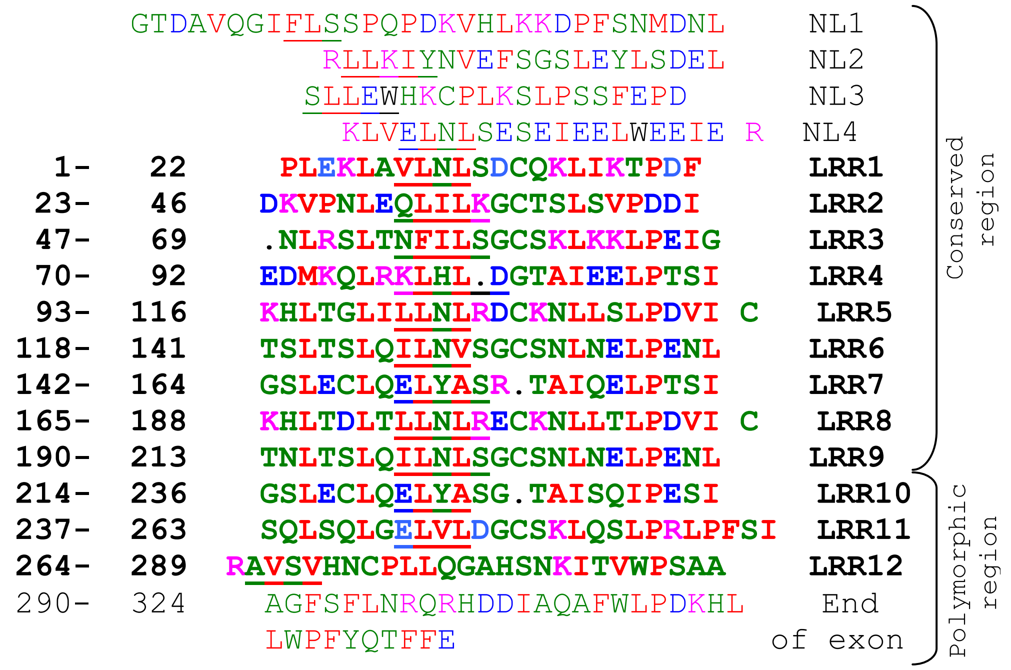
Supplemental Data

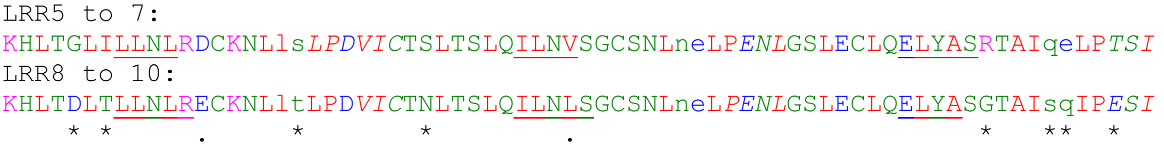
A



```
                GTDAVQGIFLSSPQPDKVHLKKDPFSNMDNL     NL1
                         RLLKIYNVEFSGSLEYLSDEL     NL2
                        SLLEWHKCPLKSLPSSFEPD       NL3
                          KLVELNLSESEIEELWEEIE R  NL4
   1-    22           PLEKLAVLNLSDCQKLIKTPDF       LRR1
  23-    46          DKVPNLEQLILKGCTSLSVPDDI       LRR2
  47-    69          .NLRSLTNFILSGCSKLKKLPEIG      LRR3
  70-    92          EDMKQLRKLHL.DGTAIEELPTSI      LRR4
  93-   116          KHLTGLILLNLRDCKNLLSLPDVI C     LRR5
 118-   141          TSLTSLQILNVSGCSNLNELPENL      LRR6
 142-   164          GSLECLQELYASR.TAIQELPTSI      LRR7
 165-   188          KHLTDLTLLNLRECKNLLTLPDVI C     LRR8
 190-   213          TNLTSLQILNLSGCSNLNELPENL      LRR9
 214-   236          GSLECLQELYASG.TAISQIPESI       LRR10
 237-   263          SQLSQLGELVLDGCSKLQSLPRLPFSI    LRR11
 264-   289         RAVSVHNCPLLQGAHSNKITVWPSAA     LRR12
 290-   324          AGFSFLNRQRHDDIAQAFWLPDKHL      End
                     LWPFYQTFFE                  of exon
```

NL1 to NL4: repeats of the NLL motifs
LRR1 to 12: repeats of the LRR motifs
Underlined: β-strand predicted structure (PSIpred)
Bolded: LRR repeats

B



```
LRR5 to 7:
KHLTGLILLNLRDCKNLlsLPDVICTSLTSLQILNVSGCSNLneLPENLGSLECLQELYASRTAIqeLPTSI
LRR8 to 10:
KHLTDLTLLNLRECKNLltLPDVICTNLTSLQILNLSGCSNLneLPENLGSLECLQELYASGTAIsqIPESI
    * *     .     *       *        .                         *   **  *
```

. : conservative mutations
* : non conservative mutations
Colors:
Blue: acid amino acids; glutamate (E), aspartate (D)
Pink: basic amino acids; lysine (K); arginine (R)
Red: the more hydrophobic non polar amino acids : leucine (L), isoleucine (I), valine (M), methionine (M), phenylalanine (F), proline (P)
Green: other polar or non-polar amino acids

Supplemental Figure S1. Alignments of repeats in the NLL (NL1 to NL4) and LRR (LRR1 to LRR12) exons in TNL1 (A) and duplication of the LRR repeats 5 to 7 and 8 to 10 (B).

```
PL3             ----------GTGGATCCTGATGTCTTTCTTATATTTTGCAGGACTTTGAACAGGACTTG
PL4             -----------------CTGACACCTTGTCTCTCCCTTACAGAACTTTGGTTGTCACACT
PL5             CAAACATATATAACACCTTGACACCTTGTCTCTCTTTTACAGGACTTTGATCGTCACTCC
                                  ***   ***   * *   ** *** ******      **

PL3             AAATATAATTCTTGTTTCCCTCCAAATGAGATTGTAGAGTGGTTCGGGCATCAAAGCAGT
PL4             ATGTATAATTCTTGTTTCCCTTCAAGCATCACTCTGGAGTGGTTTGGGGATCAAAGCAGT
PL5             ATGTATAACTCATGTTTCCCTTCAAGCATAACTCTAGAGTGGTTCGGCCATCAAAGCAAT
                *  ***** ** ********* ***     * * * ******** **  ********* *

PL3             GGCCCCTCTGTAAAAATCCCTCTACCATCAAATCTATGTGAAGACACCAACTGGATAGGA
PL4             GGCTCCTCGATAAGAGTCCCACTACCACCACATTTATATAGAGCCACTAATTGGATAGGA
PL5             GACTCCTCGGCAACAATCTCGCTACCACATAATCTAAACTTAGACAGCAATTGGATAGGA
                * * ****   ** * ** * ******    ** **     ** **  ** *********

PL3             CTGGCTTTATGTGCATACTTTTCAGTCCTTGACCACTCAACTATTGACCTTGAGAATTTG
PL4             TTGGCTTTATGCACATCCTTTTCAATCGTGGATAATCCAACTGCTGACCTAGACAATTTG
PL5             TTAGCTGTATGTGCATACTTTTCAGTCCTGGAGCATCCAACTGTCGACATTGACAATTTG
                 * *** ****  *** ******* ** * **  *  *****   *** * ** ******

PL3             AAT---CCTGAAATTTCTCACAACCTTACATGTCTATTGGAAACTGATGAAAGTTGTCTG
PL4             AAT---CCAGAAATTTCTCACCACTTAATATGTCACTTGGAGTCGGACAGAGGTACAATA
PL5             GATATTCCAGCAATTTCTCACCACCTTATATGTAATTTGGAATCAGATAGAGACAGTCTA
                 **   ** * ********** ** * * ****   *****  * **   *       *

PL3             GAATCCCTCCATGGCTATAGCACCAACAGTCAAGAATTCAAGTGGTTGTATCGTATGGGA
PL4             GAACCTCTCCATGACTACTGCACCACCAACGAAGAATTCCAATGGTTGCCTTTT---GGA
PL5             GAATCTTTGCATGACTACTGCACCACAAAGGAAGAATTCCTATGGTTGCATCTC---GGA
                *** *  * **** ***  ******  *   ********   ******  *      ***

PL3             GGATTCATTTGGCTGTCCTATATACCACGATGCTGGTTTTCAGATCAGTTGAAAGAACGA
PL4             GGATTCATTTGGGTATCCTACATACCACGAGCGTGGTTTTCAGATCAGTTGAATGAATGT
PL5             GGATTCGTTTGGGTATCCTATATACCACGAGCGTGGTTTTCAGATCAGTTGAATGAATGC
                ****** ***** * ***** *********   ******************** *** *

PL3             GGCCACCTGGAGGCTTCAATTGGAAGCGATCATGGAAGCTTGGGTGTGCATAGGTGTGGG
PL4             GATGTCCTGGAGGCTTCATTTGCAAGCGATCATGAAGCATTTACTGTGCACGAGTGTGGG
PL5             GGTGTACTAGAGGCTTCAATTGCAAGCGATCATGAGGCCTTTAGTGTGCAAAAGTGTGGG
                *     ** ********* *** ***********     **   ******   *******

PL3             CTTCGTCTTATATATCTGGAAGATGAGGAAGGGCTTAAGGAGACCATAATGCACTGCATG
PL4             CTACGTCTTGTATATCAGCATGACGAGGAAGAGATTAAGCAGACCATATTGCACTATATG
PL5             CTCCGTCTTGTATATCAGCATGATGAGGAAGAGTTTAAGCAGACCATATC----------
                ** ****** ****** * * ** ******* * ***** ********

PL3             ACCTCCTTGTCAGATATTAATCAAGGAAAAGATGAGCAATACCAGAACTGCGAGGCAGGA
PL4             ACGTCGTTGTCAGAT---AAGAAAGGAAAAAATAAGCAATGCCCCATGGGTGACACGGGA
PL5             ---TCGTTCTCAGAT---AAGAAAGGGAAAAATAAGCAACACCCTCACTGC---------
                   ** ** ******   **  **** *** ** *****  **      *

PL3             TCATCTAGTATAACTGGCAGCAACATTGTAAATCCTGTAAATCCCCATCTTGAAAGATCA
PL4             TCATCTAGTAGGCCTAGCAGCTATATTGTGAAACCT---------CATCTCGAAAGATTA
PL5             CCGCTGAACAGGAT---CAATGACACT-------------------------AAGGGT--
                 *    *  *       **   * * *                         ** * *

PL3             GAGGAGCCCAATGATAAGAAATGGGTACGATT--
PL4             GGAAGGCCTAGTGATGAGAAATGGGTATGACTCG
PL5             ---AAAC-------TAAGTACTGGA-ATAA----
                      *       * ** * ***  *  *
```

Supplemental Figure S2. Sequence alignment (ClustalW 1.8) of the PL3 to PL5 exons from TNL1 illustrating that these three exons derived from ancient duplications. Similarities between PL3 and PL4, PL3 and PL5 and PL4 and PL5 are respectively 73, 75 and 80%.

```
TNL1 R        :     GAGAAAG~AAATAATTATAGACATACCAACAAAGTCTGAGGAACC
Parsley D-box :     TACAATTCAAA~CATTGTT~~~~~~~~~~CAAACA~~~AGGAACC
```

Supplemental Figure S3. Comparison of the putative D-box from the TNL1 allele (position -3251 bp from ATG) and from the parsley *PR2* promotor as given by Rushton et al. (2002). The six base pairs critical for inducibility strength are underlined.

Supplemental Table S1. *Primers sequence, product size and position of markers of the* Ma1 *gene on the sequence of BAC 76H19 (287,717 bp).*
The position corresponds to the first base of the forward (F) primer.

Marker name	F and R primer sequences (5’→ 3’)	Product size (bp)	Position on BAC 76H19
SCAFLP3	GCAAAACCAGCCTCTGTCTC TCAGCACGTAATCTAAAGGTGG	506	3,788
SSR6	ATGGTAGCCACTTATGGAGC TTGACCTATAAAGTGATGGAAGG	402	45,096
SSR2	CCACCTCCCATCTAGAACTCC GCTAAAGTCGGCAAAGTCCA	323	107,413
PErepkin	CACAGCTTGAAACTCTTGAAGG AGAATTGCATTTTGGTGTCTCC	217	123,154
SSR1	GATTGTGAGAGTCCGTTTTCTTT ACCATCCAATGGCATCTCA	156	126,470
NSCAFLP2	AAAGGGGAAAACCCAAATTTAC GGGTCCTTTATTAGTGAATCTCTCC	327	132,620
SCAFLP2	GGACCCTGTACACTACATTAGTAAT TTAGAAGGGTGCACGTTGAGAGGCCG	202	132,941
DebNBS	GAGGCCGGAAATCTAACTACAAGT TTTTCTTCTCACCAGAGTAGCCT	907	133,136
Int2	AGGCTACTCTGGTGAGAAGAAAA AATTGAATAAAAAAACATTT	496	134,020
SSRO5I5	GAGCACATTCAAATAAAATAACA TTTCATCACGCCGAATGGCAT	283	135,856
SSRO5I12	AGCCACTGCTTTGATCCCCA CATCTTGAAAGATCAGAGGA	216	138,386
CT3-4N	TCTTGTATATCAGCATGACGAGG GCTAATCCTATCCAATTGCTGTC	458	138,957
PostGC3	ACAGGGTTAAAACCACGTAA GGACAGGTTGCATGTTAGAT	388	154,620
SSR9	CCATATTCAAACCTTTCACCG ACAACGGTGTGGCCTTCAGG	267	156,716
pIgms19	CGGGGTTCAAACTCAACAAG GTGAACAAAGCAGCACGTCT	327	172,659
SCAFLP4	TTCTCATATGGGCCATCTCCA TACGCCTCCTCTCCTGGAAATA	316	177,477
SSR12	GAACTAAAATCGAACTCAGATGC GATCTGTGAATACCAAGGGTG	324	254,593

Supplemental Table S2. *Resistance phenotype and genotype to RKN Meloidogyne spp. of material used (1) as parents for* Ma *high resolution mapping and (2) for complementation experiments.*

Species	Accession	Resistance status to…					Genotype
		M. arenaria	*M. incognita*	*M. javanica*	*M. floridensis*	*M. mayaguensis*	
Myrobalan plum (*P. cerasifera*)							
	P.2175 (1) (2)	R[a]	R	R	R	R	*Ma1 /ma*
	P.2646 (1)	S[a]	S	S	S	S	*ma/ma*
	P.2032 (2)	S	S	S	S	S	*ma/ma*
Peach (*P. persica*)							
	P.3443 (1)	S	S	S	S	S	*ma/ma*
	Nemared (1)	R	R	R/S[a]	S	-[a]	*ma/ma*
Almond x peach							
	(Garfi x Nemared)$_{22}$ (1)	R	R	R/S	S	-	*ma/ma*
Myrobalan x (almond x peach)							
	[P.2175 x (Garfi x Nemared)$_{22}$]$_{253}$ =`253' (2)	S	S	S	S	S	*ma/ma*

[a] R = resistant, S = susceptible, R/S = resistance depending on the RKN species population, - = unknown

Supplemental Table S3. *Primers used for the cDNAs of TNL1 (full-length construction), TNL2 and TNL3.*

TNL	Primer name	Sequence 5'-->3'	Target region
TNL1	Am5’-2F	CAC TTG TAA GTA CCT TTC AAA AGC	5' UTR
	TIRGC1-R1	GTT TGC CAG TTC GAC CAT TTT CG	
	TIRGC1-R2	CAA ATC CTT CGG CTT CGA GTT CGG	
	TIRNBSGC1-F	CGA ACT CGA AGC CGA AGG ATT TG	TIR-NBS
	TIRNBSGC1-R	GTC CTT TAA ATC ATC ATT TGA GAA TG	
	NBSGC1-F	CTC AAA TGA TGA TTT AAA GGA CT	NBS-NLL
	NBSNLLGC1-R	AGG AAA ATA CCT TGG ACA GCA TC	
	EpisLRR-F1	TAC CTG AAA GCA TCT CTC AGC	LRR-PL2
	EpisLRR-R1	GCA GAG CAC AGA CAA CGT AG	
	CT3-Fo	AGC AAC ATT GTA AAT CCT GTA AAT C	PL3-PL5
	CT3-Ba	CGA TCA AAG TCC CAT TTC TCA TC	
	Ic-CT3-Ba	GAT GAG AAA TGG GAC TTT GAT CG	3' UTR
TNL2	NBSGC2-F	AAA TGA GTT TGT GTA TGG ATT CG	NBS
	NBSGC2-R	GTA TAT TTC TCG GTG GTT GTA AT	
TNL3	NLR-F2	CTG CCT TCA AGT TTT GAA CCC GAT	NLL-LRR
	NLR-R	TCA GCT TAG AGG GCA AGG CCG GTC	