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a2                  MPLGEVFLAAFLQLLLDRLTPRDILNYFGNFRGVGKKLEKWRATLTTIAAVLSDADERQR 60
G14                 MPLGEVFLAAFLQLLLDRLTPRDILNYFGNFRGVGKKLEKWRATLTTIAAVLSDADERQR 60
A8                  MPLGEVFLAAFLQLLLDRLTPRDILNYFGNFRGVGKKLEKWRATLSTIAAVLSDADERQR 60
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a2                  TDDAVKLWLNNLRDLAYDVEDMLDKFATQMLKRTIEGRDQASTSNKVRNSLFKIKLNWNM 120
G14                 TDDAVKLWLNNLRDLAYDVEDMLDKFATQMLKRTIEGRDQASTSNKVRNSLFKIKLNWNM 120
A8                  TDDAVKLWLNNLRDLAYDVEDMLDKFATQMLKRTIEGRDQASTSNKVRNSLFKIKLNWDM 120
                    **********************************************************:*

a2                  NSEMKKITERLQDISDRKVKFSLKDTGTSAKESRSLPCSGVLDEKLLVGRDGDKGKIIEL 180
G14                 NSEMKKITERLQDISDRKVKFSLKDTGTSAKESRSLPCSGVLDEKLLVGRDGDKGKIIEL 180
A8                  NSEMKKITERLQDISDRKVKFGLKDTGTSAKESRSLPSSCVLDEKLVVGRDGDKGKIIEL 180
                    *********************.***************.* ******:*************

a2                  LKKSTNFGVVAIVGMPGVGKTTLAQLVFNNKDDAMKEFELKVWVSVSDDFDVVRVTKAIL 240
G14                 LKKSTNFGVVAIVGMPGVGKTTLAQLVFNNKDDAMKEFELKVWVSVSDDFDVVRVTKAIL 240
A8                  LKKSTNFGVVAIVGMPGVGKTTLAQLVFNNKDDAMKEFELKVWVSVSDDFDVVRVTKAIL 240
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a2                  ESMKPLPVQVEEFSKMQHDLSEQLRGKKFLIVLDDVWNKGDRDLNDLWLRLKSPFGVGAG 300
G14                 ESMKPLPVQVEEFSKMQHDLSEQLRGKKFLIVLDDVWNKGDRDLNDLWLRLKSPFGVGAG 300
A8                  ESMKPLPVQVEEFSKMQHDLSEQLRGKKFLIVLDDVWNKGDRDLNDLWLRLKSPFGVGAG 300
                    ************************************************************

a2                  GSKIIVTTRDLNVAKIMGATGFHNLECMANDDCLEIFERHAFGEVNSGKPVNYELIRTKI 360
G14                 GSKIIVTTRDLNVAKIMGATGFHNLECMANDDCLEIFERHAFGEVNSGKPVNYELIRTKI 360
A8                  GSKIIVTTRDLNVAKIMGATGFHNLECMANDDCLEIFERHAFGEVNSGKPVNYELIRTKI 360
                    ************************************************************

a2                  VEKCCGLPLAARTLGGLLRCKETDEWGEILDNKLWNLADNCNLPRVLELSYHYLPSHLKR 420
G14                 VEKCCGLPLAARTLGGLLRCKETDEWGEILDNKLWNLADNCNLPRVLELSYHYLPSHLKR 420
A8                  VEKCCGLPLAARTLGGLLRCKETDEWGEILDNKLWNLADNCNLPRVLELSYHYLPSHLKR 420
                    ************************************************************

a2                  CFAYCSILPNDYEFGEKQLVLLWMAEGLIQQKPDNNKQMEDLGRDYFRELLARSLFQESS 480
G14                 CFAYCSILPNDYEFGEKQLVLLWMAEGLIQQKPDNNKQMEDLGRDYFRELLARSLFQESS 480
A8                  CFAYCSILPNDYEFGQKQLVLLWMAEGLIQQKPDNNKQMEDLGRDYFRELLARSLFQESS 480
                    ***************:********************************************

a2                  KNNSRYVMHDLVSELTRWAAGEICFRLEDKQGDNLQSTCFRGARHSSFIAGEFDGVKRFE 540
G14                 KNNSRYVMHDLVSELTRWAAGEICFRLEDKQGDNLQSTCFRGARHSSFIAGEFDGVKRFE 540
A8                  KNNSRYVMHDLVSELTRWAAGEICFRLEDKQGDNLQSTCFRGARHSSFIAGEFDGVKRFE 540
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a2              DFPKAERLRTFLPLSLSYSTGWLKFLSRQVTFKLLPQLQYLRVLSFNDYKITALPESIGD 600
G14             DFPKAERLRTFLPLSLSYSTGWLKFLSRQVTFKLLPQLQYLRVLSFNDYKITALPESIGD 600
A8              DFPKAERLRTFLPLSLSYSTGWLKFLSRQVTFKLLPQLQYLRVLSFNDYKITALPESIGD 600
                ************************************************************

a2              LRLLQYLDLSYTYITSLPKSISTLYNLQTLILEHCYYLKSLLADMSNLINLRHLNNSYVS 660
G14             LRLLQYLDLSYTYITSLPKSISTLYNLQTLILEHCYYLKSLLADMSNLINLRHLNNSYVS 660
A8              LRLLQYLDLSYTYITSLPKSISTLYNLQTLILEHCYYLKSLLADMSNLINLRHLNNSYVS 660
                ************************************************************

a2              SLEGMPPNLGSLVNLQSLPNFVVSGGSDQSGIREIGPLSHLRGTLCISGLENVTDVEDAR 720
G14             SLEGMPPNLGSLVNLQSLPNFVVSGGSDQSGIREIGPLSHLRGTLCISGLENVTDVEDAR 720
A8              SLEGMPPNLGSLVNLQSLPNFVVSGGSDQSGIREIGPLSHLRGTLCISGLENVTDVEDAR 720
                ************************************************************

a2              RANLKCKERLDSLVLKWSHSSDTRETESVVLDMLEPHTKLKELTIKSYAGEEFSSWVGGP 780
G14             RANLKCKERLDSLVLKWSHSSDTRETESVVLDMLEPHTKLKELTIKSYAGEEFSSWVGGP 780
A8              RANLKCKERLDSLVLKWSHSSDTRETESVVLDMLEPHTKLKELTIKSYAGEEFSSWVGGP 780
                ************************************************************

a2              LFSNMVLVCLQKCNNCLSLPPLGQLPHLRELYISGMNAVESVGAEFYGERMLPFPVLETL 840
G14             LFSNMVLVCLQKCNNCLSLPPLGQLPHLRELYISGMNAVESVGAEFYGERMLPFPVLETL 840
A8              LFSNMVLVCLQKCNNCLSLPPLGQLPHLRELYISGMNAVESVGAEFYGERMLPFPVLETL 840
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a2              EFVEMQHWKEWLPFQADHEGGAFPCLKTLLVKKCSKLEGKLPENLNSLAKLKIVECEELV 900
G14             EFVEMQHWKEWLPFQADHEGGAFPCLKTLLVKKCSKLEGKLPENLNSLAKLKIVECEELV 900
A8              EFVEMQHWKEWLPFQADHEGGAFPCLKTLLVKKCSKLEGKLPENLNSLAKLKIVECEELV 900
                ************************************************************

a2              VSIANCKQLRQLNIDGCKVLVHTAAKVEFELLESLCLSNILEMMSLQTGELLKKGLTKVR 960
G14             VSIANCKQLRQLNIDGCKVLVHTAAKVEFELLESLCLSNISEMMSLQTGELLKKGLTKVR 960
A8              VSIANCKQLRQLNIDGCKVLVHTAAKVEFELLESLCLSNISEMMSLQTGELLKKGLTKVR 960
                **************************************** *******************

a2              DLKISGCEELTSSLKNEKGRLLQQLTSLGSLEIEDNSRLVEELGKEAEELQISKCKLEFL 1020
G14             DLKISGCEEVTSSLKNEEGRLLQQLTSLGSLEIEDNSRLVEELGKEAEELQISECKLEFL 1020
A8              DLKISGCEEVTSSLKNEEGRLLQQLTSLGSLEIEDNSRLVEELGKEAEELQISECKLEFL 1020
                *********:*******:************************************:*****

a2              ELKKCENLSKLLKGLNQLSSLQELRIHECSSLVSFPDVGLPSLKDIQITSCDSLIYFAKF 1080
G14             ELKKCENLSKLLKGLNQLSSLQELRIHECSSLVSFPDVGLPSLKDIQITSCDSLIYFAKF 1080
A8              ELKKCENLSKLLKGLNQLSSLQELRIHECSSLVSFPDVGLPSLKDIQITSCDSLIYFAKF 1080
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a2              QIPQNLRRTEIKDCKSLKSLVDEEAVSSSWSSFSHSCLEYLRIRGCESLTSLSLSGQLPR 1140
G14             QIPQNLRRTEIKDCKSLKSLVDEEAVGSSWSSFSHSCLEYLRIRGCESLMSLSLSGQLPR 1140
A8              QIPQNLRRTEIKDCKSLKSLVDEEAVGSSWSSFSHSCLEYLRIRGCESLMSLSLSGQLPR 1140
                **************************.********************** **********

a2              TLKHLDLENCDRLELIAGDGFFRDNTNDCLEYIRIWNCQNLKSLPDGLCHLSNLQTLGIG 1200
G14             TLKHLDLENCDRLELIAGDGFFRDNTNDCLEYIRIWNCQNLKSLPDGLCHLSNLQTLGIG 1200
A8              TLKHLDLENCDRLELIAGDGFFRDNTNDCLEYIRIWNCQNLKSLPDGLCHLSNLQTLGIG 1200
                ************************************************************

a2              NCGSLVSIPRLSGGRRPSNLRKIWIIGCNKLEALPEDMHNLNSLEELSIDYREGLTFPPN 1260
G14             NCGSLVSIPRLSGGRRPSNLRKIWIIGCNKLEALPEDMHNLNSLEELSIDYREGLTFPPN 1260
A8              NCGSLVSIPRLSGGRRPSNLRKIWIIGCNKLEALPEDMHNLNSLEELSIDYREGLTFPPN 1260
                ************************************************************

a2              LTSLEIGKVKSCKSLWELEWGLHRLTSLRELGIRSTDPDTVSFPPDMVRMETLFPKSLTN 1320
G14             LTSLEIGKVKSCKSLWELEWGLHRLTSLRELGIRSTDPDTVSFPPDMVRMETLFPKSLTN 1320
A8              LTSLEIGKVKSCKSLWELEWGLHRLTSLRELGIRSTDPDTVSFPPDMVRMETLFPKSLTN 1320
                ************************************************************

a2              LSIDGFPNLKKLSSKGFQFLTSLQSLDLSNCPKLASIPEEGLPPSLERLTIYECPVLKER 1380
G14             LSIDGFPNLKKLSSKGFQFLTSLQSLDLSNCPKLASIPEEGLPPSLERLTIYECPVLKER 1380
A8              LSIDGFPNLKKLSSKGFQFLTSLQSLDLSNCPKLASIPEEGLPPSLERLTIYECPVLKER 1380
                ************************************************************

a2              CQPGKGRYWHKISHIPFIWIDYKQM 1405
G14             CQPGKGRYWHKISHIPFIWIDYKQM 1405
A8              CQPGKGRYWHKISHIPFIWIDYKQM 1405
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Purple: RX-CC_like
Yellow: NB-ARC
Blue: Leucine-rich repeat domain superfamily

Fig. S3 Amino acid sequence alignment of predicted ORFs of A8, a2 and G14. Alignment was performed using ClastalW 2.1.