# AtPRK2 Promotes ROP1 Activation via RopGEFs in the Control of Polarized Pollen Tube Growth

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ABSTRACT The ROP1 GTPase-based signaling network controls tip growth in *Arabidopsis* pollen tubes. Our previous studies imply that ROP1 might be directly activated by RopGEF1, which belongs to a plant-specific family of Rho guanine nucleotide exchange factors (RopGEFs) and in turn may be activated by an unknown factor through releasing RopGEF1's auto-inhibition. In this study, we found that RopGEF1 forms a complex with ROP1 and AtPRK2, a receptor-like protein kinase previously shown to interact with RopGEFs. AtPRK2 phosphorylated RopGEF1 *in vitro* and the *atprk1,2,5* triple mutant showed defective pollen tube growth, similar to the phenotype of the *ropgef1,9,12,14* quadruple mutant. Overexpression of a *d*ominant *n*egative form of AtPRK2 (DN-PRK2) inhibited pollen germination in *Arabidopsis* and reduced pollen elongation in tobacco. The DN-PRK2-induced pollen germination defect was rescued by overexpressing a constitutively active form of RopGEF1, RopGEF1(90–457), implying that RopGEF1 acts downstream of AtPRK2. Moreover, AtPRK2 increased ROP1 activity at the apical plasma membrane whereas DN-PRK2 reduced ROP1 activity. Finally, two mutations at the C-terminal putative phosphorylation sites of RopGEF1 (RopGEF15460A and RopGEF15480A) eliminated the function of RopGEF1 *in vivo*. Taken together, our results support the hypothesis that AtPRK2 acts as a positive regulator of the ROP1 signaling pathway most likely by activating RopGEF1 through phosphorylation.

Key words: AtPRK2; RopGEF1; ROP GTPase; auto-inhibition; polarity growth.

#### INTRODUCTION

The ROP (*R*ho-like small GTPase from *p*lant) GTPase family is an important molecular switch in plant signaling (Yang, 2002; Gu et al., 2003, 2004; Yang and Fu, 2007; Lee and Yang, 2008; Yang, 2008). ROPs control polar cell growth and, as such, play a critical role in many developmental processes, including pollen tube and root hair growth, pavement cell morphogenesis, and plant responses to auxin and ABA (Lin et al., 1996; Lin and Yang, 1997; Li et al., 1999; Fu et al., 2001; Jones et al., 2002; Zheng et al., 2002; Gu et al., 2003; Fu et al., 2005; Gu et al., 2005; Hwang et al., 2005; Chang et al., 2007; Jones et al., 2007; Fu et al., 2009; Xu et al., 2010; Chen et al., 2011).

Pollen tubes are an excellent model to study the regulation of polar growth (Cheung and Wu, 2008; Yang, 2008). Three functionally redundant ROPs (ROP1, ROP3, and ROP5) are required for pollen tube polar growth (Yang, 2002, 2008). ROP1 promotes pollen tube polar growth via two counteracting pathways: the RIC4 pathway, which promotes apical F-actin assembly, and the RIC3 pathway, which promotes Ca<sup>2+</sup> signaling at the tip and subsequently increases the disassembling of apical F-actin (Gu et al., 2005). These two counteracting pathways work together to regulate F-actin dynamics and F-actin/Ca<sup>2+</sup>-dependent exocytosis (Yang and Fu, 2007; Lee and Yang, 2008; Lee et al., 2008; Yang, 2008).

Rho GTPases are mainly regulated by three classes of upstream regulators: guanine exchange factors (GEFs), GTPase activating proteins (GAPs), and guanine nucleotide dissociation inhibitors (GDIs) (Yang, 2002). GEFs activate ROPs by promoting the conversion of Rho GTPases from their GDP-bound inactive form to the GTP-bound active form. GAPs promote GTP hydrolysis and deactivate ROPs. GDIs bind to the GDP-bound form of Rho GTPases and negatively regulate Rho GTPases via preventing both guanine nucleotide exchange and Rho GTPase localization to the PM.

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Plants possess a plant-specific RhoGEF family whose members contain a highly conserved novel GEF catalytic domain, the PRONE domain, instead of the conserved PH or CZH domains found in yeast, animal, and human RhoGEFs (Berken et al., 2005; Gu et al., 2006). Fourteen members of the RopGEF family have been found in Arabidopsis thaliana and seven members are specifically or highly expressed in pollen tubes (Gu et al., 2006; Zhang and McCormick, 2007). Gu et al. transiently overexpressed five Arabidopsis RopGEFs in tobacco pollen and found that RopGEF1 overexpression induced the most severely swollen tubes, similarly to the phenotype induced by the expression of a constitutively active ROP1 (CA-ROP1) (Gu et al., 2006). The PRONE domain (amino acid 90-457) of RopGEF1 was found to exhibit high GEF activity on ROP1, while the full-length RopGEF1 protein was inactive in vitro due to the presence of an auto-inhibitory domain in the C-terminal region. Therefore, it was proposed that an in vivo mechanism must exist to release the auto-inhibition of RopGEF1 (Gu et al., 2006).

Recent studies have revealed the function of receptor-like protein kinases (RLKs) in the regulation of pollen development, germination, and pollen tube polar growth (Mu et al., 1994; Muschietti et al., 1998; Kim et al., 2002; Zhang and McCormick, 2007; Zhang et al., 2008). The first Pollen-specific Receptor-like Kinase (PRK1) was reported to play an important role in postmeiotic development of pollen in petunia (Mu et al., 1994). The tomato pollen-specific RLKs LePRK1 and LePRK2 have been proposed to receive signals from LAT52 and LeSTIG1 at different stages to promote pollen germination and pollen tube growth (Muschietti et al., 1998; Tang et al., 2002; Johnson and Preuss, 2003; Wengier et al., 2003; Tang et al., 2004; Zhang et al., 2008). Interestingly, the McCormick group found that the intracellular kinase domain of tomato pollen receptor-like kinases (PRKs) can physically interact with KPP (kinase partner protein) (Kaothien et al., 2005), whose Arabidopsis homologs were later shown to belong to the RopGEF family (Berken et al., 2005; Gu et al., 2006). KPP was found to be phosphorylated in vivo, although the kinase responsible for its phosphorylation is unknown (Kaothien et al., 2005). Importantly, the same group showed that an Arabidopsis homolog of PRKs, AtPRK2a (for simplicity, referred to as AtPRK2 here), can also interact with the pollen-specific RopGEF12 and that a phospho-mimic mutation (S510D) of RopGEF12 enhanced RopGEF12 promotion of growth depolarization (Zhang and McCormick, 2007). Co-expression studies in tobacco pollen suggested AtPRK2 could be involved in the activation of RopGEF12 (Zhang and McCormick, 2007). Similar results were found in tomato (Solanum lycopersicum) (Zhang et al., 2008). These results imply that AtPRK2 may act upstream of RopGEF12 to activate ROP signaling pathways in pollen tubes. Recent work in Arabidopsis root hairs suggests that the FER RLK acts as an upstream regulator of RAC/ROP2 signaling pathway most likely by interacting with RopGEF1 (Duan et al., 2010). Together, these studies suggest RLKs are likely to work as an upstream regulator of ROP signaling via RopGEFs. However, it remains unclear how RopGEFs are activated and how the RLKs regulate ROP activity.

In this study, we present new findings on the mechanisms employed by AtPRK2 to regulate RopGEF1 and ROP1 activities. Specifically, AtPRK2 increased ROP1 activity, and physically forms a complex with RopGEF1 and ROP1. In addition, AtPRK2 directly phosphorylated RopGEF1 and two serine-toalanine mutations in the RopGEF1 C-terminal region abolished the release of auto-inhibition, suggesting AtPRK2 may activate RopGEF1 through phosphorylation in the C-terminal region. Moreover, a constitutively active form of RopGEF1 rescued the germination deficiency induced by DN-PRK2 overexpression, suggesting RopGEF1 bridges the signaling transduction from AtPRK2 to ROP1 signaling pathways. Based on these observations, we propose that the AtPRK2 phosphorylation of RopGEF1 in its C-terminal region releases its auto-inhibition, thereby activating RopGEF1, which in turn activates ROP1. Therefore, RopGEF1 bridges the signaling transduction from AtPRK2 to ROP1 to control polarized pollen tube growth.

#### RESULTS

#### Pollen Receptor-Like Kinases (PRKs) Regulate Pollen Tube Polar Growth

A pollen RLK (AtPRK2a) has been implicated in the regulation of ROP1 signaling through its interaction of RopGEF12 in Arabidopsis (Zhang and McCormick, 2007). To further explore RLK regulation of ROP1 signaling, we surveyed a group of Arabidopsis receptor-like kinases that are homologs of the tomato LePRKs (Figure 1). Using rice genes as outgroups, we found eight Arabidopsis RLKs are closely related to LePRKs. Six out of these eight genes are highly expressed in pollen according to the Genevestigator Expression Database, and were named AtPRK1-6 (Figure 1 and Supplemental Figure 1). According to the phylogenetic tree, AtPRK1 and AtPRK2 are close to LePRK1 and LePRK2, and, although AtPRK4 and AtPRK5 are further apart, they are also derived from the same common ancestor that existed before the divergence of rice and Arabidopsis. AtPRK3 and AtPRK6 are closer to LePRK3, and diverged from the common ancestor of Arabidopsis and rice.

To test whether these AtPRKs are important for pollen tube polar growth, we transiently overexpressed full-length AtPRK1–5 (cloning AtPRK6 was unsuccessful) driven by the pollen-specific *LAT52* promoter (*pLAT52*::AtPRK) in tobacco pollen, and analyzed the width and length of pollen tubes after germination and growth for 5 h. Overexpressing (OX) AtPRK2 through 5 resulted in all cases in increased width and reduced length of pollen tubes (Table 1) as did ROP1 overexpression (Li et al., 1999), suggesting that these AtPRKs may be involved in the control of pollen tube polar growth, and may regulate ROP1 signaling pathways.



**Figure 1.** Phylogenetic Tree of Selected AtPRKs and LePRKs. LePRK1–3 from tomato, six pollen-specific (AtPRK1–6), and several non-pollen-specific AtPRKs from *Arabidopsis* were included in this tree. Rice genes are included as outgroups.

AtPRK2 overexpression induced the most severe growth depolarization with the most swollen tips (Table 1). In contrast, AtPRK1 was found to increase pollen tube length (Table 1).

### Triple *prk* and Quadruple *ropgef* Mutants Exhibit Reduced Pollen Germination

To test the role of AtPRKs in regulating pollen germination and pollen tube growth in Arabidopsis, T-DNA insertion mutant lines (Supplemental Table 1) of AtPRKs were obtained from ABRC (www.arabidopsis.org) and in vitro pollen germination and pollen tube growth were examined. Pollen from each of the prk1-1, prk1-2, prk1-2, prk2-1, and prk5-1 single homozygous mutant lines exhibited normal germination and growth. We generated pollen from the homozygous prk1-2 prk2-1 double mutant, prk2-1 prk5-1 double mutant, and prk1-2 prk2-1 prk5-1 triple mutant. Only pollen from the homozygous prk1 prk2 prk5 triple mutant line showed reduced tube elongation compared to wild-type (Figure 2B and 2H). Given additional AtPRKs are highly expressed in pollen, it is likely that one or more AtPRKs are functionally redundant with AtPRK1, AtPRK2, and AtPRK5. Similarly, none of ropgef1-1, ropgef9-1, ropgef12-1, ropgef14-1, and ropgef14-2 single knockout mutant lines exhibited altered pollen phenotype, while the homozygous ropgef1-1 ropgef9-1 ropgef12-1 ropgef14-2 quadruple mutant line showed reduced pollen tube elongation (Figure 2C and 2H),

Table 1. RLKs Induce Depolarized Growth in Pollen Tubes.

	Length <sup>a</sup>	Width <sup>a</sup>	Width/length
GFP	528±11	9.4±0.8	0.02
GFP + PRK1	861±18	10.1±1.3	0.01
GFP + PRK2	423±22	27.2±3.2	0.06
GFP + PRK3	324±15	$20.2 \pm 2.4$	0.06
GFP + PRK4	307±16	13.7±2.1	0.04
GFP + PRK5	411±21	$11.3 \pm 0.7$	0.03

The length and the maximum tip width of tobacco pollen tubes were measured 6–7 h after bombardment. <sup>a</sup> Data are the mean  $\pm$  SD.

suggesting high redundancy among these RopGEFs in the regulation of pollen tube growth. The similarity in pollen phenotype between the triple *prk* mutant and quadruple *ropgef* mutant is consistent with the notion that AtPRKs and RopGEFs may work in the same signaling pathway to regulate pollen tube growth.

#### **DN-PRK2** Inhibits Pollen Germination in Arabidopsis

Given the weak phenotype of the prk1 prk2 prk5 triple mutant, we reasoned that overexpression of a dominantnegative (DN) form of AtPRK2 (DN-PRK2) would effectively inhibit the function of redundant PRKs. Deletions of the cytoplasmic kinase domain of other RLKs have been shown to have a DN effect on the wild-type endogenous copy (Shpak et al., 2003). Therefore, we generated DN-PRK2 by deleting the kinase domain of AtPRK2 (Supplemental Figure 2) and fusing it to the pollen-specific LAT52 promoter. We introduced LAT52::DN-PRK2 in Arabidopsis and isolated 39 T<sub>1</sub> transgenic lines, which carried a Basta resistance selection marker, and analyzed the segregation ratio of the Basta resistant to Basta-sensitive T2 progenies. We anticipated that a distortion of segregation ratios from the Mendelian genetics would suggest an effect of DN-PRK2 on pollen fertility, because the LAT52 promoter is pollenspecific. Among these 39 lines, only seven exhibited a nearly 3:1 ratio, which is consistent with single-locus insertions that did not alter pollen fertility. Twenty-two lines exhibited less than 3:1 segregation ratios for Basta resistance to sensitivity, implicating a defect in pollen fertility in these lines. Three lines showed 7:1 to 10:1 ratio, and seven lines displayed ratios higher than 15:1, suggesting that they contained multiple T-DNA insertions at more than one site (Supplemental Table 2). We generated homozygous transgenic lines from lines showing a segregation ratio < 3:1, and performed the pollen phenotype analysis. Pollen from DN-PRK2 OX lines exhibited abnormally low germination rates (Supplemental Figure 2B), suggesting that AtPRKs are important for pollen germination. Since the same phenotype was observed in multiple mutants affected in ROP1 signaling (Li et al., 1999; Hwang et al., 2008), we propose AtPRKs may participate in ROP1 signaling in the modulation of pollen germination and pollen tube growth.



Figure 2. Pollen Tube Phenotypes of the Quadruple gef Mutant and Triple prk Mutant, and the DN-PRK2 OX/RopGEF1(90–457) Transgenic Plants. (A–C) Pollen tubes of Col0 (A), prk1 prk2 prk5 triple mutant (B), and gef1 gef9 gef12 gef14 quadruple mutant (C), after 5-h incubation in pollen germination medium.

(D-G) Pollen germination assay of Col0 (D), DN-PRK2 (E), DNPRK2, RopGEF1 (F), and DNPRK2, RopGEF1(90-457) (G) plants.

(H, I) Statistical analysis of pollen tube growth (H) and the germination rate of various genotypes (I).

(J) RT–PCR results suggest that the expression level of DNPRK2 does not change in all of the tested lines. Bar = 100  $\mu$ m. (A–C) same magnification and (D–G) same magnification.

#### RopGEF1(90–457) Suppresses the DN-PRK2 OX-Induced Pollen Germination Defect

RopGEF1 overexpression produces a pollen tube phenotype similar to that induced by CA-rop1 (Gu et al., 2006); thus, we sought to test whether RopGEF1 acts downstream of AtPRK2. For this purpose, we developed a constitutively active form of RopGEF1 (CA-RopGEF1). We previously showed that the PRONE domain of RopGEF1, RopGEF1(90–457), exhibits constitutive RopGEF activity *in vitro* (Gu et al., 2006). Thus, we anticipated that RopGEF1(90–457) would also be constitutively active *in*  vivo, and introduced it in Arabidopsis with a C-terminal GFP tag and driven by the LAT52 promoter. RopGEF1(90-457)–GFP overexpression (OX) induced a much greater growth depolarization in pollen tubes compared to that induced by RopGEF1 OX (data not shown), suggesting that RopGEF1(90-457) acts as an activated form of RopGEF1 in vivo. Therefore, we crossed a RopGEF1(90-457)-GFP OX line with DN-PRK2 OX line 23-12 to determine whether RopGEF1(90-457) could suppress the reduced germination phenotype induced by DN-PRK2. As expected, the pollen germination rates of DN-PRK2 OX lines were increased

in the RopGEF1(90–457)–GFP OX background (Figure 2G and 2I). Overexpression of full-length RopGEF1–GFP also showed a similar but weaker effect, compared to RopGEF1(90–457)–GFP (Figure 2F and 2I). We verified that the increased pollen germination rate was not due to altered DN-PRK2 expression levels (Figure 2J). These results imply that the full-length RopGEF1 needs to be activated, probably by AtPRK2.

#### AtPRK2 and DN-PRK2 Activate and Inhibit ROP1 Activity, Respectively

To test whether AtPRK2 acts as a positive regulator of ROP1, we determined the effect of AtPRK2 expression on ROP1 activity in tobacco pollen tubes. ROP1 activity was monitored using the ROP1 activity marker GFP-RIC4 $\Delta$ C, which specifically interacts with active ROP1 but does not induce growth depolarization in pollen tubes (Hwang et al., 2005, 2008, 2010). GFP-RIC4 C was transiently expressed together with AtPRK2a or DN-PRK2a, and PM-associated GFP-RIC4∆C fluorescence was measured as previously described (Huang et al., 2005). The average ROP1 activity in the apical PM (Intensity-Ave-PM) was calculated by means of PM GFP-RIC4∆C fluorescence standardized with the cytosolic GFP-RIC4 $\Delta$ C signal (Average-cyt) (Huang et al., 2005). Active ROP1 on the PM was presented as (Intensity-Ave-PM/Avecyt) X PM distribution. We set the active ROP1 of control pollen tubes to 100%, and calculated the relative change of ROP1 activity caused by AtPRK2 or DN-PRK2 overexpression. ROP1 activity increased by 47% in AtPRK2-overexpressing tubes, but was reduced by 26% in DN-PRK2-overexpressing pollen tubes (Figure 3A-3D). These results further support our hypothesis that AtPRK2 acts as a positive regulator of ROP1 in the control of polar growth of pollen tubes.

To confirm this hypothesis, we co-expressed DN-PRK2 with one of the ROP1 effectors, RIC4, which is directly activated by ROP1 (Wu et al., 2001; Gu et al., 2005). RIC4 overexpression induces severe tip swelling, as ROP1 overexpression does. We reasoned that, if AtPRK2 acts upstream of ROP1, overexpression of the negative form of AtPRK2, DN-RPK2, would suppress the phenotype caused by RIC4-OX, similar to the suppression of RIC4 overexpression phenotype by DN-ROP1 (Gu et al., 2005). Indeed, DN-PRK2 overexpression suppressed the GFP–RIC4-induced depolarization of pollen tube growth. Compared to GFP–RIC4 OX pollen tubes, DN-PRK2 and GFP– RIC4 co-overexpressing pollen tubes revealed reduced width and increased elongation (Figure 3E–3I).

### RopGEF1 Interacts with and Is Phosphorylated by AtPRKs

We next investigated the possible mechanisms by which AtPRKs regulate the RopGEF1/ROP1 signaling pathway. To test whether AtPRKs directly associate with RopGEF1, the kinase domains of four AtPRKs (AtPRK1, AtPRK2, AtPRK3, and AtPRK4) were cloned and fused to the C-terminus of GST and an MBP-tagged RopGEF1/RopGEF1(90–457) were

expressed in *E. coli*. The interaction was determined by pulldown assays using GST-AtPRKs-linked glutathione-beads and anti-MBP antibodies. All tested AtPRKs were able to interact with RopGEF1 and its PRONE domain, RopGEF1(90–457), through the kinase domain (Figure 4A), consistent with the genetic results that suggest functional redundancy among these AtPRKs.

The interaction of AtPRKs with RopGEF1 suggested that AtPRKs may directly phosphorylate RopGEF1. This hypothesis was tested using an *in vitro* kinase assay. As shown in Figure 4B, RopGEF1 was phosphorylated by AtPRK2 and AtPRK3, maybe also AtPRK4, while it was not phosphorylated by the control protein (GST alone was used as a negative control). To investigate whether the kinase activity of AtPRK2 or AtPRK3 was calcium-dependent, Ca<sup>2+</sup>-free conditions in the kinase assay were achieved by adding excess EGTA (10mM). The phosphorylation of RopGEF1 was not altered by EGTA inclusion (data not shown), suggesting that the phosphorylation of RopGEF1 is calcium-independent.

#### **RopGEF1 Forms a Complex with ROP1 and AtPRK2**

The physical and functional interactions between AtRPKs and RopGEF1, and between AtRPK2 and ROP1, suggest that these proteins might form complexes. We chose AtPRK2 for our further analysis because AtPRK2 overexpression induced the most severe depolarization of pollen tubes and strongly phosphorylated RopGEF1 (Table 1 and Figure 4B). To test whether AtPRK2 physically interacts with and with which form of ROP1 in vitro, the kinase domain of AtPRK2 was fused to the C-terminus of HIS tag (HIS-AtPRK2). The GTP-bound GST-ROP1 and GST-DP2 (a constitutively active form ROP1) were used as active form ROP1 (Li et al., 1999; Wu et al., 2001), the GDP-bound GST-ROP1 and GST-DN (Dominant Negative) ROP1 as inactive form (Li et al., 1999; Wu et al., 2001). All these active, inactive, and free forms of GST-ROP1 fusion proteins on glutathione-agarose beads were incubated with eluted HIS-AtPRK2. Purified fusion proteins were pulled down with GST-ROP1 and detected with HIS-antibodies. We found that AtPRK2 strongly interacts with all ROP1, GTP-ROP1, GDP-ROP1, GTP-DP2, and DN-ROP1 (Figure 4C). As it was shown that ROP1 interacts with RopGEF1 and is activated by RopGEF1 (Gu et al., 2006), we proposed that AtPRK2, RopGEF1, and ROP1 may form a complex. To test this, we performed another pull-down experiment with all these forms of GST-ROP1, HIS-AtPRK2, and MBP-RopGEF1. GST-ROP1 proteins on glutathioneagarose beads were incubated with eluted HIS-AtPRK2 and MBP-RopGEF1. After extensive washes, glutathioneagarose beads were subjected to Western blot analysis using HIS or MBP-antibody. As expected, both AtPRK2 and RopGEF1 were detected using all these forms of GST-ROP1 (Figure 4D).

To test whether the phosphorylation status of AtPRK2 may affect the formation of AtPRK2–RopGEF1–ROP1 complex, we



Figure 3. ROP1 Activity Is Positively Regulated by AtPRK2 and Negatively Regulated by DNPRK2 in Pollen Tube Growth.

(A–E) ROP1 activity was increased by AtPRK2 and decreased by DN-PRK2. The distribution of the active ROP1 marker, GFP–RIC4 and control (A), AtPRK2 OX (B), and DN-PRK2 OX (C) pollen tubes are shown. Distribution of GFP–RIC4 $\Delta$ C was enlarged in most AtPRK2 OX pollen tubes and narrowed in most DNPRK2 pollen tubes. (D) Statistical analysis of GFP–RIC4 $\Delta$ C distribution in each background compared to wild-type pollen tube. Data were collected from three independent experiments.

(F–I) DN-PRK2 suppresses RIC4-OX-induced defect in polar pollen tube growth. (E) GFP, (F) DN-PRK2+GFP, (G) DN-PRK2+GFP–RIC4, and (H) GFP–RIC4 were transiently expressed in tobacco pollen by bombardment and germinated for 5 h at RT before visualization. (I) Quantitative data of pollen tube widths from various backgrounds. Bar shows SD in (H) and (I). Scale bar = 5 µm in (A); Scale bar = 25 µm in (E).

treated the complex using alkaline phosphatase and tested their integrity. As shown in Figure 4E, the formation of the AtPRK2–RopGEF1–ROP1 complex was not markedly affected by alkaline phosphatase treatment. We also showed that mutations in the conserved kinase catalytic sites of AtPRK2 did not affect the complex formation (Figure 4F). These results suggest the interaction between AtPRK2, RopGEF1, and ROP1 is phosphorylation-independent.

### The C-Terminal Region of RopGEF1 Is Important for Its Interaction with ROP1 and AtPRK2

We next investigated how AtPRK2 regulates the RopGEF1– ROP1 signaling pathway. Our previous results suggest that the C-terminal variable region regulates the GEF activity of RopGEF1 in an auto-inhibitory manner (Gu et al., 2006). Thus, it is reasonable to postulate that the C-terminal region may be regulated by AtPRK2. First, we tested whether



Figure 4. RopGEF1 Is Phosphorylated by AtPRKs and Forms a Complex with AtPRK2 and ROP1.

(A) Both full-length RopGEF1 and RopGEF1(90–457) interact with the kinase domains of AtPRK2, AtPRK3, and AtPRK4.

(B) RopGEF1 is phosphorylated by AtPRK2, AtPRK3, and possibly AtPRK4. SOS2 was used as a positive control and GST alone was used as the negative control.

(C) The kinase domain of AtPRK2 interacts with various forms of ROP1. GDP/GTP-bound form ROP1, GTP–DP2, and DN-ROP1 were used in each reaction as indicated.

(D) The HIS-tagged kinase domain of AtPRK2, MBP–RopGEF1, and various forms of ROP1 form complexes in vitro.

(E) Interaction assay between the kinase domain of AtPRK2, RopGEF1, and ROP1 after incubation for 3, 6, 9, and 12 h with/without alkaline phosphatase.

(F) Pull-down assay to verify the interaction between ROP1, MBP-tagged ROPGEF1, and wild-type or mutated kinase domain of AtPRK2.

the C-terminal region, RopGEF1(458–548), interacts with AtPRK2, using several truncated constructs for RopGEF1 fused to the C-terminal of an MBP tag (Figure 5A). MBP–RopGEF1 was incubated with HIS–PRK2 or the truncated forms of GST–ROP1. As shown in Figure 5B, the MBP-tagged C-terminal region, MBP–RopGEF1(458–548), interacted with both ROP1 and AtPRK2. Furthermore, full-length MBP–RopGEF1 showed a strong interaction with AtPRK2, while MBP–RopGEF1(1–457) exhibited a much weaker interaction with AtPRK2. Similarly, MBP–RopGEF1(365–548) showed a strong interaction with AtPRK2 while MBP–RopGEF1(365–457) exhibited no interaction with AtPRK2 (Figure 5B). These results demonstrate that the C-terminal region of RopGEF1(458–548) is important for RopGEF1 to interact with AtPRK2.

### Phosphorylation of the C-Terminal Region Is Required for RopGEF1 Activity

Full-length RopGEF1 has no in vitro GEF activity towards ROP1. However, overexpression of RopGEF1 induces growth depolarization of pollen tubes in both Arabidopsis and tobacco (Gu et al., 2006). We reasoned that RopGEF1 activity might be regulated by phosphorylation. RopGEF1 has more than 20 predicted serine, threonine, and tyrosine phosphorylation sites (http://myhits.isb-sib.ch/cgi-bin/motif scan), including six in the C-terminal region. Because the C-terminal region of RopGEF1 is likely to be essential for its auto-inhibitory regulation (Gu et al., 2006), the six C-terminal sites of RopGEF1 were chosen for site-directed mutagenesis to test whether phosphorylation at these sites is critical for the release of auto-inhibition. If the phosphorylation of RopGEF1 is required for its in vivo function, a serine-to-alanine substitution should abolish its ability to induce growth depolarization in pollen tubes.

We generated GFP-tagged RopGEF1 constructs with a serine-to-alanine substitution at each of the six sites and transiently overexpressed these constructs in tobacco pollen tubes. Overexpression of the GFP-RopGEF1S460A mutant failed to induce depolarized pollen tube growth (Figure 6B and Supplemental Table 3), suggesting that phosphorylation at the S460 site is required for the functional activity of RopGEF1. The GFP-RopGEF1S480A mutant not only failed to cause balloon-like pollen tips, but also inhibited pollen tube elongation, similar to the effect of the dominant-negative ROP1 (DN-ROP1) mutant (Figure 6C and Supplemental Table 3), suggesting that this mutant may be dominant-negative. Four other mutations did not appear to abolish RopGEF1 activity (Figure 6D, 6E, 6G, 6H, and Supplemental Table 3).

To investigate whether these two serine phosphorylation sites (S460/S480) of RopGEF1 are conserved, we first constructed a phylogenic tree using the conserved PRONE domain in *Arabidopsis* and other dicots and monocots species (Figure 7A and Supplemental Figure 3). An alignment



Figure 5. The C-Terminal Region of RopGEF1 Is Important for Its Interaction with AtPRK2 and ROP1.

(A) A diagram of RopGEF1 motifs. The PRONE domain, S1-3 subdomains, N-terminal, and C-terminal regions of RopGEF1 are indicated.
(B) MBP-tagged truncated RopGEF1 was used in pull-down assays with the His-tagged kinase domain of AtPRK2 (His–PRK2) and various forms of GST-tagged ROP1. His–PRK2 or various GST–ROP1 included in the assay are indicated on the left. Different truncated RopGEF1 forms used in each assay are indicated above and signals were detected by anti-MBP antibodies. Proteins loaded in the assay are also shown.

between Arabidopsis RopGEF family members or RopGEF1 orthologs with the full-length amino acids revealed that S460 is shared among Brassicaceae RopGEF1 orthologs, and S480 is conserved among plant RopGEF1 orthologs (Figure 7B), but neither S460 nor S480 is conserved among other Arabidopsis RopGEFs (Supplemental Figure 4).



Figure 6. Phosphorylation in C-Terminal Regions Is Critical for RopGEF1 Activity.

Serine-to-alanine mutation of several sites in the RopGEF1 C-terminal region decreases RopGEF1 activity. Wild-type and mutant RopGEF1 were transiently expressed in tobacco pollen for 5 h before observation. Compared to GFP (A), GFP–RopGEF1wt (F) caused severe depolarization of pollen tubes with balloon-like tips. The GFP–S460A mutation (B) and GFP–S480A mutation (C) show greatly reduced RopGEF1-induced depolarization; pollen tubes overexpressing the GFP–S460A mutant are much longer than GFP–RopGEF1wt. Overexpression of GFP–S484A (D), GFP–S488A (E), GFP–S458A (G), and GFP–S501A (H) mutations caused severely depolarized pollen tubes as wild-type RopGEF1 does. Scale bars shown, and images (A–C) with the same magnification and (D–H) with the same magnification. Arrowhead indicates the tip of pollen tubes.

#### DISCUSSION

ROPs are central regulators of many important cellular processes such as cell polarity formation, cell morphogenesis, and polar cell growth (Yang, 2002, 2008), and are modulated by a number of regulators including RhoGAPs, GDIs, and RopGEFs (Yang, 2002, 2008), although little is known of how these direct regulators of ROPs are connected to extracellular signals. Recent studies suggest that RLKs directly interact with ROPs and may act upstream of RopGEFs to regulate polar growth in pollen tubes and root hairs (Zhang and McCormick, 2007; Duan et al., 2010). In this study, we provide genetic and biochemical evidence in support of the hypothesis that the *Arabidopsis* pollen RLK–AtPRK2 phosphorylates and activates RopGEF1 to regulate ROP1-dependent polar growth in pollen tubes.

Based on our findings, we propose a model to explain the regulatory mechanism for pollen tube growth (Figure 8). The GEF activity of ROPGEF1 is inhibited/disrupted by the binding of its C-terminal region to its PRONE catalytic domain. Upon AtPRK2 interaction with RopGEF1 and phosphorylation of the serine sites in the RopGEF1 C-terminal region, a conformational change is induced and the PRONE1 domain is exposed,

resulting in an active form of RopGEF1. Active RopGEF1 subsequently catalyzes the conversion of GDP-bound inactive form ROP1 into GTP active form, thereby activating ROP1 signaling pathways and promoting pollen germination and pollen tube growth (Figure 8). This model explains the observed higher activity of ROP1 in AtPRK2 OX pollen tubes and lower ROP1 activity in DN-PRK2 OX pollen tubes.

Since RopGEF1 OX pollen tubes showed severe depolarization similar to CA-ROP1 OX pollen tubes, we further propose a positive feedback regulation of RopGEF1 activity (Figure 8). In our previous study, the result that the inactive form of RopGEF1 shows the strongest interaction with GTP-bound ROP1 also supports this idea (Gu et al., 2006). We propose that, after the phosphorylation and activation of RopGEF1 by AtPRK2, the active GTP-bound ROP1 interacts with AtPRK2 and/or RopGEF1 and enhances the interaction between AtPRK2 and RopGEF1. This enhancement could be the result of an increased interaction frequency or affinity between AtPRK2 and RopGEF1. Consequently, more RopGEF1s are phosphorylated and active, as supported by the observation that RopGEF1 OX pollen tubes displayed CA-ROP1-like bulbous tips. This would also be similar to



Figure 7. The S480 Site of RopGEF1 Is Conserved in RopGEF1 Orthologs and S460 Is Conserved in Brassicaceae.
(A) A phylogenetic tree of RopGEF genes in dicots and monocots. *Arabidopsis* RopGEFs are highlighted in dark pink squares, other dicots genes are labeled by blue rhombuses, and the monocots genes are indicated by green triangles. *Selaginella* genes were included to root the tree.
(B) Alignment of the C-terminal region of RopGEF1 orthologous genes. The S460 and S480 sites are indicated by red arrows.

the mechanism regulating the Ras GEF Sos in animal cells (Margarit et al., 2003).

#### RopGEFs Directly Interact with and Are Regulated by RLKs: An Emerging Theme in RLK/ROP Signaling

An increasing number of studies suggest critical roles for *Arabidopsis* RopGEFs (Berken et al., 2005; Gu et al., 2006) in the regulation of diverse ROP-mediated processes. A recent study shows that RopGEF7 modulates the maintenance of the root stem cell niches by regulating the activity of AtRAC1

(AtROP3) and the expression of PLETHORA1 (PLT1), PLT2, and the auxin efflux protein PIN1 (Chen et al., 2011). Another *Arabidopsis* RopGEF, PIRF1 (phytochrome-interacting ROP guanine nucleotide exchange factor 1, also referred to as RopGEF11), has been found to interact with phytochromes via its conserved PRONE domain and to activate ROPs in a phytochrome-dependent manner to regulate primary root development (Shin et al., 2010). Studies in rice and legume also implicate RopGEFs in regulating the development of root hairs, cuticular papillae on the leaf surface by regulating



**Figure 8.** A Model for AtPRK2-Induced Release of RopGEF1's Auto-Inhibition and Activation of ROP1 Signaling Pathways. RopGEF1 is subjected to auto-inhibitory regulation, which is controlled by its C-terminal region. Auto-inhibition is released through the phosphorylation of the serine amino acids in its C-terminal region upon RopGEF1 interaction with AtPRK2. The phosphorylation-induced conformational change in RopGEF1 exposes the PRONE domain. Active RopGEF1 can then promote the conversion of the GDP-bound inactive form of ROP1 into its GTP-bound active form, thereby enhancing the ROP1 signaling pathways and regulating pollen germination and pollen tube growth. We also propose that the GTP form of ROP1 interacts with both RopGEF1 and AtPRK2 and somehow, through positive feedback, regulates RopGEF1 activity. The PRONE domain of RopGEF1 is shown as brown curve, and the C-terminal region is shown as a purple curve. Green arrow indicates positive regulation.

### the substrate ROP activity (Riely et al., 2011; Yoo et al., 2011; Yamaguchi et al., 2012).

The physiological significance of RopGEFs and ROPs begs the question of how RopGEFs are regulated. This study, together with several recent reports, supports an emerging theme of RLK-based RopGEF regulation at the cell surface. McCormick's group first demonstrated a physical and functional interaction between AtPRK2 and RopGEF12 and proposed that AtPRK2 functions to dock RopGEF12 to the plasma membrane of pollen tubes (Zhang and McCormick, 2007). Recently, Cheung's group showed that the RLK FERONIA (FER) interacts with RopGEF1 and is required for ROP activation and ROP-mediated root hair development (Duan et al., 2010). Our data here support the hypothesis that AtPRK2-mediated phosphorylation regulates RopGEF1 activation. This regulation is most different from AtPRK2's regulation of RopGEF12, because the functional phosphorylation sites in RopGEF1 are not conserved in RopGEF12 (see below). It is unclear why AtPRK2 regulates two different RopGEFs via distinct mechanisms. Nonetheless, these results suggest that the RLK-RopGEF connection may provide a common cell surface signaling mechanism in plants.

#### Activation of RopGEF by Phosphorylating Its C-Terminal Region and Releasing Auto-Inhibition Could Be a Common Mechanism for RopGEF Regulation

Based on our data that the C-terminal S-to-A mutations inhibited/prevented the release of RopGEF1 auto-inhibition, we propose that the phosphorylation of the serine sites in the C-terminal region of RopGEF1 releases auto-inhibition and activates RopGEF1. In addition to RopGEF1, RopGEF12 also showed C-terminal auto-inhibition in our study, and this inhibition is likely to be released by phosphorylating the C-terminal region, possibly also by AtPRK2 (Zhang and McCormick, 2007). Overexpression of wild-type RopGEF12 slightly affects the polarity of pollen tubes, while a C-terminal truncation shows a much stronger phenotype, suggesting the auto-inhibition of GEF activity is controlled by its C-terminus. Overexpression of C-terminal phosphorylation mimicking the mutation of RopGEF12 resulted in significant tip swelling, strongly suggesting that phosphorylation is likely to be critical for release of the C-terminal inhibition (Zhang and McCormick, 2007). Thus, we propose that the release of auto-inhibition by C-terminal phosphorylation could be a common mechanism for RopGEF regulation. However, the detailed mechanisms for the phosphorylation-mediated regulation may differ among different RopGEFs because different phosphorylation sites are critical for differential RopGEFs. The critical S510 phosphorylation site of RopGEF12 is conserved among several closely related RopGEFs (Zhang and McCormick, 2007) and their orthologs (Supplemental Figure 5), and the essential phosphorylation sites in the C-terminal region of RopGEF1 sites are also conserved among its orthologs (Figure 7B).

#### N-Terminal Regions May Contribute Differently to GEF Activity in Different RopGEFs

Previous results suggested that the PRONE domain of RopGEF1 is sufficient for its RopGEF activity (Gu et al., 2006), but the

same domain of RopGEF12 was not (Zhang and McCormick, 2007). We propose that the function of the various N-terminal regions among RopGEFs might be different. The N-terminal region of RopGEF1 contributed to the auto-inhibition caused mainly by the C-terminal region (Gu et al., 2006) rather than being required for GEF activity. In contrast, the N-terminal region of RopGEF12 was important for the normal GEF activity of RopGEF12; the overexpression of PRONE12 had a mild phenotype on pollen tube while overexpression of PRONE12 along with the N-terminal region of RopGEF12 caused a much stronger phenotype (Zhang and McCormick, 2007). Further studies, such as structural analysis using crystallography of full-length RopGEFs, could uncover the conformational change induced by phosphorylation and provide insights into the common and distinct mechanisms for regulating activity between these two RopGEFs.

#### Redundancy between AtRopGEF and AtPRK Family Members

Arabidopsis has 14 RopGEF members and seven members are expressed in the pollen according to previous studies (Gu et al., 2006; Zhang and McCormick, 2007). Single mutants showed no defects in pollen germination or pollen tube growth. In contrast, the ropgef1,9,12,14 quadruple mutant exhibited defective pollen tube growth, implying functional redundancy between these genes. Similarly, functional redundancy exists between AtPRK members, as indicated by the pollen tube growth deficiency in the prk1,2,5 triple mutant but not in any of the single or double mutants. It is possible that RopGEF1 may not be the only RopGEF family member that can perceive the signal from AtPRK2 and that is phosphorylated by AtPRK2, and AtPRK2 may not be the only AtPRK that can phosphorylate and activate RopGEF1. This is supported by our in vitro biochemical results that RopGEF1 interacts with and can be phosphorylated by more than one AtPRK.

#### **METHODS**

### Database Search, Sequence Alignment, and Phylogenetic Analysis

LePRK protein sequences were used to identify *Arabidopsis* and rice (*Oryza sativa* ssp. *japonica*) homology sequences by BLAST against TAIR database (www.arabidopsis.org/Blast) and phytozome database (www.phytozome.org/search. php?show=blast). Protein sequences were initially aligned using MUSCLE 3.6 (Edgar, 2004). Data generated from this alignment were loaded onto MEGA5.05 (Tamura et al., 2011) to reconstruct the rooted Maximum Likelyhood phylogenetic tree using default settings. The supporting values were estimated by using bootstrap analysis (1000 replicates). The creation of the RopGEF phylogenetic tree was performed using the same method.

#### **Site-Directed Mutagenesis**

*RopGEF1* mutations in designed sites were made using the *Fast* mutagenesis system following the manufacturer's protocols (FM111, Transgen, Beijing, CN). The resulting constructs were then verified by sequencing.

#### **Protein Expression and Purification**

The full-length and the various truncated forms of RopGEF1 were cloned in pMALC2 fusion vector, and ROP1 was cloned in pGEX-KG fusion vector (Gu et al., 2006). The kinase domains of AtPRKs were constructed in pHIS8 fusion vector. Fusion protein expression in E. coli was carried out as described previously with some modifications (Gu et al., 2006). RopGEF1 and ROP1 fusion proteins were expressed at 30°C for 4h after induction with 1 mM isopropyl-β-d-thiogalactopyranoside (IPTG). Cells were harvested by centrifugation at 5000 g for 10 min. AtPRKs fusion proteins were expressed at 16°C for 20 h after induction by 0.2 mM IPTG. For GST-fusion proteins and MBP-fusion proteins, cell pellets were re-suspended in a binding buffer (20 mM Tris, pH 7.4, 200 mM NaCl, 1 mM EDTA) and sonicated using 5-s pulses 20 times. After centrifugation at 16 000 g for 30 min, the supernatant was collected and mixed with glutathione-agarose beads (Sigma) or amylose beads (Biolabs) for GST-fusion proteins and MBP-fusion proteins, respectively. After 2-h incubation, the beads were washed with the binding buffer and the fusion protein was eluted using maltose (10 mM) or glutathione (30 mM), respectively. For His-tagged proteins, cell pellets were re-suspended in a lysis buffer (50 mM NaH<sub>2</sub>PO<sub>4</sub>, 300 mM NaCl, 10 mM imidazole, 10% glycerol (V/V), pH 8.0). After sonication and centrifugation as described above, the supernatant was mixed with Ni-NTA beads (Qiagen) for 2 h. The mixture was then washed with the wash buffer (50 mM NaH<sub>2</sub>PO<sub>4</sub>, 300 mM NaCl, 20 mM imidazole, 10% glycerol, pH 8.0). His-tagged proteins were eluted using the elution buffer (50 mM NaH<sub>2</sub>PO<sub>4</sub>, 300 mM NaCl, 250 mM imidazole, 10% glycerol, pH 8.0).

#### In Vitro Protein–Protein Interaction Assays

In vitro protein–protein interaction assay was performed as described previously (Gu et al., 2006). To detect whether ROP1, AtPRK2, and RopGEF1 formed a complex, GST–ROP1 was preloaded with GDP or GTP in a nucleotide loading buffer containing 3 mM of the corresponding nucleotide, 25 mM Tris-HCl (pH 7.5), 1 mM DTT, 10 mg ml<sup>-1</sup> BSA, and 5 mM EDTA. Approximately 10 µg of GST–ROP1 fusion proteins were bound to glutathione-conjugated agarose beads, and similar amounts of MBP–RopGEF1 and His–AtPRK2 fusion proteins were used in each assay. Beads containing GST–ROP1 fusion proteins were incubated with MBP–RopGEF1 and HIS– AtPRK2 fusion proteins in an interaction buffer containing 20 mM Hepes (pH 7.4), 5 mM MgCl<sub>2</sub>, 1 mM DTT, 0.1% Triton X-100, and 1 mM EDTA for 2 h. After binding, beads containing GST–ROP1 and bound MBP–RopGEF1 and His–AtPRK2 were washed extensively to remove unbound proteins. The bound proteins were detected using a polyclonal antibody against MBP or HIS (New England Biolabs, Beverly, MA).

#### In Vitro Kinase Assay

The substrate protein (2  $\mu$ g) was equilibrated with 1X kinase buffer containing 20 mM Tris, pH 7.4, 5 mM MgCl<sub>2</sub>, 1 mM CaCl<sub>2</sub>, 1 mM DTT, and 10  $\mu$ M ATP. Purified kinase protein and substrate were incubated in 1 kinase buffer containing 5–10  $\mu$ Ci per reaction [<sup>32p</sup>-ATP] at 30°C for 30 min. Reactions were stopped with SDS–PAGE sample buffer. Proteins were separated by SDS–PAGE and detected using autoradiography.

### Analyses of AtPRKs and RopGEF1 Overexpression Phenotype

The full-length AtPRK1–5 driven by the pollen-specific *LAT52* promoter (*pLAT52*::AtPRK) were transiently expressed in tobacco pollen, together with the *pLAT52*::GFP vector as an indicative marker. The wild-type and point mutation RopGEF1 were cloned in the *pLAT52*::GFP vector and transiently expressed in tobacco pollen. Approximately 5 h after bombardment, pollen tubes were visualized using an Olympus BX51 microscope equipped with an Olympus DP70 CCD camera (Japan). Widths and lengths of pollen tubes were measured using the AIM software (Zeiss, Germany).

Pollen tubes co-expressing GFP–RIC4 $\Delta$ C and AtPRK2/ DN-PRK2 were analyzed using laser scanning confocal microscopy under a Nikon Axioplan2 microscope (Japan) equipped with a Zeiss LSM 510 META confocal laser scanning device (Germany). 1  $\mu$ m optical sections were scanned and captured using the AIM software. Confocal laser scanning images were analyzed using the MetaMorph 4.5 software (Universal Imaging, West Chester, PA). The degree of depolarized growth was determined by measuring the diameter of the widest region of the pollen tube tip. Experiments were repeated three times and more than 30 pollen tubes were measured for each sample each time.

#### Generation of the AtPRK2-Dominant Mutant

To generate *AtPRK2*–DN construct, the ATPRK2 cDNA sequence without the cytoplasmic kinase domain was cloned into a pC1300*LAT52* vector derived from pCAMBIA1300 (CAMBIA). The construct was introduced into *Agrobacterium tumefaciens* GV3101 by electroporation and transformed into *A. thaliana* ecotype Columbia. T2 homozygous plants were selected for analysis.

#### Isolation of T-DNA Insertional Mutants

The gef1-1, gef9-1, gef12-1, gef14-1, gef14-2, prk1-1, prk1-2, prk2-1, and prk5-1 T-DNA insertion mutant lines were screened from the SIGNAL collection (http://signal.salk.edu/cgi-bin/tdnaexpress/) based on a combination of database searches and PCR amplification of T-DNA flanking regions (Supplemental Table 1). For T-DNA lines identified from the

SIGNAL collection, seeds were obtained from the Arabidopsis Biological Resource Center (http://abrc.osu.edu/order-stocks). PCR reactions were carried out to identify single plants for the T-DNA insertion with gene-specific primers and LBb1.3 primer (ATTTTGCCGATTTCGGAAC) for SALK lines or GAB-LB1 primer (CCCATTTGGACGTGAATGTAGACAC) for GABI lines.

#### SUPPLEMENTARY DATA

Supplementary Data are available at Molecular Plant Online.

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# Figure S1. DN-PRK2a overexpression reduced the germination rate of pollen grain in Arabidopsis.

(A) Schemetic diagram of the truncated AtPRK2a defined as DN-PRK2a. The signal peptide (SP), the transmembrane domain (TM), and the cytoplasm kinase domain (KD) were shown. (B) *In vitro* germination assay showed the defected pollen germination in DN-PRK2a OX lines. 8-3, 23-12, and 34-4 are three independent lines overexpressed DN-PRK2a.

		20	*	40	*	60	*	80	*	100	* 🕇	120	*	140	
RopGEF1	: VDDAMRRSIS	VTESLSLFS	SINGLNPQKA	FSVQSSPHGSP	FATH	2	ALSVASRSPR	RAPPLYSVKRNG	T	REKGIVGE	ETEKAWSYAGN	SSRRVTGVT	PERD	:	98
RopGEF2	: VEKTMRGEE													:	
RopGEF3	: VDKTMRGSE													:	1
RopGEF4	: VDRTVRNRDD													:	1
RopGEF5	: VDDLTKQSDDNNL	LSSPAVSSIIAH	KKVVPLPYL	ISASGTPYRTS	FSTTPGFSPS	SMISPKKGER	RTPYSSKDTN	KIIEKGLPSRGY	GVRRVLNNYL	GMESKLKIC\	/NPSDNADTAV	INQISKDVEEB	CKKRNSTSVI	HQKGPPKYTVS :	14
RopGEF6	: MDDISKDDGDGDC	DSCSDKLRLLSF	(EAASGGSGS	LREKLSA			PSLFSVSFSG	ISTPYRTLSFSA	STPSYSPMPL	ISPINGGRG	GERAPFLSGRN	IRERCGFGPK	KALANYLRG	:	11
RopGEF7	: VDDLTRHSSDQIF	TTLGNNGNDAP	(SIAVPVSNY	FTPSYSPSKQE	LRS	SITV	PPSPSRFKIP	HSSSVKRVLTAY	VTKNEPRLKN	LPLERSSRSS	SSERLSLEKO	MKESLNVSNLI	PGI	:	11
RopGEF8	: TDTLALKQTL-LA	EETSDGGRTTEI	DSESAGSSN	SGEEAEKHDPH	SKT		LLDFMGWNDN	SSKGGDKPTK		SPNI	LTPKKLSYLER	LENLNGFRSPH	(DRH	:	9
RopGEF9	: ADSLARKQCT-GE	ETSDGGKIATET	DSASAGSSN	YSGEEIEKLES	QNS	SKTT	LLDFIGWSDN	SS	KGQSEKPP	KSPRMT	PKKLSYLEF	(LENLNGFRSPH	(DRH	:	10
RopGEF10	: ADRLVQRQLMGEA	ETRSESEAESEY	EETEKVVAA	ETPNSRK			LSDFIGWRLS	SDTKKHSSMSDI	EFFHKVEQEK	EKPMMKSPRA	ALPKKFSY	-LAKLENMRSPS	SDRH	:	10
RopGEF11	: ADQLTQEPTNNAP	SKNRYSLKENE	LREERLSFT	EDMASGT			LSDVMQWGNK	NNEMKKESFFG-	DREKP	LLSKVTGIMI	TNNKKSSY	LDNLGAMRSPI	ARYS	:	9
RopGEF12	: ADRAGNKRNT	PLEA	AEEETLVGSM	T			LSDFMGWDFD	QAANAELESK	KDLPDDPL	IKEKLSVVTI	FKKTSY	LETLGGVKSPI	ARH	:	8
RopGEF13	: ADQLTQNPEL-AM	CKIHIVKETESE	PEKEEEPNFC	LLEDRPKKQKP	TIS		LSEVMQWNIE'	INEPR	KEKSDKKL	LTRVSSMIMS	SNNKKTTY	LESLGTTRSPI	AGRYS	:	103
RopGEF14	: EDSLSNPNSP		APPSC	FPSSRDPYRTP	ER		PLLSSRVR	HSLTDDMNKADG	TETGLDFLFA	DAKASNSVNI	TPSRSSRLWC	LSKVPSDTSP-		:	88
	D														

# Figure S2. Alignment showing the variable C-terminal region of AtRopGEFs.

The alignment was produced by MUSCLE3.6 using the full amino acid sequences of AtRopGEFs and presented by GeneDoc. The read arrows indicated the S460 and S480 sites of RopGEF1, and the blue arrow showed the S510 site in RopGEF9.

		*	20	*	40	*	60		*	80	*	100	*	<b>V</b> 2	20	*			
ROPGEF9	: 7	ADSLARKQCTGEE	TSDGGKI	ATETDSAS	AGSSNYSGEEI	EKLES	QNSSKTT <mark>I</mark> I	DFI	GWSDNS-			SKGQS	EKPPKSPRMI	PK-KLSY	I-EKLENI	NGFR <mark>SP</mark> KI	RH- :	: 100	
ROPGEF8	: 1	fd <mark>tlalkqtllae</mark>	ETSDGGRTT		-ETDSESAGSS	NSGEEAEK	hdphskt <mark>l</mark> i	DFM	GWNDNS-			SKGGD	KPTKSPNLTF	KKL <mark>S</mark> Y	<b>I</b> -EKLENI	NGFRSPKI	RH- :	: 95	
ROPGEF12	: 7	ADRAGN			KRNTPLE	AEEET	-LVGSMT <mark>L</mark> S	DFM	-GWDFDQ-	AANAELES	SKK	DLPDD	PLIKEKLSVV	TTKKTSY	IETI	GGVKSPT <i>i</i>	RH- :	: 81	
Araly1.874	: 1	ID <mark>SLALKQ</mark> T	LLAEETSDGGF	RTTETDSE-	-SAGSSNSGEE	TEKLDPH-	YSKT <mark>L</mark> I	DFM	GWNDNS-			SKGGD	KPTKSPNITF	YKKL <mark>S</mark> Y	LEKLENL-	NGFRSPKI	RH- :	: 96	
Araly1.883	: 7	AD <mark>SLARKQCTGEE</mark>	TSDGGKL	-ATETDSA	RSSNYSGEETE	KLESQ	-NSSKTT <mark>I</mark> I	DFI	GWSDNS-			SKGQS	EKPPKSPKMI	PK-KF <mark>S</mark>	<b>l</b> -ekleni	NGF <mark>RSP</mark> KI	D <mark>RH- :</mark>	: 98	
Araly1.477	: 7	ADRAGN			KRNTPME	SEDET	-lvgsmt <mark>i</mark> s	DFM	GWDFDQ-	AGNADLDS	SKK	DLSDD	plvkekls <mark>v</mark> v	TTKKT <mark>S</mark> Y	LETI	GGVKSPT <i>i</i>	A <mark>RH</mark> - :	: 81	
Bra013249	: 1	FDSLALKQALLAE	ETPDGGR	TET-	-DSESPGSSNS	GEETEKLD	RQHSKT- <mark>L</mark> F	DFM	-G <mark>W</mark> S			D	KPTTPPSVTF	YKKL <mark>S</mark> Y	L <mark>EKLENF-</mark>	NGFRSPKI	RNL :	: 89	
Bra015068	: 1	fdslalket	LLAEETSDGGF	R-TETDSE-	-SAGSSNSGEE	TEKLDPR-	YSKT <mark>L</mark> I	DFM	-GWSDNS-	SKSSD-KI	PTKSP		GLI	PK-KF <mark>S</mark>	LENL	NGFRSPK <i>i</i>	ARH- :	: 92	
Bra036671	: ]	IDSLAQKQALL	AEADAGR	-TSETDSE-	-SAGSSHSGEE	TEKLDPH-	YSKT <mark>L</mark> I	DFM	-GWSDNS-			SKGGD	KPTKSPSLTF	YKKLSY	LEKLENF-	NGFR <mark>SP</mark> KI	RH- :	: 94	
Bra003536	: 7	ADRAVS			KRSTPM	EPEEETLV	GSMT <mark>L</mark> S	DFM	-GWDFDQ-	GNEDL-DS	SKKD	MSSDD	KLVKEKLNVV	'ATKKT <mark>S</mark> }	IETI	GGVN <mark>SP</mark> T <i>I</i>	ARH- :	: 81	
Thhalv1001	: 2	ADRAGN			KRSTPRE	TEDET	-lvgsmt <mark>l</mark> s	DFM	-GWDLDQ-	SKK		DTSDD	LLVKEKLSVV	TTKKT	IETI	GGVRSPT <i>I</i>	ARH-	: 74	
POPTR_0001	: 2	ADYVTRNPSHAGH	KRNTLKEAPQ	7	PASPRE	GMEKNSED	TNASMT- <mark>L</mark> S	DFM	-GWGSEQ-	NESAA-KI	KDPFGSDEI	LKDDDRYKQ	KLTNIST	'NR-KP <mark>S</mark> }	IDNI	GALRSPT <i>i</i>	ARH-	: 106	
POPTR_0003	: 7	ad <mark>hvarnpshagh</mark>	TSNTLKE	-APQVLVSP	KEGMEKNSEDT	NASMT	<mark>L</mark> S	DFM	GWSQEQN	DTTAKKDPFG	SDEL	LKDDD	KCTQKLANIS	TNRKPS	I DNI	GASRSPT <i>i</i>	ARH- :	: 106	
POPTR_0018	: 2	ADSLAQ		-SPQLESN-	QKPEE	ELDNLTSA	ETPTSKT <mark>L</mark> S	DFM	GWKVDQGI	EANMNKTTSTI	DNM	ENCQD	KIKDKTDTTP	YKKFSY	I-EKLENI	SGLRSPTA	ARQF :	: 96	
Cucsa.0620	: 2	ADYVTQNPSQASG	KKNPSRE	-TPVSSGT-	-DKFPPGEETQ	NAAETPTSI	MT – – – – TI	DFM	NWGPDI-	ADSEA-KI	KESPPANSI	DNLPTEGEVK	HVHKLQNIVI	NNKLVSY	IENI	GGLKSPT <i>i</i>	ARH- :	: 113	
Cucsa.3592	: 2	ADGLTQNPSQ	IATRRK	PTSE-	-PPMEKLEELN	NGPETPASI	MTĪ	DFM	-GWGQDQ-	NETEM-KI	KESFGNSDI	DLNL-DSDLK	QGNKAGNIVI	'NK-KVSY	IENI	SAVRSPT <i>I</i>	ARH- :	: 104	
Vv.1782614	: 7	ADSLAQNP	SLAQTGR	-KPSAVCLP	LTGSTREETEK	NPTET	QTPTSMT <mark>L</mark> S	DFM	-GWHLMG-			DTEPG	KLNKVAI	HKKSNSY	I-DKLENI	GGLRSPTS	SRH- :	: 93	
Vv.1782737	: 5	SSL		-DPEPLNF-	PNPKEEI	EKLST	GTPQSMT <mark>I</mark> S	DFM	GWNLEK-	EDGEEKKO	GSGGNSEEI	LSKNDE	KPMTKIANII	TNKKVSY	-EKLENI	GGLRSPT <i>i</i>	\R₿-	: 95	
		d					L	DF6	g₩					Sì	6	g SP	Rh		

ROPGEF9	:	-	:	-
ROPGEF8	:	-	:	-
ROPGEF12	:	-	:	-
Araly1.874	:	-	:	-
Araly1.883	:	-	:	-
Araly1.477	:	-	:	-
Bra013249	:	S	:	90
Bra015068	:	-	:	-
Bra036671	:	-	:	-
Bra003536	:	-	:	-
Thhalv1001	:	-	:	-
POPTR_0001	:	-	:	-
POPTR 0003	:	-	:	-
POPTR 0018	:	L	:	97
Cucsa.0620	:	-	:	-
Cucsa.3592	:	-	:	-
Vv.1782614	:	-	:	-
Vv.1782737	:	-	:	-

# Figure S3. Alignment showed the C-terminal regions of the RopGEF9 Orthologous Genes.

The alignment was produced using full amino acid sequences. The read arrow indicated the conserved S510 site in RopGEF9.

	* 20 * 40	* 60	* 80 *	100 *	120 *	140 *	160	
LePRK1	MSVAYRYSNHNRHHHHHLLILFVLLLQVI	VPIKSDNNEAEI		RESKS QKNDAT	-ANMNTKVSPCDK	KTDRPN-MDNVI-CE-	NGFWFG	<b>1</b> : 88
LePRK2	MSSQKNYKNKHVLFLVMIMCSLAFV	TEANLSEPEV		LIKFRESIKYDGDP	FSTWDANVPPCVKI	DNNKPK-WNNLF-CE-	SGK <b>W</b> YG	<b>I</b> : 82
LePRK3	MAAHVLIVLFVFFSITSC	VSIGDDQV		IVEFKELLLNTSLL	DSSWKKGTNPCDNI	NNKWFEVQ-CD-	NNNNNV	L: 73
AT5G35390.	MPPMQARTLSVYNVMVPLVCLLLFF	STPTHGLSDSEA		ILKFKESLVVGQENA	LASWNAKSPPCT-	WSGVL-CN-	GGSWWR	<b>L</b> : 78
AT2G07040.	WESKCLMFVSIVSVFFMVVNG	VSETET		LKFKNSLVIGRANA	LESWNRRNPPCK-	WTGVL-CD-	RGF <b>W</b> WG	<b>L</b> : 68
AT3G42880.	MTAVLFLCFLLIC	FSFTPSLQNVSESEP		LVRFKRSVNITKGD	LNSWRTGTDPCNG	KWFGIY- <mark>C</mark> Q-	KGQTWSG	I: 71
AT3G20190.	MLTWETPVMLASNTASTKKLAFITTFLIIVLCP	VTMVMSQPQADVLPLPASDADC		LRFKDTLVNASFI	-SSWDPSISPCKRI	NSENWFCVL-CV-	TGN <b>W</b> WG	<b>L</b> : 99
AT1G50610.	MRNWEDPFTLACNTALKKNLPSCIFIIIFISVLCPVAMS	QVVVPDSDADC		LRFKDTLANGSEF	-RSWDPLSSPCQGI	NTANWFCVL-CS-	WYWWG	<b>L</b> : 93
AT5G20690.	MAAAVLNPGFFLLILLSFSI	SPSLQYVSESEP		IVRFKNSVKITKGD	LNSWREGTDPCSG	KWFCIY-CQ-	KGLTWSG	<b>I</b> : 76
AT4G31250.	MTRDDKFPIVYSLLLIVLLFV	SPIYGDGDADA		LLKFKSSLVNASSL	-GGWDSGEPPCSGI	DKGSDSKWKGVM-CS-	NGSWFA	L: 79
AT1G10850.	FASSSSSSSSSSSTVSFVVFAFTVFFC	LVTPARSSDVEA		IISLKSSIDPSNSI	SWRGTDLCN-	WOGVRECM-	NGRWSK	L: 75
AT1G60630.	HISSSSCMFFLVFAFFLISPVRS	SDVEA		LISLKSSIDPSNSI	PWRGTDPCN	WEGVKKCM-	KGRWSK	<b>L</b> : 66
AT1G72460.	MAVAWLIWPIVLSLTALSA	NSITESES		LLKFKKSLNNTKSL	-DSWTPESEPCGA	SORWIGLL-CN-	KNSWFG	: 70
AT3G50230.	MTLFFFYSLLFLLLLRI	STASLPATNYFDSFLPSDAVA		II SFKSTADLDNKL	LYSLTEPYDYCO-	WRGVD-CS-	ØDRWVR	L: 79
AT5G43020.	BLLRCNLPISGFLLFCFLFTIVA	ASSSSSSNHTKRVFHSHRDVSA		LLRFKSKADLWNKI	NTSSHFCO-	WWGVT-CY-	WVR	: 80
AT5G67200.	MTLNFFLPFFFFFILLRV	SAGAEPNYFNSLLPSDAVA		II SFKSTADLDNKL	LYSLTERYDYCO-	WRGVK-CA-	OGR	L: 77
LOC Os02q0	MARPRPPGLIAVAAAAALVAWCLCGPA	ASAAAAAGGEAGGGGAGPEGDV		LIAFRET RGPDGAPPGP	LRAWGTPAVPCRG	KASQWFGVS-CH-	GNGSWOG	<b>:</b> 98
LOC Os02q5	MPTPPSPCLFFLFLLFFMWSSHSH	LGAASDADA		ALKSALDRSDRL	PWRRDTAPALC	SSWLGVROCS-	OPPRDRR	<b>1</b> : 79
LOC Os04q5	WRHRLRLLLVVLVAAAYAAGDVAS	SSYSOPTLPAVPPVOAVRPPPAAVG	GGSHSOPTFPPRAPVRAVPPPATLVSTATP	GAL AAFLAKADPSAHL	RFPLAVSPCS-	HPAVS-CS-	ADGO	: 120
LOC Os06q0	MAOPLLLLLLAAAAAAAVAVV	AVAOTNMADAEA		MOLKKSFTNSSSL	-SSWLITNTDGDKSPCAP	GSHEMHEVV-CS-	RGKWTG	: 82
LOC Os06q4	MAGVÃAVRLLLLOAAAALALAAA	ĀĀGGPEAAT		AFRGARGPHGAPPEP	LSOWATTTPGPCAG	AGTGVSLWYCVT-CH-	ORTGOWRG	<b>1</b> : 88
LOC Os08q4	MAGAPCLLRVLAVSSCLCLLADA	ARLLAAAPAEEADA		KLKAG VDGGGA	LDTWAAGTSPCDG	GTSAWAGVV-CS-	KGSWLG	<b>1</b> : 82
LOC Os09q2	MEKSKVVVFAGRVLAIVALLLAC	CCMAAAAQGGEGARVRES		LIGFLTELAGGDKE-RAR	GIGWDASVEPCDG	NRTVWPGVG-CNG	APAGDGR	94
LOC Oslig4	MVTLLLAFRLSTLFLLLAAGA	AIAVDPDGAAAPDTAAAPDTEAAA		LIRLKASLIDPTNA	LEAWSPSSPSPPCDE	THRMPRVO-CY-	NGVLIG	<b>:</b> 90
				-	F +		-	
	+ 100 + 000	* 200			+ 2	- +	220	
I ODPK1							320	F • 240
LePRK1	* 180 * 200 CHENKGESGTI-DVDA.KD.PNFTTSVMNNFEGFIP-I	* 220 SKIAGIKTAYFTNNKFSCOIDNS	* 240 * 26 SFFEGVHWLKKTH GNNQISCKIPSVF-GQ	0 * 280 LPKITEIRENNKEGQIEDF	* 3 NQERIIDMNFANNSIQ	00 * SPIPHGLASLKPSA	320 FEG <mark>NNLC-DGP</mark>	F: 240
LePRK1 LePRK2	* 200 OPENKGISGTI-DVDA KD PNETISVMNNREGPIN-I NERN GISGTI-DUDI KE PNETISVKNKEGPIPI-I I COLOSITI-DUDI KE PNETISVKNKEGPIPI-I	* 220 SKIAGEKTAYFTNNKESGIDNS NKIPTLKSAYFSNNKESGIDNS	* 240 * 26 SFFEGMWIKKIHIGNNOISCKIPSVF-GQ NIFEGMSIKKIHIANNEFICPIPIF	0 * 280	* 3 NQERLIDMNFANMSQ RELNIQNMKFE	00 * Spiehglaslkpsa Spiepsyshlylpa	320 EEGNNLC-DGP MDGN-DGLC-CPP	F : 240 L : 213
LePRK1 LePRK2 LePRK3	* 180 * 200 Qenkçisçti-dvdakdipnettivwnNnrech Bn-i Nen Ciscti-dldi keipnettivvrnkrech Bi-i Ilggicischi-dvdvisioglevnissnsressieff	* 220 	* 240 * 26 SFFEGHWIKKHHGNNOISCKIPSVF-OQ NIFEGNSKKHHANNEFICPHPPIF DFFSKASIWKWFSRKFSCKIPSSIAK	0 * 280 LPK TEIRENKEGOIDF 	* 3 NQER_IDM.FANMS_Q RELN_QNNKFE SQPN_ATINISNNK_Q	00 * SPIPHGLA-SLKPSA SPIPPSYS-HLYLPA GLIPOSLS-KFGSNP OD DESLS-MTNDKU	320 FECNNLC-DGP YDGN-DGLC-CPP FQGN-PDLC-CNQ	F : 240 L : 213 I : 226
LePRK1 LePRK2 LePRK3 AT5G35390.	* 180 * 200 QEENKEISETI-DUDALKDIPPETISUMNNEEPIPI-I NENCOSETI-DLDIKEIPNEETISUKNKEEPIPI-I LGGICISENI-DUDU IS QGLVVNLSNSESESIPE- QEENIPISESI-DIEAISGUTSLETESEMNNKEEPEPIPI	* 220 SKIAGIKTAYFTNNKFSGOIDS NKIPTIKSAYFSNNKSSGPIDS FRIGAUSLFIDGNOFSGPIPG KKIAAKSLFIDGNOFSGPIPG	* 240 * 26 SFFEGUHWIKKI HIGNNOISEKTRSVF-GQ NIFECINSIIKKI HIANNEFIEPTEPIE DFFSKUASIWKIWFSRNKFSEKTRESI-AS DAFECIGWIKKUHAQKKFIGCTRSSV-AK	0 * 280 LPK TER ENKEGTEDF 	* 33 NOERIIDMNFANNSIO RELNIONNKFE SOPNIATINISNNKIO EHOIHLLNISNNAIT	00 * SPIPHGLA-SLKPSA SPIPPSYS-HLVLPA GLIPOSLS-KFGSNF SPIPESLS-MTDPKV	320 FEGNNLC-DGP YDGN-DGLC-CPP FQGN-FDLC-CNQ FEGN-KGLY-CKP	F : 240 L : 213 I : 226 L : 230
LePRK1 LePRK2 LePRK3 AT5G35390. AT2G07040.	* 180 * 200 OPENKGISGTI-DVDA KD PNETISVMNNFECPIPN-I NEBN GISGTI-DUDI KE PNETISVKNNFECPIPI- LGGICISGNI-DVDVIS OGLVVNLSNSFSSIPE-F OMENEISSSI-DIEALSGITSLFTSFMNKFFCFPD-F REBNEISSSI-DIEALMGNSESSIFINKFFCFPD-F	* 220 * SKIAGEKTAYFINNKSSOIDNS NKIPTIKSAYFSNNKSSOIDNS FRIGALKSIFIDGNOSSOIPPI KKIAALKSYYISNNOSOLPPI KKIAALKSYYISNNOSOLPPI KKIVALKSYYISNNOSOLPPI	* 240 * 26 SFFEG.HWIKK H GNNOISKTESVF-GQ NIFEG.NSIKK H ANDEFREPLPFF DFFSK.ASIWK WFSRNKFSKIFESI-AS DAFEG.GWIKK H EQNETESI-VAK DAFEG.GWIKK H EQNETESIS-VK	0 * 280 LPRITELRIENKIEGITDF 	* 3 NQER IDM FANNS RELIQNNKFE SQPNATINISNKTQ EHQEHLLNISNNAT RHEPNMINISNNAT	00 * SPIEHGLA-SLKPSA SPIEPSYS-HLVLPA GLIPOSLS-KFGSNF SPIESLS-MTDPKV COENSFS-TMPKL COENSFS-TMPKL	320 FEGNNLC-DGP YDGN-DGLC-CPP FQGN-FDLC-CNQ FEGN-KGLC-CKP FEGN-KGLC-CKP	F : 240 L : 213 I : 226 L : 230 L : 220 L : 228
LePRK1 LePRK2 LePRK3 AT5G35390. AT2G07040. AT3G42880. AT3G42880.	* 180 * 200 QUENKGISCTI-DVDALKD PNETISVMNNREGIEN-I NENGISCTI-DLDI KE PNETISVKNKFEGELEI- LGGGGSNLDVDVISGGGRVNLSNSSSSDE-F QMENEISSI-DLEALSGTSETTSFMNKFKGPFE-F RENIELSSI-DLEALMGINSESSFINNKFKGPFE-F HTRIGISTI-NIEDIKDPNLFTELDNNLLSGPLP-F OF COUTEKI-DIPLALKNIFTSFMNKFKGSIBS-	* 220 SK AGE KTAYFTIN NKFSCO DNS NK PTLKSA FSNNKFSCP DQN 7-FRIGATKSFF DCNOSSCO PPT 7-FK AAKSJISN OG DE PKT 7-FK VALKSJISN OG DE PKT 7-FK PCKSFE JSNNODE PKT 7-FK PCKSFE JSNNODE PAD	* 240 * 26 SFFEG.HWIKKHHGNNOISGKIPSVF-GQ NIFEG.NSIKKHHANNEFIGPLPPIF DFFSKJASIWKHFSRIKFIGKIPSSI-AS DAFEG.GWIKKHHGKNFIGIPSSI-AK DAFEG.GWIKKHHEONNFIGEFTSI-VK DFFKETPOIRVEIDNRLSKIPASI-AQ	0 * 280 LPKTERENKECTOF 	* 33 NOER IDM FANGS O RELNIONNKFO RHUHLNISNNA T 	O PIPHGLA-SLKPSA SPIPSYS-HLYLPA CLPOSLS-KFGSNP SPIESLS-MTDPKV SOIDNSFS-TMDPKL SPIESLS-MTDPKL SPIESLS-MTDPKL SPIESLS-MTDPKL	320 EGNNLC-DGP YDGN-DGLC-GPP YDGN-PDLC-CNQ EGN-KGLY-CKP FEGN-KGLC-CKP FEGN-QRLC-CSP FSCN-KNLC-CPP	F : 240 I : 213 I : 226 I : 230 I : 220 I : 228 I : 228 I : 252
LePRK1 LePRK2 LePRK3 AT5G35390. AT2G07040. AT3G42880. AT3G20190. AT3G20190.	* 180 * 200 CDENKGISGTI-DVDALKDIPNFETESVMNNNFEGPLEN-I NEGNICSGTI-DLDIKEIPNETEVFKNKFEGPLEI-I LGGICISGNL-DVDVISSOGEVVNISSNSFSSIPE- QMENLEISGI-DIEALSGITSKTSFMNKKFEGPLE- RVENLEISGI-DIEALMGINSKSSFINNKFKGFEE-F HTRECISGII-NIEDIKUPNISTEFLDNLISGPLEP- QEGUCITEKL-DLEPLALKNKFTSFFNNKFKGSPS- OFGUCITEKL-DLEPLALKNKFTSFFNNKFKGSPS-	* 220 3 SK AGEKTAVFTINKFSCO DN NK PTIXSAVFSNNKFSCO DO 7FK GALKSLF DONOSCO PFI 7KK AALKSLYISNNOSDLE PKK 7KK VALKSLYISNNOSDLE PKK 7FK PGLKSLISNNOSDLE PKI KNFGALKSLYISNNSFSCF PAI KNFGALKSLYISNNFFSCF PAI	* 240 * 26 SFFEGUHWIKKIH GNNOISCKIPSVF-GQ NIFEGUNS KKIH ANNEFICPLEPIF DFFSKJASUKUFSRNKFSKITESU-AS DAFEGUWIKKIH AONKFICOIPSSV-AK DAFDCUWIKKIH EONRISCKIPASI-MQ DFFKETPOLKRVFIDNRLSCKIPASI-MQ DAFDCUHHUKKILIANAAFRSTESSI-AS	0 * 280 	* 33 NQER IDM FANSS 	00 * PPHCLASLKPSA PIPPSYS-HLYLPA PIPPSISKFGSNF SIPPSISMTDPKV SIPIFISDRKNLEMK PIPESISNMDPYS PIPFIFISLSNMDPYS	320 FECNNLC-DGP YDGN-DGLC-CPP FQGN-PDLC-CNQ FEGN-KGLY-CKP FEGN-KGC-CKP FEGN-QRLC-CSP FSGN-KNLC-CPP	F : 240 L : 213 I : 226 L : 230 L : 220 L : 228 L : 252 I : 246
LePRK1 LePRK2 LePRK3 AT5G35390. AT3G42880. AT3G42880. AT3G20190. AT1G50610. AT5G20600	* 200 CDENKGISGTI-DVDA KDIPNETISVMNNREGPIPN-I NEBN GISGTI-DLDI KEIPNETISVKNNREGPIPI-I LGGICISGNI-DVDVISGGISVKNSFSSSIE-F QMENEFISSI-DIEALSGISSIFTSFMNKFFGFPE-F HUTRIGISGI-DIEALSGISSIFTSFMNKFFGFPE-F HUTRIGISGI-DIEALSGISSIFTSFMNKFRGPE-F UTRIGISGIT-NIEDIKDIPNETISFMNKFRGPE-F QEGGCITKL-DLEFIAALKNETISFMNKFRGSPE- QEGGCITKL-NLDPUVVKNETISFMNNKFNGPP-F QEGGCITKL-NLDPUVVKNETISFMNNKFNGPP-F	+ 220 SKIAGEKTAYFINNKSSCODNS NKIPTIKSAYFSNNKSSCODNS FRIGALKSIFIDGNOSSCOPPI KRIAALKSYYSNNOSCOPPI KRIVALKSYYSNNOSCOPPI FKIPGLKSITISNNSTSCADI KRFGLKSITISNNSTSCPPI KRFGLKSITISNNRTSCPPI	* 240 * 26 SFFEG HWIKK H GNNOIS KIPSVF-GQ NIFEG NS KKH H ANNEFE PLPFF DFFSK AS WKHWFSR KFSK HESI-AS DAFEG GWIKK H AOKKFC TISSV-AK DAFEG GWIKK H EQNET STISSI-AY DFFKETPO KKVFI DNRLSK HASI-MQ DAFEG PLIKK LIANNAFR STISSI-AY DAFEG PLIKK LIANNAFR STISSI-AY	0 * 280 LPRTTELRENKEGOTOF 	* 33 NOERIIDM FANNS O RELUQONKFE SOPNATINISNAT SOPNATINISNAT ATDGNKVIKSIDISNA CKUSISSENDIE KOKDIKLASFENDIE QCKDIKLASFENDIE QCKDIKLASFENDIE	00 * PPGVSSLKPSA PPGVSHLVLPA LIPOSISKFGSNF FIPESISMTDFKU OIPNSFSTMDFKI EIPISISMDFVS FIPESISNMDFVS FIPES	320 FEGNNIG-DGP MDGN-DGG-CPP PQGN-PDL-CNQ FEGN-KGLY-CKP EGN-KGLG-CKP EGN-QRG-CSP EGN-QRG-CSP EGN-RGC-DAP FAGN-KGC-DAP	F : 240 L : 213 I : 226 L : 230 L : 220 L : 228 L : 252 L : 246 V : 233
LePRK1 LePRK3 AT5G35390. AT2G07040. AT3G20190. AT3G20190. AT1G50610. AT5G20690. AT4G31250	* 180 * 200 CDENKGISCTI-DVDA KDIPNETTISVMNNEEGIEN-I NEMIGISCTI-DVDA KDIPNETTISVMNNEEGIEN-I LEGGGISSNI-DVDVIS OG RVVNLSNNSESSIBE-F CMENIEISSI-DIEA SGITSLEVTSFMNKEEGEPD-F RENIEISSI-DIEA MGINSLESSFINKEEGEPD-F GUEGGITSKI-NIED KDIPNLETTESFMNKENSYES- OEGGGITSKI-NLOPIVEKNETTISFMNNNENSYEQ- HTTRIGISTI-VLDPIVEKNETTISFMNNNENSYEQ- HTTRIGISTI-VLDPIVENNETTISFMNNNENSYEQ- HTTRIGISTI-VLDPIVENNETTISFMNNNENSYEQ- HTTRIGISTI-VLDPIVENNETTISFMNNNENSYEQ- HTTRIGISTI-VLDPIVENNETTISFMNNNENSYEQ-	* 220 SK AGE KTAYFINNK SCODNS NK PTLKSA FONKSSOD DN TRIGALKSF DCNOSSOD PPI KK AKSYLSNNO GDP ERI KK VALKSYLSNNO DDE PKI KK PCKSF JONNSSOD ADI KRFTSLKSYLSNNR SCE PAI KRFTSLKSYLSNNR SCE PAI KRFTSLKSYLSNNR SCE PAI KRFTSLKSYLSNNR SCE PAI	* 240 * 26 SFFEG HWIKK H GNNOISCKIPSVF-GQ NIFEG NS KKIH ANNEFICPLEPIF DFFSK AS WKIMFSRIKFSKIFESI-AS DAFEG GWIKKIH EQNNFISEIFTSI-VK DAFGG GWIKKIH EQNNFISEIFTSI-VK DFFKETPO KRIVE DNRLSKIFASI-AY DAFLG PLIKKIL ANNAFRSTIPSSI-AY DAFLG VLIKKIL ANNAFRSTIPSSI-AS DFFKDVSKI KRIVE DHKFESSIFSSI-AS	0 * 280 LPKTTE RENNKE CIEDF 	* 33 NQER IDM FANSS 	00 * PPHCLASLKPSA SPIPPSYSHLYLPA CIPOSISKFGSNF SPIPESLSMTDPKI SPIPESLSMTDPKI SPIPESLSMNDPKS SPIPESLSNMDPKS SPIPESLSNMDPKS SPIPESLSNMDPKS SPIPESLSNMDPKS SPIPESLSNMDPKS SPIPESLSNMDPKS SPIPESLSNMDPKS SPIPESLSNMDPKS SPIPESLSNMDPKS SPIPESLSNMDPKS SPIPESLSLMNTPKS SPIPESL	320 EECN-NIC-DCP DCN-DCC-CPP CON-PDC-CPP ECN-KGY-KP ECN-KGY-KP ECN-KGC-CPP ECN-KGC-DAP IAON-KGC-DAP ILTEN-EYC-CPP	F : 240 L : 213 I : 226 L : 230 L : 220 L : 228 L : 252 L : 246 L : 233 U : 233
LePRK1 LePRK3 AT5G35390. AT2G07040. AT3G20190. AT3G20190. AT1G50610. AT5G20690. AT4G31250.	* 180 * 200 CDENKGISGTI-DVDALKD PNETISVMNNNFERIE ILGGICISGTI-DLDIKE PNETISVMNNNFERIE ILGGICISGNI-DVDVISKOGVWNISNSFSSIPE- OXENIEISGSI-DIEANGGINSESSOFINKFKCPBE- HTRIGISGTI-NIEDIKD PNETIFILDNLISCPEPI- QEGGCITEKL-DLEPIAAKNETISFMNNFROPIE- HTRIGISGTI-NIEDIKD PNETIFILDNLISCPEPI- HTRIGISGTI-NIEDIKD PNETIFILDNLISCPEPI- RENNSISSEL-DVQAGSRGKSTSFMNNFROPIE- NTRIGISGTI-TVDDIKD PNEKTREDNLISCPEPI- RENSISSEL-DVQAGSRGKSTSFMNNFFCKPRG	* 220 SK AGL TA FINNKSSC DNS NK PT SS PENKSSC DDS KK AALSS T DS SS DDS KK VALSS T DS SS D AD KK VALSS T SN SS D AD KK SS T SN SS D AD KRFS SS T SN SS D AD KRFS SS T SN SS SS P AD	* 240 * 26 SFFEG HWIKK H GNNOISCKIPSVF-GQ NIFEG NS KK H ANNEFE PLPIF	0 * 280 LPRITERENKECTOP 	* 33 NOER IDM FANNS O 	* PIPHCLASLKPSA PIPFSYSHLYLPA SLIPQSISKFGSMF PIPESLSMTDPKV OIPNSFSTMDPKV EIPITISDRKNLEAK PIPESLRNMDPVS PIPESLRNMDPVS RIPESLRNMDFYS OIPDESLACHNIFY PIPELIG-LMNIFF	320 ECNNLDGP VDCNDGC CO CCNDUL NO ECNKGI KP ECNKGI SP ECNKGI SP ECNKGI SP ECNKGI SP ECN	F : 240 L : 213 I : 226 L : 230 L : 220 L : 228 L : 252 L : 246 V : 233 L : 233 L : 233 L : 233
LePRK1 LePRK2 LePRK3 AT5G35390. AT3G07040. AT3G20190. AT3G20190. AT1G50610. AT4G31250. AT1G10850. AT1G60630	* 180 * 200 CDENKGISGTI-DVDA KDIPNETISVMNNREGPIN-I NEBN GISGTI-DLDI KEPPNETISVKNNREGPIE-I LGGIGISGNI-DVDVISQGIRVMISNSFSSIE-F QENIEISSI-DIEALSGISIFISSISTER HUTRIGISGI-DIEALSGISSIFISSISTER HUTRIGISGI-DIEALSGISSIFISSISTER HUTRIGISGI-DIEALSGISSIFISSISTER HUTRIGISGI-DIEALSGISSIFISSISTER HUTRIGISGI-NESSISTER CEGGCITKL-DLEFIALKNETISFMNNKINGPPO- HUTRIGISGI-VOALSGIRGISSIFIKNISSISSIP-I VENINTSSI-NESSING DORVUSFKASLSSIP-I VENINTSSIFIENEN NOT DORVUSFKASLSSIPII	* 220 * SK AGE KTALFINNK SGO DNS NK PT KSALFSNNK SGO DNS FRIGALSS FIDGNO SGO PPI FRIGALSS FIDGNO GCO PGI KK VALKS YLSNNO DLE PKI FK PGLS I SNNS SGE ADI FK PGLS I SNNS SGE PAI FK PGLS I SNNS SGE PAI SG VNLS YLDNNS SGEPPE	* 240 * 26 SFFEG HWIKK H GNNOISKIPSVF-GQ NIFEG NSIKK H ANNEFE PLPTF DFFSK AS WKIWFSR KFSK HESI-AS DAFEG GWIKK H AOKKT CIESSV-AK DAFEG GWIKK H EQNFISEITSSI-W DAFEG HIKK LIANAFR SISSI-MAY DAFEG PLIKK LIANAFR SISSI-MAY	0 * 280 LPRTTELRENKEGOIDF 	* 33 NQER I DM FANNS O 	CO * PPGVSSLKPSA PPGVSHLVLPA PPGVSKFGSNF PPESLSMTDPKV PUPSFSTMDPKI PPSLSMDPVS PPESLSNMDPVS PPESLSNMDPVS PVPQSIADKKNLAVN RIPLFIGLMNIFF PUPPLRALKOPDESS PPPOALNEFNESS	320 DECN-DGLC-DGP OCN-DGLC-DGP CON-DGLC-CO CON-DGLC-CN ECN-KGLC-KP ECN-KGLC-KP ECN-KGLC-GP BACN-KGLC-DP BACN-KGLC-AP TSN-KGLC-AP TSN-KGLC-AP TSN-KGLC-AP TSN-KGLC-AP	F : 240 I : 213 I : 226 I : 220 I : 220 I : 220 I : 228 I : 252 I : 246 V : 233 I : 233 I : 229 I : 229 I : 229 I : 229 I : 220 I : 223 I : 223 I : 220 I : 220 I : 223 I : 220 I :
LePRK1 LePRK2 LePRK3 AT5G35390. AT2G07040. AT3G20190. AT3G20190. AT1G50610. AT4G31250. AT4G31250. AT1G10850. AT1G60630.	* 180 * 200 CPENKGISGTI-DVDA KDIPNETTISVMNNTEGITN-I NEMIGISGTI-DVDA KDIPNETTISVFNNTEGITN-I LGGGGSSNI-DVDVIS QGLVVNLSNNSFSSBEF ROMIFISSI-DIEAISGTSLFTSFMNKFFGFPD-F HTRICISGTI-NIEDIKDIPNLRTREDNILSGPDP-E OEGSGTGKL-NLEPIKDIPNLRTREGNNNFNSPE- HTRICISGTI-NIEDIKDIPNLRTREGNNNFNSPE-F HTRICISGTI-NIEDIKDIPNLRTREGNNNFNSPE-F CEGSGTGKL-NLEPIKDISSESSFMNNFNSPE-F HTRICISGTI-NIEDIKDIPNLRTRESFMNNFNSPE-F HTRICISGTI-NIEDIKDIPNLRTRESFMNNFNSPE-F UEGSGTGKL-NLEPIVALKNERTISFMNNFNSPE-F HTRICISGTI-VDDIKDISSESFMNNFNSPE-F HTRICISGTI-VDDIKDIPNLRTRESFMNNFNSPE-F HTRICISGTI-VDDIKDISSESFMNNFNSPE-F HTRICISGTI-VDDIKDIPNLRTRESFMNNFNSPE-F HTRICISGTI-VDDIKDISSESFMNNFNSPE-F HTRICISGTI-VDDIKDISSESFMNNFNSPE-F HTRICISGTI-VDDIKDISSESFMNNFNSPE-F HTRICISSEL-VPNLNTSSESFMN-F HTRICISGLINGKSINGIDDERVESFKGSLSGSTEN-I VEPNNNSSELNGKSINGIDDERVESFKGSSLSGSTEN-I	* 220 SK LAG KTAYFINNK SGO DNS NK PTLKSA FSNNK SGO DP FRIGALSK JISNN G GD PI KK LAKS JISNN G DLE PKI KK PCKSL JISNN G DLE PKI KK PCKSL JISNN FSGE AD KRFTSLKS JISNN FSGE PAI KRFTSLKS JISNN FSGE DI SGUVNLKS JINNN SGEPES SGUVNLKS JINNN SGEPES	* 240 * 26 SFFEG HWIKK H GNOISCKIPSVF-GQ NIFEC NS KKI H ANNEFICPLEPIF DFFSK AS WKIWFSRKFFGKIESSI-AS DAFEG GWIKK H EONNFISEIFTSI-VK DAFGG GWIKK H EONNFISEIFTSI-VK DAFGC HKKIL ANNAFRSTESSI-AS DFFKD SKIKRFJDHKKFESIESSI-AS DFFKD SKIKRFJDHKFESIESSI-CK SLTS- HRIKTIFISGRESSIESSI-LR SLTS- HRIKTIFISGRESSI-LR SLTS- HRIKTIFISGRESSI-LR SLTS- HRIKTIFISGRESSI-LR	0 * 280 LPRITE RENKE CIEDF 	* 33 NQER IDM FANSSO 	* PHGLASLKPSA PIPSYS-HLYLPA LIPOSISKFGSNE PIPSSISMTDPKU OIPNSFSTMDPKI PIPSISMNDPVS PIPSSISNMDPVS PIPSSISNMDPVS PIPSSISNMDPVS PIPSISNMDPVS PIPSISNMDPVS PIPSISNMDPVS PIPSISNMDPVS PIPSISNMDPVS PIPSISNMDPVS PIPSISNMDPVS PIPSISNMDPVS PIPSISNMDPVS PIPSISNMDPVS PIPSISNMDPVS PIPSISNMDPVS PIPSISNMDPVS PIPSIS	320 FECN-NLC-DCP CON-DCLC-CP CON-FDUC-CP FECN-KGLC-CKP FECN-KGLC-CKP FECN-KGLC-CKP FECN-KGLC-CP FECN-KGLC-DAP LTSN-KGLC-CP FECN-KGLC-CP FTN-VALC-CP FTN-VALC-CP FTN-LAC-CP FTN-LAC-CP	F : 240 L : 213 L : 226 L : 220 L : 220 L : 228 L : 252 L : 252 L : 233 L : 233 L : 229 L : 220 V : 233 L : 229 L : 220
LePRK1 LePRK2 LePRK3 AT5G35390. AT2G07040. AT3G42880. AT3G20490. AT1G50610. AT4G31250. AT1G10850. AT1G60630. AT1G72460. AT3G50230	* 180 * 200 CDENKGISGTI-DVDA KD PNETISVMNNNFEPIEN-I NEDN GISGTI-DLDI KE PNETISVMNNNFEPIEN- LGGIGISGN L-DVDVIS QGEVINISM SFSSIPE OMENIELSSI-DIEANG NS.RSJFINNKFEPEE HTRIGISGI-NIEUKD PNETISIONNKFESEE GEGGGTGKL-DLEPIAAKNETISFMNNKFESEE HTRIGISGI-NIEUKD PNETISIONNKFESEE HTRIGISGI-NIEUKD PNETISIONNKFESEE CEGGGTGKL-DLEPIAAKNETISFMNNFEPEE HTRIGISGI-NIEUKD PNETISIONNKFESEE TRENSISSEL-DVQA GSRGLKSTSFMNNFEPEE VEYNIGSSI-NEKSINQ DQLFVGFKASLSSIP-I VEYNINGSL-NEKSINQ DQLFVGFKASLSSIPE-I CEGGGISKV-DVAFKDIDGEVGFKASLSSIPE-I CEGGGISKV-DVAFKDIDGEVGFKASLSSIPE-I	* 220 SK AGU TA FINNK SCO DNS NK PT KSA FINNK SCO DNS KK VALKS FINNK SCO SCO PPI KK VALKS FINN SCO SCO PI KNFGALKS FINN SCO AD KNFGALKS FINN SCO PAI KNFGALKS FINN SCO PAI SCO VNLKS FINN DNN FINN DNN FINN FINN DNN SCO PAI SCO VNLKS FINN DNN FINN FINN FINN FINN FINN FINN	* 240 * 26 SFFEG HWIKK H GNNOISCKTPSVF-GQ NIFEG NS KK H ANBEF PLPFIF DFFSK JASK MK HFSKKFSKIPSSI-AS DAFEG GWIKK H AQKKFSKIPSSI-AS DAFEG GWIKK H EQNNFIE PIPSI-VK DAFDG HH KKIL ANAFRSISSI-AY DAFLG PL KK LI ANAFRSISSI-AY DAFLG VL KK FI DHKFESISSI-AY DAFLG VL KK FI DHKFESISSI-TQ DAFSK KA LK H EGRESE FIESI-KK SLTS- HRIKTIV SKRFSKTPSI-LR SLTS- HRIKTIV SKRFSKTPSI-LR DYFET VS KKAW SNRFSKTPSI-LR	0 * 280 LPKITERENKEGOIDF 	* 3 NQER IDM FANNS O 	* PIPHCLASLKPSA PIPSYS-HLYLPA PIPSYS-KFGSNF PIPESLSMTDPKV OIPNSFSTMDPKV PIPESLSMDPVS PIPESLRNMDPVS PIPESLRNMDFVS PIPESLRNMIFF OIPLIGA-LMNIFF OIPLIRALKOFDESS PIPPCLLKFDAKT PUPLWKLLPENASS	320 DECN NUC - DGP VDCN DGC NO CGN DUC NO DECN KGU NO DECN KGU SP DECN KGU SP DECN KGU SP DECN KGU SP SGN KGU SP TCN NAC DQ TCN NAC DQ TCN NAC DQ TCN NAC DQ SSN SCU SP SSN SCU SP SSN SCU SP	F : 240 L : 213 I : 226 L : 230 L : 220 L : 228 L : 252 L : 246 V : 233 I : 229 I : 220 L : 224 C : 233 I : 229 I : 224 C : 233 I : 220 I : 224 C : 233 I : 220 I : 233 I : 233 I : 220 I : 233 I : 233 I : 220 I : 233 I :
LePRK1 LePRK2 LePRK3 AT5G35390. AT3G07040. AT3G20190. AT3G20190. AT4G31250. AT4G31250. AT1G10850. AT1G72460. AT3G50230. AT5G43020	* 180 * 200 OPENKGISGTI-DVDA KD PNETISVMNNREGPIN-I NEBN GISGTI-DUDI KD PNETISVFN KFEGPIFI- L GGIGISGNI-DVDVIS QGLVVNISN SFSSIFE-F QENIEISSI-DIEA GG TSLTD SFMN KFFGFPE-F HVTRIGISGTI-DIEDIKD PNLTTISFMN KFFGFPE-F HVTRIGISGTI-DIEDIKD PNLTTISFMN KFFGFPE-F HVTRIGISGTI-NIEDIKD PNLTTISFMN KFFGFPE-F HVTRIGISGTI-NIEDIKD PNLTTISFMN KFFGFPE-F HVTRIGISGTI-NIEDIKD PNLTTISFMN KFFGFPE-F OFGGCTTKL-DLEFIAAKNLTTISFMN KFFGFPE-F HVTRIGISGI-FKSSINGDOLFVISSKASSISSIN-I VENINISSEL-DVQA GSIRGLKSISFMN HFFGKIPFG VESININISSISFMEXSINGDOLFVISSKASSISSIN-I OFGGCTSKV-DVAFIKD PSLTTISIMN SFSDIPF-I DEGCGTSKV-DVAFIKD PSLTTISIMN SFSDIPFI VESNINISSEL-SSNCDOLFVISSKASSISFD-I VESNINISSENSKV-DVAFIKD PSLTTISIMN SFSDIPFI	* 220 * SK AGE KTANFINNK SGO DNS NK PT KSA YESNNK SGO DP FRIGALSS FIDGNOSGO PP FRIGALSS FIDGNOSGO PP KK VALSS YIGSNOSGE AD FRIPGLS I SISNS SGE AD FRIPGLS VIGSNNR SGE PA FRIPGLS VIGSNNR SGE PA FRIPGLS VIGSNNR SGE PA FRIPGLS VIGSNNR SGE PA SG VNLS VIDSNS SGE PA	* 240 * 26 SFFEG HWIKK H GNNOISCKIPSVF-GQ NIFEG NSIKK H ANNEFE PLPTF DFFSK AS WKIWFSR KFSK HESI-AS DAFEC GWIKK H AOKFT COISSV-AK DAFEC GWIKK H EQNET STAS DAFEC HIKK LIANAFR SISSI-MAY DAFEC HIKK LIANAFR SISSI-MAY DAFEC HIKK LIANAFR SISSI-MAY DAFEC HIKK LIANAFR SISSI-MAY DAFEC FLIKK LIANAFR SISSI-MAY DAFEC FLIKK LIANAFR SISSI-MAY DAFEC FLIKK LIANAFR SISSI-MAY DAFEC SISSI-MAY DAFEC SISSI-MAY DAFEC SISSI-MAY SISSI-RITYVISR SKISSI-SISSI-SI DIFET VS KKAWISN HFSCHISSI-SI SILS- RTTED SFNFSSISSI-SI SILS-RTTED SFNFSSISSI-SI SILS-RTTED SFNFSSISSI-SISSI-SISSI-SIS SILS-CHARTEN SIN HFSCHISSI-SIS	0 * 280 LPRTTELRENNKEGOTOF 	* 33 	CO * PPGVSSLKPSA PPGVSHLVLPA PPGVSKFGSNF PPESLSMDPKN PPSFSTMDPKN PPSISMDPVS PPESLSNMDPVS PPESLSNMDPVS PPGLRALKOPDESS SHPPGALNENESS SHPPGL-KFDAKT PVPVVLLEFGISS NDVVVVLLEFGISS	320 DECN NUC - DGP VDCN - DGUC DGP CON - PDUC PO ECN KCU Y- KP ECN KCU Y- KP ECN KCU KP SCN KUC CP SCN KCU AP TCN VAUC CP TCN VAUC CP ACN SCU AK SSN FOUC AK SSN FOUC AK	F : 240 L : 213 I : 226 L : 220 L : 220 L : 222 L : 246 V : 233 I : 229 I : 229 I : 229 I : 220 L : 224 L : 224 J : 224 J : 224 J : 223 J : 223 J : 223 J : 233 J : 233 J : 234 J : 226 J : 235 J : 23
LePRK1 LePRK2 LePRK3 AT5G35390. AT2G07040. AT3G20190. AT3G20190. AT4G50610. AT4G31250. AT1G10850. AT1G10850. AT1G7260. AT3G50230. AT5G43020.	* 180 * 200 CPENKGISGTI-DVDA KD PNETISVMNNFECPIPN-I NEMN GISGTI-DVDA KD PNETISVMNNFECPIPI-I LGGIGLSCNI-DVDVIS QGLVVNLSNSFSSBEE-F QXENEDISGSI-DIEALSGTSLFTSFMNKFECPIPI- RENDISGSI-DIEALSGTSLFTSFMNKFECPIP-F HVTRIGSGTI-NIEDKD PNLRTREIDNILSGPLEP-F QEGCGITCKL-NLDPVPKNLRTISFMNNFNGVEQ-V HTRIGISGTI-TVDD KD PNLKTREISFMNNFNGVEQ-V HTRIGISGTI-NVDVKNLRTISFMNNFNGVEQ-V HTRIGISGTI-VDD KD PNLKTREISFNNFNFGVEQ-I HTRIGISGTI-VDD KD PNLKTREISFNNFNFGVEQ-I HTRIGISGTI-VDVKNLRTISFNNFNFGVEQ-I HTRIGISGTI-VDVKNLRTISFNNFNFGVEQ-I HTRIGISGTI-VDVKNLRTISFNNFNFGVEQ-I HTRIGISGTI-VDVKNLRTISFNNFNFGVEQ-I HTRIGISGTI-VDVKNLGSRGVGVKNLSSBFN-I VEYNNTSSL-NEKSING DQLRVUSFKASISGSTEN-I UGGCGRSF-SPETISRIDQLRVUSLENSISGSTED-I VEGVTGRL-IPDSVNKDQLEVSSLKNTSIGPLEP-F	* 220 SKIAGI KTAYFININK SGC DNS NKI PTLKSÅ FSNNKSGP DON FRIGALSSI FDGNOSG DPI KKIALSSI JSNNOGDLE PKI KKIPCLSSI JSNNOGDLE PKI KKIPCLSSI JSNNOGDLE PKI KRFTSLSSI JSNNGSSG ADI KRFTSLSSI JSNNRSSG PAI KRFTSLSSI JSNNRSSG PAI KRFTSLSSI JSNNRSSG PAI SGUVNLSV JNNNSSGPPS SGUVNLSV JINNNSSGPPS SGUVNLSV JNNNSSGPPS SGUVNLSV JNNNSSGPPS	* 240 * 26 SFFEG HWIKK H GNOISCKIPSVF-GQ NIFEC NS KKI H ANNEFIC PLPTF PFSK AS WKIWFSRKFFGCFESSI-AS DAFEG GWIKK H ECNNFISEITSI-VK DAFGG GWIKK H ECNNFISEITSI-VK DAFGC HVIK H ANAFRSTESSI-AY DAFLG PL KKIL ANAFRSTESSI-AS DFFKOSKI KRIF DHKFFSSISSI-IR SITS- HRIKTIFISGRESSISSI-IR SITS- HRIKTIFISGRESSISSI-IR SITS- HRIKTIFISGRESSISSI-IR SITS- HRIKTIFISGRESSISSI-IR SITS- HRIKTIFISGRESSISSI-IR SITS- HRIKTIFISGRESSISSI-IR SITS- HRIKTIFISGRESSI-IR SITS- HRIKTIFISGRESSISSI-IR SITS- HRIKTIFISGRESSISSI-IR SITS- HRIKTIFISGRESSISI-IR SITS- HRIKTIFISGRESSISI-IR SITS- HRIKTIFISGRESSISSI-IR SITS- HRIKTIFISGRESSISI	0 * 280 LPRITE RENNKE CIEDF 	* 33 NQER IDM FANSSO 	**************************************	320 FECN-NLC-DCP DGN-DGL-CPP CON-PDJC-CPP ECN-KGL-CPP ECN-KGL-CPP ECN-KGL-CPP ECN-KGL-CPP ECN-KGL-CPP CSN-KGL-CPP TON-KGL-CPP TON-VALC-CPQ TON-I	F : 240 I : 213 I : 226 L : 220 L : 220 L : 220 L : 228 I : 252 L : 252 I : 246 V : 233 I : 229 I : 220 I : 224 I : 233 V : 234 I :
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LOC Os09g2	: FPP	P			PPPSSGE	NDGKRRRRART	1CLGYVLLGAG	VAAFVLYM	-MCSKRRR	RPSGVGGKTAATT	ETSSSVTPG	KSAYSLPMS	EERMNATAA	AAAAVARATPA	SLVVLQRSG	<ul> <li>: 359</li> </ul>
LOC Osllg4	: SGAGA	ААААРС	GPAHT		AMPPMSAAD	YFAVQEETSVFVVM	1GIIMLVVLIV.	AGAMVLML	-RQDEGTST	ASSGYEHPAIGA	PSGNLSVPH	AAGAAASAQ	LVTMEQGGS	GAAGGAGGVGG	VGGAR	- : 366
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LePRK3	: SDMGD	LVVVNDEKO	GIFGMPDI	Mka <mark>aaevlg</mark> n-	GG	LGSAYKALLGNGVI	LSVVVKRLRET	NKFNKE	C-FDAEIRR	RLARIR <mark>H</mark> KN <b>IL</b> OP	LAYHYGKEEKI	VVSEYIPKG	SLLYLFHG-	-D-RGTAHAQ	NWCIRVKIILGVANGM	: 446
AT5G35390.	: VENTK	ISFLREDRE	EKFDLQD	lka <mark>s</mark> aeilg <mark>s-</mark>	GC	FCASYKAVLSSG-Q	OMMVVKRFKQM	NNAGRD	E-FQEHMKR	RLGRLMHHN <b>LL</b> SI	VAYYYRKEEKI	l <b>v</b> Cd <b>f</b> aerg	SLAINIES-	-N-QSLGKPS	D <mark>W</mark> PTRLK <mark>I</mark> VKGVAKGL	: 469
AT2G07040.	: IHTTK	LSFLRDDKC	GKFELQDI	LLKAS <mark>A</mark> EILG <mark>S</mark> -	GC	FGASYKTLLSNG-S	SV <mark>MVVKR</mark> FKHM	NSAGID	E-FQEHMKR	RLGRLN <mark>H</mark> EN <b>LL</b> PI	VAYYYKKEEKL	FVSDFVANG	SLAAHLHG-	-H-KSLGQPS	D <mark>W</mark> PTRFN <mark>I</mark> VKGVGRGL	: 450
AT3G42880.	: SGMGD	IIMVNSEKO	GSFGLPDI	.mka <mark>aaevlg</mark> n-	GS	LGSAYKAVMANG-I	LS <mark>VVVKR</mark> IRDM	NKLARE.	A-FDTEMQR	RFGKLR <mark>H</mark> PN <b>VL</b> TP	LAYHYRREEKI	VVSEYMPKS	SILYVIHG-	-D-RGVYHSE	T <mark>W</mark> ATRLK <mark>I</mark> IQGVARGM	: 470
AT3G20190.	: PDQNK	LLFIQDDIÇ	2REDLQDI	llra <mark>sa</mark> evlg <mark>s-</mark>	GS	FGSSYKTGINSG-Q	0MLVVKRYKHM	NNVGRD	e-fhehmrr	RLGRLK <mark>:</mark> PN <b>LL</b> PI	VAYYYRREEKI	LIAEFMPNR	SLASHILA-	-N-HSVDQPG	D <mark>W</mark> PTRLK <b>I</b> IQGVAKGL	: 484
AT1G50610.	: DPGGR	LLFVRDDIÇ	2RFDLQD	llra <mark>sa</mark> evlg <mark>s-</mark>	GT	FGASYKAAISSG-Q	2TLVVKRYKHM	NNVGRD	e-fhehmrr	RLGRLNHPNILPL	VAYYYRREEKI	lvtefmpns	SLASHILA-	NNSAG	DWITRLKIIKGVAKGL	: 484
AT5G20690.	: GGMGD	IIMVNTDKC	GSEGLPDI	MKAAAEVLGN-	GS	LGSAYKAVMTTG-I	LSVVVKRIRDM	NQLARE	P-FDVEMRR	REGKLRHPNILTP	LAMHYRREDKI	VVSEYMPKS	SILLYVILLIG-	-D-RGIYHSE	TWATRIKUIQGVAHGM	496
AT4G31250.	: GDQRK	HFVRNDQE	SRITLQD	ALRASAEVLGS-	GG	FGSSYKAALSSC-F	RAVVVKRFRFM	SNIGRE	E-FYDHMKK	AIGRESEPN LEPL	IAFYYRKEFK.	LVINTISNG	SLANLILA-	-N-RTPGQVV	DWPIRLKIVRGVTRGL	: 4/8
ATIG10850.	: GAVGT	LVELGTSDSGET	LVVRNTMED.	LIKASAETLGR-	G1	LGSTYKAVMESG-F	TVTVKRLKNA.	RIPRME.	E-FKRHVEI	LGQLKEPNLVPL	RAMFQAREERI	LVIDIFPNG	SHFTLIHG-	-TRASGSGKP	HWTSCI.KIAEDIASAL	: 4/0
ATIG60050.	- GSVGI	VEIGRDII		MKA AAUVI ONI	CCCCNDDDCCCC	LGSTINAVNESG-P		GFPRMD	L-INKHIEI	LGREAGPNEVPE	KANFQANERCI LANUERODIKI	IVEENUDNU	SEFSELEC-	-SKVSGSGKP	HWI SCLAHAEDLAMGL	: 403
ATIG/2400.	. AGISD	ITECCECCCCCE		MDA GAELLOD	GGGSNRFRSSGG	VGSALNEVLSING-V		NGALMOND	V-FDREIRA		LANEOSNOR I	UTVENODNC	STENT TOC	-C-DECKARD	UNTROLY AFDUAOAL	407
AT5GJ0250.	. TRACE	VECACEAL		MTASAFI I CR.	сэ •		TWTWKRIGT	RI AIISDE	K-FENQUEI	WEAT CHANTWRT	PAYFOAKEPPT	I TYDYL PMC	STCCTWFC	_T_KCCDATD		. 180
AT5G67200	· PNSCN	IVECGESRS		MRASAFLICR-		VCITYKAVI DNO-I	TWTWKRLDAA	KTAVTSEE	A-RENHMET	VCCLEHTNINPT	RSMFOSNCERI	TTYDYHPNG	STENLTRO-	-S-RSSRAKP	HMTSCIKIAEDVAQGI	. 507
LOC 0s02a0	DEHGR	VEW0ESRE	(	TRASAEVICS	GN	FGSSYKATLOER-F	PAVVVKREKDM	NGWGRE	D-ESEHMBB	REGRESSENTERV	VAYLYKKDEKT	TTDYTTNG	STAHFLEG-	NRGSE	DØGKBURTTRGTARGI	. 493
LOC 0s02q5	: EGIGK	VFCGGVAF	EMYSIFE	LRASAETLCR-	CE	VESTYKAVMETE-F	TIVTVKRMBEP	AAGAA	E-LGRRAEF	LGRURHPNWAL	RAMFOAKEBRI	VYDYYPNG	STESLIEGS	SSRTSSKGKP	HWTSCMKHAEDVAAGI	: 490
LOC Os04q5	: ERSGC	TECAGEGA	ASYSLEO	MRASAEVLGR-	GS	VGTTYKAVI DGR-I	VVIVKRLDAA	KIGAAALEAE.	A-BEONMDA	VGRUR	RAFOAKEBRI	VYDYOPNG	STYSLING-	-S-RSSRAKP	HWTSCLKHAEDIGOGL	: 551
LOC Os06q0	: GGAGD	LVIVNNCKO	GVEGLTDI	MKA <mark>AAEVIG</mark> S-	GG	HGSAYKAVMANG-V	/AVVVKRARDM	NRATKD.	A-FEAEMKR	RIGAMSHANILPP	LAYHYRRDEKI	LVYEYIPKG	SLLYVLHG-	-D-RGMDYAG	DWPTRLKVAVGVARGT	: 477
LOC Os06q4	: DDHGR	LVFIQEGRE	RFELEDI	LIRASAEVLGS-	GS	FGASYKATLVEG-Q	SMVVKRFKEM	NGVGRQ	D-FNEHMRR	RLGRLV <b>H</b> PN <b>LL</b> PV	VAYLYKKDEKI	FVTEYMVNG	SLAHLLHG-	GSSMAA	DWPRRLK <b>I</b> IKGVTRGI	: 494
LOC Os08g4	: GEQGR	TFVRDDDF	RGRFFELQD	IKASAEVIGA-	AN	LGVCYRATLTGG-H	is <mark>vvvkr</mark> fkem	NRVGKE	D-FEEHMRR	RLGRLSHPN <b>LL</b> PL	ISYYYRKEEKI	<b>H</b> HDYVPNK	SLAHLLHG-	-E-GRRVKKL	H <mark>W</mark> PARLK <b>L</b> VKGVARAL	: 520
LOC_Os09g2	: TAAST	/MTLNTAAAAAAEAAF	RKLRFEDI	LLRSPAELLGR-	<b>C</b> R	FGSAYKVVVPGG-A	AALAVKRVKDA.	AGAEEE	EEFRRRMER	RVGKAR <b>H</b> PA <b>VL</b> PP	LAFYCAMQEKI	VVYEFLGHG	S <b>L</b> AKLLHG-	-S-IESSQVA	DWPARLH <mark>I</mark> ASKVADGM	: 502
LOC_Os11g4	: KQVAE	FVLMSNAAC	GEFGIPEI	MKASAEVLGN-	GT	LGSAYKAAMRNG-V	/T <mark>V</mark> AVKRMRDM	NRVGRA	E-FEEHIRM	1LGELRHPNVLSP	VGYHYRKEEKI	IVSEFMPRG	SILYVLHG-	-D-QSPERVV	DWPARMR <b>I</b> AVGVVRGL	: 501
			6	56 a Ae 6G	a	G Y4a 6 or	6 VKR		f	a Hunee	a5 E L	6 5	sL Ha	6	W 6 a	

	66	50 *	680	*	700	*	720	*	740	*	760	*	780	*	800	*	820	
LePRK1 :	LYI	YNELPSLT	-A		PHGHLKSSNVL	LNESYDPL	LTDYALL	PVVNLEHAQE	EHMIAYKS	PEFK-	HN	G-R-IIRKN <b>D</b> V	WTLGILII	EMLTGKFPS	NFLQQGKGSDT	DLATWVRSV	VNEDMT :	: 593
LePRK2 :	LYI	YNELPSLT	-s		PHGHLKSSNVL	LTENFEAV	LTDYALL	PVVNAEHAHE	EHMISYKA	PELK-	QS	G-K-VNRKTDV	WTLGMLII	EILTGKFPS	NLLGKGTQDSD	DLATWVNTI	LGGESS :	: 570
LePRK3 :	KFI	HSEFGSYD			PHGNLKSSNIL	I SANNEPL	TDYAFY	-PLVNNSQAVQ	SLFAYKS	PEAI·	LN	Q-Q-VIPKS <b>D</b> W	YCLGIII	EILTGKFPS	QYLSNQKFTGT	DVAQWVQSA	IEENRV :	: 559
AT5G35390. :	FΥΙ	HQDLPSLM	A		PHGHLKSSNVL	LTKTEEPL	LTDYGLI	PLINQEKAQN	1HMAAYRS	PEYL-	QH1	R-R-IIKKT <b>D</b> V	WGLGILII	LEILTGKFPA	NFSQSSEE	DLASWVNSG	FHGVWA :	: 579
AT2G07040. :	LYI	HKNLPSLM	-A		PHGHLKSSNVL	LSEKFEPL	LMDYGLI	PMINEESAQE	ELMVAYKS	PEYV-	KQ	S-R-VIKKT <mark>D</mark> V	WGLGVLII	EILTGKLLE	SFSQVDKESEE	DLASWVRSS	FKGEWT :	: 563
AT3G42880. :	DFI	HEEFASYD	L		PHGNLKSSNVL	LSETYEPL	SDYAFL	PLLQPNNASC	)ALFAFKS	PEFV-	QN	Q-Q-VSPKSDW	YCLGIIVI	EVMTGKEPS	QYLNTGK-GGT	DIVEWVQSS	IAQHKE :	: 582
AT3G20190. :	GYI	FNELTTLT	I		PHGHLKSSNVV	LDESF <b>D</b> PL	LTDYALR	PVMNSEQSHN	JLMISYKS	PEYS-	LK	G-H-LTKKT <b>D</b> V	WCLGVLII	ELLTGRFPE	NYLSQGYDANM	SLVTWVSNM	IVKEKKT :	: 597
AT1G50610. :	SYI	FDELPTLT			PHGHMKSSNIV	LDDSFEPL	LTDYALR	-PMMSSEHAHN	JFMTAYKS	PEYR-	PSI	KGQIITK <mark>KT</mark> DV	WCFGVLII	EVLTGREPE	NYLTQGYDSNM	SLVTWVNDM	VKEKKT :	: 599
AT5G20690. :	KFI	HEEFASYD	L		PHGNLKSSNVL	LSETYDPL	SDYAFL	PLLQPSNASC	)alfafkt	PEFA-	QT(	Q-Q-VSHKS <b>D</b> V	YCLGIIII	EILTGKFPS	QYLNNGK-GGT	DIVQWVQSS	VAEQKE :	: 608
AT4G31250. :	AYI	YRVFPDLN	L		PHGHLKSSNVL	LDPNFEPL	LTDYALV	-PVVNRDQSQC	)FMVAYKA	PEFT-	QQ	D-R-TSRRSDW	WSLGILII	EILTGKFPA	NYLRQGKGADD	ELAAWVESV	ARTEWT :	: 591
AT1G10850. :	LYI	HQNPG	L		THGNLKSSNVL	LGPDFDSC	LTDYGLS		ETSAVSLFYKA	PE <mark>CR</mark> -	DP1	R-KASIQPA <b>DV</b>	YSFGVLLI	ELLTGRTPF	QDLVQEYGS	DISRWVRAV	REEETE :	: 582
AT1G60630. :	VYI	HQNPG	L	'	THGNLKSSNVL	LGPDFESC	LTDYGLS	DIHDPYSIEI	DTSAASLFYKA	PECR-	DL1	R-KASIQPA <b>D</b> V	YSFGVLLI	ELLTGRTSF	KDLVHKYGS	DISTWVRAV	REEETE :	: 575
AT1G72460. :	WYI	HRELGFLN	L		PHGNLKSSNIF	LAEDGOPL	ISEFGLQ	KLINPDAQSQ	28LVAFKS	PE <mark>A</mark> D-	RD(	G-T-VSAKSDW	FSFGVVVI	EILTGKFPS	QYAGLNRAGGA	NLVEWLGSA	LEQGGW :	: 580
AT3G50230. :	ΗYΙ	HQSSAKF			HGNLKSTNIL	LGHDEEAC	VTDYCLS	VITDSSVPPN	ND-PDISSYKA	PEIR-	KS	IDSRPISKCDV	YSFGVFLI	ELLTGKTAS	RQPIMEPN	DMLDWVRAM	IRQEEER :	: 608
AT5G43020. :	SYI	HQAWQ	L	'	VHGNLKSSNVL	LGQDFDAC	ADYCLVALAT	NPPTTSNDGQE	ED-ADAAAYKP	PEAR-	НК	SLNYQSVKADW	YSFGILLI	ELLTGKOPS	KIPVLPLD	EMIEWVRKV	REEGEK :	: 605
AT5G67200. :	ΥYI	HQTSSALV			HGNLKSTNIL	LGQDFEAC	LTDYCLS	-VITDSSSASE	PDDPDSSSYKA	PEIR-	KS	S-RRPISKC <b>D</b> V	YSFGVLIE	ELLTGKNAS	RHPFMAPH	DMLDWVRAM	IREEEEG :	: 619
LOC Os02g0 :	GHI	YDELPMLT			PHGHLKSSNVL	I DGDMBAV	ISDYALV	-PVVTASAAAQ	0VMVAYKA	PECVAAA-	AA	G-K-PSKKSDW	WSLGILII	EVLTGKEPA	NYLRQGRQDNA	DLAGWVSSV	VSEERT :	: 609
LOC Os02q5 :	VH	HQSPPAGI	v		HGNLKPSNVL	LGPDEESC	LTDYGLV	-PTILPSHADI	LASSTSVLYRA	PET	RT	A-HAFIPAS <b>D</b> V	YSFGVLLI	ELLTGKAPF	QDLMEMHSD	DIPSWVRAV	REEETE :	: 603
LOC Os04q5 :	AYI	HQASR	L	'	VHGNIKSSNVL	LGSDFDAC	TDNCLA	-FLLESSEVKI	DDAAYRA	PENM-	KSI	N-RRLTPKSDI	YAFGILLI	ELISGKPPL	QHSVLVAT	NLQTYVQSA	.RDDGV- :	: 657
LOC Os06q0 :	AFI	HGELAGHE	v		PHGNLKSANIL	LAPDEPL	IVDFGYS	-GLINHMQSPN	ISMIARRA	PECA-	AGI	H-P-VGAKADW	YCLGIVLI	ELLTGKFPS	LYLQNAK-GGT	DLVMWATSA	IADGYE :	: 589
LOC Os06q4 :	AHI	YDELPMLT	v		PHGHLKSSNVL	I DAAF <b>B</b> PI	LSDYALV	- PVMTPRHAAQ	OVMVAYKS	PECG-	ET	G-R-PSKKSDW	WSLGILII	EVLTGKFPA	NYHRQGR-TGT	DLAGWVHSV	VREEWT :	: 606
LOC Os08g4 :	QYI	YDELPMLT	v		PHGHLKSSNIL	LNDRFEPL	LTDYSLV	- PVMNQSHSAC	)LMVAFKS	PERR-	QF	G-R-SSKKSDW	WCLGILII	EILTGRPPS	YDPPPQPEAATANO	GDLVGAVASI	PEGEWL :	: 636
LOC Os09g2 :	AFN	HGALRGGDGDGDGA	NANLSFSSSYE	EDEAGGAI	AHGNLKASNII	FTATMPC	ISEYGVT	-APPPPSSAP	A			ALRADV	RAYGVLLI	ELLTGKATA	ADGA	ELSRWVTAV	IREEWT :	: 617
LOC Oslig4 :	SYI	HEKLGIPA	-MRLVSMTGAD	FDAPPPPP	PHGNLKSGNIL	DAHLEPR	UDYGFF	-PLVNTSOAPH	HAMFAFRS	PEAAS	SAAAAGAGAAAOR	A-A-LSARSDW	YCLGIVLI	ELVTGKEPS	OYLLTAR-GGT	DVVOWAASA	VAGGTE :	: 641
	6	5	_		HG 6Ks N6	1 E	6 d			pe		D6	G6 61	LE663G4 p		6		
		*	840	*	860	*	880	*	900	*	920	*						

LePRK1				669
LePRK2	÷			642
LePRK3	÷			612
AT5G35390.	÷		÷	662
AT2G07040.	÷			647
AT3G42880.	÷		÷	633
AT3G20190.	÷			679
AT1G50610.	÷		÷	686
AT5G20690.	÷	E-ELIDPEIVNNTESMROWVELLRVGAACIASNPDERLDWREAVRR EOVKT		659
AT4G31250.	÷			676
AT1G10850.	:	SGEEPTSSGNEASEEK OALIS ATVOVTIOPDN PVNREVLKMORDARAEAPFSSNSSEHSPGRWSDTVOSLPRDDOVSI	:	663
AT1G60630.	:	VSEELNASEEK OALLT ATACVAVKPEN PAV REVLKNYKDARAEAALFSFNSSDHSPGRWSDTIOSLPREDHMSI	:	652
AT1G72460.	:		:	644
AT3G50230.	:	SENGLEMMTOTACLCRV-TSPEORPTMKEVIKMOEIKGSVV-MTEENEKFLENEKFL	:	660
AT5G43020.	:	KNGNWREDRDKFGMLTEVAVACSL-ASPEORPTWWOVLKMPOELKEAAVMECELVMDSANSESS	:	669
AT5G67200.	:	TENREGMTETACLORV-TSPEORPTMROVIKMOEIKESVMAEENDPFRENDPFRENDPFR	:	669
LOC Os02q0	:	G-EVFDKDMAAAGAGAEDDVLKI-HVGLCCCDADVDCWEIKTAIAREEIRVPDPTPTPAAAADAAEPSPSTTTTTNSGETRS	:	692
LOC Os02q5	:	SGGESASAGGTEEK GALIS AAAOVVADPAR PTTPEVI RMUREARAEAM-SSSNSSDRSPARWSDAVOVOMGMGVPRDOGELGGLT	:	690
LOC Os04q5	:	DVER_SMIVDLASACVR-SSPESRPTAWOVLKMOCVKEADTAGDNDSDLTSNS	:	710
LOC Os06q0	:	R-DLFDKAITSAWKFALPDWARWRWAVDCVETDADK-PDWKVAAARWEEVVAAAMATVRERHQAAGGESSRSSSHAQYVRDGSMORITSVGERSSRRGSNDYSS	:	693
LOC Os06q4	:	G-EVFDQEMRGARGGEGEVVKILK/GLCCCESDVDK-WDIRDALAR EELRERDAGAGADDSSAASSVASGGGGGEASRSHSS	:	688
LOC Os08q4	:	E-KVVDADMIRKWEDEESKGEVVKLIKIGMACCEAAVDSRWEIKTAVESTEELKGGKEEDANDEHSFYSSIDGDEFASVAIN	:	717
LOC Os09g2	:	A-EVFDRAMLSSAGAGGDTVASEQR/VRLLQVAMRCIDDASSPSPPPTVREVAGMUNAIREEDDMSLSSEADDMSLSSEA	:	687
LOC Osllg4	:	Q-EVVDPVVAAGAGPAAVRLLR/GVRCTIPEPESRPSMADVARMVEQVAGGGGGGASAGPAAVRLLR/GVRCTIPEPESRPSMADVARMVEQVAGGGGGGAS	:	697

Figure S4. Alignment data used to produce the PRKs phylogenetic tree in Figure 1A. The alignment was produced by MUSCLE 3.6 and presented by

GeneDoc without adjustment.

RopGEF1 : RopGEF2 :	* EIEMMKERF <mark>A</mark> KLLL ELETMKERFSKLLL	20 * .GEDMSC <mark>GGK</mark> GV <mark>C</mark> TALAISNAIT .GEDMSC <mark>SGKGVC</mark> TAV <mark>T</mark> ISNAIT	40 * 6 NISATVFGELWRLEPLAPOKKAN NLYATVFGONLRLEPLEIEOKTI	0 * MRRETEWILCVSDSIVE WKREYNCLLSVCDYLFE	80 * LIPSIQFP-GEGTYSI FIEKSONLS-NEATVO	100 * METRPRSDIYANLEAL MESRPRADIYINLEAL	12 KT ANT DM : 118 KT SMT MEA : 118
RopGEF3 :	ELETMKERFAKLLI	.GEDMSG <mark>SGKGVC</mark> TAV <mark>T</mark> ISNAIT	NLYATVFGÖ <mark>NL</mark> RLEPL <mark>ETEKRAI</mark>	MKRENNCLESVCDYIVE	FIPRCONLS-NCATVEV	MESRPRADIYINLPALR	KLOSMIMEA : 118
RopGEF4 :	ELEMMRERFAKLLI	.GEDMSG <mark>SGKGVC</mark> TAVTVSN <mark>S</mark> IT	NLYATVFGÖSLRLOPLSTEKKDI	MKRENNCFVSICDYIVE	VIPRSLCTNVEI	TETKIRSDIIMSIPALR	KLONMIMEI : 114
RopGEF5 :	DVEMMKERFAKLLI	.GEDMSGSGKGVCTALAISNAIT	NLCATIFGOLWRLEPLSSEKKEN	MRRENEVILSVSDHIVE	LTPSTOTYP-DCNKFEV	MECRPREDITINLPALR	KLONMILDI : 118
RopGEF6	EIELLKER <mark>MA</mark> KLLI	GEDMSG <mark>SGEGVCE</mark> ALAISNAIT	NLYAAIEGOWRLEPIPSEKKIN	NRRETEVILSVSDHTVE	LVPSFONFP-NCNKIDV	MNCR PRSDLFTCLEALR	KIDNMITEI : 118
RopGEF7	EVEMMKERF <mark>S</mark> KLLI	GEDMSG <mark>SGNGVC</mark> TALAISNAIT	NICATIFGOIMRLEPIPTEKKEN	NRREMEWILCVSDHTVE	MTPTWCTFP-DCTKLDI		KIDNMITEI : 118
RopGEF9 : RopGEF10 :	ETEMMKDRFTKLLL DMEVMKERFAKLLL	JGEDMSGGGAGVSSALALSNAII JGEDMSGGGKGV <mark>S</mark> SALALSNAIT JGEDMSG <mark>GGTGET</mark> SALALSNAIT	NIAASIFGEOTKLOPMAPDRAA KIADSMFGEOMKLOPMAPETKEN	NKEIDWIISVIDHVE NKEIDWIISVIDHVE NRKENGWIISVIDHIVQ	FVPSQCISK-ECVCTPI FVPSQCISK-ECVCTPI FVPSRCMGK-NCQFTPI	VTROBODILINIEADR VTROBODILINIEADR	KIDAMIIDI : 118 KIDAMIIDI : 118 KIDSVILET : 118
RopGEF11 :	AMEQMKEKFSKLLI	.GEDMSG <mark>CCK</mark> GV <mark>S</mark> SALALSNAIT	NLAASAFGEORRLEPMAVDRKTE	NRREIGWLISVADYIVE	FAPTQCTNK-DCTSMD	ST QRTDLC LE L	KURAMITOC : 118
RopGEF12 :	DMEQMKERFSKLLI	.GED <mark>N</mark> SG <mark>CCK</mark> GV <mark>S</mark> SALALSNAIT	NLAASVFGEORRLEPMPABRRAF	NRREIDWLISVTDYVE	FAPSQCKNK-DCTNMD	TT QRTDLH LE L	KURAMITOC : 118
RopGEF13 :	ELEOMKDKFAKLLI	.GEDMSG <b>GSK</b> GVSSALALSNAIT	NLAASAFGEIRRLEAISEDKKEE	NRREIGWLISVTDHIVE	FSPTHCTNE-DCSSMD	TT QRTDLH LE L	KURAMITOC : 118
RopGEF14 :	DVEAMKEKFSKLLI	.GEDVTG <mark>GCK</mark> GV <mark>OV</mark> ALALSNAVT	HLATSIFGELMKLEPLCEFKKOP	NRRENDWLLSPINYNIE	LVPSKONDA-NGRSLDI	TP ABADIHU LE IC	KLDSMLTET : 118
Araly1.314 :	AMEOMKEKFSKLLI	.GEDMSG <mark>G</mark> FKGV <mark>S</mark> SALALSNAIT	NLAASAFGEORRLEPMAADRKTF	NRREIGWLISVAdhive	FAPTQOTNK-DGTSMDV	ST CETDILC LE I	KLDAMLIDC : 118
Araly1.479 :	EKECMKERISKLLL	.GEDNSGGEKGVSSALALSNAIT	NIAASVEGEORRLEPMPABRRAH	WRREIGWLISVIEYVV	FAPSOCKNK-DOTNME	TT CRIDINS IF I	KUTEMILDC : 118
Araly1.479 :	EKECMKEKFAKLLL	.GEDMSG <mark>GSK</mark> GVSSALALSNAIT	NISASAFGELRRLEPISEDRKEH	WRREIGWLISVICHIVE	FSPIHHTNE-DOSSMOV		KUTEMILDC : 118
Araly1.483 :	ELEMMRERFAKLLL	.GEDMSG <mark>S</mark> CKGVCTAV <mark>T</mark> VSN <mark>S</mark> IT	NI <mark>Y</mark> ATVFGQ <mark>SL</mark> RLQPI <mark>STE</mark> KK <mark>E</mark> I	WKREMNCFMSICCHYIVE	VIPRSLOTNVPI		KUTMIMEI : 114
Araly1.485 : Araly1.486 : Araly1.488 :	EIELLKER <mark>MA</mark> KLLL EVEMMKERF <mark>S</mark> KLLL DIEVMKERFNKLLL	GEDMSC <mark>S</mark> GEGVCPALAISNAIT GEDMSCSGNGVCTALAISNAIT GEDMSCCCDCVTSALAISNAIT	NLYAAILGOOWRLEPIPSEKKSN NLCATLFGOLWRLEPLPTEKKEN KLARSMEGEOMKLOPMYPERKEI	MRREIEVILSVSDHIVE MRREMEVILCVSDHIVE MRKEMDVI SVMCHIVE	LVPSFONFP-NONKIEV MTPTWOTFP-DCTKLEI EVPSKOMCK-NOOFTPI	MNCRPRSDLFTCLPALR MTCRRSDLYMLPALR	KLOHMITEI : 118 KLONMILEI : 118 KLONMILEI : 118
Araly1.490 :	ELETMKERFAKLLI	.GEDMSG <mark>SCK</mark> GV <mark>C</mark> TAV <mark>T</mark> ISNAIT	NLYATVFGQNIRLËPLETEKRAN	NKREMNÖLLSVODYIVE	FIPRCONLS-NGATVOV	MESRPEADIYENLEADR	KIDSMIMEA : 118
Araly1.490 :	EIEMMKERFAKLLI	.GEDMSG <mark>GCK</mark> GV <mark>C</mark> TALAISNAIT	NL <mark>S</mark> ATVFGELMRLEPLAPOKKAN	NRRELENLLÖVSDSIVE	LIPSLOHFP-GGGTYOI	METRPESDIYANLEADR	KIDAMIIDM : 118
Araly1.49/ : Araly1.861 : Araly1.874 :	DVDMMKERFAKLLI DVDMMKERFAKLLI DMEMMKDRFAKLLI	.GEDMSGSGKGVCTAVHVSNSIT .GEDMSGSGKGVCTALAISNAIT .GEDMSG <mark>G</mark> GKGV <mark>S</mark> SALALSNAIT	NIYATVEGOSIRLOPISTERRE NICATIFGOIMRLEPISSERRE NI <mark>A</mark> ASIFGE <mark>OT</mark> KLOPMPQER <mark>OVE</mark>	NKRENNCHUSICLY VE WRREMEWILSVSCHIVE WKKEI <mark>DWLISVECHIVE</mark>	UTPRSLCINVS LTPSTCTYP-DONKFOV FVPSQCTSK-EGVCTS	TC PREDIE LEAD VI ORGDIL IEAD	KUNMILDI : 114 KUNMILDI : 118 KUNMILDT : 118
Araly1.883 :	ETEMMKDRFTKLLI	.GEDMSG <mark>CCKGVS</mark> SALALSNAIT	NI <mark>A</mark> ASIFGE <mark>QT</mark> KLQPM <b>APD</b> RR <mark>A</mark> H	KKELEN ISVI HIVE	FVPSQCISK-EGVCTOI	VT QEGDIL IF I	KLOAMIIDT : 118
Bra000971 :	ELETMKERFSKLLI	.GEDMSG <mark>SCKGVC</mark> TAV <mark>I</mark> ISNAIT	NL <mark>Y</mark> ATVFGQ <mark>NL</mark> RLEPL <mark>ETE</mark> KR <mark>A</mark> H	KKEVKCIISVCIYIVE	FIPRCOSLS-NGTTVOV	ES PEADIYI IF I	KLOSMIMEA : 118
Bra002246 :	DMEAMKARFAKLLI	.GEDMSG <b>GSE</b> GVBSALALS <mark>V</mark> AIT	NIADSVFGEOVKLOPM <b>YPE</b> WKK	KKEVNLISVV HIVO	FVPSKOMGK-NGAFTOI	VT QEDDIL IF I	KLOSMITET : 118
Bra003536	DMEQMKERFSKLLI	.GED <mark>N</mark> SC <mark>CEK</mark> GV <mark>C</mark> SALALSNAIT	NLAASVFGE <mark>OR</mark> RLÊPM <mark>PAD</mark> RR <mark>A</mark>	NRREIDWLLSVIDYVY	FAPSQCKNK-DGTTMDI	MTTROGNOLHMALEAL R	KLDAMLIDC : 118
Bra004945	ELEMMRERFAKLLI	.GEDMSC <mark>SEK</mark> GV <mark>C</mark> TAV <u>T</u> VSN <mark>S</mark> IT	NL <mark>Y</mark> ATVFGO <mark>SI</mark> RLOPISTEKKDI	NKREWNCFVSICDYIVE	VISRSLGNNVDI	TETALESDILMALEAL R	KLDNMLMDI : 114
Bra007183 : Bra009152 :	EVELIKER <mark>MA</mark> KILI DVDMMKERFAKILI	.GEDMSG <mark>GER</mark> GVISALALSNAII .GEDMSG <mark>SGE</mark> GV <mark>CF</mark> ALAISNAIT .GEDMSG <mark>SGK</mark> GV <mark>C</mark> TALAISNAIT	NIYAAILGO WRIEPIPSEKKI NICATIFGO <mark>IW</mark> RIEPIPSEKKA	NRREIEVLISVSCHIVE NRREIEVLISVSCHIVE	LVPSFONIP-NCSKIDV LTPSTOTYP-DCKKFDV	NC PRODUCTOR	KIDNMITEI : 118 KIDNMIIDV : 118
Bra009621 :	EIEMMKERFSKLLI	,GEDMSG <mark>SCNGVC</mark> TALAISNAIT	NLCATLFGQLWRLEPIPKEKKD	KREVEWILCVSDHIVE	MTPIWCTFP-DCTKLDI	TC PESDIY LEAD	KLONMILEI : 118
Bra013249 :	DTDMMKDRFAKLLI	,GEDMSG <mark>GCKGVS</mark> SALALSNAIT	NLAASIFGEQTKLQPMPQDRQAR	KkeidwilsvTdhive	FVPSKCTNK-DCVCTDI	VT QEGDIL IP D	KLOTMIIDT : 118
Bra015010 :	EIEMMKERFAKLLI	,GEDMSG <mark>GCKGVC</mark> TALAISNAIT	NLSATVFGELWRLEPLAPCKKAN	KreiewilcvCdsive	LIPSTCOFPGGCGTYDI	ET PESDIYA LEAD	KLOAMIIDM : 119
Bra015068 : Bra018956 : Bra020048	DTEMIKDRFAKLLI AMDOMKEKFSKLLI	GEDMSG <mark>GGK</mark> GV <mark>S</mark> SALALSNAIT GEDMSG <mark>GK</mark> GV <mark>S</mark> SALALSNAIT	NLAASIFGE <mark>OT</mark> KLOPM <mark>PODROAB</mark> NLAASAFGEORLEPMAADRKAB	NKKBIDWLISVTCHIVE NRREIGWLISVACHIVE	FVPSQCMSK-DCVCTPI FAPTQCTNK-DCTSMPV	VTROEGDILUNIFAIR STROETDILCNIFAIR	KLDAMLIDT : 118 KLDAMLIDC : 118 KLDAMLIDC : 119
Bra021162 :	EQMKERFAKLLI	MSG <mark>GE</mark> GV <mark>S</mark> SALALSNAIT	NISASAFGEORRIEPISEDRKEF	MRREIGWLISVTCHIVE	FSPIQCTNK-DCSSIPV	NTTROEGDIVSNIEAU	KEDVMETDC : 101
Bra027189 :		.GEDMSG <mark>GE</mark> KGV <mark>S</mark> SALALSNAVT	NISASAFGEORRIEPISEDRKEF	MRRENGWLISVTCHIVE	FSPIQCTNK-DCSSIPV	NTTROETDIVSNIEAU	NEDVMETDC : 116
Bra030396 :	AMEQMKERFSKLLL	.GEDMSGCGKGVSSALALSNAIT	NLAASAFGEORLEPMPADRKAN	MARENGWINSVADHUVE	FABLQCTNK-DOSSMOV	TT QETDILC VEAU	KU AGUIDC : 118
Bra036671 :	LKDRFAKLLL	.GEDMSGCGKGVSSALALSNAIT	NLAASIFGEOTKLOPMPODR <mark>OA</mark> B	Makenewilsvidhuve	FVPSQCTSK-DOVCTOL	VT QEGDIL IFAU	KU AMUIDT : 114
Bra037342 :	ELETMKERFAKLLL	.GEDMSG <mark>S</mark> GKGVCTAV <mark>T</mark> ISNAIT	NL <mark>Y</mark> ATVFGO <mark>NL</mark> RLEPL <b>ETE</b> KR <mark>A</mark> I	Makenavcinsvcdynve	FIBRCOSLS-NOTTVOV	ES PEADIY LEAU	KU SMUMEV : 118
Cucsa.0620 : Cucsa.0666 :	ETEQMKERFAKLLL EIEMMKERF <mark>S</mark> KLLL DIDIMKAKFAKLLL	.GEDMSG <mark>GGK</mark> GV <mark>S</mark> SALALSNAIT .GEDMSGCGNGVCTALAISNAIT .GEDMSGCKGVSSALAISNAIT	NI <mark>A</mark> ASVFGE <mark>OW</mark> RLEPM <mark>SVE</mark> RK <mark>A</mark> F NICATLFGQLMRLEPLPSEKKLM NIACVIEDLLOKIENISPOKKAB	WRKEIDLLLSVTDYIVE WRRENDWLLCVSDHIVE WRREIEWEISVWDHIVE	FVPSQCKSK-DCTNMBI LTPTWCTFP-DCSKLBV FVPSKCTSK-DCTDMBI	VTROSNDIH IFALR MTCRPSSDIY NLFALR VTLOSKOU I FRANK	KLDAMLIDC : 118 KLDAMLIEI : 118 KLDAMLISY : 118
Cucsa.1193 :	EVEMMKERFAKLLI	.GEDMSG <mark>GCKGVC</mark> TALAISNAIT	NI <mark>S</mark> ASVFGE <mark>LM</mark> RLEPL <mark>APO</mark> KRAM	WHREMEWILCVCDSIVE	LVPIVOPFP-GGTY	MMSKPRSDIHMNLFALK	KT DALILGI : 118
Cucsa.1355 :	EMEMMKERFAKLLI	.GEDMSG <mark>SCKGVC</mark> TAV <mark>T</mark> ISNAIT	NIYATVFGONIKLEPL <b>PPE</b> KKAM	WKREMSCLLSVCDYIVE	FFTLSOTLE-DGTSLOV	INSRQRSDICINLFALQ	KT DMMILDI : 118
Cucsa.1363 : Cucsa.1758 : Cucsa.3592 :	EMELMKERFAKLLI ETEMMKERF <mark>S</mark> KLLI EME <mark>Q</mark> MKERFAKLLI	.GEDMSCSG <mark>K</mark> GVSTALAISNSII .GEDMSG <mark>SGN</mark> GV <mark>C</mark> TALAISNAIT .GEDMSG <mark>GCK</mark> GV <mark>S</mark> SALALSNAIT	NICATIFGOLWRLEFIPRERAS NICGSVFGQLMRLEFIEAERKAN NIAASVFGE <mark>QM</mark> RLEPM <mark>SVE</mark> RKAE	WGREMEFLICVSLHIVE WGREMEFLICVSNHIVE WRKEI <mark>DL</mark> LISVTDYIVE	LIPSF TFP-DGSKLOV LIPIW TFP-DGTKLOI FVPSQCKSK-DGTNMOI	TC PRSDIY NEAD VT QENDUH IEAD	KUCHMILDI : 118 KUCHMILDI : 118 KUCHMILDC : 118
mgv1a00322 :	EMEMMK <mark>G</mark> RFAKLLI	,GEDMSG <mark>SCK</mark> GV <mark>CF</mark> ALAISNAIT	NLCATVFGQLMRLEPIAAEKKIN	MQRENGWINCVSDYNVE	FTPSWCTVP-DCSKLDV	AT PRODUCE AT A VACOR SDIT	KUDAMITSI : 118
mgv1a00378 :	EIDMMKERFAKLLI	,GEDMSG <mark>GCK</mark> GVOTALAISNAIT	NLSATVFGELWRLEPMAPCKKAN	MCRENEWINSVSDSNVE	LVPSTCHLP-GCGTYDI		Kudamitsi : 118
mgv1a00399 :	EAELMKERFAKLLI	,GEDMSG <mark>GCK</mark> GV <mark>G</mark> TALAISNAIT	NLAASVFGELWKLEPLAPCKKSN	MQRENEWINCVSDSNVE	LVPSVCEFS-GCGSFDI		Kudamitsi : 118
mgv1a00461 : mgv1a00530 : mgv1a00594 :	ENEMMKERFAKLLI - LORSTOKVPVSPL	.GEDMSG <mark>CGNGVC</mark> TALAISNAIT .G <mark>NNGAKSSAKDRHG</mark> .GAKSSAKDRHG	NLCATLFGQ <mark>IWRLEPLKPD</mark> KK <mark>SM SASVFGEOSKLEPMSPERKAP NUCHTIFCOTMELEPTOTEKVY</mark>	NRRENEWLICVSDHIVE NKKEIGWLISVADYVE	LIPSWOTFP-DCTKLDI FVPSQOKAK-DCSTMDI	MTS PRSDLYSNLEALC MVTQQRKDLL IFAL	KLONMILEI : 118 KLOAMILGT : 107
mgv1a00334 : mgv1a00778 : mgv1a02184 :	ELELMKERFSKLLL	.GQDMSG <mark>C</mark> G <mark>K</mark> GV <mark>S</mark> SAV <mark>T</mark> ISNAIT	NI <mark>Y</mark> ASIFGQ <mark>HQ</mark> RLEPLQFE	NRKEIDWLISVTDYNVE NRKENNCLISVCDYNVE	FVASKCKAK-DESTMBV FSPSLCHLK-DETTIBV	MATROSNODHMNIFADR MSSRPRSDIYINLFADR	KIDAMILDC : 67 KIDAMILDI : 118
mgv1a02262 :	EMDMMKERFAKLLI	.GEDMSGSCKGVCAALTISNAIT	NICATIFGQVWRLEPIPCEKKS	NQRENEWLICVSDHIVE	FTPSWOTFP-DETRLEV	TC PRODET MEAN	KE NGE EI : 118
mgv1a02280 :	DMELMKERF <mark>S</mark> KLLI	.GEDMSGCCKGVSSALALSNAVT	NIAASVFGEQSKLEPMSADRKAP	MKKEIDWLISVTDYIVE	FVPSQOKSK-DETNMEI	VTOORRDEL MEAN	KE VMIIGV : 118
mgv1a02642 :	-MELMKEKFAKLLI	.GEDMSG <mark>C</mark> CKGVSSALALSNAIT	NIAASAFGEQKRLEPMSPEMKAP	MKKEIDWLISVTDHIVE	FVPSKOKAK-DESNMEI	VTOORRDEL MEAN	KE AMILEC : 117
POPTR 0001 :	-MEQMKERFAKLLL	.GEDMSG <mark>GGKGVS</mark> SALALSNAIT	NI <mark>AASVFGEORRLEPMSPERKAF</mark>	MIREIDWLLSVTCHIVE	LVPSQCKSK-DCSSMDI	MVTROSNDIHMNIFALR	KLDAMILDS : 117
POPTR 0002 :	EIEIMRERFAKLLL	.GEDMSGGG <mark>GGTC</mark> TA <mark>A</mark> AISNAIT	NISASVFGELMKLEPLAPCKKAN	MKREMEWLLCVSDSIVE	LVPSMCEFP-GCGTYDV	MVAOPSDIYVNLFALK	KLDAMIISI : 118
POPTR 0002	EIEIMKERFSKILL	.GEDMSGSCKGVGTAVTISNAIT	NIVATVFCONLELFPLKPEKKS	MKREMEVLLSVCDVIVE	FIDKSCNLR-DCTALO	MESERSDIY NLFALK	KLDAMITEV : 118
POPTR 0003 :	-MEQMKERFAKLLI	.GEDMSG <mark>GCK</mark> GV <mark>S</mark> SALALSNAIT	NIAASVFGE <mark>OR</mark> RLEPM <mark>SPE</mark> RKAH	MIREIDWLLSVICHVVE	LVPSQCKSK-DCSNMBI	MVTRORNDIHMNIFALR	KLDAMLIDS : 117
POPTR 0004 :	EVEMMKERFAKLLI	.GEDMSG <mark>GCK</mark> GV <mark>C</mark> TALAISNAIT	NISATVFGELWRLEPLALCKKSN	Mkremewllcvsdsive	LVPSICQFP-GCGTYDV	MATRPRSDIYVNLFALK	KLDAMLITM : 118
POPTR_0005 :	EIALMKERFAKLLI	.GEDMSGCGOGVCTAVAISNAIT	NLSASVFGELMRLEPLAPORKVN	NGREMEWILCISISIVE	LVPSMOEFP-GEGTYDV	VPRPSSDY LEAD	KU AGUISI : 118
POPTR_0006 :	ETEMMKERF <mark>S</mark> KLLI	.GEDMSGCGNGVCTALAISNAIT	NLCATLFGQLMRLEPL <mark>PLEKKAN</mark>	MRREMEWILCVSDHIVE	LMPSWOTFP-DESKLDV	TCGPSSDY LEAD	KU NMILEI : 118
POPTR 0008 :	EIDMIKERFAKLLI	.GEDMSG <mark>S</mark> GKGVCTALAISNAIT	NLCGTIYGQLMRLEPL <mark>PEE</mark> KK <mark>S</mark> N	MRREMEILLCVGDHIVE	LIPSWOTFP-DESKLDV	TCPPSSDFI LEAD	KU NMILEV : 118
POPTR_0009 :	EVEMMKERFAKLLI	,GEDMSG <mark>GCK</mark> GV <mark>C</mark> TALAISNAIT	NL <mark>S</mark> ATVFGE <mark>LW</mark> RLEPL <mark>LPOKKS</mark> N	WKREMEVILCVSDSIVE	LVPSMOQFP-GGGTYDV	MATEPRSDLYVNLPAL	KLDAMIISM : 118
POPTR_0010 :	EIDMMKERFAKLLI	,GEDMSG <mark>SCKGVC</mark> TALAISNAIT	NLCGHVFGOLWRLEPLPAEKKSN	WRREMEILLCVGDHIVE	LIPSWOTFP-DGSKLDV	MTCELRSDLFINLPALS	KLDNMILEV : 118
POPTR_0014 :	ENEMMKERFSKLLI	,GEDMSGSCKGVCTAV <mark>T</mark> ISNAIT	NLYATVFGONURLEPIKPEKKSN	WKREMDOL SVODVIVE	FIPKSONLO-DGTVLDV	MESEPET DTHINLPAL	KLDAMIMEV : 118
POPTR_0016	ETEMMKERFSKLLI	.GEDMSGCCNGVCTALAISNAIT	NICATLFGQLMRLEPIAPEKKAN	NRREVEWFLCVSDHVVE	LMPSWCTFP-DGSKLDV	MTCRPESDIYINDEADR	KIONMILEI : 118
POPTR_0018	DMELMKERFAKLLI	.GEDMSGCCKGVSSALALSNAIT	NIAASVFGE <mark>OK</mark> KLEPM <mark>NPE</mark> RKAN	NRKEIDWIISVTDHIVE	FVPSQC-SK-DGIDMDI	MTRQESDILMNDEADR	KIOTTIIIDL : 117
Thhalv1000 : Thhalv1000 :	DTEMMKDRFAKILI EFETMKER <mark>ES</mark> KILI	.GEDMSGSGKGVCIAVIVSNSII .GEDMSGGGKGVSSALALSNAIT .GEDMSG <mark>SGK</mark> GV <mark>CI</mark> AV <mark>T</mark> ISNAIT	NLAASIFGEOTKLOPMPOLR <mark>OA</mark> NL <mark>AASIFGEOTKLOPMPOLROAB</mark> NL <mark>YATVEGONL</mark> RLEPLEIERKTN	KKELDWELSVEDHUVE KKELDWELSVEDHUVE KKELNNCLESVEDYLFE	FVPSQCTSK-DCVCTPI FIPKSCNLS-NGATVDV	VTROEGDLANIE I MESRPEADIY LEAD	KUDAMIIDT : 118 KUDAMIMEA : 118
Thhalv1001 :	EVELIKERMAKILI	,GEDMSG <mark>SCE</mark> GV <mark>CF</mark> ALAISNAIT	NLYAAILGOOWRLEPLPSEKKT	KRSEIEVLISVSDHIVE	LVPSF0SFP-NCSKID	NNCEPESDIFTCLEADE	KLONNITEI : 118
Thhalv1001 :	AMEQMKERFSKILI	,GEDMSG <mark>GCK</mark> GV <mark>S</mark> SALALSNAIT	NLAASAFGEORRLEPMAALRKAB	KREIGWLISVADHIVE	FADDQCTNK-DCSSMDV	NTTEORTDILCNIEADE	KLOANILDC : 118
Thhalv1001 :	DVDMMKERFAKILI	,GEDMSG <mark>SCK</mark> GV <mark>C</mark> TALAISNAIT	NLEATIFGOLWRLEPLSSVKKEN	KREVEWLISVSDHIVE	LTPST0TYP-DCKKFDV	NTCEPEFDIFENLEADE	KLONNILEI : 118
Thhalv1001 : Thhalv1001 : Thbalv1001 :	EIEMMKERFSKLLL DMEVMKERFAKLLL	GEDMSG <mark>SGNGVC</mark> TALAISNAIT GEDMSGGGEGVTSALALSNAIT	NI <mark>C</mark> ATLFGQ <mark>LW</mark> RLEPL <b>PTE</b> KK <mark>E</mark> N NI <mark>AD</mark> SMFGEHMKLQPMYPETKEI	MRREMEWLLCVSDHIVE MRKEMNWLLSVVDHIVQ	MTPTWOTFP-DOSKLDI FVPSROMAK-NOTFTDI FARSOCKNK-DOTNMOL	TCRPRSDIY LEAD VT QCDDLL IFAD TT COTOL IFAD	KLONMLLEI : 118 KLOSVLLET : 118 KLOSVLLET : 118
Thhalv1001 :	DMECMKERFSKLLI	.GEDNSG <mark>CCK</mark> GV <mark>S</mark> SALALSNAIT	NIAASVEGEORRIEPMPAERRAE	WRREIDWLIAVEDYVVE	FAPSQCKNK-DGTNMBI	NTTRORTOLHMNIFALX	KL AMITOC : 118
Thhalv1002 :	IHECMKERFAKLLI	.GEDMSG <mark>CCK</mark> GV <mark>S</mark> SALALSNAVT	NISASAEGEORRIEPMSEERKKE	WRREIGWLISVEDHIVE	FSPTQCTNK-NGSSMBV	NTTRORTOLVSNIFALX	KL AMITOC : 118
Thhalv1002 : Thhalv1002 :	ETERONOMIA AND	GEDMSGGGKGVCTALAISNAIT		NRREVEWIICVSDSIVE NRREVEWIICVSDSIVE NRREVEWIICVSDSIVE	LIPSICQFP-GCGTYDI LIPSICQFP-GCGTYDI LIPSICQFP-GCGTYDI	METR PRODUYANLEADR METR PRODUYANLEADR	KUDAMIIDM : 60 KUDAMIIDM : 60
Thhalv1002 : Vv.1782614 : Vv.1782686 :	EVEQIRERFAKLLI EIEMMKERFSKLLI	.GEDMSGSGKGVCTAV <mark>H</mark> ISNAIT .GEDMSG <mark>RGT</mark> GV <mark>S</mark> SALALSNAIT .GEDMSG <mark>SGKGVC</mark> TALAISNAIT	NLVATVFGQNIRLEPIETEKRAI NLAASVFGE <mark>Q</mark> WKLEPM <b>SAE</b> RKAN NL <mark>C</mark> ATIFGQLWRLEPLPPEKKSN	AKRENNCLISVCDYHVE MRKDIDLLISVADYHVE MRRENELLICVSDHIVO	FIBRCONLS-NEATVEV LVESQOTAK-DETTMEV LIESWOTFP-DESKLEV	NES PRADIY LEAD VS QRKDLL LEAD TC PRSDIF LEAD	KUISKUINEA : 114 KUIAMUIEH : 118 KUINMUIEI : 118
Vv.1782737 : Vv.1783220 :	EAEMMKERF <mark>S</mark> KLLL	GEDMSCHCKGV <mark>S</mark> SALALSNAIT GEDMSCCKGVCTALAISNAIT	NVAASVFGELRRLEPMPVERKTN NLSATVFGELMRLEPLAPCKKAN	MRREIDWLLSVSDHIVE MCREMEWLLCVSDSIVE	MVE-QORSK-DOTSMEV LVESIOQFP-GOGTYEV	MVTRORCOLLANIFALR MATRORSOLY MLFALR	KLDAMLIDT : 113 KLDAMLISM : 118 KLDAMLISM : 118
Vv.1783965 : LOC_Os01g4 :	DIEMMKERF <mark>S</mark> KLLL EIDLVKEKFAKLLL	GEDMSG <mark>CGN</mark> GVCTALAISNAIT GEDMSG <mark>CGN</mark> GVCTALAISNAIT GEDMSG <mark>TGKGVS</mark> SALALSNAIT	NICATLFGQLWRLEPIPAEKKAN NLAASVFGEORRLEPMSADRAF	WRRENEWLLCVSDHIVE W <mark>N</mark> KEIDWLLSVIDHIVE	LIPSWCTFP-DCSKLEV FVPSQCAST-DCTSMEV	TC PRSDLY LEAD GTQQRRDLL IEAD	KLONMI EV : 118 KLOAMI EY : 118
LOC_OS01g5 : LOC_OS01g6 : LOC_OS02g1 :	EMELMKERFAKLLI EMEMMKERFAKLLI D <mark>LDV</mark> MKERFAKLLI	.GEDMSGSGKGVPSALAVSNAIT .GEDMSGSGKGVCTALAI <mark>A</mark> NAIT .GEDMSG <mark>T</mark> GKGV <mark>S</mark> SALALSNAIT	NIAASVEGEORKLEPMAPLEKGE NICATIFGQLMRLEPLPPEKKAN NLAASVFGEHRKLEPMAPDTKEE	NKKENGWLLSVALH VE WRRENGWLLCVSDHIVE WKKENGWLLSVEDHIVE	FVARROVLD-NOVEMOV LVPTWOSFP-DGTRLOV FVPTROTAE-NGTTMPI	STACERDICAL FALL STACERDICAL VEAL	KUTHMITEI : 118 KUTHMITEI : 118 KUTAMITGY : 118
LOC_Os04g4 :	ELQLIKERFSKLLI	.GEDMSG <mark>SCK</mark> GV <mark>S</mark> TAVAISNAIT	NLYATVFGGCHRLEPILAEKRSN	KRENDOLLSVODYIVE	LFPSKBIMP-DCTVRBV	AT PRODY LEADE	KUDDANDEI : 118
LOC_Os05g3 :	EMEMMKERFAKLLI	.GEDMSG <mark>GCK</mark> GVCTALAISNAIT	NLCATIFGOLWRLEPILPEKKTN	KRENDWLLOVSDHIVE	LVPTWCTFP-DCSKLBI	TS PRODY LEAD	KUDHANDEI : 118
LOC_Os05g4 :	DAEMVREKFSKLLI	.GEDMSGTCKGVSSALALSNAIT	NLAASVFGEORRLOPMAADOKAF	KRENDWLLSVSDHIVE	FVPSKCVSE-DCSTMBI	ITOORDION LEAD	KUDAANDEY : 118
LOC_0s07g2 : LOC_0s09g3 :	EMELMKEKYTKLLL EVDMMKERFAKLLL	.GEDMSG <mark>SGK</mark> GVCTAVAISNAIT .GEDMSG <mark>SCK</mark> GVCTALAISNAIT .CEDMSGCCKCVCTALAISNAIT	NLYATVFGTCHRLÖPIPEKKAN NLSATVFGELWRLEPMASARKAN	MNRENDCLESICEYIVE MTRENDVLESVALSIVE	FS KV AMP-DCSTHD LT SI ELPDGCGOF FY SS TI D-DCTVU	ATŠPESDIL LE LE VP PESDIY LE L	KLETMILEI : 118 KLEAMILAM : 119
GRMZM2G059 : GRMZM2G065 :	DIDIMK <mark>D</mark> KFAKLLI EMEMMKERFAKLLI	.GEDMSGGGGGGVCTAVATSNATT .GEDMSG <mark>TGKGVS</mark> SALALSNATT .GEDMSG <mark>SG</mark> KGV <mark>C</mark> TALAISNATT	NIAASIFGE <mark>OR</mark> RLEPH <b>SAE</b> RRAA NLCGIIFGOLMRLEPI <mark>PPE</mark> KKAN	NREIDULISVACHIVE NREMDULISVACHIVE	FSPSQCVSE-DCTNIEV LV9TWCSFP-DCTRL91	GTQQEGDIL IPAL TSTPESDIY LPAL	KIDAMILEY : 118 KIDAMILEI : 118
GRMZM2G071 :	EMELVKERF <mark>S</mark> KLLI	GEDMSGCCKGVCTÀVAISNAIT	NLYATVFGSCHKLEPIPACKAN	WTRENDCLISVCDYIVQ	FYPSTOTLP-DCTKVDV	MATRPRSDIYINLPADE	KLDAMIIDI : 118
GRMZM2G087 :	ELQLIKERF <mark>S</mark> KLLI	GEDMSGSCKGVSI <mark>S</mark> VAISNAIT	NLYATVFGSCHRIKPIPPEKKSN	MRENDCLISVCDYIVE	FFPSKBILP-DCSIRDV	MATRPRSDIYVNLPADE	KLDDMIIEI : 118
GRMZM2G105 :	EID <mark>M</mark> MKERFAKLLI	GEDMSG <mark>SCKGVCTALAIS<u>NAIT</u></mark>	NLSATVFGE <mark>LNRLEPLAKARKAN</mark>	MTRENENLISVSDSIVE	LTPSIQELPEGCQQFDV	MVPRPRTDIYMNLPADK	KLDAMIIAM : 119
GRMZM2G131 : GRMZM2G132 : GRMZM2G144 ·	EMELMKEKYTKLLL EMDLMKEKFAKLLL EMEMMKERESKILL	.GEDMSG <mark>SGKGVC</mark> TAVAISN <mark>S</mark> IT .GEDMSG <mark>SGKGVF</mark> SALALSNAVT .GEDMSGSGKGVCTALATSNAVT	NLYATVFGTCHRLEPISPEKRSN NLAASVFGEORKLEPMAPDRKGI NLCATVFGOTMRLEPIPPEKKA	NNRENDCLESICEYIVE NKRENGWLESIADHIVE NRREDCLESIADHIVE	FSEIVEAMP-DESTHD FVAKKEVLD-NETEMBU	MATSPRSDILMNLPALE MGTQQRRDDQANIPALE MTSPRSDIM	KLETMILGI : 118 KLTMLLDY : 118 KLONMLERT : 118
GRMZM2G158	EIDMMKERFAKLLI	.GEDMSG <mark>SCK</mark> GV <mark>C</mark> TALAISNAIT	NISATVFGELMRLEPLATARKAN	NTRENEWLISVADSIVE	LTPSICELPEGEGQESV	MVPRPRSDIYMNLPATX	KL AMILAM : 119
GRMZM2G173	ELDVMKEKFAKLLI	.GEDMSG <mark>TCK</mark> GV <mark>F</mark> SALALSNAVT	NIAASVFGEHRKLEPMAPDTKE	NKRENGWLISVTDHIVE	FVPTRHTSE-NGITMEI	MSTACERDIAMNTPATE	KL AMILGY : 118
GRMZM2G359 : GRMZM2G377 : GRMZM2G442 :	DADIVREKFSKLLI DAEKVREKFSKLLI ELDVMKEKFSKLLI	GEDMSCTGRGVTSALALSNAIT GEDMSGTGRGVTSALALSNAIT GEDMSG <mark>TGR</mark> GV <mark>P</mark> SALALS <u>NAIT</u>	HARS OF GEORELOF HAREOKSE NIAASVEGEORELOF HADDOKSE NIAASVEGEORELEF HAPDEKEE	NKKEVDWIDSVADHIVE NKKEVDWIDSVADHIVE NKREVGWIDSVTDIJVE	FVPSQCVAE-NETCM3 FVPSQCVAE-NETSVD FVPTRCTAE-NETTM3	MITQORODI KUNIDALA MITQORODI OMNIDALA MSTACRADI AMNIDALA	KLDAMLIEY : 118 KLDAMLIEY : 118
Selmol.431 :	EAEIMKERFARLLL	.GEDMSC <mark>GAK</mark> GV <mark>S</mark> TALALSNAIT	NISASVFG <mark>NLW</mark> KLEPI <mark>ATSRR</mark> N	NKRENNWLVSVIDYIVE	LVPTWOTFP-DCSSVDI	VVANPRPDIQINLPATR	KEOMMEDC : 118
Selmol.623 :	EVEMMKERFARLLL	.GEDMSC <mark>GSKGVC</mark> TALAISNAIT	NISASVFGELWRLEPISVEKKK	NRRENEWIDSVIDHIVE	LVPTWOTFP-DCSSVDV	VVSNPRADLHINLPATR	KEOMMEDEC : 118
Selmol.627 :	EVEMMKEKFAKLLL	.GEDMSC <mark>GAKGVC</mark> TALAISNAIT	NIAASVFGELWRLEPISHERKT	NRRENEWIDSVSDYVE	LVPSWOSFR-DCSNUDV	VVTRPSDIHINLPATR	KEOTMEDES : 118
Selmol.629 :	EIEMMKERF <mark>S</mark> KLLI	.GEDMSC <mark>SC</mark> KGVCTALAISNALT	NI <mark>AASVFGE</mark> LWRLEPLSHERKLI	NORDONWIDSVCDHUVD	FVPSFHSVT-DCTSLD	MISRPESDIHUNIEAR	kelami ea : 118
	e 111	.g gggv a a sna t	n a g l p	W e6 6 62	P G e6	R D6 n6Pal	k6d 6L

	0 *	140	* 160 *	180		* 20	00	220	*	2
RopGEF1 : RopGEF2 :	LDASSDTDE LDSSQKTDE	YT-DR-GIVLGDC YA-EE-GSLSMKS	DKDSYNSPASV TRSATGSFRKVIVQ	RQEDK	WLPCPKV WLPIPLV	PPN <b>GL</b> SEEARKE PLO <b>GL</b> SEKARKO	(LQQCRDFANO) LKSKRESTNOI	LKAALAINSGV H <mark>KAAMAINSSI</mark>	LAENEIEDFYLETLPK LGENDIEDSYMATLPK	S : 21 S : 21
RopGEF3 : RopGEF4 :	LDSBQNTBC DSBTENBC	YA-EE-GSLSMKS YV-ER-GSSSMNS	ARSSTGSFRKVIVÇ GG-GGRDSGTFRKVVVÇ	RKEEK.	WLFVPLV WLFVPCV	PSEGISDKARKO PAEGISEEERKH	RHKRESTNOL	HKAAMAINSSI HKAALAINDST	ISENEIEDSYMTTLPK INDNDIEDSYLTTLPK	C : 21 S : 21
RopGEF5 : RopGEF6 :	ASSKKTS SSGETS	VV-DQ-GIVASEN	DGSASFRRKIÇ		WLEVPRL	APN <mark>GL</mark> IEEASTI ESD <b>GL</b> IEOTSIJE	NHKRECATO	LKAAMAINSLA IKAOMSINSIA	LTENDVEKSYLETLEK LAENEVEOSYLEALEK	N : 21
RopGEF7 :	LDSSEETOP	VV-DQ-GIMAHESAA	DGSSSFRKSFQ	RQEDK	WLPVPRV	SPG <mark>GI</mark> QENSRKO	QUQHKRDCTNO	LKAAMAINSIT	LADMEIRESYLESLER	K 21
RopGEF9 :	DNSRG-HNS	V-SR-DSEEG	20AR-NE	TKD	NLPPVKV	PPNGI SESARRI	1 HFQKDSVSQ	QKAAMAINAQV QKAAMAINAQV	LSEMAIPDSYIESLPK	N : 20
RopGEF10 : RopGEF11 :	NSKD-QKD KSKD-QD	VV-PR-DMEDA	DHWG-DW CET	ENDERN	%LFVVKV %LFAVKV	PTDGLSEESRR/ PPNGLSEISRR		'LKAATAINAHV LKAAMAIN <mark>AQ</mark> V	ISENHVEENYIDSLER ISENEIPESYLESLER	N : 20 N : 20
RopGEF12 : RopGEF13 :	ENSKD-QS55 KSKD-QD55	SVI-SK-DSPDL VV-TP-GSPES	DGP ENSN-SI	RNDERW RNDDKW	WIPTVKV	PPD <b>GI</b> SEASRRE PPK <b>GI</b> SETLKRE	TIQYCKDCVNOV	LKAAMAINAQV LNSAMAINSQV	IFENEIPESYIDSLPK ITENEIPESYIDSLPK	N : 20 K : 20
RopGEF14 : Araly1.314 :	I SMVNTOP	YS-EI-GSRA YV-KK-DSPDS	EGT SET	SESKR	WLFSPOV WLFAVKV	PKPGISNSGRKE PPNGISEISRRE	LDKGKVVYOV	FKATKAINENI LKAAMAINAOV	ILSNPVEIVIKEAUPK ISSNEIBESYLESIPK	S : 20 N : 20
Araly1.477 : Araly1.479 :	ENSKD-QSPC	SYV-SK-DSPDS	DGP RNSN-S7	RNDD 80	WIPTVKV WIPTVKV	PPD <mark>GL</mark> SEASRR PPK <b>GL</b> SETLKB	T QYCKDCVNOV	LKAAMAIN <mark>AQ</mark> V	LFENEIPESYIDSLPK TENEIPESYIDSLPK	N : 20
Araly1.483 :	LDSSTENDF	VV-ER-GSSSMNS	SG-GGRDSGTFRKVVVQ	KDEK	WLPVPCV	PAE <mark>GI</mark> SEEERKI	ILRHKRDCASOI	HKAALAINDST	INDNDIEDSYLTTLEK	S 21
Araly1.485 : Araly1.486 :	IDSPEETPE	VV-DQ-GIV-AAES	DGSSSFRKSFÇ	EQEDRO	WLPVPRV	SPGGIQENSRK	QLQHKRDCTNOI	LKAAMAINSIT	LADNEIRESYLESLPR	K : 21
Araly1.488 : Araly1.490 :	LISIQNTIF	A-EE-GSLSMKS	ARSSTGSFRKVIVÇ	RKEER	WLPVPLV	PPEGLSDKARK	UKNKRESTNOI	HKAAMAINSSI	ISEMEIPESYMTTLPK	C : 21
Araly1.490 : Araly1.497 :	BARSDTRE BSRTENBR	9WT-DR-GIVLGEC 9WV-ER-GSSSMNS	DKDSYNSPASV SG-GGRDSGTFRKVVVÇ	RQEDRO	%LPCPKV %LPVPCV	PPNGI SEESRKI PAE <mark>GI</mark> SEEERKI	(DQQCRDFANO) IRHKRDCASOI	EKAALAINSGV H <mark>KAALAIN</mark> DST	LADNEIBDPYLETLEK INDNDIEDSYLTTLEK	S : 21 S : 21
Araly1.861 : Araly1.874 :	ASSKKTSS NSRG-HNSS	VV-DQ-GIVASEN VV-SR-DSEEG	DGÇ QQAR-N	RQEEKW RTNDKW	WLFVPRL WLFPVKI	APN <b>GL</b> EEARTH EPG <b>GL</b> SEPARR	INHKRECATO TYFORDSVTOV	IKAAMAINSLA QKAAMAINAQV	LTENDVEETYLETLPK LSENAIFESYIDSLPK	N : 21 N : 20
Araly1.883 : Bra000971 :	BONGRG-HNDR SIGONTOP	VV-SR-DSEEG	KQBAR-NBAR-NBAR-NBARB	R TKD KO KEEKO	WLPPVKV WLPVPLV	PLN <mark>GL</mark> SESARR PREGISDIARKO	HFOKDSVSOV	QKAAMAINAQV HKAAMAINSSI	ISDNAIDDSYIESUPK ISDNEIDDSYNATUPK	N : 20 C : 21
Bra002246 :	LDNSKD-QKDS	VV-PR-DVEDT	SNИG-DИ DN	RDEN	NLFVVKV	PSDGLSEESRKI		LKAATAINDVV	ISEMNIPDNYIDSLPK	N : 20
Bra004945 :	LDGSTENDF	WV-ER-GSSSMNS	NN-GGRDSGSFRKVVVQ	RKDEK	WLPVPCV	PAEGI SENERKI	ILRHKEDCANOL	HKAALAINDST	INDNDIEDSYLTTLEK	S : 21
Bra007183 :	DSBEGTBR	VV-DQ-GVVASES	ARF	EDGDK	WLPLPRV	SDGISEQTRK	DHTRDFTNO	LKACM <mark>SIN</mark> SIA	LADNEVEQAYLEALEK	N : 21
Bra009152 : Bra009621 :	LOSSEETOP	VU-DQ-GIVSSEN	DGSSSFRKRIQ DGSSSFRKSFQ	RQEERW	%LFVPRL	SPG <mark>GI</mark> QENSRKÇ	DIQHKRDCTNQ1	LKAAMAINSVS LKAAMAINSIT	LADMEIRESYLESLER	R : 21
Bra013249 : Bra015010 :	LDGDSDTDF	YT-DR-GIGLGDC	KQP EK-ESFDSPASRGGGCGRPSP	RQEEK	NLPCPKV	PPG <b>GL</b> SDPARR PPN <mark>GL</mark> SEETRKE	A YFQRDSVTQ A QQCRDFANQI	QKAAMAINAQV EKAALAIN <mark>AG</mark> V	LASNEIEDPYLETLER	S: 22
Bra015068 : Bra018956 :	LONGKG-HNOR LOKSKD-QNOR	YV-SR-DSEEG YV-KK-DSPDS	KQAS-NA GET	RSNDRW	%LPPVKV %LPAVKV	PPG <b>GI</b> SEPARR PPN <mark>GI</mark> SEISRR	ALYFONDSVTON FLQSQNECVNOV	QKAAMAINAQV LKAAMAINAQV	LSENAIRESYIDSLPK LSENEIRETYLESLPK	N : 20 N : 20
Bra020048 : Bra021162 :	HSSKD-QKD	YV-PR-DVEDT	ENWG-DW LTSN-ST	RDDN	WLFVVKV WLFTVKV	PSDGISEESRKI PPTGISETSKTE	LIHSOKDSVSOV LISOKECVSOV	LKAATAINAVV LESAMAINAEV	ISENHIEDNYIDSLPK ISONEIEESYIDSLPK	N : 20 K : 19
Bra027189 : Bra030396 :	KaKD-QD31	YV-TT-DSPEH	LN SE	ENNDRW RNDERW	%LPTVKV %LPAVKV	PPN <mark>GI</mark> SETSKRI PPN <b>GI</b> SEMSRBI	LSONECVSOV	IKSALAINAEV Ikaamainaov	ISONETRESYIDSLEK ISONETRESYLESIEK	N : 20 N : 20
Bra036671 : Bra037342 ·	L N RG-HN	VV-SR-DSEEG	KQAS-N	R SNDK	WLPPVKV	PPG <mark>GI</mark> SEPARKI	TYFORDSVTO	OKAAMAINAOV	ISEMAIPESYIDSLPK SEMETEDSYMATLPK	N : 20
Cucsa.0620 :	L DNSKD-QSBF	VV-SR-DSNES	NKP	RKDDK	WLPTPKV	TNGLSENSRK	MQYQKDCVNOV	LKAAMAINAQV	ISEMEIRENYIESLEK	N : 20
Cucsa.1164 :	DQIGK-LHID	V-DQ-GILAPET VV-SR-DDESA	CDC KDC 	EQLER	//LPVPRV	PERCENSION PROFESSION	ULFQNESVNOI	LKAAMA IN <mark>AQ</mark> V	ITENEVPESTIESLPK	N : 20
Cucsa.1193 : Cucsa.1355 :	I GGBCHTBE	YYA-EK-GSMSSNS	NRSRSGSFRRLSI	QKEEK	WLFCPKV WLFVPCI	PADGI SEDARKI PSC <mark>GI</mark> SENARKI	e qocrdctno. Hrnkrecanoi	HKAAMAINSNV HKAAMAINSTI	LABNEVBAAMETLER	S : 21 S : 21
Cucsa.1363 : Cucsa.1758 :	ESSADTER IDSSVDSEC	YV-DQ-GIVSSDG CVI-DQ-GILAT	DGSSSFRKIVÇ DQTDASSSFRKLLE	RQQEKW	WLFVPRV WLFIPRV	EAG <mark>GI</mark> GEDSRKO ENG <mark>GI</mark> SEASTRE	IHHTRDCTNOI ILQHKRDCTNOI	lkavmainnia Lkaamainsvt	LNDMEVRESYLETLPK LADNDVEISYLEGLPK	N : 21 N : 21
Cucsa.3592 : mgv1a00322 :	LDNSKD-QNSC LDGSTNTSC	YV-SR-DANDS YI-EQ-GVTPPET	ΕΚN DGSVSYRKAΙΩ	KRNDK QADK	WLPTAKV WLPVPRV	PPNGLSDMSRKI PSG <mark>GL</mark> PEDSRK	TQYQKDCVNQV THTRECASOI	LKAAMAINAQI LKAAMAINSTS	ISENEIPEDYIESLPK ISENDVPDSYTETLPK	N : 20 N : 21
mgv1a00378 : mgv1a00399 :	GGRDTR GGRHDTR	YV-DR-GIVVDDC YV-DR-GTVVADG	DKYSSDVMCGRPSV ERIIEPYQCSPSRTRPSV	RQEEKW TLEEKW	WLPCPKV WLPFPKV	PGK <mark>GI</mark> SEDARKI PAN <b>GI</b> SEETRNI	QQCRDCTNOI	LKAALAINGNV LKAAVAINSTV	LAENDIESAYMETLEK LSENEVEOVYLESLEK	N : 21 S : 22
mgv1a00461 : mgv1a00530 :	DSSESSEE	YV-EQ-GILTPEGDG	SGSGSSSSFRKILF KGSGSSSSFRKILF	ORNE K	%LPIPRV %LPTVKV	PG <mark>GLEENARK</mark> PNGLSEESSOI	ALQHREDSTNOL	lkaamainsta lkasmainahi	LADNDIBESYLEALPK ISDNDIBESYLESLPK	N : 21 N : 19
mgv1a00594 : mgv1a00778 :	LOSEESCOR INSKD-QNDR	YV-DQ-GIVASEA	GGF GK-TT	SQED	WLFVPRL WIFTPKV	SPG <mark>GI</mark> SEESRA PN <b>GI</b> SEVTRA	IQHKRDSTNOI	LKA <mark>VMAIN</mark> SAT LKAAMAINAOV	LAENDIEDSYLEALPK LSENGIEDNYIEALPK	N : 21 N : 15
mgv1a02184 : mgv1a02262 :	ESSQETS GSKKTS	YA-EQ-GSISAKS YV-DQGGIVAAET	IRSGSFRKIVQPQPQ DGSVSFEKAIF	RKEEKW ROEDKW	WLFVPCL WLFVPRV	SPD <mark>GI</mark> SEKSKK HG <b>GI</b> SECSRK	I ROKEDRANO	HKAAMAINSSI Ikaatsintia	LAENQIPESYMASLPK LADNEVPESYMETLPK	S : 21 N : 21
mgv1a02280 : mgv1a02642 :	IDNETN-EQUE IDNEKD-QNEI	KYV-KRDA YV-SS-TEEES	DDS 2QGK-NF	ERNDER	WLPSVKV WIPTPKV	PPN <b>GI</b> SEESRHI PPN <b>GI</b> SEVSRKV	DQKQHEAVNQV DQYQHDSVNQV	LKA <mark>S</mark> MAINAQI LKAAMAINAQV	LSDMEIFDNYIETLPK LSEMEIFESYIESLPK	N : 20 N : 20
POPTR 0001 : POPTR 0002 :	LONGKD-QNOC	YV-SR-DSPES	EKB GD-DVIEE-FPVPSSLRRPPI	RTDDK	%LPTVKV %LPFPKV	PPD <mark>GI</mark> SERATKI PPN <b>GI</b> SEELTKI	TQYOKDSVNOV	LKAAMAINAQI LKAAMAINSSV	ISOMEIPENYIESLPK IAOMEIPDTYFENLPK	N : 20 S : 22
POPTR 0002 : POPTR 0003 :	BBSBQDRBB NAKD-OND	YA-EQ-GSMSSNS WV-SR-DSPES	IRSGSFRRVVIÇ EKBG-TF	RKEEK	NVPVPCV NLPTVKV	PHD <mark>GI</mark> SEKSRKE PEDGI SERAKKE	HRHKRDCAYO	HKAAMAINSSI LKAAMAINAOI	ITOMEIRHSYMASLPK ISPNEIRENYIESLPK	S : 21
POPTR 0004 : POPTR 0005 :	DGBSETBE	WA-DR-GIVVG	DG-GDCDT-YPSGISGGRPSI	RQEDK	%LPCPKV	PPD <mark>GL</mark> SEDARKE	QQCRDCTNOI	LKAAMAINSSV IKAALAINNSV	IVENEIPTAYMETLPK LAEMEIPDTYESSLPK	N : 22
POPTR 0006 :	LDSDDNTDD	YV-DQ-GILAPDT	DGSASFRRTLQ	RÕEEKW	NLFVPQV	PEGGLHENSRK	QHKRDSTNO	LKAAMAINSIT	LAENEIPESYLEALPK LAENDURDSYLEALPK	N : 21
POPTR 0009 :	LDGBCETBR	V-DR-GIVVA	DG-GDCDA-YPSGISGGRPSI	ROEEKW	WLPCPKV	PPNGI SDDARKI	QQCRDCTNO	LKAAMAINSSV	IVENEIPTAYMETLPK	N : 22
POPTR 0014 :	LDSSQDTBP	A-EQ-GSMSSNS	ILSGSFRRVIVC	KEEK	WVPVPCV	SGGI SEKSRKI	IRHKRDCAYO	HKASMAINSSI	LASSELLETYIASLEK	S 21
POPTR 0018 :	DQDGS-QNDE	VV-SKDE	DGLEQGTPF	NDD	VIPTVKV	QNGLADVTRR	NQFQKDSVNO	LKAAMAINAQV	ISENEIFENYIESLPK	N 20
Thhalv1000 :	LDNSRG-HTDP	VV-SR-DSEEG	KQAR-N	RTNDER	WLPPVKV	P <b>PG<mark>GL</mark>SEPARRI</b>	1 YFQKDSVTQV	QKAAMAINAQV	LSEMAIPESYIDSLPK	N : 20
Thhalv1000 : Thhalv1001 :	SBQKTBR BSBGETBR	9 <b>W</b> A-EE-GSLSMKS 9 <b>W</b> V-DQ-GIVAAES	ΓRSATGSFRKVIVÇ ARF	EDGD	%LPIPLV %LPLPRV	PSQ <b>GI</b> SDKARK PSD <mark>GI</mark> TEQARKI	DHTRDFTNOI	HKAAMAINSSI LKA <mark>O</mark> M <mark>SIN</mark> SIA	labodiedsymetlek Laboeveqpylealek	S : 21 N : 21
Thhalv1001 : Thhalv1001 :	I KIKD-QNII ITSIKKTIT	YV-KK-DSPDS YV-DQ-GIVASEN	SEΊ DGSASFRRKIΩ	RNDEKW	%LPAVKV %LPVPRL	EPN <b>GI</b> SEISREI APN <b>GI</b> GEEARTI	TIQSQUECVNOV ELNHKRECATQI	ikaamainaqv ikaamainsvs	LSENEIRESYLESLPK LAENDVRESYLETLPK	N : 20 N : 21
Thhalv1001 : Thhalv1001 :	LDSBEETER LDNBKD-QKDR	YV-DQ-GIMAHESAA- YV-PR-EVEDT	DGÇ EKNG-DŴ	RQEDEN	WLPVPRV WLPVVKV	SPG <mark>GI</mark> QENSRKÇ FSD <b>GI</b> SEESRRI	DONOKOSVAOV	LKAAMAINSIT LKAA <mark>T</mark> AINASV	INDMEIPESYLESLPR ISEMRIEDDYIDSLPH	K : 21 N : 20
Thhalv1001 : Thhalv1001 :	EKSKD-QSS EKSKD-OSS	SWV-SK-DSPDS SWV-SK-DSPDS	ENP ENP	RNDDR	WIPTVKV WIPTVKV	PPD <mark>GL</mark> SEASRRE PPD <b>GL</b> SEASRRE	T QYQKDCVNOV	IKAAMAINAQV IKAAMAINAOV	IFBNEIRESYIDSUPK FFNEIRESYIDSUPK	N : 20 N : 20
Thhalv1002 : Thhalv1002 :	NARSD-QDD	T-DR-GIV-LGEC	LNIN-TI	RNDDR	%LPTVKV %LPCPKV	PPK <mark>GI</mark> SETTKRI PPNGISOETEKI		LKAAMAINAEV IKAALAINSGV	ISONEIPESYIDSLPK TAEMETPDPYIEALPH	N : 20
Thhalv1002 :	L ASSDTER	T-DR-GIV-LGEC	AYNSPASV	RQEDK	WLPCPKV	PPNGL SOETRKI	(LQQCRDFANO)	LKAALAINSGV	LABNEIEDPYLEALPK	S : 15
Thhalv1002 :	L SEQNTER	MA-EE-GSLSMKS	ARSATGSFRKVIVÇ	KEEK	WLPVPLV	SEGISDKARK	RNKRESTNO	HKAAMAINSSI	ISONEIRESYMATLEK	C : 21
Vv.1782686 :	LDGSTNTSC	V-DQ-GIIAPET	DGSASFRKPIÇ	RQEEK	WLPVPRV	PRGISDASKA	LNHKRESANOI	lkaama in sna	LABNEVEESFLEALPK	N : 21
Vv.1783220 :	ENSKD-QKSE EGSCETSE	YV-DR-GIIVA	SRQ EA-DNHDA-YPLSASSGRPSI	RQEEK	"LPCPKV	PPNGLSEVIRK PPN <mark>GL</mark> SEDARKI	REQUINE CENTRAL CONTRACT NOT	lkaamainaqi Lkaamainssv	LASNEIFENYIESLER LASNEIFTAYLETLER	N : 20. N : 22
Vv.1783447 : Vv.1783965 :	LOSSKETOR	VA-EQ-GKLVSATRA VV-DQ-GILAPDT	Ç DGÇ	RPDEKN	%LFVPCI %LFVPRV	PG <mark>GI</mark> SEKARKI PG <mark>GI</mark> HENSRK	DIKHTRDCANQI QIQHKRDCTNQI	HKAAM <mark>SIN</mark> SSI Ikaama <mark>in</mark> sta	LADNKIEDSYIAALPK LADNEIEESYIEVLPK	S : 21 N : 21
LOC_Os01g4 : LOC Os01g5 :	LDNSKD-EQDE LDNSKD-RNSE	VV-KK-DADEG VV-KR-DSCSDS	ЕКGD-АБ DEС	RQGDK	WIPTVRV WIPIVKV	PE <b>GI</b> PDASKKI PG <b>GI</b> SPASEGI	NILHQKDLVGQV NIQHQKELVNQV	LKAAMAINADV LKAAMAINANC	ITENEIPGEYIETLPK Imenaipesyleslpk	N : 20 N : 20
LOC_Os01g6 : LOC_Os02g1 :	DESERDPER MENEVD-OSER	YV-EQ-GICAPDC	DGBASFRAAFB	RDEK	WLPVPRV WMPTVKV	PEGERDKARK( AEGERDVIRK)	QIQHKRDCANOI	LKAALAINSNA LKAAMAINAOV	LABNEVRESYLESLPK IVENEIREVYIESLPK	N : 21 K : 20
LOC_Os04g4 :	LDSBQKTBD	WVNDK-GQKDSCA	AABAAPCRPVSF		WLFVPCV	TKP <mark>GL</mark> TESARRI	ROKHDCASO	HKAAMAINNGV UKAAMAINSNA	LASIRIPELYKOTLPK	C : 21
LOC_0s05g4 :	LINSKD-KODE	VV-SKDA	SESEKGNTF	RODDRO	MLPTVRV	PGGLSDASRK	VQHQKDLVNQV	LKAAMAINANV	LMONDVEEAYIESLPK	N : 20
LOC_0s09g3 :	I GIKETH	VV-DR-GIVVDDS	GGPFSSSSSSCGRPSV	QEEK	%LPCPRV	PREISEDARRE	OQUERDCANO	IKAAMAINSDV	LADNEIFEVYLESIOK	S 22
GRMZM2G059 :	SIGE-AQDE	YV-AK-DADGGED	ni 3001m8888FRRSTF DDE	STCD	NIPTVRV	DGGL SGKARKE	UQHQKDLVGQV	IKAAMAINADV	TABNE I PEEVIES LPK	N : 20
GRMZM2G065 : GRMZM2G071 :	ESERDPDE L SEQKADE	YA-EQ-GIA-APDC YA-DA-GTRSFGS	UGBASFRVAFF	RNDER	MLPVPRV MLPVPCV	PG <b>GU</b> HNKTRK PDA <b>GI</b> TDKARKI	QHKRDCANQI QQRRDCANQI	HKAAMAINSNT HKAAV <mark>SIN</mark> SGV	LABNEVEEPYIDSLEK IGDNEVEESEMAVLEK	N 21 S 22
GRMZM2G087 : GRMZM2G105 :	INGSKGTER IDGSKGTER	YVNDK-GQK YV-DR-GVMVEDS	DDSVATPCRPVSH GGPFPSSSSSSSSCGRPSV	RGEER	%LFVPCV %LFCPRV	AKPGLUETARRI PK <mark>GI</mark> SEDS <u>RR</u> F	JEQQKRDCASOI (EQQSRDCANO)	HKAAMAINNAV LKAAMAINSDV	LAD IR FDLYKEALPK LADNE FEMYLETLPK	C : 21 S : 22
GRMZM2G131 : GRMZM2G132 :	SPHKPP NPKE-RNP	A-DQRNQSFKES VV-KR-DSCS	KKSFÇ ESEN-EE	ESEDKO SDE C	%LFEPCV %IPIVKV	EDS <b>GI</b> SDCMHRE FG <mark>GI</mark> SKTSRGV	EDQQKRDQASQI ILHQKELVNOV	HRMAM <mark>EIN</mark> SSI LKAAMAINANC	ISBNOVELSYLETLPK DMSNSIEDTYIDTLPK	S : 20 N : 20
GRMZM2G144 : GRMZM2G158 :	EGORDVDE IGSKDTDE	YV-DQ-GICAPDC YV-DR-GVMVEDS	DSPFPSSSSSSCGRPSV	RDDR	WLPVPHV WLPCPRV	PHG <mark>GI</mark> REATRE PFK <mark>GI</mark> SEDARRE	LEHREDCASOL COOSEDCANOL	IKAAMAINSNA IKAAMAINSDV	LABNAVEVSYLDSLEK LABNEIEEVYLETUES	N : 21 N : 22
GRMZM2G173 : GRMZM2G359	M N AD-QT	ME-KG-GDNDA	DEPGKGNVF		METVKV METVRU	SE <b>GI</b> SDVTRKI	ONHINDLVAO	IKAAMAINAQV IKAAMAINANI	NVENEIPEVYIESIPK Meneveesynesipk	K : 20
GRMZM2G377 :	LOSEAG-KORE	A-SKDA	DGPGKGSTP		0 LPTVRV	PPDGISGAYSKI	I QNOKDLVAOV	IKAAMAINANV	DMEMEVRESYTESLPK	N : 20
Selmo1.431 :	ES QTPor	VU-DOEHMVCC	KDKAPNRPSVS	HEG	ALFVPKV	PSGISDEAKK	LHCKESTSO	FKAAMAINSQI	ISDNEVEDAYLEALEK	N : 21
Selmo1.627 :	DSYKETD	YV-EQ-GIILS	EK-DDSNKNNNMQHSLQ	QEEK	WLFTPRV	PPN <mark>GI</mark> SDEARKS	ONCROCTSO	LKAAVA <b>IN</b> GQV	ISBNEVEDLEWESINK	N : 21
seimoi.029 :	6d eF	Y Y	or-1676222291876222222222222222222222222222222222222	arrd <u>a</u> a M	w6P 6	∎iG <b>GI</b> EEKS <u>KR</u> p G6	A∎QNQ <u>B</u> BCTN <b>O</b> 6 Q€	kaa aIN	6 6 P 6P4	ja : 21:

Des CEE1	40 *	260 *	280	* 300 *	320 *	340 *
RopGEF2 : RopGEF3 :	CKASTG AIYRH	TS SGR SPECIEDC	HEALQLADEVEAS YTTE	RK-ACL-NNSKSS	NN-VKD MS-DKN-YVLAERA NNM-VKD MS-DKN-YVLAERA	SLLFCLKORYEELSOTSIDI : 319
RopGEF4 : RopGEF5 :	CKASVGLVIYKQI	CTAEKEYPDOLLDILKITSE	HEALELADKVDASLVTVF	RK-TGGLTHSKSS	NDM-MKDISN-DKN-HILAAR	SLLFCLKORYEELSOSSIDI : 318
RopGEF6 : RopGEF7 :	GRSCLGDFLYRNI	-ISDNFSADHILESIDLSSE	LAVVENANEVEASNYVVI	RR-AHSRHTR	MGMIVKE/MG-DKR-EIFAERA	SLLIRIKORFEGIROTALIT : 310
RopGEF8 : RopGEF9 :	GRASIGISIYKSI	TEEWFDPEOFLAMLDMSTE	HKVLDIKNRIDASVVIV HKVLDIKNRIDASVVIV	RK-LHT-KDTKSS	MGS-AVSIEKR-ELFEERA MGS-AVSIEKR-ELFEERA	TILVLIKOKFEGLPOSSIDI : 307
RopGEF10 :	GKTSLGDFLYKSI GBASLGTVTYRM	TEESFDPDYFVSFLDLSTE	HKVLDIKNRIÐASMVIØP	RK-MCQ-KEKDGKSQ	NGS-TVSEKR-ELFEVRA	TILVMIKOOFEGIPOSSIEV : 309
RopGEF12 : RopGEF13 :	GRASIGIQMYKNI GRASIGIMTYRMI	-TVDFFDPDQFLSSMDMSSE	HKIVDIKNRIÐASIIIWH HKTIDIKNKEÐASVVIV	RK-MVY-KDNXSSAF	WAS-GVSIEKR-EVFEERA	TILLIKORYEGISOSSIDI : 306
RopGEF14 : Aralv1.314 :	GKNSIGDELYKMI GRASIGDVIYRMI	-AVESATVDEIFISLNLGTE	AA ETV K PSA FAN	EITEQGSNGKSPV-AS -MVO-KDT-SP	MSF-AKDPLS-EIGRN-ESLLNRA MGS-TVSEKR-EOFEER	A RTOISSHEN PHEFLA : 316
Araly1.477 : Aralv1.479 :	GRASIGIQMYKNI GRASIGDMIYRMI	-TVDFFDPDOFLSSMDMSSE	CH <mark>KIVDLKNRID</mark> ASIIIWH CHKILDLKNKE <b>D</b> ASVVIN	(RK-MVY-KDSKSSAF RK-IVO-IDNKSSSF	MAS-GVSUEKR-EVFEERA MST-NLSUDKR-OOLEERJ	TILLIIKORYEGISOSALDI : 306 ATHOLIKOEFEGISOSTIDI : 309
Araly1.483 : Araly1.485 :	GKASVGEVIYKQI GRSCLGEFLYRNI	CHAEKSYPDOLLDVLKITSE - SDNSSADHLLESIDLSSE	HEALELADKVDASIVTYF LALVEMANEVDASMYVYF	RK-TGGLTHSKSS	MDM-MKDGN-DKN-HILAARO MGMIVKEOMG-DKR-EIFAERO	ASLLFCHKORYFELSOTSIDI : 318 SILIRIKORFEGIROTALDT : 310
Araly1.486 : Araly1.488 :	GRSCLGDLIYRYI GKTSLGDFLYKSI	-SSDQFSPECLIDCLDLSSE -TEECFDPDYFVSFLDLSTE	YQATETAN EVESSTYLWE HKVLDIKNETEASMVIW	KR-TNS-KPATNTKTS (RK-MCQ-KEKDGKSQ	WEM-VKELMVDDKL-ELMADRA MGS-TVSLEKR-ELFEVRA	SILLSINGREEGIPOTALOM : 322 TILVMINGGEEGIPOSSIEV : 309
Araly1.490 : Araly1.490 :	GKSSVGDSIYR <mark>Y</mark> M GKECLGEIIYQYL	SGSGREFPEQULDCLNIASE -TANKESPECULDCLDLSSE	HEAVQLADRVEASMYTWF HQTLEIANRIEAAVYVWF	RK-ACL-SNSKSS CK-NGRKLSS	WNM-VKDIMT-DKN-YVMAERA NGGKVKGIVS-DRN-DFLVQRA	STLIFCLKORYFELSOTSIDI : 319 STLIQSIRIRFEGIPOTTIOM : 314
Araly1.497 : Araly1.861 :	GKASVGIVIYKQI GRSCIGDVIYRYI	CTAEKFYPDQLLDILKITSF -TSDKFSAECLLDCLDLSSF	HEALELADKVEASLVTWF HIALDIANRVEASLYVWF	RK-TGGLTHSKSS RR-VQT-KLGVNNNPKLT	WDM-MKDIGN-DKN-HILAARD WEM-VKEIMG-DKR-GLLVERS	SLIFCLKORYFELSOTSIDI : 318 TILIRCLKORFFSLTOTSIDI : 320
Araly1.874 : Araly1.883 :	GRASIGISIYKSI GRVSIGISIYKSI	-TEEWFDPEQFLSMLDLSTE -TEEWFDPEQFLSTLDLSTE	CHKVLDIKNRIÐASVVIØÐ CHKVLDVKNRIÐASIVIØÐ	(RK-LHT-KDTKSS (RK-LHL-KDNKSS	MGS-AVSUEKR-ELFEERA MGS-AVSUEKR-ELFEERA	STILVLIKOKFFGLPOSSIDI : 307 STILVLIKOKFFGLPOSSIDI : 307
Bra000971 : Bra002246 :	GKSSVGLSIYRYM GKTILGDFLYKIL	SGSGREFPEKLIDCLNIASE - IDEHEDPDYFLSFLDLSTE	HEAVQLADRVDASMYTWF HKVLDLKNRIDASMVLWF	RK-ACL-SNSKNS RK-MNQ-KEKDGR <mark>S</mark> Q	MNL-VKDUMT-DKN-YVMAERA MGS-SVSUERR-ELLEVRA	MILLECHRORMEELSONSDI : 319 MILLECHROMEGIPOSSDEV : 309
Bra003536 : Bra004945 :	GRASIGIQMYKNI GKASVGIVIYKQI	- IVEFENPDQFINSMOMSSE CTAEKEYPDQLIDI <mark>IK</mark> ISSE	CHKILDIKNKIDASIII// CHEALEIADKVDASIVT//F	(RK-MVQ-KDNKPSAF) (RK-TGGLAHSKSS	MAS-GVSDEKR-EVFEERA MDM-MKDUGN-DKN-HILAARU	NTILLINKHRYFGISOSSIDI : 307 RSLLFCHKORFFELSOTSIDI : 318
Bra006510 : Bra007183 :	CRISIC LINKS CRSCIC FLYRN	-TDEYEDPGYFLSSCDLSTF -TSDNESADYLLESIDLSSF	HKVIDIKNSIDASHVIN HAVVEMANSVDASHYIN	RR-MNHREQ RR-GHS-RHASPT	MGS-FVSEKR-ELFEVRV MGMIVREVMG-DKR-QIFAGRA	SILISIKOREEGIROTALIT : 312
Bra009152 : Bra009621 :	CRSCIG VIYRYI CRSCIGILIYRYI	-SSDQESPEYLIDCLDLSSE	H QAIEIAN SVESSIYU H QAIEIAN SVESSIYL ØF	KR-VQT-KLGVNNPHLS KR-SNS-KPATNTKTS	MEM-VKDIMG-DRR-GLLVERS MEM-VKEIMV-DEKLEVMADRA	SLLISIKORFEGLPOTALDM : 321
Bra015010 :	CKECLGEI HQYI	-TANKESPECILDCIDLSSE	HQTLEIANRIE-AVHVWF	QKKG KLSS	NGS-AVSEREELFEERA NSGKVKG VN-DRN-EFLAQRA	TLLQSIRIREGLPOTTLOM : 325
Bra015068 : Bra018956 :	CRASLGIVIYKMI	-TVEMEDADOFI IEMDLSSE	HKILDIKNRIDASIVIZH	RK-MVQ-KDTKSA	MGS-AVSEKR-EDFEERA MGS-TVSTEKR-EQFEERA	TILLIALGEGISOSTICI : 304
Bra020048 : Bra021162 :	CRVSLGDTIYRM	-TLDMFDAEQFILEMDLTSF	HKILELKNKI BASVVIV	RK-IVQ-KDNISSSI	ST-NLSOEKR-QLLEERO	ATTIFL KOVEG SOSTLII: 292
Bra030396 :	GRASLGIVIYKMI	-TVEMEDADOFI IEMDLSSE	HKILDIKNKIDASIVIN	RK-MVQ-KDTKSP	GS-GVSTEKR-EQFEERA	TILLIKOGFFGISOSSIDI : 304
Bra037342 :	CKSSVGCSIYRYN	SGSGR FPEKLIDSLNIAS	HEAVQLAD V DASMYT	RK-ACL-SNSINS	NN-VKD MT-DKN-YVMAERA	STLLFCLKORYELSONSUI : 303
Cucsa.0666 :	RACIGULIYRY	-SDH-SPECLIDCLEMSS	HOATEIANEV DASIYV7	KR-TNS-KPSKSS	MEM-VKE MV-DKR-ELLAE	TILLCHKORFEGIPOTTLOM : 315
Cucsa.1193 :	CKACLG IIYRY	-TADH-SPECLIDCLDLSS	HHTLE IANRI BASIHIYE	CK-DHKRPT	SGKVKG VG-DKS-NNLARA	TLLDSIRLREGGLPOTALDM : 317
Cucsa.1363 :	CRACLGEVIYRYI	TSEHFSSEYLLDCLDLSSE		RR-AHS-KPARSS	MEM-VKDIMI-DKR-EFLAERA	GLIHSLKORFESITOTTET : 315
Cucsa.3592 : mgv1a00322 :	GRASIGISIYKSI	-TVEFFDPDQFLSSMDLTSE	HKILDIKORIBASIVIW HVALETANEVBAATYVZ	RK-MNQ-KDGST	WGS-AVSVEKR-ELFEERA	TILLIAHREEGIPOSSICI : 306
mgv1a00378 : mgv1a00399 :	GKDCLGDIIYRYI EKACLGDILYRYI	-TADOFAPECILDOMDLSSE -THDOFSPDCILDYLDLSSE	HTVDVANR DAVHVY VSTDIAR PTA HEV	TKEKKKKKKT MaYOKGSE	WGGKMKGFGA-DKN-QSLACRA MGSTVKG VV-DKT-KLFAHRO	TLLHSIRHRFEGLPOTALOM : 318
mgv1a00461 :	GKASLGILIHRYI GKSSLGESTYRGI	-NSDOYSPECILIDCLDLSSE	HHALEIANRVEATIHVWF	RK-TNS-KPLNHSKSS BK-LHH-KDGKAA-	WEI-VKDUVI-DKR-ELLASRA	TILLCIKORFEGIPOTTIOT : 323
mgv1a00594 : mgv1a00778 :	CKTSIG LIHRYI CRASIG ATYKII	NNSEQESPECII DOLDLSSI HEDFEDPDCLISSIDLST	NHALEIANRVDASIYIV KI DIKNKIPASVVIV	RK-LIP-KQTTNRSNSKSS RK-MNA-KDTKSS	MEM-VKDFVS-DKRVQLAADRA MGS-GVSVE-KR-ELLEDRA	TILLCIKORFEGIPOETIOT : 320
mgv1a02184 : mgv1a02262 :	GKASVGITIYRHM GRACLGIVIYRYI	YSAEKESPDHLLDSLNLSSI -ISENESSKCLLDCLDISSE	DLEALELADKVDASMYTY HAALEIANKVDAAIYVY	RK-M-G-MTSKSS RR-QHP-KSPARPSKSS	MDM-VKD MS-DKN-HILAERA MEM-VRG VV-DKS-ELLAERA	TLLFCLKORYFELSOTTLDT : 319 SLLISIKORFEGLSOTTLDA : 320
mgv1a02280 : mgv1a02642 :	GRASIGESIYKSI GRASIGESMYKSI	-TVEFFDPLQFLSTMDLSSE -TDEYFDPDYFLSSIDLSSE	HKVLDIKNRIÐASIVIØF HKLIDIKNKIÐASVVIØF	RK-MHHKADSKSSN- RK-MLA-KDNKSS	MGS-AISLEKR-ELFEERA MGS-AVSLEKR-EIFEDRA	STILLLIKOOFFGIPOSSIEI : 303 STILLLIKHRFFGLPOSILII : 306
POPTR_0001 : POPTR_0002 :	GRASIGILAYRSI GKACIGRIMYRYI	-TLEYFDPDQFLSTMDISSE -TAKHFSPDYDLDYLDVSSE	HKILDIKNRIÐASIVIW YTTIÐIANRIÐAASHFWS	RK-MNQ-KDSKSA SEKYLNRYLGRARDGRSS	WGS-AVS <mark>I</mark> EKR-ELFEERA WGGKVKGFVG-EKR-KLLAKRA	TILLLERORFEGIPOSSLOV : 306 ILIHNIRLEFEGIPOTALDA : 328
POPTR_0002 : POPTR_0003 :	GRASIGITIYRYI GRASIGISAYRSI	CTADGESPDHLIDCINIASE -TLEYEDPDQEISTMDISSE	HEALELADRVDASMYTWF HKILDLKNRIDAST <mark>V</mark> TWF	RK-ACL-SSKSS RK-MNQ-KDGKSA	MDM-VKD MS-DKN-HVLAERA MGS-AVSUEKR-ELFEERA	STILFCIKORYFELSOFSLIT : 316 STILLIKORFFGLPOSSLIV : 306
POPTR_0004 : POPTR_0005 :	GKACLGDIIYRYI GKACLGRIMYHYI	-TAEKFSPECILDCLDLSTE -TAKHFSPDYLLDYLDLSSE	HHTLEIANRVEAAVHIW FTTLEIANRIEAATHFWS	QM-DHR-KKHSS SQN-YQNGWSS	WGGKVKGFVA-DKN-QILAQRA MSGKVKGFVG-EKR-KLLAKRA	TLIQSIRLRYEGIPOTALOM : 321 FVIMHNIRLRFEGIPOTALOV : 320
POPTR_0006 : POPTR_0008 :	GKASIGILIYRYI GRACIGILVYRYI	-SSDQFYPECLIDCLDLSSF -TSDQFSAECLIDCLDLSSF	HQATELANRV <b>D</b> ASTYTZF HVALETANRVDSSTYVZF	KR-TNY-KPASSTNRSSSKSS RR-AHS-RPTKSS	MEL-VKEIMA-DKR-ELLADRA MEM-VKDIMV-DKR-ELLAERA	SLLLCHKORFEGLPOHTLOM : 323 SLLLSHKHRFENLTOTALDT : 315
POPTR_0009 : POPTR_0010 :	GRPOLGDIIYRYI GRACLGDLVYRYI	-TAEQHSPDRLIDCLDLSTE -TSDQHSAECLIDCLDLSSE	HHTLEIANSIDAAVHVOI HVALDIANSVDSAIYVOI	QN-DHK-KKHSS RR-AHS-RPTKSS	MGGKVKGFVT-DKN-QILAQNA MEM-VKDIIV-DKR-ELLAENA	SILLSHAQWEENLTOITHOT : 315
POPTR 0014 : POPTR 0016 :	GRASIGDTIYRYI GKASIGDLIYRCI	YTADKESPGHLIDCLNIASE -SSDQEYPECLIDCLDLSSE	HEALQIADRVDASMYT7 IllaielanrvdasiyN7	RK-ACL-SHSKSS KK-TNS-KPVNSTNRSKSS	NN-VKDMS-DKN-HILAERA MEL-MKELMV-DKR-DLLADRA	ITLLFCHKORYFELSOTSLDT : 317 ISLLLCHKORFEGIPOTTLDM : 321
POPTR_0018 : Thhalv1000 :	erasigisiyksi erasvgiviykoj	-TVEYEDPEQELSTMOMSTE CTAEKEYPDQLLDILKITSE	HKVLDIKNRIDASIVI70 HEALEIADKVDASIVI70	RK-MNQ-KDGKST RK-TGGLAHSKSS	MGS-AVSEXR-ELFEERA MDM-MKD GG-DXN-HILAAR	NTILLINKORFEGISOSSIDI : 306 RSLIFCIKORYEELSOBSIDI : 318
Thhalv1000 : Thhalv1000 :	CRASIGUSIYRSI CRASTGUSIYRYM	TSSGK LPEKLDCLKIVS	HEALQIADEVBASVYTVE	RK-LHL-RDNRSS RK-ACL-SNSKSS	NGS-AVSEKR-ELFEERA NNM-VKD MS-DKN-YVLAERA	SLLFCLKORYEELSOTSLDI : 307
Thhalv1001 :	GRASLGIVIYRMI	-TVEMEDADQFI IEMDLSSE	HKILDIKNRIDASVVIVI	RK-MVQ-KDTKSP	GS-TVSEKR-EQFEERA	TILLIKOGFEGISOSALDI : 304
Thhalv1001 :	GRSCIGCLIYRYI	- SDQ SPEYLLDCLDLSS	QALEIAN SSIY	KR-SNS-KPATNTKTS	MEM-VKE VG-DKK-GLIVES	SLILSHOREGEPOTALOM : 321
Thhalv1001 : Thhalv1001 :	CRASICOMYRNI	-TVDWEDPDQFLST	HKIVDIKNSIDASIVI HKIVDIKNSIDASIVI	RK-MVH-KDSKSAAF	MAS-GVSIEKR-EVFEERA MAS-GVSIEKR-EVFEERA	TILLILKORYEGISOSSIDI : 309
Thhalv1002 : Thhalv1002 :	GRASIGUTIYEMI	-TLDIFDAEQFLLEMDLSSE	HKVLDIKKKFBASVVIV HOTLFIANSVBAAVHVV	RK-IVQ-KDNKSSSF	ST-NLSVEKR-QLLEER	ATILLIKOGEEGISOSTIDI : 309
Thhalv1002 : Thhalv1002 :	GKECLGEIIYHYI GKECLGEIIYHYI	-TADKESPECILDCLDLSTE	HOTLE IAN EVENAVHVYF	QK-NGRRRKQHKLSS	NSGKVKGLVN-DRN-DFLVCRA	TLLQSIRIREGLPOTTIOM : 258
Thhalv1002 : Vv.1782614 :	CKSSVGISIYRYM CRASIGISIYKSI	SSSGREFPEQLIDCLNIATE	HEAVQLADRVDASMYTWF HKVLEFKNKIDASIVIV	RK-ACL-SNSKNS	MNM-VKD MT-DKN-YLMAERA MGS-AVSEKR-ELFEERA	TILIFCIKORYELSOUSIDI : 315
Vv.1782686 : Vv.1782737 :	GRACLGDIIYRYI GRASLGDSIYKSI	-TSDOFSSECLIDCLDLSSE -TVDHEDFGOFLSTMDLSSN	HVALEIANRVDASTYVØF IRKILDEKNRIDASTVIØF	RR-THH-KPMTNPNRSTASS RK-MHN-KDGSA	MEM-VKDUMG-DKR-ELLAERA MAS-AVSUEKR-ELFEERA	SIFLSIKORFIGLTOTTLDT : 323
Vv.1783220 : Vv.1783447 :	GKACLGEIIYRYI GRAGLGEAIYRFM	-TAEQESPECIIDCLDLSSE NTSDKESPDQLMDYLHISSE	HHTLEIANRIDAAVHV?P HEALELADRVDASMYT?P	QKDWKKKRST RKK-ACV-AHSKSS	NGGKVKG VA-DKN-QFLAIRA NDM-VKQIIT-DKN-YVLAERA	STLLHSLRLRFEGLPOTALDM : 321 SSLLFCLKORYEELSOFSLDA : 315
Vv.1783965 : LOC_Os01g4 :	CKSSIGDLIHRYV CRSSIGDSIYKII	-ISDQFSPEYILACLDLSSE -IDDHFDPNEILSSVDLSTE	HQALEIANRVEASVYVWF HKIVDIKORIEASVVIWG	RK-TNS-KPSRSS RK-ISNKLS	WEI-VKDIMV-DKR-ELLAERA WGP-GVSLEKR-EQFEERA	SILHOMKORFEGLPOTTLDM : 315 DTVLLILKHOFEGVPOSSIDI : 304
LOC_Os01g5 : LOC_Os01g6 :	GRASIGDALYRII GRATIGDIIYRYI	-TDVEFDPDVFLSTVDLTSE -TSDHFSPECLDCLDLSTF	HKILDIKORIÐASVIIWN YQALEIANRVÐASVYVØF	IRK-VHN-KDGKSA RR-IAA-KPASVLGRGRSS	WGS-AVSQEKR-EQFEERAG MGM-VKDUII-DKR-ELLAERA	TILLIIKHRYEGIPOSTIDI : 305 GLLICIKORFFGLTOTSIDM : 321
LOC_Os02g1 : LOC_Os04g4 :	GKTSIGDAIYRSI GRASVGDLIYRHM	- DEEFDPIEFLEGVDLSTE SFPGKFSPEYLLDRLEISSE	HKVLDLKNRIÐASTIIWF HDALEAADRVÐAAMHVØF	(RK-MQT-KQEAKSS RKK-ASQ-GHSRSP	WGS-IISFEKR-EQFEERA WSA-VKEUMS-DKN-VMLASRA	STILHLIKLQFEGTPOSCIDI : 301 SDVLICIKORFEGISOTTIDA : 318
LOC_0s05g3 : LOC_0s05g4 :	GRATIGDIIYRYI GKSTIGDSMYKII	-TSDQESEDCLIDCLDLSSE -TEDHENPEELLGTVDMSAE	YQALETANRVEASIYVW YNIIDIKNRIEASVVIWC	RK-GTS-GAASRNKSS RK-MVH-KEGKLS	MGI-VKDUIM-DKRDDLLADRA MGH-GVKFEKR-EKFEARA	IGLIMCIKORFEGITOTSLDT : 319 INVILLIKHRFEGIAOSALDI : 307
LOC_0s07g2 : LOC_0s09g3 :	CRVGVGDATYRYN CKSCLGEIIYRYI	SAGDQHSPDHLINFLNLSSE - AEQHSPECLIDCLDLSSE	HEADENADRYDAANYY HHTLEVANRIDAANHYN	ASMTVVSK- L-GQK-KSTPQAKSKKS	MEN-VTEWNA-DWN-LILASE MGGKVKGUVG-D-EXS-HVLSQE	ASLELCHKORFEGLSOFTEDT : 309 DGLLQSIRLRYEGLPOESEDM : 328
LOC_Os10g4 : GRMZM2G059 :	GRASVGDGVYRAM GRSILGDSMYKII	LGAEKFSPEYLLDOLDMSSE -TDDVFDPNELLQSVDLSTE	HEADAMADRVƏAAMYVƏ HKIVDIKORIDASVVIDH	RK-ISNKLS	MGA-VKEUVADDKN-VMLAGRA MGPAGVSIEKR-EEFEERA	TALLILKHREEGIPOSALII : 304
GRMZM2G065 : GRMZM2G071 :	CRASVGISVYRV	LGADKE SPEFLI DTLDISSE		RK-ASG-SHGKLP	MSK-VKEIAA-DKN-VTLANRA	SLLCIKHREGISOTTOT : 325
GRMZM2GU8/ : GRMZM2G105 :	GKSCLGEIIYRYI	TAEQ: SPECII DOLDISSE	HT EVAN R EAH W	LGQK KS	NGGKVKG VG-DNS-HTLSER	NGLLOSIRLEYEGLPOTSLOM : 321
GRMZM2G131 : GRMZM2G132 :	GRASIGIALYRII	-TDVE-DPDDFLSTVDLTSF	HKILDIKORIEASVIIW	RK-VHN-KDGKSS	MEN-VIEINA-DMN-LVIASRO MGS-AVSQEKR-EQFEERA CI UKR NA D	TILLIKHREGIPOSTICI : 310
GRMZM2G144 : GRMZM2G158 :	KSCIGEIIYRYI	TAEOFSPECLIDOLDLSSE	HT EVAN BOGA HV	LK-GQK-KSTPQAKSKIS	GI-VKDUVM-D-RR-DLLAERA MGGKVKG VG-DKEKS-HTLSERA	DG LOS RLYEG PORSE M : 314
GRMZM2G359 :	CKSTIGISAYKLI	TDDCTDAEELLRSVDLSD	SIVE KNRVE STV	KK-MTH-KDSKLS	MGH-NARHEKR-GMFEGRA	NVILLIKHREGIAOSALDI : 301
GRMZM2G442 : Selmol /21	CKTSIGDAIYRSI	TEETFDPLEFLAGMDLSTE	HKVIDIKNRIDASTVIN	RK-MQT-KDSKSS	NSS-IVSFE-KR-EQFEERA	TILHLIKLOFEGTPOSCHOI : 300
Selmo1.623 : Selmo1.627 ·	GRSSIGEGEYRCI	-SFEC SPEALLATLIMAS	HILELAN BUDAALHTW HNALEAAN BUDAALH	RK-VSSARSS	GGLMKD VG-DR-ETLIARA	STLLICIKHKFEGLPOTILDI : 314 SLLISFKORFEGLPOSVIDV : 319
Selmol.629 :	ARAN G T YG	-RQEHESPDALLSSLDLSTE	HSALEVANE OSALH V 2h 4 2a W	KK-ESSGSHKESRYS	S Ra	SLLLCIRORFEGLPOTVLDV : 319 4 P q3 Ld



# Figure S5. Alignment data used to produce the RopGEFs phylogenetic tree in Figure 7A. The alignment was produced by MUSCLE 3.6 and presented by GeneDoc without adjustment.

Mutant line ID	Bar <sup>R</sup>	Bar <sup>s</sup>	Bar <sup>R</sup> :Bar <sup>S</sup>
LDN-1	72	15	4.8 :1
LDN-2	68	2	34 :1
LDN-3	<b>69</b>	35	2 :1
LDN-4	152	22	7 :1
LDN-5	172	48	3.6 :1
LDN-6	98	24	4 :1
LDN-7	117	57	2 :1
LDN-8	<b>98</b>	56	1.8 :1
LDN-9	100	0	$\sim$
LDN-10	53	20	2.7 :1
LDN-11	112	44	2.5 :1
LDN-12	48	11	4.4 :1
LDN-13	64	1	64 :1
LDN-14	51	3	17 :1
LDN-15	<b>46</b>	23	2 :1
LDN-16	109	31	3.5 :1
LDN-17	42	39	1.1 :1
LDN-18	53	5	10.6 :1
LDN-19	120	<b>50</b>	2.4 :1
LDN-20	98	<b>50</b>	2 :1
LDN-21	53	29	1.8 :1
LDN-22	47	1	47 :1
LDN-23	92	57	1.6 :1
LDN-24	165	62	2.7 ;1
LDN-25	79	33	2.4 :1
LDN-26	65	0	$\sim$
LDN-27	52	23	2.3 :1
LDN-28	67	32	2.1 :1
LDN-29	53	6	8.8 :1
LDN-30	73	31	2.4 ;1
LDN-31	61	23	2.7 :1
LDN-32	53	23	2.3 :1
LDN-33	NA	NA	NA
LDN-34	42	21	2 :1
LDN-35	66	21	3.1 :1
LDN-36	103	7	14.7 :1
LDN-37	85	30	2.8 :1
LDN-38	67	27	2.5 :1
LDN-39	70	28	2.5 ;1
LDN-40	41	11	3.7 :1

 Table S1:The Segregation Ratios of the LAT52:DNPRK2 T2 plants

Genes	AGI number	Alleles	Accession No.	Background	Marker	Insert. posi.	mRNA levels (by RT PCR)
RopGEF1	At4g38430	ropgef1-1 (586B11)	GABI_586B11	Col	Sulfadiazine	3rd Exon	not detectable
RopGEF9	At4g13240	ropgef9-1 (717A10)	GABI_717A10	Col	Sulfadiazine	5th Exon	not detectable
RopGEF12	At1g79860	ropgef12-1 (103614)	SALK_103614	Col	Kan (2:1)	4th Exon	not detectable
RopGEF14	At1g31650	ropgef14-1 (064617)	SALK_064617	Col	Kan (3:1)	1st Intron	suppression
		ropgef14-2 (046067)	SALK_046067	Col	Kan (lost)	1st Intron	not detectable
AtPRK1	At5g35390	prk1-1	SALK_112241	Col	Kan(3:1)	1st Exon	not detectable
		prk1-2	SALK_054149	Col	Kan(3:1)	1st Exon	not detectable
AtPRK2	At2g07040	prk2-1	SALK_110661	Col	Kan(lost)	1st Exon	suppression
AtPRK5	At1g50610	prk5-1	SALK_016815	Col	Kan(lost)	3rd Exon	suppression

#### Table S2. Information of the ropgef and prk T-DNA Insertion Mutants

	Length <sup>a</sup>	Width <sup>a</sup>	Width/Length
GFP	469 ± 11	9.1±0.8	0.02
GFP-GEF1	21±7	29.4±4	1.41
GFP-S458A	39±11	39.9±8	1.03
GFP-S460A	422±89	13.8±2.3	0.03
GFP-S480A	174±40	5.7±0.5	0.03
GFP-S484A	63±15	11.3±0.7	0.58
GFP-S488A	70±12	35.6±0.7	0.51
GFP-S501A	24±5	22.7±3.8	0.94

 Table S3. Phosphorylation in C-terminal regions is critical for RopGEF1 activity

The length and the maximum tip width of tobacco pollen tubes were measured 6 hours after bombardment. <sup>a</sup>Data are the mean  $\pm$  SD.