```
ORF_A6               1 MALGEVFLGAFLQLLLDRLTPREILEYFGNFRGVGQKLEKWRTTLSTIGA     50
                       ||||||||.||||||||||||||||||.||||||||||||||||||||||
XP_009379454.1       1 MALGEVFLAAFLQLLLDRLTPREILEYLGNFRGVGQKLEKWRTTLSTIGA     50

ORF_A6              51 VLSDAEERQLTEGGVKLWLHDLRDLAYDIEDMLDKFAIQMLKRMIEGRDQ    100
                       |||||||||||||||||||.|||||||||||||||||.||||||||||||
XP_009379454.1      51 VLSDAEERQLTEGGVKLWLDDLRDLAYDIEDMLDKFATQMLKRMIEGRDQ    100

ORF_A6             101 GSTSRK--------------------------------------------    106
                       .|.|||
XP_009379454.1     101 ASPSRKVRRSFYKVKLSFDMNSEMKKITKRLQDISERKDKFGLKDTGTSA    150

ORF_A6             107 --------------------------------------------------    106

XP_009379454.1     151 KESRSLPSSDVLDEKLVVGRDGDKGKIIELLSRKYEHADAVNFGVVAIVG    200

ORF_A6             107 --------------------------------------------------    106

XP_009379454.1     201 MAGVGKTTLAQLVFNNKDDAMKDIELKVWVSVSDDFDVVRVTKAILESIT    250

ORF_A6             107 -RP-----------------------------------------------    108
                        ||
XP_009379454.1     251 SRPVQVEEFSKMQHDLSEQLRGKKFLIVLDDIWDKDDYDLYDLWTRLQSP    300

ORF_A6             109 --------------------------------------------------    108

XP_009379454.1     301 FGVGAGGSKIIVTTRDRNVAKITGAAGVHNLECMADDDCMEIFERHAFGE    350

ORF_A6             109 --------------------------------------------------    108

XP_009379454.1     351 INNGKPVNYEVIRTKIVGKCCGLPLAARTLGGLLRRQEKEEWGEILDNKL    400

ORF_A6             109 --------------------------------------------------    108

XP_009379454.1     401 WNLADKSGLLPVLKLSYHYLPSHLKRCFAYCSILPNDYEFGEKQLVLLWM    450

ORF_A6             109 --------------------------------------------------    108

XP_009379454.1     451 AEGLIQQKHDDNKQMEDLGRDYFRELLARSLFQESSKNNSRYVMHDLVND    500

ORF_A6             109 --------------------------------------------------    108

XP_009379454.1     501 LARWAAGEICFRLEDKQGDNLQSTCFRRARHSSFIAGQFDGVMRFEDFPK    550

ORF_A6             109 --------------------------------------------------    108

XP_009379454.1     551 AERLRTSLPLSLSDSRGWYKYLSRKVTFELLPQLQYLRVLSFNGYRITEL    600
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ORF_A6            109 --------------------------------------------------    108

XP_009379454.1    601 PKSIGDLRLLQYLDLSYTLITSLPKSTSTLYYLQTLILEGCDELKSLPVN    650

ORF_A6            109 --------------------------------------------------    108

XP_009379454.1    651 MSNLIKLRHLNNSGASSLEGMPLQLGRLTNLQSLPLFVASEGSDQSGIRE    700

ORF_A6            109 --------------------------------------------------    108

XP_009379454.1    701 IGPLLHLRGALCLSRLENVTDVEDARRANLKCKERLDSLVLEWSRSRDTR    750

ORF_A6            109 --------------------------------------------------    108

XP_009379454.1    751 ETESTVLDMLQPHTKIKELTIKRYAGKEFSSWVGGSFFSNMVLVRLEECN    800

ORF_A6            109 ---------------------------------GECILPFPLLEILEFLD    125
                                                       |||:|.|||||||||:|
XP_009379454.1    801 NCLLLPPLGQLPHLKELYIRGMNAVESVGPEFYGECVLAFPLLEILEFVD    850

ORF_A6            126 KQHWKVWLPFQLDHGSGCFPCLKRLSIKECSKLE----------------    159
                      .||||||||||||||||.||||||||||:|||||
XP_009379454.1    851 MQHWKVWLPFQLDHGSGVFPCLKRLSIKKCSKLEGKLPENLDLLAKLEIV    900

ORF_A6            160 -----------------------------DAKVEFELLEYLCLSNISEVM    180
                                                   ||:|||||||.|.||||||||
XP_009379454.1    901 ECEELAVSIVNYKQLRQLNIKGCKVLVHTDAEVEFELLESLRLSNISEVM    950

ORF_A6            181 SLETGELFRKGLSKVTYLKISGCEKLMSSFKNEARLLQQLTSLGRLEIEG    230
                      ||:||||.|||||||..|||:|||||.||:|||.||||:||||||||||.
XP_009379454.1    951 SLQTGELLRKGLSKVRDLKINGCEKLTSSWKNEGRLLQRLTSLGRLEIED   1000

ORF_A6            231 NSRLVEELGEEAEELLQLQILECKLKFLELNKCENLVKLPKGLNQLSSLQ    280
                      |||||||||||||||||||||||||:||:|.|||||:|||||||||||||
XP_009379454.1   1001 NSRLVEELGEEAEELLQLQILECKLEFLQLKKCENLLKLPKGLNQLSSLQ   1050

ORF_A6            281 ELCIHECSSLVSFPDVGLPPSLKNIKIRKCDSLIYFAKFQIPQNLKIIDI    330
                      ||.|:||||||||||||||||||:|.||:|.||||||||||||||:.|:|
XP_009379454.1   1051 ELRIYECSSLVSFPDVGLPPSLKDIDIRRCHSLIYFAKFQIPQNLRRINI   1100

ORF_A6            331 GDCKSLKSLVDEEECERLGLIAPNGFFSDNTNHCLECIDMFGCQNLKSLP    380
                      .:|||||||||||||||:|||||||||:||||||||.|.::.||||||||
XP_009379454.1   1101 ENCKSLKSLVDEEECERVGLIAPNGFFNDNTNHCLEYIQIWNCQNLKSLP   1150

ORF_A6            381 DGLCHLSNLQELDIRECGSLVSILRLSGGRRPSNLIQIHIENCEKFEALP    430
                      ||||||||||.|.|.:|||||||.|||||||||||..|.|   .|..|||
XP_009379454.1   1151 DGLCHLSNLQTLIIGDCGSLVSIPRLSGGRRPSNLRWIVI---WKLVALP   1197
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ORF_A6            431 EDMHNLNSLETLSIDYREGLIFPPNLTSLVIWKVKSY-------------    467
                      ||||||||||.|.|||||||.||||||||.||||||.
XP_009379454.1   1198 EDMHNLNSLEELRIDYREGLTFPPNLTSLTIWKVKSCKSLWELEWGLQRL   1247

ORF_A6            468 ---------PDTVSFPPNMVRMETLLPKSLTRLVINDFPNLKKLSSEGFQ    508
                               ||||||||:|||||||||||||.|:|..|||||||||:||:
XP_009379454.1   1248 TSLIIYGEDPDTVSFPPDMVRMETLLPKSLTELIIVGFPNLKKLSSKGFE   1297

ORF_A6            509 FLTSLQYLGLWNCPKLASIPEEGLPPSLEELWIYGCPVLKERCQPGKGRY    558
                      ||||||.|.|..||||||||||.||||||||.||.|||||||||||||||
XP_009379454.1   1298 FLTSLQSLQLSKCPKLASIPEESLPPSLEELSIYRCPVLKERCQPGKGRY   1347

ORF_A6            559 WHKISHIPYIRIDDKEYSEDENEQKRYINGIAYFLSFHGHVFVWFFIKNG    608
                      ||||||||.|.||.:..
XP_009379454.1   1348 WHKISHIPCILIDCQPI---------------------------------   1364

ORF_A6            609 FAAFINHRQSFDNVVILSAPIEEHAGEVKFEAMVSSLPKEIVCDILLRLP    658

XP_009379454.1   1365 --------------------------------------------------   1364

ORF_A6            659 PKALIRCTSVSKPWNSMIKNPSVVHTHLRHTIDFNQFGTHHLLLRDNPVE    708

XP_009379454.1   1365 --------------------------------------------------   1364

ORF_A6            709 QNYYLHLDNHAFDEYCKLEYPSVSKRNRFPRVVYSLARGLWSSPRSFDPI    758

XP_009379454.1   1365 --------------------------------------------------   1364

ORF_A6            759 WCSLNDGRYQNFILAIDVDSDGNSIAMFTTTRGRNCPEDFLDIWVMKEYG    808

XP_009379454.1   1365 --------------------------------------------------   1364

ORF_A6            809 IEDSWAKLITLKSTGSGKKGALQALMF    835

XP_009379454.1   1365 ---------------------------   1364
```

Purple：RX-CC_like
Yellow：NB-ARC
Blue：　Leucine-rich repeat domain superfamily
Red：　F-box domain

Fig. S2 Pairwise alignment of deduced amino acid sequences between A6, a predicted ORF within *Alt* region, and XP_009379454.1.1, the gene most similar to A6, as revealed by a database search. Alignment was performed using Needle.