcRG_076
38,785 DcRG_077
39,843 DcRG_078
40,247 DcRG_079
40,339 DcRG_080
43,132 DcRG_081
43,910 .
Chr_3
0,000 .
0,432 DcRG_082
0,452 DcRG_083
0,594 DcRG_084
0,750 DcRG_085
0,803 DcRG_086
0,809 DcRG_087
1,577 DcRG_088
1,714 DcRG_089
1,722 DcRG_090
2,131 DcRG_091
2,687 DcRG_092
4,466 DcRG_093
5,581 DcRG_094
7,913 DcRG_095
15,204 DcRG_096
16,595 DcRG_097
16,601 DcRG_098
16,603 DcRG_099
22,467 DcRG_100
23,628 DcRG_101
26,523 DcRG_102
29,960 DcRG_103
30,494 DcRG_104
30,687 DcRG_105
33,646 DcRG_106
35,030 DcRG_107
35,034 DcRG_108
35,039 DcRG_109
35,496 DcRG_110
39,490 DcRG_111
41,575 DcRG_112
43,464 DcRG_113
43,613 DcRG_114
43,619 DcRG_115
43,623 DcRG_116
43,626 DcRG_117
43,630 DcRG_118
43,634 DcRG_119
45,239 DcRG_120
45,251 DcRG_121
45,518 DcRG_122
45,524 DcRG_123
46,619 DcRG_124
46,950 DcRG_125
48,014 DcRG_126
48,362 DcRG_127
48,383 DcRG_128
48,533 DcRG_129
48,915 DcRG_130
49,028 DcRG_131
49,239 DcRG_132
49,321 DcRG_133
50,310 .
Chr_4
0,000 .
9,400 DcRG_134
10,197 DcRG_135
10,913 DcRG_136
10,979 DcRG_137
11,162 DcRG_138
11,346 DcRG_139
13,387 DcRG_140
15,163 DcRG_141
15,178 DcRG_142
15,189 DcRG_143
15,210 DcRG_144
15,445 DcRG_145
16,125 DcRG_146
16,820 DcRG_147
17,398 DcRG_148
17,795 DcRG_149
18,650 DcRG_150
18,705 DcRG_151
19,039 DcRG_152
19,281 DcRG_153
23,073 DcRG_154
23,088 DcRG_155
24,240 DcRG_156
25,286 DcRG_157
29,504 DcRG_158
32,742 DcRG_159
34,485 DcRG_160
34,493 DcRG_161
34,499 DcRG_162
34,985 DcRG_163
35,920 .
Chr_5
0,000 .
0,381 DcRG_164
4,036 DcRG_165
9,192 DcRG_166
10,930 DcRG_167
12,380 DcRG_168
13,287 DcRG_169
22,006 DcRG_170
28,135 DcRG_171
31,110 DcRG_172
31,241 DcRG_173
31,852 DcRG_174
32,105 DcRG_175
32,112 DcRG_176
33,584 DcRG_177
34,451 DcRG_178
39,512 DcRG_179
40,782 DcRG_180
40,785 DcRG_181
40,922 DcRG_182
41,037 DcRG_183
41,046 DcRG_184
41,072 DcRG_185
41,080 DcRG_186
41,085 DcRG_187
41,104 DcRG_188
41,179 DcRG_189
41,960 .

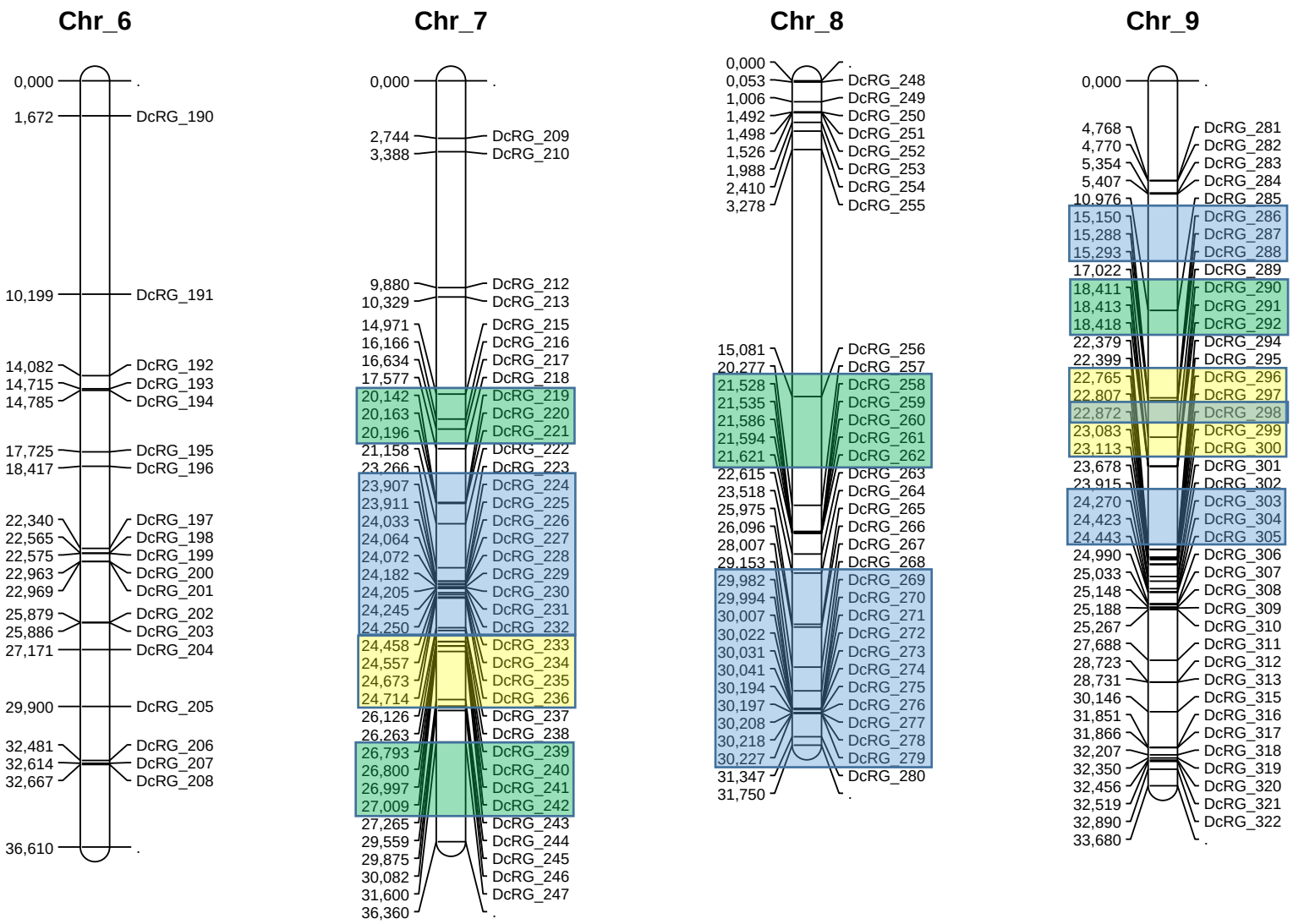


Figure 1. Carrot R gene map. Schematic map presentation of the genomic localization of the 320 carrot R genes listed in Suppl. Table 1. Figures on the left side of the bars show the start position of the CDS of each R gene in Mb (mega base pairs). R gene clusters are presented in coloured boxes (NLR - blue, RLP - yellow, KIN - green).

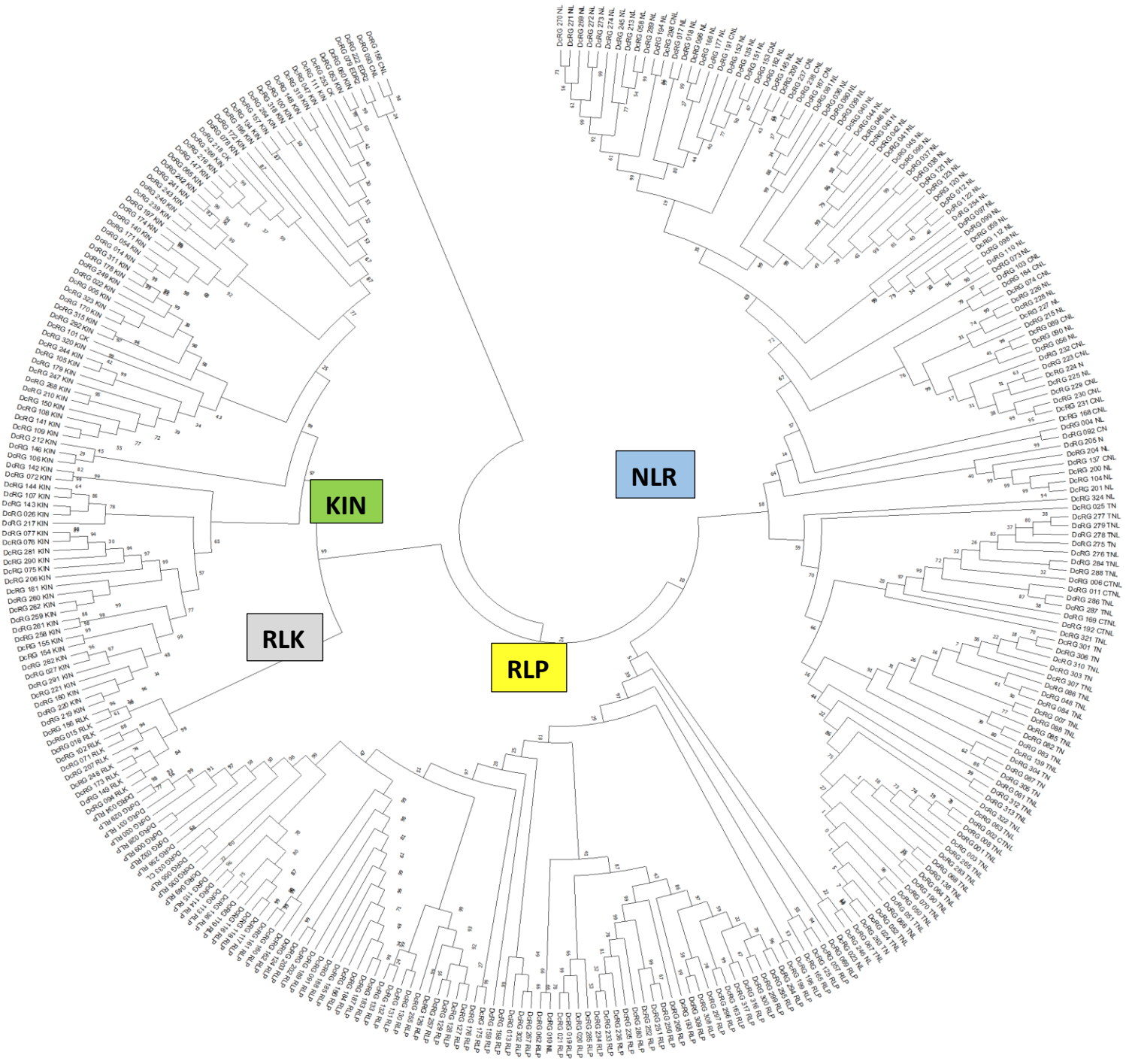


Figure 2. Phylogenetic analysis of 320 deduced *Daucus carota* R proteins and their grouping in clades (NLR, RLP, RLK and KIN). Multiple sequence alignment by MUSCLE (MEGA-X). Neighbor-joining method and n=1000 replicates for bootstrapping were applied (MEGA-X). Bootstrap values are shown next to each node.

Suppl. Table 1. List of 320 *Daucus carota* R gene models sorted by their physical position on the assembled nine carrot chromosomes according to the carrot whole genome sequence assembly vers.2 (Iorizzo et al. 2016). NLR gene clusters are shaded in blue, RLP clusters in yellow, and KIN clusters in green, respectively (for cluster definition, see methods). NA – Not annotated in carrot genome sequence vers.2

			Genomic coordinates[3)]						
Gene name[1)]	**Chrom.**	**Class[2)]**	**Strand**	**Start**	**Stop**	**Locus name[4)]**	**Prediction (GeMoMa)[5)]**	**Exon no.**	**AA[6)]**
DcRG_001	Chr_1	**TNL**	-	3334635	3351268	DCAR_001225	GLYMA.03G087500.2.WM82.A2.V1_R3	6	817
DcRG_002	Chr_1	***CTNL***	-	3374751	3378828	NA	SOLYC05G006630.2.1.ITAG2.4_R9	5	1153
DcRG_003	Chr_1	**TNL**	-	3386037	3390016	NA	AT1G63870.1.TAIR10_R9	4	1025
DcRG_004	Chr_1	**NL**	-	4017929	4029504	DCAR_001279	POTRI.005G042900.1.V3.0_R0	3	1247
DcRG_005	Chr_1	**KIN**	+	14125232	14131946	DCAR_001366	GLYMA.09G181400.1.WM82.A2.V1_R6	3	659
DcRG_006	Chr_1	***CTNL***	+	15285224	15290985	DCAR_001436	POTRI.019G001700.1.V3.0_R1	6	1156
DcRG_007	Chr_1	**TNL**	-	15948244	15953280	NA	AT5G40100.1.TAIR10_R4	5	965
DcRG_008	Chr_1	**TNL**	+	19308075	19312726	DCAR_001691	SOLYC09G007710.2.1.ITAG2.4_R7	5	1226
DcRG_009	Chr_1	**RLP**	-	21268604	21271345	DCAR_001832	POTRI.009G112000.1.V3.0_R9	2	884
DcRG_010	Chr_1	**NL**	+	24550403	24551521	DCAR_002050	GLYMA.06G319700.1.WM82.A2.V1_R5	1	373
DcRG_011	Chr_1	***CTNL***	-	27479966	27485197	DCAR_002255	POTRI.005G206400.1.V3.0_R5	6	1180
DcRG_012	Chr_1	**NL**	+	30042291	30045532	NA	AT1G58410.1.TAIR10_R0	2	949
DcRG_013	Chr_1	**RLP**	-	31167439	31169202	DCAR_002613	AT5G23400.1.TAIR10_R0	1	588
DcRG_014	Chr_1	**KIN**	+	33733961	33736555	DCAR_002886	AT5G39030.1.TAIR10_R8	1	865
DcRG_015	Chr_1	**RLK**	+	38784490	38787184	DCAR_003427	POTRI.013G158800.1.V3.0_R6	2	639
DcRG_016	Chr_1	**RLK**	+	39874385	39877096	DCAR_003536	POTRI.013G158800.1.V3.0_R9	2	647
DcRG_017	Chr_1	**NL**	-	40335091	40337429	DCAR_003581	SOLYC07G039390.1.1.ITAG2.4_R8	4	405
DcRG_018	Chr_1	**NL**	-	40354145	40356865	DCAR_003582	SOLYC04G009660.2.1.ITAG2.4_R7	1	907
DcRG_019	Chr_1	**RLP**	-	41620093	41623047	DCAR_003743	AT2G34930.1.TAIR10_R1	1	985
DcRG_020	Chr_1	**RLP**	-	41625658	41628633	DCAR_003744	AT2G34930.1.TAIR10_R0	1	992
DcRG_021	Chr_1	**RLP**	-	41630254	41633226	DCAR_003745	AT2G34930.1.TAIR10_R2	1	991
DcRG_022	Chr_1	**KIN**	-	44989248	44999805	DCAR_004129	GLYMA.07G096100.1.WM82.A2.V1_R4	3	725
DcRG_023	Chr_1	**NL**	-	47059885	47063792	DCAR_004352	POTRI.002G056100.1.V3.0_R1	4	796

			Genomic coordinates[3)]						
Gene name[1)]	**Chrom.**	**Class[2)]**	**Strand**	**Start**	**Stop**	**Locus name[4)]**	**Prediction (GeMoMa)[5)]**	**Exon no.**	**AA[6)]**
DcRG_024	Chr_1	**TNL**	-	47313350	47317926	NA	SOLYC09G092410.2.1.ITAG2.4_R3	5	1099
DcRG_025	Chr_1	**TN**	+	47833334	47835138	NA	GLYMA.02G023800.1.WM82.A2.V1_R3	2	339
DcRG_026	Chr_1	**KIN**	-	48680869	48683436	DCAR_004501	GLYMA.05G237100.1.WM82.A2.V1_R1	3	654
DcRG_027	Chr_1	**KIN**	+	49412713	49413804	DCAR_004576	GLYMA.07G095100.1.WM82.A2.V1_R9	1	364
DcRG_028	Chr_1	**RLP**	+	50256662	50259553	NA	AT1G47890.1.TAIR10_R8	1	964
DcRG_029	Chr_1	**RLP**	+	50267963	50270839	NA	POTRI.001G389100.1.V3.0_R2	1	959
DcRG_030	Chr_1	**RLP**	+	50281594	50284452	DCAR_004673	POTRI.011G104900.1.V3.0_R5	1	953
DcRG_031	Chr_1	**RLP**	+	50300950	50303859	NA	AT1G47890.1.TAIR10_R7	1	970
DcRG_032	Chr_1	**RLP**	+	50321690	50331579	NA	POTRI.001G389100.1.V3.0_R1	2	1053
DcRG_033	Chr_1	***CL***	+	50337331	50340131	DCAR_004675	POTRI.001G389100.1.V3.0_R9	3	899
DcRG_034	Chr_1	**RLP**	+	50352172	50355033	NA	POTRI.001G389100.1.V3.0_R0	1	954
DcRG_035	Chr_1	**RLP**	-	50383733	50386504	DCAR_004682	POTRI.001G389100.1.V3.0_R5	2	899
DcRG_036	Chr_2	**NL**	+	58662	61556	DCAR_004830	AT5G43470.1.TAIR10_R5	2	884
DcRG_037	Chr_2	**NL**	-	211201	213883	DCAR_004846	AT1G10920.1.TAIR10_R2	3	841
DcRG_038	Chr_2	**NL**	-	280061	283927	DCAR_004853	SOLYC12G096920.1.1.ITAG2.4_R4	3	955
DcRG_039	Chr_2	**NL**	-	938672	942000	DCAR_004872	AT1G59780.1.TAIR10_R5	2	946
DcRG_040	Chr_2	**NL**	-	1152442	1155392	DCAR_004880	AT1G10920.1.TAIR10_R5	2	855
DcRG_041	Chr_2	**NL**	-	2492204	2495294	DCAR_004969	GLYMA.08G247900.1.WM82.A2.V1_R5	5	866
DcRG_042	Chr_2	**NL**	+	2503242	2506744	DCAR_004970	AT1G10920.1.TAIR10_R9	3	850
DcRG_043	Chr_2	**N**	+	2541539	2544772	DCAR_004976	AT5G43470.1.TAIR10_R9	2	952
DcRG_044	Chr_2	**NL**	+	2559352	2562670	DCAR_004978	AT1G58410.1.TAIR10_R8	2	947
DcRG_045	Chr_2	**NL**	+	2610685	2620387	DCAR_004985	AT1G58807.1.TAIR10_R2	4	976
DcRG_046	Chr_2	**NL**	+	2625176	2628516	DCAR_004988	AT1G59780.1.TAIR10_R6	3	909
DcRG_047	Chr_2	**KIN**	+	4062037	4063385	DCAR_005050	PGSC0003DMT400023005.V4.03_R5	5	259
DcRG_048	Chr_2	**TNL**	+	8605381	8610012	NA	AT5G17970.1.TAIR10_R8	4	790
DcRG_049	Chr_2	**RLP**	+	8887832	8890630	DCAR_005187	AT3G24982.1.TAIR10_R9	1	933
DcRG_050	Chr_2	**TNL**	+	9014191	9018101	DCAR_005188	SOLYC09G092410.2.1.ITAG2.4_R6	6	1014

			Genomic coordinates[3)]						
Gene name[1)]	**Chrom.**	**Class[2)]**	**Strand**	**Start**	**Stop**	**Locus name[4)]**	**Prediction (GeMoMa)[5)]**	**Exon no.**	**AA[6)]**
DcRG_051	Chr_2	**TNL**	+	9061979	9065369	DCAR_005190	GLYMA.16G085700.1.WM82.A2.V1_R6	4	985
DcRG_052	Chr_2	**TNL**	-	9847210	9852422	DCAR_005216	POTRI.019G001700.1.V3.0_R5	7	968
DcRG_053	Chr_2	**KIN**	+	11987487	11989819	DCAR_005345	PGSC0003DMT400023009.V4.03_R2	6	406
DcRG_054	Chr_2	**KIN**	+	17857017	17859611	DCAR_005745	AT5G39030.1.TAIR10_R6	1	865
DcRG_055	Chr_2	**RLP**	+	18187570	18190523	DCAR_005778	POTRI.009G112000.1.V3.0_R8	3	859
DcRG_056	Chr_2	**NL**	+	18270956	18274006	DCAR_005785	POTRI.015G121800.1.V3.0_R2	1	1017
DcRG_057	Chr_2	**RLP**	+	18742636	18743808	DCAR_005830	POTRI.011G023500.1.V3.0_R2	1	391
DcRG_058	Chr_2	**NL**	-	18805419	18808028	DCAR_005833	SOLYC04G009110.1.1.ITAG2.4_R6	1	870
DcRG_059	Chr_2	**NL**	-	20184081	20186635	DCAR_005938	PGSC0003DMT400047507.V4.03_R3	2	842
DcRG_060	Chr_2	**KIN**	-	20426714	20430070	NA	PGSC0003DMT400023009.V4.03_R1	6	402
DcRG_061	Chr_2	**TNL**	+	23902080	23906583	NA	AT5G45210.1.TAIR10_R2	4	754
DcRG_062	Chr_2	**RLP**	-	24115847	24116929	DCAR_006300	GLYMA.13G005800.1.WM82.A2.V1_R4	1	361
DcRG_063	Chr_2	**TNL**	-	25095215	25099092	NA	POTRI.T127700.1.V3.0_R9	4	934
DcRG_064	Chr_2	**TNL**	-	25318472	25323739	NA	SOLYC05G006630.2.1.ITAG2.4_R2	5	1301
DcRG_065	Chr_2	**KIN**	+	25932552	25937554	DCAR_006481	PGSC0003DMT400002807.V4.03_R2	5	402
DcRG_066	Chr_2	**TNL**	+	26026896	26031279	DCAR_006494	POTRI.019G001700.1.V3.0_R9	5	1143
DcRG_067	Chr_2	**TNL**	+	26037273	26039281	NA	POTRI.T001400.1.V3.0_R9	3	572
DcRG_068	Chr_2	**TNL**	-	26320625	26324534	NA	SOLYC05G007850.1.1.ITAG2.4_R6	4	1076
DcRG_069	Chr_2	**RLP**	-	26326546	26331048	NA	POTRI.T005300.1.V3.0_R3	4	512
DcRG_070	Chr_2	**TNL**	-	26349468	26354227	NA	POTRI.T001500.1.V3.0_R7	5	1245
DcRG_071	Chr_2	**RLK**	+	29218504	29220472	DCAR_006860	POTRI.013G158800.1.V3.0_R7	2	605
DcRG_072	Chr_2	**KIN**	-	32816767	32820124	DCAR_007260	SOLYC03G119240.2.1.ITAG2.4_R4	4	658
DcRG_073	Chr_2	**NL**	+	35123060	35125756	DCAR_007540	GLYMA.01G010500.1.WM82.A2.V1_R2	1	899
DcRG_074	Chr_2	**CNL**	+	38170622	38174623	DCAR_007914	GLYMA.03G075200.1.WM82.A2.V1_R0	1	1334
DcRG_075	Chr_2	**KIN**	-	38765036	38767053	DCAR_007999	GLYMA.08G044300.1.WM82.A2.V1_R8	2	642
DcRG_076	Chr_2	**KIN**	-	38772867	38774833	DCAR_008001	AT1G66920.1.TAIR10_R5	2	622
DcRG_077	Chr_2	**KIN**	-	38784684	38786650	DCAR_008003	AT1G66920.1.TAIR10_R4	2	621

			Genomic coordinates[3)]						
Gene name[1)]	**Chrom.**	**Class[2)]**	**Strand**	**Start**	**Stop**	**Locus name[4)]**	**Prediction (GeMoMa)[5)]**	**Exon no.**	**AA[6)]**
DcRG_078	Chr_2	**KIN**	-	39842813	39844439	DCAR_008139	PGSC0003DMT400002807.V4.03_R1	5	398
DcRG_079	Chr_2	**EDR2***	+	40247417	40257126	DCAR_008189	SOLYC12G096050.1.1.ITAG2.4_R0	22	723
DcRG_080	Chr_2	**NL**	+	40338741	40341735	DCAR_008200	GLYMA.15G168500.2.WM82.A2.V1_R0	2	938
DcRG_081	Chr_2	**NL**	-	43131647	43134988	DCAR_008568	GLYMA.15G168500.2.WM82.A2.V1_R4	2	947
DcRG_082	Chr_3	**TN**	-	431859	433745	NA	AT1G72890.1.TAIR10_R4	2	418
DcRG_083	Chr_3	**TNL**	-	452369	457048	NA	AT2G14080.1.TAIR10_R3	4	1158
DcRG_084	Chr_3	**TNL**	-	593784	597788	NA	AT1G63870.1.TAIR10_R7	4	1014
DcRG_085	Chr_3	**TNL**	+	749747	764287	NA	SOLYC05G006630.2.1.ITAG2.4_R6	5	1300
DcRG_086	Chr_3	**TNL**	+	803446	807170	NA	AT1G63870.1.TAIR10_R5	4	1073
DcRG_087	Chr_3	**TN**	+	808952	810503	NA	AT1G66090.1.TAIR10_R2	2	486
DcRG_088	Chr_3	**TNL**	+	1576802	1580958	NA	AT5G17680.1.TAIR10_R9	4	1120
DcRG_089	Chr_3	**CNL**	-	1713748	1718604	DCAR_008832	POTRI.018G003500.1.V3.0_R3	3	889
DcRG_090	Chr_3	**NL**	-	1721885	1725366	DCAR_008833	PGSC0003DMT400079343.V4.03_R0	4	597
DcRG_091	Chr_3	**RLP**	+	2131140	2133680	DCAR_008878	AT2G33060.1.TAIR10_R4	2	815
DcRG_092	Chr_3	**CN**	+	2687353	2689026	DCAR_008924	PGSC0003DMT400028241.V4.03_R0	1	558
DcRG_093	Chr_3	**CNL**	-	4465596	4470353	DCAR_009112	POTRI.003G101000.1.V3.0_R1	1	1586
DcRG_094	Chr_3	**RLK**	-	5580948	5584234	DCAR_009226	POTRI.019G131500.1.V3.0_R2	2	657
DcRG_095	Chr_3	**NL**	+	7912809	7916087	DCAR_009477	AT1G59620.1.TAIR10_R5	3	951
DcRG_096	Chr_3	**NL**	-	15204254	15206854	NA	AT3G46730.1.TAIR10_R4	1	867
DcRG_097	Chr_3	**NL**	+	16594988	16596481	DCAR_010221	PGSC0003DMT400005733.V4.03_R3	1	498
DcRG_098	Chr_3	**NL**	+	16600738	16602243	DCAR_010221	PGSC0003DMT400005733.V4.03_R1	1	502
DcRG_099	Chr_3	**NL**	+	16602695	16605097	DCAR_010221	PGSC0003DMT400047507.V4.03_R1	1	801
DcRG_100	Chr_3	**KIN**	-	22467470	22470490	DCAR_010403	PGSC0003DMT400023009.V4.03_R0	6	384
DcRG_101	Chr_3	***CK***	+	23628357	23630908	NA	POTRI.004G096900.1.V3.0_R7	2	619
DcRG_102	Chr_3	**RLK**	-	26522846	26524976	DCAR_010637	POTRI.019G131500.1.V3.0_R3	2	617
DcRG_103	Chr_3	**CNL**	+	29959620	29962208	DCAR_010879	PGSC0003DMT400043963.V4.03_R6	1	863
DcRG_104	Chr_3	**NL**	-	30494490	30502892	DCAR_010928	POTRI.007G039300.1.V3.0_R1	5	822

			Genomic coordinates[3)]						
Gene name[1)]	**Chrom.**	**Class[2)]**	**Strand**	**Start**	**Stop**	**Locus name[4)]**	**Prediction (GeMoMa)[5)]**	**Exon no.**	**AA[6)]**
DcRG_105	Chr_3	**KIN**	+	30686966	30691050	DCAR_010945	AT1G18390.1.TAIR10_R7	3	702
DcRG_106	Chr_3	**KIN**	+	33645917	33648382	DCAR_011214	PGSC0003DMT400079581.V4.03_R1	6	542
DcRG_107	Chr_3	**KIN**	+	35029913	35032685	DCAR_011361	GLYMA.07G094500.5.WM82.A2.V1_R1	2	637
DcRG_108	Chr_3	**KIN**	-	35034031	35036812	DCAR_011362	SOLYC12G036330.1.1.ITAG2.4_R7	5	629
DcRG_109	Chr_3	**KIN**	-	35038969	35041349	DCAR_011363	SOLYC03G119240.2.1.ITAG2.4_R3	3	621
DcPG_110	Chr_3	**NL**	+	35496072	35497775	DCAR_011401	PGSC0003DMT400005733.V4.03_R6	1	568
DcPG_111	Chr_3	**KIN**	+	39490394	39493207	NA	PGSC0003DMT400023009.V4.03_R4	6	367
DcPG_112	Chr_3	**NL**	-	41574966	41577572	DCAR_011885	PGSC0003DMT400047504.V4.03_R2	2	826
DcRG_113	Chr_3	**RLP**	+	43463639	43469780	DCAR_012065	POTRI.001G389100.1.V3.0_R8	3	846
DcRG_114	Chr_3	**RLP**	-	43613175	43615967	DCAR_012081	POTRI.001G389100.1.V3.0_R7	2	896
DcRG_115	Chr_3	**RLP**	-	43619007	43621433	NA	AT3G28890.1.TAIR10_R1	1	809
DcRG_116	Chr_3	**RLP**	-	43622571	43625189	DCAR_012082	POTRI.001G389100.1.V3.0_R6	2	842
DcRG_117	Chr_3	**RLP**	-	43625963	43628533	DCAR_012082	AT3G11080.1.TAIR10_R3	1	857
DcRG_118	Chr_3	**RLP**	-	43630268	43632838	DCAR_012083	AT3G11080.1.TAIR10_R4	1	857
DcRG_119	Chr_3	**RLP**	-	43633910	43636552	DCAR_012084	AT4G13880.1.TAIR10_R9	2	803
DcRG_120	Chr_3	**NL**	+	45238656	45241851	NA	GLYMA.18G269500.1.WM82.A2.V1_R1	2	949
DcRG_121	Chr_3	**NL**	+	45250607	45253911	NA	GLYMA.15G168500.2.WM82.A2.V1_R6	2	948
DcRG_122	Chr_3	**NL**	-	45518004	45521342	NA	AT1G58410.1.TAIR10_R9	2	963
DcRG_123	Chr_3	**NL**	-	45523712	45527297	NA	AT1G50180.1.TAIR10_R9	4	857
DcRG_124	Chr_3	**RLP**	-	46618509	46622364	DCAR_012405	POTRI.001G389100.1.V3.0_R4	2	964
DcRG_125	Chr_3	**RLP**	-	46950016	46951215	DCAR_012446	POTRI.011G023500.1.V3.0_R1	1	400
DcRG_126	Chr_3	**RLP**	+	48014155	48017131	NA	AT5G25910.1.TAIR10_R3	2	904
DcRG_127	Chr_3	**RLP**	-	48361703	48366009	NA	AT5G25910.1.TAIR10_R4	3	852
DcRG_128	Chr_3	**RLP**	-	48383310	48386225	NA	AT5G25910.1.TAIR10_R2	3	859
DcRG_129	Chr_3	**RLP**	+	48532959	48535924	NA	AT5G25910.1.TAIR10_R1	2	922
DcRG_130	Chr_3	**RLP**	+	48914598	48922543	DCAR_012595	AT3G24900.1.TAIR10_R7	2	846
DcRG_131	Chr_3	**RLP**	+	49027920	49034372	NA	AT2G32660.1.TAIR10_R9	2	675

			Genomic coordinates[3)]						
Gene name[1)]	**Chrom.**	**Class[2)]**	**Strand**	**Start**	**Stop**	**Locus name[4)]**	**Prediction (GeMoMa)[5)]**	**Exon no.**	**AA[6)]**
DcRG_132	Chr_3	**RLP**	+	49238871	49241530	DCAR_012608	AT3G23120.1.TAIR10_R4	2	855
DcRG_133	Chr_3	**RLP**	+	49320867	49324434	DCAR_012610	AT5G40170.1.TAIR10_R7	3	860
DcRG_134	Chr_4	**KIN**	-	9400357	9401528	DCAR_015659	PGSC0003DMT400023008.V4.03_R8	4	246
DcRG_135	Chr_4	**NL**	-	10196825	10199416	DCAR_015581	AT3G46710.1.TAIR10_R3	1	864
DcRG_136	Chr_4	**RLP**	-	10912755	10915271	DCAR_015528	POTRI.011G104900.1.V3.0_R9	1	839
DcRG_137	Chr_4	**CNL**	-	10979036	10983290	DCAR_015522	POTRI.007G039300.1.V3.0_R2	5	840
DcRG_138	Chr_4	**TNL**	+	11162302	11167515	NA	SOLYC05G006630.2.1.ITAG2.4_R8	5	1098
DcRG_139	Chr_4	**TNL**	+	11345889	11350028	NA	AT5G17680.1.TAIR10_R5	4	1109
DcRG_140	Chr_4	**KIN**	+	13387215	13389872	DCAR_015328	AT5G39030.1.TAIR10_R3	1	886
DcRG_141	Chr_4	**KIN**	+	15162639	15172670	DCAR_015152	SOLYC12G036330.1.1.ITAG2.4_R1	4	659
DcRG_142	Chr_4	**KIN**	-	15178142	15186369	DCAR_015151	GLYMA.07G094100.1.WM82.A2.V1_R3	3	756
DcRG_143	Chr_4	**KIN**	-	15188694	15191151	DCAR_015150	GLYMA.05G237100.1.WM82.A2.V1_R0	3	670
DcRG_144	Chr_4	**KIN**	-	15210137	15213261	DCAR_015147	GLYMA.05G237100.1.WM82.A2.V1_R4	3	582
DcRG_145	Chr_4	**NL**	-	15444997	15447666	DCAR_015124	POTRI.003G149800.1.V3.0_R0	1	890
DcRG_146	Chr_4	**KIN**	+	16125082	16127526	DCAR_015038	PGSC0003DMT400079581.V4.03_R2	7	567
DcRG_147	Chr_4	**KIN**	-	16820179	16821932	DCAR_014957	PGSC0003DMT400002806.V4.03_R5	4	351
DcRG_148	Chr_4	**KIN**	+	17397624	17398755	DCAR_014899	PGSC0003DMT400023008.V4.03_R7	4	251
DcRG_149	Chr_4	**RLK**	-	17794504	17797891	DCAR_014853	POTRI.013G158800.1.V3.0_R4	2	633
DcRG_150	Chr_4	**KIN**	-	18649658	18655105	NA	SOLYC03G119240.2.1.ITAG2.4_R0	4	673
DcRG_151	Chr_4	**NL**	-	18705101	18707740	NA	SOLYC04G009260.1.1.ITAG2.4_R0	1	880
DcRG_152	Chr_4	**NL**	+	19038730	19041485	DCAR_014749	SOLYC04G009150.1.1.ITAG2.4_R2	2	861
DcRG_153	Chr_4	**CNL**	-	19280907	19283498	DCAR_014736	SOLYC04G009660.2.1.ITAG2.4_R0	1	864
DcRG_154	Chr_4	**KIN**	-	23072876	23075938	DCAR_014295	AT5G38240.1.TAIR10_R6	2	664
DcRG_155	Chr_4	**KIN**	-	23088254	23091497	DCAR_014293	AT5G38240.1.TAIR10_R3	2	637
DcRG_156	Chr_4	**RLK**	-	24239998	24243673	DCAR_014170	POTRI.013G158800.1.V3.0_R8	2	625
DcRG_157	Chr_4	**KIN**	-	25285981	25290620	NA	PGSC0003DMT400023009.V4.03_R9	6	402
DcRG_158	Chr_4	**CNL**	+	29504495	29508370	DCAR_013527	POTRI.003G101000.1.V3.0_R0	1	1292

			Genomic coordinates[3)]						
Gene name[1)]	**Chrom.**	**Class[2)]**	**Strand**	**Start**	**Stop**	**Locus name[4)]**	**Prediction (GeMoMa)[5)]**	**Exon no.**	**AA[6)]**
DcRG_159	Chr_4	**RLP**	-	32742140	32744629	DCAR_013113	AT1G74190.1.TAIR10_R9	1	830
DcRG_160	Chr_4	**RLP**	+	34485335	34488235	DCAR_012890	POTRI.016G126900.1.V3.0_R2	1	967
DcRG_161	Chr_4	**RLP**	+	34492526	34495417	DCAR_012889	POTRI.016G126900.1.V3.0_R4	1	964
DcRG_162	Chr_4	**RLP**	+	34499027	34501933	DCAR_012888	POTRI.016G126900.1.V3.0_R0	1	969
DcRG_163	Chr_4	**RLP**	-	34985004	34987841	DCAR_012836	SOLYC07G008590.1.1.ITAG2.4_R6	1	946
DcRG_164	Chr_5	**CNL**	+	381436	384306	DCAR_016111	POTRI.015G121800.1.V3.0_R0	1	957
DcRG_165	Chr_5	**RLP**	-	4035831	4037048	DCAR_016491	GLYMA.20G127300.1.WM82.A2.V1_R2	1	406
DcRG_166	Chr_5	**NL**	-	9192370	9195015	NA	AT3G46730.1.TAIR10_R0	1	882
DcRG_167	Chr_5	**CNL**	+	10929855	10933017	DCAR_017046	GLYMA.15G168500.2.WM82.A2.V1_R1	2	921
DcRG_168	Chr_5	**CNL**	-	12380413	12383112	DCAR_017175	POTRI.006G147100.1.V3.0_R0	3	866
DcRG_169	Chr_5	***CTNL***	+	13287323	13292347	DCAR_017232	GLYMA.03G088100.2.WM82.A2.V1_R5	8	884
DcRG_170	Chr_5	**KIN**	+	22006152	22007384	DCAR_017641	PGSC0003DMT400067987.V4.03_R5	1	411
DcRG_171	Chr_5	**KIN**	+	28134725	28137265	DCAR_018279	AT5G39030.1.TAIR10_R7	1	847
DcRG_172	Chr_5	**KIN**	+	31110250	31113746	DCAR_018558	PGSC0003DMT400002807.V4.03_R8	5	404
DcRG_173	Chr_5	**RLK**	-	31240587	31243000	DCAR_018578	POTRI.013G158800.1.V3.0_R0	2	641
DcRG_174	Chr_5	**KIN**	-	31851624	31854293	DCAR_018647	AT5G39030.1.TAIR10_R2	1	890
DcRG_175	Chr_5	**RLP**	-	32105374	32108775	DCAR_018680	POTRI.009G112000.1.V3.0_R6	1	1134
DcRG_176	Chr_5	**RLP**	-	32111721	32114933	DCAR_018681	AT1G47890.1.TAIR10_R9	1	1071
DcRG_177	Chr_5	**NL**	+	33584182	33586779	DCAR_018824	SOLYC04G009660.2.1.ITAG2.4_R3	2	846
DcRG_178	Chr_5	**KIN**	-	34451354	34452550	DCAR_018917	PGSC0003DMT400067987.V4.03_R1	1	399
DcRG_179	Chr_5	**KIN**	+	39512287	39514695	DCAR_019492	POTRI.012G054700.1.V3.0_R9	2	396
DcRG_180	Chr_5	**KIN**	-	40781784	40784888	DCAR_019649	GLYMA.07G094500.5.WM82.A2.V1_R4	2	601
DcRG_181	Chr_5	**KIN**	+	40785361	40787483	DCAR_019650	AT1G66910.1.TAIR10_R8	2	636
DcRG_182	Chr_5	**NL**	-	40921822	40924557	DCAR_019675	POTRI.002G216800.1.V3.0_R0	1	912
DcRG_183	Chr_5	**RLP**	+	41036760	41039498	DCAR_019688	POTRI.016G126900.1.V3.0_R6	1	913
DcRG_184	Chr_5	**RLP**	+	41045834	41048543	DCAR_019690	POTRI.016G126900.1.V3.0_R7	2	893
DcRG_185	Chr_5	**RLP**	+	41072410	41075146	DCAR_019691	GLYMA.09G145600.1.WM82.A2.V1_R5	2	871

			Genomic coordinates[3)]						
Gene name[1)]	**Chrom.**	**Class[2)]**	**Strand**	**Start**	**Stop**	**Locus name[4)]**	**Prediction (GeMoMa)[5)]**	**Exon no.**	**AA[6)]**
DcRG_186	Chr_5	**RLP**	+	41079818	41082706	DCAR_019692	GLYMA.09G145600.1.WM82.A2.V1_R3	1	963
DcRG_187	Chr_5	**RLP**	+	41085142	41087892	DCAR_019693	POTRI.016G126900.1.V3.0_R5	1	917
DcRG_188	Chr_5	**RLP**	+	41104317	41112751	DCAR_019698	AT4G13810.1.TAIR10_R7	2	860
DcRG_189	Chr_5	**RLP**	-	41178696	41181500	DCAR_019710	POTRI.016G126900.1.V3.0_R1	1	935
DcRG_190	Chr_6	**TNL**	-	1672431	1677920	DCAR_023109	AT4G12010.1.TAIR10_R4	5	1202
DcRG_191	Chr_6	**CNL**	-	10198845	10201457	DCAR_022573	SOLYC04G009150.1.1.ITAG2.4_R4	1	871
DcRG_192	Chr_6	***CTNL***	-	14082355	14092519	DCAR_022321	POTRI.019G001700.1.V3.0_R6	5	1109
DcRG_193	Chr_6	**RLP**	+	14714744	14722626	DCAR_022265	AT2G34930.1.TAIR10_R5	2	1021
DcRG_194	Chr_6	**NL**	+	14785298	14787241	DCAR_022256	SOLYC07G039390.1.1.ITAG2.4_R4	4	393
DcRG_195	Chr_6	**RLP**	+	17725227	17726369	DCAR_021995	GLYMA.20G127300.1.WM82.A2.V1_R0	1	381
DcRG_196	Chr_6	**KIN**	+	18417261	18419669	NA	PGSC0003DMT400023006.V4.03_R9	4	234
DcRG_197	Chr_6	**KIN**	+	22339780	22342317	DCAR_021517	AT5G39030.1.TAIR10_R9	1	846
DcRG_198	Chr_6	**RLP**	-	22565102	22567021	DCAR_021489	AT5G23400.1.TAIR10_R3	1	640
DcRG_199	Chr_6	**RLP**	-	22574733	22575995	DCAR_021488	GLYMA.20G127300.1.WM82.A2.V1_R1	1	421
DcRG_200	Chr_6	**NL**	+	22963077	22967507	DCAR_021434	POTRI.007G039300.1.V3.0_R3	6	809
DcRG_201	Chr_6	**NL**	+	22968646	22973544	DCAR_021433	POTRI.007G039300.1.V3.0_R0	5	827
DcRG_202	Chr_6	**RLP**	-	25879400	25882168	DCAR_021097	POTRI.T092000.1.V3.0_R9	2	810
DcRG_203	Chr_6	**RLP**	-	25886193	25889105	DCAR_021096	POTRI.016G126900.1.V3.0_R3	1	971
DcRG_204	Chr_6	**NL**	-	27171479	27174536	DCAR_020939	GLYMA.14G079500.1.WM82.A2.V1_R0	5	832
DcRG_205	Chr_6	**N**	-	29899947	29900948	DCAR_020607	AT4G19060.1.TAIR10_R0	1	334
DcRG_206	Chr_6	**KIN**	-	32480969	32483315	NA	AT1G66910.1.TAIR10_R9	2	663
DcRG_207	Chr_6	**RLK**	-	32614297	32617063	DCAR_020297	POTRI.013G158800.1.V3.0_R3	2	627
DcRG_208	Chr_6	**RLP**	+	32666721	32669779	DCAR_020292	SOLYC07G008600.1.1.ITAG2.4_R0	2	989
DcRG_209	Chr_7	**NL**	-	2743772	2747464	DCAR_023561	GLYMA.01G171000.1.WM82.A2.V1_R1	2	870
DcRG_210	Chr_7	**KIN**	+	3388041	3392288	DCAR_023631	GLYMA.09G116300.2.WM82.A2.V1_R1	3	629
DcRG_212	Chr_7	**KIN**	-	9880464	9882796	DCAR_024142	PGSC0003DMT400079581.V4.03_R0	6	431
DcRG_213	Chr_7	**NL**	-	10329028	10331628	DCAR_024175	SOLYC04G009120.1.1.ITAG2.4_R2	4	671

			Genomic coordinates[3)]						
Gene name[1)]	**Chrom.**	**Class[2)]**	**Strand**	**Start**	**Stop**	**Locus name[4)]**	**Prediction (GeMoMa)[5)]**	**Exon no.**	**AA[6)]**
DcRG_215	Chr_7	**NL**	+	14970860	14974237	DCAR_024486	AT3G14470.1.TAIR10_R4	1	1126
DcRG_216	Chr_7	**KIN**	-	16165740	16171443	DCAR_024551	PGSC0003DMT400002807.V4.03_R4	5	500
DcRG_217	Chr_7	**KIN**	+	16633579	16636386	DCAR_024598	SOLYC02G086210.2.1.ITAG2.4_R3	3	600
DcRG_218	Chr_7	***CK***	-	17576626	17584590	DCAR_024644	PGSC0003DMT400002807.V4.03_R3	5	444
DcRG_219	Chr_7	**KIN**	-	20141986	20142993	DCAR_024858	GLYMA.07G095700.1.WM82.A2.V1_R6	1	336
DcRG_220	Chr_7	**KIN**	+	20162811	20166302	DCAR_024862	GLYMA.07G094500.5.WM82.A2.V1_R5	2	614
DcRG_221	Chr_7	**KIN**	-	20196041	20199899	NA	GLYMA.07G095000.1.WM82.A2.V1_R7	2	602
DcRG_222	Chr_7	**EDR2***	-	21158149	21170460	DCAR_024947	POTRI.003G100600.1.V3.0_R0	22	725
DcRG_223	Chr_7	**CNL**	+	23266220	23269705	DCAR_031533	AT3G14470.1.TAIR10_R6	1	1162
DcRG_224	Chr_7	**N**	+	23906942	23907955	DCAR_025118	PGSC0003DMT400050981.V4.03_R0	1	338
DcRG_225	Chr_7	**NL**	+	23910837	23914322	DCAR_025119	GLYMA.03G075200.1.WM82.A2.V1_R2	1	1162
DcRG_226	Chr_7	**NL**	+	24033063	24036572	NA	POTRI.018G003500.1.V3.0_R6	3	926
DcRG_227	Chr_7	**NL**	+	24063911	24067470	DCAR_025136	POTRI.001G029300.1.V3.0_R9	2	1165
DcRG_228	Chr_7	**NL**	+	24071521	24075364	DCAR_025137	POTRI.015G121800.1.V3.0_R1	3	926
DcRG_229	Chr_7	**CNL**	-	24182183	24185614	DCAR_025154	PGSC0003DMT400043963.V4.03_R2	2	1102
DcRG_230	Chr_7	**CNL**	-	24204879	24208310	DCAR_025158	POTRI.001G029300.1.V3.0_R6	1	1144
DcRG_231	Chr_7	**CNL**	-	24245002	24248466	DCAR_025161	POTRI.001G029300.1.V3.0_R3	1	1155
DcRG_232	Chr_7	**CNL**	-	24249990	24253496	DCAR_025162	PGSC0003DMT400043963.V4.03_R3	2	1121
DcRG_233	Chr_7	**RLP**	+	24458287	24466889	NA	SOLYC12G005620.1.1.ITAG2.4_R1	2	614
DcRG_234	Chr_7	**RLP**	+	24557336	24560593	NA	POTRI.015G024800.1.V3.0_R1	2	1065
DcRG_235	Chr_7	**RLP**	-	24673090	24676308	NA	POTRI.015G028600.1.V3.0_R7	3	1005
DcRG_236	Chr_7	**RLP**	-	24714263	24717556	NA	POTRI.015G024600.1.V3.0_R1	1	1098
DcRG_237	Chr_7	**CNL**	-	26125618	26129129	DCAR_025331	POTRI.018G138500.1.V3.0_R7	3	968
DcRG_238	Chr_7	**CNL**	-	26263229	26266696	DCAR_025337	POTRI.018G138500.1.V3.0_R4	3	948
DcRG_239	Chr_7	**KIN**	-	26793064	26795577	DCAR_025396	AT5G39020.1.TAIR10_R5	1	838
DcRG_240	Chr_7	**KIN**	-	26800147	26802678	DCAR_025397	AT5G39030.1.TAIR10_R5	1	844
DcRG_241	Chr_7	**KIN**	-	26997007	26999559	DCAR_025418	AT5G39030.1.TAIR10_R1	1	851

			Genomic coordinates[3)]						
Gene name[1)]	**Chrom.**	**Class[2)]**	**Strand**	**Start**	**Stop**	**Locus name[4)]**	**Prediction (GeMoMa)[5)]**	**Exon no.**	**AA[6)]**
DcRG_242	Chr_7	**KIN**	-	27009412	27011979	DCAR_025419	AT5G39030.1.TAIR10_R0	1	856
DcRG_243	Chr_7	**KIN**	+	27264645	27267206	DCAR_025444	AT5G39030.1.TAIR10_R4	1	854
DcRG_244	Chr_7	**KIN**	-	29559054	29562867	DCAR_025671	GLYMA.09G116300.2.WM82.A2.V1_R7	3	694
DcRG_245	Chr_7	**NL**	+	29874881	29877481	DCAR_025716	SOLYC04G009660.2.1.ITAG2.4_R6	2	856
DcRG_246	Chr_7	**NL**	+	30082257	30083785	NA	POTRI.T001400.1.V3.0_R4	4	406
DcRG_247	Chr_7	**KIN**	+	31600066	31605352	DCAR_025904	SOLYC02G086270.2.1.ITAG2.4_R0	4	948
DcRG_248	Chr_8	**RLK**	+	52996	55126	DCAR_028931	POTRI.019G131500.1.V3.0_R1	2	642
DcRG_249	Chr_8	**KIN**	+	1005839	1006858	DCAR_028838	PGSC0003DMT400067987.V4.03_R0	1	340
DcRG_250	Chr_8	**RLP**	+	1491967	1495891	NA	POTRI.015G025800.1.V3.0_R6	3	1047
DcRG_251	Chr_8	**RLP**	+	1497877	1500759	NA	POTRI.015G024600.1.V3.0_R5	1	961
DcRG_252	Chr_8	**RLP**	+	1526473	1530802	NA	POTRI.015G025800.1.V3.0_R8	4	845
DcRG_253	Chr_8	***CK***	-	1988272	1990892	DCAR_028743	PGSC0003DMT400023009.V4.03_R3	6	373
DcRG_254	Chr_8	**NL**	+	2409633	2411897	DCAR_028713	PGSC0003DMT400047507.V4.03_R4	1	755
DcRG_255	Chr_8	**RLP**	+	3277998	3280631	DCAR_028661	AT5G25910.1.TAIR10_R0	2	846
DcRG_256	Chr_8	**RLP**	-	15081403	15084282	DCAR_028105	POTRI.009G112000.1.V3.0_R2	1	960
DcRG_257	Chr_8	**RLP**	+	20277198	20279895	NA	AT3G23110.1.TAIR10_R9	2	822
DcRG_258	Chr_8	**KIN**	-	21527561	21534304	DCAR_027586	GLYMA.07G094500.2.WM82.A2.V1_R9	4	631
DcRG_259	Chr_8	**KIN**	+	21534833	21537254	DCAR_027585	GLYMA.07G094100.1.WM82.A2.V1_R9	2	655
DcRG_260	Chr_8	**KIN**	-	21586442	21590197	DCAR_027574	GLYMA.09G182200.1.WM82.A2.V1_R5	4	538
DcRG_261	Chr_8	**KIN**	+	21594123	21596404	DCAR_027573	GLYMA.07G094500.5.WM82.A2.V1_R6	2	616
DcRG_262	Chr_8	**KIN**	-	21620875	21621960	DCAR_027568	GLYMA.07G095700.1.WM82.A2.V1_R9	1	362
DcRG_263	Chr_8	**TN**	+	22614613	22616761	NA	POTRI.T112700.1.V3.0_R4	2	544
DcRG_264	Chr_8	**KIN**	+	23518222	23521194	DCAR_027395	PGSC0003DMT400023009.V4.03_R5	6	421
DcRG_265	Chr_8	**TNL**	-	25975380	25979796	DCAR_027115	SOLYC09G092410.2.1.ITAG2.4_R9	5	1114
DcRG_266	Chr_8	**KIN**	-	26096075	26101852	DCAR_027102	PGSC0003DMT400002807.V4.03_R5	5	492
DcRG_267	Chr_8	**RLP**	-	28006751	28008529	DCAR_026875	AT5G23400.1.TAIR10_R1	1	593
DcRG_268	Chr_8	**KIN**	+	29153059	29155931	DCAR_026747	GLYMA.09G116300.2.WM82.A2.V1_R4	2	614

			Genomic coordinates[3)]						
Gene name[1)]	**Chrom.**	**Class[2)]**	**Strand**	**Start**	**Stop**	**Locus name[4)]**	**Prediction (GeMoMa)[5)]**	**Exon no.**	**AA[6)]**
DcRG_269	Chr_8	**NL**	-	29981804	29985804	DCAR_026651	SOLYC04G009690.1.1.ITAG2.4_R7	2	859
DcRG_270	Chr_8	**NL**	-	29994173	29996725	DCAR_026650	POTRI.003G149800.1.V3.0_R8	1	851
DcRG_271	Chr_8	**NL**	-	30007354	30009897	DCAR_026649	POTRI.003G149800.1.V3.0_R7	1	848
DcRG_272	Chr_8	**NL**	-	30022204	30024783	DCAR_026647	SOLYC04G009250.1.1.ITAG2.4_R9	1	860
DcRG_273	Chr_8	**NL**	-	30030611	30033437	DCAR_026646	GLYMA.01G010500.1.WM82.A2.V1_R8	2	861
DcRG_274	Chr_8	**NL**	-	30041115	30043715	DCAR_026645	SOLYC04G009660.2.1.ITAG2.4_R9	2	850
DcRG_275	Chr_8	**TN**	-	30194345	30196181	NA	POTRI.T112700.1.V3.0_R1	2	528
DcRG_276	Chr_8	**TNL**	-	30196984	30202575	DCAR_026632	POTRI.005G206400.1.V3.0_R7	8	1102
DcRG_277	Chr_8	**TNL**	-	30207704	30213355	DCAR_026631	POTRI.005G206400.1.V3.0_R1	6	1173
DcRG_278	Chr_8	**TNL**	-	30218198	30222649	DCAR_026630	GLYMA.03G077400.1.WM82.A2.V1_R0	5	1161
DcRG_279	Chr_8	**TNL**	-	30227120	30233089	DCAR_026630	POTRI.005G206400.1.V3.0_R0	6	1123
DcRG_280	Chr_8	**RLP**	+	31346764	31350006	NA	POTRI.015G024600.1.V3.0_R2	1	1081
DcRG_281	Chr_9	**KIN**	-	4767644	4769636	DCAR_029326	AT1G66920.1.TAIR10_R6	2	626
DcRG_282	Chr_9	**KIN**	+	4769885	4772336	DCAR_029327	GLYMA.07G094500.5.WM82.A2.V1_R9	2	653
DcRG_283	Chr_9	**TNL**	+	5354137	5358211	DCAR_029356	SOLYC05G007850.1.1.ITAG2.4_R3	4	1130
DcRG_284	Chr_9	**TNL**	-	5406512	5411097	DCAR_029364	POTRI.005G206400.1.V3.0_R3	6	1135
DcRG_285	Chr_9	**RLP**	-	10975964	10979104	DCAR_029693	POTRI.015G024600.1.V3.0_R6	1	1047
DcRG_286	Chr_9	**TNL**	-	15150058	15155738	DCAR_029849	POTRI.T001500.1.V3.0_R8	5	994
DcRG_287	Chr_9	**TNL**	-	15288383	15292500	DCAR_029841	POTRI.005G206400.1.V3.0_R2	6	1145
DcRG_288	Chr_9	**TNL**	-	15293469	15297400	DCAR_029841	GLYMA.16G087100.1.WM82.A2.V1_R1	5	1115
DcRG_289	Chr_9	**NL**	+	17022468	17025047	DCAR_029804	SOLYC04G009260.1.1.ITAG2.4_R9	1	860
DcRG_290	Chr_9	**KIN**	-	18411219	18413262	NA	GLYMA.08G044300.1.WM82.A2.V1_R6	2	631
DcRG_291	Chr_9	**KIN**	+	18413446	18415951	DCAR_029973	GLYMA.05G237100.1.WM82.A2.V1_R7	2	670
DcRG_292	Chr_9	**KIN**	+	18417593	18420040	NA	GLYMA.20G119600.1.WM82.A2.V1_R7	3	575
DcRG_294	Chr_9	**RLP**	+	22378825	22381671	DCAR_030240	POTRI.015G024600.1.V3.0_R9	1	949
DcRG_295	Chr_9	**RLP**	+	22399093	22403137	DCAR_030241	POTRI.015G025100.1.V3.0_R6	3	987
DcRG_296	Chr_9	**RLP**	-	22765296	22768211	DCAR_030271	SOLYC07G008600.1.1.ITAG2.4_R9	1	972

			Genomic coordinates[3)]						
Gene name[1)]	**Chrom.**	**Class[2)]**	**Strand**	**Start**	**Stop**	**Locus name[4)]**	**Prediction (GeMoMa)[5)]**	**Exon no.**	**AA[6)]**
DcRG_297	Chr_9	**RLP**	-	22806645	22809486	DCAR_030276	POTRI.015G028600.1.V3.0_R8	3	836
DcRG_298	Chr_9	**CNL**	-	22872395	22875076	DCAR_030282	SOLYC04G009660.2.1.ITAG2.4_R8	1	894
DcRG_299	Chr_9	**RLP**	+	23083373	23086000	DCAR_030294	AT2G34930.1.TAIR10_R9	2	862
DcRG_300	Chr_9	**RLP**	+	23113481	23116288	DCAR_030298	POTRI.015G024600.1.V3.0_R7	1	936
DcRG_301	Chr_9	**TN**	-	23678226	23679887	NA	AT1G66090.1.TAIR10_R0	2	483
DcRG_302	Chr_9	**RLP**	+	23914898	23916658	DCAR_030350	AT5G23400.1.TAIR10_R2	1	587
DcRG_303	Chr_9	**TN**	+	24270402	24275569	NA	AT5G48780.1.TAIR10_R1	3	641
DcRG_304	Chr_9	**TN**	-	24423185	24426677	NA	AT4G04110.1.TAIR10_R4	4	252
DcRG_305	Chr_9	**TN**	-	24443468	24445550	NA	AT1G72890.2.TAIR10_R0	5	476
DcRG_306	Chr_9	**TN**	+	24990017	24991343	NA	AT1G72890.1.TAIR10_R2	2	383
DcRG_307	Chr_9	**TNL**	+	25033379	25039407	DCAR_030397	AT5G41750.1.TAIR10_R9	4	1081
DcRG_308	Chr_9	**RLP**	+	25147901	25149565	DCAR_030412	SOLYC12G005620.1.1.ITAG2.4_R7	1	555
DcRG_309	Chr_9	**RLP**	+	25187555	25189219	NA	SOLYC12G005620.1.1.ITAG2.4_R8	1	555
DcRG_310	Chr_9	**TNL**	-	25266572	25272274	NA	AT5G45210.1.TAIR10_R1	4	704
DcRG_311	Chr_9	**KIN**	-	27687655	27688860	DCAR_030583	PGSC0003DMT400067987.V4.03_R4	1	402
DcRG_312	Chr_9	**TNL**	-	28722716	28727938	DCAR_030671	GLYMA.08G293600.10.WM82.A2.V1_R1	6	1284
DcRG_313	Chr_9	**TNL**	-	28730851	28739956	DCAR_030672	SOLYC05G006630.2.1.ITAG2.4_R4	6	1198
DcRG_315	Chr_9	**KIN**	+	30146336	30149634	DCAR_030820	SOLYC05G010530.2.1.ITAG2.4_R9	4	370
DcRG_316	Chr_9	**RLP**	-	31851146	31853776	DCAR_031009	SOBIC.009G012900.1.V3.1_R9	1	877
DcRG_317	Chr_9	**RLP**	+	31865894	31868533	DCAR_031012	AT2G34930.1.TAIR10_R7	1	880
DcRG_318	Chr_9	**KIN**	+	32206922	32209658	DCAR_031037	PGSC0003DMT400023009.V4.03_R6	5	420
DcRG_319	Chr_9	**KIN**	-	32350016	32352409	DCAR_031050	PGSC0003DMT400023009.V4.03_R7	5	426
DcRG_320	Chr_9	**KIN**	+	32455717	32457660	DCAR_031067	POTRI.010G035300.1.V3.0_R0	1	648
DcRG_321	Chr_9	**TNL**	+	32519349	32525701	DCAR_031076	SOLYC05G006620.2.1.ITAG2.4_R0	5	1428
DcRG_322	Chr_9	**TNL**	+	32890459	32894388	NA	AT1G72840.2.TAIR10_R5	4	1153
DcRG_323	Contig_S190.1	**KIN**	+	104964	106058	DCAR_031991	PGSC0003DMT400067987.V4.03_R9	1	365
DcRG_324	Contig_ S72.1	**NL**	-	12023	13532	DCAR_032355	POTRI.T001400.1.V3.0_R6	4	418

[1)] Gene numbers 211, 214, 293, and 314 are not existing

[2)] Class assignment according to DRAGO 3 / PRGdb 4.0 database (Calle-Garcia et al. 2022). Unknown domain combinations are in italics (for details, see Table 2). *assignment after BLAST P

[3)] Genomic coordinates and [4)] DCAR locus names according to the carrot whole genome sequence assembly vers.2

[5)] AT - *Arabidopsis thaliana*; GLYMA - *Glycine max*, POTRI - *Populus trichocarpa*, SOLYC - *Solanum lycopersicum*; SOBIC - *Sorghum bicolor*, PGSC - *Solanum tuberosum*

[6)] Protein length (AA - Amino Acids)