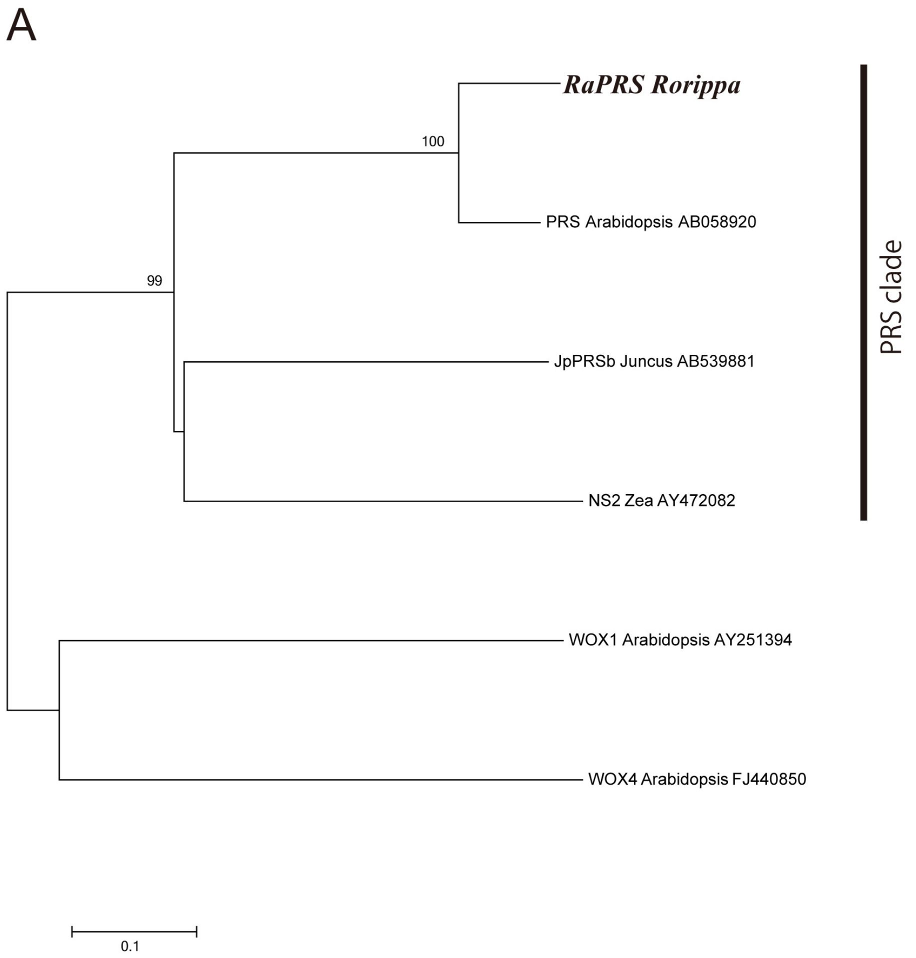
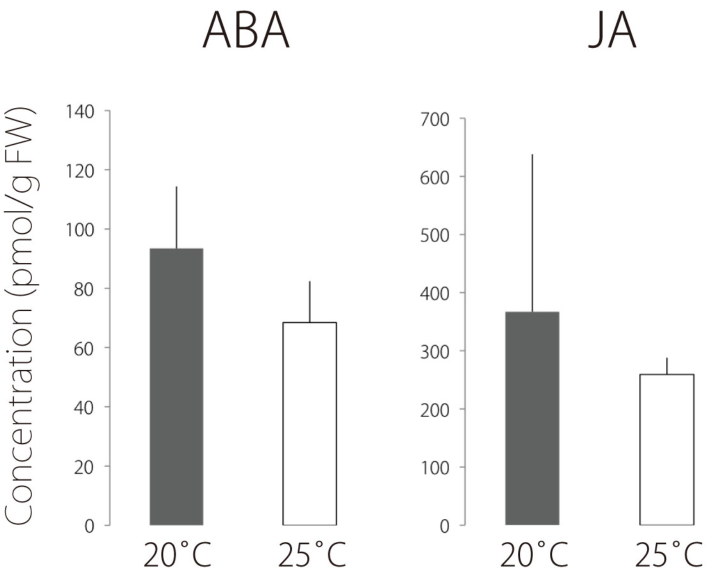
**Supplemental Figure 1.** Gross morphology of leaves at 15˚C.
Leaves from an in vitro culture plant grown at 15˚C. Bar = 2 cm.



B

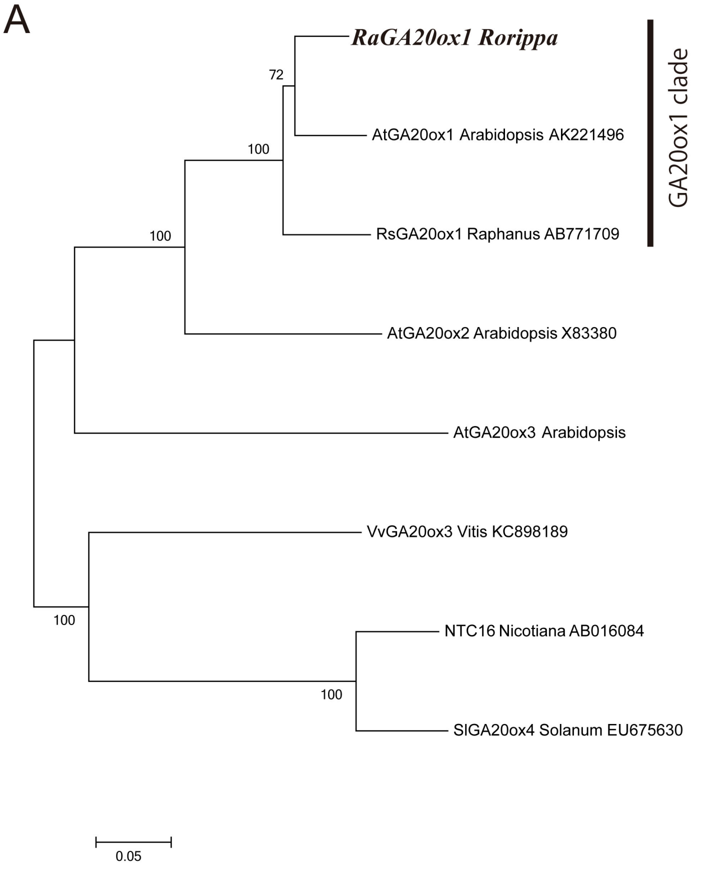
```
RaPRS_Rorippa       ------TRWCPTPEQLMILEEMYRSGIRTPNAVQIQQITAHLAFYGRIEGKNVFYWFQNH 54
PRS_Arabidopsis     MSPVASTRWCPTPEQLMILEEMYRSGIRTPNAVQIQQITAHLAFYGRIEGKNVFYWFQNH 60
JpPRSb_Juncus       MPPTRTTRWCPTPEQLMILEEMYRNGLQTPNAPQIQQITAHLSCYGRIEGKNVFYWFQNH 60
NS2_Zea             MPQTPSTRWCPTPEQLMILEEMYRSGVRTPNAAEIQQITAHLAYYGRIEGKNVFYWFQNH 60
                          ******************.*::**** :********: ****************

                    KARDRQKLRKKLAKQLHQQQHQFQHQFQQLK----PKPLS-MMSQPIN---NNITDHHNP 106
                    KARDRQKLRKKLAKQLHQQQHQLQLQLQQIK----PKPISSMISQPVN---KNIIDHHNP 113
                    KARDRQKMRRKL--------HSMSVLYAQSA----AHYHNSVHHQFVD---QRFVSPPP- 104
                    KARERQRLRRRLCARHQQQYAQQQQQATAAAPASSPNSSATLLAPPAAGGSSAPCVHPAV 120
                    ***:**::*::*         . .           .:    :         .

                    YHHHHH--------PYDHMSFSCCSHPSPMCLPNQ-----VCNIPNSLS--VFC------ 145
                    YHHHHHNHHHNHHRPYDHMSFDCCSHPSPMCLPHQGTG--VGEAPSKVMNEYYCTKSGAE 171
                    --------------PFGHP-FMETQKTSPLPFYHQGAP--IQEAAIVHDPASNYFIGTER 147
                    MQLHHHHHPYATSFSMPHLGYLGQQAATVTPVLNPAAAGMVDLAGAGAGNRATGAGGAYG 180
                                  .  *  :   . .:   . :      :

                    ------------------------------------------------------------
                    EILMQKSITGPNSSYGRDWMMMMDMGPRPSYPSSSSS---------PISCCNMMMSSPKI 222
                    NVHMAH----------FDWTMMMGMHEAAG----------------VSSCCR-------- 173
                    GGAGLYNSCSSNQLEVWDATEPMDHCNASCGAASGSSDEGGAAHLQLPACCRR------- 233

                    --------------------------------
                    PLKTLELFPISSINSKQDSTKL---------- 244
                    PLKTLDLFPTKVSQGVDD-------------- 191
                    PLKTLDLFPTKSTGLKDECSSSKSSSCSTSTN 265
```

**Supplemental Figure 2.** A phylogenetic tree and alignments of *PRS* orthologs. (A) A phylogenetic tree of *PRS* orthologs resulting from Neighbor-joining method by MEGA. (B) Identical or similar amino acid residues were indicated by asterisks and colons, respectively. The bootstrap values are indicated on branches (only those more than 50% are indicated on the tree).



**Supplemental Figure 3.** Plant hormone profiles.

Accumulation levels of ABA and JA in leaf primordia at 20˚C and 25˚C.



B

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RaGA20ox1_Rorippa        MAVSCVTTSLEEEVKPRLDFGNIQTPLIFNPSILNLQPNIPNQFIWPDDE 50
ATGA20ox1_Arabidopsis    MAVSFVTTSPEEEDKPKLGLGNIQTPLIFNPSMLNLQANIPNQFIWPDDE 50
RsGA20ox1_Raphanus       MAVSCVRTSSEQEHTPKLGLGNSQSPLIFNPSMLNLQPNIPDQFIWPDHE 50
                         **** * ** *:* .*:*.:** *:*******:****.***:******.*

                         KPSIDVPELEVPLIDLKKFMSDPVSPSSSTLEASRLISEACTKHGFFLVV 100
                         KPSINVLELDVPLIDLQNLLSDP----SSTLDASRLISEACKKHGFFLVV 96
                         KPCTEAPELEVPLIDLKDFLSNSSSP-SATLEASRLISEACSKHGFFLVV 99
                         **. :. **:******:.::*:.    *:**:*********.********

                         NHGINEALISDAHEYMGRFFDMPLSVKQRVLRKPGESCGYASSFTGRFST 150
                         NHGISEELISDAHEYTSRFFDMPLSEKQRVLRKSGESVGYASSFTGRFST 146
                         NHGISEELISDAHEYMARFFDMPLSEKQRVQRKPGESCGYASSFTGRFST 149
                         ****.* ******** .******** **** **.*** ************

                         KLPWKETLSFRFSDEKSLSKTVEDYFCDALGHGFEPFGKVYQEYCEAMSS 200
                         KLPWKETLSFRFCDDMSRSKSVQDYFCDALGHGFQPFGKVYQEYCEAMSS 196
                         KLPWKETLSFRFCDDKNSPNTVQDYFCHALGHEFEPLGKVYQEYCEAMSF 199
                         ************.*: . .::*:****.**** *:*:************

                         LSLKIMELLGLSLGVNRDYFREFFEENDSIMRLNYYPPCQKPDLTLGTGP 250
                         LSLKIMELLGLSLGVKRDYFREFFGENDSIMRLNYYPPCIKPDLTLGTGP 246
                         LSLKIMELLGLSLGVSRDYFRAFFEENDSIMRLNYYPPCQKPDLTLGTGP 249
                         ***************.***** ** ************** **********

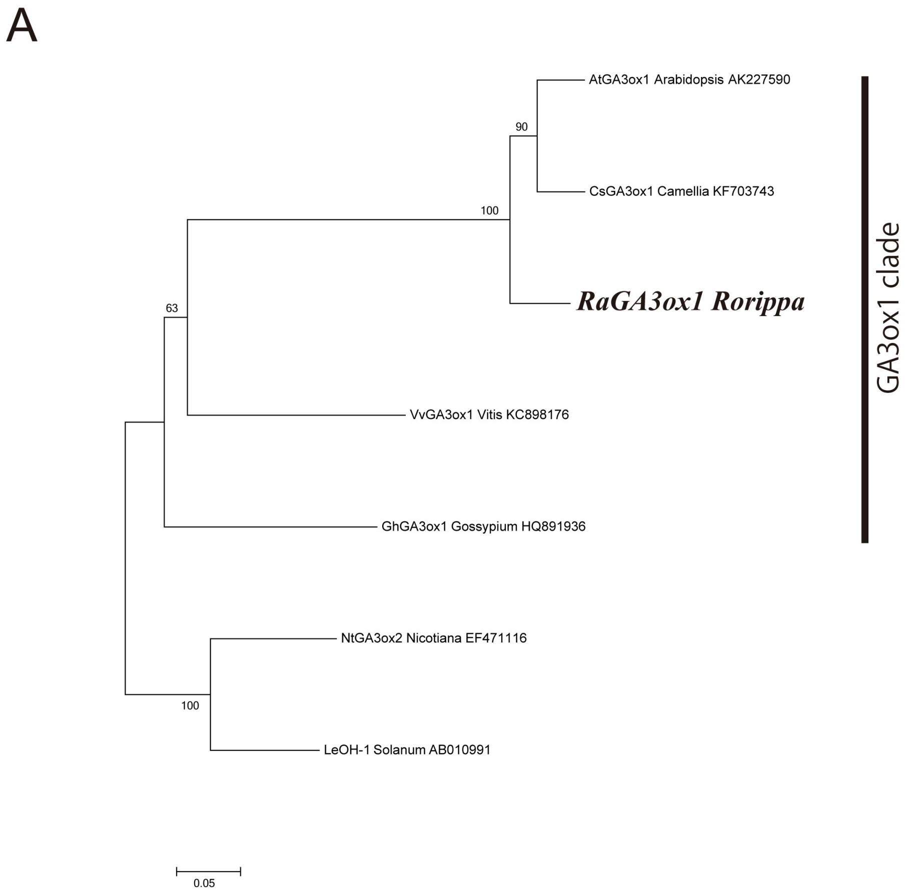
                         HCDPTSLTILHQDHVNGLQVFVENQWRSIRPNPKAFVVNIGDTFMALSNN 300
                         HCDPTSLTILHQDHVNGLQVFVENQWRSIRPNPKAFVVNIGDTFMALSND 296
                         HCDPTSLTILHQDHVNGLQVLVENQWRSISPNPKAFVVNIGDTFMALSNN 299
                         ********************:******** *******************:

                         RYKSCLHRAVVNCESERKSLAFFLCPRKDRVVKPPRELLDSITPRRYPDF 350
                         RYKSCLHRAVVNSESERKSLAFFLCPKKDRVVTPPRELLDSITSRRYPDF 346
                         RYKSCLHRAVVNSRSERKSLAFFLCPKKDRVVKPPRELLNSITPRRYPDF 349
                         ************..************:*****.******:***.******

                         TWSLFLEFTQKHYRADMNTLQAFSDWLTNKPI 382
                         TWSMFLEFTQKHYRADMNTLQAFSDWLT-KPI 377
                         TWSMLLEFTQKHYRADMNTLQAFSDWLTDKPI 381
                         ***::************************ ***
```

**Supplemental Figure 4.** A phylogenetic tree and alignments of *GA20ox1* orthologs.

(A) A phylogenetic tree of *GA20ox1* orthologs resulting from Neighbor-joining method by MEGA. (B) Identical or similar amino acid residues were indicated by asterisks and colons, respectively. The bootstrap values are indicated on branches (only those more than 50% are indicated on the tree).



B

```
AtGA3ox1_Arabidopsis       MPAMLTDVFRGHPIHLPHSHIPDFTSLRELPDSYKWTPKDDLLFSAAPSPPATGENIPLI 60
CsGA3ox1_Camellia          MPAMLTDVFRGHPIHLPHSHQPDFTSLRELPDSYSWTPKDDILFAAAPSPPTAVETIPLI 60
RaGA3ox1_Rorippa           MPTMLTDVFRGHPIHLPHSHQPDFTALRELPDSYTWTPKDDILFPAAPSPPAASETIPLI 60
                           **:***************** ****:********.******:**.******:: *.****

                           DLDHPDATNQIGHACRTWGAFQISNHGVPLGLLQDIEFLTGSLFGLPVQRKLKSARSETG 120
                           DLDHPDAANQIGHACRTWGAFQIANHGVPLSLLQDVEFLTESLFGLPVKRKLKAARSETG 120
                           DLNQPDAANQIGRACRTWGAFQIANHGVPLGLLEDIEFLTSSLFRLPVQRKLKAARSDTG 120
                           **::***:****:**********:******.**:*:**** *** ***:****:***:**

                           VSGYGVARIASFFNKQMWSEGFTITGSPLNDFRKLWPQHHLNYCDIVEEYEEHMKKLASK 180
                           VSGYGVARIASFFNKQMWSEGFTITGSPLNDFRKLWPQDHLNYCDIVEEYEERMKKLASK 180
                           VSGYGVARIASFFNKQMWSEGFTITGSPLNDFRKLWPQLHLNYCDIVEEYEEQMRKLASK 180
                           ************************************** *************:*:*****

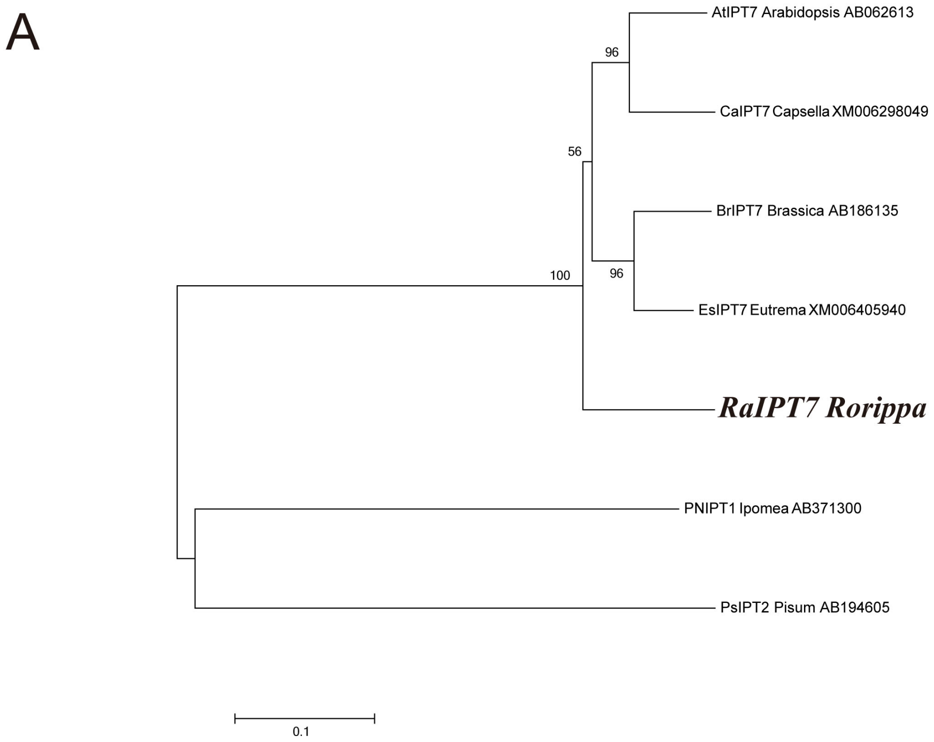
                           LMWLALNSLGVSEEDIEWASLSSDLNWAQAALQLNHYPVCPEPDRAMGLAAHTDSTLLTI 240
                           LMWLALNSLGVTEEDVEWARLTSDLSWAQAALQLNHYPVCPEPDRAMGLAAHTDSTLLTI 240
                           LLWLVLNSLGVSEEDVKWARLNSDSNWAQAALQLNHYPVCPQPDQAMGLAAHTDSTLLTI 240
                           *:**.******:***::** *.** .***************:**:***************

                           LYQNNTAGLQVFRDDLGWVTVPPFPGSLVVNVGDLFHILSNGLFKSVLHRARVNQTRARL 300
                           LYQNNTAGLQVFRDDLGWITVPPVPGSLVVNVGDLFHILSNGLFKSVLHRARVNQTRARL 300
                           LYQNNTAGLQVFRDDLGWVTVPPVPGSLVVNVGDLLHILSNGLFKSVLHRARVNQTRSRF 300
                           ******************:****.***********:*********************:*:

                           SVAFLWGPQSDIKISPVPKLVSPVESPLYQSVTWKEYLRTKATHFNKALSMIRNHREE 358
                           SVAFLWGPQSDIKISPVPKLVSPLESPLYRSVTWREYLQTKATHFNKALSMIRNHREE 358
                           SVAFLWGPQSDIQISPIPKLVGPFESPLYQSVTWTHYLQIKATHFNKALSMIE--RKD 356
                           ************:***:****.*.*****:**** .**: ************.  *::
```

**Supplemental Figure 5.** A phylogenetic tree and alignments of *GA3ox1* orthologs.

(A) A phylogenetic tree of *GA3ox1* orthologs resulting from Neighbor-joining method by MEGA. (B) Identical or similar amino acid residues were indicated by asterisks and colons, respectively. The bootstrap values are indicated on branches (only those more than 50% are indicated on the tree).



B

```
AtIPT7_Arabidopsis      MKFSISSLKQVQPILCFKNKLSKVNVNSFLHPKEKVIFVMGATGSGKSRLAIDLATRFQG 60
CaIPT7_Capsella         MKFSISALRQVQPILSFKNKLSMVNVNSFLNPKEKVVFVMGATGSGKSRLAIDLATRFQS 60
BrIPT7_Brassica         MKFSISAMKQVQPILSFKNKLSMVNVNSFLRPQEKVVFVMGATGSGKSRLAIDLATRFQT 60
RaIPT7_Rorippa          ------------------------------------------------------------

                        EIINSDKIQLYKGLDVLTNKVTPKECRGVPHHLLGVFDSEAGNLTATQYSRLASQAISKL 120
                        EVINSDKIQLYKGLDVLTNKVTPQECRGVPHHLLGVFDSEFGNLTATQYSNLASQAITKL 120
                        EIINSDKIQVYKGLDVLTNKVTPQECRGVPHHLLGVFDSEAGNLTATDFCRLASQEISTL 120
                        ------------------------------------------------------------

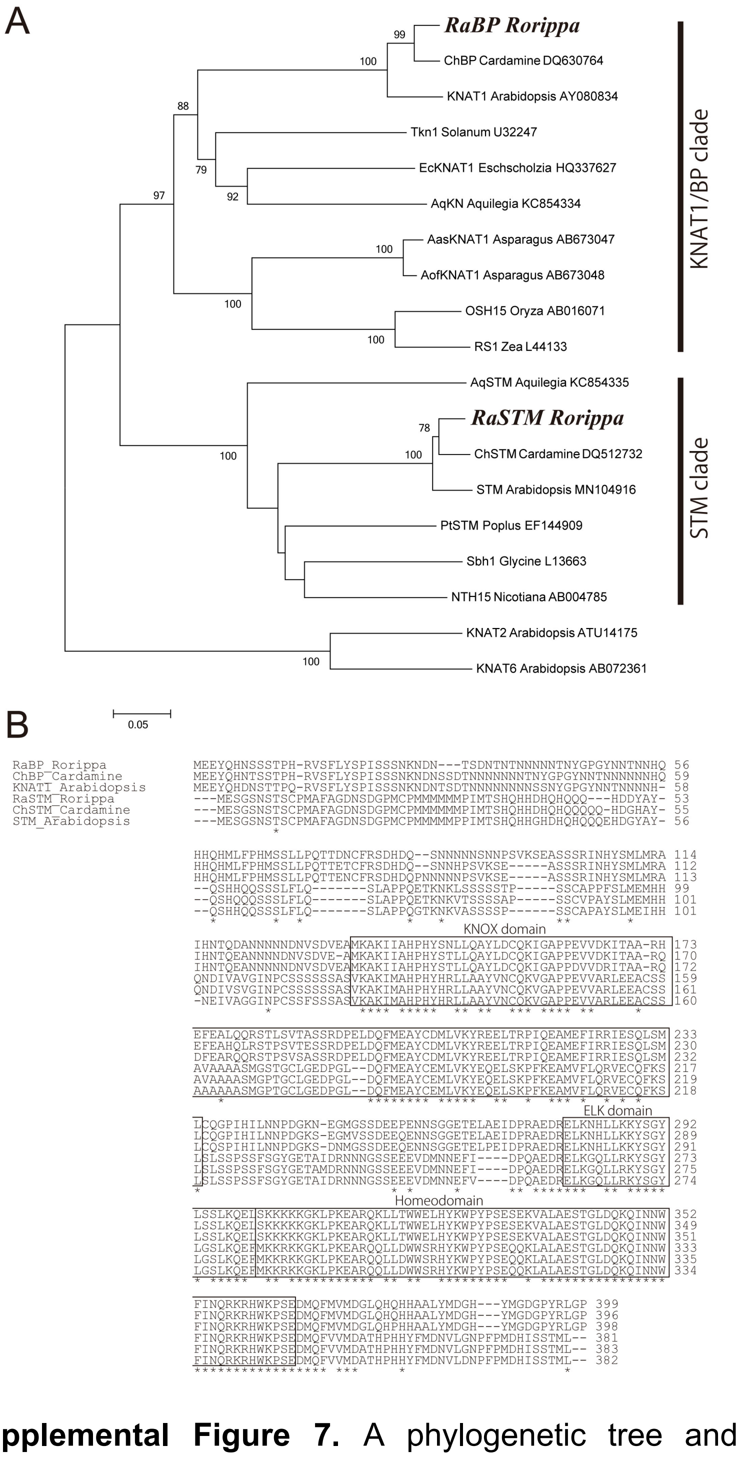
                        SANNKLPIVAGGSNSYIEALVNHSSGFLLNNYDCCFIWVDVSLPVLNSFVSKRVDRMMEA 180
                        SANHKLPIVAGGSNSYIEALANHSAGFLLNNYECCFIWVDVSLPVLNSFVSKRVDRMMEA 180
                        SANNKLPIVAGGSNSYIEALANHSSGFLLNKYQCCFIWVDVSLPVLNSFVSKRVDRMMEA 180
                        -------------------------------------WVDVSLPVLNSFVSKRVDRMMEA 23
                                                             ***********************

                        GLLEEVREVFNPKANYSVGIRRAIGVPELHEYLRNESLVDRATKSKMLDVAVKNIKKNTE 240
                        GLLEEVREVFNPKADYSVGIRRAIGVPELHEYLRYESLVDSATQRMMLDVAVKNIKKNTE 240
                        GLLEEVREVHDPKADYSVGIRRAIGVPELHEYLCYESLVDRGTQRKMLDAAVKKIKENTE 240
                        GLLKEVREMFNPIADYSVGLRRAIGVPELHEYLQYESLVDTATQKKMLHLAVEKIKKNTE 83
                        ***:****:.:* *:****:*************  ***** .*:  **. **::**:***

                        ILACRQLKKIQRLHKKWKMSMHRVDATEVFLKRNVEEQDEAWENLVARPSERIVDKFYNN 300
                        ILACRQLKKIQRLNKKWKLSMHRVDATEVFLKRNVEEQDEAWESLVARPSERIVDKFYNN 300
                        ILACRQLLKIQRLSKKWKLSMHRVDATEVFLKRTEEEADEAWENLVARQTKRIVDKFCDN 300
                        ILACRQLQKIQQLNKKWNFSIHRLDATEVFLKSNEEEADEAWEKLVARPSEIIVEKFYNN 143
                        ******* ***:* ***::*:**:******** . ** *****.**** :: **:** :*

                        N-NQLKND-DVEHCL----AASYGGGSGSRAHNMI 329
                        NSNQVKNDHDVEHCL----AASYGGGSGTRAHNMI 331
                        Q--VMKND-DVEHCLTSIGAASYGGGSGSRAHNMV 332
                        K---MKNNDVHEHCLTT--IGTYGGESGHRAHNLI 173
                        :   :**:   ****     .:*** ** ****::
```

**Supplemental Figure 6.** A phylogenetic tree and alignments of *IPT7* orthologs. (A) A phylogenetic tree of *IPT7* orthologs resulting from Neighbor-joining method by MEGA. (B) Identical or similar amino acid residues were indicated by asterisks and colons, respectively. The bootstrap values are indicated on branches (only those more than 50% are indicated on the tree).



```
RaBP_Rorippa        MEEYQHNSSSTPH-RVSFLYSPISSSNKNDN---TSDNTNTNNNNNTNYGPGYNNTNNHQ 56
ChBP_Cardamine      MEEYQHNTSSTPH-RVSFLYSPISSSNKNDNSSDTNNNNNNNTNYGPGYNNTNNNNNNHQ 59
KNAT1_Arabidopsis   MEEYQHDNSTTPQ-RVSFLYSPISSSNKNDNTSDTNNNNNNNNSSNYGPGYNNTNNNNH- 58
RaSTM_Rorippa       ---MESGSNSTSCPMAFAGDNSDGPMCPMMMMMMPIMTSHQHHDHQHQQQ---HDDYAY- 53
ChSTM_Cardamine     ---MESGSNSTSCPMAFAGDNSDGPMCPMMMMMMPIMTSHQHHDHQHQQQQQ-HDGHAY- 55
STM_Arabidopsis     ---MESGSNSTSCPMAFAGDNSDGPMCPMMMMMPPIMTSHQHHGHDHQHQQQEHDGYAY- 56
                              *

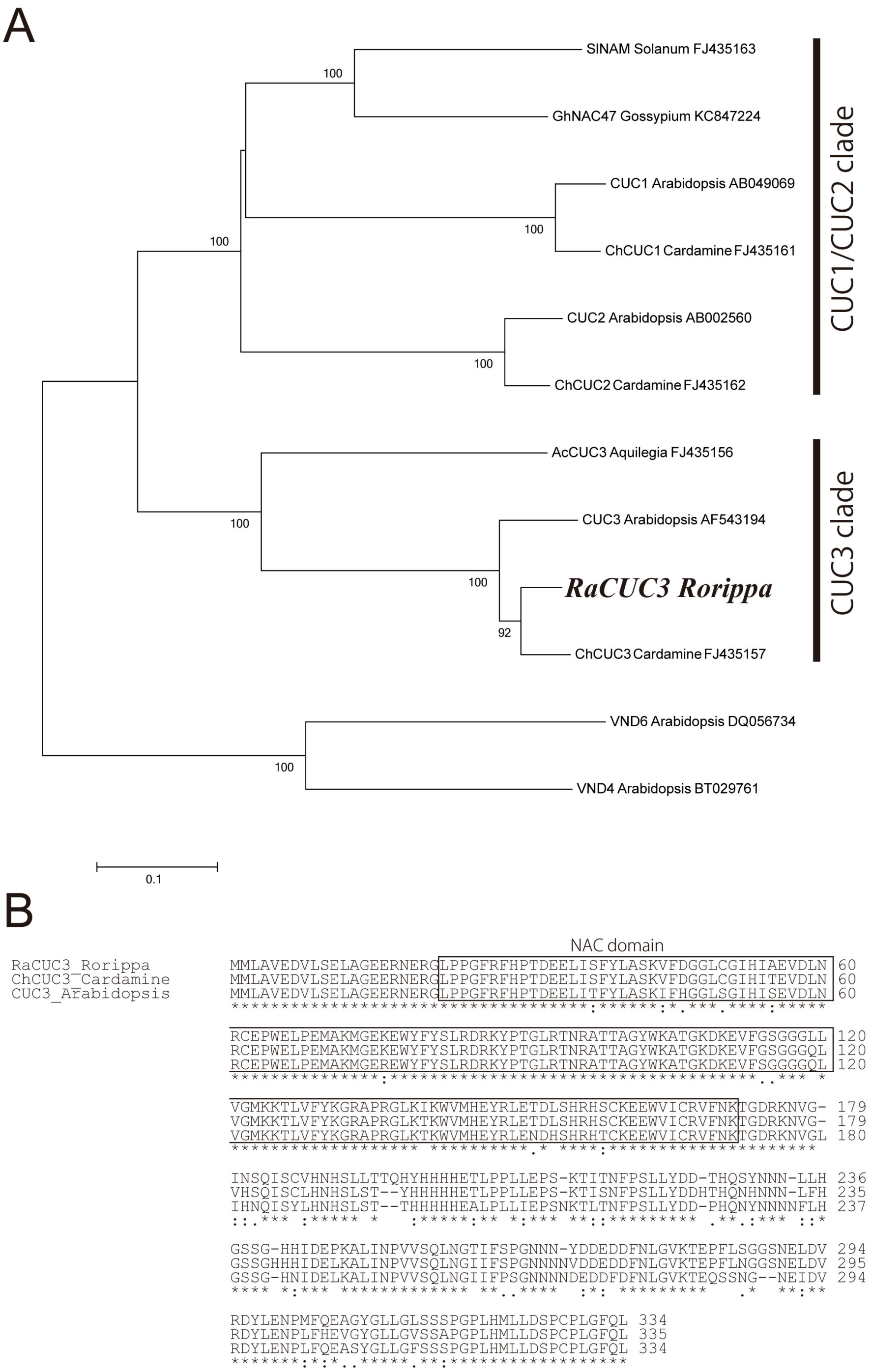
                    HHQHMLFPHMSSLLPQTTDNCFRSDHDQ--SNNNNNSNNPSVKSEASSSRINHYSMLMRA 114
                    HHQHMLFPHMSSLLPQTTETCFRSDHDQ--SNNHPSVKSE-----ASSSRINHYSMLMRA 112
                    HHQHMLFPHMSSLLPQTTENCFRSDHDQPNNNNNPSVKSE-----ASSSRINHYSMLMRA 113
                    --QSHHQQSSSLFLQ-------SLAPPQETKNKLSSSSSTP-----SSCAPPFSLMEMHH 99
                    --QSHQQQSSSLFLQ-------SLAPPQETKNKVTSSSSAP-----SSCVPAYSLMEMHH 101
                    --QSHHQQSSSLFLQ-------SLAPPQGTKNKVASSSSP------SSCAPAYSLMEIHH 101
                      *       *  *             *   *              **       *
                                                       KNOX domain
                    IHNTQDANNNNNDNVSDVEAMKAKIIAHPHYSNLLQAYLDCQKIGAPPEVVDKITAA-RH 173
                    IHNTQEANNNNNDNVSDVE-AMKAKIIAHPHYSTLLQAYLDCQKIGAPPEVVDKITAA-RQ 170
                    IHNTQEANNNNNDNVSDVEAMKAKIIAHPHYSTLLQAYLDCQKIGAPPDVVDRITAA-RQ 172
                    QNDIVAVGINPCSSSSSSASVKAKIMAHPHYHRLLAAYVNCQKVGAPPEVVARLEEACSS 159
                    QNDIVSVGINPCSSSSSSASVKAKIMAHPHYHRLLAAYVNCQKVGAPPEVVARLEEACSS 161
                    -NEIVAGGINPCSSFSSSASVKAKIMAHPHYHRLLAAYVNCQKVGAPPEVVARLEEACSS 160
                             *           **** *****  ** **  *** **** **     *

                    EFEALQQRSTLSVTASSRDPELDQFMEAYCDMLVKYREELTRPIQEAMEFIRRIESQLSM 233
                    EFEAHQLRSTPSVTESSRDPELDQFMEAYCDMLVKYREELTRPIQEAMEFIRRIESQLSM 230
                    DFEARQQRSTPSVSASSRDPELDQFMEAYCDMLVKYREELTRPIQEAMEFIRRIESQLSM 232
                    AVAAAASMGSTGCLGEDPGL--DQFMEAYCEMLVKYEQELSKPFKEAMVFLQRVECQFKS 217
                    AVAAAASMGPTGCLGEDPGL--DQFMEAYCEMLVKYEQELSKPFKEAMVFLQRVECQFKS 219
                    AAAAAASMGPTGCLGEDPGL--DQFMEAYCEMLVKYEQELSKPFKEAMVFLQRVECQFKS 218
                       *                  ******** *****  **  *  *** *  * * *
                                                                  ELK domain
                    LCQGPIHILNNPDGKN-EGMGSSDEEPENNSGGETELAEIDPRAEDRELKNHLLKKYSGY 292
                    LCQGPIHILNNPDGKS-EGMVSSDEEQENNSGGETELAEIDPRAEDRELKNHLLKKYSGY 289
                    LCQSPIHILNNPDGKS-DNMGSSDEEQENNSGGETELPEIDPRAEDRELKNHLLKKYSGY 291
                    LSLSSPSSFSGYGETAIDRNNNGSSEEEVDMNNEFI----DPQAEDRELKGQLLRKYSGY 273
                    LSLSSPSSFSGYGETAMDRNNNGSSEEEVDMNNEFI----DPQAEDRELKGQLLRKYSGY 275
                    LSLSSPSSFSGYGETAIDRNNNGSSEEEVDMNNEFV----DPQAEDRELKGQLLRKYSGY 274
                    *                        * *     *      ** *******  ** *****
                                            Homeodomain
                    LSSLKQELSKKKKKGKLPKEARQKLLTWWELHYKWPYPSESEKVALAESTGLDQKQINNW 352
                    LSSLKQELSKKKKKGKLPKEARQKLLTWWELHYKWPYPSESEKVALAESTGLDQKQINNW 349
                    LSSLKQELSKKKKKGKLPKEARQKLLTWWELHYKWPYPSESEKVALAESTGLDQKQINNW 351
                    LGSLKQEFMKKRKKGKLPKEARQQLLDWWSRHYKWPYPSEQQKLALAESTGLDQKQINNW 333
                    LGSLKQEFMKKRKKGKLPKEARQQLLDWWSRHYKWPYPSEQQKLALAESTGLDQKQINNW 335
                    LGSLKQEFMKKRKKGKLPKEARQQLLDWWSRHYKWPYPSEQQKLALAESTGLDQKQINNW 334
                    * *****  ** *********** ** **  *********  * ****************

                    FINQRKRHWKPSEDMQFMVMDGLQHQHHAALYMDGH---YMGDGPYRLGP 399
                    FINQRKRHWKPSEDMQFMVMDGLQHQHHAALYMDGH---YMGDGPYRLGP 396
                    FINQRKRHWKPSEDMQFMVMDGLQHPHHAALYMDGH---YMGDGPYRLGP 398
                    FINQRKRHWKPSEDMQFVVMDATHPHHYFMDNVLGNPFPMDHISSTML-- 381
                    FINQRKRHWKPSEDMQFVVMDATHPHHYFMDNVLGNPFPMDHISSTML-- 383
                    FINQRKRHWKPSEDMQFVVMDATHPHHYFMDNVLDNPFPMDHISSTML-- 382
                    ***************** ***     *                    *
```

**Supplemental Figure 7.** A phylogenetic tree and alignments of *KNOX1* orthologs.

(A) A phylogenetic tree of *KNOX1* orthologs resulting from Neighbor-joining method by MEGA. (B) Identical or similar amino acid residues were indicated by asterisks and colons, respectively. The bootstrap values are indicated on branches (only those more than 50% are indicated on the tree).



```
RaCUC3_Rorippa          MMLAVEDVLSELAGEERNERGLPPGFRFHPTDEELISFYLASKVFDGGLCGIHIAEVDLN 60
ChCUC3_Cardamine        MMLAVEDVLSELAGEERNERGLPPGFRFHPTDEELISFYLASKVFDGGLCGIHITEVDLN 60
CUC3_Arabidopsis        MMLAVEDVLSELAGEERNERGLPPGFRFHPTDEELITFYLASKIFHGGLSGIHISEVDLN 60
                        ************************************:******:*.***.****:*****

                        RCEPWELPEMAKMGEKEWYFYSLRDRKYPTGLRTNRATTAGYWKATGKDKEVFGSGGGLL 120
                        RCEPWELPEMAKMGEKEWYFYSLRDRKYPTGLRTNRATTAGYWKATGKDKEVFGSGGGQL 120
                        RCEPWELPEMAKMGEREWYFYSLRDRKYPTGLRTNRATTAGYWKATGKDKEVFSGGGGQL 120
                        ***************:*************************************..*** *

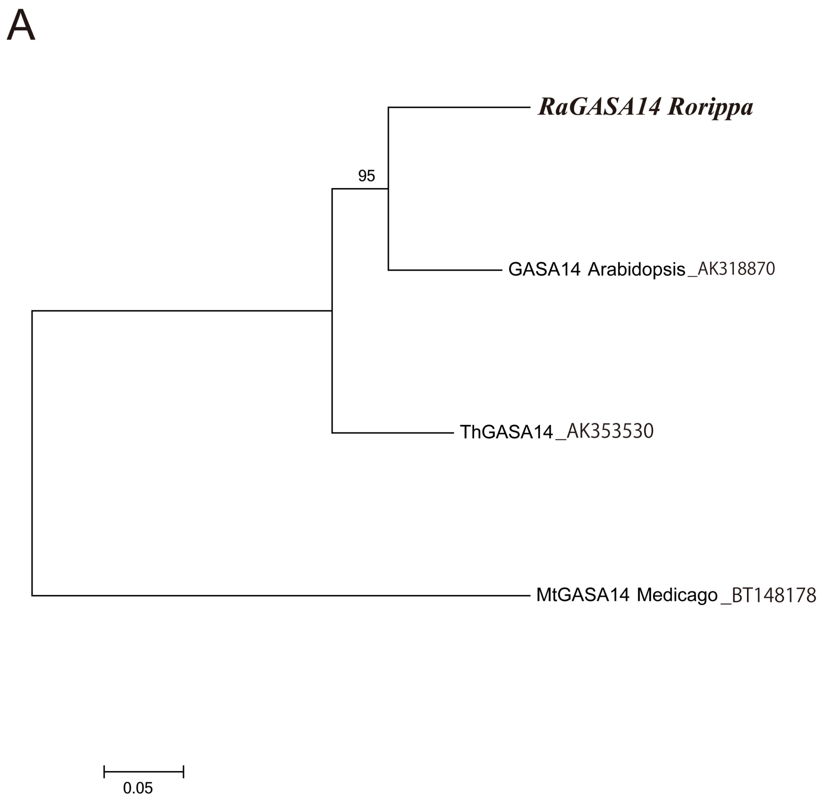
                        VGMKKTLVFYKGRAPRGLKIKWVMHEYRLETDLSHRHSCKEEWVICRVFNKTGDRKNVG- 179
                        VGMKKTLVFYKGRAPRGLKTKWVMHEYRLETDLSHRHSCKEEWVICRVFNKTGDRKNVG- 179
                        VGMKKTLVFYKGRAPRGLKTKWVMHEYRLENDHSHRHTCKEEWVICRVFNKTGDRKNVGL 180
                        ******************* **********.* ****:*********************

                        INSQISCVHNHSLLTTQHYHHHHETLPPLLEPS-KTITNFPSLLYDD-THQSYNNN-LLH 236
                        VHSQISCLHNHSLST--YHHHHHETLPPLLEPS-KTISNFPSLLYDDHTHQNHNNN-LFH 235
                        IHNQISYLHNHSLST--THHHHHEALPLLIEPSNKTLTNFPSLLYDD-PHQNYNNNNFLH 237
                        ::.*** :***** *   :*****:** *:*** **::********* .**.:*** ::*

                        GSSG-HHIDEPKALINPVVSQLNGTIFSPGNNN-YDDEDDFNLGVKTEPFLSGGSNELDV 294
                        GSSGHHHIDELKALINPVVSQLNGIIFSPGNNNNVDDEDDFNLGVKTEPFLNGGSNELDV 295
                        GSSG-HNIDELKALINPVVSQLNGIIFPSGNNNNDEDDFDFNLGVKTEQSSNG--NEIDV 294
                        **** *:*** ************* **..****  :*: *********   .*  **:**

                        RDYLENPMFQEAGYGLLGLSSSPGPLHMLLDSPCPLGFQL 334
                        RDYLENPLFHEVGYGLLGVSSAPGPLHMLLDSPCPLGFQL 335
                        RDYLENPLFQEASYGLLGFSSSPGPLHMLLDSPCPLGFQL 334
                        *******:*:*..*****.**:******************
```

**Supplemental Figure 8.** A phylogenetic tree and alignments of *CUC* orthologs. (A) A phylogenetic tree of *CUC* orthologs resulting from Neighbor-joining method by MEGA. (B) Identical or similar amino acid residues were indicated by asterisks and colons, respectively. The bootstrap values are indicated on branches (only those more than 50% are indicated on the tree).



B

```
RaGASA14_Rorippa          MALSLLSVFIFLH----VFTNVIFAASNEESKALGSLPTPTPQNPQ---- 42
GASA14_Arabidopsis        MALSLLSVFIFFH----VFTNVVFAASNEESNALVSLPTPTLPSPSPATK 46
ThGASA14_Thellungiella    MAFSLLSVFIFLQ----VFTNVVFAASDEESKTLVSLPTPP---PT---- 39
MtGASA14_Medicago         MLQKMVSKSIFLLGIFLVLATKVYSY-DEDLKIVVNYVNPTAP-PSPIVT 48
                          *  .::*  **:     *::. :::  :*: : : .  .*.   *

                          -PSPAIKQPTP-LYKPPTLPTTP-----IKPPTTTPPIQP---------P 76
                          PPSPALKPPTP-SYKPPTLPTTP-----IKPPTTKPPVKP---------P 81
                          --SPAIKPPSP-SYKPPTLPTIP-----IKPPTTIPPVKPPTTLPPVKPP 81
                          PPSPVKAPPTPPLVKSPPIVKAPSPPLVKTPPYQSPPVKP-------TPP 91
                            **.   *:*   *.*.: . *      .**   **::*         *

                          ITPVTPAKPPVKSYPTPLVKPPTTPTVQPPTYKPPTPPFKPPTTSPVKPP 126
                          TIPVTPVKPPVS-----------------------TPPIKLP---PVQPP 105
                          TSPVTPTKPPVKSYP--------------------IPPVKPPTAPLVKPP 111
                          IVKSPPSPPLVKS----------------------PPYQSPPIVKAPSPP 119
                              .*  * *.                        *  . *     .**

                          TYKPPTPSIKPPS--------VQPPTYKPPTPPVKPPTISPVQPPTYKPP 168
                          TYKPPTPTVKPPS--------VQPPTYKPPTPTVKPPTTSPVKPPT---- 143
                          TYKPPTPTVKPPTTPLIKPPPVQPPTYKPPTPLVKPPTTTPVTTPP--PV 159
                          LVKPTPPIVKSPP---------SPPLVKTPPYQSPPIVKAPPTPPP-IVK 159
                            **..* :*.*.         .**  *.*.    * . :*  .*.

                          TPPVKPPPVQPPTYKPPTPPLKPPTTPPVKPPTPPPARTGIDCVSLCGTR 218
                          TPPVQSPPVQP-------------PTAPPVKPPTPPPVRTRIDCVPLCGTR 181
                          KPPVNPTPTHP-----------VKPPVAPAKPPTPP----RIDCVSLCGTR 195
                          TPPYQSPPIVK-------------PPVAPSPPPTPI-VKSWKDCIPLCGYR 196
                          .** :..*               *...*  ****       **:.*** *

                          CSKHSRINRCMRACVTCCYRCKCVPPGTYGNKEKCGSCYANMKTYGGKPK 268
                          CGQHSRKNVCMRACVTCCYRCKCVPPGTYGNKEKCGSCYANMKTRGGKSK 231
                          CGQHSRKNICMRACVTCCYRCKCVPPGTYGNKEKCGSCYANMKTRGGKPK 245
                          CQKHSRQNTCIRACMTCCDRCKCVPPGTYGNREKCGKCYTDMVTHGNRPK 246
                          * :*** * *:***:*** ************:****.**::* * *.:.*

                          CP 270
                          CP 233
                          CP 247
                          CP 248
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**Supplemental Figure 9.** A phylogenetic tree and alignments of *GASA14* orthologs.

(A) A phylogenetic tree of *GASA14* orthologs resulting from Neighbor-joining method by MEGA. (B) Identical or similar amino acid residues were indicated by asterisks and colons, respectively. The bootstrap values are indicated on branches (only those more than 50% are indicated on the tree).

**Supplemental Table1.** Functional categorization by GO annotation.

| up-regulated in dissected leaf condtion (630 genes) | | | | up-regulated in simple leaf condtion (471 genes) | | | |
|---|---|---|---|---|---|---|---|
| Keyword Category | Functional Category | Annotation Count | Gene Count | Keyword Category | Functional Category | Annotation Count | Gene Count |
| GO Cellular Component | other intracellular components | 1048 | 415 | GO Cellular Component | other cytoplasmic components | 206 | 160 |
| GO Cellular Component | other cytoplasmic components | 938 | 421 | GO Cellular Component | other intracellular components | 160 | 104 |
| GO Cellular Component | chloroplast | 566 | 279 | GO Cellular Component | nucleus | 141 | 135 |
| GO Cellular Component | ribosome | 374 | 151 | GO Cellular Component | chloroplast | 107 | 77 |
| GO Cellular Component | plastid | 364 | 177 | GO Cellular Component | other membranes | 83 | 62 |
| GO Cellular Component | cytosol | 360 | 231 | GO Cellular Component | extracellular | 67 | 61 |
| GO Cellular Component | other membranes | 278 | 198 | GO Cellular Component | plasma membrane | 65 | 64 |
| GO Cellular Component | nucleus | 261 | 202 | GO Cellular Component | plastid | 50 | 36 |
| GO Cellular Component | mitochondria | 127 | 104 | GO Cellular Component | mitochondria | 40 | 36 |
| GO Cellular Component | plasma membrane | 112 | 110 | GO Cellular Component | cytosol | 37 | 37 |
| GO Cellular Component | other cellular components | 105 | 104 | GO Cellular Component | other cellular components | 28 | 27 |
| GO Cellular Component | extracellular | 58 | 55 | GO Cellular Component | Golgi apparatus | 22 | 22 |
| GO Cellular Component | cell wall | 50 | 47 | GO Cellular Component | cell wall | 22 | 19 |
| GO Cellular Component | Golgi apparatus | 14 | 12 | GO Cellular Component | ribosome | 21 | 17 |
| GO Cellular Component | ER | 9 | 9 | GO Cellular Component | ER | 14 | 14 |
| GO Cellular Component | unknown cellular components | 4 | 4 | GO Cellular Component | unknown cellular components | 12 | 12 |
| GO Molecular Function | other binding | 242 | 194 | GO Molecular Function | other enzyme activity | 196 | 107 |
| GO Molecular Function | nucleotide binding | 215 | 165 | GO Molecular Function | other binding | 165 | 118 |
| GO Molecular Function | other enzyme activity | 213 | 117 | GO Molecular Function | transferase activity | 154 | 70 |
| GO Molecular Function | hydrolase activity | 201 | 108 | GO Molecular Function | hydrolase activity | 108 | 65 |
| GO Molecular Function | structural molecule activity | 149 | 147 | GO Molecular Function | unknown molecular functions | 83 | 83 |
| GO Molecular Function | DNA or RNA binding | 141 | 114 | GO Molecular Function | protein binding | 75 | 66 |
| GO Molecular Function | protein binding | 95 | 84 | GO Molecular Function | nucleotide binding | 61 | 51 |
| GO Molecular Function | transferase activity | 89 | 56 | GO Molecular Function | transporter activity | 55 | 28 |
| GO Molecular Function | unknown molecular functions | 54 | 54 | GO Molecular Function | kinase activity | 51 | 20 |
| GO Molecular Function | nucleic acid binding | 44 | 44 | GO Molecular Function | DNA or RNA binding | 44 | 38 |
| GO Molecular Function | transporter activity | 43 | 27 | GO Molecular Function | transcription factor activity | 39 | 39 |
| GO Molecular Function | kinase activity | 17 | 10 | GO Molecular Function | other molecular functions | 28 | 24 |
| GO Molecular Function | other molecular functions | 12 | 11 | GO Molecular Function | structural molecule activity | 12 | 11 |
| GO Molecular Function | transcription factor activity | 8 | 8 | GO Molecular Function | nucleic acid binding | 6 | 6 |
| GO Molecular Function | receptor binding or activity | 1 | 1 | GO Molecular Function | receptor binding or activity | 0 | 0 |
| GO Biological Process | other cellular processes | 1844 | 518 | GO Biological Process | other cellular processes | 926 | 304 |
| GO Biological Process | other metabolic processes | 1494 | 500 | GO Biological Process | other metabolic processes | 725 | 298 |
| GO Biological Process | protein metabolism | 411 | 290 | GO Biological Process | response to stress | 342 | 134 |
| GO Biological Process | cell organization and biogenesis | 370 | 186 | GO Biological Process | response to abiotic or biotic stimulus | 285 | 119 |
| GO Biological Process | response to abiotic or biotic stimulus | 328 | 152 | GO Biological Process | other biological processes | 213 | 116 |
| GO Biological Process | developmental processes | 318 | 157 | GO Biological Process | transport | 158 | 77 |
| GO Biological Process | response to stress | 299 | 150 | GO Biological Process | developmental processes | 119 | 69 |
| GO Biological Process | other biological processes | 269 | 189 | GO Biological Process | signal transduction | 107 | 50 |
| GO Biological Process | transport | 183 | 123 | GO Biological Process | protein metabolism | 98 | 81 |
| GO Biological Process | transcription,DNA-dependent | 89 | 59 | GO Biological Process | cell organization and biogenesis | 78 | 50 |
| GO Biological Process | electron transport or energy pathways | 88 | 70 | GO Biological Process | unknown biological processes | 69 | 69 |
| GO Biological Process | unknown biological processes | 67 | 67 | GO Biological Process | transcription,DNA-dependent | 58 | 46 |
| GO Biological Process | DNA or RNA metabolism | 48 | 25 | GO Biological Process | DNA or RNA metabolism | 21 | 8 |
| GO Biological Process | signal transduction | 35 | 21 | GO Biological Process | electron transport or energy pathways | 18 | 16 |

**Supplemental Table 2.** List of oligonucleotide primers used in this study.

| Number | Name | Sequence (5'-3') |
|---|---|---|
| 1 | RaGA20ox1_F | ATTACTTCTGCGATGCGTTG |
| 2 | RaGA20ox1_R | GTGATTTCCTCTCGCTCTCG |
| 3 | RaGA20ox1_5RACE1 | CATGTCCCAACGCATCGCAGAAGTA |
| 4 | RaGA20ox1_3RACE | AAACCCGGTGAGAGTTGTGGCTACG |
| 5 | RaGA20ox1_RT_F | CGAGACTAATCTCTGAGGCCTGTAC |
| 6 | RaGA20ox1_RT_R | TGATATAAGCGCCTCGTTGATG |
| 7 | RaGA3ox1_F1 | CGTACCTTTGGGACTTCTCG |
| 8 | RaGA3ox1_R1 | TGACCCAACCAAGATCATCA |
| 9 | RaGA3ox1_5RACE | AGGGGAACCGGTGATGGTGAAACCT |
| 10 | RaGA3ox1_3RACE | TTTCACCATCACCGGTTCCCCTCTC |
| 11 | RaGA3ox1_RT_F | AATAAGCAAATGTGGTCTGAAGGTT |
| 12 | RaGA3ox1_RT_R | GGGCCAAAGTTTACGGAAGTC |
| 13 | RaSTM_F1 | ATGGAGAGTGGTTCCAACAG |
| 14 | RaSTM1_R1 | AAGCATGGTTGAGGAGATGT |
| 15 | RaSTM_RT_F | TGGTGGAGCCGACACTACAA |
| 16 | RaSTM_RT_R | GCCAGTGCCAGCTTTTGC |
| 17 | RaBP_F1 | TCCTGGTTACAATAATACTAA |
| 18 | RaBP_R1 | TCAATACGACGTATAAACTC |
| 19 | RaBP_5RACE1 | CGGAGGGGTTGTTGTTGTTGTTGG |
| 20 | RaBP_5RACE2 | GAGGAAGAAGAGAACTCATATGTG |
| 21 | RaBP_3RACE1 | CACATATGAGTTCTCTTCTTCCTC |
| 22 | RaBP_3RACE2 | CCAACAACAACAACAACCCCTCCG |
| 23 | RaBP_RT_F | CAAAGAGGCAAGGCAGAAGCT |
| 24 | RaBP_RT_R | GGATACGGCCACTTGTAATGC |
| 25 | RaCUC3_F1 | AAGTGGGTCATGCATGAG |
| 26 | RaCUC3_R1 | GCTTTGAGCTCGTCGATG |
| 27 | RaCUC3_F2 | GAGTGTTCAATAAAACAGG |
| 28 | RaCUC3_R2 | CCTGATGATCCATGGAGGAG |
| 29 | RaCUC3_F0.5 | AGTAAAAGATGATGCTTG |
| 30 | RaCUC3_R0.5 | TCCAAGGGCCAAGATTCTA |
| 31 | RaCUC3_RT_F | TGACGAGCCCAAAGCCTTAAT |
| 32 | RaCUC3_RT_R | AGAGAAAATGGTGCCGTTAAGC |
| 33 | RaIPT7_F1 | ttgggtcgacgtttccttac |
| 34 | RaIPT7_R1 | tcggggtaaatgtcacacct |
| 35 | RaIPT7_5RACE | AATCCTGCTTCCATCATTCG |
| 32 | RaIPT7_RT_F | CCGAATGATGGAAGCAGGAT |
| 33 | RaIPT7_RT_R | CCGAATAATCTGCTATTGGATTGA |
| 34 | RaGASA14_5RACE1 | TCCCAGTTCTTGCTGGAGGTGGTGT |
| 35 | RaGASA14_5RACE2 | TGGAGGTGGTGTTGGTGGTTTGACC |
| 36 | RaGASA14_RT_F | GTGCTGCTACCGCTGCAA |
| 37 | RaGASA14_RT-R | CACACTTCTCCTTGTTACCGTACGT |
| 38 | RaPRS_F | CAACGAGGTGGTGTCCAAC |
| 39 | RaPRS_R | TTTGTTGTCTTTTCTTTAAAGTTTGG |