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Natural diversity in the model legume *Medicago truncatula* allows identifying distinct genetic mechanisms conferring partial resistance to Verticillium wilt.

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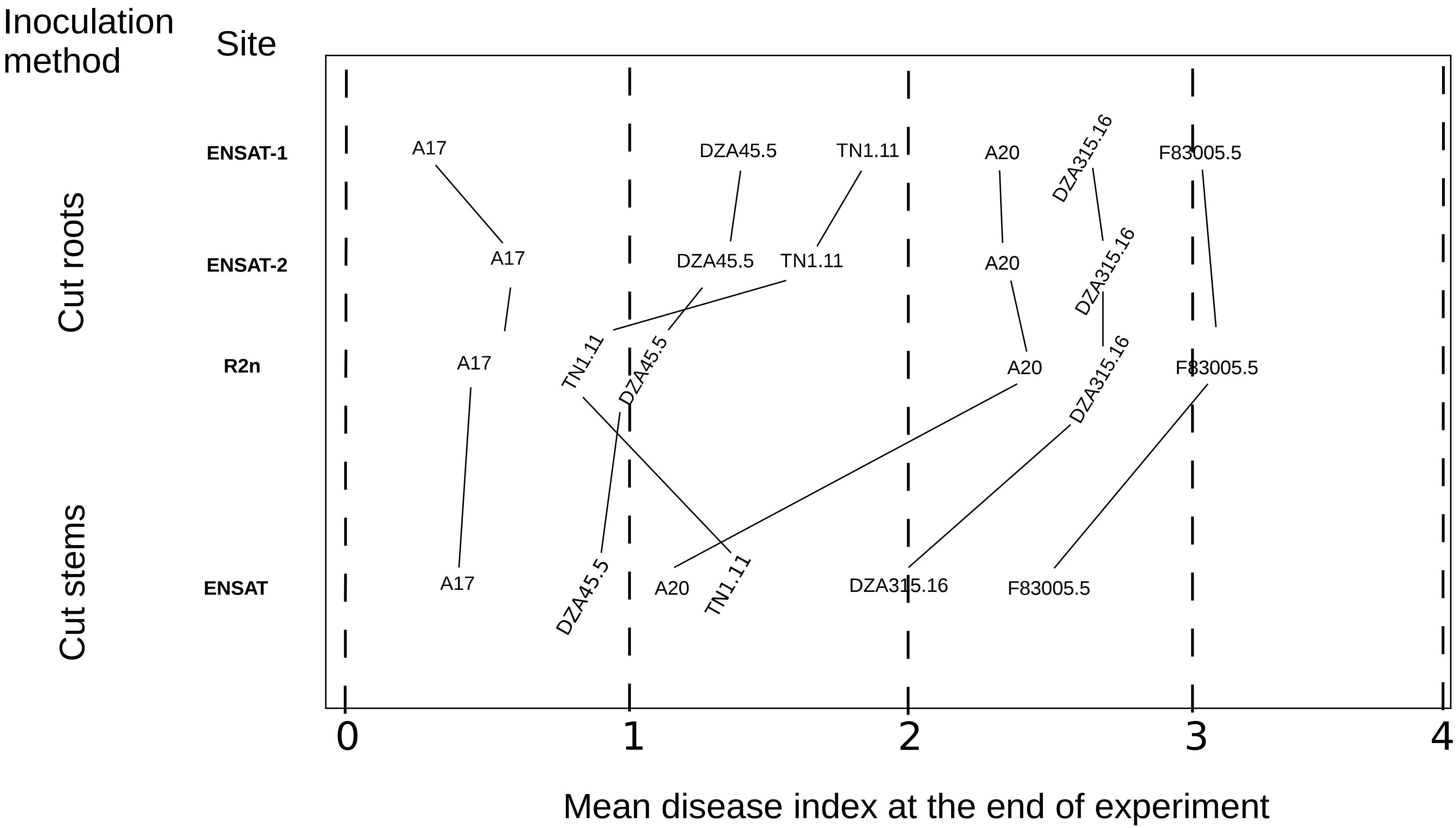


Figure S1. Comparisons of the quantitative resistance levels of six *Medicago truncatula* lines depending on inoculation method with *Verticillium albo-atrum*. The widely used tolerance assay in *M. sativa* based on infection after stem cuttings ('Cut stems' inoculation method; Molinero- Demilly et al., 2007) is compared to the one based on infection after roots cuttings in Jiffy pots ('Cut roots' inoculation method). The new inoculation method based on cut roots was tested at three different sites. *M. truncatula* accessions are drawn at their corresponding average score within each site, and lines allow easy comparisons of scores ranges between environments for each accession. Fifteen plants per line were inoculated for cut stems inoculation method, 12 to 15 plants per line were used for cut roots inoculation method.

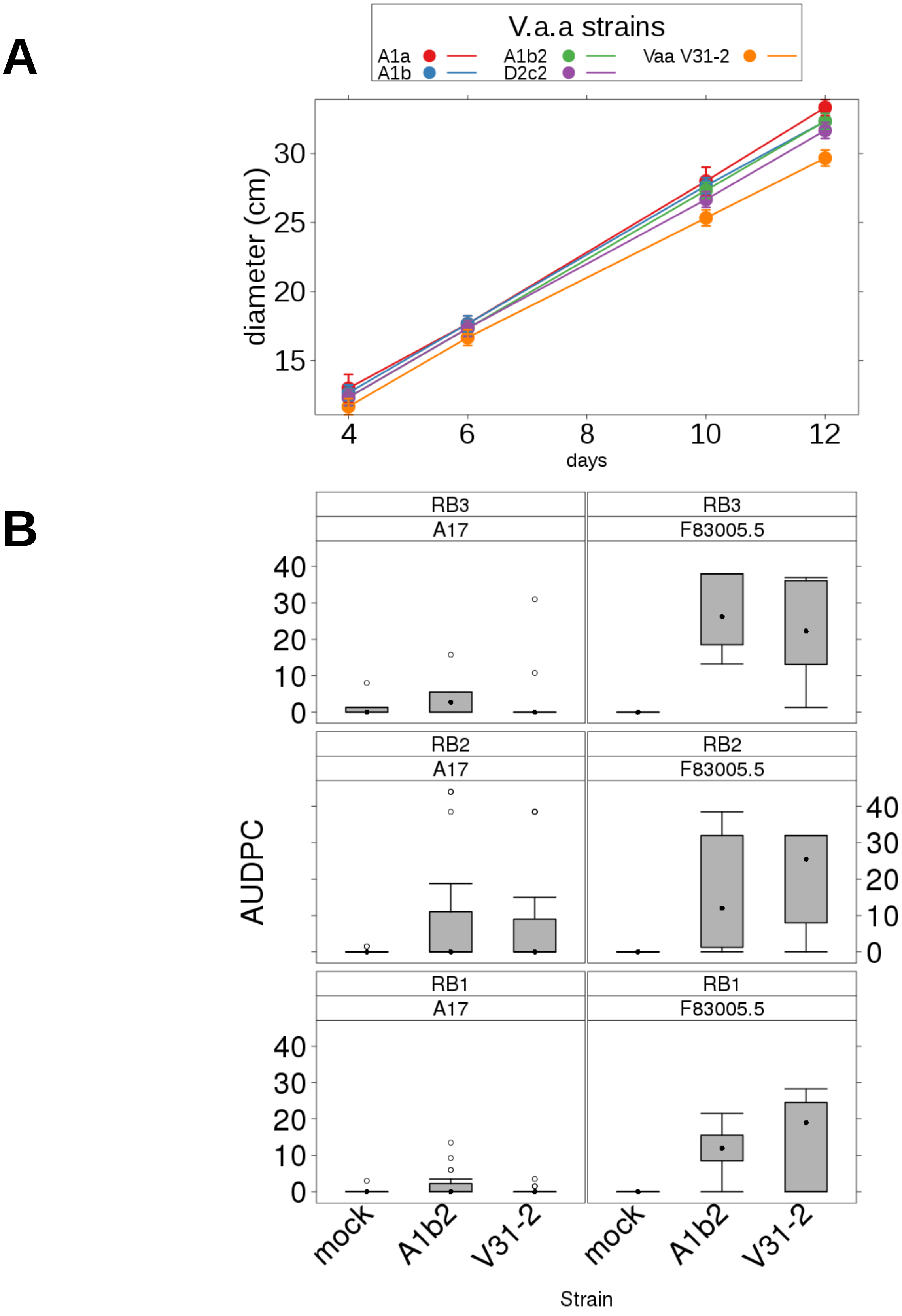


Fig. S2. Analysis of the growth and aggressiveness of four monosporic isolates of *V. albo-atrum* expressing the Green Fluorescent Protein gene in comparison to the wild-type strain V31-2.

A Radial growth on PDA medium was determined for 12 days. Data are means (± SD) of three independent experiments **B** Aggressiveness of the A1b2 GFP-expressing strain and corresponding wild strain V31-2 as assessed through AUDPC in the susceptible *M. truncatula* line F83005.5 or resistant line Jemalong-A17, following root inoculation in hydroponic culture. Data were obtained from 3 independent experiments (RB1, RB2, RB3).

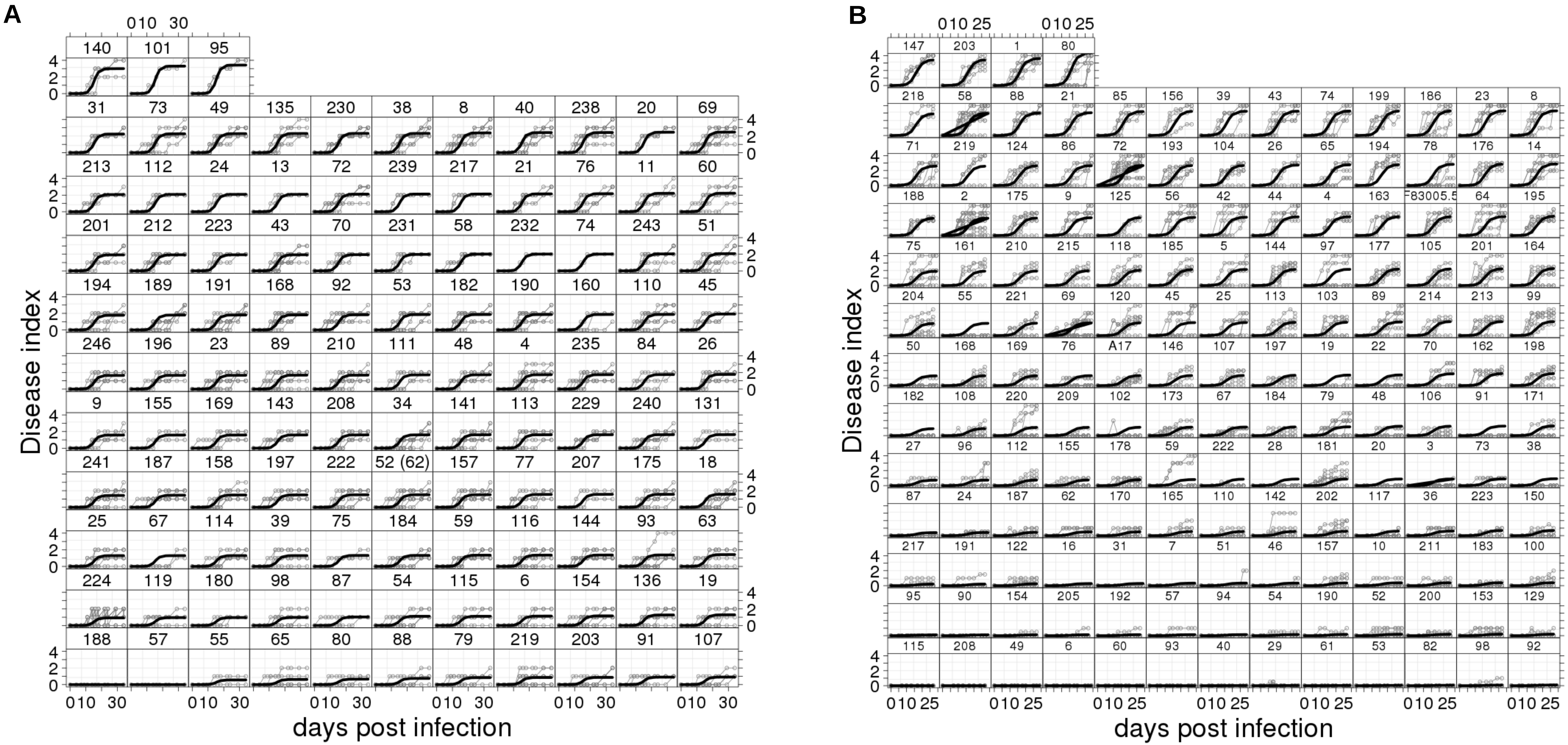


Fig. S3. Example of model fitting for wilting symptoms in 113 LR4 RILs at R2N site (**A**) and 158 LR5 RILs at ENSAT site (**B**).
RIL genotypes are ordered by increasing maximum disease index, from bottom left to top right. For LR5, the parental genotypes Jemalong-A17 and F83005.5 are included.

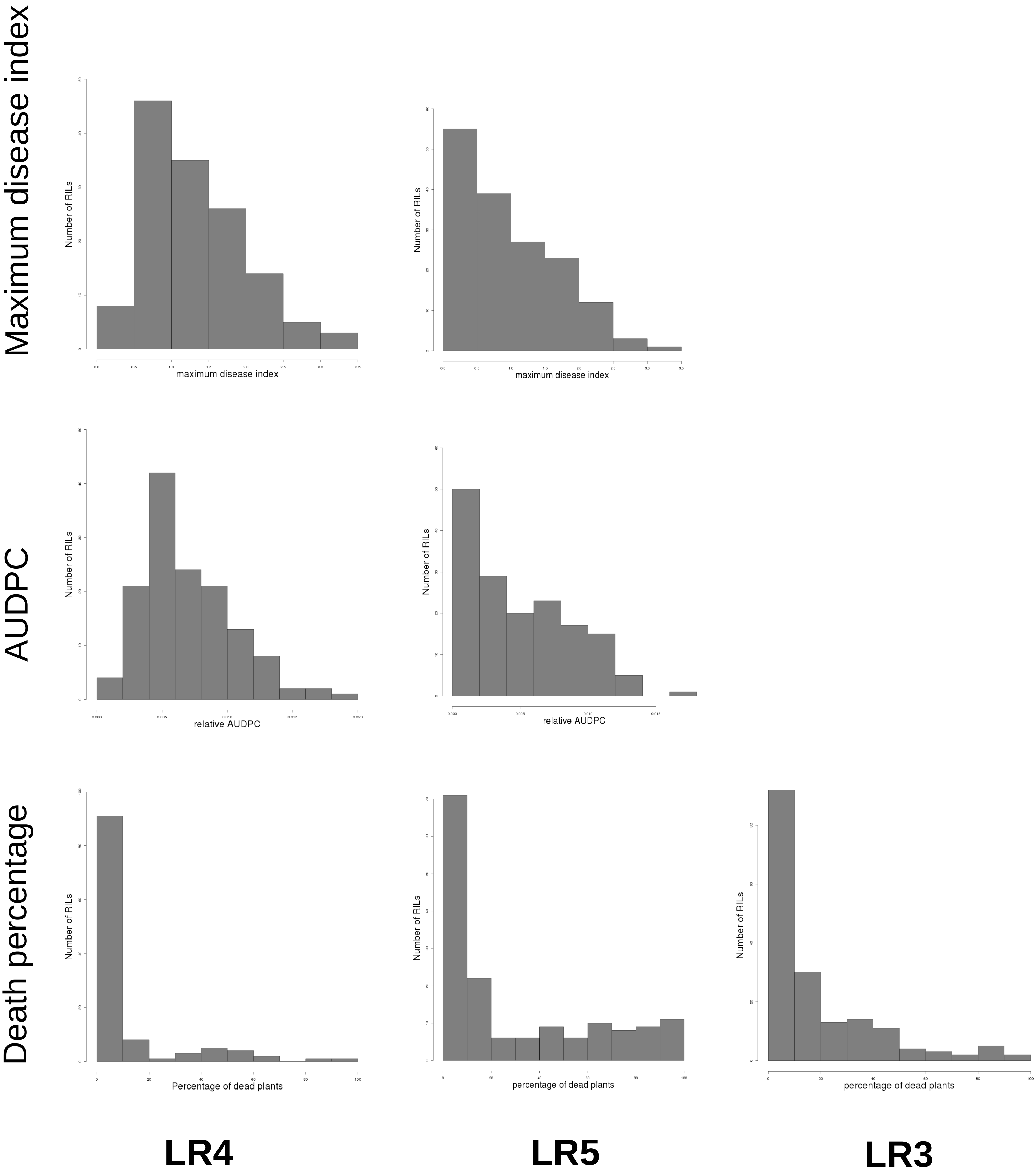


Fig. S4. Distribution of disease evaluation parameters in LR3, LR4 and LR5 RILs upon infection with *V. albo-atrum* V31-2.

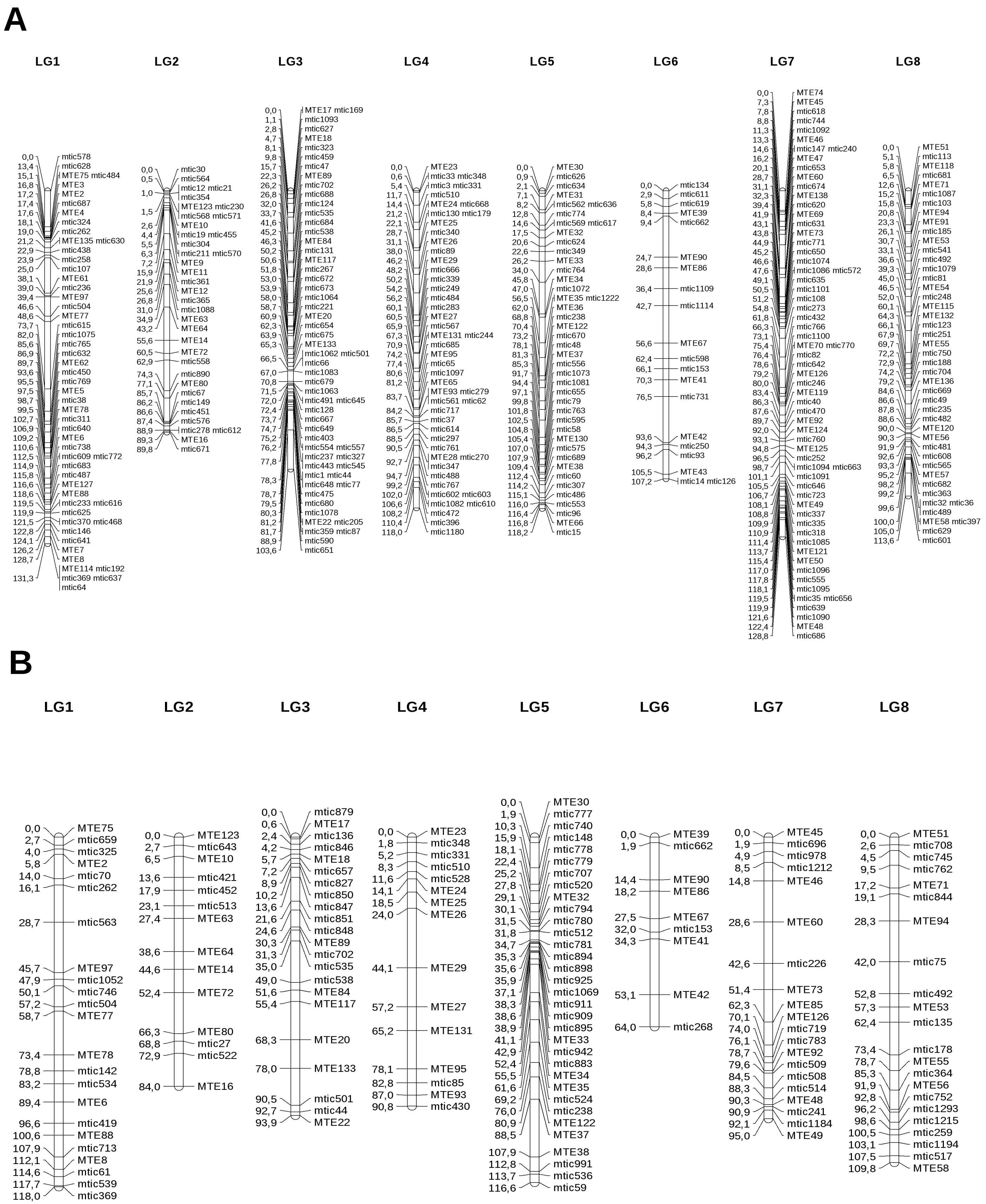


Fig. S5. Dense genetic maps for (A) A17 X DZA315.16 (LR4) and (B) A17 X F83005.5 (LR5) RILs populations of *Medicago truncatula*

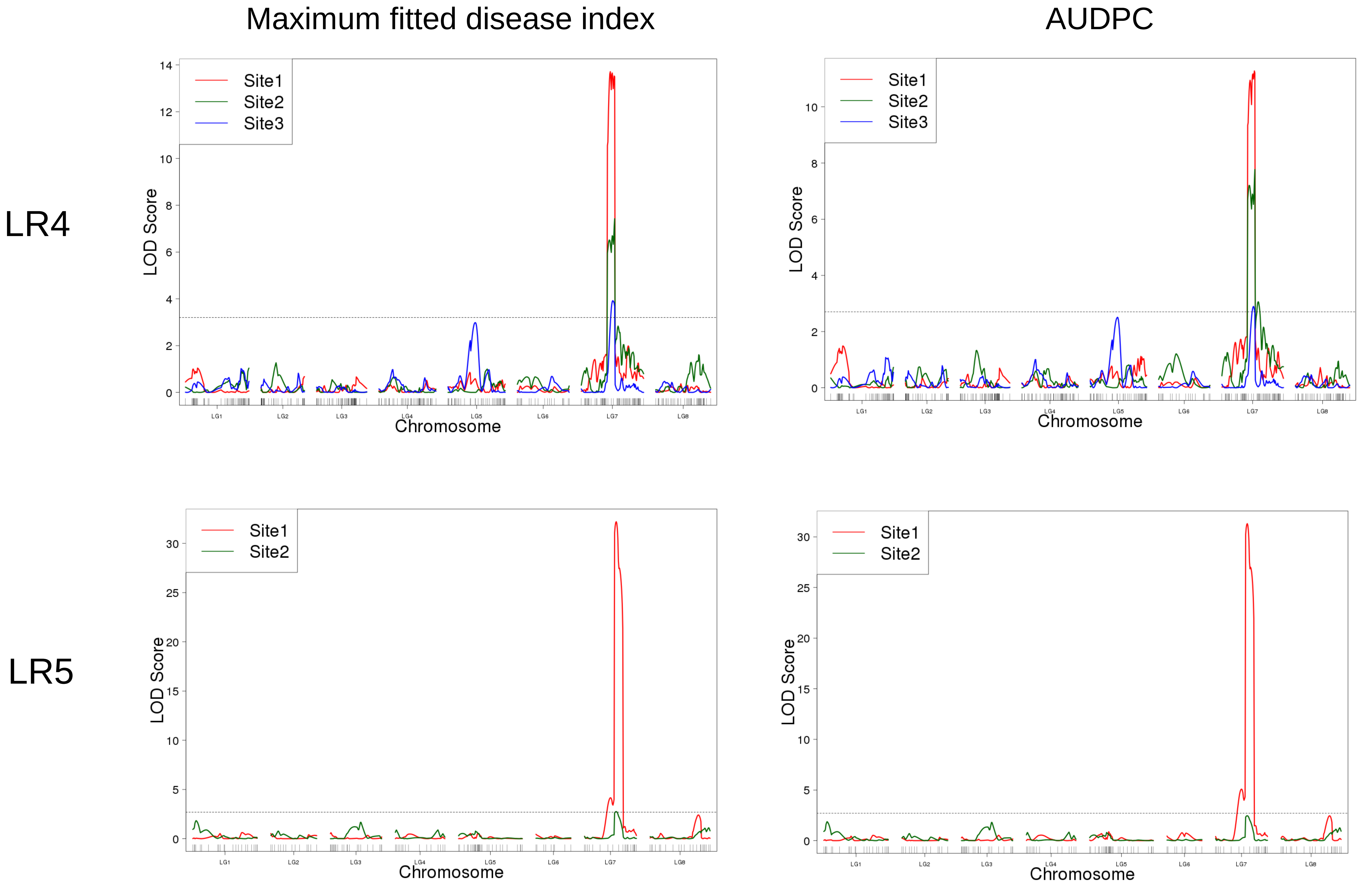
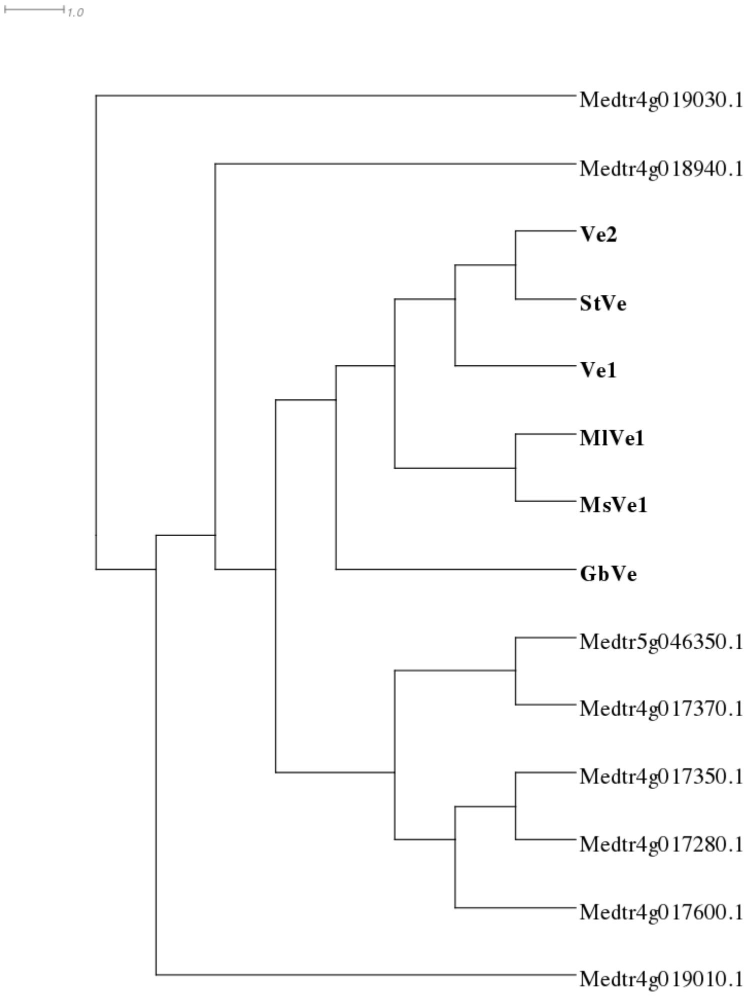


Fig. S6. Whole-genome scans for QTL detection for *Verticillium* resistance assessed through maximum disease index (MDI) and AUDPC parameters in LR4 and LR5 populations, for each site.

Log-likelihood (LOD) score for MDI and AUDPC, as identified by Multiple QTL Mapping, are plotted against the whole-genome of *Medicago truncatula* for LR5 and LR4 RIL populations. Significance of QTL is indicated by a LOD score above the threshold values, determined by permutation analysis at the genome-wise significance level of 0.05.

A



B

	Ve2	StVe	GbVe	MsVe1	MlVe1	Medtr4g017280.1	Medtr4g017350.1	Medtr4g017370.1	Medtr5g046350.1
Ve1	83	80	48	49	49	46	46	46	43
Ve2		86	50	49	49	44	44	44	43
StVe		50	50	49	49	44	44	44	43
GbVe				42	42	42	44	41	42
MsVe1					96	42	42	41	41
MlVe1						42.00	42	42	42
Medtr4g017280.1							83	69	70
Medtr4g017350.1								70	69
Medtr4g017370.1									91

C

Functional domain A

```
            Ve1  MKMMATLYFLWLLLIPSFQILSGYHIFLV   29
Medtr4g017370.1  ..MRAHLTFL.LFLIPFSLINSSSNIFLV
Medtr4g017350.1  ..MRAHIVFL.LFFIPFSLIISSSNKFLV
Medtr4g017280.1  ..MIAHIIFW.LFLIPFSIINSSSNNFVV
Medtr5g046350.1  ..MRAHIIF.WLFFMLFSSINSSTNNFLL
           GbVe MMISPFSWIFFNAFLVAAFFTI...HLVLV
```

Functional domain B

```
            Ve1  SSQCLDDQKSLLLQFKGSLQYDSTLSKKLAKWND   63
Medtr4g017370.1  NGYCQGHERSLLLHLKNSLIFNPAKSSKLVNWNQ
Medtr4g017350.1  NGYCHGHEHSLLLQLKNSLIFNPTKSSKLVHWNQ
Medtr4g017280.1  NGYCHGHQRSLLLQLKNNLIFNSEISSKLVHWKQ
Medtr5g046350.1  NGNCRGHQRAVLLQLKNNLIFNPEKSSKLVHWNQ
           GbVe  SGQCQRDQGQLLLELKSS..FNSTSLGKLQKWNQ
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```
            Ve1  MTSECCNWNGVTCNLFGHVIALELDDETISSGIE   97
Medtr4g017370.1  NDDDCCQWNGVTC.IEGHVTALDLSHESISGGLN
Medtr4g017350.1  SDDDCCQWHGVTC.KQGHVTVLDLSQESISGGLN
Medtr4g017280.1  SEHDCCQWDGVTC.KDGHVTALDLSQESISGGLN
Medtr5g046350.1  SEYDCCKWHGVTCK.DGHVTALDLSQESISGGLN
           GbVe  .TTDCCFWDGVTCDASGRVIGLDLSNQSISGAID
```

```
            Ve1  NSSALFSLQYLESLNLADNMFNVGIP  123
Medtr4g017370.1  ASSSLFSLQYLQSLNLALNDFHSMMP
Medtr4g017350.1  DSSALFSLQYLQSLNLAFNHFRSVIP
Medtr4g017280.1  DSSALFSLQYLQSLNLALNKFNSVIP
Medtr5g046350.1  DSSAIFSLQ...GLNLAFNKFNFVIP
           GbVe  DSSGLFRFQHLQQLNLAYNRLMATFP
```

Functional domain B (continued)

```
          Ve1   VGIANLTNLKYLNLSNAGFVGQIP   147
Medtr4g017370.1   QELHQLQNLRYLNFSNAGFQGQIP
Medtr4g017350.1   QDLHRLHNLRYLNLSNAGFKGQVP
Medtr4g017280.1   QALHKLQNLSYLNLSDAGFDGYVP
Medtr5g046350.1   QALHKLQNLRYLNLSDAGFEEQVP
           GbVe   TGFDKLENLSYLNLSNAGFTGQIP

          Ve1   ITLSRLTRLVTLDLSTILPFFDQP   171
Medtr4g017370.1   TEIFHLKRLVTLDLSSSF.TSHHV
Medtr4g017350.1   EEISHLKRLVILDFSSKF.ISLQN
Medtr4g017280.1   IEISHLTRLVTLDLSSTF.ISHQS
Medtr5g046350.1   KEIAHLTRLVTLDLSSLI.TSRQN
           GbVe   AVISRMTRLVTLDLS-VSSLLGRS

          Ve1   LKLENPNLSHFIENSTELRELYLDGVDLSSQRT   204
Medtr4g017370.1   LKLENPNIGMFMKNFTDITKLYLDGVAISASGE
Medtr4g017350.1   LKLEKPNIGMLVQNLTDITELYLDGVAISARGE
Medtr4g017280.1   LKLAKQNMAILVKNLTNIIELYLDGVAICTSGE
Medtr5g046350.1   LKLENPNIEMLVKNLTDITELYLDGVAISSSGD
           GbVe   LTLEKPKLEMLVQNLTKLKFLHLDGVNIRATGN

          Ve1   EWCQSLSLHLPNLTVLSLRDCQISGPLD   232
Medtr4g017370.1   EWGRSLYP.LGGLRVLSMSSCNLSGPID
Medtr4g017350.1   EWGHPLSL.LKGLRVLSMSSCNLSGPID
Medtr4g017280.1   EWGRALSS.LEGLRVLSMSSCNLSGPID
Medtr5g046350.1   EWGRALSL.LEGVRVLSMSSCNLSGPID
           GbVe   EWCRALS.SLTDLQVLSMSNCNLSGPID
```

Functional domain B (continued)

Ve1	ESLSKLHFLSLVQLDQNNLSSTVP	256
Medtr4g017370.1	SSLARLQSLSVLKLSHNNLSSIVP	
Medtr4g017350.1	SSLAKLQSLSIVKLSQNKLFTTVP	
Medtr4g017280.1	SSLVKLQSLSLLKLSHNKLSCIVP	
Medtr5g046350.1	SSLAKLQSLSVLRLNNNKLSSKVP	
GbVe	SSISKLRSLSVIRLDNNNLSTSVP	

Ve1	EYFANFSNLTTLTLGSCNLQGTFP	280
Medtr4g017370.1	SSLARLQSLSVLKLSHNNLSSIVP	
Medtr4g017350.1	SSLAKLQSLSIVKLSQNKLFTTVP	
Medtr4g017280.1	SSLVKLQSLSLLKLSHNKLSCIVP	
Medtr5g046350.1	DSFANFSNLTILEISSCGLNGFFP	
GbVe	EFFAEFPNLTSLHLSTSGLRGGLP	

Ve1	ERIFQVSVLESLDLSINKLLRGSIP	305
Medtr4g017370.1	KDIFQIHTLKVLDISYNQNLNGSLP	
Medtr4g017350.1	KDIFQIHTLKVLDMSNNQNLYGSLP	
Medtr4g017280.1	KDIFQIHKLNVLDISDNQNLNGSLP	
Medtr5g046350.1	KEIFQIHTLKVLDISDNQNLSGSLP	
GbVe	AEVLKIPTLQILDLSNNELLEGSFQ	

Ve1	IFFRNGSLRRISLSYTNFSGSLP	328
Medtr4g017370.1	DFSTLASLKYLNLADTNFSGPLP	
Medtr4g017350.1	DFPPFAYLHYLNLNNTNFLGPLP	
Medtr4g017280.1	DFPPLASLHYLNLTNTNFSGPLP	
Medtr5g046350.1	DFSPLASLKYLNLADTNFSGPLP	
GbVe	EFPSNGSLQTLTLSGTKFGGQVP	

Functional domain B (continued)

```
            Ve1   ESISNHQNLSRLELSNCNFYGSIP   352
Medtr4g017370.1   NTISNLKHLSTIDLSHCQFNGTLP
Medtr4g017350.1   NTISNLKQISTIDLSYCKFNGTIP
Medtr4g017280.1   NTISNLKQLSTIDLSYCQFNGTLP
Medtr5g046350.1   NTISNLKHLSTIDLSHCQFNGTLP
           GbVe   DSIGNLGQLTRIELASCNFSGPIP

            Ve1   STMANLRNLGYLDFSFNNFTGSIP   376
Medtr4g017370.1   SSMSKLTQLVYLDLSFNNFTGLLP
Medtr4g017350.1   NSMSELTQLVYLDMSSNNLTGPLP
Medtr4g017280.1   SSMSELTQLVYLDMSSNYLTGPLP
Medtr5g046350.1   SSMSELTQLVYLDLSFNNFTGLLP
           GbVe   KAVKKLTQLVYLDFSSNSFSGPIP

            Ve1    YFRLSKKLTYLDLSRNGLTGLLS   399
Medtr4g017370.1    SLSMSKNLRYISLLRNYLSGNLP
Medtr4g017350.1    SFNMSKNLTYLSLFLNHLSGDLP
Medtr4g017280.1    SFNMSKNLTYLSLFLNHLSGDLP
Medtr5g046350.1    SLR....................
           GbVe    SFSSSRNLTQLNLAYNRLNGTIH

            Ve1   RAHFEGLSELVHINLGNNLLSGSLP   424
Medtr4g017370.1   SNHFEGLINLVSINLGFNSFNGSVP
Medtr4g017350.1   SSHFEGLKNLVIVDLGFNYFTGNIP
Medtr4g017280.1   SSHFEGLQNLVSIDLGFNSFKGKMP
Medtr5g046350.1   ................FNSFNGSVP
           GbVe   STDWSVLSNLVSIDLRNNKLSGTIP
```

Functional domain B (continued)

```
            Ve1    AYIFELPSLQQLFLYRNQFVGQVD    448
Medtr4g017370.1    SSVLKLPCLRELKLPYNKLSGILG
Medtr4g017350.1    SSLLKLPYLRELMLPFNQLSGVLS
Medtr4g017280.1    SSLLKLPYLRELKLPFNQIGGLLV
Medtr5g046350.1    SSVLKLPCLRELKLPYNKLCGILG
           GbVe    PTLFGIPSLQKISLSQNRFNGSLG

            Ve1   EFRNASSSPLDTVDLTNNHLNGSIP    473
Medtr4g017370.1   EFHNASSPLLEMIDLSNNYLQGPIP
Medtr4g017350.1   EFDNASLPVLEMLDLGSNNLQGHVP
Medtr4g017280.1   EFDIAS.SVLEMLDLGSNNLQGHIP
Medtr5g046350.1   EFHNASSPLLEMIDLSNNYLEGPIP
           GbVe   DLRGKTTLLLDTLDLSSNMLQGQFP

            Ve1    KSMFEIERLKVLSLSSNFFRGTVP    497
Medtr4g017370.1    LSIFNLQTLRFIQLSSNKFNGTVK
Medtr4g017350.1    FSLFNLRTLRVFQLSSNKFNGTIQ
Medtr4g017280.1    VSVFNLRKLRVLQLSSNKLNGTIQ
Medtr5g046350.1    LSIFNLQTLRFIQLSSNKFNGTVK
           GbVe    MFVFELQGLKILTISSNKFSGFIQ

            Ve1   LDLIGRLSNLSRLELSYNKLTVDAS    522
Medtr4g017370.1   LDVIRKLSNLTVLGLSYNNLLVDVN
Medtr4g017350.1   LNVLQRLRNLNVLGLSHNNLSIDVN
Medtr4g017280.1   LDIIRRLSNLTVLGLSNNFLSIDVN
Medtr5g046350.1   LDVIRRLSNLTVLGLSYNNILVDVN
           GbVe   WTDIQKLRNLSNLDLSYNNLSIDAT
```

Functional domain B (continued)

```
            Ve1   SSNSTSFT.FPQLNILKLASCRLQKFPD   549
Medtr4g017370.1   FKYDHNMSSFPKMRILDLESCKLLQIPS
Medtr4g017350.1   FRDNHDLSPFPEIKDLMLASCKLKGIPS
Medtr4g017280.1   FRDDHQLSLFREIRVVQLASCNLRGIPS
Medtr5g046350.1   FKYDHNMSSFPKMRILDLESCKLLQIPS
           GbVe   STNSALST.FPNITTLKLASCNLKKFPG


            Ve1   .LKNQSWMMHLDLSDNQILGAIP   571
Medtr4g017370.1   FLKNQSTILSIHMADNNIEGPIP
Medtr4g017350.1   FLRNQSKLLFLDLSSNGIEGPIP
Medtr4g017280.1   FLRNQSKLLFLDISRNDIEGSIP
Medtr5g046350.1   FLKNQSTILSIHMADNNIEGPIP
           GbVe   FLKTQVKLNHLDLSKNQMSGEIP


            Ve1   NWIWGIGGGGLTHLNLSFNQL-EYVEQ   597
Medtr4g017370.1   KWIWQLES..LVSLNLSHNYFTGLEES
Medtr4g017350.1   NWIWKLES..LLSLNLSKNSLTNFEES
Medtr4g017280.1   NWIWKHES..LLNLNLSKNSLTNFEET
Medtr5g046350.1   KWIWQLES..LVSLNLSHNYFTGLEES
           GbVe   NWVWEIKN..LAYLNLSQNSLMKFEGP


            Ve1   .YTASSNLVVLDLHSNRLKGDLLIP 622
Medtr4g017370.1   FSNFSSNLNTVDLSYNNLQGPIPLV
Medtr4g017350.1   IWNLSSNLYLVDLSFNKLQGPISFI
Medtr4g017280.1   SWNLSSNLYMVDLSFNRLQGPISFI
Medtr5g046350.1   FSNFSSNLNTVDLSYNNLQGPIPLV
           GbVe   FLSITSTLTVVDLHGNQLQGQIDRL
```

Functional domain B (continued)

```
          Ve1   PCTAIYVNYSSNNLNNSIPTDIG   645
Medtr4g017370.1   PKYAAYLDYSSNNFSSIIPPDIG
Medtr4g017350.1   PKYAFYLDYSSNKLSSIIHPDIG
Medtr4g017280.1   PKHAFYLDYSSNKLSSIVQPDIG
Medtr5g046350.1   PKYAAYLDYSSNNFSSIIRPDIG
           GbVe   PQYATYLDYSRNNFSSVLPRDIG
```

```
          Ve1   KSLGFASFFSVANNGITGIIP   666
Medtr4g017370.1   NHLPYMTFMFLSNNKFQGQIH
Medtr4g017350.1   NYLPAINILFLSNNSFKGEID
Medtr4g017280.1   NYLPAINILFLSNNSFKGEID
Medtr5g046350.1   NHLPYMTFMFLSNNKFQGQIH
           GbVe   DFLQFAYFFSISDNNFHGSIP
```

```
          Ve1   ESICNCSYLQVLDFSNNALSGTIP   690
Medtr4g017370.1   DSFCNATSLRLLDLSHNNFLGKIP
Medtr4g017350.1   ESLCNASSLRLLDLSYNNFDGKIP
Medtr4g017280.1   ESLCNASYLRLLDLSYNNFDGKIP
Medtr5g046350.1   DSFCNASSLRLLDLSHNNFVGTIP
           GbVe   ESICKSSYLQVLDLSNNSLSGSIP
```

```
          Ve1   PCLLEYSTKLGVLNLGNNKLNGVIP   715
Medtr4g017370.1   KCFEALSSNLRVLNFGGNKLRGQIP
Medtr4g017350.1   KCFATLSSKLRMLNFGGNKLHGHIP
Medtr4g017280.1   KCFATLSSRLLMLNFEGNKLHGHIP
Medtr5g046350.1   KCFEALSSSLRVLNFGGNKLRGQIP
           GbVe   ECLIQMSVSLGVLNLRRNNLTGNIS
```

Functional domain B (continued)

```
            Ve1   DSFSIG.CALQTLDLSANNLQGRLP   739
Medtr4g017370.1   SSMFPNLCALRFVDLNDNLLGGPIP
Medtr4g017350.1   DTISPNSCALRYLNLNDNLLDGSIP
Medtr4g017280.1   DIISPNSCALRYLNLNDNLLNGSIP
Medtr5g046350.1   SSMFPNLCALRFVDLNDNLLGGPIP
           GbVe   DTFPEN.CLLQTLVLNRNLLRGKVP

            Ve1   KSIVNCKLLEVLNVGNNRLVDHFP   763
Medtr4g017370.1   KSLINCKELQVLNLGKNALTGRFP
Medtr4g017350.1   KSLVNCNKLQVLNLGNNFLSDRFP
Medtr4g017280.1   KSLVNCNKLQVLNLGNNFLSDRFP
Medtr5g046350.1   TSLINCKELQVLNLEKNALTGRFP
           GbVe   KSLVSCKMLEVLDLGNNQINDTFP

            Ve1   CMLRNSNSLRVLVLRSNKFYGNLM   787
Medtr4g017370.1   CFLSKIPTLRIMVLRSNKLHGSIR
Medtr4g017350.1   CFLSNISNLRIMILRSNKMHGSIG
Medtr4g017280.1   CFLSNISTLRIMVLRSNKLHGSIG
Medtr5g046350.1   CFLSKIPTLRIMVLRSNKLHGSIR
           GbVe   CHLKNISSLRVLVLRGNKFNGNVH

            Ve1   CDVTRNSWQNLQIIDIASNNFTGVLN   813
Medtr4g017370.1   CPNSTGYWKMLHIVDLARNNFSGMIS
Medtr4g017350.1   CPNSTGDWEMLHIVDLASNNFNGTIP
Medtr4g017280.1   CPTRTGDWKMLHIVDLASNNLNGRIP
Medtr5g046350.1   CPNSTGYWKMLHIVDLACNNFSGMIS
           GbVe   CS.ERSPWPMLQIVDLSSNSFSGRLH
```

Functional domain B (continued)

```
                                            Ve1   AEFFSNWRGMMVADDYVETGRNHIQ  838

                                Medtr4g017370.1   SALLNSWQAMMRDEDVLGPEFGSLF

                                Medtr4g017350.1   VALLNSWKAMMRDEGVLRKELGHLF

                                Medtr4g017280.1   VSLLNSWKAMMRDEDVLGTELGHLF

                                Medtr5g046350.1   SALLNSWQAMMRDEDVLGPEFGSLF

                                           GbVe   EACLSTWKAMRAAESETLSELNHLQ


                                                                             867

   Ve1YEFLQ.................................LSKLY............YQDTVTLTIKGMELELVKI

 .70  FEVYDNYHQMGFKDVVRMMEKFCAKQVAQLLLNMSHSDLYQVFSDRTAEHVDLGRYQESIIIVNKGHQMKLVKV

 .50  FDIDDNFHPMSFKALLPDLDKHVSMNLIKLLANMSRSIIDQEY....AKFKILARYQDTIIIVNKGQQMNVVKI

 .80  FDIDDNFHPMSFKAMLPALDKRVSTNLIPFLENMSRSIIDQEY....AKLKILARYQVSINIVNKGHQMKLVKI
 350  FEVYDNYHQMGFKDVVRMMEKFCAKQVTQLLLNMSHSDLYQVFSDRTAEHVDLGRYQESIIIVNKGHQMKLVKV

GbVe  FKVLK.................................LNQFY............YQDAITVTMKGLELELLKI


                                                  Ve1   LRVFTSIDFSSNRFQGAIP  886

                                      Medtr4g017370.1   QTAFTYVDMSSNYLEGQIP

                                      Medtr4g017350.1   QSTFTYVDMSSNYLGGPIP

                                      Medtr4g017280.1   QSALTYVDMSSNYLEGPIP

                                      Medtr5g046350.1   QTAFTYVDMSSNYLEGQIP

                                                 GbVe   LTVFTSIDISRNNFEGPIP


                                             Ve1   DAIGNLSSLYVLNLSHNALEGPIP  910

                                 Medtr4g017370.1   DELMQFKALMALNLSHNALTGHIP

                                 Medtr4g017350.1   DVLMRFKALNALNLSHNALTGHIP

                                 Medtr4g017280.1   NELMQFKALNALNLSHNALMGHIP

                                 Medtr5g046350.1   DELMQFKALMALNLSHNALTGHIP

                                            GbVe   EVIGTFKALYVLNFSHNAFTGSIP
```

Functional domain B (continued)

Ve1	KSIGKLQMLESLDLSTNHLSGEIP	934
Medtr4g017370.1	SSVENLKHLECMDLSNNSLNGEIP	
Medtr4g017350.1	SSVENLKHLESMDLSNNSLNGEIP	
Medtr4g017280.1	SLVGNLKNLESMDISNNSLNGEIP	
Medtr5g046350.1	SSVENLKHLESMDLSNNSLNGEIP	
GbVe	PSLGNLSQLESLDLSSNSFDGEIP	

Ve1	SELASLTFLAALNLSFNKLFGKIP	958
Medtr4g017370.1	QGLSSLSFLAYMNLSFNHLVGRIP	
Medtr4g017350.1	QGLSSLSFLAYMNLSFNHLVGRIP	
Medtr4g017280.1	QELSSLSFLAYMNLSFNHLVGRIP	
Medtr5g046350.1	QGLSSLSFLAYMNLSFNHLVGRIP	
GbVe	IQLANLNFISFLNVSNNKLEGQIP	

Ve1	STNQFQTFSADSFEGNSGLCGLPLNNSCQSNG...SA	992
Medtr4g017370.1	LGTQIQSFDVDSFKGNEGLCGPPLTTNCDDGGVQGLP	
Medtr4g017350.1	LGTQIQTFDVDSFAGNEGLCGPPLTKICE......PP	
Medtr4g017280.1	LGTQIQTFDVDSFEGNEGLCGPPLTKICE......LP	
Medtr5g046350.1	LGTQIQSFDVDSFKGNEGLCGPPLTTNCDDGGVQGLP	
GbVe	RSTQIQSFSEASFENNKGLCGLPLTTDCV.NG...TS	

Functional domain C

Ve1	SESLPPPTPLPDSDDEWE	1010
Medtr4g017370.1	PPASELSPCHNDSSIDWN	
Medtr4g017350.1	QPASETPHSQNESFVEWS	
Medtr4g017280.1	QSASETPHSQNESFVEWS	
Medtr5g046350.1	PPASELSPCHNNSSIDWN	
GbVe	PKPRTTQEFQPADEFDWQ	

Functional domain D	Ve1	FIFAAVGYIVGAANTISVVWF	1031
	Medtr4g017370.1	FLSVELGFIFGLGIFILPLVC	
	Medtr4g017350.1	FISIELGFFFGFGVFILPVFC	
	Medtr4g017280.1	FISIELGFLFGFGVFILPVFC	
	Medtr5g046350.1	FLSVELGFIFGLGIFILPLVC	
	GbVe	FIFIGVGFGVGAALFVAPLIF	

Functional domain E	Ve1	YKPVKKWFDKHMEKCLLWFSRK	1053
	Medtr4g017370.1	LMKWRLWYSNHADEMLHRFIPQLDFVYEQHEGKRCRSLRWRY	
	Medtr4g017350.1	WKKLRLWYSKHVDEMLYRFIPRLDFVYEQHEGKRYKTLKWMY	
	Medtr4g017280.1	WKKLRLWYSKHVDEMLYRFIPRLDFVYEQHEGKRYKTLKWMY	
	Medtr5g046350.1	LMKWRLWYSNRADEMLHRFIPQLDFVYEQHEGKRCRSLRWRY	
	GbVe	WKTASKWVDEIVDKILEVVLPKLGRTYTCPGDRKVDEDENLE	

Fig. S7. Identification of four *Medicago truncatula* paralogs putatively orthologous to *Ve Verticillium* resistance genes.

A Phylogenetic tree comparing MtVe candidates proteins to functionally validated Ve homologs in other plant species. **B** Percentage of amino-acid similarities of four MtVe candidates proteins deduced from cDNA sequence with functionally validated Ve homologs in other plant species. **C** Conservation of functional protein domain in the primary structure of Ve1, GbVe and four MtVe candidates proteins. Primary structure of the Ve1, GbVe and our four MtVe candidates proteins are deduced from cDNA sequence. The Ve polypeptides have been divided into domains A–E by Kawchuk et al. (2001) and alignments are drawn to comply with this classification. Highlighted are the hydrophobic amino acids (purple) of the putative signal peptide domain A and membrane-associated domain D; conserved L/I (red), G (green), and potential Nglycosylation sites (blue) within the LRR domain B; neutral and acidic amino acids (gray) of domain C; and neutral and basic amino acids (yellow) of domain E.

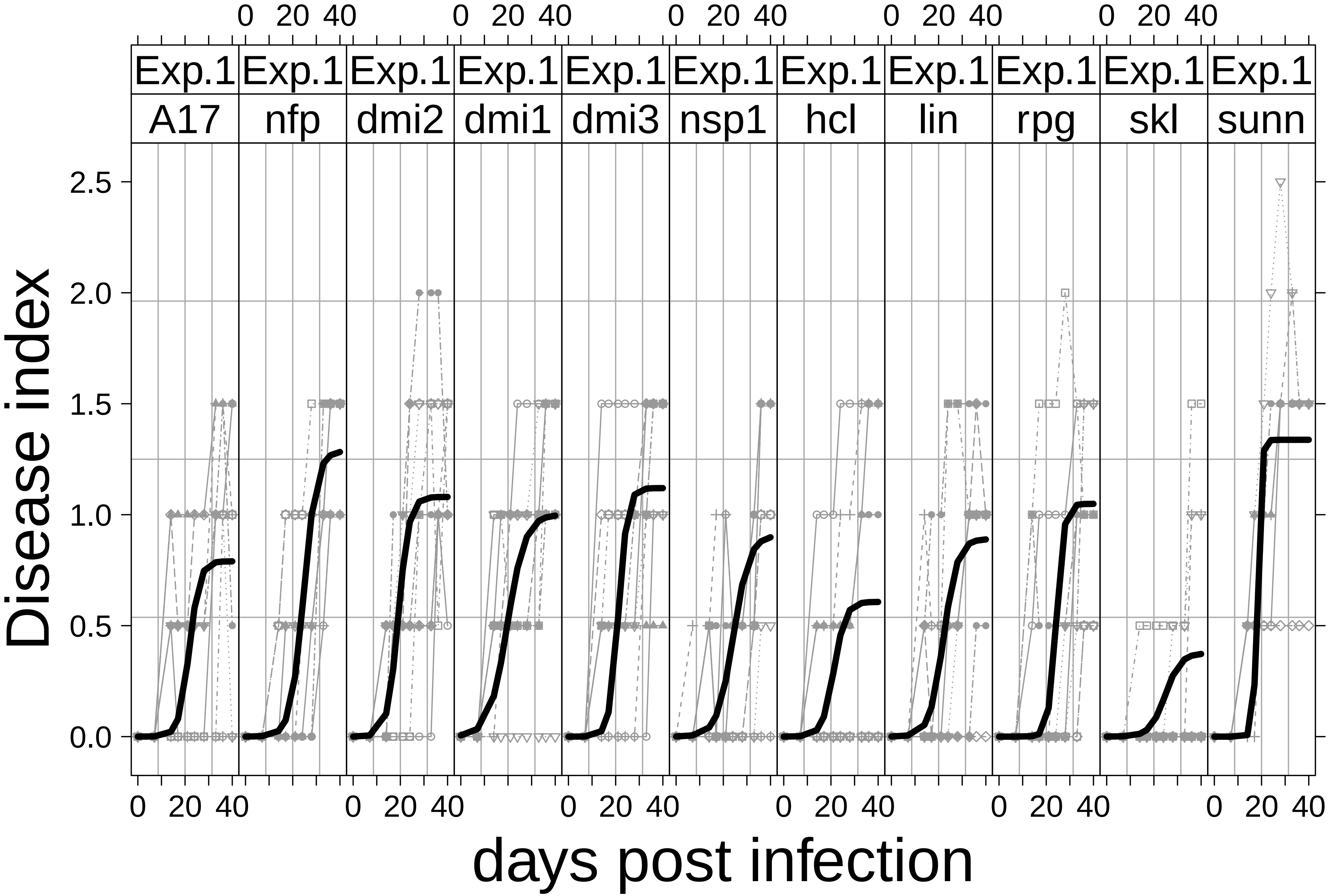

Fig. S8. Response to *Verticillium albo-atrum* inoculation of *Medicago truncatula* nodulation mutants.
Mutants are in the Jemalong-A17 (resistant) genetic background. Disease symptoms were scored with eight to ten plants per inoculation. F83005.5 was used as susceptibility control.
Similar results were obtained in three independent experiments.

Table S1: Variance analysis for functional disease parameters in the Core Collection 32, including Jemalong-A17.

			Disease curve modelling		
		df	maximum disease index	time to 50% disease [d]	rate of disease progression [d]
CC32	Biol. repeat	1	NS	<.0001	NS
	Genotype	32	<.0001	0.0213	NS

NS : non significant at alpha=1%