**File S4.**  Five sets of amino acid alignments of closely linked putative effector peptides and called secreted RxLR effectors within the same gene families.

**Set 1**

|  |  |  |
| --- | --- | --- |
| PmGH34\_PBPs\_010 | g537330 | Secreted RxLR effector |
| PmGH34\_PBPs\_010 | g537340 | Putative effector peptide |

>g537330

MNKAFLHIRNLRVTILLAVVIFQSCISATSTDFPIINSSSLYLTSRLDQNVVQNKRNLRI

HVLATTEDSSDERGINLGATTVAKLKDLTTSATQKLEKFAVSAKLKTLKNNQLATDKSFA

KFDVGTSKSNVFESARFQKWFNSVHKAYKQNVEESEVAVVTTLTKHYGDESLTKLLSEAK

TIPNTKVIAEKLEDARLTKWLTEQKSVDDIFNLLKLDETGENIFKSPLLSSWVNYANKFQ

KNPDEIMFSTLKTHFDDETLAKMLIVAKEDSSNIATKLEKVEFDQWLNSGKTSDDVFKLL

SLNDDTGNLLKNPIFKTWVLYVTKTGKQSPYDAVFSKLLARYDDLSLAKLIYAAKRDHAM

SSIARNLEAAQLKAWSKSGKSSDDVFKLLSLEKVGGVDLLKRSLLNVWMAYVKMLKKNSD

EVLLSKLKLRHSDEWLVKMLLVAEKDYRSKDIAKRLQGSLQKTWINDGKTADDVFNLLKL

GTGDLVFTSPMWSTWNTYVDKTKQTEP

>g537340

MYLVLKAQFGEEKFKTIIDKAKTNMITKNIADKLQEEAWRSEGKTMDDIFKLLKLGEKGD

KFVESPMLTTWISYVTTLEKLKEKPNEFVAISYLEKRFGDLTLARILSTEKHQHSRIPET

VVADLQQLQFRQWMNKGVDPKYLSNWLVSDTSNMPGKLLVTLDFSDFYKIHGVPFY

CLUSTAL O(1.2.4) multiple sequence alignment

g537330 MNKAFLHIRNLRVTILLAVVIFQSCISATSTDFPIINSSSLYLTSRLDQNVVQNKRNLRI 60

g537340 ------------------------------------------------------------ 0

g537330 HVLATTEDSSDERGINLGATTVAKLKDLTTSATQKLEKFAVSAKLKTLKNNQLATDKSFA 120

g537340 ------------------------------------------------------------ 0

g537330 KFDVGTSKSNVFESARFQKWFNSVHKAYKQNVEESEVAVVTTLTKHYGDESLTKLLSEAK 180

g537340 --------------------------------------MYLVLKAQFGEEKFKTIIDKAK 22

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g537330 TIPNTKVIAEKLEDARLTKWLTEQKSVDDIFNLLKLDETGENIFKSPLLSSWVNYANKFQ 240

g537340 TNMITKNIADKLQ---EEAWRSEGKTMDDIFKLLKLGEKGDKFVESPMLTTWISYVTTLE 79

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g537330 K---NPDE-IMFSTLKTHFDDETLAKMLIVAKEDSSN----IATKLEKVEFDQWLNSGKT 292

g537340 KLKEKPNEFVAISYLEKRFGDLTLARILSTEKHQHSRIPETVVADLQQLQFRQWMNKGVD 139

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g537330 SDDVFKLLSL--NDDTGNLLKNPIFKTWVLYVTKTGKQSPYDAVFSKLLARYDDLSLAKL 350

g537340 PKYLSNWLVSDTSNMPGKLLVTLDFSDFYK---IH--GVPFY------------------ 176

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g537330 IYAAKRDHAMSSIARNLEAAQLKAWSKSGKSSDDVFKLLSLEKVGGVDLLKRSLLNVWMA 410

g537340 ------------------------------------------------------------ 176

g537330 YVKMLKKNSDEVLLSKLKLRHSDEWLVKMLLVAEKDYRSKDIAKRLQGSLQKTWINDGKT 470

g537340 ------------------------------------------------------------ 176

g537330 ADDVFNLLKLGTGDLVFTSPMWSTWNTYVDKTKQTEP 507

g537340 ------------------------------------- 176

**Set 2**

|  |  |  |
| --- | --- | --- |
| PmGH34\_PBPs\_010 | g539450 | Putative effector peptide |
| PmGH34\_PBPs\_010 | g539460 | Putative effector peptide |
| PmGH34\_PBPs\_010 | g539470 | Secreted RxLR effector |
| PmGH34\_PBPs\_010 | g539480 | Secreted RxLR effector |

>g539450

MLNDWVRKKVSADGIFIRLQLDKTGYKLLESPRLITWVKYADALNIKTQGTSAPAISKLT

DYYGDAALARMIEVAKKNPSSKNIASDLETMQFNYWVNSFATPDEVFILLELRFGRDKLL

DNPLFSTWLNYITFFDGTHPSI

>g539460

MASNQPVFAVEDEVIIHSRQLLRTNVAMGDEHEERYPEPPYSKIETLKSLFTPKTISEDM

INRWLKNKKSVDKVFVRLKLENTPEDKLLENPHFITWINYAKALNSETGSPSWSTVSKLT

KYYDDDDIARIIETAKQTPGMEALASDLHTQQFQYWLHIAKKPEYVFRSLRLIDAKEELL

RNPSKNPLFMIWLDYVKYYNKHKDRKKGYLSTLGTRFWFDDDEISTMVKVAKKTPSTTEF

AKQLRAEQVDRWFTYGWPPSKVWKYLRFDVVGDDLLASPEFKLLSTYVDRFNKKNPDNKT

TVVTALNEYSRRTTSTAILAALRSKTSDLTNQVETALIKLWLTKYDPTEVFKILNLHQSR

TKLLKNPLLITWGKYVYAFNVKNPNKRATPVEILRNQFGDRELYKMLVKKNNAPSLKKP

>g539470

MTLHHVYLIAFAIMVNITVGFPSHIVSKLPTFFADEQVIFSKRFLRTASDVIEENEERAP

QLPISKIETLKSLTTSANIPDDMFNRWVKKKKSVDKVFIRLSLNKKEEKLLNNPHFVTWI

NYVKALDAATDGPSWTAISKLTKYYGDRDVAKVIEAAKKKPGMEKIADDLHAQQFQYWLN

SYDTDTPYYVFRSLALPFDYYKPLENPLFLSWIDYVNFFNKNRSPKDQEGFLATLGTKYM

YNDNGISKLVEAAKKKPNTMDFGEKLRAEQIERSLANGVSPTDVWGYLKYDVVGGKVFDS

PNFKTLATYVDRFNTKHPGKETTLASVIMNHYYTNDPTNVVINVLKNTKPGTEQIVKQVQ

AEVFNIWEKSDVDPSLAFVKLALHKTPSELFSNPLFNTWTAYVNVLNAKNPNMRTEVVDV

LRARFGDSTLSKMLAEAKAVPSSKDLATKLKASLLAKMTTEDKPPVNAN

>g539480

MHPLYLAFLIAFTLFASVHASHSPTFVVEDENKGDIDSRRFLNANSAVNEERLPQLPTSN

IEKIKSFTTPATISDDIFNRWVKEKKSVDKVFVRLNLKTTKQDKLVENPHFVTWIKYVKA

LDAKTEGPSSSAVSKLTEYYGDRVVAQIIEGVKIKPGMEKLASDLQTQQFQYWLHQYMSQ

TPDGVFRSLGLGFEMAKLLENPSKNPLFMTWINYVKFYNKHAKIDGYLPTLGAKFRYNDN

EISRMVEVARKTPSTMEFAKKLRAEQVDRWFTYGWHPSKVWLNLRHDVDGKNVFASPEFK

LLSTYVDRFNTKYPDKKITVVSALNEYSRRTTSKAILTALRSKTPDITNQVETALIKLWL

TKYDPTEVFKILNLHQSRTKLLKNPLLITWGKYVYAFNMKNPNKRTTPMEILRNQFGEKK

LYKMLVLEKNVPSS

CLUSTAL O(1.2.4) multiple sequence alignment

g539460 ------------------------MASNQPVFAVEDEVIIHSRQLLRTNVAMGDEHEERY 36

g539470 MTLHHVYLIAFAIMVNITVGFPSHIVSKLPTFFA-DEQVIFSKRFLRTASDVIEENEERA 59

 :.\*: \*.\* . \*\* :\*.\*:::\*\*\* : :\*:\*\*\*

g539460 PEPPYSKIETLKSLFTPKTISEDMINRWLKNKKSVDKVFVRLKLENTPEDKLLENPHFIT 96

g539470 PQLPISKIETLKSLTTSANIPDDMFNRWVKKKKSVDKVFIRLSLNK-KEEKLLNNPHFVT 118

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g539460 WINYAKALNSETGSPSWSTVSKLTKYYDDDDIARIIETAKQTPGMEALASDLHTQQFQYW 156

g539470 WINYVKALDAATDGPSWTAISKLTKYYGDRDVAKVIEAAKKKPGMEKIADDLHAQQFQYW 178

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g539460 LHIA--KKPEYVFRSLRLIDAKEELLRNPSKNPLFMIWLDYVKYYNKHKD--RKKGYLST 212

g539470 LNSYDTDTPYYVFRSLALPFD----YYKPLENPLFLSWIDYVNFFNKNRSPKDQEGFLAT 234

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g539460 LGTRFWFDDDEISTMVKVAKKTPSTTEFAKQLRAEQVDRWFTYGWPPSKVWKYLRFDVVG 272

g539470 LGTKYMYNDNGISKLVEAAKKKPNTMDFGEKLRAEQIERSLANGVSPTDVWGYLKYDVVG 294

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g539460 DDLLASPEFKLLSTYVDRFNKKNPDNKTTVVTAL-NEYSRRTTSTAIL---AALRSKTSD 328

g539470 GKVFDSPNFKTLATYVDRFNTKHPGKETTLASVIMNHYYTNDPTNVVINVLKNTKPGTEQ 354

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g539460 LTNQVETALIKLWLT-KYDPTEVFKILNLHQSRTKLLKNPLLITWGKYVYAFNVKNPNKR 387

g539470 IVKQVQAEVFNIWEKSDVDPSLAFVKLALHKTPSELFSNPLFNTWTAYVNVLNAKNPNMR 414

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g539460 ATPVEILRNQFGDRELYKMLVKKNNAPSLKKP----------------------- 419

g539470 TEVVDVLRARFGDSTLSKMLAEAKAVPSSKDLATKLKASLLAKMTTEDKPPVNAN 469

 : \*::\*\* :\*\*\* \* \*\*\*.: : .\*\* \*.

CLUSTAL O(1.2.4) multiple sequence alignment

g539450 ------------------------------------------------------------ 0

g539470 MTLHHVYLIAFAIMVNITVGFPSHIVSKLPTFFADEQVIFSKRFLRTASDVIEENEERAP 60

g539450 ----------------------MLNDWVRKKVSADGIFIRLQLDKTGYKLLESPRLITWV 38

g539470 QLPISKIETLKSLTTSANIPDDMFNRWVKKKKSVDKVFIRLSLNKKEEKLLNNPHFVTWI 120

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g539450 KYADALNIKTQGTSAPAISKLTDYYGDAALARMIEVAKKNPSSKNIASDLETMQFNYWVN 98

g539470 NYVKALDAATDGPSWTAISKLTKYYGDRDVAKVIEAAKKKPGMEKIADDLHAQQFQYWLN 180

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g539450 SFATPDE--VFILLELRFGRDKLLDNPLFSTWLNYITFFDGTHPSI-------------- 142

g539470 SYDTDTPYYVFRSLALPFDYYKPLENPLFLSWIDYVNFFNKNRSPKDQEGFLATLGTKYM 240

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g539450 ------------------------------------------------------------ 142

g539470 YNDNGISKLVEAAKKKPNTMDFGEKLRAEQIERSLANGVSPTDVWGYLKYDVVGGKVFDS 300

g539450 ------------------------------------------------------------ 142

g539470 PNFKTLATYVDRFNTKHPGKETTLASVIMNHYYTNDPTNVVINVLKNTKPGTEQIVKQVQ 360

g539450 ------------------------------------------------------------ 142

g539470 AEVFNIWEKSDVDPSLAFVKLALHKTPSELFSNPLFNTWTAYVNVLNAKNPNMRTEVVDV 420

g539450 ------------------------------------------------- 142

g539470 LRARFGDSTLSKMLAEAKAVPSSKDLATKLKASLLAKMTTEDKPPVNAN 469

CLUSTAL O(1.2.4) multiple sequence alignment

g539470 -MTLHHVYLIAFAIMVNITVGFPSHIVSKLPTFFADE---QVIFSKRFLRTASDVIEENE 56

g539480 MHPLYLAFLIAFTLFAS-------VHASHSPTFVVEDENKGDIDSRRFLNANS---AVNE 50

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g539470 ERAPQLPISKIETLKSLTTSANIPDDMFNRWVKKKKSVDKVFIRLSLNK-KEEKLLNNPH 115

g539480 ERLPQLPTSNIEKIKSFTTPATISDDIFNRWVKEKKSVDKVFVRLNLKTTKQDKLVENPH 110

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g539470 FVTWINYVKALDAATDGPSWTAISKLTKYYGDRDVAKVIEAAKKKPGMEKIADDLHAQQF 175

g539480 FVTWIKYVKALDAKTEGPSSSAVSKLTEYYGDRVVAQIIEGVKIKPGMEKLASDLQTQQF 170

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g539470 QYWLNSYDTDTPYYVFRSLALPFDYYK----PLENPLFLSWIDYVNFFNKNRSPKDQEGF 231

g539480 QYWLHQYMSQTPDGVFRSLGLGFEMAKLLENPSKNPLFMTWINYVKFYNKHA---KIDGY 227

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g539470 LATLGTKYMYNDNGISKLVEAAKKKPNTMDFGEKLRAEQIERSLANGVSPTDVWGYLKYD 291

g539480 LPTLGAKFRYNDNEISRMVEVARKTPSTMEFAKKLRAEQVDRWFTYGWHPSKVWLNLRHD 287

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g539470 VVGGKVFDSPNFKTLATYVDRFNTKHPGKETTLASVIMNHYYTNDPTNVVINVLKNTKPG 351

g539480 VDGKNVFASPEFKLLSTYVDRFNTKYPDKKITVVSAL-NEYSRRTTSKAILTALR---SK 343

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g539470 TEQIVKQVQAEVFNIWEKSDVDPSLAFVKLALHKTPSELFSNPLFNTWTAYVNVLNAKNP 411

g539480 TPDITNQVETALIKLWLT-KYDPTEVFKILNLHQSRTKLLKNPLLITWGKYVYAFNMKNP 402

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g539470 NMRTEVVDVLRARFGDSTLSKMLAEAKAVPSSKDLATKLKASLLAKMTTEDKPPVNAN 469

g539480 NKRTTPMEILRNQFGEKKLYKMLVLEKNVPSS-------------------------- 434

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CLUSTAL O(1.2.4) multiple sequence alignment

g539480 MHPLYLAFLIAFTLFASVHASHSPTFVVEDENKGDIDSRRFLNANSA---VNEERLPQLP 57

g539460 ------------------MASNQPVFAVEDEV--IIHSRQLLRTNVAMGDEHEERYPEPP 40

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g539480 TSNIEKIKSFTTPATISDDIFNRWVKEKKSVDKVFVRLNLKTTKQDKLVENPHFVTWIKY 117

g539460 YSKIETLKSLFTPKTISEDMINRWLKNKKSVDKVFVRLKLENTPEDKLLENPHFITWINY 100

 \*:\*\*.:\*\*: \*\* \*\*\*:\*::\*\*\*:\*:\*\*\*\*\*\*\*\*\*\*\*:\*:.\* :\*\*\*:\*\*\*\*\*:\*\*\*:\*

g539480 VKALDAKTEGPSSSAVSKLTEYYGDRVVAQIIEGVKIKPGMEKLASDLQTQQFQYWLHQY 177

g539460 AKALNSETGSPSWSTVSKLTKYYDDDDIARIIETAKQTPGMEALASDLHTQQFQYWLHI- 159

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g539480 MSQTPDGVFRSLGLGFEMAKLLENPSKNPLFMTWINYVKFYNKHA-KIDGYLPTLGAKFR 236

g539460 -AKKPEYVFRSLRLIDAKEELLRNPSKNPLFMIWLDYVKYYNKHKDRKKGYLSTLGTRFW 218

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g539480 YNDNEISRMVEVARKTPSTMEFAKKLRAEQVDRWFTYGWHPSKVWLNLRHDVDGKNVFAS 296

g539460 FDDDEISTMVKVAKKTPSTTEFAKQLRAEQVDRWFTYGWPPSKVWKYLRFDVVGDDLLAS 278

 ::\*:\*\*\* \*\*:\*\*:\*\*\*\*\* \*\*\*\*:\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\* \*\*.\*\* \*.:::\*\*

g539480 PEFKLLSTYVDRFNTKYPDKKITVVSALNEYSRRTTSKAILTALRSKTPDITNQVETALI 356

g539460 PEFKLLSTYVDRFNKKNPDNKTTVVTALNEYSRRTTSTAILAALRSKTSDLTNQVETALI 338

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*.\* \*\*:\* \*\*\*:\*\*\*\*\*\*\*\*\*\*\*.\*\*\*:\*\*\*\*\*\* \*:\*\*\*\*\*\*\*\*\*

g539480 KLWLTKYDPTEVFKILNLHQSRTKLLKNPLLITWGKYVYAFNMKNPNKRTTPMEILRNQF 416

g539460 KLWLTKYDPTEVFKILNLHQSRTKLLKNPLLITWGKYVYAFNVKNPNKRATPVEILRNQF 398

 \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*:\*\*\*\*\*\*:\*\*:\*\*\*\*\*\*\*

g539480 GEKKLYKMLVLEKNVPSS--- 434

g539460 GDRELYKMLVKKNNAPSLKKP 419

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CLUSTAL O(1.2.4) multiple sequence alignment

g539480 MHPLYLAFLIAFTLFASVHASHSPTFVVEDENKGDIDSRRFLNANSAVNEERLPQLPTSN 60

g539450 ------------------------------------------------------------ 0

g539480 IEKIKSFTTPATISDDIFNRWVKEKKSVDKVFVRLNLKTTKQDKLVENPHFVTWIKYVKA 120

g539450 ----------------MLNDWVRKKVSADGIFIRLQLDKTG-YKLLESPRLITWVKYADA 43

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g539480 LDAKTEGPSSSAVSKLTEYYGDRVVAQIIEGVKIKPGMEKLASDLQTQQFQYWLHQYMSQ 180

g539450 LNIKTQGTSAPAISKLTDYYGDAALARMIEVAKKNPSSKNIASDLETMQFNYWVNSFA-- 101

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g539480 TPDGVFRSLGLGFEMAKLLENPSKNPLFMTWINYVKFYNKHAKIDGYLPTLGAKFRYNDN 240

g539450 TPDEVFILLELRFGRDKLLD----NPLFSTWLNYITFFDGTHPSI--------------- 142

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g539480 EISRMVEVARKTPSTMEFAKKLRAEQVDRWFTYGWHPSKVWLNLRHDVDGKNVFASPEFK 300

g539450 ------------------------------------------------------------ 142

g539480 LLSTYVDRFNTKYPDKKITVVSALNEYSRRTTSKAILTALRSKTPDITNQVETALIKLWL 360

g539450 ------------------------------------------------------------ 142

g539480 TKYDPTEVFKILNLHQSRTKLLKNPLLITWGKYVYAFNMKNPNKRTTPMEILRNQFGEKK 420

g539450 ------------------------------------------------------------ 142

g539480 LYKMLVLEKNVPSS 434

g539450 -------------- 142

**Set 3**

|  |  |  |
| --- | --- | --- |
| PmGH34\_PBPs\_010 | g539590 | Putative effector peptide |
| PmGH34\_PBPs\_010 | g539600 | Putative effector peptide |
| PmGH34\_PBPs\_010 | g539610 | Putative effector peptide |
| PmGH34\_PBPs\_010 | g539620 | Secreted RxLR effector |

>g539590

MKIGKMMETEWMKHSLNKKYSPKDTFVHLGLKAAGDDVLISPAFKIWTRYLDAFNARYPE

QKVTMIDGLTANFTYQGLLWVFQTAKKDQTIEKLVKTLQENLIDKWVTLKEKPEDLKRIL

HHIEIGEEMIQRYMTKIPSVNVS

>g539600

MWLDSGETTDDVFKLLKLDDEVHFYTFQDKVLLTTWVSYVNAFFAKNPGQKDELFSALKL

RFEDRPLNEILNIAKTFPSIESAANKIQTDKIQNYLVNNVSSKRVFELLGLSEDRNHILD

SPLFQSWMQYVEAYSKKNPSKLES

>g539610

METLKSLFTPKTISDDMFNRWLKNKKSVDKVFVRLNLQNTPEDKLLENPYFTTWINYAKA

LNAETGSPSWSTVSKLTEYYDDDIIARIIEAAKKTPGMEVLASDLHTQQFQYWLHFATKP

EYVFRSLRLTDAKEELLKNPSKNPLFMLWLDYVNFYNKNMKNHQEGYLSTLGTRVWFDDD

DIFTMVEVARKTPSTMEFAKKLRAEQVDRWFTYGWHPSKVWLYLRRDVNGKNVFASPEFK

LLSTYVDRFNKKNPNEKTTVVSALNEYFRRTSTKAILAALRSKPPDISNKVETALIKTWL

TKYDPIKVFETLNLHRSRTKLLQNPLLITWGKYVYAYNVKNPDKRTTPMEILREQFGDRE

LYKMLVKKKNVPTLKNP

>g539620

MHPLYLAFLIAFTLFASVHASHSPTFVVEDENKGDIDSRRFLNANSAVNEERLPQLPTSS

IEKIKSFTTPATISDDIFNRWVKEKKSVDKVFVRLNLKTTKQDKLVENPHFVTWIKYVKA

LDAKTEGPSSSAVSKLTEYYGDRVVAQIIEGVKIKPGMEKLASDLQTQQFQYWLHQYMSQ

TPDGVFRSLGLGFEMAKLLENPSKNPLFMTWINYVKFYNKHAKIDGYLPTLGAKFRYNDN

EISRMVEVARKTPSTMEFAKKLRAEQVDRWFTYGWHPSKVWLNLRHDVDGKNVFASPEFK

LLSTYVDRFNTKYPDKKITVVSALNEYYRSTTSKAILTALRSKTPDITNQVEAALIKLWL

TKYDPTQVFKILNLQQSRTKLLKNPLLITWGKYVYAFNMKYPNKRTTPMEILRNQFGEKK

LYKMLVLEKNVPSS

CLUSTAL O(1.2.4) multiple sequence alignment

g539610 ------------------------------------------------------------ 0

g539620 MHPLYLAFLIAFTLFASVHASHSPTFVVEDENKGDIDSRRFLNANSAVNEERLPQLPTSS 60

g539610 METLKSLFTPKTISDDMFNRWLKNKKSVDKVFVRLNLQNTPEDKLLENPYFTTWINYAKA 60

g539620 IEKIKSFTTPATISDDIFNRWVKEKKSVDKVFVRLNLKTTKQDKLVENPHFVTWIKYVKA 120

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g539610 LNAETGSPSWSTVSKLTEYYDDDIIARIIEAAKKTPGMEVLASDLHTQQFQYWLHF--AT 118

g539620 LDAKTEGPSSSAVSKLTEYYGDRVVAQIIEGVKIKPGMEKLASDLQTQQFQYWLHQYMSQ 180

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g539610 KPEYVFRSLRLTDAKEELLKNPSKNPLFMLWLDYVNFYNKNMKNHQEGYLSTLGTRVWFD 178

g539620 TPDGVFRSLGLGFEMAKLLENPSKNPLFMTWINYVKFYNKHA--KIDGYLPTLGAKFRYN 238

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g539610 DDDIFTMVEVARKTPSTMEFAKKLRAEQVDRWFTYGWHPSKVWLYLRRDVNGKNVFASPE 238

g539620 DNEISRMVEVARKTPSTMEFAKKLRAEQVDRWFTYGWHPSKVWLNLRHDVDGKNVFASPE 298

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g539610 FKLLSTYVDRFNKKNPNEKTTVVSALNEYFRRTSTKAILAALRSKPPDISNKVETALIKT 298

g539620 FKLLSTYVDRFNTKYPDKKITVVSALNEYYRSTTSKAILTALRSKTPDITNQVEAALIKL 358

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g539610 WLTKYDPIKVFETLNLHRSRTKLLQNPLLITWGKYVYAYNVKNPDKRTTPMEILREQFGD 358

g539620 WLTKYDPTQVFKILNLQQSRTKLLKNPLLITWGKYVYAFNMKYPNKRTTPMEILRNQFGE 418

 \*\*\*\*\*\*\* :\*\*: \*\*\*::\*\*\*\*\*\*:\*\*\*\*\*\*\*\*\*\*\*\*\*:\*:\* \*:\*\*\*\*\*\*\*\*\*\*:\*\*\*:

g539610 RELYKMLVKKKNVPTLKNP 377

g539620 KKLYKMLVLEKNVPSS--- 434

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CLUSTAL O(1.2.4) multiple sequence alignment

g539600 ------------------------------------------------------------ 0

g539620 MHPLYLAFLIAFTLFASVHASHSPTFVVEDENKGDIDSRRFLNANSAVNEERLPQLPTSS 60

g539600 -------------------MWLDSGETTDDVFKLLKLDDEVHFYTFQDKVLLTTWVSYVN 41

g539620 IEKIKSFTTPATISDDIFNRWVKEKKSVDKVFVRLNLKTTKQ-DKLVENPHFVTWIKYVK 119

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g539600 AFFAKNPGQKDELFSALKLRFEDRPLNEILNIAKTFPSIESAANKIQTDKIQNYLVNNVS 101

g539620 ALDAKTEGPSSSAVSKLTEYYGDRVVAQIIEGVKIKPGMEKLASDLQTQQFQYWLHQYMS 179

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g539600 --SKRVFELLGLSEDRNHIL----DSPLFQSWMQYVEAYSKKNPS--------------- 140

g539620 QTPDGVFRSLGLGFEMAKLLENPSKNPLFMTWINYVKFYNKHAKIDGYLPTLGAKFRYND 239

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g539600 ------------------------------------------------------------ 140

g539620 NEISRMVEVARKTPSTMEFAKKLRAEQVDRWFTYGWHPSKVWLNLRHDVDGKNVFASPEF 299

g539600 ------------------------------------------------------------ 140

g539620 KLLSTYVDRFNTKYPDKKITVVSALNEYYRSTTSKAILTALRSKTPDITNQVEAALIKLW 359

g539600 --------------------------------------------KLES------------ 144

g539620 LTKYDPTQVFKILNLQQSRTKLLKNPLLITWGKYVYAFNMKYPNKRTTPMEILRNQFGEK 419

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g539600 --------------- 144

g539620 KLYKMLVLEKNVPSS 434

CLUSTAL O(1.2.4) multiple sequence alignment

g539590 ------------------------------------------------------------ 0

g539620 MHPLYLAFLIAFTLFASVHASHSPTFVVEDENKGDIDSRRFLNANSAVNEERLPQLPTSS 60

g539590 ------------------------------------------------------------ 0

g539620 IEKIKSFTTPATISDDIFNRWVKEKKSVDKVFVRLNLKTTKQDKLVENPHFVTWIKYVKA 120

g539590 ------------------------------------------------------------ 0

g539620 LDAKTEGPSSSAVSKLTEYYGDRVVAQIIEGVKIKPGMEKLASDLQTQQFQYWLHQYMSQ 180

g539590 ------------------------------------------------------------ 0

g539620 TPDGVFRSLGLGFEMAKLLENPSKNPLFMTWINYVKFYNKHAKIDGYLPTLGAKFRYNDN 240

g539590 ---------------MKIGKMMETEWMKHSLNKKYSPKDTFVHLGLKAAGDDVLISPAFK 45

g539620 EISRMVEVARKTPSTMEFAKKLRAEQVDRWFTYGWHPSKVWLNLRHDVDGKNVFASPEFK 300

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g539590 IWTRYLDAFNARYPEQKVTMIDGLTANFTYQGLLWVFQTAKKDQTIEKLVKTLQENLIDK 105

g539620 LLSTYVDRFNTKYPDKKITVVSALNEYYRSTTSKAILTALR--SKTPDITNQVEAALIKL 358

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g539590 WVTLKEKPEDLKRILHHIEIGEEMIQ------------RYMTKIPSVNVS---------- 143

g539620 WLTKYDPTQ-VFKILNLQQSRTKLLKNPLLITWGKYVYAFNMKYPNKRTTPMEILRNQFG 417

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g539590 ----------------- 143

g539620 EKKLYKMLVLEKNVPSS 434

**Set 4**

|  |  |  |
| --- | --- | --- |
| PmGH34\_PBPs\_023 | g580280 | Secreted RxLR effector |
| PmGH34\_PBPs\_023 | g580290 | Putative effector peptide |

>g580280

MRLSHILVFATTFLASTTALSPSATTPLKALRALHEGNNNGGRILRIHEPVDEDTGDNKE

ERGGGVNNFLNKFRYQSQGAHGADDLNPTLVQQLRNNPRLFEQMRTNDVLRGNIFSAWRG

VKLHSGEVKAAMKNHGYTKEEYKQFVREYKNFKPEDLSF

>g580290

MSIYPEGLPRALHEGNNYGGRVLRIHEPIDEDKSGNQEERGGGTNFLNRFRYQSQGAHGA

EDLNQVTMARNYLQDNPTLFNRIRSDSDKRYETYSIWRGMKYHSDEVKRAMKAHGLDDDE

VRKFVNEYKAFKPATLSFKVFFWHSSLVRLLLFYLSFNSP

CLUSTAL O(1.2.4) multiple sequence alignment

g580280 MRLSHILVFATTFLASTTALSPSATTPLKALRALHEGNNNGGRILRIHEPVDEDTGDNKE 60

g580290 ----------------------MSIYPEGLPRALHEGNNYGGRVLRIHEPIDEDKSGNQE 38

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g580280 ERGGGVNNFLNKFRYQSQGAHGADDLNPTLV--QQLRNNPRLFEQMRTNDVLRGNIFSAW 118

g580290 ERGGG-TNFLNRFRYQSQGAHGAEDLNQVTMARNYLQDNPTLFNRIRSDSDKRYETYSIW 97

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g580280 RGVKLHSGEVKAAMKNHGYTKEEYKQFVREYKNFKPEDLSF------------------- 159

g580290 RGMKYHSDEVKRAMKAHGLDDDEVRKFVNEYKAFKPATLSFKVFFWHSSLVRLLLFYLSF 157

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g580280 --- 159

g580290 NSP 160

**Set 5**

|  |  |  |
| --- | --- | --- |
| PmGH34\_PBPs\_023 | g581580 | Secreted RxLR effector |
| PmGH34\_PBPs\_023 | g581590 | Putative effector peptide |
| PmGH34\_PBPs\_023 | g581600 | Secreted RxLR effector |
| PmGH34\_PBPs\_023 | g581610 | Secreted RxLR effector |

>g581580

MRLQYIMLMVLATLVTSNGVVSGVPVVRATEDVQLWKAADANLINTVNTEHVQPKRKRFL

RTGDTKTTDYVYDPTKKKVFIEDKLHKSLTNPKKAKKLYKRWYKRGYSVKLVTRTLNQGA

NKDVVDVYDELAKGYAAYYKKKST

>g581590

MESLYRCLQQRSELNLPTAATTMNLRYVLLVVTATIIANISIASADNAKFVKLNSVPSAQ

NEQHEFVRSLLEDDEDNAVTKPGSPRFMEQKLQKALTNPKKTAKLYEYWAQKGYTAKQIS

SEMGQTENRELSQTFTKLSKGYATYLKNRK

>g581600

MHLHYVMVMIVAILAAASGVLEAKVMDTNLRNVDASTPINSINTVPTEISSTRKLRGAAT

NADKTNVHYYPSKGKKKPFIEVRIKKALSNPKKTRKLYEQWYQSGFTPKQVARGLTQDDN

RGLDGTYKRVAKGYAKFVKEKRSQQQTM

>g581610

MRLHYVLVMVAATLAAVNGVSEAKVMDTNLRNIEDVAPINSINTAPTEISSTRKLRGADT

NVDKTNVHYYPSKGKKKPFIEVRIKKALSNPKKTRKLYAQWYQSGFTPKQVARGLTQDEN

RGLDETYKRVAKGYAVYVKEKRSPQQTM

CLUSTAL O(1.2.4) multiple sequence alignment

g581580 ----------------------MRLQYIMLMVLATLVTSNGVVSGVPVVRATEDVQLWKA 38

g581590 MESLYRCLQQRSELNLPTAATTMNLRYVLLVVTATIIANISIASA--------------- 45

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g581580 ADANLINTVNTEHVQPKRKRFLRTGDTKTTDYVYDPTKKKVFIEDKLHKSLTNPKKAKKL 98

g581590 DNAKFVKLNSVPSAQNEQHEFVRSLLEDDEDNAVTKPGSPRFMEQKLQKALTNPKKTAKL 105

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g581580 YKRWYKRGYSVKLVTRTLNQGANKDVVDVYDELAKGYAAYYKKKST 144

g581590 YEYWAQKGYTAKQISSEMGQTENRELSQTFTKLSKGYATYLKNRK- 150

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CLUSTAL O(1.2.4) multiple sequence alignment

g581590 MESLYRCLQQRSELNLPTAATTMNLRYVLLVVTATIIANISIASAD-----------NAK 49

g581600 ----------------------MHLHYVMVMIVAILAAASGVLEAKVMDTNLRNVDASTP 38

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g581590 FVKLNSVPSAQNEQHEFVRSLLEDDEDNA---VTKPGSPRFMEQKLQKALTNPKKTAKLY 106

g581600 INSINTVPTEISSTRKLRGAATNADKTNVHYYPSKGKKKPFIEVRIKKALSNPKKTRKLY 98

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g581590 EYWAQKGYTAKQISSEMGQTENRELSQTFTKLSKGYATYLKNRK------ 150

g581600 EQWYQSGFTPKQVARGLTQDDNRGLDGTYKRVAKGYAKFVKEKRSQQQTM 148

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CLUSTAL O(1.2.4) multiple sequence alignment

g581590 MESLYRCLQQRSELNLPTAATTMNLRYVLLVVTATIIANISIASAD-----------NAK 49

g581610 ----------------------MRLHYVLVMVAATLAAVNGVSEAKVMDTNLRNIEDVAP 38

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g581590 FVKLNSVPSAQNEQHEFVRSLLEDDED---NAVTKPGSPRFMEQKLQKALTNPKKTAKLY 106

g581610 INSINTAPTEISSTRKLRGADTNVDKTNVHYYPSKGKKKPFIEVRIKKALSNPKKTRKLY 98

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g581590 EYWAQKGYTAKQISSEMGQTENRELSQTFTKLSKGYATYLKNRK------ 150

g581610 AQWYQSGFTPKQVARGLTQDENRGLDETYKRVAKGYAVYVKEKRSPQQTM 148

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CLUSTAL O(1.2.4) multiple sequence alignment

g581580 MRLQYIMLMVLATLVTSNGVVSGVPVVRATEDVQLWKAADANLINTVNTEHVQPKRKRFL 60

g581600 MHLHYVMVMIVAILAAASGVLEAKVMD-----TNLRNVDASTPINSINTVPTEISSTRKL 55

g581610 MRLHYVLVMVAATLAAVNGVSEAKVMD-----TNLRNIEDVAPINSINTAPTEISSTRKL 55

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g581580 RTGD----TKTTDYVYDPTKKKVFIEDKLHKSLTNPKKAKKLYKRWYKRGYSVKLVTRTL 116

g581600 RGAATNADKTNVHYYPSKGKKKPFIEVRIKKALSNPKKTRKLYEQWYQSGFTPKQVARGL 115

g581610 RGADTNVDKTNVHYYPSKGKKKPFIEVRIKKALSNPKKTRKLYAQWYQSGFTPKQVARGL 115

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g581580 NQGANKDVVDVYDELAKGYAAYYKKKST----- 144

g581600 TQDDNRGLDGTYKRVAKGYAKFVKEKRSQQQTM 148

g581610 TQDENRGLDETYKRVAKGYAVYVKEKRSPQQTM 148

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CLUSTAL O(1.2.4) multiple sequence alignment

g581600 MHLHYVMVMIVAILAAASGVLEAKVMDTNLRNVDASTPINSINTVPTEISSTRKLRGAAT 60

g581610 MRLHYVLVMVAATLAAVNGVSEAKVMDTNLRNIEDVAPINSINTAPTEISSTRKLRGADT 60

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g581600 NADKTNVHYYPSKGKKKPFIEVRIKKALSNPKKTRKLYEQWYQSGFTPKQVARGLTQDDN 120

g581610 NVDKTNVHYYPSKGKKKPFIEVRIKKALSNPKKTRKLYAQWYQSGFTPKQVARGLTQDEN 120

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g581600 RGLDGTYKRVAKGYAKFVKEKRSQQQTM 148

g581610 RGLDETYKRVAKGYAVYVKEKRSPQQTM 148

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