**Description of Data Files**

**Data File 1 (D1):** Genotypic data of the F2 population CB46-Null x FN-2-9-04. One-hundred nineteen F2 lines were genotyped for single-nucleotide polymorphism markers using the Cowpea iSelect Consortium Array containing 51128 SNPs, 17208 SNPs were polymorphic between the parents (susceptible: CB46-Null and resistant: FN-2-9-04) and in the population. Locus\_name, chr, cM stand for SNP marker, chromosome and centi-Morgan, respectively. H, A and B stand for heterozygous loci, unfavorable allele from susceptible parent and favorable allele from resistant parent, respectively.

**Data File 2 (D2):** Phenotypic data of the F2:3 population CB46-Null x FN-2-9-04 obtained through phenotyping 119 F2:3 families for response to root-galling caused by root-knot nematode (RKN) species *Meloidogyne incognita* (isolate Beltran) in the field with soil infested with this nematode. This nematode isolate is avirulent to gene *Rk*. Data files 1 and 2 were used to map quantitative trait loci associated with resistance to root-galling caused by this nematode.

**Data File 3 (D3):** Phenotypic data of the F2:3 population CB46-Null x FN-2-9-04 obtained through phenotyping 119 F2:3 families for response to root-galling caused by RKN species *M. javanica* (isolate Project 811) in the field with soil infested with this nematode. This nematode isolate is virulent to gene *Rk*. Data files 1 and 3 were used to map quantitative trait loci (QTL) associated with resistance to root-galling caused by this nematode.

**Data File 4 (D4):** Phenotypic data of the F2 population CB46-Null x FN-2-9-04 obtained through phenotyping 119 F2 lines for response to egg-mass production by RKN species *M. javanica* (isolate Project 811) in seedling growth-pouches plant inoculation with this nematode. This nematode isolate is virulent to gene *Rk*. Data files 1 and 4 were used to map QTL associated with resistance to egg-mass production by this nematode.

**Data File 5 (D5):** Phenotypic data of the F2 population CB46-Null x FN-2-9-04 obtained through phenotyping 119 F2 lines for response to root-galling by RKN species *M. javanica* (isolate Project 811) in greenhouse plant inoculation with this nematode. This nematode isolate is virulent to gene *Rk*. Data files 1 and 5 were used to map quantitative trait loci (QTL) associated with resistance to root-galling caused by this nematode.

**Data File 6 (D6):** Genotypic data of the F2 population CB46 x FN-2-9-04. One hundred thirty-seven F2 lines were genotyped for single-nucleotide polymorphism markers using the Cowpea iSelect Consortium Array containing 51128 SNPs, of which 17903 SNPs were polymorphic between the parents (susceptible: CB46 and resistant: FN-2-9-04) and in the population. Locus\_name, chr, cM stand for SNP marker, chromosome and centi-Morgan, respectively. H, A and B stand for heterozygous loci, unfavorable allele from susceptible parent and favorable allele from resistant parent, respectively.

**Data File 7 (D7):** Phenotypic data of the F2 population CB46 x FN-2-9-04 obtained through phenotyping 137 F2 lines for response to root-galling by RKN species *M. javanica* (isolate Project 811) in greenhouse plant inoculation with this nematode. This nematode isolate is virulent to gene *Rk*. Data files 6 and 7 were used to map QTL associated with resistance to root-galling by this nematode.

**Data File 8 (D8):** Genotypic data of the F2 population CB46 x FN-2-9-04. From the genotypic data in data file 6 (n = 137), a subset of genotypic data for 105 F2 lines of this population was created to match the corresponding number and lines phenotyped for egg-mass production (data file 9). Locus\_name, chr, cM stand for SNP marker, chromosome and centi-Morgan, respectively. H, A and B stand for heterozygous loci, unfavorable allele from susceptible parents and favorable allele from resistant parent, respectively.

**Data File 9 (D9):** Phenotypic data of the F2 population CB46 x FN-2-9-04 obtained through phenotyping 105 F2 lines for response to egg-mass production by RKN species *M. javanica* (isolate Project 811) in seedling growth-pouches plant inoculation with this nematode. This nematode isolate is virulent to gene *Rk*. Data files 8 and 9 were used to map QTL associated with resistance to egg-mass production by this nematode.