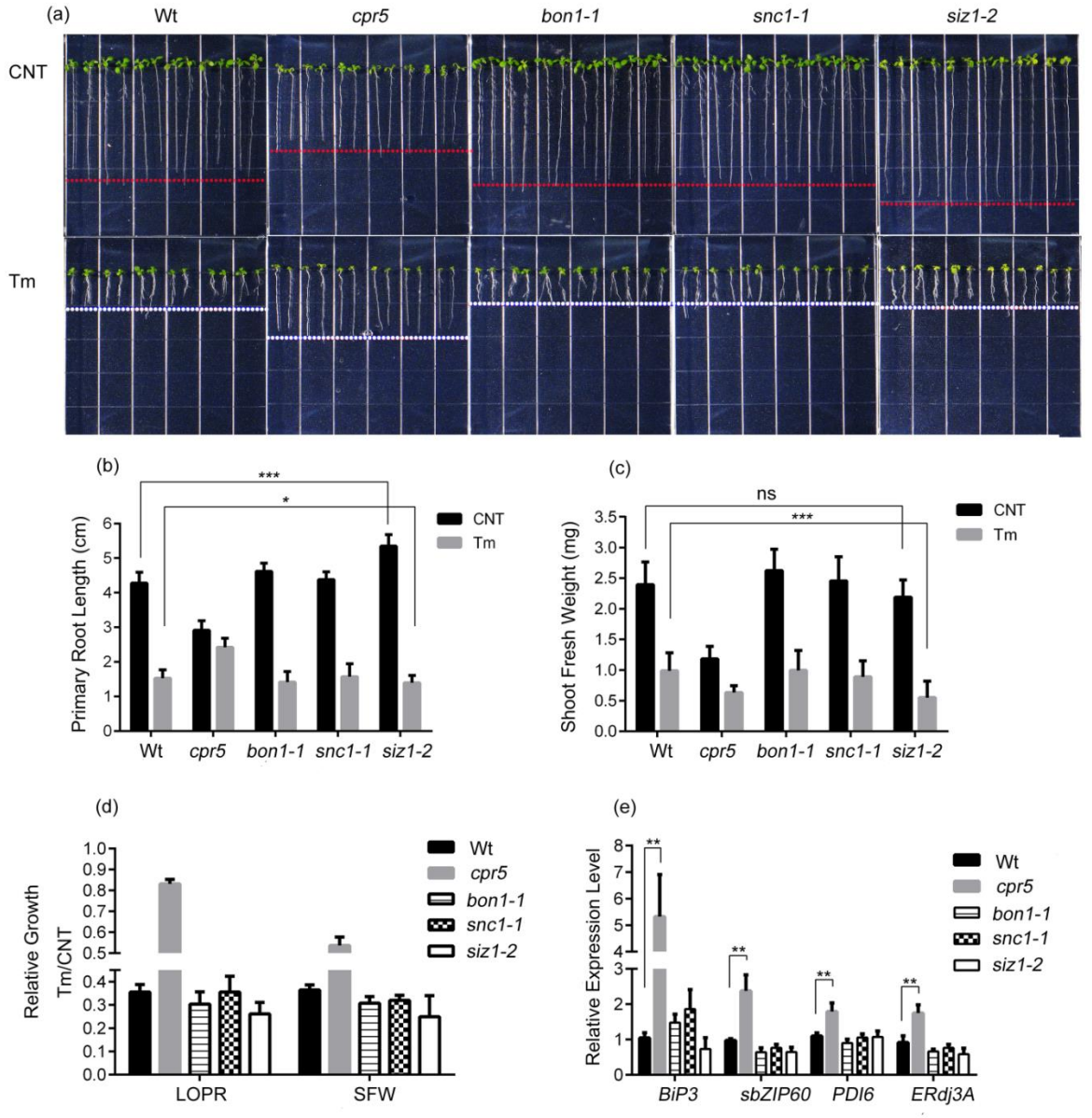


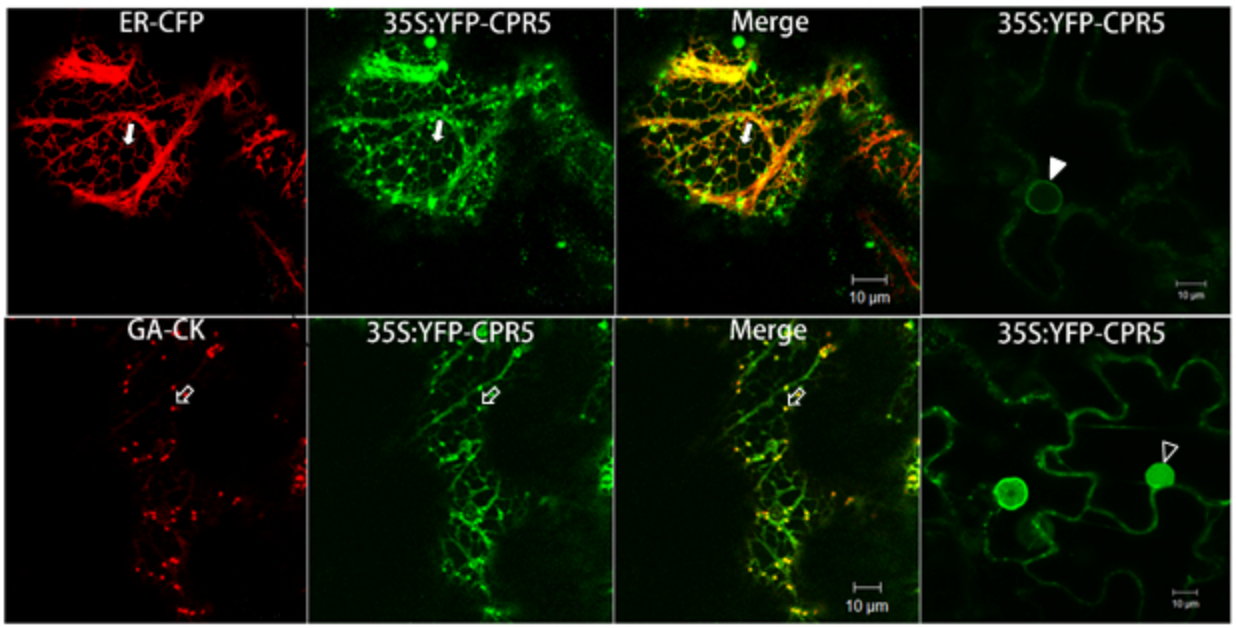
Figure S1. High SA content mutants do not show the ER stress tolerance phenotype of *cpr5*.

(a) The indicated genotypes were germinated on 1/2 LS medium containing 0.0005% DMSO (Control, CNT) or 50 ng/mL Tm for 12 days vertically. **(b)** Measurement of primary root length (cm). **(c)** Quantification of shoot fresh weight (mg). **(d)** The relative growth rate of seedlings as indicated in (a). n=24 for each genotype. **(e)** Relative expression of UPR marker genes *BiP3*, *PDI*, *ERdj3A* and spliced bZIP60 (*sbZIP60*) in Wt and high SA-content mutants estimated by qRT-PCR analyses in 12-day-old seedlings under normal growth condition. The relative gene expression represents the expression level of each gene in the mutants divided by that in Wt, both of which were normalized to the expression of UBQ10. The values shown were relative to Wt which was set to 1. Error bars represent SD from three biological replicates. **P<0.001. *P<0.05; **P<0.001; ***P<0.0001; ns: not significant.

(a)

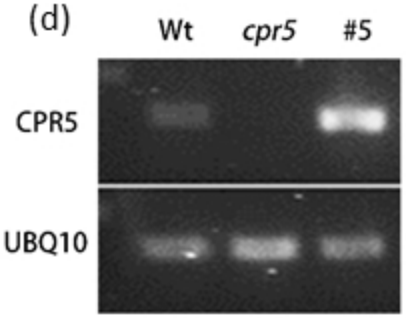
MEALLLPPSPEPQNQITNPANSKPNHQSGDVHKDETMMMKKKKDTNPSNLEKRKLKGKKKEIMDNDEASSSYCSTSS
TSNSNSTKRVTRVVHRLRNPMRLGMARRSVGERQAEKLAKPLGFSLAAFANMVIARKNAAGQNVYVDDLVEIFATLV
EESLANVYGNKLGSFATNFEQTFSSTLKILKLTNECANPHQSNNNDGGSCNLDRSTIDGCSDTELFERETSSATSAYEVM
QGSATATSLMNELALFEETLQLSCVPPRSSAMALTTDERFLKEQTRANDLKTVEIGLQIRELRCKETALGLKFESNNLGKA
ALELDVSKAAFRAEKFKTELEDTRKEEMVTRIMDWLLVSVFSMLASMVLGVYNFSIKRIEDATSVCDQSEEKSSSWWVP
KQVSSINSGFNTFICRVRVVWVQIFFGVLMIIVFTYFLNKRSSGTKQTMPISFIVLFLGIFCGVSGKLCVDTLGGDGKLWLIV
WEVFCLLQFVANVFTLALYGLMFGPINVTQETRSNRCNSMFPYWARRSVVYVVILFVLPVINGLLPFATFGEWRDFAM
YHLHGGSDYA

(b)



(c)

(d)



Supporting Information Legends

Figure S1. High SA content mutants do not show the ER stress tolerance phenotype of *cpr5*.

(a) The indicated genotypes were germinated on 1/2 LS medium containing 0.0005% DMSO (Control, CNT) or 50 ng/mL Tm for 12 days vertically.

(b) Measurement of primary root length (cm).

(c) Quantification of shoot fresh weight (mg).

(d) The relative growth rate of seedlings as indicated in (a). n=24 for each genotype.

(e) Relative expression of UPR marker genes *BiP3*, *PDI*, *ERdj3A* and spliced bZIP60 (*sbZIP60*) in Wt and high SA-content mutants estimated by qRT-PCR analyses in 12-day-old seedlings under normal growth condition. The relative gene expression represents the expression level of each gene in the mutants divided by that in Wt, both of which were normalized to the expression of UBQ10. The values shown were relative to Wt which was set to 1. Error bars represent SD from three biological replicates. **P<0.001.

Figure S2. The subcellular localization of CPR5 in the ER, Golgi, and nucleoplasm is suggestive of activation of CPR5 by proteolysis.

(a) Amino acid sequence of CPR5. The blue characters indicate a putative bipartite nuclear-localization signal. The 5 predicted transmembrane domains are

underlined. The red character (W) indicates the position of the point mutation in the *cpr5* allele used in this work (Trp477stop).

(b) Confocal analyses of YFP-CPR5 in tobacco leaf epidermal cells expressing either an ER marker, ER-CFP, or a Golgi marker, GA-CK. As supported by colocalization of the punctate structures labelled by YFP-CPR5, CPR5 is localized at the Golgi (hollow arrow) in addition to the ER localization. We have also verified that in some cells YFP-CPR5 is at the nuclear envelope (top right corner image, solid arrowhead) and in the nucleoplasm (bottom right corner image, hollow arrowhead).

(c) Complementation of *cpr5* by 35S:YFP-CPR5. Wt, *cpr5*, 35S:YFP-CPR5/*cpr5*#5 plants were grown on the soil for 4 weeks. The YFP-CPR5 fusion complements the *cpr5* phenotype.

(d) Semi-quantitative RT-PCR analyses of *CPR5* and *UBQ10* transcript in Wt, *cpr5* and 35S:YFP-CPR5/*cpr5*#5 show that YFP-CPR5 is expressed at higher levels compared to Wt.

Figure S3. Proposed working model of roles of CPR5 in growth-ER stress defense tradeoff through SA and UPR.

(**a**) CPR5 supports in growth in physiological conditions as well as under ER-stress inducing conditions by antagonizing SA which harnesses the UPR channels to repress growth. Therefore, in the balance of growth-defense tradeoffs (**b**), successful allocation of the plant's resources to either growth or defense for survival depends on opposite roles of CPR5 and SA.

Table S1. Primers list.

Table S1. Primers list.

Primers	Sequence (5'–3')	Gene	Purpose
CS3770 WT F	TGGCAAACTCTGGCTAATAGTcTg	At5g64930	Genotyping *cpr5-2* and RT-PCR
CS3770 Mutation F	TGGCAAACTCTGGCTAATAGTcTa	At5g64930	Genotyping *cpr5-2*
CS3770 R	TCAAGCATAGTCAGACCCACCAT	At5g64930	Genotyping *cpr5-2* and RT-PCR
WiscDsLox420D09 RP	TATCTCCGATCCATCGTTGAC	At2g17520	genotyping *atire1a*
WiscDsLox420D09 LP	CAAAATCTTCAGTGCTAGCGG	At2g17520	genotyping *atire1a*
WiscDsLox LB	AACGTCCGCAATGTGTTATTAAGTTG		genotyping *atire1a*
SAIL_238_F07 RP	GAAGGAAAACGGACATCCTTC	At5g24360	genotyping *atire1b-1*
SAIL_238_F07 LP	CCTCTCGAACCCTTCAGGTAC	At5g24360	genotyping *atire1b-1*
SAIL LB	TCATAACCAATCTCGATACAC		genotyping *atire1b-1*
SALK_050203 RP	CACAGCATCATCGTCTCCTTC	At1g42990	genotyping *bzip60*
SALK_050203 LB	GGAAGAAAAGTCCTCTCGGAG	At1g42990	genotyping *bzip60*
SALK_132285 RP	TATCCCCTAACAGGATACGGC	At3g10800	genotyping *bzip28*
SALK_132285 LP	TTTATCATCATTTTGGTCGCC	At3g10800	genotyping *bzip28*
SALK_LB	ATTTTGCCGATTTCGGAAC		genotyping SALK lines
sid2-2 F	TTCAACCACCTGGTGCAC	At1g74710	genotyping *sid2-2*
sid2-2 R	TGTTGCACTCTTGCAAGC	At1g74710	genotyping *sid2-2*
UBQ10-qP For	GGCCTTGTATAATCCCTGATGAATAAG	At4g05320	qRT-PCR
UBQ10-qP Rev	AAAGAGATAACAGGAACGGAAACATAGT	At4g05320	qRT-PCR
BiP3-qP For	CGAAACGTCTGATTGGAAGAA	At1g09080	qRT-PCR
BiP3-qP Rev	GGCTTCCCATCTTTGTTCAC	At1g09080	qRT-PCR
AtERdi3A-qP For	CCCACCGCCCATATTTTG	AT3G0890	qRT-PCR

Primers	Sequence (5'–3')	Gene	Purpose
AtERdj3A-qP Rev	TGAAAGCGAAGAGCGTTGATC	AT3G0890	qRT-PCR
PDI6-qP For	CGAAGTGGCTTTGTCATTCCA	At1g77510	qRT-PCR
PDI6-qP Rev	GCGGTTGCGTCCAATTTT	At1g77510	qRT-PCR
sbZIP60-qP For	GGAGACGATGATGCTGTGGCT	At1g42990	qRT-PCR
sbZIP60-qP Rev	CAGGGAACCCAACAGCAGACT	At1g42990	qRT-PCR
UBQ10 For	TCAATTCTCTCTACCGTGATCAAGATGCA	At4g05320	RT-PCR
UBQ10 Rev	GGTGTCAGAACTCTCCACCTCAAGAGTA	At4g05320	RT-PCR
CPR5 F	ATGGAAGCCCTCCTCCTCCCTCCT	At5g64930	35S:YFP-CPR5/CPR5ΔTMD and Y2H
CPR5 R	TCAAGCATAGTCAGACCCACCAT	At5g64930	35S:YFP-CPR5
CPR5ΔTMD R	TCATGTGACCATCTCTTCTTTTCTTGTATC	At5g64930	35S:YFP-CPR5ΔTMD and Y2H
sbZIP60 F	ATGGCGGAGGAATTTGGAA	At1g42990	FRET
sbZIP60 R	TCACGCCGCAAGGGTTAAGATT	At1g42990	FRET
bZIP28ΔTMD F	ATGACGGAATCAACATCCGTGGTTG	At3g10800	FRET
bZIP28ΔTMD R	TCACTTCTTGAGCTTACTTTTACCCTCA	At3g10800	FRET
sbZIP60ΔAD F	CCAACTAGCGATTCTGGCTC	At1g42990	Y2H
Primers	**Sequence (5'–3')**	**Gene**	**Purpose**
sbZIP60ΔAD R	TCACGCCGCAAGGGTTAAGAT	At1g42990	Y2H
bZIP28ΔTMDΔAD F	gaCGCATCATCCTCCCCTGAATCA	At3g10800	Y2H
bZIP28ΔTMDΔAD R	TCACTTCTTGAGCTTACTTTTACCC	At3g10800	Y2H