

Table S2

List of RXLR effector candidates used in this study. PexRD, PexRD family members (nr), *Agrobacterium tumefaciens* clones, known genes, the *Phytophthora infestans* strain and amino acid sequences are presented. PexRD and *A. tumefaciens* clones correspond to Table 2.

PexRD	nr	A. tum clone	Known gene	P.i strain	Sequence (without signal peptide)
RD1	1	195-2		88069	LSAHRAQIMNVATSDLI SPIESTVQDDNCDRQLRGFYATENTDPVNNQDTAHEDGEERVNVA TVLGGKDEAWDDALMRLAYQHWFDGGKTS DGMRLIMDLPAKGEALRHPNWGKYIKYLEFVKE KKKEAADAAA VAALKRRRTYRGWYVDGKTEKDVRKIFGLPATGKAKNHPNWADFQEYLNVVR EYSKVVFVK*
RD2	1	11-8		88069	LSTTTGVQAAANLVGPAQRLLRKHHTAAENDDDDSEARALNTEKMKTMKAGMTVDDYAAKLLK TDKIAAAAANSARAMEKLGETLKMKKLLRYLNYVAEHTAV*
RD6	1	41-3	IpiO1-K143N	88069	VSSNLNTAVNYASTSKIRFLSTEYNADEKRSLRGDYNNEVTKEPNTSDEERAFSISKSAEYV KMLYGFKLGFSPRTQSKTVLRYEDKLF TALYKSGETPRSLRTKHLDKASASVFFNRFKNWY DKNVGPS*
	2	41-10	IpiO2 ¹	88069	VSSNLNTAVNYASTSKIRFLSTEYNADEKRSLRGDYNNEVTKEPNTSDEERAFSISKSAEYV KMLYGFKLGFSPRTQSKTVLRYEDKLF TALYKLGETPISLRTKHLDKASGSVFFNRFKNWY DKNVGPS*
	3	39-6	IpiO4 ²	CU3	TAGNDASTSKIRFLSTEYNADEKRSLRGDYNNEVTKEPNTADEERAFSISNSVEKVKLGLYA LKIAFSPRTQSKTVLRYEDKLF TYLHKSGETPAS YKNKHPDKASAGVFFNRFKNWYDKNVGP S*
RD7	1	Avr3a-KI	Avr3a ³	88069	IDQTKVLVYGT PAHYIHDSAGRLLRKN EENEETSEERAPNFNLANLNEEMFNVAALTKRAD AKKLAKQLMGNDKLADAA YIWWQHNRVTL DQIDTFLKLASKTQGAKYNQIYNSYMMHLGLTG Y*
	2	Avr3a-EI	Avr3a-K80E ⁴	88069 ⁴	IDQTKVLVYGT PAHYIHDSAGRLLRKN EENEETSEERAPNFNLANLNEEMFNVAAL TERAD AKKLAKQLMGNDKLADAA YMWWQHNRVTL DQIDTFLKLASKTQGAKYNQIYNSYMMHLGLTG Y*
	3	Pex147-2	Avr3a paralogue ³	88069	IDQTKVLMYGS PAHYIHDSAGRLLRKN EEESEETSEERAPNFNLATLNEEMFDVAALTKKAD AKKLAKQLMGNGKLADAA YIWWQHNRVTL DQIDAF LKLASSKTQGARYNRIYNSCYMMHLGL TGF*
	4	Pex147-3	Avr3a paralogue ³	88069	IDQTKVLMYGT PAHYIHDSAGRRLRKN EENEETSEERAPNFNLANLNEE IFNVAALTKKAD AKKLAKQLMGNDKMAKAA YVWWQHNGVTP SQIDTFLKLASGKTQGARYNEIYNSYLMHLGLT AY*

RD8	1	95-1	88069	AAEASEPMPNIAKYASPEVSVHLGAEREKRLRLRFDSDNDYRDDDDDEEERANAANLNFVNDKLTV YVNKAQKRRTANNVSGSLLNYFKRLEAYGYSPVKLGNRIPEEYDNLRLMLYRSWYYHNK*
RD9	1	217-3	IPO-0	GEASAAVVLATSPPAATAVPSASPASTSRSGRNLRQKMVDELKNVKLRKSPAGKDKNSTRGT PPPLELNEVDVDEEDDVQDPQAAGKAKGCSICERSFTVFRAKHTCKICAQKICDDCSKNRM KLNRRLEKKGSRLCDPCARSYIHADNGSGEDTFPDSPTLMSIHSEDTMTHKQGDNSGLSR RHSVPAKTLSSLIRNKDKTSVSNVSTAIQVNNAGSSKMQATTRTQVKRIVHLSHLRTRHWMS LLAIAVLVTLRVIYYNRRIGVEGSAVPSDTASPSSFVERALDNLLSMRTLGTLYLLGLVLFDE LSRPKGSKIQVKRQHKKRRRRSSGQQRERTKSSLSDTSVASKRHAVDSSAPPSPQTSQDDD LEVTLIEQNHEEEGF'LDKLVGALDEGARARAPDGNLGLGCFMATCNVICGLFVGFGRATSF AGSTVGAYF'TSIEHNLEAWPVPSSNTWKEQSVRSVIEHEVVLGVADVGGKKKPCSRCLLR LLWFVQFVEACVRLTLIESTEDNCYNGASKAYEETLGKRHPWLVRKGVNTALGSIPTRSHIL NELHTGDGDMELLTKAHAQLVIVITELKAVFEEHALTDLK*
RD10	1	96-1	88069	QPTTTEVAVPDVVYSRYTAEIAGDFVSKRKLADKAADQVVSTEERGVTGFYVPRRLN*
RD11	1	21-1	88069	LPADAGKVIHENGADTRIPTHVHDQRLRRVRNDEGELTEERTGGLLDKIKSVVKKITPEKA VTKFKEKDI'NPEWLKIKHKVREAKGQGYK*
	2	43-1	CU9	LPADAGKVIHENGADTRIPTHVHDQRLRRVRNDEGELTEERTGGLLDK*
RD12	1	101-2	88069	LTTTVADTAQTATSILTPVLAGEPNKHVTTRSLRTHPIADSDDGEERLLNGMTDFVKYHAGK MNPEQLYKYLKLGQGRGQ'EAYKHKNYASYIKKSKKWWKNQ*
	2	103-2	CU2	LTTTVADTAQTATSILTPVLAGEPNKHVTTRSLRTHPIADSDDGEERLLNGMTDFVKYHAGK MNPEQLYKYLKLGQGRGQ'EAYKHKNYASYIKKSKKWWKNQ*
RD13	1	98-3	88069	NEATDIMRQLRVGKAVASLFENQHQSTRELEEKIMQEDDNKPNEVQAD'TTKFRVRRRLSPN YVELIERRGPLKEARAIR
	2	98-4	88069	NEATDIMRQLRVGKAVASLFENQHQSTRELEEKIMQEDDNKPNEVQAD'TTKFRVRRRLSPN YVELIE*
RD14	1	99-1	88069	AALGPPKSSEGTHETASLLRLNAVQPVE'ETGNQEERTINFASIKKIVPGTSAFKNAQALKAS QKAALKAQDAAKRKAAVDKWFQFESDEF'LFTAAPPSWVRKKMHPDKVREYFASLGKSGDDV SMIVKRYDNYRQTIPTKK*
	2	99-4	88069	AALGPPKSSEGTHETARLLRLNAVQPVE'ETGNQEERTINFASIKKIVPGTSAFKNAQALKAS QKAALKAQDAAKRKAAVDKWFQFESDEF'LFTAAPPSWVRKKMHPDKVREYFASLGKSGDDV SMIVKRYDNYRQTIPTKK*
	3	99-5	88069	AALGPPKSSEGTHETARLLRLNAVQPVE'ETGNQEERTINFASIKKIVPGTSAFKNAQALKAS QKAALKAQDAAKRKAAVDKWFQFESDEF'LFTAALPSWAGKKMHPDKVREYFASLGKSGDDV SMIVKRYDNYRQTIPTKK*

RD16	1	59-1	88069	AVAETSNDINTMNNNQEFARSLRNTEERSIAAILAEAGEEDRAAWRINYRAWYKAKLTPTQV KTVLGVSQAEMNNVAKQLQRLYLGYYSFYTAMEKKKKEKKRLATP*
	2	56-2	CU6	AVAETSNDINTMNNNQEFARSLRSNTEERSIAAIFAEAGEEDRAAWRINYRAWYKAKLTPTQ VKTVLGVSQAEMNNVAKQLQRLYLGYYSFYTAMEKKKKEKKRLATP*
RD17	1	MKB-4	88069	KKQQRTRVLRKQLTNLRFDLVSAEIEAETERILAQMKRVDDEIAALSPSAVTFESTAQKIID LDHEMLSRVTNVTFLGQVAADKETRDACKADEVIEDFSVQRSMRADVYKAVNTLYKSAAYQ KLNTVTQRYVHRLVQDFERNGLQLPGEKQKEVQAWKQKLSKLGIQFQONLSEETIEVQFLHD ELKGLSNDFIAALEKGDDGKYKIALSYPTVFPILNTCTVESTTRKAVEYAFNRRCISTNVAIL EEMLEIRHKVALALGYENHAAVLEQRMETPANVKKFLSDLDNKLVLAKKDLDDLKKE ADCEQNEWKFDGKINMWDFRFYMDQYVKKHCSIDSEKLEFYPLTHVTTELLSMYQELLSLK FVEISQPHVWHKDVRMFAVYDARPGKAGNLVGHFYLDLFPFRAGKYGHAACFTLQOQSCINSAG VREYPAAAMVANFNAPTKSKPSLLGHQEVVITYFHEFGHVMHCLCSEVDIPRFAGTRVERDFV EAPSQMLENWCWEKEPLQRLSSHJETGEKLSDDLITRLISTKNVNTGLLNKRQLLFAIFDQT IHSKPKANTAQLLKQLQTEIMLIDMTPETNFAGSFGHLAGGYDAQYGYMWSEVFSMDMFVS RFKKEGLMNPKTGLAYRELILARGGSVDASVMLKDFLGRAPNQDAFLLSKLMPRV
	2	MKA-1	90128	KKQQRTRVLRKQLTNLRFDLVSAEIEAETERILAQMKRVDDEIAALSPSAVTFENTAQKIID LDHEMLSRVTNVTFLGQVAADKETRDACKADEVIEDFSVQRSMRADVYKAVNTLYKSAAYQ KLNTVTQRYVHRLVQDFERNGLQLPGEKQKEVQAWKQKLSKLGIQFQONLSEETIEVQFLRD ELKGLSNDFIAALEKGDDGKYKIALSYPTVFPILNTCTVESTTRKAVEYAFNRRCISTNVAIL EEMLEIRHKVALALGYENHAAVLEQRMETPANVKKFLSDLDNKLVLAKKDLDDLKKE ADCEQNEWKFDGKINMWDFRFYMDQYVKKHCSIDSEKLEFYPLTHVTTELLSMYQELLSLK FVEISQPHVWHKDVRMFAVYDARPGKVGNLVGHFYLDLFPFRAGKYGHAACFTLQOQSCINSAG VREYPAAAMVANFNAPTKSKPSLLGHQEVVITYFHEFGHVMHCLCSEVDIPRFAGTRVERDFV EAPSQMLENWCWEKEPLQRLSSHJETGEKLSDDLITRLISTKNVNTGLLNKRQLLFAIFDQT IHSKPKANTAQLLKQLQTEIMLIDMTPETNFAGSFGHLAGGYDAQYGYMWSEVFSMDMFVS RFKKEGLMNPKTGLAYRELILARGGSVDASVMLKDFLGRAPNQDAFLLSKGLKVDASSSFEL KL*
RD21	1	64-2	88069	IPVIKEANQAMLANGPLPSIVNTEGGRLLRGVKKRRTAEREVQEERMSGAKLSEKQKQFLKWF FRGSDTRVKGRSWR*
RD22	1	68-2	88069	TEVTRTALANSVQTKTSTISLYSPTTESYRFLRARKNEDASDEERGISNVARIKEKIFKLM KIAMPSIKKVLAVVGDVLFK*
	2	66-1	CU9	TEVTRTALANSVQTKTSTISLYNPTTENYRFLRARKNEDAADDEERGLSNVARIKEKIFKLM KIAMPSIKKVLAVVGDVLFK*

RD24	1	113-1	88069	VSTEANGQVALSTSKGQLAGERAEENSIVRSLRAVETSEDEEERDLLGLFAKSKLKKMMKS ESFKLKRFGWDDFTVGYIREKLNKYPDLLLLNYLNVYKKAGNEIVRHANNPNKVTFSNKVR ARIYKTNS*
	2	116-1	CU5	VSTEANGQVALSTSKGQLVSERAEENSIVRSLRAVETSEDEEERDLLGLFAKSKLKKMMKS ESFKLKRFGWDDFTVGYIREKLNKYPDLLLLNYLNVHKKAGDEIVRHAHNPKNKVTFSNKVQ ARIYNPNS*
RD26	1	119-1	88069	TSPKPKDLIQRRSGRVLRADATYNQATNAVDEERASIPELISKLGKSMKWFQKYLATRRLR LKAVQMNLDNVVEKLVKEGVDPNRAYKVLKLLKSDSNQFVGMHETGEYKLWHKLVTAQKKYP KWNLYA*
	2	118-1	90128	TSPKPKDLIQRRSGRVLRADATYNQATNAVDEERASIPELISKLGKSVKWFQKYLATRRLR LKAVQMNLDNVVEKLVKEGVDPNRAYKVVKLLKSDSNQFVCMHETGEYKLWHKLVTAQKKYP KWNLYA*
RD27	1	143-2	IPO-0	SDQNSNVASITSQVQRLLRTHHATIKVNADSEERFLTEPPLTTDEMAMMMKAGKSKNAYAFE LGIAGQMAFDINSGLPDIETFKKTFEFQKYEYFYMNFLNDRKDDDYKPLVEMIKKNGETEA FKTLLVKVEDNVSKKASPSAIVKLDPLNREQAIVEKIELALKKNQALNKNKASLETIEHTV RMAAKSKPSTWKIFKIIPRLKLLKLR*
RD28	1	176-2	88069	ESTVVINLRASGEERAYAFVDKIKSLFSRPGISQKVESLQKNPAMVKNLEKAALSQKSSKV RDWFMHMYNNSKRDRFFILATLVMFPIGVWAVVTNYRR*
RD31	1	120-1	88069	RQTAANIMYPVLDGEQNVLGKRSRSLRTHDMRVSTVEDQEGDEERIFRRFTDWIKYLFNKMNP QLHTYLGLDGXGETAYKHKNYPIYLMKSKK*
RD36	1	45-1	88069	ACAHSRHLRANGKDALWNYDTSGGINSIVADDEERVVNFSGIKRWLKELFKNWSQRNKKIPE GTEYDFFTGNYQQNAQKQTRSA*
	2	45-10	88069	ACAHSRHLRVNGKDALWNYDTSGGINSIVADDEERVVSFSGIKRWLKELFKNWS*
RD39/40	1	169-4	88069	FPIPDSRPLSKTSPDTVAPRSLRVEAQEVIQSGRGDGYGGFWKNVAQSTNKIVKRPDIKIS KLIAAAKKAKAMTKS
	2	170-1	88069	FPIPDSRPLSKTSPDTVAPRSLRVEAQEVIQSGRGDGYGGFWKNVQSTNKIVKRPDIKIG KLIEAAKKAKAMTKS*
	3	89-2	88069	FPIPDSRPLSKTSPDTGATRSRVEAQEVIQSGRGDGYGGFWKNVFPSTSKI IKKPDIKIS KLIAAAKKAKAMTKS*
	4	89-9	88069	SRPLSKTSPDTVATRSRVEAQEVIQSGRGDGYGGFWKNIPSTNKI IKKPDIKISKLIEAA KKAKK
	5	89-7	88069	FPIPDSRPLSKTSPDTVATRSRVEAQEVIQSGRGDGYGGFWKNVFPSTNKI IKKPDIKIS KLIAAAKKAKAMTKS*

RD41	1	91-3	88069	AFLNPDETRLLSDTFTKRSLRVAGQEVARGDRGEEIVRVIVQSTNKIFKRPAEKDMSKLI AAKIAMLEKKMAKLSFVGKEAAK*
	2	91-5	88069	ALLNPDETRLLSDTFTKRSLRVAGQEAARGEIIVRVTAQSTNKIFKRPAEKDMSKLL EAAKALLEKRMAELSKVIKKPAK*
	3	91-7	88069	AFLNPDETRLLPDTFTKRSLRVAGQEVARGDRGEEIVRVIVQSTNKIFKRPAEKDMSK LIAAKIAMLEKKMAKLYSSVRRQRSSL*
	4	91-10	88069	AFPNPDETRLLSDTFTKRSLRVAGQEAARGEIIVRVTAQSTNKIFKRPAEKDMSKLL EAAKALLEKRMAELSFVGKEAAK*
	5	92-7	90128	AFPNPDETRLLSDTFTKRSLRVAGQEAARGEIIVRVTAQSTNKIFKRPAEKDMSKLL EAAKALLEKRMAELSKVIKKPAK*
RD45	1	184-2	90128	IPNHTTESQLLSKASPDPAKRSLRNAGQQVV*
	2	215-3	CU4	IPNHTTESQLLSKASPDPAKRSLRNAGQQVQSRPTDGNNGGVFKAFSGTNKLIKLP DMKISNVLEAAKVKKLEMDKLLKLIKSSK*
RD46	1	92-4	CU4	ALLNPDETRLLSDTFTKRSLRVAGQEVARGDRGEEIVRVIVQSTNKIFKRPAEKDMSK LIAAKIAMLEKKMAKLSFVGKKAAC*
	2	92-12	CU4	ALPNPDETRLLPDTFTKRSLRVAGQEVARGDRGEEIVRVIVQSTNKIFKRPAEKDMSK LIAAKIAMLEKKMAKLSFVGKEAAK*
RD49	1	186-2	88069	RSATEHAQLMVSQSELDQPTRWNVADKRLLRANDGTNAEEERGMADIATKMKTWTQ SLKTHVGSSKPFQIAAQKWRNTKVQRMIKKGISDTALFENKVTPEFFKALRLKPLKQ SSVTNNPALNKYRAYKSFYESKIKTAAT*
RD50	1	191-1	88069	SDSEKAAKISNDQVLSGRQLIDTVAKDNKKRLPRAYKDAEDDSEDSKNVKPTADSK HADESEDSQEEERFSLIQTSNQPRYYWWFQHHTPLDVRRDLELTADTINPIKRSVY TGYVDYYEDHCSYYENRKEEFCKAEDF*
	2	191-6	88069	SDSEKAAKISNDQVPSGRQLIDTVAKDNKKRLRAYKDAEDDSEDSKNVKPTADSK HADESEDSQEEERFSLIQTSNQPRYYWWFQHHTPLDVRRNLELTADTINPIKRSVY TGYVDYYEDHCSYYENRKEEFCKAEDF*

References

¹ Pieterse CMJ, Van West P, Verbakel HM, Brasse PWHM, Van Den Berg Velthuis G, C. M., et al. (1994) Structure and genomic organization of the ipiB and ipiO gene clusters of *Phytophthora infestans*. *Gene* 138: 67-77.

² van de Vondervoort, Bouwmeester and Govers. Unpublished results.

³ Armstrong MR, Whisson SC, Pritchard L, Bos JIB, Venter E, et al. (2005) An ancestral oomycete locus contains late blight avirulence gene Avr3a, encoding a protein that is recognized in the host cytoplasm. *Proc Natl Acad Sci U S A* 102: 7766-7771.

⁴ Bos JIB, Kanneganti T-D, Young C, Cakir C, Huitema E, et al. (2006) The C-terminal half of *Phytophthora infestans* RXLR effector AVR3a is sufficient to trigger R3a-mediated hypersensitivity and suppress INF1-induced cell death in *Nicotiana benthamiana*. *Plant Journal* 48: 165-176.