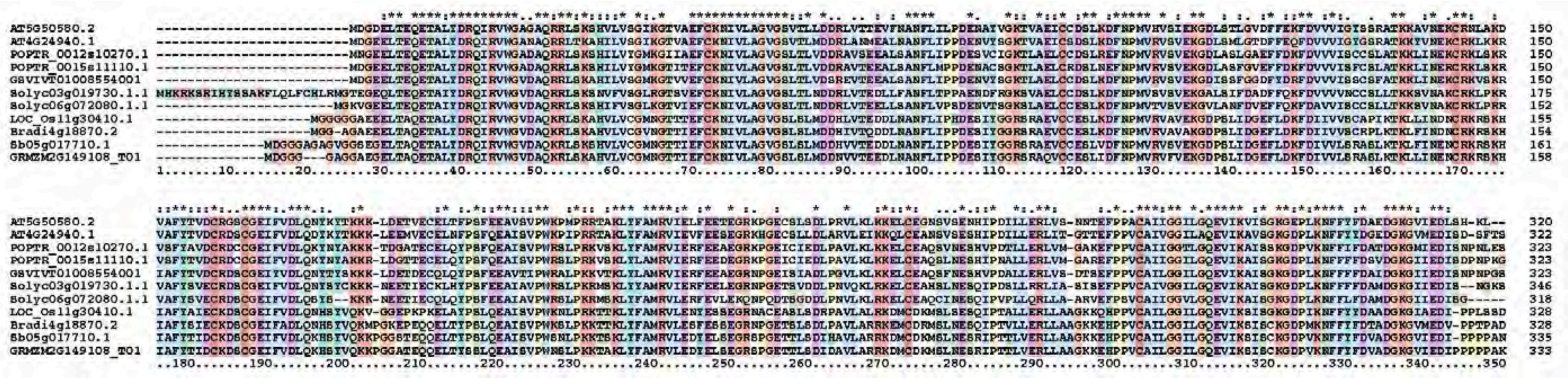

```
                                                 :** ****:*********..**:**:*:::* *:.*    **************::* *.. .. : : ****    *.   *:: *::* :** :***** * : **  : :. :* ::** :*:.  .  **  :* .**:  :
AT5G50580.2        -------------------------MDGDELTEQETALYDRQIRVWGAGAQRRLSKSHVLVSGIKGTVAEFCKNIVLAGVGSVTLLDDRLVTTEVFNANFLILPDENAYVGKTVAEICCDSLKDFNPMVHVSIEKGDLSTLGVDFFEKFDVVVIGISSRATKKAVNEKCRNLAKD   150
AT4G24940.1        -------------------------MDGEELTEQETALYDRQIRVWGANAQRRLTKAHILVSGIKGTVAEFCKNIVLAGVGSVTLMDDRLANMEALNANFLIPPDENVYSGKTVAEICSDSLKDFNPMVRVSVEKGDLSMLGTDFFEQFDVVVIGYGSRATKKYVNEKCRKLKKR   150
POPTR_0012s10270.1 -------------------------MNGEELTEQETALYDRQIRVWGADAQRRLSKSHILVYGMKGIIAEFCKNIVLAGVGSLTLVDDRAVSEEALSANFLIPPDESVCIGKTLAELCCDSLREFNPMVRVSVEKGDLASLGAEFFDKFDVVVISCCSLATKKLINEKCRKLSKR   150
POPTR_0015s11110.1 -------------------------MDGEELTEQETALYDRQIRVWGADAQRRLSKSHILVYGMKGTITEFCKNIVLAGVGSLTLVDDRAVTEEALSANFLMPPDENACSGKTLAELCRDSLNEFNPMVRVSVEKGDLASFGVEFFDKFDVVVISFCSLATKKLINERCRKLSKR   150
GSVIVT01008554001  -------------------------MDGEELTEQETALYDRQIRVWGVDAQRRLSKAHILVSGMKGTVVEFCKNIVLAGVGSLTLVDSREVTEEALSANFLIPPDENVYSGKTLAELCCDSLKDFNPMVRVSVEKGDISSFGGDFYDRFDVVVISSCSFATKKLINEKCRKVSKR   150
Solyc03g019730.1.1 MHKRKSRIHYSSAKFLQLFCHLRMGTEGEQLTEQETAIYDRQIRVWGVDAQRRLSKSNVFVSGLRGTSVEFCKNIVLAGVGSLTLNDDRLVTEDLLFANFLTPPAENDFRGKSVAELCCDSLKDFNPMVSVSVEKGALSIFDADFFQKFDVVVVNCCSLLTKKSVNAKCRKLPKR   175
Solyc06g072080.1.1 -----------------------MGKVGEELTEQETAIYDRQIRVWGVDAQRRLSKSHIFVSGLKGTVIEFCKNIVLAGVGSLTLNDDRLVTEELLSANFLVPSDENVTSGKSLAELCCESLKDFNPMVTVSVEKGVLANFDVEFFQKFDAVVISCCSLLTKKSVNAKCRKLPRR   152
LOC_Os11g30410.1   --------------------MGGGGGAEEELTAQETALYDRQIRVWGVDAQKRLSKAHVLVCGMNGTTTEFCKNIVLAGVGSLSLMDDHLVTEDDLNANFLIPHDESIYGGRSRAEVCCESLKDFNPMVRVAVEKGDPSLIDGEFLDKFDIIVVSCAPIKTKLLINDNCRKRSKH   155
Bradi4g18870.2     --------------------MGG-AGAEEELTAQETALYDRQIRVWGVDAQKRLSKAHVLVCGVNGTTIEFCKNIVLAGVGSLSLMDDHIVTQDDLNANFLIPPDESIYGGRSRAEVCCESLKDFNPMVRVAVAKGDPSLIDGEFLDRFDIIVVSCRPLKTKLFINDNCRKRSKH   154
Sb05g017710.1      --------------MDGGGAGAGVGGSEGELTAQETALYDRQIRVWGVDAQKRLSKSHVLVCGMNGTTIEFCKNIVLAGVGSLSLMDDHVVTEDDLNANFLIPPDESIYGGRSRAEVCCESLVDFNPMVRVSVEKGDPSLIDGEFLDKFDIVVLSRASLKTKLFINENCRKRSKH   161
GRMZM2G149108_T01  --------------MDGGG---GAGGAEGELTAQETALYDRQIRVWGVDAQKRLSKAHVLVCGMNGTTIEFCKNIVLAGVGSLSLMDDNVVTEEDLNANFLIPPDESIYGGRSRAQVCCESLIDFNPMVRVFVEKGDPSLIDGEFLDKFDIVVLSRASLKTKLLINENCRKRSKH   158
                   1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150.......160.......170.....

                   ::**:::*:..****:.***.:.  :*         :* :.*::**:::**  :*:: :*** ****:* :*  * :.  :    *   *   :*::*:  ...*.::*  *:.**:     :.*..***:** *.***** :* **:*:**** :*  ****: **:
AT5G50580.2        VAFYTVDCRGSCGEIFVDLQNYKYTKKK-LDETVECELTFPSFEEAVSVPWKPMPRRTAKLYFAMRVIELFEETEGRKPGECSLSDLPRVLKLKKELCEGNSVSENHIPDILLERLVS-NNTEFPPACAIIGGILGQEVIKVISGKGEPLKNFFYFDAEDGKGVIEDLSH-KL--   320
AT4G24940.1        VAFYTVDCRDSCGEIFVDLQDYKYTKKK-LEEMVECELNFPSFQEAISVPWKPIPRRTAKLYFAMRVIEVFEESEGRKHGECSLLDLARVLEIKKQLCEANSVSESHIPDILLERLIT-GTTEFPPVCAIVGGILAQEVIKAVSGKGDPLKNFFYYDGEDGKGVMEDISD-SFTS   322
POPTR_0012s10270.1 VSFYAVDCRDCCGEIFVDLQKYNYAKKK-TDGATECELQYPSFQEAISVPWRSLPRKVSKLYFAMRVIERFEEAEGRKPGEICIEDLPAVLKLKKELCEAQSVNESHVPDTLLERLVM-GAKEFPPVCAIIGGTLGQEVIKAISSKGDPVKNFFIFDATDGKGMIEDISNPNLES   323
POPTR_0015s11110.1 VSFYTVDCRDCCGEIFVDLQKYNYAKKR-LDGTTECELQYPSFQEAISVPWRSLPRKVSKLYLAMRVIERFEEDEGRKPGEICIEDLPAVLKLKKELCEAQSLNESHIPNALLERLVM-GAREFPPVCAIIGGILGQEVIKAISGKGDPLKNFFFFDSVDGKGIIEDISDPNPKG   323
GSVIVT01008554001  IAFYTVDCRDSCGEIYVDLQNYTYSKKK-LDETDECQLQYPSFEEAVTIPWRALPKKVTKLYLAMRVIERFEEAEGRNPGEISIADLPGVLKLKKELCEAQSFNESHVPDALLERLVS-DTSEFPPVCAILGGILGQEVIKAISGKGDPLKNFFFFDAIDGKGIIEDISNPNPGS   323
Solyc03g019730.1.1 VAFYSVECRDSCGEIFVDLQNYSYCKKK-NEETIECKLHYPSFEEAIAVPWRSLPKRMSKLYYAMRVIERFEELEGRNPGETSVDDLPNVQKLRKELCEAHSLNESQIPDSLLRRLIA-SISEFPPVCAIVGGILGQEVIKAISGKGDPLKNFFFFDAMDGKGIIEDIS--NGKS   346
Solyc06g072080.1.1 VAFYSVECRDSCGEIFVDLQSYS--KKK-NEETIECQLQYPSFEEAIAVPWRSLPKRMSKLYFAMRVLERFEVLEKQNPQDTSGDDLPNVLKLRKELCEAQCINESQIPVPLLQRLLA-ARVEFPSVCAIIGGVLGQEVIKAISGKGDPLKNFFLFDAMDGKGIIEDISG-----   318
LOC_Os11g30410.1   IAFYAIECKDSCGEIFVDLQNHSYVQKV-GGEPKPKELAYPSLQEAISVPWKNLPRKTTKLYFAMRVLENYESSEGRNACEASLSDRPAVLALRKDMCDKMSLSESQIPTALLERLLAAGKKQHPPVCAILGGILGQEVIKSISGKGDPIKNFFYYDAADGKGIAEDI-PPLSSD   328
Bradi4g18870.2     IAFYSIECKDSCGEIFADLQNHSYVQKMPGKEPEQQELTYPSLQEAISVPWKSLPKKTTKLYFAMRVLESFESSEGRNPGETSLSDLPAVLARRKEMCDRMSLNESQIPTVLLERLLAAGKKEHPPVCAILGGILGQEVIKSISCKGDPMKNFFYFDTADGKGVMEDV-PPTPAD   328
Sb05g017710.1      IAFYTIDCKDSCGEIFVDLQKHSYVQKKPGGSTEQQELTYPSLQEAISVPWSNLPKKTSKLYFAMRVLEDYELSEGRSPGETTLSDIHAVLARRKDMCDKMSLNESRIPTTLVERLLAAGKKEHPPVCAILGGILGQEVIKSISCKGDPVKNFFYFDVADGKGVIEDI-PPPPAN   335
GRMZM2G149108_T01  IAFYTIDCKDSCGEIFVDLQKHSYVQKKPGGATEQQELTYSSLQEAISVPWNSLPKKTAKLYFAMRVLEDYELSEGRSPGETTLSDIDAVLARRKDMCDKMSLNESRIPTTLVERLLAAGKKEHPPVCAILGGILGQEVIKSISCKGDPVKNFFYFDVADGKGVIEDIPPPPPAK   333
                   ..180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300.......310.......320.......330.......340.......350
```

Fig. S1 Alignment of SUMO activating enzyme subunit 1 (SAE1) protein sequences