

Spatiotemporal formation of the large vacuole regulated by the BIN2-VLG module is required for female gametophyte development in *Arabidopsis*

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Abstract

The large vacuole (LV) is a key organelle in plant cells. The *VG* gene encodes a *Vesicle GTPase* (VG) protein that is involved in the formation of the LV. *VG* is controlled by the *BIN2*-*VLG* module. *BIN2* is a member of the *BRASSINOSTEROID INSENSITIVE2 (BIN2)* family and *VLG* is a member of the *VLG* family. *BIN2* and *VLG* interact with each other and regulate the formation of the LV. *BIN2* and *VLG* are expressed in different tissues and at different stages of plant development. *BIN2* and *VLG* are also involved in the regulation of other cellular processes such as endocytosis and vesicle trafficking. The *BIN2*-*VLG* module plays a key role in the formation of the LV and its function is conserved across different plant species. The *BIN2*-*VLG* module may also play a role in other cellular processes.

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Introduction

AGAM-like genes are found in most eukaryotes (FG) (Wang et al., 2012). They are involved in various biological processes, including cell cycle regulation, DNA repair, and gene expression. AGAM-like genes are also found in plants, where they play a role in growth and development. In humans, AGAM-like genes have been implicated in various diseases, including cancer and neurological disorders. AGAM-like genes are also found in other organisms, such as yeast and nematodes. The function of AGAM-like genes is not fully understood, but they are believed to be involved in regulating gene expression and protein synthesis.

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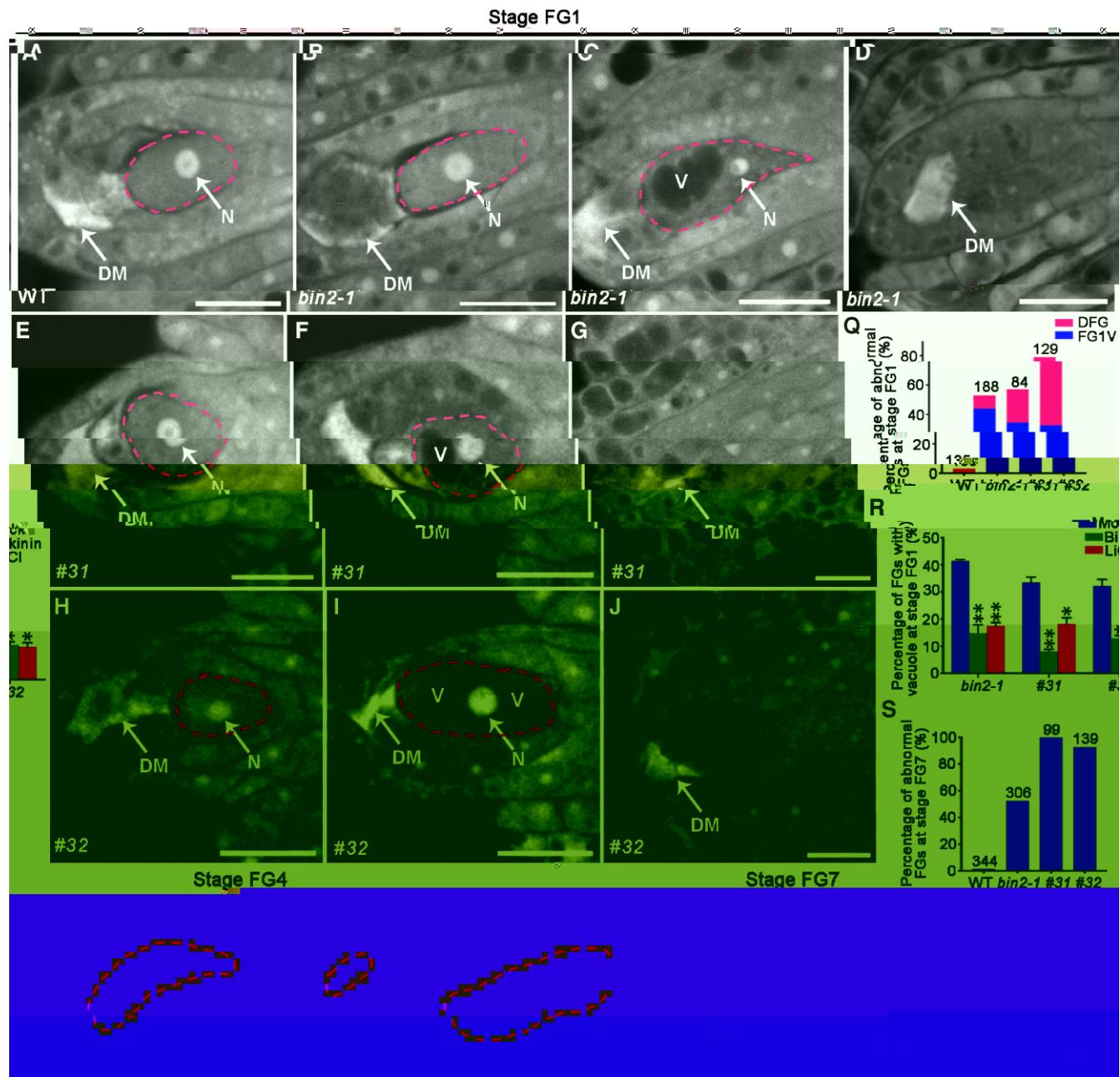


Figure 1 Bin2-1 affects FG localization. Panels A–D show Stage FG1 confocal images of WT and *bin2-1* genotypes. Panels E–H show Stage FG4 confocal images of #31 and #32 genotypes. Panels I–L show Stage FG7 confocal images of WT, *bin2-1*, #31, and #32 genotypes. Panels Q and R are bar graphs showing the percentage of embryos with abnormal FG localization at Stage FG1 and Stage FG7, respectively. **P < 0.01.

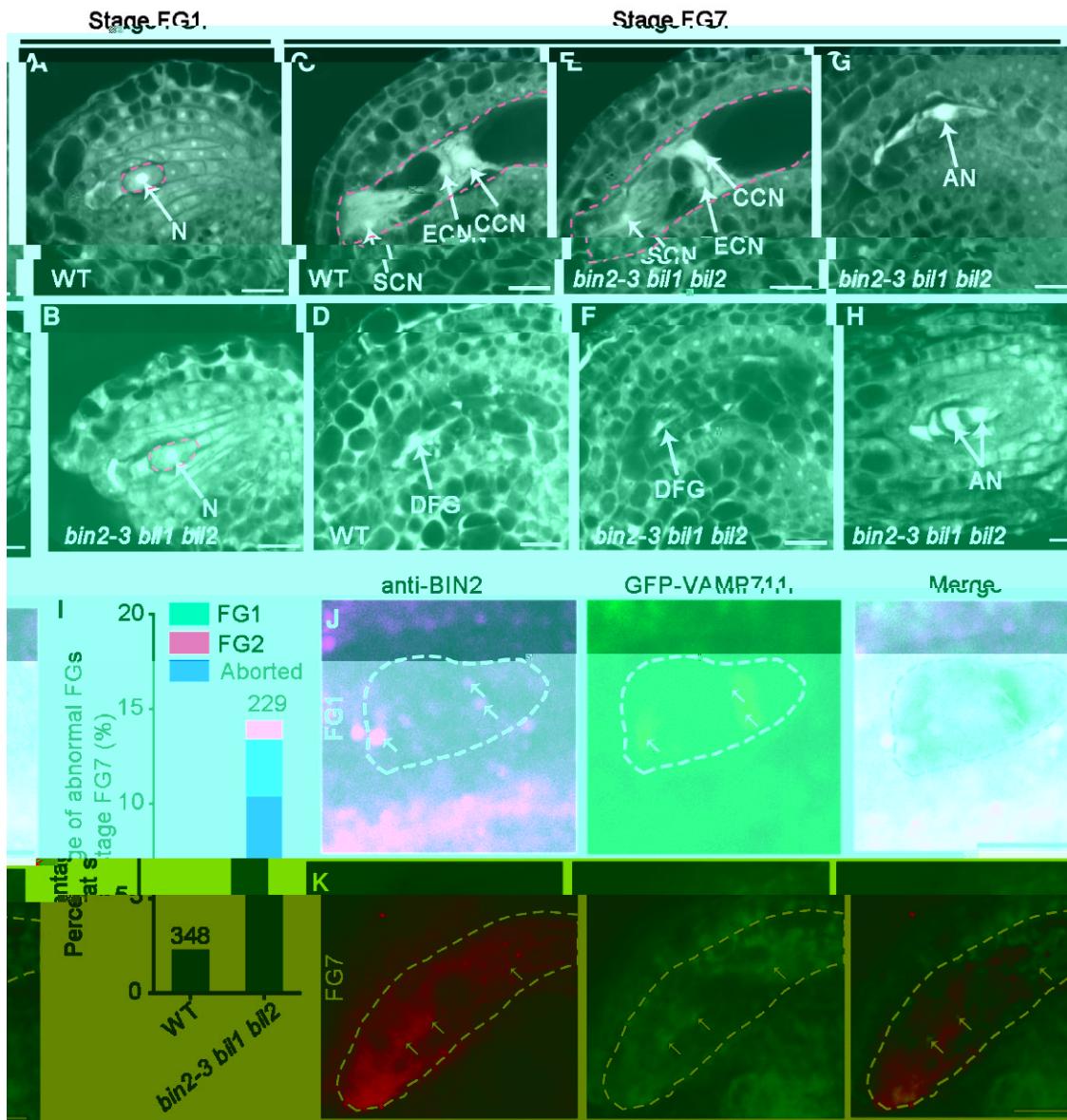


Figure 2 Bin2-3 bil1 bil2 affects flower development. (A–I) Fluorescence microscopy images of WT (A–D) and *bin2-3 bil1 bil2* (E–H) flowers at Stage FG1 (A, E), Stage FG7 (B, F), and imbibition stage 2–3 (C, G). (B, F) Dashed boxes indicate regions shown at higher magnification in (E, H). (D, F) Arrows indicate ECN. (E, H) Arrows indicate CCN. (G) Arrows indicate DFG. (I) Quantification of the percentage of abnormal flowers. (J–K) Fluorescence microscopy images of *bin2-3 bil1 bil2* flowers at Stage FG7. (J) Anti-BIN2 staining. (K) GFP-VAMP711 staining. (L) Bar graph showing the percentage of aborted flowers. Data represent mean \pm SD. $n = 10$ m.

Figure 3: *bin2-3 bil1 bil2* affects flower development. (A–D) Fluorescence microscopy images of *bin2-3 bil1 bil2* flowers at Stage FG1. (E–H) Fluorescence microscopy images of *bin2-3 bil1 bil2* flowers at Stage FG7. (I–L) Fluorescence microscopy images of *bin2-3 bil1 bil2* flowers at Stage FG1. (M–P) Fluorescence microscopy images of *bin2-3 bil1 bil2* flowers at Stage FG7. (Q) Bar graph showing the percentage of aborted flowers. Data represent mean \pm SD. $n = 10$ m.

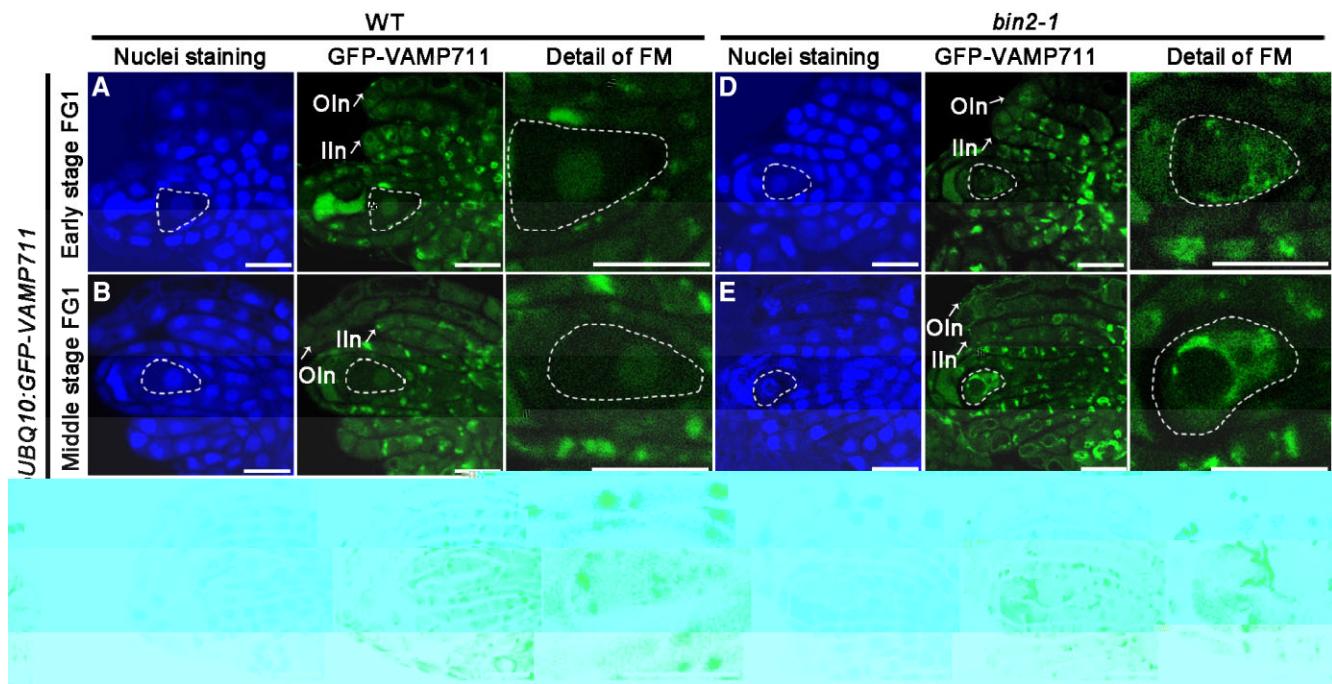


Figure 3 Early stage FG1 (A–C), middle stage FG1 (B, E), detail of FM (C, F). Scale bar = 10 μm.

(A–F) Early stage FG1 (A, D), middle stage FG1 (B, E), detail of FM (C, F). Scale bar = 10 μm.

Figure 3 Early stage FG1 (A–C), middle stage FG1 (B, E), detail of FM (C, F). Scale bar = 10 μm.

Figure 3 Early stage FG1 (A–C), middle stage FG1 (B, E), detail of FM (C, F). Scale bar = 10 μm.

BIN2 participates in female gametophyte development mainly by regulating vacuole formation

Figure 3 Early stage FG1 (A–C), middle stage FG1 (B, E), detail of FM (C, F). Scale bar = 10 μm.

BIN2 interacts with VLG both in vitro and in vivo

Figure 3 Early stage FG1 (A–C), middle stage FG1 (B, E), detail of FM (C, F). Scale bar = 10 μm.

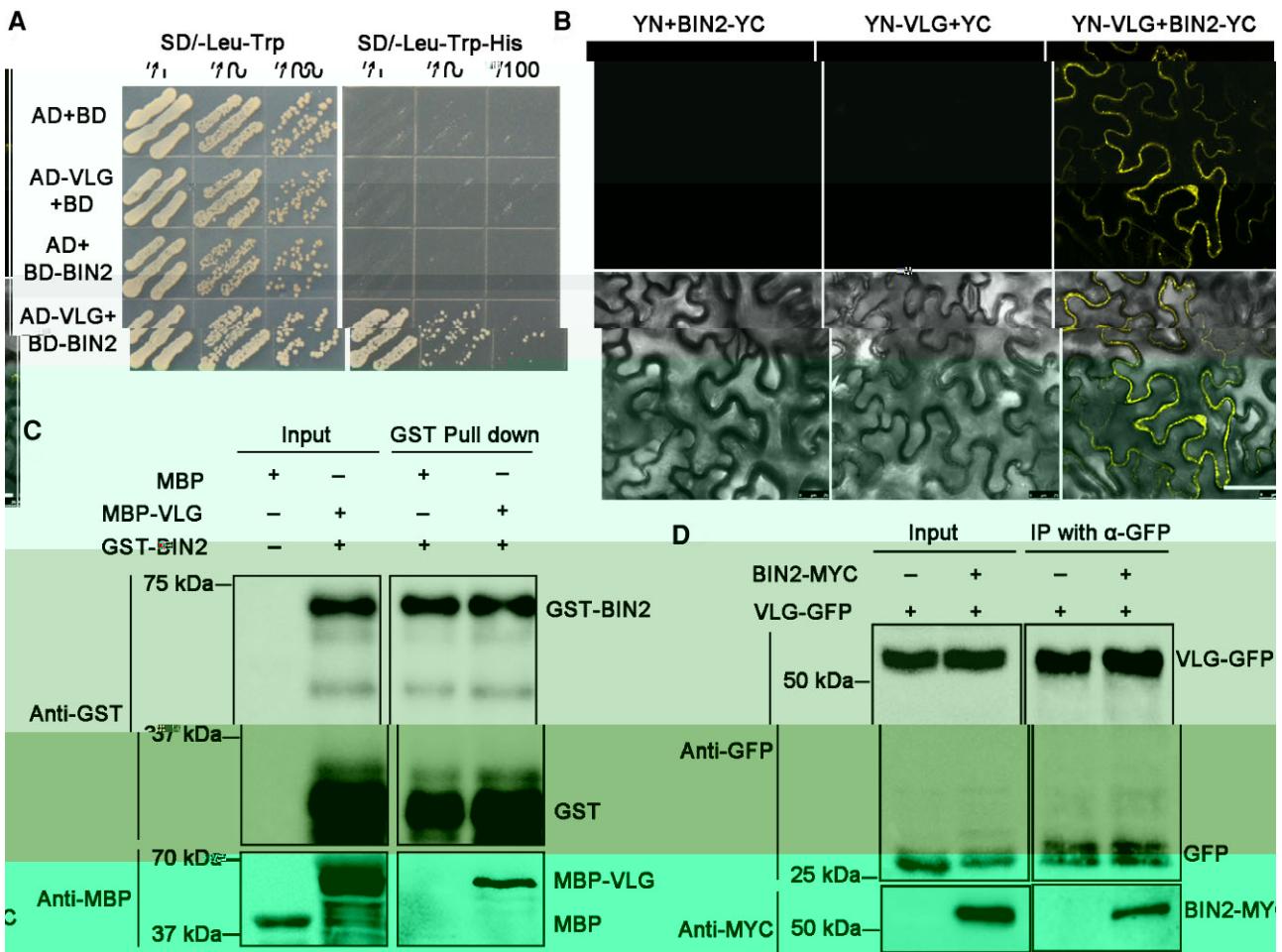


Figure 4 BI 2. (A) (B) (C) (D)

BIN2 positively regulates VLG abundance and influences large vacuole formation

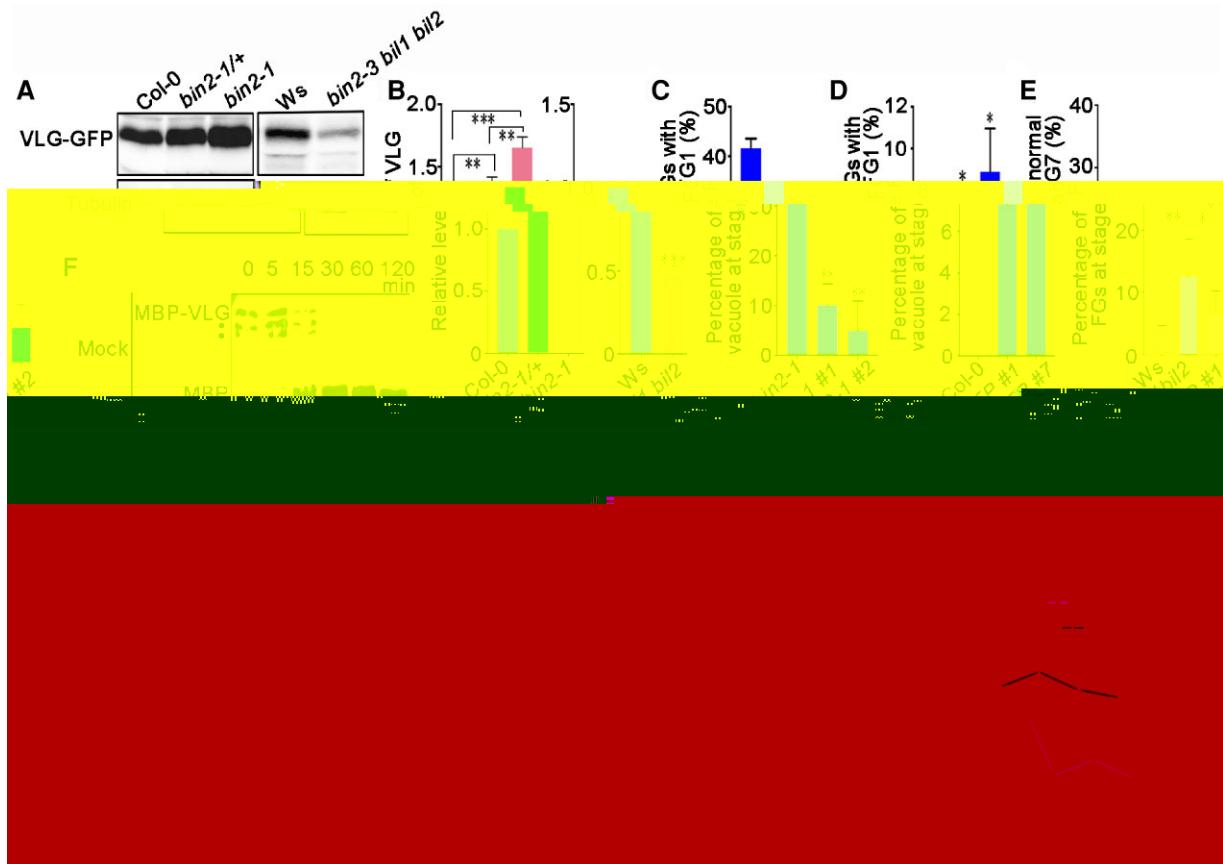


Figure 5 BIN2 enhances VLG stability via phosphorylation. (A) Western blot analysis of VLG-GFP expression in Col-0, bin2-1, bin2-1*, Ws, and bin2-3 bil1 bil2 genotypes. (B) Quantification of VLG levels in (A). (C-E) Flow cytometry analysis of cell cycle distribution (G1 with G2/M) and FG vacuole formation in Col-0, bin2-1, bin2-1*, Ws, and bin2-3 bil1 bil2 genotypes. (F) Time course of MBP-VLG protein levels. Error bars represent standard deviation. Statistical significance relative to Col-0: **P < 0.01, ***P < 0.001.

Panel F shows a Western blot of MBP-VLG protein levels at 0, 15, 30, 60, and 120 minutes. The protein level decreases over time, with a significant reduction after 15 minutes. The loading control is Tubulin.

BIN2 enhances VLG stability via phosphorylation

Panel F shows a Western blot of VLG:VLG-GFP protein levels in Col-0, bin2-1, bin2-1*, Ws, and bin2-3 bil1 bil2 genotypes. The protein level is significantly reduced in the bin2-1, bin2-1*, and bin2-3 bil1 bil2 genotypes compared to Col-0 and Ws. The loading control is Tubulin. Panel G shows a bar graph of VLG:VLG-GFP protein levels. Panel H shows a bar graph of FG staining. Panel I shows a bar graph of G2/M. Panel J shows a bar graph of G1 with G2/M. Panel K shows a bar graph of percent of cells showing FG staining. Panel L shows a bar graph of FG staining. Panel M shows a bar graph of G2/M. Panel N shows a bar graph of G1 with G2/M. Panel O shows a bar graph of percent of cells showing FG staining. Panel P shows a bar graph of FG staining. Panel Q shows a bar graph of G2/M. Panel R shows a bar graph of G1 with G2/M. Panel S shows a bar graph of percent of cells showing FG staining. Panel T shows a bar graph of FG staining. Panel U shows a bar graph of G2/M. Panel V shows a bar graph of G1 with G2/M. Panel W shows a bar graph of percent of cells showing FG staining. Panel X shows a bar graph of FG staining. Panel Y shows a bar graph of G2/M. Panel Z shows a bar graph of G1 with G2/M. Panel AA shows a bar graph of percent of cells showing FG staining. Panel BB shows a bar graph of FG staining. Panel CC shows a bar graph of G2/M. Panel DD shows a bar graph of G1 with G2/M. Panel EE shows a bar graph of percent of cells showing FG staining. Panel FF shows a bar graph of FG staining. Panel GG shows a bar graph of G2/M. Panel HH shows a bar graph of G1 with G2/M. Panel II shows a bar graph of percent of cells showing FG staining. Panel JJ shows a bar graph of FG staining. Panel KK shows a bar graph of G2/M. Panel LL shows a bar graph of G1 with G2/M. Panel MM shows a bar graph of percent of cells showing FG staining. Panel NN shows a bar graph of FG staining. Panel OO shows a bar graph of G2/M. Panel PP shows a bar graph of G1 with G2/M. Panel QQ shows a bar graph of percent of cells showing FG staining. Panel RR shows a bar graph of FG staining. Panel SS shows a bar graph of G2/M. Panel TT shows a bar graph of G1 with G2/M. Panel UU shows a bar graph of percent of cells showing FG staining. Panel VV shows a bar graph of FG staining. Panel WW shows a bar graph of G2/M. Panel XX shows a bar graph of G1 with G2/M. Panel YY shows a bar graph of percent of cells showing FG staining. Panel ZZ shows a bar graph of FG staining.

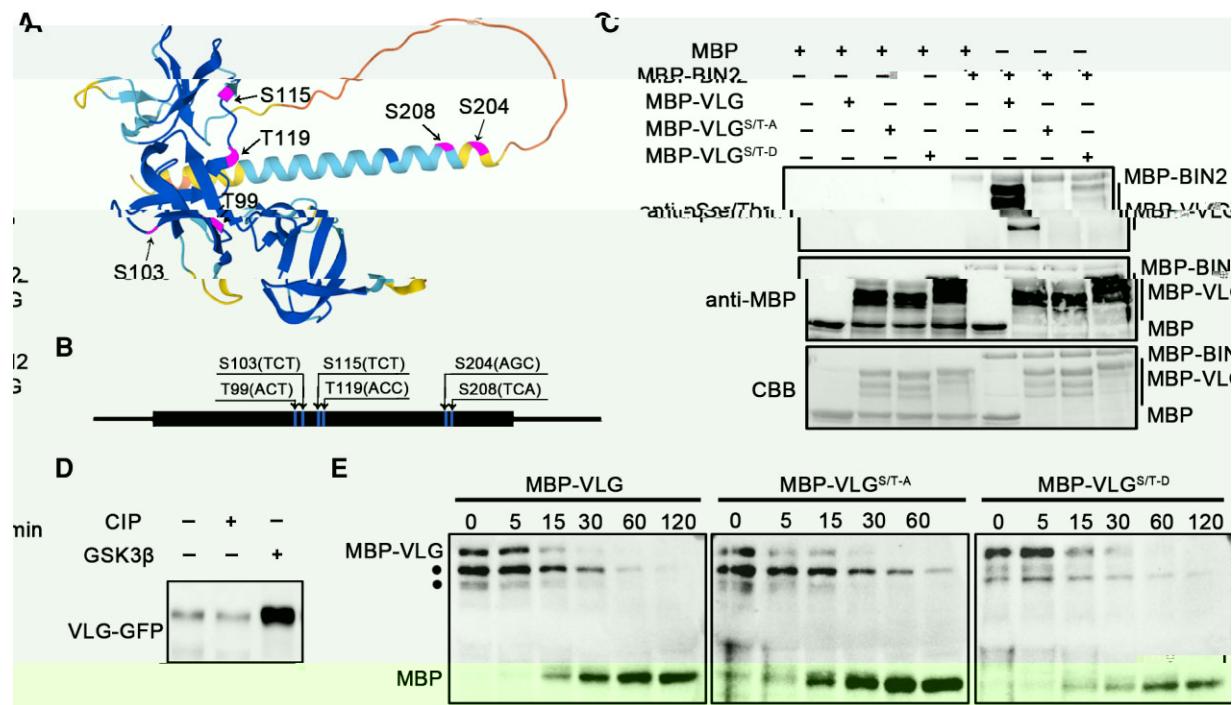


Figure 6 BIN2 modulates FG vacuole formation. (A) Schematic representation of the MBP-BIN2-VLG complex. (B) Sequence of the MBP-BIN2-VLG construct showing the positions of the mutations. (C) Western blot analysis of MBP, MBP-BIN2, MBP-VLG, MBP-VLG^{S/T-A}, and MBP-VLG^{S/T-D} using anti-MBP and anti-MBP-BIN2 antibodies. (D) Western blot analysis of VLG-GFP expression under CIP and GSK3 β conditions. (E) SDS-PAGE analysis of MBP-VLG, MBP-VLG^{S/T-A}, and MBP-VLG^{S/T-D} at time points 0, 5, 15, 30, 60, and 120 min.

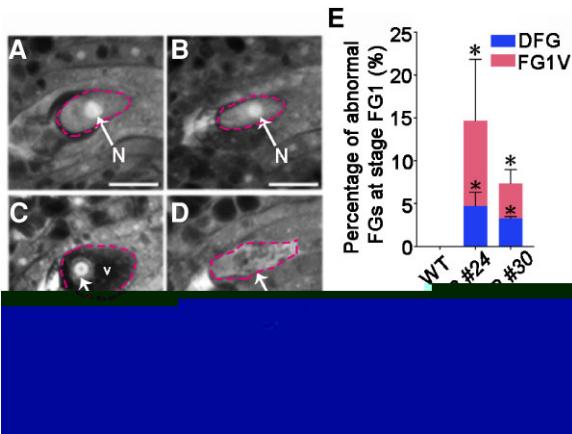
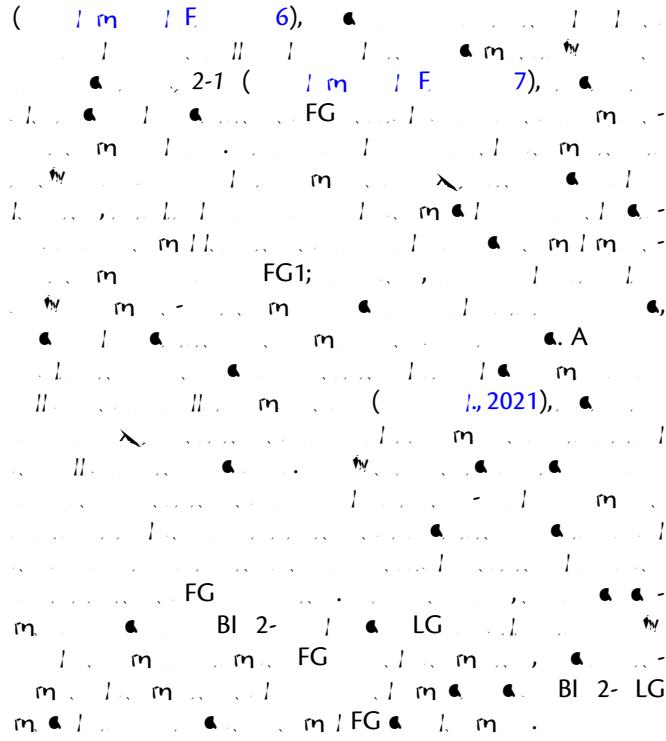


Figure 7 Analysis of FG1 and FG1V expression in pollen grains. (A–D) Fluorescence micrographs of pollen grains at different stages (I, II, III, IV) showing FG1 and FG1V expression. (E) Quantification of the percentage of abnormal FG1 at stage FG1 (%). The legend indicates DFG (blue) and FG1V (red). Data points are: WT (~1%), #24 (~15%, *), and #30 (~8%, *). Error bars represent standard deviation. Statistical significance was determined by Student's *t*-test relative to WT. *P < 0.05.



Materials and methods

Plant materials and growth conditions

Arabidopsis thaliana (Columbia-0, L, N, m, I, 2-1 (L, 1998; L, 2019), C-0, V-2, A, 2-1 (L, 2001), P, DD45:GFP (L, 2012), P, FM1:GUS (H, 2005; L, 2020), P, STK:BIN2*-GFP (L, 2019), P, 35S:BIN2-M C (L, 2019), 2-3, 1, 2, 1 m (L, 2009), V-2, P, KNU:KNU-VENUS (L, 2004; L, 2018). All A. thaliana were grown under long-day conditions (16 h light/8 h dark) at 22°C. C. elegans (16 L/18 A) were grown at 20°C in 90 μm/L m⁻² (F L LED 8-16-65/A22B/24, L).

DNA manipulation

P, UBIQ10:GFP-VAMP711 (L, 2019). G, VAMP711 (L, 2019). E, VAMP711 (L, 2019). D, VAMP711 (L, 2019). P, UBIQ10:GFP-GW (L, 2019). P, UBIQ10:GFP-VAMP711. All lines were transformed into C. elegans (L, 2019). P, 35S:VLG-GFP (CD, 747-1, m/fi). m, VLG (CD, 747-1, m/fi). CAMBIA1302 (L, 2022). BII, S1, BIN2 (L, 2019).

N¹ N²(B) m F 3
L m C A ACTIN7(A 5G09810)
L , (2019; J , 2020). All X.
m m m m m m m m m m m m
L a. L m ID 1.

Confocal laser scanning microscopy

L m m m m m m m m m m m
(C , 1997; L , 2005). D m m
m fix m 30 m 4% m m
a 12.5 m m (H 6.9).
a fix m m m m m m m m m m
m l m a a a a a a a a a a a
10%, 20%, 40%, 60%, 80%, 90% (10 m). A
90% m m m m m m m m m m
m a m m m m m m m m m m
2:1 (/)

II II IV B1 50 mM
 HCl , H 8.0, 500 mM, 1 mM MgCl_2 , 10 mM
 ED A, 5 mM D, 2 mM F, 1X
 1(), 1(), 30 m.
 18,514 10 m 4C,
 10 μL
 -GF - (C m) m III
 10 μL
 -GF - (C m) 3 4C.
 A B1, 100 C 10 m. A
 30- μL L 100 m. A
 m. A 100 C (A ;
 AB0001; 1:3000 (A)
 (A ; AB0005; 1:3000 (A).

Cell-free degradation assay

F 0.1 7-a-1a. 1
 mm a 1 a (B1).
 (25 mM HCl , H 7.5, 10 mM Cl_2 , 10 mM MgCl_2 ,
 5 mM D, 0.4 mM F, 10 mM A) a 1 a.
 30 m. 1 μM B-LG m.
 22 C
 fi m a m m m m a L a
 100 C 10 m. II
 D-AGE. (B1) (A ;
 AB0029; 1:3000 (A)
 (A ; AB0029; 1:3000 (A).

CIP and GSK treatment assays

F Cl m, LG-GF m mm
 GF - a m m a
 B1 a Cl (m) a
 2 μL Cl (E B, 1). 500 μL Cl
 (50 mM HCl , H 7.5, 5 mM MgCl_2 , 1 mM D, 1 mM
 F, 0.1% -40). 60 m 37 C.
 a m m Cl F G K3 β m,
 LG-GF m mm
 GF - a m m a m m B1
 a 2 μL G K3 β . 300 μL G K3 β
 60 m 37 C m a
 m (IC m). a m m a
 m m B1 a m a m a
 100 C 10 m. A 20- μL L
 -GF - (A ; AB0005; 1:3000 (A).

kinase treatment assay

NB-LG NB-BI 2 m mm
 fi NB - NB -
 5 μM NB NB-BI 2 m m a 20 μL
 fi NB NB-LG 30 C 1 m m
 fi (25 mM HCl , H 7.4, 12 mM MgCl_2 , 1 mM D
 a

1 mM A) (I, 2019). m m a m a L a
 100 C 10 m. A 15- μL L
 m m m m m m m m
 -NB (A m ; AB0029; 1:3000 (A)
 (A m ; AB17464; 1:4,000 (A).

Immunoblot assay

F 1 m 7-a-1a. a
 L m a fi m a a a a
 2X D m m m m m
 30 m. 18,514 10 m
 4C. a m m a m m a
 10 m 10 μL a
 10% D-AGE a
 m m m m m m m m
 BI 2 (A ; A 163203; 1:5,000 (A). 1 m I
 F 2B, a -GF a (A ;
 AB0005; 1:5,000 (A) a a a
 (A m , N20045; 1:5,000 (A). F 5, A
 a H 4C
 G m m G (H+L) H (B; B-AB0102;
 1:5,000) G m m G (H+L) H (B; B-AB0101; 1:5,000). All a m a 5% m
 m m (B 1% m -20). m
 BI - AD C m D. Im
 (I D) I LG a L
 a L F 5, A a H m fi a
 Im L m (B - a) (I, 2019).

Root mitosis analysis

I m m 1/2XN m m 7-10 a
 fix. C fix. (100% : 1 : 1
 a = 3:1) (B, 2014). m 1
 m m m m m m m m
 a a H₂ a a a a a a
 20 m 37 C. a a m m a a a
 a a a a a a a a
 a a a a a a a a
 a a a a a a a a
 a a a a a a a a
 45 C. 30, m 20 μL 60% a a a
 m m m m m m m a a a
 -20 C C fix. m m m m m m m
 m m m m m m m m m
 5-10 m. A a 7-10 μL DA I, m m
 m m m m m m m m
 A a A2 m (B, 2014).

Accession numbers

m m m m m m m m
 ACTIN7 (A 5G09810), AGP18 (A 4G37450), AGL23
 (A 1G65360), AOG1 (A 5G57790), ATKIN-1 (A 3G63480),
 BIN2 (A 4G18710), BIL1 (A 2G30980), BIL2 (A 1G06390),
 BUB3.1 (A 3G19590), C CA1;1 (A 1G44110), C CB2;3

(A 1G20610), C CD2;1 (A 2G22490), C CD3;1 (A 4G34160), DD45 (A 2G21740), D AD (A 5G51330), FM1 (A 4G12250), KNU (A 5G14010), MOS7 (A 5G05680), PRL (A 4G02060), SNAIL1 (A 5G61770), SWA1 (A 2G47990), SWA2 (A 1G72440), • VLG (A 2G17740).

Supplemental data

- Supplemental Figure S1.
- Supplemental Figure S2. BIN2
- Supplemental Figure S3. BI 2
- Supplemental Figure S4.
- Supplemental Figure S5. F m / m
- Supplemental Figure S6. A 1 G 1 L 1 m / m
- Supplemental Figure S7.
- Supplemental Figure S8. C 4 L 1 m / BI 2 • LG
- Supplemental Figure S9. Ex m / VLG
- Supplemental Figure S10. Ia fi m / LG m / m (M).
- Supplemental Figure S11.
- Supplemental Figure S12. Ia fi m / LG
- Supplemental Data Set S1.
- Supplemental Data Set S2.

Acknowledgments

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