

Table S1. LRR-RLPs with known functions in plant immunity or development used in this study for HMM profile construction and phylogenetic analyses.

Gene	Genbank accession number	Specie	RLP Structure*	Protein length (aa)	Subcellular location	Function	Reference
<i>Cf-9</i>	AAA65235	<i>Solanum pimpinellifolium</i>	SP-LRR-TM	863	Cell membrane	Plant immunity	[64]
<i>Cf-2</i>	AAC15779	<i>Solanum pimpinellifolium</i>	SP-LRR-TM	1112	Cell membrane	Plant immunity	[65]
<i>Cf-4</i>	CAA05268	<i>Solanum habrochaites</i>	SP-LRR-TM	806	Cell membrane	Plant immunity	[66]
<i>Cf-5</i>	AAC78591	<i>Solanum lycopersicum</i>	SP-LRR-TM	968	Cell membrane	Plant immunity	[67]
<i>CLV2</i>	AAF02654	<i>Arabidopsis thaliana</i>	SP-LRR-TM	720	Cell membrane	Development	[68]
<i>Fea2</i>	AAL17871	<i>Zea mays</i>	SP-LRR-TM	613	Cell membrane	Development	[69]
<i>Hcr9-4E</i>	CAA05269	<i>Solanum habrochaites</i>	SP-LRR-TM	855	Cell membrane	Plant immunity	[70]
<i>EIX2</i>	AAR28378	<i>Solanum lycopersicum</i>	SP-LRR-TM	1021	Cell membrane	Plant immunity	[71]
<i>HcrVf2</i>	CAC40826	<i>Malus floribunda</i>	SP-LRR-TM	980	Cell membrane	Plant immunity	[72]
<i>Vel</i>	ACR33106	<i>Solanum lycopersicum</i>	SP-LRR-TM	1053	Cell membrane	Plant immunity	[73]
<i>ReMAX</i>	NP_001322741	<i>Arabidopsis thaliana</i>	SP-LRR-TM	1077	Cell membrane	Plant immunity	[74]
<i>RFO2</i>	NP_173168	<i>Arabidopsis thaliana</i>	LRR-TM	756	Cell membrane	Plant immunity	[49]
<i>RLP30</i>	NP_187187	<i>Arabidopsis thaliana</i>	SP-LRR-TM	786	Cell membrane	Plant immunity	[75]
<i>RBPG1</i>	NP_189138	<i>Arabidopsis thaliana</i>	SP-LRR-TM	890	Cell membrane	Plant immunity	[76]
<i>ELR</i>	QED40966	<i>Solanum microdontum</i>	SP-LRR-TM	1093	Cell membrane	Plant immunity	[77]
<i>RLM2</i>	AJG42078	<i>Brassica napus</i>	SP-LRR-TM	925	Cell membrane	Plant immunity	[78]
<i>CuRe1</i>	XP_025888168	<i>Solanum lycopersicum</i>	SP-LRR-TM	1121	Cell membrane	Plant immunity	[79]
<i>I-7</i>	AKR80573	<i>Solanum pennellii</i>	SP-LRR-TM	966	Cell membrane	Plant immunity	[22]
<i>I</i>	Solyc11g011180	<i>Solanum pimpinellifolium</i>	SP-LRR-TM	994	Cell membrane	Plant immunity	[23]
<i>RLP23</i>	NP_180827	<i>Arabidopsis thaliana</i>	SP-LRR-TM	890	Cell membrane	Plant immunity	[80]

* SP, signal peptide; LRR, leucine rich repeat domain; TM, transmembrane domain. The signal peptide and protein domains were identified with the SMART and InterProScan programs. The subcellular localization was predicted using the DeepLoc program.

64. Jones, D.A.; Thomas, C.M.; Hammond-Kosack, K.E.; Balint-Kurti, P.J.; Jones, J.D.G. Isolation of the tomato Cf-9 gene for resistance to *Cladosporium fulvum* by Transposon Tagging. *Science* 1994, 266, 789–793. <https://doi.org/10.1126/science.7973631>.

65. Dixon, M.S.; Jones, D.A.; Keddie, J.S.; Thomas, C.M.; Harrison, K.; Jones, J.D.G. The tomato Cf-2 disease resistance locus comprises two functional genes encoding leucine-rich repeat proteins. *Cell* 1996, 84, 451–459. [https://doi.org/10.1016/S0092-8674\(00\)81290-8](https://doi.org/10.1016/S0092-8674(00)81290-8).
66. Thomas, C.M.; Jones, D.A.; Parniske, M.; Harrison, K.; Balint-Kurti, P.; Hatzixanthis, K.; Jones, J.D. Characterization of the tomato Cf-4 Gene for resistance to *Cladosporium Fulvum* identifies sequences that determine recognitional specificity in Cf-4 and Cf-9. *Plant Cell* 1997, 9, 2209–2224. <https://doi.org/10.1105/tpc.9.12.2209>.
67. Dixon, M.S.; Hatzixanthis, K.; Jones, D.A.; Harrison, K.; Jones, J.D.G. The tomato Cf-5 disease resistance gene and six homologs show pronounced allelic variation in leucine-rich repeat copy number. *Plant Cell* 1998, 10, 1915–1925. <https://doi.org/10.1105/tpc.10.11.1915>.
68. Jeong, S.; Trotochaud, A.E.; Clark, S.E. The Arabidopsis CLAVATA2 gene encodes a receptor-like protein required for the stability of the CLAVATA1 receptor-like kinase. *Plant Cell* 1999, 11, 1925–1933. <https://doi.org/10.1105/tpc.11.10.1925>.
69. Taguchi-Shiobara, F.; Yuan, Z.; Hake, S.; Jackson, D. The fasciated ear2 gene encodes a leucine-rich repeat receptor-like protein that regulates shoot meristem proliferation in maize. *Genes Dev.* 2001, 15, 2755–2766. <https://doi.org/10.1101/gad.208501>.
70. Westerink, N.; Brandwagt, B.F.; De Wit, P.J.G.M.; Joosten, M.H.A.J. *Cladosporium fulvum* circumvents the second functional resistance gene homologue at the Cf-4 Locus (Hcr9-4E) by secretion of a stable Avr4E isoform. *Mol. Microbiol.* 2004, 54, 533–545. <https://doi.org/10.1111/j.1365-2958.2004.04288.x>.
71. Ron, M.; Avni, A. The receptor for the fungal elicitor ethylene-inducing xylanase is a member of a resistance-like gene fam-ily in tomato. *Plant Cell* 2004, 16, 1604–1615. <https://doi.org/10.1105/tpc.022475>.
72. Belfanti, E.; Silfverberg-Dilworth, E.; Tartarini, S.; Patocchi, A.; Barbieri, M.; Zhu, J.; Vinatzer, B.A.; Gianfranceschi, L.; Gessler, C.; Sansavini, S. The HcrVf2 gene from a wild apple confers scab resistance to a transgenic cultivated variety. *Proc. Natl. Acad. Sci. USA* 2004, 101, 886–890. <https://doi.org/10.1073/pnas.0304808101>.
73. Fradin, E.F.; Zhang, Z.; Ayala, J.C.J.; Castroverde, C.D.M.; Nazar, R.N.; Robb, J.; Liu, C.M.; Thomma, B.P.H.J. Genetic dissection of *Verticillium* wilt resistance mediated by tomato Ve1. *Plant Physiol.* 2009, 150, 320–332. <https://doi.org/10.1104/pp.109.136762>.
74. Jehle, A.K.; Lipschis, M.; Albert, M.; Fallahzadeh-Mamaghani, V.; Fürst, U.; Mueller, K.; Felix, G. The Receptor-like protein ReMAX of Arabidopsis detects the microbe-associated molecular pattern eMax from *Xanthomonas*. *Plant Cell* 2013, 25, 2330–2340. <https://doi.org/10.1105/tpc.113.110833>.
75. Zhang, W.; Fraiture, M.; Kolb, D.; Löffelhardt, B.; Desaki, Y.; Boutrot, F.F.G.; Tör, M.; Zipfel, C.; Gust, A.A.; Brunner, F. Arabidopsis RECEPTOR-LIKE PROTEIN30 and receptor-like kinase suppressor of BIR1-1/EVERSHED mediate innate immunity to necrotrophic fungi. *Plant Cell* 2013, 25, 4227–4241. <https://doi.org/10.1105/tpc.113.117010>.
76. Zhang, L.; Kars, I.; Essenstam, B.; Liebrand, T.W.H.; Wagemakers, L.; Elberse, J.; Tagkalaki, P.; Tjoitang, D.; van den Ackerveken, G.; van Kan, J.A.L. Fungal endopolygalacturonases are recognized as microbe-associated molecular patterns by the Arabidopsis receptor-like protein responsiveness to botrytis polygalacturonases1. *Plant Physiol.* 2014, 164, 352–364. <https://doi.org/10.1104/pp.113.230698>.
77. Du, J.; Verzaux, E.; Chaparro-Garcia, A.; Bijsterbosch, G.; Keizer, L.C.P.; Zhou, J.; Liebrand, T.W.H.; Xie, C.; Govers, F.; Robatzek, S.; et al. Elicitin recognition confers enhanced resistance to *Phytophthora infestans* in potato. *Nat. Plants* 2015, 1, 15034. <https://doi.org/10.1038/nplants.2015.34>.

78. Larkan, N.J.; Ma, L.; Borhan, M.H. The Brassica napus receptor-like protein RLM2 is encoded by a second allele of the LepR3/Rlm2 blackleg resistance locus. *Plant Biotechnol. J.* 2015, 13, 983–992. <https://doi.org/10.1111/pbi.12341>.
79. Hegenauer, V.; Fürst, U.; Kaiser, B.; Smoker, M.; Zipfel, C.; Felix, G.; Stahl, M.; Albert, M. Detection of the plant parasite *Cuscuta reflexa* by a tomato cell surface receptor. *Science* 2016, 353, 478–481.
80. Ono, E.; Mise, K.; Takano, Y. RLP23 is required for Arabidopsis immunity against the grey mould pathogen *Botrytis Cinerea*. *Sci. Rep.* 2020, 10, 13798. <https://doi.org/10.1038/s41598-020-70485-1>.

Table S2. Primers used for the RT-qPCR assays.

Primer name	Primer orientation	Primer sequence
MaLRR-RLP58 F	Forward	5'-ATGGCAGCATTCCGGAGGTG-3'
MaLRR-RLP58 R	Reverse	5'-TCAGTGATGCTAACGCTTGAG-3'
MaLRR-RLP74 F	Forward	5'-TTGCCTACGATGCTACCGTC-3'
MaLRR-RLP74 R	Reverse	5'-AAGGTCAAGGTATTCCAGACC-3'
MaLRR-RLP78 F	Forward	5'-TTGGTGCATCGGCGTACTG-3'
MaLRR-RLP78 R	Reverse	5'-TCTCCTGATCGATATCACTGC-3'

C3 subdomain

Clv2	1	SYNLSMVGIDLSDNLLHGETPEAIFRQKNLEYLNLSYNFTEGQIPR-EKIPRIKALDI
Fea2	1	GYDQATTGIDLSGNELCGEIPEGVVDKLEYLNLSYNYLAGQIPAGLGGGRHLHILDF
RFO2	1	NQIFSLPPYIRRNNLKGSIPIEVGQIKVLVLELSHNYLSGIIPHELSKLTSLERLDL
ReMAX	1	GDILRYMHGIDLSSNELSGEIPIEGDLQNISSLNLSNRLTGSIPTDS-SKLKGLSIDL
CuRe1	1	GNILKYMSGIDLSSNRLTGEIPVEIGNVSNIALNLSHNNHNGRIPNIFSNLQETESLDL
I	1	GSIDYMSGIDLSCNQLSGHIPKEISNLTOIALNLSHNNHGTTLISAFSKLTNLETSLDL
RBPG1	1	ENYLTSSATIDLSGNLEGEIPESGLLKALIALNLSNNAFTGHIPLSLANLKKIESLDL
RLP23	1	AKALTSYALIDFSGNLEGOIPESGLLKALIAANNNAFTGHIPLSMANLENLESIDM
RLM2	1	VEILYIYTAIDFSENEFEGVTPSSGLLKELVNLSCNAFTGRISSMGNLSLESIDL
RLP30	1	LRIPYFFRAIDFSGNREFGNIPESGLLKELVNLSCNFTSNIPQSLANLTNLEILDL
HcrVf2	1	TKILGFVKMDLSCNFMYEIPEEETGLLAIQYLNLSNNRFTGRIPSKIGSVAQLESIDF
EIX2	1	KNALLYLKIDLSSNVLVGGIPKEIAEWRELSSNLSRNNDLNGTIVEGIGQMKLESIDL
Vel	1	VKILRVFTSIDFSSNRFQGAIPDAIGNLSSILYVLNLSHNALEGPIPKSICKLQMLLESIDL
Cf-2	1	VEILSLYTVIDLSSNKFEGHIPSVGDLIAIRILNLSHNAIQGYIPSSGLSLSILESIDL
Cf-5	1	VEILSLYTIIDLSSNKFEGHIPSVGDLIAIRVLNLSHNAIQGYIPSSGLSLSILESIDL
Cf-4	1	VEILDSNMIINLSKNRFEGHIPSIIGDLVGLRTNLNLSHNVLEGHIPASFQNLVLESIDL
Cf-9	1	VEILDSNMIINLSKNRFEGHIPSIIGDLVGLRTNLNLSHNVLEGHIPASFQNLVLESIDL
Hcr9-4E	1	VEIFTFNMIIINLSKNRFEGRIPIIGDLVGLRTNLNLSHNVLEGHIPVSQNLVLESIDL
ELR	1	QRISTIMTTIDLSSNHFEGVTPKTKDLSSLWLLNLSHNNLGHIPMELGQNLTEALDL
I-7	1	MRITSIMTSVDLSSNREFGDIPIISGLNLSLVLNLSHNSFRGHIPAEFTKLCQLEALDL

D domain

Clv2	60	SHNSLSGQVIGNISAPPGLTILNLSHNCFSGIT-EKEGLGKFPFG-ALAGNPELCVE---
Fea2	61	SHNGLSGENPPGLAAMTVLEVLNLSYNLSGPIPF-----TTKFPG-ALAGNPELCVG---
RFO2	61	SNHLSGRIPWSLITSLHMSYFNVNNSLDGPPIF-TESQFDITFPQANIKGNPILCGGILL
ReMAX	61	SNNKLDGSIPPALADLNSLGVLNLSYNLSGGEIP-FKGHLVTFDERSYIGNAHLCCGLFTN
CuRe1	61	SCNRINGSIPVGLLELNSLAVFSAYNNLSGAPDFKAQFCTFNKSYEGNPFLCGYPLD
I	61	SYNNLTGNIPTQLDLTLAVFSAHNNLTGTTPQPIAOEFTFNESYEGNPFLCGBPPI
RBPG1	61	SSNQLSGTIPNGLGLFLFLAYLNNVSHNQLNGEIP-QGTQITGQPKSSEEGNAGLCGEPLQ
RLP23	61	SRNQLSGTIPNGLGSTIFLAYLNNVSHNQLTGEIP-QGTQITGQSKSSEEGNAGLCGPPLK
RLM2	61	SRNKLGAIPQELGNLSYLAYNMFSHNQLAGLIP-GGTQFRTQPCSSEKDNPGLYGPSLE
RLP30	61	SRNQLSGHIPRDLGSLFLSTNMFSHNQLGEPVP-LGTQFQSQHCSSTMDNLRLYGL--E
HcrVf2	61	SMNQLDGEIPPSYITLTFLSHNLNLSYNNLTGRIP-ESTQLQSLDQSSSEVGN-ELCCGAPLN
EIX2	61	SRNQLSGMIPVGLSNLTFLSVLDLSNNHLSGRIP-SSTQLQSFDRSYSGNAOLCGEPPL
Vel	61	STNHLSGEIPSELASLTFLAALNLSFNKLEFGKIP-STNQFOTFSADSEGNISGLCGPLN
Cf-2	61	SFNQLSGEIPQQLASLTFFLEFLNLSHNYLQGCIP-QGEPQFRTFESNSYEGNDGLRGYPVS
Cf-5	61	SFNQLSGEIPQQLASLTFFLEVLNLSHNYLQGCIP-QGEPQFRTFESNSYEGNDGLRGYPVS
Cf-4	61	SSNKLSGEIPQQLASLTFFLEVLNLSHNNHVGCIIP-KGKQFDSFGNLSYCGNDGLRGEPPLS
Cf-9	61	SSNKLSGEIPQQLASLTFFLEVLNLSHNNHVGCIIP-KGKQFDSFGNLSYCGNDGLRGEPPLS
Hcr9-4E	61	SSNKLSGAIPQQLASLTFFLEVLNLSHNNHVGCIIP-KGKQFDSFGNLSYCGNDGLRGEPPLS
ELR	61	SWNWLHGKIPQELTRNFLAVLNLSQNHVVGPIIP-QGEPQFNTFENDSYCGNLDLCGEPLS
I-7	61	SWNRILIGEIPGQLSSLTFFLEVLNLSYNHLAIGRIIP-IGKQFNTFPNDSYCGNPDLCCGEPLS

Clv2	115	TPGSK
Fea2	112	KGCSE
RFO2	120	TSCKA
ReMAX	120	KNCIS
CuRe1	121	NKCGM
I	121	ISCTE
RBPG1	120	ESCFG
RLP23	120	ESCFG
RLM2	120	EVCVD
RLP30	118	KICGK
HcrVf2	119	KNCSE
EIX2	120	E-CPG
Vel	120	NSCQS
Cf-2	120	KGCGK
Cf-5	120	KGCGK
Cf-4	120	KLCGG
Cf-9	120	KLCGG
Hcr9-4E	120	THCGG
ELR	120	KQCET
I-7	120	MECGN

Figure S1. ClustalO alignment of the C3-D region of 20 LRR-RLPs with known functions. The C3 subdomain and D domain used by Kang and Yeom [27] are underlined. This region was used for the HMM profile construction. Identical amino acids are shaded in black, and conserved substitutions are shaded in gray.

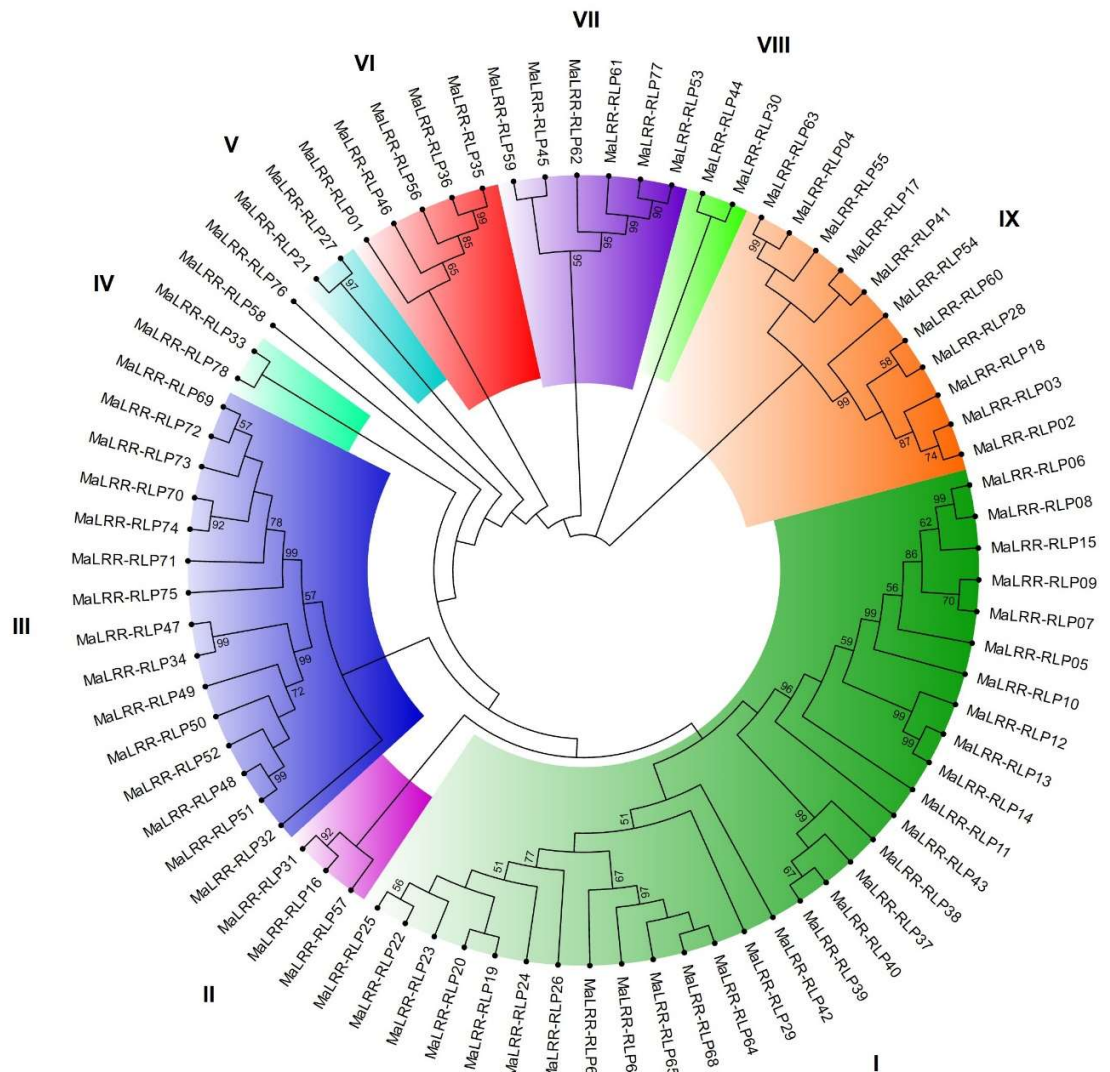


Figure S2. Maximum-likelihood phylogenetic tree of the banana LRR-RLP family. The roman numerals in bold indicate major clades of the phylogenetic tree. Numbers on the branches indicate the percentage of 100 bootstrap replications supporting the particular nodes, and only those $\geq 50\%$ are shown. The C3-F region of LRR-RLPs was used for phylogenetic tree construction.

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I      MT-----NSKIVYWWLLILFMANGWLCCYCCLNEERTALLQKANKINYSTH-----DYLSSWEANETSDDCCW 64
I-7   MEYQQL---LAFCFYSLEFVQSQFAYAGKHLCPRDQAFYLLQFKQCLTVDPNAYDCENKARSKTLSW---NVTGDCCEW 74
MaLRR-RLP74 MGFPLRFLSSSLCLLALLLHRATVT---SGCFSMERFALLDFKAGIHDH-----YNRLSS---WVGODCCAW 62
MaLRR-RLP75 MGFPLRFLSSSLCLLALLLQRAVT---SGCFSMERFALLDFKAGIHDH-----QNRLSS---WVGODCCAW 62

I      EGVICSNSTRRVVETSVIAKQISSEQLGNFTTRDDMLRNWLFNASLFIPFKNLKNIPGHSLSAGWVKNEGFEKRPFR 144
I-7   DGVTCNGLTGHVILCLDLSCELI-----GTINAN-----SSITKLS 110
MaLRR-RLP74 EGVICCATTGHVVMMLDRNTNINYPWKL-----RGERMN-----SSLLALS 102
MaLRR-RLP75 AGVICRATTGHVVKLDLRNTNTLQAL-----RGERMN-----SSLLALS 102

I      KLERLDLSCNOFNRS-IFQSSQLSSLSLNLSSNNAPRSEM-----WFTDNKIGSGSR--- 199
I-7   HLQRLNLASNEFNDFPLGNSTSELSSLTHNLSDSGIFNERKMIIPGLCRLSKLISLDLSGSYIQ-----VGRTTET 182
MaLRR-RLP74 HLERLDLSENFDSGIRIPEFIFGSKFKLRYLNLSSNTNM---GGIPARLGNLSSLHVLDLSDALHFT---SHVNLHL 174
MaLRR-RLP75 HLRHLDLSENFDSGIRIPEFIFGSKFKLRYLNLSSNTYFM---GGIPARLGNLSSLYVLDLSDALYVDDYNGYFVQNLDL 179

I      SLLHNLTHLEVLLFDYVYASFELPKKFPSSLRKLSLOGTNVFGN-ITDSOLFHLPLNLOVLRRLGDNPSLTGT-LPNEHWNF 229
I-7   SHTTSL-----KHLDLSGLNLTDPVDWFSSVNMPLSLQVLSMSVSGLDITIP-ASVVHINF 228
MaLRR-RLP74 SHTTSL-----KHLDLSEINLTVPVDWFSSVNMPLSLQVLSMSVSGLDITIP-ASVVHWNF 233
MaLRR-RLP75 SHTTSL-----KHLDLSEINLTVPVDWFSSVNMPLSLQVLSMSVSGLDITIP-ASVVHWNF 233

I      SRPTKKLNIRSRFQSFENEEFGAARNFYLLDGITLCKNFLRSSGVMSLKVLSVACCS-LNGTTPROGLCKLKYL 308
I-7   -SKSVLE-----LDFSYTGIFGVPPDSIGLQSLWRNLNENCH-LSGSIPESFGNLTIT 312
MaLRR-RLP74 -SSSTVLDLSSNHEFDTLPKW-LGNITSLTHLDFYSGYGVIPDAIGDLGSITFLDGDNQ-LEGTVPRSMVDLRSL 304
MaLRR-RLP75 -SSSTVLDLSSNHEFDTLPKW-LGNVSGITSLGLSCCEPLGTIPDAIGDLGSITFLNGLNELLGIVPR-SMANLHL 310

I      EELSLSRNSFTGKLPACLRNLTFRVIDLTQNOITGNIA-----LSPLSLLSLEYLITN 364
I-7   RELILSGNFTGNLSTHSKLNKLWNLSLNNHFRGSLPESIGNLTAIRELISDNISFAGYVPSV-IGLKNLKLDSLSLS 391
MaLRR-RLP74 KELHMQCNRNLGNLSDLEQMNLLILDLQSNLHRSMPSSVGVKFSNMTLELNAGNSVGGVLSEHFENLTRLRLDLG 384
MaLRR-RLP75 KELDLNVNQLSGTLTGWLEQNTNLIVLNLNLSNLDNGSVVPASVGVKFSNLTGLYGGNSLGGVISEAHFESITKLRVLDLFD 390

I      NNFEVETISFESFANHSLKLFVADYNS-VIVQTTSKMIPKFOLEALSLFNSSQMPNFLSHQHHLRLIRLSKCNIGGDFP 443
I-7   NNFESSIPD-----IFANFSELYSLDFHSSNNEVGFPPYSIATL-----THLDGLELQNNSTFGPLP 447
MaLRR-RLP74 NPITTSIG-----QSWVPPFQLRVYDL-----TKCQLGPPQFP 416
MaLRR-RLP75 NSITVSIG-----QSWVPPFQLRVIYL-----SNCHLGPQFP 422

I      NWLLENPKLGEVYLDGNAFTGSLQLPFLPLNLKAFDLSNNKIRGQLEPNLGSFPN-LVISTMSSNMPLGLLSSFADMQ 522
I-7   SNISGFG-----NLFNLDLSFNLHLCATEPWLQFQPSL--MSLSVQANKFTGELPNENRST 502
MaLRR-RLP74 EWLQFQT-----QIEKLYLADCKIAGTMAWLWNSSSTITLDELSSNQIGGKLPSISKFTK 473
MaLRR-RLP75 EWLRFQT-----QTQELTMHDKIAATIEENFWFNSSSTVTLVDLSDNRICGRLPSSISFAR 479

I      SVECDLSYNKLGELPTRLARK-----SKLYLRLSNNMKLGEIPFASANINN-FNYLYLDG 580
I-7   SWPFDLSYNNLHCBTPYWMLSMMWNSLDLSHNLFTFEKQVHSEYLSYLNENNELQGLPHQSTCDLIN-LEELILAQ 581
MaLRR-RLP74 LW-ILYLDLSNRFEGLPTML-PSTLDTLFLSNNSFTGQ-LPIWPD--VQSVALSNNMGLGGLSSSICQWTGCGLEYLDSN 548
MaLRR-RLP75 LE-EYLDLSNIFEGELPAML-PSLDTLYLSNNSFTGQ-LPVWPH--VSLALLSNNMGLGGLSSSICRWTY-LRVLVLSG 553

I      NNFSGEIPQTLSTAPLRLTLDLSYNNLSGNIPSWIGLEWLDISENNLVGVTFPSCFSSFRDLKHLYLSKKNLQGEFN--MFS 658
I-7   NNFNESIPDCLGNSNR-----LTSILDRMNNFRGEIPTFTIP--RGLEYLGLYGNQLRGQVPRSLVN 641
MaLRR-RLP74 NNLFGEIPYCLGKSLQ-----NLKILNLGNHFSGEIPHTIGFLSLGWHQLKNNFSFSGELPLSLKN 610
MaLRR-RLP75 NNLFGEIPYCLGESLQ-----DLSTLSANNHFSGEIPNTIGFLTEKLLQLKNNFSFSGELPLSLQN 615

I      NSGLRVLDLGDNNFSGSIPKWLGS--SGITILLKGNLQGTITHTPLC--HASYLRLIMPLSHNNLSGPIPRCFGNIMQOE 734
I-7   RLSLVALDLGNKLNLTPEINLE-KLPNLQVLLILKSNLFGPHGDLESEFPFPELRIFDLSPNGFTGTSSNLKFSFRGM 720
MaLRR-RLP74 CGLRFLDLAQNMFVGSITPWTGDNLQQLVVLRLRNSNMFSGVIFWOLA--RFEKLOILDIANNNFSIPHNIQN-LSTM 687
MaLRR-RLP75 CENLQFLDLAQNMFVGSITPWTGDNLQQLVVLRLRNSNMFSGVIFWOLA--QLGRLOILDIANNTFSGSIPHNFQN-FSTM 692

I      DIIELYPYSSSFGSSVFETFGGDTAIEVESSIMSSSTLLLLDNYVWVCAEFMTKHNITYSVEGSIWYMSGIDLSNQNLG 814
I-7   MDA-----DEGKSG-----ISRARNRTRRDYLYHV-SLVTKGNEFD--MRITSTMSVLDLSSNRFEG 774
MaLRR-RLP74 RST-----SQYNDFCYDELQVFTKGQDLVYKCSIKLMSKMDLSNNLSLG 732
MaLRR-RLP75 AST-----SDNGTEIYDLFDISTKGDLYIK-DLDDLKSLDLSNNRLIG 736

I      HTPKEISNLTQIRALNLSNHHTCHILSAFSKLLNIESLDLSYNNLGNIPTQLDITTLAVFSVAHNNLTGTTQPIAQ 894
I-7   DIPNSIGNLSSEVILNLSHNSFRCHIPAEFTKLQQLBALDLSNNRLIGELPGOLSSITLLEVNLNLSNLAGRIPTGK-Q 853
MaLRR-RLP74 ETPKGIQDLACLKNLNLNRNYLQKIPAEIIGGMKLSLESLDLSINDLSGSIPELSVLYSYLNLNLSYNNLSGRIPTGR-Q 811
MaLRR-RLP75 DIPKEIGDLACLKNLNLNRNHLKGIKIPGIGGMKLSLESLDLSINDLSGSIPELSVLYSYLNLNLSYNNLSGRIPTGH-Q 815

I      FGTFF-NESSYEGNPFLCGPPLISCTEKEKEPKSPLEPECCEDDTGFLD-IELFYISFLVAFANV---VLATVVLWVNP 969
I-7   FNTFPND-SYCGNPDLCCGPELSMECGNNNESPLERDSDDDDDSFMSGFTREAVAICGCGMIFGLLIGALMFLLEPR 932
MaLRR-RLP74 LOTLNDPSIYMGNADLCGPPTSKSCFDNKTQIIOEHEKE-----ISDWLWFIYSLVLGFMGFWIFFGILF---LRD 882
MaLRR-RLP75 LOTLNDPSIYMGNANLCGPPTSKSCHNNKTAQNNIOEYEKE-----ISDWLWFIYSLVLGFMGFWIFFGILF---LRD 886

I      YWRNWFYIVVEYMYSCYFFASK---M----- 994
I-7   KW---YVKFAEDIAQIAAKKRTRQKKIRQRRGVRMN 966
MaLRR-RLP74 ANRHAYFHEIDDVYDWVWVQ*----- 903
MaLRR-RLP75 ANRYAYFRMIDDMYDRINWVQQLILRLFER*----- 918

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Figure S3. ClustalO alignment of I-7, I, MaLRR-RLP74 and MaLRR-RLP75. Identical amino acids are shaded in black and conservative substitutions are shaded in gray.