Title: Proteolytic processing of SERK3/BAK1 regulates plant immunity, development and
 cell death

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- **33 Running title:** BAK1 cleavage regulates its multiple functions
- 34 **One-sentence summary:**
- 35 Arabidopsis BAK1, a co-receptor of multiple receptor-like kinases undergoes proteolytic
- 36 cleavage process, which is essential for its functions in plant immunity, growth and cell death
- 37 control.
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39 Abstract

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Plants have evolved many receptor-like kinases (RLKs) to sense extrinsic and intrinsic cues. The 41 signaling pathways mediated by multiple leucine-rich repeat (LRR) RLK (LRR-RLK) receptors 42 require ligand-induced receptor-coreceptor heterodimerization and transphosphorylation with 43 BAK1/SERK family LRR-RLKs. Here we reveal an additional layer of regulation of BAK1 via a 44 Ca²⁺-dependent proteolytic cleavage process that is conserved in Arabidopsis thaliana, Nicotiana 45 benthamiana and Saccharomyces cerevisiae. The proteolytic cleavage of BAK1 is intrinsically 46 regulated in response to developmental cues and immune stimulation. The surface-exposed 47 aspartic acid (D²⁸⁷) residue of BAK1 is critical for its proteolytic cleavage and plays an essential 48 role in BAK1-regulated plant immunity, growth hormone brassinosteroid-mediated responses 49 and cell death containment. BAK1^{D287A} mutation impairs BAK1 phosphorylation on its substrate 50 BIK1, and its plasma membrane (PM) localization. Intriguingly, it aggravates BAK1 51 overexpression-triggered cell death independent of BIK1, suggesting that maintaining 52 homeostasis of BAK1 through a proteolytic process is crucial to control plant growth and 53 54 immunity. Our data reveal that in addition to layered transphosphorylation in the receptor complexes, the proteolytic cleavage is an important regulatory process for the proper functions of 55 56 the shared co-receptor BAK1 in diverse cellular signaling pathways.

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58 Introduction

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Plants growing in their natural habitats are at constant risks for various potential attacks. 60 61 meanwhile maintaining their active growth. To adapt, sessile plants have evolved a large number of cell surface-resident receptor-like kinases (RLKs) to sense extrinsic and intrinsic cues and 62 elicit distinct biological responses (Shiu and Bleecker, 2003). A typical RLK usually contains a 63 variable extracellular domain that perceives either self- or non-self signals on the cell surface, a 64 single transmembrane domain, and an intracellular kinase domain that is important to relay 65 signaling. A large portion of RLKs contains an extracellular leucine-rich repeat (LRR) domain 66 with different number of LRR repeats. For example, the Arabidopsis thaliana genome encodes 67 more than 200 LRR-RLKs that regulate a wide range of biological processes from plant growth, 68 symbiosis immunity (Belkhadir al., 69 development, to et 2014). The LRR-RLK 70 BRASSINOSTEROID INSENSITIVE 1 (BRI1) is the receptor of plant hormone brassinosteroids (BRs), important in growth and development (Li and Chory, 1997; Belkhadir et 71 al., 2006). Some LRR-RLKs function as pattern-recognition receptors (PRRs) that recognize 72 microbe-associated molecular patterns (MAMPs) and induce the first line of plant immunity 73 (Macho and Zipfel, 2014; Yu et al., 2017). Arabidopsis PRRs FLAGELLIN-SENSING 2 (FLS2) 74 and ELONGATION FACTOR-TU (EF-Tu) RECEPTOR (EFR) recognize bacterial flagellin and 75 76 EF-Tu, respectively, and initiate the convergent plant immune signaling (Gomez-Gomez and Boller, 2000; Zipfel et al., 2006; Boller and Felix, 2009). 77

A group of LRR-RLKs, named SOMATIC EMBRYOGENESIS RECEPTOR KINASES 78 (SERKs) with five members in Arabidopsis, function as shared co-receptors of multiple LRR-79 80 RLKs (Liebrand et al., 2014; Ma et al., 2016; He et al., 2018). SERK3, also known as BRI1-ASSOCIATED RECEPTOR KINASE 1 (BAK1), was originally identified as a BRI1 interacting 81 82 protein that mediates BR signaling (Li et al., 2002; Nam and Li, 2002). SERK1 and SERK4 were 83 also found to interact with BRI1 and mutation of SERK1, SERK3/BAK1 and SERK4 rendered plants insensitive to BR treatment (Karlova et al., 2006; He et al., 2007; Gou et al., 2012). 84 SERK3/BAK1 was also shown to dimerize with FLS2 upon flagellin perception and plays a key 85 86 role in flagellin-activated responses (Chinchilla et al., 2007; Heese et al., 2007). SERK3/BAK1 87 also heterodimerizes with several other PRRs, including EFR and PEP1 RECEPTOR 1 (PEPR1)

that perceives endogenous danger peptide PEPs (Postel et al., 2010; Roux et al., 2011). SERK4,
but not SERK1 nor SERK2, performs a function redundant with that of SERK3/BAK1 in
mediating PRR signaling (Roux et al., 2011). The crystal structure analysis indicates that BAK1
family RLKs are involved in ligand sensing through contacting the BRI1-BR- or FLS2-flagellinbinding interface respectively, and function as co-receptors (Santiago et al., 2013; Sun et al., 2013).

Recent studies have revealed additional functions of SERKs as co-receptors of different 94 LRR-RLK 95 receptors in regulating plant development and growth, including PHYTOSULFOKINE (PSK) RECEPTOR 1 (PSKR1) recognizing peptide hormone PSK for root 96 growth (Wang et al., 2015), the ERECTA (ER) family sensing EPIDERMAL PATTERNING 97 FACTORS (EPFs) for cell fate specification in stomatal patterning (Meng et al., 2015), the 98 99 HAESA (HAE) family perceiving INFLORESCENCE DEFICIENT IN ABSCISSION (IDA) for floral organ abscission (Meng et al., 2016; Santiago et al., 2016), ROOT MERISTEM GROWTH 100 FACTOR (RGF) receptors perceiving peptide hormones RGF for regulating root meristem 101 development (Ou et al., 2016; Song et al., 2016), EXCESS MICROSPOROCYTES1 (EMS1) 102 103 perceiving TAPETUM DETERMINANT1(TPD1) in controlling anther cell fate determination (Li et al., 2017). In addition, SERK3/BAK1 and SERK4 (also named BAK1-LIKE 1, BKK1) 104 105 negatively regulate cell death in a BR-independent manner, and the Arabidopsis bak1serk4 mutant exhibits a seedling lethality and constitutive defense responses (He et al., 2007; 106 107 Kemmerling et al., 2007). Recent studies suggest the involvement of protein N-glycosylation and nucleocytoplasmic trafficking in the cell death control regulated by BAK1 and SERK4 (de 108 109 Oliveira et al., 2016; Du et al., 2016). Interestingly, excessive expression of BAK1 or its ectodomain could also trigger cell death in Arabidopsis with constitutive activation of defense 110 111 (Dominguez-Ferreras et al., 2015). Thus, the homeostasis of BAK1 is important for its functions in plant growth and immunity. 112

A common theme for BAK1-associated RLK complex activation is rapid heterodimerization and transphosphorylation upon the cognate ligand perception (Wang et al., 2008; Perraki et al., 2018). Members of receptor-like cytoplasmic kinases (RLCKs), including BOTRYTIS-INDUCED KINASE 1 (BIK1), associate with multiple RLKs and can be phosphorylated by BAK1 (Lu et al., 2010; Zhang et al., 2010). It has been reported that members of mammalian receptor tyrosine kinases (RTKs) involved in growth regulation, and Toll-like 119 receptors (TLRs) involved in innate immunity, require proteolytic cleavage for activation (Park et al., 2008; Ancot et al., 2009; Chen and Hung, 2015). Recently, several plant RLKs, including 120 121 rice LRR-RLK XANTHOMONAS RESISTANCE 21 (XA21) (Park and Ronald, 2012), Arabidopsis LYSM domain containing RLK CHITIN ELICITOR RECEPTOR KINASE 1 122 (CERK1) (Petutschnig et al., 2014), and legume RLK SYMBIOSIS RECEPTOR-LIKE KINASE 123 (SYMRK) (Antolin-Llovera et al., 2014), are shown to undergo proteolytic cleavage. In this 124 study, we report that BAK1 and other SERKs undergo Ca²⁺-dependent proteolytic cleavage by a 125 conserved protease(s) present in both plants and yeast. Bacteria or MAMP treatment promotes 126 the accumulation of cleaved BAK1, which occurs between the transmembrane domain and 127 ectodomain. Through an extensive mutagenesis screen, we identified the aspartate residue (D^{287}) 128 of BAK1 as an important site for its proteolytic cleavage. The BAK1^{D287A} mutation is impaired 129 in FLS2-mediated immunity, BRI1-mediated BR signaling and cell death control. Our data 130 suggest the proteolytic cleavage of plasma membrane-resident RLKs as a common mechanism in 131 the regulation of intracellular signaling. 132

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135 **Results**

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137 BAK1 undergoes Ca²⁺-dependent proteolytic cleavage

When the carboxyl (C)-terminal hemagglutinin (HA)-tagged BAK1 under the control of the 35S 138 promoter was expressed in Arabidopsis Col-0 protoplasts, we observed a major protein band 139 with a molecular weight (MW) of \sim 75 kilodalton (kD) corresponding to the full-length (FL) 140 glycosylated BAK1-HA proteins, along with at least three polypeptide bands with MW ranging 141 from 42 to 50 kD in an immunoblot (Fig. 1A). The truncated BAK1 fragments were also 142 observed when BAK1 was tagged with FLAG (Supplemental Figure S1A) or GFP (Fig. S1B) at 143 its C-terminus and expressed in protoplasts, and when BAK1 was expressed in transgenic 144 Arabidopsis plants under the control of either the 35S promoter (35S::BAK1-HA) (Fig. 1B) or its 145 native BAK1 promoter (*pBAK1::BAK1-GFP*) (Fig. 1C). To eliminate the potential complication 146 from the C-terminal epitope tag (Ntoukakis et al., 2011), we expressed BAK1 without any tag in 147 Arabidopsis protoplasts and also observed the truncated fragments of BAK1 detected by anti (α)-148 BAK1 polyclonal antibodies directing against the C-terminal peptide (DSTSQIENEYPSGPR) in 149 150 an immunoblot (Fig. 1D). Notably, among the truncated BAK1 polypeptide bands, the one with the MW of ~48 kD (~50 kD for HA- or FLAG-tagged BAK1 and ~75 kD for GFP-tagged BAK1) 151 was the most abundant in different expression systems and named as C-terminal fragment (CTF) 152 of BAK1. 153

To determine if BAK1^{CTF} was derived from proteolytic cleavage or non-specific protein 154 degradation, we applied different chemical inhibitors, including protease inhibitors, to explore 155 the biochemical requirements for the formation of BAK1^{CTF}. The calcium (Ca²⁺) chelating 156 agents ethylenediaminetetraacetic acid (EDTA) and ethylene glycol tetra-acetic acid (EGTA) 157 blocked the production of BAK1^{CTF} (Fig. 1E). In addition, the Ca²⁺ channel blockers lanthanum 158 chloride (LaCl₃) and gadolinium chloride (GdCl₃) markedly compromised the production of 159 BAK1^{CTF}, suggesting the involvement of Ca²⁺ in the formation of BAK1^{CTF} (Fig. 1E). MG132, a 160 commonly used cell-permeable proteasome inhibitor, also blocked the production of BAK1^{CTF} 161 (Fig. 1F). However, lactacystin, a specific 26S proteasome inhibitor that binds and inhibits 162 catalytic subunits of the proteasome (Fenteany et al., 1995), did not affect the production of 163 BAK1^{CTF} (Fig. 1F), suggesting the effect of MG132 on BAK1 cleavage may not be caused by its 164 inhibition on the 26S proteasome. Notably, lactacystin has no reported effect on serine or 165



Figure 1. Proteolytic processing of BAK1 in plants by a conserved protease

(A) Expression of BAK1-HA in Arabidopsis protoplasts. Protein extracts from Arabidopsis protoplasts transfected with 35S::BAK1-HA or a control vector (Ctrl) were analyzed by Western blot (WB) with an α-HA antibody. The upper band corresponding to the full-length BAK1 protein was indicated by FL, and the lower band corresponding to the C-terminal fragment of BAK1 was indicated by CTF, and labeled with a red star. (B & C) BAK1^{CTF} is produced in Arabidopsis transgenic plants. Protein extracts from 355::BAK1-HA (B) and pBAK1::BAK1-GFP (C) transgenic plants were analyzed by WB with respective α -HA and α -GFP antibodies. Wild-type Col-0 Arabidopsis was used as Ctrl. (D) Non-tagged BAK1^{CTF} is produced in Arabidopsis protoplasts. Protein extracts from Arabidopsis protoplasts transfected with 35S::BAK1 were analyzed by WB with an α-BAK1 antibody. (E & F) Effects of chemical inhibitors on the production of BAK1^{CTF}. 1 mM EDTA, 1 mM EGTA, 1 mM LaCl₃, 0.5 mM GdCl₃, 2 µM MG132 or 2 µM Lactacystin was added immediately after protoplast transfection with 35S::BAK1-FLAG. Protein extracts were analyzed by WB with an α-FLAG antibody. Lactacystin and MG132 were stored in DMSO, and other chemicals were stored in H₂O. (G) Effects of Calpain inhibitors on the production of BAK1^{CTF}. 20 µM ALLN, Calpian inhibitor III, Calpeptin, PD150606 or EST (Calbiochem, cat.# 208733) was added immediately after protoplast transfection with 355::BAK1-FLAG. Protein extracts were analyzed by WB with an α-FLAG antibody. EST was stored in ethanol (ETOH), and other inhibitors were stored in DMSO. (H & I) BAK1^{CTF} is produced in Nicotiana benthamiana and Saccharomyces cerevisiae. Protein extracts from N. benthamiana transiently expressing 35S::BAK1-HA (H) and S. cerevisiae expressing pGAL1::BAK1-HA (I) were analyzed by WB with q-HA antibodies. (J) Proteolytic cleavage is conserved in SERK family members. Protein extracts from Arabidopsis protoplasts expressing FLAG-tagged SERK1, SERK2, SERK3 (BAK1) or SERK4 were analyzed by WB with α-FLAG antibodies.

The above experiments were repeated three times with similar results.

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166 cysteine proteases whereas MG132 could also inhibit the activity of certain proteases, including

167 calpains (Tsubuki et al., 1996), a family of cytosolic calcium-dependent cysteine proteases that

- regulate a wide variety of cellular processes (Zatz and Starling, 2005; Ono and Sorimachi, 2012).
- 169 The Arabidopsis genome encodes one calpain gene *DEK1*, mutant of which is embryonic lethal

170 (Lid et al., 2005; Johnson et al., 2008), making it difficult to genetically assess the role of calpain in BAK1 cleavage. However, by using a wide collection of calpain inhibitors, we could show 171 that pretreatment of certain calpain inhibitors, such as ALLN, calpain inhibitor III, calpeptin, or 172 EST but not PD150606 nor the solvent DMSO and ethanol (ETOH) controls blocked the 173 production of BAK1^{CTF} (Fig. 1G). The data suggest that BAK1 undergoes Ca²⁺-dependent 174 cleavage in Arabidopsis, and calpain is a potential candidate that mediates BAK1 proteolytic 175 cleavage. The protease that cleaves BAK1 is conserved in plants and yeast since BAK1^{CTF} was 176 observed when it was expressed in Nicotiana benthamiana (Fig. 1H) or Saccharomyces 177 cerevisiae (Fig. 1I and S1C). Other SERK members, including SERK1, SERK2 and SERK4, 178 also produced cleaved products when they were expressed in Arabidopsis protoplasts (Fig. 1J). 179 BAK1 bears strong kinase activity. Pretreatment of the kinase inhibitor K252a did not affect the 180 formation of BAK1^{CTF} (Fig. S1D). Consistently, HA-tagged BAK1 kinase inactive mutant 181 (BAK1^{KM}-HA) produced BAK1^{CTF} similar as the wild-type (WT) BAK1-HA (Fig. S1E), 182 suggesting that the kinase activity may not be required for the BAK1 cleavage. 183

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185 BAK1 cleavage is MAMP-induced

As a co-receptor, BAK1 plays an important role in multiple cellular processes, including 186 MAMP-mediated immunity and BR-mediated growth and development (Ma et al., 2016). We 187 examined whether BAK1 cleavage is regulated upon the cognate ligand perception and signaling 188 189 activation. When we treated the *pBAK1::BAK1-GFP* plants with the nonpathogenic bacterium Pseudomonas syringae pv. Tomato (Pst) DC3000 hrcC, the abundance of BAK1^{CTF} was 190 increased at 3, 6, and 12 hours post-inoculation (hpi) (Fig. 2A). Pst hrcC is a type III secretion 191 mutant strain of Pst DC3000, which is defective in secretion of type III effectors, but possesses a 192 193 variety of MAMPs. Furthermore, using the α -BAK1 antibody, we were able to detect both the endogenous BAK1^{FL} proteins and BAK1^{CTF} in WT Col-0 plants (Fig. 2B). Notably, Pst hrcC 194 treatment enhanced the abundance of the endogenous BAK1^{CTF} proteins (Fig. 2B). Treatment of 195 purified MAMP flg22, the synthesized 22-amino-acid peptide derived from bacterial flagellin, 196 also induced the production of BAK1^{CTF} in Col-0 plants (Fig. 2B). Only a small portion of 197 endogenous BAK1 is cleaved in the cells (Fig. 2B). The abundance of BAK1^{CTF} was gradually 198 reduced during the plant maturation process from the seedling to adult stages (Fig. 2C). 199 BAK1^{CTF} was mostly abundant at 8 to 13 days post-germination (dpg), indicating a potential 200



Figure 2. Regulation of BAK1^{CTF} production

(A) Production of BAK1^{CTF} in *pBAK1::BAK-GFP* transgenic plants upon *Pst hrcC* infection. Four-week-old soil-grown *Arabidopsis pBAK1::BAK-GFP* transgenic plants were hand-inoculated with *Pst hrcC* at 5×10^5 cfu. Total proteins from inoculated leaf extracts were analyzed by WB with an α -GFP antibody. hpi, hours post inoculation. (B) Production of BAK1^{CTF} in WT plants upon infections. Four-week-old soil-grown *Arabidopsis* Col-0 plants were hand-inoculated with *Pst hrcC* at 5×10^5 cfu or 1 µM flg22. Total proteins from inoculated leaf extracted leaf extracts were analyzed by WB with an α -BAK1 antibody. (C) Developmental regulation of BAK1^{CTF} production. Total proteins extracted from *Arabidopsis* 35S::*BAK1-HA* transgenic plants at different growth stages from 8 through 35 days post germination (dpg) on ½ MS plates were analyzed by WB with an α -HA antibody. (D) BAK1^{CTF} production in different tissues. Total proteins extracted from different tissues of two-month-old soil-grown *35S::BAK1-HA* transgenic plants were analyzed by WB with an α -HA antibody. (E) BAK1^{CTF} production in different tissues. Total proteins extracted from different tissues of two-month-old soil-grown *35S::BAK1-HA* transgenic plants were analyzed by WB with an α -HA antibody. (E) BAK1^{CTF} production in different tissues. Total proteins extracted from different tissues of two-month-old soil-grown *35S::BAK1-HA* transgenic plants were analyzed by WB with an α -HA antibody. (E) BAK1^{CTF} production in different tissues. Total proteins extracted from different tissues of two-month-old soil-grown *35S::BAK1-HA* transgenic plants were analyzed by WB with an α -HA antibody. (E) BAK1^{CTF} production in different tissues. Total proteins extracted from different tissues of two-month-old soil-grown *35S::BAK1-HA* transgenic plants were analyzed by WB with an α -HA antibody. F: flowers, S: stem; CL: cauline leaves; RL: roots.

The above experiments were repeated three times with similar results.

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201 endogenous regulatory mechanism during plant growth and development underlying the BAK1

- cleavage (Fig. 2C). Additionally, we observed that BAK1^{CTF} was mostly observed in rosette and
- 203 cauline leaves, but it was less abundant in stems, flowers and roots of four-week-old 35S::BAK1-

HA transgenic plants (Fig. 2D). Taken together, the data indicate that BAK1 cleavage is a
 temporo-spatially regulated process and is also regulated upon pathogen recognition.

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207 **BAK1**^{D287} is required for the production of BAK1^{CTF}.

BAK1 possesses an extracellular LRR domain €, a transmembrane domain (T), a juxtamembrane 208 domain (J) and an intracellular kinase domain (K) (Fig. 3A). To map the BAK1 cleavage region, 209 we first compared the expression pattern of BAK1^{FL} proteins with different BAK1 truncations, 210 including the BAK1 kinase domain (BAK1^K), the juxtamembrane and kinase domains (BAK1^{JK}), 211 and the juxtamembrane, transmembrane and kinase domains (BAK1^{TJK}) (Fig. S2A). BAK1^{TJK} 212 exhibited a migration pattern similar to that of BAK1^{CTF} in an immunoblot detected by an α -213 BAK1 antibody (Fig. S2B), indicating that the BAK1 proteolytic cleavage may occur close to the 214 transmembrane domain. We then performed an extensive alanine substitution mutagenesis screen 215 to systemically mutate 35 residues in this region with each construct carrying three- or four-216 amino-acid substitution to alanine (A) (Fig. S2C). However, none of these mutations blocked the 217 BAK1 cleavage (Fig. S2D). We extended our mutagenesis screen to the neighboring regions, in 218 particular, the motifs showing certain homology to the cleavage sites of mammalian receptor 219 tyrosine kinases (RTKs) by proteases (Fig. 3A). Notably, substitution of a four-amino-acid 220 sequence at the residues 284-287 (BAK1^{VASD}) to alanine blocked the production of BAK1^{CTF} 221 (Fig. 3A & 3B). Subsequent single-amino-acid substitution among these residues indicated that 222 the aspartate-to-alanine mutation at the residue 287 (BAK1^{D287A}) was sufficient to block the 223 production of BAK1^{CTF} (Fig. 3C). When transiently expressed in N. benthamiana, BAK1^{D287A} 224 also blocked the production of BAK1^{CTF} (Fig. 3D). We further generated Arabidopsis transgenic 225 plants stably expressing HA-tagged BAK1^{D287A} under the control of the 35S promoter 226 (35S::BAK1^{D287A}-HA) (Fig. 3E) and GFP-tagged BAK1^{D287A} under the control of its native BAK1 227 promoter (pBAK1::BAK1^{D287A}-GFP) (Fig. 3F). BAK1^{CTF} was no longer detected in either 228 35S::BAK1^{D287A}-HA or pBAK1::BAK1^{D287A}-GFP transgenic plants (Fig. 3E & 3F). Aspartate is a 229 negatively charged amino acid. We also substituted aspartate to the negatively charged glutamate. 230 Similarly, aspartate-to-glutamate (BAK1^{D287E}) substitution blocked the production of BAK1^{CTF} 231 (Fig. 3G), suggesting that blocking of the cleavage in BAK1^{D287A} was not due to the loss of 232 negative charge in residue 287. The aspartate 287 residue locates in the beginning of BAK1 233 kinase domain and is a surface-exposed residue according to the published BAK1 kinase domain 234





(A) Scheme of BAK1 protein domains and sites for mutagenesis. E: extracellular LRR domain; T: transmembrane domain; J: juxtamembrane domain; K: intracellular kinase domain. (B) VASD residues are required for BAK1 cleavage. *Arabidopsis* protoplasts expressing HA-tagged BAK1 mutants, in which the indicated four amino acids were mutagenized to alanine, were analyzed by WB with an α -HA antibody. (C) D287 residue is required for BAK1 cleavage in *Arabidopsis* protoplasts. (D) D287 residue is required for BAK1 cleavage in *N. benthamiana*. *N. benthamiana* leaves transiently expressing HA-tagged BAK1 or BAK1^{D287A} mutant were analyzed by WB with α -HA antibody. (E) D287 residue is required for BAK1 cleavage in *Arabidopsis* 35S::BAK1-HA transgenic plants. (F) D287 residue is required for BAK1 cleavage in *Arabidopsis* 35S::BAK1-HA transgenic plants. (F) D287 residue is required for BAK1 cleavage in *Arabidopsis* 35S::BAK1-HA transgenic plants. (F) D287 residue is required for BAK1 cleavage in *Arabidopsis* 35S::BAK1-HA transgenic plants. (F) D287 residue is required for BAK1 cleavage in *Arabidopsis* pbaK1::BAK1-GFP transgenic plants. (G) D287E mutation blocks BAK1 cleavage in *Arabidopsis* protoplasts. (H) D287 residue of BAK1 is conserved among *Arabidopsis* SERKs. (I) BAK1 D287 corresponding residue in other SERK members is required for cleavage in *Arabidopsis* protoplasts.

The above experiments were repeated three times with similar results.

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structure (Yan et al., 2012). BAK1^{D287} is also conserved among SERKs (Fig. 3H). To determine if this site is required for proteolytic cleavage of other SERKs, we substituted the cognate aspartate residue to alanine in SERK1, SERK2 and SERK4, and found that the corresponding cleaved fragment in SERK4 and SERK2 was reduced (Fig. 3I). The data indicate that the conserved aspartate residue is required for the proteolytic cleavage of BAK1 and probablySERK4 and SERK2.

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242 BAK1^{D287} is required for PTI signaling and responses.

BAK1 plays an important role in PTI signaling and the bak1-4 mutant shows compromised 243 immune responses (Chinchilla et al., 2007; Roux et al., 2011). To determine whether the 244 cleavage is required for BAK1 function in PTI signaling, we generated the transgenic plants 245 carrying the WT BAK1 or BAK1^{D287A} under the control of the native BAK1 promoter in the bak1-246 4 mutant (pBAK1::BAK1/bak1 or pBAK1::BAK1^{D287A}/bak1). Multiple transgenic lines were 247 obtained and two representative lines for each construct with a comparable BAK1 expression 248 level between WT BAK1 and BAK1^{D287A} were used to systematically characterize PTI responses 249 (Fig. S3). As shown in Fig. 4, *pBAK1::BAK1/bak1*, but not *pBAK1::BAK1^{D287A}/bak1* transgenic 250 plants, were able to complement the deficiency of the flg22-induced MAPK activation (Fig. 4A), 251 ROS production (Fig. 4B) and callose deposition (Fig. 4C) in the bak1-4 mutant. Pre-treatment 252 of flg22 protected the WT Col-0 and pBAK1::BAK1/bak1 transgenic plants to the infection of the 253 virulent bacterium Pst DC3000 as indicated by the reduced in planta bacterial multiplication (Fig. 254 4D). However, similar to the *bak1-4* mutant, the *pBAK1::BAK1^{D287A}/bak1* transgenic plants lost 255 the flg22-mediated resistance against Pst DC3000 infection. Taken together, the data indicate 256 that BAK1^{D287}-mediated cleavage is critical for BAK1-dependent PTI responses. 257

258 BAK1 directly transphosphorylates BIK1 to relay PTI signaling (Lin et al., 2014). The pBAK1::BAK1/bak1, but not pBAK1::BAK1^{D287A}/bak1, transgenic plants restored the deficiency 259 of flg22-induced BIK1 phosphorylation in the *bak1-4* mutant evidenced by phosphoprotein 260 mobility shift in immunoblots (Fig. 4E). When BAK1 was expressed in Arabidopsis bak1-4 261 protoplasts and immunoprecipitated for a kinase assay, the *in vivo* expressed BAK1^{D287A} showed 262 reduced autophosphorylation compared to WT BAK1 (Fig. 4F). In addition, in vivo expressed 263 BAK1^{D287A} showed reduced transphosphorylation activities towards BIK1^{KM} (Fig. 4F), 264 consistent with the reduced BIK1 phosphorylation upon flg22 treatment (Fig. 4E). Notably, the 265 cleaved BAK1^{CTF} also possessed autophosphorylation activity (Fig. 4F). Interestingly, an *in vitro* 266 kinase assay showed that the cytosolic domain of BAK1 (BAK1^{CD}) and BAK1^{CD D287A} fused 267 with maltose-binding protein (MBP) purified from Escherichia coli possessed similar 268 autophosphorylation and trans-phosphorylation activities towards BIK1 (Fig. 4G), suggesting 269



Figure 4. Compromised immune responses in pBAK1::BAK1^{D287A}/bak1 transgenic plants

(A) flg22-induced MAPK activation. Two-week-old seedlings of WT Col-0, bak1-4, pBAK1::BAK1/bak1 and pBAK1::BAK1/bak1 were treated with 100 nM flg22 for 15 min. Phosphorylated MPK3 (pMPK3) and MPK6 (pMPK6) were detected by WB with an α-pERK antibody (top). Protein loading is shown by Coomassie Brilliant Blue (CBB) staining for RuBisCo (RBC) (bottom). (B) flg22-induced ROS production. Leaf discs from four leaves (technical repeats) of each of six five-week-old plants (biological repeats) of indicated genotypes were treated with 100 nM flg22, and ROS production was detected at the indicated time points. The data are shown as the mean ± SD from six biological repeats. (C) fig22-induced callose deposition. Leaves of four-week-old plants were collected for aniline blue staining 12 hr after inoculation with 500 nM flg22. Callose deposits were counted using ImageJ 1.43U software (http://rsb.info.nih.gov/ij/). The data are shown as the mean ± SD from six biological repeats. (D) flg22-mediated resistance to bacterial infection. Four-week-old plants were pretreated with 200 nM of flg22 or water and then infected with Pst DC3000 at 5×10^5 cfu/ml. The bacterial growth assays were performed 2 days after infection. The data are shown as the mean \pm SD from three biological repeats. The asterisks indicate statistical significance compared to H₂O pretreatment by using student's *t*-test (P<0.05). (E) flg22-induced BIK1 mobility shift. Arabidopsis protoplasts isolated from Col-0, bak1-4 mutant, pBAK1::BAK1/bak1 and pBAK1::BAK1^{D287A}/bak1 transgenic plants were used to express BIK1-HA and treated with 100 nM flg22 for 15 min. Mobility shift of BIK1 was detected by WB with an α-HA antibody (top). Equal loading of protein was indicated by CBB staining towards RBC (bottom). pBIK1, phosphorylated BIK1. (F) The kinase activity of BAK1 and BAK1^{D287A}. Full length BAK1-FLAG or BAK1^{D287A}-FLAG were expressed in Arabidopsis Col-0 protoplasts and precipitated with an α-FLAG antibody. Kinase activity of the precipitated proteins were detected using GST-BIK1^{KM} (kinase mutant) as a substrate. Phosphorylation was detected by autoradiography (top), and the protein loading is shown by WB with an α-FLAG antibody (bottom). (G) The *in vitro* kinase activity of the cytosolic domain of BAK1 and BAK1^{D287A}. GST-BIK1^{KM} protein was used as a substrate and MBP-BAK1^{CD} (cytosolic domain) or its D287A mutant was used as the kinase in an *in vitro* kinase assay. Phosphorylation was detected by autoradiography (top), and the protein loading is shown by CBB staining (bottom). The above experiments were repeated three times with similar results.

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that BAK1^{D287A} is a functionally competent kinase, and BAK1^{D287} mainly regulates its activity *in vivo*.

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BAK1 plays an important role in BR signaling and the bak1-4 mutant resembles the weak bri1 274 mutant with compacted rosette leaves and short petioles compared to WT Col-0 plants (Li et al., 275 276 2002; Nam and Li, 2002). The transgenic plants of *pBAK1::BAK1/bak1*, but not pBAK1::BAK1^{D287A}/bak1, restored the growth defect of bak1-4 to WT Col-0 (Fig. S3). When 277 grown in the dark, hypocotyls of *pBAK1::BAK1^{D287A}/bak1* transgenic plants and *bak1-4* were 278 shorter than those of *pBAK1::BAK1/bak1* transgenic plants and WT Col-0 in the absence or 279 presence of brassinazole (BRZ), an inhibitor of BR biosynthesis (Fig. 5A & 5B), suggesting an 280 important role of BAK1^{D287} in mediating BR signaling. BAK1 positively regulates BR signaling 281 by heterodimerization and transphosphorylation with BRI1 (Li et al., 2002; Nam and Li, 2002). 282 Overexpression of functional BAK1 partially alleviates the growth defects of the bri1 mutants. 283 We generated Arabidopsis transgenic plants expressing BAK1 or BAK1^{D287A} under the control of 284 the 35S promoter in the bri1-5 mutant (35S::BAK1/bri1-5 and 35S::BAK1^{D287A}/bri1-5). Multiple 285 transgenic lines were obtained and two lines of each construct with comparable BAK1 protein 286 levels were selected for further study (Fig. 5C & 5D). As previously reported, overexpression of 287 BAK1 in bri1-5 partially rescued the dwarf phenotype of bri1-5 with relatively big leaves, 288 elongated stems, and long siliques compared to bri1-5 (Nam and Li, 2002). In contrast, 289 overexpression of BAK1^{D287A} in *bri1-5* did not recover the dwarf phenotype of *bri1-5*, instead 290 enhanced the growth defects of bri1-5. The 35S::BAK1^{D287A}/bri1-5 transgenic plants were sterile 291 (Fig. 5C). Taken together, the data suggest that BAK1^{D287} is required for BAK1 function in BR 292 293 signaling.

BAK1 together with SERK4 (also called BAK1-LIKE 1 [BKK1]) play a redundant role 294 295 in the regulation of cell death and the bak1/serk4 mutant is seedling lethal associated with spontaneous cell death and constitutive H₂O₂ production (He et al., 2007). To assess the 296 requirement of BAK1^{D287} in BAK1/SERK4-regulated cell death, we transformed pBAK1::BAK1 297 and *pBAK1::BAK1^{D287A}* into the Arabidopsis *BAK1-4^{+/-}SERK4-1^{-/-}* mutant and examined the 298 growth phenotypes of T1 generation of transgenic plants. We further differentiated BAK1 WT 299 $(BAK1^{+/+})$, BAK1 heterozygous $(BAK1^{+/-})$ and BAK1 mutant $(BAK1^{-/-})$ genotypes by genotyping 300 T-DNA insertions in the transgenic plants. Transgenic plants of pBAK1::BAK1 and 301 *pBAK1::BAK1^{D287A}* in *BAK1^{+/+}SERK4^{-/-}* or *BAK1^{+/-}SERK4^{-/-}* backgrounds displayed normal 302 growth phenotype as the WT Col-0 plants (Fig. 5E). However, pBAK1::BAK1^{D287A} transgenic 303 plants in the BAK1^{-/-}SERK4^{-/-} background showed growth defects with much short petioles, and 304



Figure 5. BAK1 D287 is critical for BR signaling and cell death control

(A) The reduced hypocotyl length of *pBAK1::BAK1^{D287A}/bak1* transgenic plants. The seedlings of WT, *bak1-4* and transgenic plants were grown in the dark for 5 days on ½ MS plats without or with 1 μ M of BRZ. (B) Quantification of the hypocotyl length shown in (A). The data are shown as the mean ± SD from 20 biological repeats. The different letters indicate statistically significant difference analyzed with one-way ANOVA followed by Tukey's test (P<0.05). (C) BAK1^{D287A} mutant cannot restore *bri1-5* dwarf defect. Transgenic plants of *355::BAK1* and *355::BAK1^{D287A}* in *bri1-5* background were taken photos at two months old. The individual leaves and siliques are shown in the middle and bottom. (D) Expression of BAK1 protein in rosette leaves from four-week-old plants of (C) was detected by WB with an α-BAK1 antibody. (E) D287 is important for BAK1 function in cell death control. Arabidopsis *BAK1^{+/-}SERK4^{-/-}* plants were transformed with *pBAK1::BAK1* or *pBAK1::BAK1^{D287A}*. Plants of T₁ generation after selection of BAK1 or BAK1^{10287A} transgene were genotyped for endogenous genomic BAK1. Pictures were taken four weeks after germination. *BAK1^{+/+}SERK4^{-/-}* (BAK1: WT, SERK4: mutant); *BAK1^{+/-}SERK4^{-/-}* (BAK1: heterozygous, SERK4: mutant); *BAK1^{-/-}SERK4^{-/-}* (BAK1: mutant, SERK4: mutant). Scale bars, 1 cm.

The above experiments were repeated three times with similar results.

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- small leaves compared to the WT Col-0 plants (Fig. 5E). Notably, there are variations of growth
- defects of $pBAK1::BAK1^{D287A}$ in the $BAK1^{-/-}SERK4^{-/-}$ background, with plants similar to or better
- than $BAK1^{-/-}SERK4^{-/-}$ (Fig. 5E). Thus, BAK1^{D287} is partially required for BAK1/SERK4-mediated
- 308 cell death. In addition, silencing of SERK4 in bak1-4, but not in WT Col-0 plants, using the

309 Agrobacterium-mediated virus-induced gene silencing (VIGS) triggers severe growth defects and cell death (de Oliveira et al., 2016) (Fig. S4A). Silencing of SERK4 in pBAK1::BAK1/bak1 310 311 transgenic plants via VIGS did not trigger growth defects, whereas silencing of SERK4 in *pBAK1::BAK1^{D287A}/bak1* transgenic plants exhibited severe growth defects with chlorotic leaves 312 and dwarfism (Fig. S4A). Trypan blue staining revealed spontaneous cell death in bak1-4 and 313 *pBAK1::BAK1^{D287A}/bak1* transgenic plants but not in Col-0 and *pBAK1::BAK1/bak1* transgenic 314 plants upon silencing of SERK4 (Fig. S4B). Additionally, RT-quantitative PCR (RT-qPCR) 315 analysis indicated that transcripts of *pathogenesis-related protein 1 (PR1)* and *PR2* were 316 significantly increased in bak1-4 and pBAK1::BAK1^{D287A}/bak1 plants compared to Col-0 and 317 *pBAK1::BAK1/bak1* plants upon silencing of *SERK4* (Fig. S4C). The data further elaborated that 318 BAK1^{D287} is required for BAK1 and SERK4-regulated cell death. 319

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321 BAK1^{D287} is required for BAK1 plasma membrane localization.

BAK1 is a plasma membrane-localized protein (Li et al., 2002; Nam and Li, 2002), that is also 322 likely localized to endosomal compartments (Russinova et al., 2004). We tested whether D287A 323 is important for BAK1 localization by generating *pBAK1::BAK1-GFP* and *pBAK1::BAK1^{D287A}*-324 GFP transgenic plants. As reported previously, BAK1-GFP was mainly localized in the plasma 325 membrane, where it colocalized with FM4-64, a lipophilic dye that labels plasma membrane 326 (Fig. 6A, top panels, &6B). However, the plasma membrane localization of BAK1^{D287A}-GFP was 327 greatly reduced in the *pBAK1::BAK1^{D287A}-GFP* transgenic plants (Fig. 6A, bottom panels & 6B). 328 The BAK1^{D287A}-GFP protein appeared retained in the endoplasmic reticulum (ER) as 329 330 corroborated by colocalization analyses using the ER marker mCherry-HDEL (Nelson et al., 2007) (Fig. 6C) and the ER-Tracker Red (Fig. S5). The reduced plasma membrane localization 331 of BAK1^{D287A} was also documented by protein fractionation assay. BAK1-HA and BAK1^{D287A}-332 HA were transiently expressed in N. benthamiana, and total proteins and plasma membrane-333 enriched fractions were analyzed with an α-HA immunoblot. The HA-tagged RLK PSKR1 was 334 co-expressed with BAK1-HA or BAK1^{D287A}-HA as a control for the plasma membrane-localized 335 proteins (Ladwig et al., 2015). Immunoblot for endogenous MPK6 with an α-MPK6 antibody 336 was used as a cytoplasmic protein control (Collins et al., 2017). Significantly, compared to WT 337 BAK1, the amount of BAK1^{D287A} in the plasma membrane-enriched fraction was greatly 338 reduced, although the amount of PSKR1 in the plasma membrane-enriched fraction stayed the 339



Figure 6. D287 is critical for the plasma membrane localization of BAK1

(A) Subcellular localization of BAK1-GFP (top panel) and BAK1^{D287A}-GFP (bottom panel) in root epidermis of five-day-old *Arabidopsis* seedlings. The plasma membrane was stained with FM4-64 (2 μ M). (B) Pearson's correlation coefficient (*r* value) for the colocalization between GFP and FM4-64 fluorescence in the plasma membrane. These values were measured in 15 cells. Error bars indicate mean ± SD. P-value (*t*-test), * P<0.01. (C) Colocalization of BAK1^{D287A}-GFP with endoplasmic reticulum (ER) marker, mCherry-HDEL. Scale bars, 20 μ m. (D) Leaves of four-week-old *N. benthamiana* were hand-inoculated with Agrobacteria carrying *355::BAK1-HA* or *355::BAK1^{D287A}-HA* together with *355::PSKR1-HA*. BAK1 from total proteins and enriched plasma membrane (PM) proteins were analyzed by WB with an α -HA antibody. Cytosolic MPK6 was detected by α -MPK6 WB. PSKR1 is a plasma membrane-localized protein. The above experiments were repeated three times with similar results.

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same when it was co-expressed with BAK1 or BAK1^{D287A} (Fig. 6D). Thus, D287 is essential for
BAK1 to localize in the plasma membrane, where it functions as a co-receptor to activate diverse
signaling pathways.

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Overexpression of *BAK1*^{D287A} triggers SOBIR1-dependent and BIK1-independent cell death. 344 Overexpression of BAK1 under a double 35S (2x35S) promoter in Arabidopsis triggers plant 345 dwarfism accompanied with cell death (Dominguez-Ferreras et al., 2015). Consistently, transient 346 expression of 2x35S::BAK1 triggered cell death in N. benthamiana. Expression of 347 2x35S::BAK1^{D287A} clearly aggravated the occurrence of cell death in N. benthamiana (Fig. 7A). 348 The elevated cell death by $2x35S::BAKI^{D287A}$ was also indicated by the autofluorescence signals 349 under the UV light (Fig. 7B) and the electrolyte leakage (Fig. 7C). We did not detect cell death 350 when BAK1 was under the control of a single 35S promoter (35S::BAK1). However, 351 35S::BAK1^{D287A} triggered cell death when transiently expressed in N. benthamiana (Fig. 7A, 7B 352 & 7C). No cell death was observed when *BAK1* or *BAK1*^{D287A} was expressed under the control of 353 its native promoter (*pBAK1::BAK1 or pBAK1::BAK1^{D287A}*) (Fig. 7A, 7B & 7C). The occurrence 354 of cell death by overexpression of BAK1 appeared to be correlated with the level of BAK1 355 proteins as 2x35S::BAK1 produced more BAK1 proteins, including both BAK1^{FL} and BAK1^{CTF}. 356 than 35S::BAK1 (Fig. 7A). We further generated Arabidopsis transgenic plants overexpressing 357 BAK1 and BAK1^{D287A} under the control of the 35S promoter in the Col-0 (WT) background. 358 Among 39 *35S*::*BAK1* plants with positive signals by α-BAK1 immunoblots, 33% (13 out of 39) 359 of transgenic plants were small and showed dwarfism. However, 64% (9 out of 14) of 360 35S::BAK1^{D287A} transgenic plants were small and dwarfed (Fig. 7D). The small plants were 361 associated with cell death as stained by trypan blue and H₂O₂ accumulation as stained by DAB 362 (Fig. 7E). RT-qPCR analysis revealed that the expression of *PR1* and *PR2* was elevated in the 363 35S::BAK1^{D287A} transgenic plants than that in 35S::BAK1 plants (Fig. 7F). Taken together, our 364 365 data indicate that cleavage of BAK1 might be a way to alleviate cell death when BAK protein level is high in plants. 366

367 BIK1 is a key component downstream of BAK1 in plant immunity (Lin et al., 2013; Liang and Zhou, 2018). We tested whether cell death caused by overexpression of BAK1 or BAK1^{D287A} 368 depends on BIK1 by transferring 35S::BAK1 or 35S::BAK1^{D287A} into the bik1 mutant. Compared 369 to WT plants, the bik1 mutant did not reduce the portion of small plants of 35S::BAK1 or 370 35S::BAK1^{D287A} transgenic plants (Fig. 7G), indicating that cell death caused by over-expression 371 of BAK1 or BAK1^{D287A} is BIK1-independent. Thus, it is likely that cleavage of over-produced 372 BAK1 negatively regulates cell death independently of flg22-triggered signaling. It has been 373 reported that overexpression of BAK1-triggered cell death is dependent on SOBIR1 (Suppressor 374



Figure 7. Over-production of BAK1 ^{D287A} enhances SoBIR1-dependent cell death

(A) Expression of BAK1 and BAK1^{D287A} under different promoters in N. benthamiana. Leaves of four-week-old N. benthamiana were hand-inoculated with Agrobacteria carrying 35S::GFP, 2x35S::BAK1, 2x35S::BAK1^{D287A}, 35S::BAK1, 35S::BAK1, D287A, pBAK1::BAK1 or pBAK1::BAK1^{D287A}. Pictures were taken under UV light (left) or visible light (right) three days after inoculation. Two days after inoculation and before cell death progressed, protein levels of BAK1 were analyzed by WB with an α-BAK1 antibody (bottom). BAK1 proteins from 2x355::BAK1 (2) and 2x355::BAK1^{D287A} (3) were detected by WB using SuperSignalTM West Pico Chemiluminescent Substrate, and BAK1 proteins from 355::BAK1 (4) and 355::BAK1^{D287A} (5) were detected using Thermo ScientificTM SuperSignalTM West Femto Maximum Sensitivity Substrate. (B) The fluorescent signal from the circled areas in (A) was obtained under the UV light and was quantified as means ± SD from ten biological repeats. The asterisks indicate statistical significance by using student's t-test (P<0.05). (C) Measurement of electrolyte leakage of leaf discs from (A). Data are shown as means ± SD from three biological repeats. The asterisks indicate statistical significance by using student's t-test (P<0.05). (D) Overexpression of BAK1 and BAK1^{D287A} in Arabidopsis. Arabidopsis plants overexpressing 355::BAK1 or 355::BAK1^{D287A} were taken photos at four-week-old stage. Each phenotype of T₁ generation plants was calculated as a percentage to the total transgenic plants of that genotype. (E) Cell death and H₂O₂ accumulation in the leaves of four-week-old plants were examined by trypan blue and DAB staining respectively. B: normal-looking plants; S: small plants. (F) Expression levels of PR genes in one-week-old transgenic plants were determined by qRT-PCR. The data are shown as means ± SD from three biological repeats. The asterisks indicate statistical significance by using student's t-test (P<0.05). (G) BAK1 and BAK1^{D287A} cell death is SoBIR1-dependent and BIK1-independent. 35S::BAK1 and 35S::BAK1^{D287A} were transformed into sobir1 and bik1 mutant backgrounds. Each phenotype of T1 generation at four-week-old stage was calculated as a percentage as in (D). The above experiments were repeated three times with similar results.

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Of BIR1-1), which encodes an LRR-RLK (Gao et al., 2009; Dominguez-Ferreras et al., 2015).
We examined whether overexpression of BAK1^{D287A}-triggered cell death also requires SOBIR1
by transferring 35S::BAK1 or 35S::BAK1^{D287A} into the *sobir1* mutant. Significantly, the ratio of

dwarfed plants in *sobir1* was reduced for both 35S::BAK1 (33% to 10%) and 35S::BAK1^{D287A}

379 (64% to 17%) transgenic plants compared to WT plants (Fig. 7G). Thus, over-expression of
 BAK1^{D287A} causes a SOBIR1-dependent, but BIK1-independent cell death.

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383 Discussion

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In animal studies, members of cell surface proteins have been observed to undergo multi-layered 385 proteolytic cleavage processes to regulate transmembrane protein functions (Hayashida et al., 386 2010). For example, proteolytic cleavage of some RTKs upon ligand binding triggers their 387 nuclear translocation to execute their functions in the nucleus (Carpenter and Liao, 2013). 388 Immune receptors TLR7 and TLR9 are ectodomain-cleaved and form the functional receptors in 389 the endolysosome (Ewald et al., 2008; Park et al., 2008; Petes et al., 2017). Similarly, rice LRR-390 RLK XA21, which confers broad-spectrum immunity to the Gram-negative bacterial pathogens, 391 is cleaved and the intracellular domain is likely translocated to the nucleus, where it interacts 392 with transcription factors for immune activation (Park and Ronald, 2012). The legume RLK 393 394 SYMRK undergoes proteolytic cleavage and the cleaved ectodomain promotes the formation of a complex with NOD-FACTOR RECEPTOR 5 (NFR5), which is involved in root symbiosis 395 (Antolin-Llovera et al., 2014). Arabidopsis chitin receptor RLK CERK1 is also likely cleaved, 396 and a mutation that blocks cleavage generates a novel function of CERK1 in chitin-independent 397 398 cell death control (Petutschnig et al., 2014). An ATP-binding proteomics analysis predicted that two uncharacterized LRR-RLKs (At3g02880 and At5g16590) exist in leaves only as cytoplasmic 399 400 domains, suggesting that the extracellular domains are cleaved (Villamor et al., 2013). We show here that the shared coreceptor BAK1, and likely other SERK family members, are cleaved by a 401 402 conserved protease in eukaryotes (Fig. 1). Importantly, this cleavage is enhanced by pathogen or MAMP treatments (Fig. 2), suggesting that the BAK1 cleavage is involved in plant responses to 403 404 pathogen attacks. Together with previous findings, the proteolytic cleavage of plant RLKs is likely another layer of regulatory mechanism in addition to the well-studied phosphorylation, 405 406 which controls RLK activation.

We have observed that BAK1 cleavage is Ca^{2+} -dependent (Fig. 1E), and multiple calpain inhibitors blocked BAK1 cleavage *in vivo* (Fig. 1G). Since the mutation of plant calpain DEK1 is embryonic lethal (Lid et al., 2005; Johnson et al., 2008), we attempted to silence Arabidopsis *DEK1* with VIGS. However, we did not observe the change of BAK1 cleavage in *DEK1*-silenced plants compared to control plants (Supplemental Figure S6). Notably, *DEK1*-silenced plants were phenotypically similar to control plants. It is possible that the reduced DEK1 level in *DEK1*-silenced plants is sufficient for its normal functions. Despite extensive studies on 414 mammalian calpains, the sequence and structural determinants of cleavage targets are little understood (Johnson et al., 2005), and no substrates of calpain in plants have been reported yet. 415 416 Plant RLKs are functional counterparts of mammalian RTKs, cleavage of which is stimulated by caspases, metalloproteases, y-secretase complex or mRNA splicing (Ancot et al., 2009; Chen and 417 Hung, 2015). The most prevalent mechanism of RTK cleavages occurs within the membrane 418 through the action of a multisubunit γ -secretase complex (Carpenter and Liao, 2013). BAK1 419 cleavage likely occurs within or immediately after the transmembrane domain (Fig. S2B). 420 Arabidopsis also contains genes coding for γ -secretase homologous with the conserved amino 421 acid motifs essential for enzymatic activities (Smolarkiewicz et al., 2014). However, the 422 functions of γ -secretase subunits in plants are largely unknown. In a forward genetic screen for 423 suppressors of the growth phenotype of a weak brassinosteroid insensitive 1 allele bri1-5, BRS1 424 was identified and demonstrated as a secreted and active serine carboxypeptidase (Li et al., 2001; 425 Zhou and Li, 2005). Although BRS1's substrates remain unknown, this work reconciles the 426 importance of proteolytic cleavage processes in BR signaling. The proteolytic cleavage of BAK1 427 is required for its function in BR signaling and overexpression of BAK1^{D287A} fails to alleviate the 428 growth defects of bri1-5 (Fig. 5C & 5D). It remains possible that BRS1 proteolytically processes 429 BAK1 or plays a role in the BAK1 cleavage. 430

431 We have identified D287 as an important site for BAK1 cleavage (Fig. 3). This site is conserved among other SERK family members and likely required for SERK2 and SERK4 432 433 cleavage (Fig. 3I). D287 locates at the beginning of BAK1 kinase domain (Fig. 3A). BAK1 is a type I integral membrane protein with a single transmembrane domain, an extra-cytoplasmic 434 435 receptor domain and a cytoplasmic kinase domain. Based on the molecular weight, BAK1 cleaved products are bigger than the predicted products of cytoplasmic domain (Fig. S2A & 436 437 S2B). D287 may not be the cleavage site, but it is essential for the protease-mediated cleavage. Importantly, D287 is essential for BAK1 functions in plant immunity (Fig. 4), BR responses 438 (Fig. 5A-C) and cell death control (Fig. 5D & 5E). Interestingly, the BAK1^{D287A} mutant 439 exhibited an unaltered in vitro kinase activity (Fig. 4G), suggesting that BAK1^{D287A} is still a 440 functional protein. There are several possibilities to explain why BAK1 cleavage is required for 441 its normal functions. Similar with XA21 (Park and Ronald, 2012), the cleaved BAK1 may be 442 released from the plasma membrane and translocated to the nucleus or other subcellular 443 compartments to execute the functions. However, we have not observed a claimable nuclear 444

localization of BAK1. It is also possible that the activated cytoplasmic domain of BAK1 is 445 released to cytoplasm, where it phosphorylates different substrates for bifurcating its different 446 447 functions. Additionally, the cleaved BAK1 ectodomain may have a higher affinity for the extracellular LRR domains of FLS2 and BRI1 than the full-length BAK1, and may promote the 448 ligand-induced receptor complex formation. We have observed that the BAK1 ^{D287A} mutant has a 449 reduced plasma membrane localization (Fig. 6). The cleaved BAK1 fragments may facilitate the 450 translocation of BAK1 to the plasma membrane. The BAK1^{D287A} mutant is likely trapped in the 451 endoplasmic reticulum (ER) during protein maturation process (Fig. 6C & 6D). ER-mediated 452 protein quality control is essential for the abundance and signaling of some LRR-RLKs, such as 453 EFR and BRI1 (Liu and Li, 2014; Tintor and Saijo, 2014). 454

Overexpression of BAK1 or its ectodomain in Arabidopsis triggers growth defects and 455 constitutive activation of defense and cell death (Dominguez-Ferreras et al., 2015). It has been 456 postulated that this cell death might be caused by unbalanced regulatory interactions, such as 457 insufficient amount of the BAK1-INTERACTING RECEPTOR-LIKE KINASE 1 (BIR1), which 458 can suppress BAK1 activity (Gao et al., 2009; Dominguez-Ferreras et al., 2015; Liu et al., 2016). 459 We observed that overexpression of the BAK1^{D287A} mutant caused more extensive cell death 460 than WT BAK1 in N. benthamiana and Arabidopsis when they were expressed at the same level 461 462 (Fig. 7A-F). These data suggest that BAK1 cleavage might provide a means to avoid the detrimental effect of BAK1 overproduction. Both BAK1 and BAK1^{D287A}-induced cell death 463 464 depends on SOBIR1 (Fig. 7G), which mediates bir1-induced cell death (Gao et al., 2009). SOBIR1 appears to be specifically required for immune responses triggered by certain LRR 465 466 receptor-like proteins (LRR-RLPs), not LRR-RLKs (Liebrand et al., 2014). Thus, BAK1 overexpression-activated defense is likely mediated by a different mechanism with BAK1-467 468 mediated PTI in which BAK1 functions as a coreceptor of multiple LRR-RLKs. Indeed, BAK1 overexpression-activated defence is independent of a key PTI regulatory protein BIK1 (Fig. 7G). 469 470 Thus, cleavage of BAK1 may have dual roles in plant immunity: mediating BIK1-dependent PTI signaling and attenuating SOBIR1-dependent autoimmunity. Notably, Dominguez-Ferreras et al. 471 also observed the presence of multiple BAK1 polypeptides in BAK1 overexpression and WT 472 plant extracts, and speculated that they were the products of proteolytic cleavage (Dominguez-473 Ferreras et al., 2015). 474

475 Pathogen effector-mediated proteolytic cleavage is a common mechanism in the activation or attenuation of plant immunity (Dean, 2011; Pogany et al., 2015; Hou et al., 2018). 476 477 P. syringae effector AvrPphB, a cysteine protease, can cleave Arabidopsis RLCK AVRPPHB SUSCEPTIBLE 1 (PBS1) to initiate cytoplasmic immune receptor RESISTANCE TO P. 478 SYRINGAE 5 (RPS5)-specified effector-triggered immunity (ETI) and cleave PBS1-like (PBL) 479 kinases BIK1, PBL1, and PBL2 to inhibit PTI (Shao et al., 2003; Zhang et al., 2010). 480 Interestingly, P. syringae effector HopB1 binds to FLS2 and cleaves immune-activated BAK1 to 481 inhibit plant immunity (Li et al., 2016). In this study, we show that BAK1 proteolytic cleavage is 482 dependent on a host-originated protease(s). In contrast to the HopB1-mediated BAK1 cleavage 483 which occurs within the kinase domain between Arg297 and Gly298 (Li et al., 2016), the 484 conserved eukaryotic protease-mediated BAK1 cleavage identified in this study occurs likely 485 within the transmembrane domain, and the cleaved BAK1^{CTF} has a normal kinase activity as the 486 WT BAK1 (Fig. 4F). In the case of HopB1-mediated cleavage, the phosphorylation status of 487 BAK1 is critical as two kinase-dead mutants (BAK1^{K317E} and BAK1^{D416N} in the ATP-binding 488 site and catalytic site, respectively) and a phospho-site mutant of BAK1 (BAK1^{T455A}) are 489 resistant to cleavage by HopB1 (Li et al., 2016). In contrast, our studies show that the host 490 protease-mediated BAK1 cleavage does not require BAK1 kinase activity (Fig. S1D & S1E). 491 Similarly, the proteolytic cleavage at the ectodomain of mammalian EPIDERMAL GROWTH 492 FACTOR RECEPTOR (EGFR) does not require its kinase activity (Chen et al., 2008; Liao and 493 494 Carpenter, 2012). These findings show that plants use a different type of protease with bacterial effector HopB1 to cleave BAK1 for a distinct function. 495

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497 Materials and Methods

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Plant materials, growth conditions and treatments. The following *Arabidopsis thaliana* mutant lines have been described previously: *bik1* (Salk_005291), *sobir1-12, bak1-4, serk4-1* and *bak1/SERK4*^{+/-} in Col-0 background (Gao et al., 2009; Lu et al., 2010; de Oliveira et al., 2016), *bri1-5* in Ws-0 background (Lin et al., 2013). Arabidopsis plants were grown in soil (Metro Mix 366) in a growth room with 23°C, 45% relative humidity, 85 μE m⁻² s⁻¹ light and a photoperiod of 12 hr light /12 hr dark for four weeks before protoplast isolation. To grow Arabidopsis seedlings on medium, the seeds were surface-sterilized with 50% bleach for 15 min, washed with sterilized ddH_2O and then placed on the plates with half-strength Murashige and Skoog medium ($\frac{1}{2}$ MS) containing 0.5% sucrose, 0.8% agar and 2.5 mM MES at pH 5.7. The plates were first stored at 4°C for 3 days in the dark for seed stratification, and then moved to the growth room for different periods of time depending on the experiments.

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Plasmid construction and generation of transgenic plants. Protoplasts expression vectors 511 pHBT-35S::BAK1-HA, pHBT-35S::BAK1-FLAG, pHBT-35S::BAK1-GFP, pHBT-35S::SERK1-512 FLAG, pHBT-35S::SERK2-FLAG, pHBT-35S::SERK4-FLAG, pHBT-35S::BIK1-HA, pHBT-513 35S::FLS2-HA, protein expression vectors pMAL-BAK1^{CD}, pGST-BIK1^{KM}, and VIGS vector 514 pYL156-SERK4 were reported previously (Shan et al., 2008; Lu et al., 2010; Lu et al., 2011; Lin 515 et al., 2013; Zhou et al., 2014; Meng et al., 2015; de Oliveira et al., 2016; Meng et al., 2016). The 516 517 yeast expression vector *pESC-BAK1-MYC* and binary vector *pPZP212-pBAK1:BAK1-GFP* were obtained from Dr. Jianming Li (Nam and Li, 2002). The binary vector pMDC32-2x35S::BAK1 518 was obtained from Dr. Chinchilla Delphine (Dominguez-Ferreras et al., 2015). The yeast 519 expression vector pYES2-BAK1-HA was generated by sub-cloning BAK1-HA from pHBT-520 521 35S::BAK1-HA into a modified pYES2 vector using primers listed in Table S1. Non-tagged fulllength or truncated BAK1 in pHBT was cloned using pHBT-35S::BAK1-FLAG as the template 522 523 and primers listed in Table S1. To construct pCB302-35S::BAK1 and pCB302-35S::BAK1-HA binary vectors for Agrobacterium-mediated transformation in Arabidopsis, BAK1 was sub-cloned 524 525 into a modified plant transformation binary vector pCB302 derivative under the control of the 35S promoter with or without an HA-epitope tag at its C-terminus. To construct pHBT-526 527 pBAK1::BAK1-GFP and pCB302-pBAK1::BAK1, the 35S promoter in pHBT-35S::BAK1-GFP or pCB302-35S::BAK1 was substituted with the 1.5kb BAK1 promoter that was amplified by 528 529 PCR from Col-0 genomic DNA. BAK1/SERK point mutation variants were generated by sitedirected mutagenesis with primers listed in Table S1 and using respective BAK1 or SERK4 530 531 constructs as the templates. Full-length PSKR1 was amplified by PCR from Col-0 cDNA and cloned into a modified plant expression vector *pCAMBIA1300* with a HA tag. 532

The *BAK1* transgenic plants were generated by *Agrobacterium*-mediated transformation of Col-0, *bri1-5*, *sobir1-12*, *bik1* or *bak1/SRK4*^{+/-}, and screened with the herbicide BASTA (resistance conferred by the *pCB302* binary vector), antibiotic kanamycin (*pPZP212*) or hygromycin (*pMDC32*). BAK1 expression was detected by RT-PCR or Western blot with α -HA, 537 α -GFP or α -BAK1 antibodies. The homozygous lines were selected based on the survival ratio 538 of T₂ and T₃ generation plants after BASTA spray or antibiotic selection.

539 $pBAK1::BAK1^{D287A}$ -GFP plants expressing the ER marker were generated by 540 Agrobacterium-mediated transformation with p2x35S::mCherry-HDEL (CD3-959, ER-rk) 541 (Nelson et al., 2007). T1 plants were selected on kanamycin and transferred to $\frac{1}{2}$ MS without 542 antibiotic for 2 days before imaging.

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Arabidopsis protoplast and *Nicotiana benthamiana* transient assays. For Arabidopsis protoplast transient expression, protoplasts were transfected with genes in the *pHBT* vector and incubated for 12 hr (He et al., 2007). The cell extracts were added with $2 \times SDS$ loading buffer and subjected to immunoblot analysis.

For N. benthamiana transient expression, Agrobacterium tumefaciens strain GV3101 548 containing binary vector was cultured overnight in LB medium at 28 °C. Bacteria were harvested 549 by centrifugation and resuspended with buffer (10 mM MES, pH 5.7, 10 mM MgCl₂, 200 µM 550 acetosyringone) at $A_{600} = 0.75$. Leaves of four-week-old soil-grown N. benthamiana were hand-551 infiltrated using a needleless syringe with Agrobacterium cultures. Leaf samples were collected 552 36 hr after infiltration for protein isolation and immunoblot analysis. The cell death phenotype 553 was observed and leaf pictures were taken three days after infiltration under UV light with a 554 ChemiDoc system. 555

For electrolyte leakage assays, eight leaf discs (0.5 cm diameter) excised from *N*. *benthamiana* four days after infiltration was termed as one sample and was pre-floated in 10 ml of ddH₂O for 10-15 min to eliminate wounding effect. The ddH₂O was then exchanged and electrolyte leakage was measured using a conductivity meter (VWR; Traceable Conductivity Meter) as the average of three samples (n= 3).

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In vitro phosphorylation, immunocomplex kinase and *in vivo* MAP kinase assays. For *in vitro* kinase assay, reactions were performed in 30 μ l of kinase buffer (20 mM Tris-HCl, pH 7.5, 10 mM MgCl₂, 5 mM EGTA, 100 mM NaCl, and 1 mM DTT) containing 10 μ g of fusion proteins with 0.1 mM cold ATP and 5 μ Ci [³²P]- γ -ATP at room temperature for 3 hr with gentle shaking. The reactions were stopped by adding 4 x SDS loading buffer. The phosphorylation of fusion proteins was analyzed by autoradiography after separation with 12% SDS-PAGE.

568 For immunocomplex kinase assay, protoplasts were lysed with 0.5 mL of IP buffer (50 mM Tris·HCl, pH 7.5, 150 mM NaCl, 5 mM EDTA, 1 mM DTT, 2 mM NaF, 2 mM Na₃VO₃, 1% 569 570 Triton, and a protease inhibitor mixture from Roche). After centrifugation at 12,470 g for 10 min at 4°C, the supernatant was incubated with an α-FLAG antibody for 2 hr and then with protein-571 G-agarose beads for another 2 hr at 4°C with gentle shaking. The beads were collected and 572 washed once with IP buffer and once with kinase buffer (20 mM Tris·HCl, pH 7.5, 20 mM 573 MgCl₂, 5 mM EDTA, and 1 mM DTT). The kinase reactions were performed in 20 µl of kinase 574 buffer with 2 µg of GST fusion proteins, 0.1 mM cold ATP, and 5 µCi of $[^{32}P]-\gamma$ -ATP at room 575 temperature for 1 hr with gentle shaking. The phosphorylation of GST fusion proteins was 576 analyzed by 10% SDS-PAGE. 577

578 For detecting MAP kinase activity *in vivo*, two-week-old seedlings grown on $\frac{1}{2}$ MS 579 medium were transferred to water overnight and then treated with 100 nM flg22 or H₂O for the 580 times indicated and frozen in liquid nitrogen. The seedlings were homogenized in IP buffer and 581 equal amount of total protein was electrophoresed on 10% SDS–PAGE. An α -pERK antibody 582 (1:2,000) (Cell Signaling) was used to detect phosphorylation status of MPK3 and MPK6 with 583 an immunoblot.

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Measurement of ROS production. Four leaves of each of six five-week-old Arabidopsis plants 585 were excised into leaf discs of 0.25 cm^2 , following an overnight incubation in 96-well plate with 586 587 100 μ l of H₂O to eliminate the wounding effect. H₂O was replaced by 100 μ l of reaction solution containing 50 µM luminol and 10 µg/ml horseradish peroxidase (Sigma) supplemented with 100 588 nM flg22. The luminescence was measured with a luminometer (Perkin Elmer, 2030 Multilabel 589 Reader, Victor X3) immediately after adding the solution, with a 2 min interval reading time for 590 591 a period of 60 min. The measurement value of ROS production from 24 leaf discs per treatment was indicated as the mean of RLU (Relative Light Units). 592

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Callose deposition. The leaves of four-week-old plants were incubated with 500 nM flg22 for 12 hr at room temperature. Leaves were immediately cleared in alcoholic lactophenol [95% ethanol: lactophenol (phenol: glycerol: lactic acid: H_2O 1:1:1:1)=2:1] overnight. Samples were subsequently rinsed with 50% ethanol and H_2O . Cleared leaves were stained with 0.01% aniline blue in 0.15 M phosphate buffer (pH 9.5) and the callose deposits were visualized under a UV filter using a fluorescence microscope. Callose deposits were counted using ImageJ 1.43U
software (http://rsb.info.nih.gov/ij/). The number of deposits was expressed as the mean of six
different leaf areas with standard error.

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Pathogen infection assays. Pseudomonas syringae pv. tomato DC3000 strain was cultured 603 overnight at 28°C in KB medium with 50 µg/ml rifampicin. Bacteria were collected, washed and 604 diluted to the desired density with H2O. Four-week-old Arabidopsis leaves were pre-inoculated 605 with 200 nM flg22 or H₂O control for 24 hr and then infiltrated with bacteria at a concentration 606 of 5 x 10^5 cfu/ml using a needleless syringe. To measure bacterial growth, two leaf discs were 607 ground in 100 µl of H₂O and serial dilutions were plated on KB medium with appropriate 608 antibiotics. Bacterial colony forming units (cfu) were counted two days after incubation at 28°C. 609 610 Each data point is shown as triplicates.

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Trypan blue and DAB staining. For trypan blue staining, the leaves of four-week-old plants 612 were excised and subsequently immersed in boiled lactophenol (lactic acid: glycerol: liquid 613 614 phenol: distilled water 1:1:1:1) solution with 0.25 mg/ml trypan blue for 1 min. The stained leaves were destained with 95% ethanol/lactophenol solution, and washed with 50% ethanol. For 615 616 DAB staining, the leaves of four-week-old plants were immersed in 1 mg/ml DAB (3,3'diaminobenzidine) (pH 3.8) solution with low vacuum pressure for 30 min, followed by an 617 618 overnight incubation at room temperature in the dark. The stained leaves were fixed and cleared in alcoholic lactophenol (95% ethanol: lactic acid: phenol 2:1:1) at 65 °C, and rinsed once with 619 620 50% ethanol and twice with H₂O. The destained leaves were subjected to microscopic observation. 621

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Agrobacterium-mediated virus-induced gene silencing assay. Plasmids containing binary TRV vectors pTRV-RNA1 and pTRV-RNA2 derivative pYL156-SERK4 were introduced into Agrobacterium tumefaciens strain GV3101 by electroporation. Agrobacterium cultures were first grown overnight in LB medium containing 50 µg/ml kanamycin and 25 µg/ml gentamicin and then sub-cultured in fresh LB medium containing 50 µg/ml kanamycin and 25 µg/ml gentamicin supplemented with 10 mM MES and 20 µM acetosyringone overnight at 28 °C in a roller drum. Cells were pelleted by 4,200 rpm centrifugation, resuspended in a solution containing 10 mM 630 MgCl₂, 10 mM MES and 200 μ M acetosyringone, adjusted to A₆₀₀=1.5 and incubated at 25 °C 631 for at least 3 hr. Agrobacterium cultures containing *pTRV*–*RNA1* and *pYL156*–*SERK4* were 632 mixed in a 1:1 ratio and inoculated into the first pair of true leaves of two-week-old soil-grown 633 plants using a needleless syringe.

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Plasma membrane protein enrichment. Enrichment of plasma membrane proteins was 635 performed as reported (Lee, 2017) with modifications. Briefly, N. benthamiana leaves weighing 636 about 1g were ground in liquid N₂, and further lysed with 10 mL of ice-cold extraction buffer 637 containing 100 mM Tris-HCl pH 8.8, 150 mM NaCl, 1 mM EDTA, 20% glycerol, 0.75% 638 polyvinylpolypyrrolidone (PVPP), 20 mM NaF, 2 mM Na₃VO₄, 1 mM PMSF, and 1 complete 639 protease inhibitor cocktail (Roche) per 50 mL. The lysate was centrifuged at 10,000 g at 4 °C for 640 641 10 min to pellet and remove intact cells, cell debris, and intact organelles. Microsomal membranes were then separated by ultracentrifugation at 100,000 g for 30 min at 4 °C and 642 treated with detergent Brij58 (0.02%) to invert plasma membrane vesicles and release 643 contaminating contents (Collins et al., 2017). Pellets were washed with extraction buffer and 644 645 subjected to a final ultracentrifugation step to collect the enriched plasma membrane fraction.

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647 Confocal microscopy and image analysis.

Five to seven-day-old Arabidopsis seedlings were imaged using Leica SP8X inverted confocal 648 649 microscope equipped with a HC PL APO CS2 40×/1.10 water-corrected objective. The excitation wavelength was 488 nm for both GFP and FM4-64, and 561 nm for mCherry by using 650 651 the white light laser. Emission was detected at 500–530 nm or 495-540 nm for GFP, 570–670 nm for FM4-64 and 600-700 nm for mCherry by using Leica hybrid detectors. Autofluorescence was 652 653 removed by adjusting the time gate window between 1 and 4.5 ns or 0.3 and 6 ns. Intensities were manipulated with the Leica LAS-X standard software and FIJI software. The Pearson's 654 655 correlation co-efficient (r value) was calculated using coloc-2 plugin included in Fiji software. ER-Tracker Red (BODIPY TR Glibenclamide; Life-Technologies) was used to stain ER in 656 657 Arabidopsis roots following the manufacturer's protocol.

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659 Accession Numbers

Sequence data from this article can be found in the Arabidopsis TAIR database under the
following accession numbers: SERK1, AT1G71830; SERK2, AT1G34210; BAK1/SERK3,
AT4G33430; SERK4, AT2G13790; FLS2, AT5G46330; BRI1, AT4G39400; BIK1, AT2G39660;
SOBIR1, AT2G31880.

664

665 Supplemental Data

- 666 Supplemental Figure S1. Production of C-terminal BAK1 fragments
- 667 Supplemental Figure S2. Identification of BAK1 cleavage site by mutational analyses
- 668 Supplemental Figure S3. Phenotype of BAK1^{D287A} transgenic plants
- 669 Supplemental Figure S4. The D287 site is critical for BAK1/SERK4-mediated cell death
- 670 Supplemental Figure S5. Colocalization of BAK1^{D287A}-GFP with endoplasmic reticulum (ER)
- 671 marker
- 672 Supplemental Figure S6. The proteolytic cleavage of BAK1 in *DEK1*-silenced Arabidopsis
- 673 Supplemental Table S1. Primers for point mutations, gene cloning, genotyping and RT-qPCR
- 674

675 Figure Legends

Figure 1. Proteolytic processing of BAK1 in plants by a conserved protease

(A) Expression of BAK1-HA in Arabidopsis protoplasts. Protein extracts from Arabidopsis 677 protoplasts transfected with 35S::BAK1-HA or a control vector (Ctrl) were analyzed by Western 678 blot (WB) with an α-HA antibody. The upper band corresponding to the full-length BAK1 679 680 protein was indicated by FL, and the lower band corresponding to the C-terminal fragment of BAK1 was indicated by CTF, and labeled with a red star. (B & C) BAK1^{CTF} is produced in 681 Arabidopsis transgenic plants. Protein extracts from 35S::BAK1-HA (B) and pBAK1::BAK1-GFP 682 (C) transgenic plants were analyzed by WB with respective α -HA and α -GFP antibodies. Wild-683 type Col-0 Arabidopsis was used as Ctrl. (D) Non-tagged BAK1^{CTF} is produced in Arabidopsis 684 protoplasts. Protein extracts from Arabidopsis protoplasts transfected with 35S::BAK1 were 685 analyzed by WB with an α -BAK1 antibody. (E & F) Effects of chemical inhibitors on the 686 production of BAK1^{CTF}. 1 mM EDTA, 1 mM EGTA, 1 mM LaCl₃, 0.5 mM GdCl₃, 2 µM 687 MG132 or 2 µM Lactacystin was added immediately after protoplast transfection with 688 35S::BAK1-FLAG. Protein extracts were analyzed by WB with an α-FLAG antibody. Lactacystin 689 and MG132 were stored in DMSO, and other chemicals were stored in H₂O. (G) Effects of 690

Calpain inhibitors on the production of BAK1^{CTF}. 20 µM ALLN, Calpian inhibitor III, Calpeptin, 691 PD150606 or EST (Calbiochem, cat.# 208733) was added immediately after protoplast 692 693 transfection with 35S::BAK1-FLAG. Protein extracts were analyzed by WB with an α -FLAG antibody. EST was stored in ethanol (ETOH), and other inhibitors were stored in DMSO. (H & I) 694 BAK1^{CTF} is produced in *Nicotiana benthamiana* and *Saccharomyces cerevisiae*. Protein extracts 695 from N. benthamiana transiently expressing 35S::BAK1-HA (H) and S. cerevisiae expressing 696 697 pGAL1::BAK1-HA (I) were analyzed by WB with α -HA antibodies. (J) Proteolytic cleavage is conserved in SERK family members. Protein extracts from Arabidopsis protoplasts expressing 698 FLAG-tagged SERK1, SERK2, SERK3 (BAK1) or SERK4 were analyzed by WB with α-FLAG 699 antibodies. 700

701 The above experiments were repeated three times with similar results.

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703 Figure 2. Regulation of BAK1^{CTF} production

(A) Production of BAK1^{CTF} in *pBAK1::BAK-GFP* transgenic plants upon *Pst hrcC* infection. 704 Four-week-old soil-grown Arabidopsis pBAK1::BAK-GFP transgenic plants were hand-705 inoculated with Pst hrcC at 5 \times 10⁵ cfu. Total proteins from inoculated leaf extracts were 706 analyzed by WB with an α -GFP antibody. hpi, hours post inoculation. (B) Production of 707 BAK1^{CTF} in WT plants upon infections. Four-week-old soil-grown Arabidopsis Col-0 plants 708 were hand-inoculated with Pst hrcC at 5 \times 10⁵ cfu or 1 μ M flg22. Total proteins from 709 inoculated leaf extracts were analyzed by WB with an α -BAK1 antibody. (C) Developmental 710 regulation of BAK1^{CTF} production. Total proteins extracted from Arabidopsis 35S::BAK1-HA 711 transgenic plants at different growth stages from 8 through 35 days post germination (dpg) on $\frac{1}{2}$ 712 MS plates were analyzed by WB with an α -HA antibody. (D) BAK1^{CTF} production in different 713 tissues. Total proteins extracted from different tissues of two-month-old soil-grown 35S::BAK1-714 715 HA transgenic plants were analyzed by WB with an α -HA antibody. F: flowers, S: stem; CL: cauline leaves; RL: rosette leaves; R: roots. 716

- 717 The above experiments were repeated three times with similar results.
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719 Figure 3. The D287A mutation of BAK1 blocks its cleavage

720 (A) Scheme of BAK1 protein domains and sites for mutagenesis. E: extracellular LRR domain;

721 T: transmembrane domain; J: juxtamembrane domain; K: intracellular kinase domain. (B) VASD

722 residues are required for BAK1 cleavage. Arabidopsis protoplasts expressing HA-tagged BAK1 mutants, in which the indicated four amino acids were mutagenized to alanine, were analyzed by 723 724 WB with an α -HA antibody. (C) D287 residue is required for BAK1 cleavage in Arabidopsis protoplasts. (D) D287 residue is required for BAK1 cleavage in N. benthamiana. N. benthamiana 725 leaves transiently expressing HA-tagged BAK1 or BAK1^{D287A} mutant were analyzed by WB 726 with α -HA antibody. (E) D287 residue is required for BAK1 cleavage in Arabidopsis 727 35S::BAK1-HA transgenic plants. (F) D287 residue is required for BAK1 cleavage in 728 Arabidopsis *pBAK1::BAK1-GFP* transgenic plants. (G) D287E mutation blocks BAK1 cleavage 729 in Arabidopsis protoplasts. (H) D287 residue of BAK1 is conserved among Arabidopsis SERKs. 730 (I) BAK1 D287 corresponding residue in other SERK members is required for cleavage in 731 Arabidopsis protoplasts. 732

733 The above experiments were repeated three times with similar results.

734

Figure 4. Compromised immune responses in *pBAK1::BAK1^{D287A}/bak1* transgenic plants

(A) flg22-induced MAPK activation. Two-week-old seedlings of WT Col-0, bak1-4, 736 pBAK1::BAK1/bak1 and pBAK1::BAK1^{D287A}/bak1 were treated with 100 nM flg22 for 15 min. 737 Phosphorylated MPK3 (pMPK3) and MPK6 (pMPK6) were detected by WB with an α-pERK 738 739 antibody (top). Protein loading is shown by Coomassie Brilliant Blue (CBB) staining for RuBisCo (RBC) (bottom). (B) flg22-induced ROS production. Leaf discs from four leaves 740 741 (technical repeats) of each of six five-week-old plants (biological repeats) of indicated genotypes were treated with 100 nM flg22, and ROS production was detected at the indicated time points. 742 743 The data are shown as the mean \pm SD from six biological repeats. (C) flg22-induced callose deposition. Leaves of four-week-old plants were collected for aniline blue staining 12 hr after 744 745 inoculation with 500 nM flg22. Callose deposits were counted using ImageJ 1.43U software (http://rsb.info.nih.gov/ij/). The data are shown as the mean \pm SD from six biological repeats. (D) 746 flg22-mediated resistance to bacterial infection. Four-week-old plants were pretreated with 200 747 nM of flg22 or water and then infected with *Pst* DC3000 at 5×10^5 cfu/ml. The bacterial growth 748 assays were performed 2 days after infection. The data are shown as the mean \pm SD from three 749 biological repeats. The asterisks indicate statistical significance compared to H₂O pretreatment 750 by using student's t-test (P < 0.05). (E) flg22-induced BIK1 mobility shift. Arabidopsis 751 Col-0, 752 protoplasts isolated from bak1-4 mutant, pBAK1::BAK1/bak1 and

pBAK1::BAK1^{D287A}/bak1 transgenic plants were used to express BIK1-HA and treated with 100 753 nM flg22 for 15 min. Mobility shift of BIK1 was detected by WB with an α-HA antibody (top). 754 755 Equal loading of protein was indicated by CBB staining towards RBC (bottom). pBIK1, phosphorylated BIK1. (F) The kinase activity of BAK1 and BAK1^{D287A}. Full length BAK1-756 FLAG or BAK1^{D287A}-FLAG were expressed in Arabidopsis Col-0 protoplasts and precipitated 757 with an α-FLAG antibody. Kinase activity of the precipitated proteins were detected using GST-758 BIK1^{KM} (kinase mutant) as a substrate. Phosphorylation was detected by autoradiography (top), 759 and the protein loading is shown by WB with an α-FLAG antibody (bottom). (G) The *in vitro* 760 kinase activity of the cytosolic domain of BAK1 and BAK1^{D287A}. GST-BIK1^{KM} protein was used 761 as a substrate and MBP-BAK1^{CD} (cytosolic domain) or its D287A mutant was used as the kinase 762 in an in vitro kinase assay. Phosphorylation was detected by autoradiography (top), and the 763 764 protein loading is shown by CBB staining (bottom).

765 The above experiments were repeated three times with similar results.

766

767 Figure 5. BAK1 D287 is critical for BR signaling and cell death control

(A) The reduced hypocotyl length of $pBAK1::BAK1^{D287A}/bak1$ transgenic plants. The seedlings 768 of WT, *bak1-4* and transgenic plants were grown in the dark for 5 days on ½ MS plats without or 769 with 1 µM of BRZ. (B) Quantification of the hypocotyl length shown in (A). The data are shown 770 as the mean \pm SD from 20 biological repeats. The different letters indicate statistically significant 771 difference analyzed with one-way ANOVA followed by Tukey's test (P<0.05). (C) BAK1^{D287A} 772 mutant cannot restore bri1-5 dwarf defect. Transgenic plants of 35S::BAK1 and 35S::BAK1^{D287A} 773 in bri1-5 background were taken photos at two months old. The individual leaves and siliques 774 are shown in the middle and bottom. (D) Expression of BAK1 protein in rosette leaves from 775 four-week-old plants of (C) was detected by WB with an α-BAK1 antibody. (E) D287 is 776 important for BAK1 function in cell death control. Arabidopsis BAK1^{+/-}SERK4^{-/-} plants were 777 transformed with *pBAK1::BAK1* or *pBAK1::BAK1*^{D287A}. Plants of T₁ generation after selection of 778 BAK1 or BAK1^{D287A} transgene were genotyped for endogenous genomic BAK1. Pictures were 779 taken four weeks after germination. BAK1^{+/+}SERK4^{-/-} (BAK1: WT, SERK4: mutant); BAK1^{+/-} 780 SERK4^{-/-} (BAK1: heterozygous, SERK4: mutant); BAK1^{-/-}SERK4^{-/-} (BAK1: mutant, SERK4: 781 782 mutant). Scale bars, 1 cm.

783 The above experiments were repeated three times with similar results.

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785 Figure 6. D287 is critical for the plasma membrane localization of BAK1

(A) Subcellular localization of BAK1-GFP (top panel) and BAK1^{D287A}-GFP (bottom panel) in 786 root epidermis of five-day-old Arabidopsis seedlings. The plasma membrane was stained with 787 788 FM4-64 (2 μ M). (B) Pearson's correlation coefficient (r value) for the colocalization between GFP and FM4-64 fluorescence in the plasma membrane. These values were measured in 15 cells. 789 Error bars indicate mean \pm SD. P-value (*t*-test), * P<0.01. (C) Colocalization of BAK1^{D287A}-GFP 790 with endoplasmic reticulum (ER) marker, mCherry-HDEL. Scale bars, 20 um. (D) Leaves of 791 four-week-old N. benthamiana were hand-inoculated with Agrobacteria carrying 35S::BAK1-HA 792 or 35S::BAK1^{D287A}-HA together with 35S::PSKR1-HA. BAK1 from total proteins and enriched 793 plasma membrane (PM) proteins were analyzed by WB with an α-HA antibody. Cytosolic 794

795 MPK6 was detected by α -MPK6 WB. PSKR1 is a plasma membrane-localized protein.

796 The above experiments were repeated three times with similar results.

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798 Figure 7. Over-production of BAK1 ^{D287A} enhances SoBIR1-dependent cell death

(A) Expression of BAK1 and BAK1^{D287A} under different promoters in *N. benthamiana*. Leaves 799 of four-week-old N. benthamiana were hand-inoculated with Agrobacteria carrying 35S::GFP, 800 $2x35S::BAK1^{D287A}$. 35S::BAK1^{D287A}. 801 2x35S::BAK1. 35S::BAK1, pBAK1::BAK1 or pBAK1::BAK1^{D287A}. Pictures were taken under UV light (left) or visible light (right) three days 802 after inoculation. Two days after inoculation and before cell death progressed, protein levels of 803 BAK1 were analyzed by WB with an α-BAK1 antibody (bottom). BAK1 proteins from 804 2x35S::BAK1 (2) and 2x35S::BAK1^{D287A} (3) were detected by WB using SuperSignalTM West 805 Pico Chemiluminescent Substrate, and BAK1 proteins from 35S::BAK1 (4) and 35S::BAK1^{D287A} 806 (5) were detected using Thermo ScientificTM SuperSignalTM West Femto Maximum Sensitivity 807 Substrate. (B) The fluorescent signal from the circled areas in (A) was obtained under the UV 808 light and was quantified as means ± SD from ten biological repeats. The asterisks indicate 809 statistical significance by using student's *t*-test (P<0.05). (C) Measurement of electrolyte leakage 810 of leaf discs from (A). Data are shown as means \pm SD from three biological repeats. The 811 asterisks indicate statistical significance by using student's *t*-test (P<0.05). (D) Overexpression 812 of BAK1 and BAK1^{D287A} in Arabidopsis. Arabidopsis plants overexpressing 35S::BAK1 or 813 35S::BAK1^{D287A} were taken photos at four-week-old stage. Each phenotype of T_1 generation 814

815 plants was calculated as a percentage to the total transgenic plants of that genotype. (E) Cell death and H₂O₂ accumulation in the leaves of four-week-old plants were examined by trypan 816 817 blue and DAB staining respectively. B: normal-looking plants; S: small plants. (F) Expression levels of PR genes in one-week-old transgenic plants were determined by RT-qPCR. The data 818 are shown as means \pm SD from three biological repeats. The asterisks indicate statistical 819 significance by using student's *t*-test (P<0.05). (G) BAK1 and BAK1^{D287A} cell death is SoBIR1-820 dependent and BIK1-independent. 35S::BAK1 and 35S::BAK1^{D287A} were transformed into sobir1 821 and *bik1* mutant backgrounds. Each phenotype of T_1 generation at four-week-old stage was 822 823 calculated as a percentage as in (D).

824 The above experiments were repeated three times with similar results.

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Acknowledgements: We thank Jianming Li and Delphine Chinchilla for providing materials. The work was supported by National Institutes of Health (NIH) (R01GM092893) and the National Science Foundation (NSF) (IOS-1252539) to P.H., NIH (R01GM097247), the Robert A. Welch foundation (A-1795) to L.S., the Young Eastern Scholar (QD2016035) and Shanghai Sailing Program (17YF1406400) to J.Z., China Scholar Council to P. W. and G. X., and the Research Foundation-Flanders (G022516N and G0E5718N) to E.R. The authors have declared no conflict of interests.

Parsed Citations

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