Legends for supplemental data

Table S1 The list of primers used in this study. F and R indicate forward and reverse primers.

Fig. S1 The BlastP between AtSAG and other homologous proteins from *Glycine max* (XP_003522398.1), *Vitis vinifera* (XP_002282819.2), and *Ricinus communis* (XP_002515436.1). The asterisk marked letters indicates the VWA domain components, the straight lines indicate regions of AAA and VWA domains in MDN1domain, and the black arrow indicates the T-DNA insertion site.

Fig. S2 The protein accumulation of ABI3 and ABI5 in WT and *sag* mutant seeds germinated for 2.5-day on 1/2 MS with or without 0.5 μM ABA. The black arrows in the right side indicate ABI3 and ABI5, respectively. – and + indicate without and with 0.5 μM ABA, respetively.

Fig. S3 The expression analysis of *AtSAG* in *abi5* germinated seeds compared to WT.

Fig. S4 The expression analysis of *AtSAG* in *mapk4* and 35S:MKS1 plants by genevestigator analysis (A), and the expression of MAPK4 in WT and *sag* mutant seeds germinated for 2.5-day on 1/2 MS with or without 0.5 μM ABA (B).

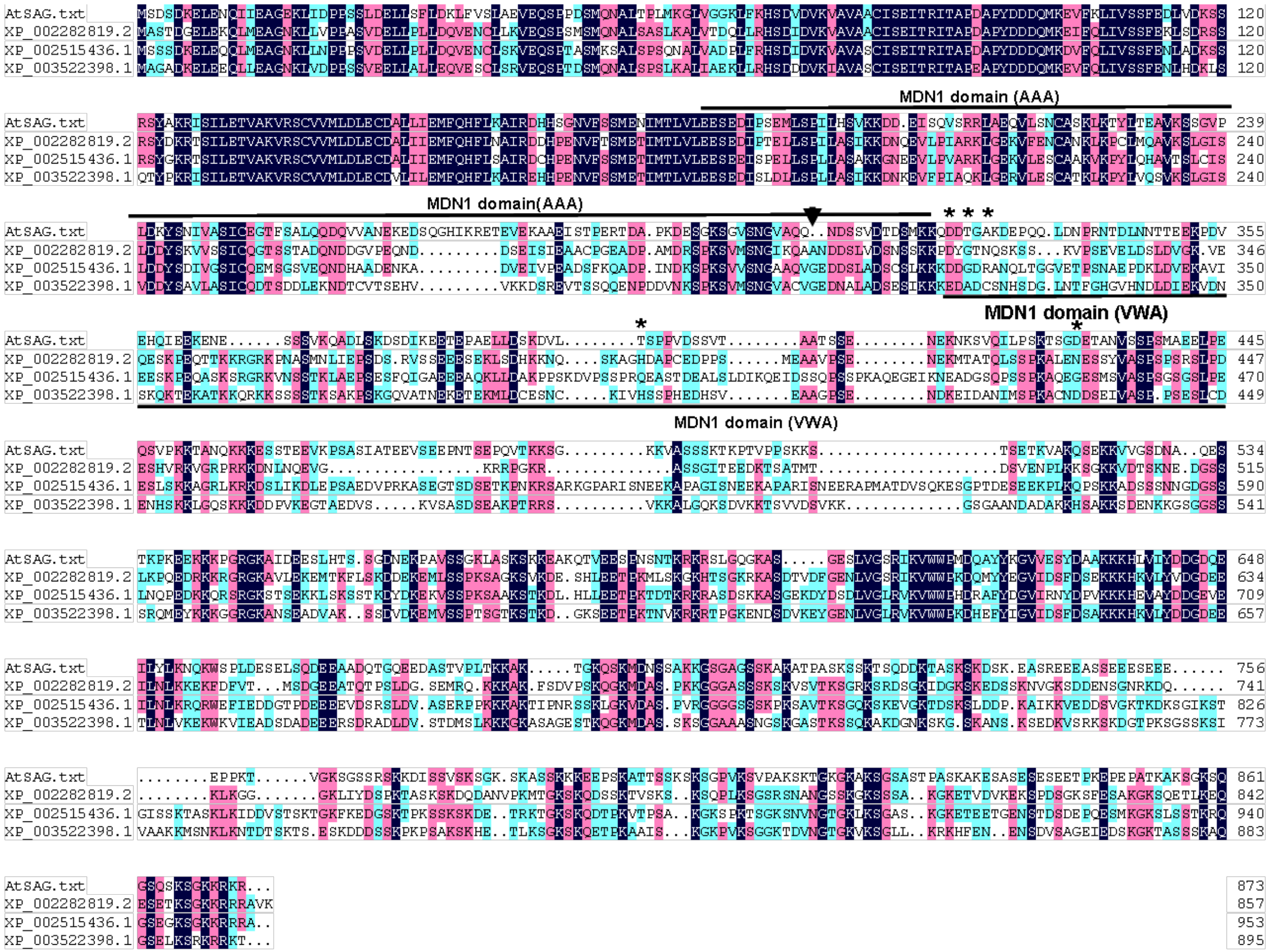
Fig. S5 The SDS-PAGE of coinmmunoparticipaed proteins from 35S:AtSAG-GFP and 35S:GFP seeds germinated for 2.5-day on 1/2 MS with 0.5 μM ABA**.** 1 and 2 indicated two independent repeats. The sequenced bands were marked in red box.

Supplementary data

Table S1 The list of primers used in this study.

Primer Name	Primer Sequence
NCED3-F	GCTGCGGTTTCTGGGAGAT
NCED3-R	GTCGGAGCTTTGAGAAGACGAT
NCED5-F	CCTCCGTTAGTTTCACCAACACT
NCED5-R	GGTGTGTCGGAGACGGAGTT
CYC707A1-F	CTCACTCTCTTCGCCGGAAG
CYC707A1-R	GGAGGGAGTGGGAGTTTGGAA
CYC707A2-F	CGTCTCTCACATCGAGCTCCTT
CYC707A2-R	GAGGGTGTTGATGGACTTTTGG
ABI3-F	TACTCCGTTTGTGTTCCTCAG
ABI3-R	GTTTCTCCGATTTGGGTTTGG
ABI5-F	AACCTAATCCAACCCGAACC
ABI5-R	ACCCTCCTCCTCCTGTCC
EM1-F	TCAAATGGTATGCGGTTATG
EM1-R	TATCACAAGTAAGACACGAAG
EM6-F	TGTCTCGTTTGTTTTCCAG
EM6-R	CACTATGTTGAGAATCCAC
RD29A-F	TGATCGATGCACCAGGCGTAAC
RD29A-R	CCCTGGTGGAATAATTTCCTCCG
RAB18-F	GAGCACCACGAGAAGAAGG
RAB18-R	GCACAATACAACGACCGAATG
ATS1-F	ATTACGGACTTAGTGTTC
ATS1-R	CTTGTGTATGTTGTGTATG
Ole2-F	CCACTATTTCTCCTCTTC
Ole2-R	TTCTCCTCTTAGCATACT
Ole4-F	AACTACGAAGATGATGTC
Ole4-R	GCTATAAGTGCCAAGATT
At3G22640-F	AAGGACAAGAAGAAGAAG
At3G22640-R	CGAGAGTATAGTGAATGG
At4G36700-F	GCTGTTATCTTGGAATGT
At4G36700-R	CTTCTCTTCTTCTTCTTCA
At2S4-F	CCAATACAGAAATGTCAGA
At2S4-R	GATGTCGTCTTCCATATC

Fig. S1



```
AtSAG.txt       MSDSDKELENQIIEAGEKLIDPESSLDELLSFLDKLFVSLAEVEQSEPDSMQNALTPLMKGLVGGKLFKHSDVDVKVAVAACISEITRITAPDAPYDDDQMKEVFKLIVSSFEDLVDKSS 120
XP_002282819.2  MASTDGELEKQLMEAGNKLLVPEASVDELLPLLDQVENCLLKVEQSESMSMQNALSASLKALVTDQLLRHSDIDVKVAVAACISEITRITAPDAPYDDDQMKEIFQLIVSSFEKLSDRSS 120
XP_002515436.1  MSSSDKELEQQLMEAGNKLLNPEPSVDELLPLLDQVENCLSKVEQSPTASMKSALSPSQNALVADPLFRHSDIDVKVAVASCISEITRITAPDAPYDDDQMKDVFQLIVSSFENLADKSS 120
XP_003522398.1  MAGADKELEEQLLEAGNKLVDPESSVEELLALLEQVESCLSRVEQSPTDSMQNALSPSLKALIAEKLLRHSDDDVKIAVASCISEITRITAPEAPYDDDQMKEVFQLIVSSFENLHDKLS 120

AtSAG.txt       RSYAKRISILETVAKVRSCVVMLDLECDALLIEMFQHFLKAIRDHHSGNVFSSMENIMTLVLEESEDIPSEMLSPILHSVKKDD.EISQVSRRLAEQVLSNCASKLKTYLTEAVKSSGVP 239
XP_002282819.2  RSYDKRTSILETVAKVRSCVVMLDLECDALIIEMFQHFLNAIRDDHPENVFTSMETIMTLVLEESEDIPTELLSPILASIKKDNQEVLPIARKLGEKVFENCANKLKPCLMQAVKSLGIS 240
XP_002515436.1  RSYGKRTSILETVAKVRSCVVMLDLECDALIIEMFQHFLSAIRDCHPENVFSSMETIMTLVLEESEEISPELLSPLLASAKKGNEEVLPVARKLGEKVLESCAAKVKPYLQHAVTSLCIS 240
XP_003522398.1  QTYPKRISILETVAKVRSCVVMLDLECDVLILEMFQHFLKAIREHHPENVFSSMETIMTLVLEESEDISLDLLSPLLASIKKDNKEVFPIAQKLGERVLESCATKLKPYLVQSVKSLGIS 240

AtSAG.txt       LDKYSNIVASICEGTFSALQQDQVVANEKEDSQGHIKRETEVEKAAEISTPERTDA.PKDESGKSGVSNGVAQQ..NDSSVDTDSMKKQDDTGAKDEPQQ.LDNPRNTDLNNTTEEKPDV 355
XP_002282819.2  LDDYSKVVSSICQGTSSTADQNDDGVPEQND.........DSEISIEAACPGEADP.AMDRSPKSVMSNGIKQAANDDSLVDSNSSKKPDYGTNQSKSS...KVPSEVELDSLDVGK.VE 346
XP_002515436.1  LDDYSDIVGSICQEMSGSVEQNDHAADENKA.........DVEIVPEADSFKQADP.INDKSPKSVVSNGAAQVGEDDSLADSCSLKKKDDGDRANQLTGGVETPSNAEPDKLDVEKAVI 350
XP_003522398.1  VDDYSAVLASICQDTSDDLEKNDTCVTSEHV.........VKKDSREVTSSQQENPDDVNKSPKSVMSNGVACVGEDNALADSESIKKKEDADCSNHSDG.LNTFGHGVHNDLDIEKVDN 350

AtSAG.txt       EHQIEEKENE......SSSVKQADLSKDSDIKEETEPAELLDSKDVL........TSPPVDSSVT........AATSSE........NEKNKSVQILPSKTSGDETANVSSESMAEELPE 445
XP_002282819.2  QESKPEQTTKKRGRKPNASMNLIEPSDS.RVSSEEESEKLSDHKKNQ....SKAGHDAPCEDPPS......MEAAVPSE........NEKMTATQLSSPKALENESSYVASPSPSRSLPD 447
XP_002515436.1  EESKPEQASKSRGRKVNSSTKLAEPSESFQIGAEEEAQKLLDAKPPSKDVPSSPRQEASTDEALSLDIKQEIDSSQPSSPKAQEGEIKNEADGSQPSSPKAQEGESMSVASPSGSGSLPE 470
XP_003522398.1  SKQKTEKATKKQRKKSSSSTKSAKPSKGQVATNEKETEKMLDCESNC.....KIVHSSPHEDHSV.......EAAGPSE........NDKEIDANIMSPKACNDDSEIVASP.PSESLCD 449

AtSAG.txt       QSVPKKTANQKKKESSTEEVKPSASIATEEVSEEPNTSEPQVTKKSG.........KKVASSSKTKPTVPPSKKS....................TSETKVAKQSEKKVVGSDNA..QES 534
XP_002282819.2  ESHVRKVGRPRKKDNLNQEVG.................KRRPGKR..............ASSGITEEDKTSATMT....................DSVENPLKKSGKKVDTSKNE.DGSS 515
XP_002515436.1  ESLSKKAGRLKRKDSLIKDLEPSAEDVPRKASEGTSDSETKPNKRSARKGPARISNEEKAPAGISNEEKAPARISNEERAPMATDVSQKESGPTDESEEKPLKQPSKKADSSSNNGDGSS 590
XP_003522398.1  ENHSKKLGQSKKKDDPVKEGTAEDVS.....KVSASDSEAKPTRRS..........VKKALGQKSDVKKTSVVDSVKK.............GSGAANDADAKKHSAKKSDENKKGSGGSS 541

AtSAG.txt       TKPKEEKKKPGRGKAIDEESLHTS.SGDNEKPAVSSGKLASKSKKEAKQTVEESPNSNTKRKRSLGQGKAS.....GESLVGSRIKVWWPMDQAYYKGVVESYDAAKKKHLVIYDDGDQE 648
XP_002282819.2  LKPQEDRKKRGRGKAVLEKEMTKFLSKDDEKEMLSSPKSAGKSVKDE.SHLEETPKMLSKGKHTSGKRKASDTVDFGENLVGSRIKVWWPKDQMYYEGVIDSFDSEKKKHKVLYVDGDEE 634
XP_002515436.1  LNQPEDKKQRSRGKSTSEKKLSKSSTKDYDKEKVSSPKSAAKSTKDL.HLLEETPKTDTKRKRASDSKKASGEKDYDSDLVGLRVKVWWPHDRAFYDGVIRNYDPVKKKHEVAYDDGEVE 709
XP_003522398.1  SRQMEYKKKGGRGKANSEADVAK..SSDVDKEMVSSPTSGTKSTKD..GKSEETPKTNVKRKRTPGKENDSDVKEYGENLVGLRVKVWWPKDHEFYIGVIDSFDSAKKKHKVLYDDGDEE 657

AtSAG.txt       ILYLKNQKWSPLDESELSQDEEAADQTGQEEDASTVPLTKKAK.....TGKQSKMDNSSAKKGSGAGSSKAKATPASKSSKTSQDDKTASKSKDSK.EASREEEASSEEESEEE...... 756
XP_002282819.2  ILNLKKEKFDFVT...MSDGEEATQTPSLDG.SEMRQ.KKKAK.FSDVPSKQGKMDAS.PKKGGGASSSKSKVSVTKSGRKSRDSGKIDGKSKEDSSKNVGKSDDENSGNRKDQ...... 741
XP_002515436.1  ILNLKRQRWEFIEDDGTPDEEEEVDSRSLDV.ASERPPKKKAKTIPNRSSKLGKVDAS.PVRGGGGSSSKPKSAVTKSGQKSKEVGKTDSKSLDDP.KAIKKVEDDSVGKTKDKSGIKST 826
XP_003522398.1  TLNLVKEKWKVIEADSDADEEERSDRADLDV.STDMSLKKKGKASAGESTKQGKMDAS.SKSGGAAASNGSKGASTKSSQKAKDGNKSKG.SKANS.KSEDKVSRKSKDGTPKSGSSKSI 773

AtSAG.txt       ........EPPKT......VGKSGSSRSKKDISSVSKSGK.SKASSKKKEEPSKATTSSKSKSGPVKSVPAKSKTGKGKAKSGSASTPASKAKESASESESEETPKEPEPATKAKSGKSQ 861
XP_002282819.2  ........KLKGG.......GKLIYDSPKTASKSKDQDANVPKMTGKSKQDSSKTVSKS..KSQPLKSGSRSNANGSSKGKSSSA..KGKETVDVKEKSPDSGKSFESAKGKSQETLKEQ 842
XP_002515436.1  GISSKTASKLKIDDVSTSKTGKFKEDGSKTPKSSKSKDE..TRKTGKSKQDTPKVTPSA..KGKSPKTSGKSNVNGTGKLKSGAS..KGKETEETGENSTDSDEPQESMKGKSLSSTKRQ 940
XP_003522398.1  VAAKKMSNKLKNTDTSKTS.ESKDDDSSKPKPSAKSKHE..TLKSGKSKQETPKAAIS...KGKPVKSGGKTDVNGTGKVKSGLL..KRKHFEN..ENSDVSAGEIEDSKGKTASSSKAQ 883

AtSAG.txt       GSQSKSGKKRKR...  873
XP_002282819.2  ESETKSGKKRRRAVK  857
XP_002515436.1  GSEGKSGKKRRRA..  953
XP_003522398.1  GSELKSRKRRKT...  895
```

Fig. S2

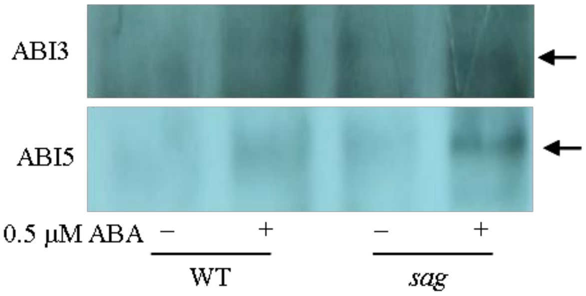


Fig. S3

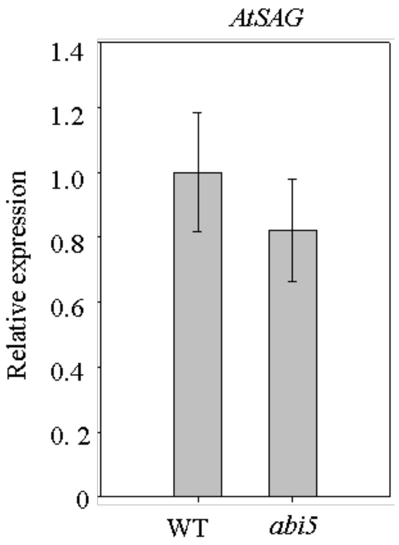


Fig. S4

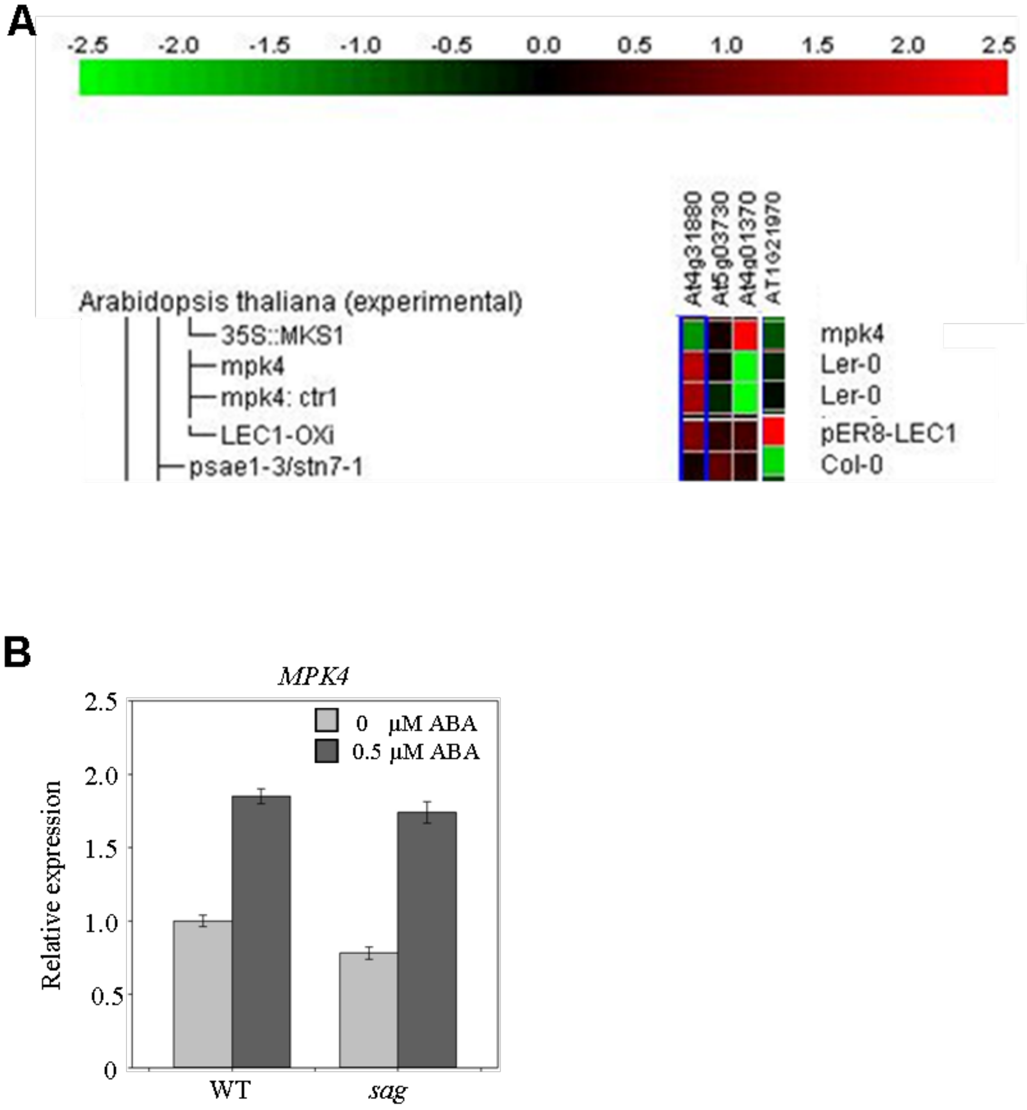

A
-2.5
-2.0
-1.5
-1.0
-0.5
0.0
0.5
1.0
1.5
2.0
2.5
At4g31880
At5g03730
At4g01370
AT1G21970
Arabidopsis thaliana (experimental)
35S::MKS1
mpk4
mpk4: ctr1
LEC1-OXi
psae1-3/stn7-1
mpk4
Ler-0
Ler-0
pER8-LEC1
Col-0
B
MPK4
0 µM ABA
0.5 µM ABA
Relative expression
2.5
2.0
1.5
1.0
0.5
0
WT
sag

Fig. S5